

Immune Epitope Database NEWSLETTER

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<http://www.immuneEPITOPE.org>

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IEDB 2.0 Beta

The new IEDB 2.0 Beta website was unveiled at the start of June. As one can see by comparing the new home page in Figure 1 to the old home page in Figure 2, the IEDB home page has been significantly redesigned. The popular “Simple Search” has been further simplified and moved to a prominent place on the home page. A breakdown of the data contents is listed in the middle panel under the heading of “Summary Metrics”. The user can view items under each category by clicking on the corresponding number in the Count column. The user can also access the Analysis Resource, which contains epitope prediction and analysis tools, directly from this page. The pull-down menus have been reorganized to enhance usability.

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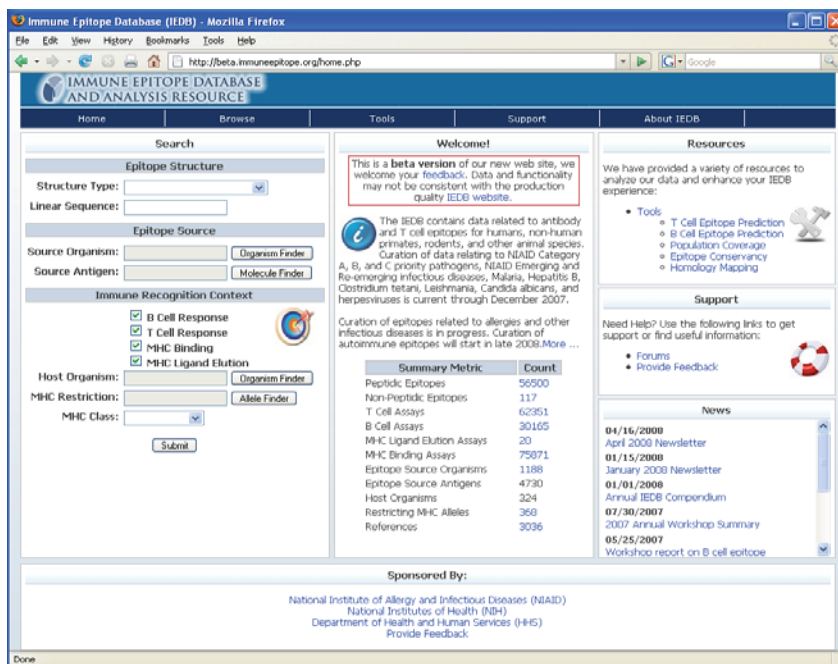


Figure 1. The new IEDB 2.0 Beta Home Page



Figure 2. Current IEDB Home Page

2008 Conference Wrap-Up:



Figure 3. Senior Curators Xin Dong and Nima Salimi staff the IEDB booth at the AAI Annual Meeting in San Diego this past April

The IEDB exhibit booth was present at three conferences this spring. The first appearance was at the AAI Annual Meeting held as part of the Experimental Biology Conference in San Diego on April 5 – 9. IEDB staff members were present to introduce the resource to new users, answer questions from current users, and demonstrate features of the new IEDB 2.0 website. In addition, the IEDB sponsored a two-hour user workshop on April 8. The presentation included an overview of the project, a demonstration of the website's query capabilities, a tour of the Analysis Resource, and a demonstration of the IEDB 2.0 alpha system. Audience participation and interaction was encouraged, and a number of insightful questions were posed and answered. This was the third time that LIAI had presented and staffed an IEDB exhibit booth at this particular meeting and the second time conducting an IEDB user workshop.

The IEDB exhibit booth appeared for the first time at two other conferences this year – the Eleventh Annual Conference on Vaccine Research held May 5 – 7 in Baltimore, and the American Society for Microbiology General Meeting held June 1 – 4 in Boston. Many at the Vaccine conference were already familiar with the IEDB and had the opportunity to learn more about it and to provide feedback. Participants at the ASM meeting were less familiar with the IEDB, giving the IEDB staff members the opportunity to introduce it to many more people.

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The Beta site does not yet have all the functionality of the current production site, such as advanced search and the text-based quick search, but features will be added in two updates scheduled for September and December 2008. Current features include Browse by MHC Allele, Browse by Source Organism, the complete Analysis Resource, forum, help, and feedback.

Likewise, the current Beta site does not contain all the data in the production site. The balance of the data will be transferred over the coming months as the fields are migrated from the old data schema to the new one. Data from the ongoing curation activities are being added to the Beta site periodically. No new data are being added to the current production website.

Readers can check out the beta site at <http://beta.immuneepitope.org>. The development team invites your comments on the new website, which can be sent using the “Provide Feedback” link at the center bottom of the web page. Comments can also be sent to L_iedbadmin@saic.com.

Recent Publications

A systematic assessment of MHC class II peptide binding predictions and evaluation of a consensus approach.

Wang P, Sidney J, Dow C, Mothé B, Sette A, Peters B.
PLoS Comput Biol. 2008 Apr 4;4(4):e1000048.

PMID: 18389056

The identification of MHC class II restricted peptide epitopes is an important goal in immunological research. A number of computational tools have been developed for this purpose, but there is a lack of large-scale systematic evaluation of their performance. Herein, we used a comprehensive dataset consisting of more than 10,000 previously unpublished MHC-peptide binding affinities, 29 peptide/MHC crystal structures, and 664 peptides experimentally tested for CD4+ T cell responses to systematically evaluate the performances of publicly available MHC class II binding prediction tools. While in selected instances the best tools were associated with AUC values up to 0.86, in general, class II predictions did not perform as well as historically noted for class I predictions. It appears that the ability of MHC class II molecules to bind variable length peptides, which requires the correct assignment of peptide binding cores, is a critical factor limiting the performance of existing prediction tools. To improve performance, we implemented a consensus prediction approach that combines methods with top performances. We show that this consensus approach achieved best overall performance. Finally, we make the large datasets used publicly available as a benchmark to facilitate further development of MHC class II binding peptide prediction methods.

Meeting Report: NIH Workshop on the Tuberculosis Immune Epitope Database.

Ernst JD, Lewinsohn DM, Behar S, Blythe M, Schlesinger LS, Kornfeld H, Sette A.
Tuberculosis (Edinb). 2008 Jul;88(4):366-70. Epub 2007 Dec 18.

PMID: 18068490

The Immune Epitope Database (IEDB), an online resource available at <http://immuneepitope.org/>, contains data on T cell and B cells epitopes of multiple pathogens, including M. tuberculosis. A workshop held in June, 2007 reviewed the existing database, discussed the utility of reference sets of epitopes, and identified knowledge gaps pertaining to epitopes and immune responses in tuberculosis.

Upcoming Conferences

Tumor Immunology: New Perspectives

December 2-5, 2008
Miami, Florida, USA

www.aacr.org/home/scientists/meetings--workshops/special-conferences/tumor-immunology-new-perspectives.aspx



Frontiers in Immunology Research

January 8-11, 2009
Alcapulco, Mexico

www.firnweb.com



3rd International Biocuration Conference

April 16-19, 2009
Berlin, Germany

<http://projects.embl.org/sdbv/events/BiocurationMeeting/index.html>



The 96th Annual Meeting of The American Association of Immunologists

May 8-12, 2009
Seattle, Washington, USA

www.immunology2009.org

Recent Publications (cont.)

Immune epitope database analysis resource (IEDB-AR).

Zhang Q, Wang P, Kim Y, Haste-Andersen P, Beaver J, Bourne PE, Bui HH, Buus S, Frankild S, Greenbaum J, Lund O, Lundegaard C, Nielsen M, Ponomarenko J, Sette A, Zhu Z, Peters B.

Nucleic Acids Res. 2008 Jul 1;36(Web Server issue):W513-8. Epub 2008 May 31.

PMID: 18515843 [PubMed - in process]

We present a new release of the immune epitope database analysis resource (IEDB-AR, <http://tools.immuneepitope.org>), a repository of web-based tools for the prediction and analysis of immune epitopes. New functionalities have been added to most of the previously implemented tools, and a total of eight new tools were added, including two B-cell epitope prediction tools, four T-cell epitope prediction tools, and two analysis tools.

Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan.

Nielsen M, Lundegaard C, Blicher T, Peters B, Sette A, Justesen S, Buus S, Lund O.
PLoS Comput Biol. 2008 Jul 4;4(7):e1000107.

PMID: 18604266

CD4 positive T helper cells control many aspects of specific immunity. These cells are specific for peptides derived from protein antigens and presented by molecules of the extremely polymorphic major histocompatibility complex (MHC) class II system. The identification of peptides that bind to MHC class II molecules is therefore of pivotal importance for rational discovery of immune epitopes. HLA-DR is a prominent example of a human MHC class II. Here, we present a method, NetMHCIIpan, that allows for pan-specific predictions of peptide binding to any HLA-DR molecule of known sequence. The method is derived from a large compilation of quantitative HLA-DR binding events covering 14 of the more than 500 known HLA-DR alleles. Taking both peptide and HLA sequence information into account, the method can generalize and predict peptide binding also for HLA-DR molecules where experimental data is absent. Validation of the method includes identification of endogenously derived HLA class II ligands, cross-validation, leave-one-molecule-out, and binding motif identification for hitherto uncharacterized HLA-DR molecules. The validation shows that the method can successfully predict binding for HLA-DR molecules-even in the absence of specific data for the particular molecule in question. Moreover, when compared to TEPITOPE, currently the only other publicly available prediction method aiming at providing broad HLA-DR allelic coverage, NetMHCIIpan performs equivalently for alleles included in the training of TEPITOPE while outperforming TEPITOPE on novel alleles. We propose that the method can be used to identify those hitherto uncharacterized alleles, which should be addressed experimentally in future updates of the method to cover the polymorphism of HLA-DR most efficiently. We thus conclude that the presented method meets the challenge of keeping up with the MHC polymorphism discovery rate and that it can be used to sample the MHC "space," enabling a highly efficient iterative process for improving MHC class II binding predictions.

Curation Update

Curation of data relating to NIAID Category A, B, and C priority pathogens, NIAID emerging and re-emerging infectious diseases (<http://www3.niaid.nih.gov/research/topics/emerging/list.htm>), Malaria, Hepatitis B, Clostridium tetani, Leishmania, Candida albicans, and herpesvirus is current for articles appearing in PubMed as of the end of April 2008. The curation staff is working on new references in the aforementioned categories that have appeared in PubMed as of 30 June 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 iedb_help@liai.org.

Tidbits from the 2007 IEDB Annual Compendium

This third Annual Compendium of the Immune Epitope Database and Analysis Resource is available as a pdf file on the IEDB website (<http://www.immuneepitope.org/export/doc/iedbAnnualCompendium2007.pdf>). It consists of three sections. The first section contains a list of the antibody and T cell epitope information in the database as of 23 January 2008. The second section lists and describes the various features of the IEDB website available at the end of 2007. The third section lists the scientific publications in 2007 for which the IEDB played a contributory role.

Many new references and many new pathogens were added to the IEDB in 2007. Of the 848 source species listed in the compendium, 275 were added in 2007. In addition, the number of distinct B cell epitopes increased by 5489, from 4122 to 9611, and the number of distinct T cell epitopes increased by 10538, from 16738 to 27276.

Contact Information

The Immune Epitope Database & Analysis Resource is supported by a contract from the National Institute of Allergy & Infectious Disease, NIH, DHHS (Contract HH-SN266200400006C). The newsletter is distributed four times a year. We welcome communication from the users of the IEDB database and invite suggestions for articles in future issues. To subscribe to the IEDB newsletter or to contact project staff, send your email information to the email address below.

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