Immune Epitope Database
NEWSLETTER

IEDB 2.0

After six months as a Beta site, the new IEDB 2.0 became the official Immune Epitope Database website on February 4, 2009. The url was also changed to www.iedb.org, although the www.immuneepitope.org address still works. Major changes have been made to the home page, browse and query functionality, query reporting features, accessing tools, and submitting data.

Inside this Issue

The home page has been completely redesigned, as seen in Figure 1. Besides providing a general description of the IEDB project, the home page displays system level status and notification of scheduled updates and maintenance. The page contains a commonly used search capability easily accessible on the left-hand side. Introductory information, summary metrics of the data, available resources, user support, and project-related news can also be accessed from the page.

Summary Metrics are displayed in the center column of the screen. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, MHC ligand elution, and MHC binding), epitope source organisms, epitope source antigens, host organisms, restricting MHC alleles, and references.

The browse and query capabilities have been overhauled. Browsing by MHC Allele now groups alleles by source organism, MHC class, and locus, and browsing by epitope source organism now aggregates data at higher taxonomic levels (e.g. all epitopes from bacteria). The advanced search feature has been replaced by detailed specialized queries for epitope structure, B cells, T cells, MHC binding, and MHC ligand elution. These make it possible to search for all fields in the database on a single page. Less commonly used fields are initially collapsed into logical subcategories.

Conferences

The IEDB exhibit booth was present at two conferences this spring. The first appearance was at the Twelfth Annual Conference on Vaccine Research held in Baltimore on April 27- 29. The second was at the AAI Annual Meeting in Seattle on May 8 - 12. The IEDB presented a one-hour workshop at the meeting to demonstrate the new 2.0 features, introduce new users to its capabilities, and assist current users in better utilizing its features. Those coming by the booth were able to avail themselves of a redesigned IEDB brochure and four new one-page handouts on the tools in the Analysis Resource and the tuberculosis, malaria and influenza meta-analyses.

Figure 1. The new IEDB 2.0 Home Page

The Fifth Annual Immune Epitope Database and Discovery Workshop was held March 10 and 11, 2009 at the Silver Spring Hilton Hotel in Silver Spring, Maryland. The meeting provided an opportunity for the contractors of the Immune Epitope Database and Analysis Resource (IEDB) and the Large Scale Antibody and T Cell Epitope Discovery Programs to present their project status and plans and to discuss common interests. The two-day meeting started with a presentation of the status of the IEDB, followed by fourteen 40 minute presentations by the Large-Scale Antibody and T Cell Epitope Discovery contractor teams. This meeting was the last in the series as the Epitope Discovery contracts are expiring in 2009. The Executive Summary of the Meeting Report is posted on the IEDB website, and contains further details of the IEDB presentation.

All types of queries now generate a common report page in a simplified format. Assays relating to the same epitope structure that are reported in different references are grouped together into a summary view of the epitope. Similar summary views of all assays and epitopes relating to a given source organism or MHC allele are also available. In table views of the data, which list multiple assays side by side, the information from groups of database fields is collapsed into a narrative that is easier to view compared to a sparsely populated table with many columns. This was implemented for the immunization narrative and the object descriptions. In addition, naming conventions have been updated throughout the site for increased consistency and to improve the data representation.

A more complete description of the new IEDB 2.0 features can be found in the 2008 Annual Compendium that is posted on the IEDB website.

Recent Publications

ElliPro: a new structure-based tool for the prediction of antibody epitopes.

Ponomarenko J, Bui HH, Li W, Fusseder N, Bourne PE, Sette A, Peters B.

BACKGROUND: Reliable prediction of antibody, or B-cell, epitopes remains challenging yet highly desirable for the design of vaccines and immunodiagnostics. A correlation between antigenicity, solvent accessibility, and flexibility in proteins was demonstrated. Subsequently, Thornton and colleagues proposed a method for identifying continuous epitopes in the protein regions protruding from the protein's globular surface. The aim of this work was to implement that method as a web-tool and evaluate its performance on discontinuous epitopes known from the structures of antibody-protein complexes. RESULTS: Here we present ElliPro, a web-tool that implements Thornton's method and, together with a residue clustering algorithm, the MODELLER program and the Jmol viewer, allows the prediction and visualization of antibody epitopes in a given protein sequence or structure. ElliPro has been tested on a benchmark dataset of discontinuous inferred from 3D structures of antibody-protein complexes. In comparison with six other structure-based methods that can be used for epitope prediction, ElliPro performed the best and gave an AUC value of 0.732, when the most significant prediction was considered for each protein. Since the rank of the best prediction was at most in the top three for more than 70% of proteins and never exceeded five, ElliPro is considered a useful research tool for identifying antibody epitopes in protein antigens. ElliPro is available at http://tools.immuneepitope.org/tools/ElliPro. CONCLUSION: The results from ElliPro suggest that further research on antibody epitopes considering more features that discriminate epitopes from non-epitopes may further improve predictions. As ElliPro is based on the geometrical properties of protein structure and does not require training, it might be more generally applied for predicting different types of protein-protein interactions.

Meta-analysis of immune epitope data for all Plasmodia: overview and applications for malarial immuno-biology and vaccine-related issues.

Vaughan K, Blythe M, Greenbaum J, Zhang Q, Peters B, Doolan DL, Sette A.

We present a comprehensive meta-analysis of more than 500 references, describing nearly 5000 unique B cell and T cell epitopes derived from the Plasmodium genus, and detailing thousands of immunological assays. This is the first inventory of epitope data related to malaria-specific immunology, plasmodial pathogenesis, and vaccine performance. The survey included host and pathogen species distribution of epitopes, the number of antibody vs. CD4(+) and CD8(+) T cell epitopes, the genomic distribution of recognized epitopes, variance among epitopes from different parasite strains, and the characterization of protective epitopes and of epitopes associated with parasite evasion of the host immune response. The results identify knowledge gaps and areas for further investigation. This information has relevance to issues, such as the identification of epitopes and antigens associated with protective immunity, the design and development of candidate malaria vaccines, and characterization of immune response to strain polymorphisms.

The curation guidelines of the immune epitope database and analysis resource.

Vita R, Peters B, Sette A.

Cytometry A. 2008 Nov; 73(11): 1066-70.

PMID: 18688821

The IEDB houses antibody and T cell epitope data and makes them accessible and searchable. The curation of literature references requires explicit guidelines in order to capture the data in an objective and consistent manner. Description of these guidelines ensures transparency of the database and facilitates direct submissions to the database.

IEDB Usage Continues to Grow in 2008

The number of users to the IEDB website as measured by visits per month continued increasing in 2008 as seen in the figure below. The linear trend line indicates a growth of approximately 4000 visits per month each year for the past three years.

Another perspective of the growth of the IEDB website usage can be seen by examining the average visits per month. In 2006, its first year of operation, the IEDB had an average of 3147 visits per month. In 2007, this figure increased to 6271, and in 2008, the average gained over 4000 visits to reach 10,338 visits per month.

$$y = 321.71x + 1428.9$$
$$R^2 = 0.8877$$

IEDB Usage
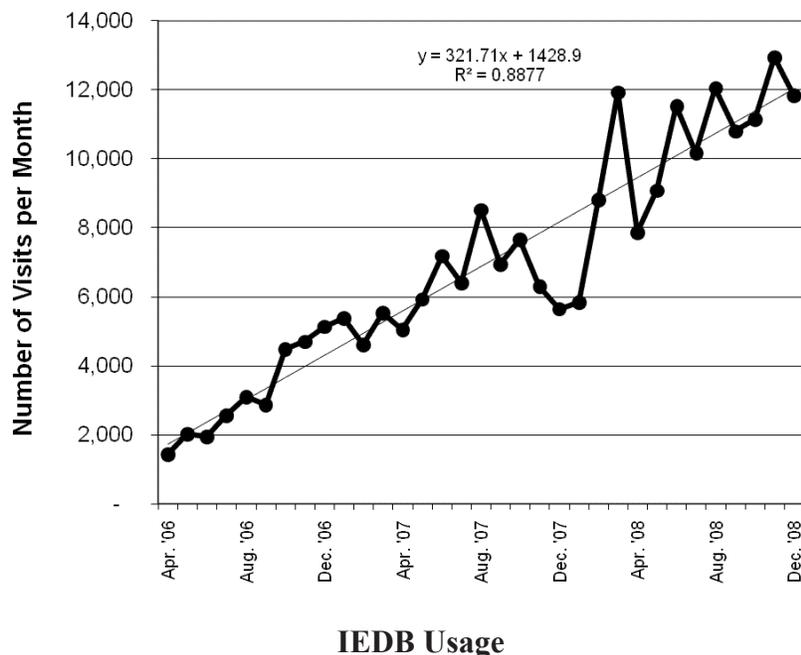
Ontology and Data Structure Revisions

At the heart of the IEDB 2.0 redesign is a new ontology. An ontology is a formal representation of a set of concepts within a domain and the relationships between those concepts. The IEDB's ontology, the Ontology of Immune Epitopes (ONTIE), has been completely revised and is now built upon the Ontology of Biomedical Investigations (OBI, http://obi-ontology.org). This integration into a larger ontology effort promises enhanced ability to connect data from the IEDB with other resources storing experimental information. All data captured by the IEDB were evaluated to determine how they should be represented in ontological terms. The figure below gives a high level overview of the ontology.
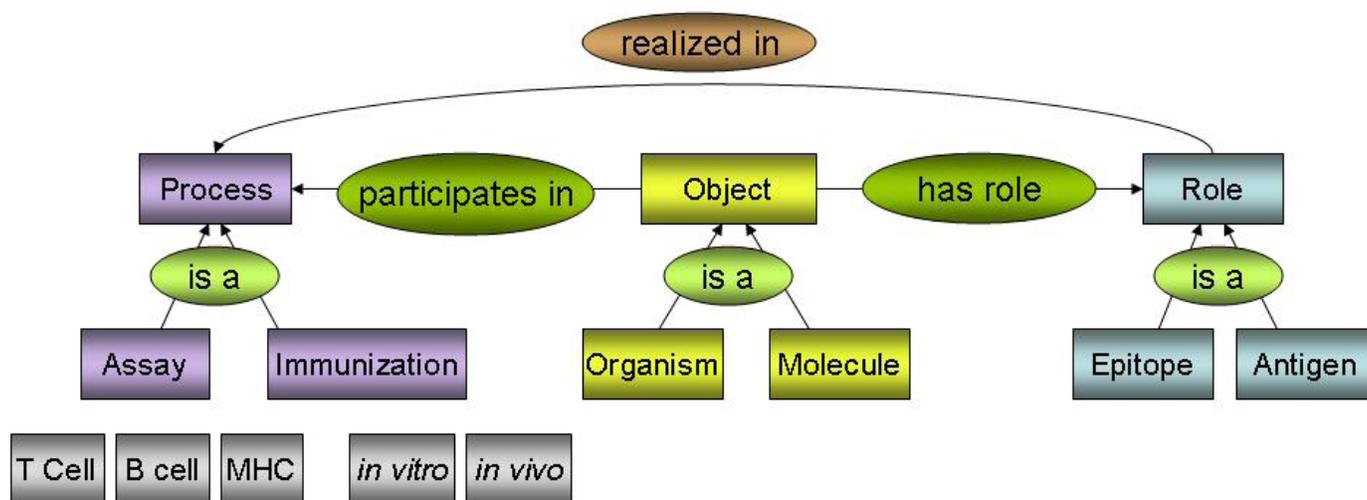
High-level overview of the new IEDB Ontology of Immune Epitopes (ONTIE)

As a result of this endeavor, the database has been restructured, and the resulting database structure is easier to update and maintain over time. Specifically, instead of having individual database tables for epitopes, antigens, immunogens and so forth, a single table is utilized to capture all types of objects. These are referenced from the process table (one for each assay), and assigned a specific role in the assay, such as antigen or immunogen. All immunization procedures and assays now exist as distinct processes that occur either *in vivo* or *in vitro* and have defined participants playing defined roles.

This fourth Annual Compendium of the Immune Epitope Database and Analysis Resource is available as a pdf file on the IEDB website (http://www.iedb.org/doc/iedbAnnualCompendium2008.pdf). It consists of four sections. The first section contains a list of antibody and T cell epitope information in the database as of 14 January 2009. The second section lists the many new features and changes found in IEDB 2.0, a major database and website revision implemented during 2008. The third section describes the features of the IEDB 2.0 website. The fourth section lists the scientific publications in 2008 and 2007 for which the IEDB played a contributory role.

Many new references and many new pathogens were added to the IEDB in 2008. Of the 1402 species/strains listed, 326 were added in 2008. In addition, the number of B cell epitopes increased by 3681, from 10,102 to 13,783, and the number of T cell epitopes increased by 3368, from 20,817 to 24,185.

Data Submission Tool

The data submission tool (DST) is designed to be used by researchers to facilitate submission of data to the IEDB without an in-depth knowledge of curation rules or the required XML data format. The initial version of the DST allows users to submit data in a tab-delimited spreadsheet format using a set of predefined template files designed to accommodate the data submitted by the Epitope Discovery Groups so far. The templates cover over 80% of the anticipated cases based on previous curation experience. Microsoft Excel can be used to easily edit the template files. Available on-line documentation includes a field-by-field guide for each data type that describes the fields, the valid choices, and whether the field is optional or required. Upon submission of the completed spreadsheet(s), the submitter is provided with (1) a validation report summarizing all formatting and/or reporting errors or omissions that are contained in the data, and (2) an official IEDB submission identification number to be used to reference the submission in publications. An online alpha version of the DST can be accessed at http://submission.iedb.org/. Most of the Epitope Discovery contractors who deposited data in the IEDB prior to the Annual Meeting did so using DST.

Curation Update

Curation of data relating to NIAID Category A, B, and C priority pathogens, NIAID emerging and re-emerging infectious diseases, Malaria, Hepatitis B, Clostridium tetani, Leishmania, Candida albicans, and herpesvirus is current for articles appearing in PubMed as of the end of September 2008. In addition, the curation team has continued curating references related to allergen and other infectious diseases. All reference categories will continue to be updated quarterly. Curation of autoimmune diseases will start in 2009. Users are invited to bring references to our attention that are potentially relevant to the IEDB but do not appear in the database. References that are deemed to meet the IEDB criteria for curation will be queued for processing in accordance to our NIH-directed priorities. Citations should be sent to help@iedb.org

The IEDB Team of 2008

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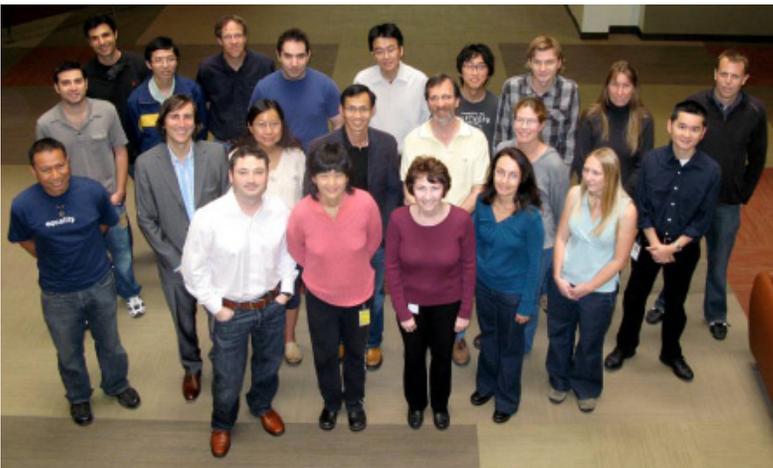& Immunology
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