

Immune Epitope Database NEWSLETTER

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<http://www.immuneEPITOPE.org>

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Curation Update

Curation of data relating to NIAID Category A, B, and C priority pathogens, including Influenza, is current for articles appearing in PubMed as of the end of September 2006. The curation of NIAID emerging and re-emerging infectious diseases is over 95% complete. The curation of Malaria literature is in progress, and will be followed by Clostridium tetani, Hepatitis B, Candida albicans, and Leishmania. The list of Category A-C pathogens, emerging/re-emerging infectious diseases, and malaria references will be updated in February 2007. The IEDB curation team will start curating allergen epitopes later this year and expect to have them completed by the end of 2007.

IEDB Discussion Forums



Find the IEDB forums in the navigation bar under RESOURCES

A primary mission of the IEDB is to support an ongoing dialogue with experimentalists and informatics experts in the immunology community. Online, we have provided a bulletin board system known as the IEDB Forums. These forums do not require formal registration or logins to browse, and are provided purely as an open meeting place

to ask questions or find answers to questions posed by others. If you do register, you can post questions to IEDB staff or the user community in general, and expect an email alert when your question is answered. In addition, you can set your account to watch specific threads for activities. Finally, you can use your web browsers Really Simple Syndication (RSS) feature to subscribe to the IEDB forums which allows you to see a listing of threads at a glance.

While we moderate the forums to make sure that nothing patently offensive is posted, we do not edit or limit the scope or content of user's posts. The goal of the online forums is to provide an open, casual and lightly structured environment to easily ask questions or to initiate an ongoing discussion about issues related to immune epitope discovery, ways to use the database or tools in the analysis resource, or suggestions to IEDB staff as to how to improve the database. We'll even seek out experts to your questions if we can not answer them ourselves.

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Third Annual Immune Epitope Database & Discovery Workshop

November 7-8, 2007
Bethesda, Maryland



The Third Annual Immune Epitope Database and Discovery Workshop was held November 7 and 8, 2006 at the Marriott North

Bethesda Hotel and Conference Center in North Bethesda, 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 and was followed by a presentation on the NIH Tetramer Core Facility and fourteen 40 minute presentations by the Large-Scale Antibody and T Cell Epitope Discovery contractor teams.

The Workshop concluded with a discussion session, which dealt with data submission from the Discovery groups to the IEDB. The process for submitting data was reviewed and a tentative submission policy was introduced. The IEDB project team reiterated its commitment to assist the Discovery groups with the direct submission process.

The Fourth Annual Immune Epitope Database and Discovery Workshop will be held on November 14 and 15, 2007 in San Diego, California.

IEDB In the News

Study gives tool to scientists studying Flu Vaccines

By Bruce Lieberman
Union Tribune Staff Writer
January 2, 2007

Scientists still have huge gaps in their knowledge of the flu virus, a disease that kills 36,000 Americans each year, a new study shows.

The examination by San Diego researchers is the most comprehensive to date on what scientists know about antibody and T-cell epitopes for the influenza A virus. Antibody epitopes and T-cell epitopes are the sites on the surface of the flu virus that are recognized by the immune system.

The paper is published online this week in the journal *The Proceedings of the National Academy of Sciences*.

More insights are needed about these epitopes before scientists can develop better vaccines against the world's broad array of influenza A viruses – the most common type of flu virus and the cause of the most serious epidemics in history. The avian flu, H5N1,

“This study is interesting for what it shows we know and do not know,” said Anthony S. Fauci, director of the National Institute of Allergy and Infectious Diseases...”

is an influenza A virus.

The study “gives researchers ways of sharing knowledge and information never available before,” said Alessandro Sette, director of the Center for Infectious Disease at the La Jolla Institute for Allergy and Immunology and one of the study's authors.

“It's a huge resource to speed up things.”

Scientists at the institute examined a compilation of studies of 58 influenza A strains that detailed 600 antibody and T-cell epitopes.

One goal of the study was to identify how many epitopes were common to the strains.

“If we can find shared epitopes, it may be possible to develop an influenza vaccine with greater cross-protection for many different viruses,” Sette said.

The study found hundreds of epitopes that are similar from strain to strain. But it remains to be seen whether they are similar

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Recent Publications

Proc Natl Acad Sci U S A. 2007 Jan 2;104(1):246-51.

Ab and T cell epitopes of influenza A virus, knowledge and opportunities

Bui HH, Peters B, Assarsson E, Mbawuike I, Sette A

Communicated by Howard M. Grey, La Jolla Institute for Allergy and Immunology, San Diego, CA, November 1, 2006 (received for review October 1, 2006)

The Immune Epitope Database and Analysis Resources (IEDB) (www.immuneepitope.org) was recently developed to capture epitope related data. IEDB also hosts various bioinformatics tools that can be used to identify novel epitopes as well as to analyze and visualize existing epitope data. Herein, a comprehensive analysis was undertaken (i) to compile and inventory existing knowledge regarding influenza A epitopes and (ii) to determine possible cross-reactivities of identified epitopes among avian H5N1 and human influenza strains. At present, IEDB contains >600 different epitopes derived from 58 different strains and 10 influenza A proteins. By using the IEDB analysis resources, conservancy analyses were performed, and several conserved and possibly cross-reactive epitopes were identified. Significant gaps in the current knowledge were also revealed, including paucity of Ab epitopes in comparison with T cell epitopes, limited number of epitopes reported for avian influenza strains/subtypes, and limited number of epitopes reported from proteins other than hemagglutinin and nucleoprotein. This analysis provides a resource for researchers to access existing influenza epitope data. At the same time, the analysis illustrates gaps in our collective knowledge that should inspire directions for further study of immunity against the influenza A virus.

PMID: 17200302 [PubMed - in process]

J Mol Recognit. 2007 Jan 5; [Epub ahead of print]

Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools.

Greenbaum JA, Andersen PH, Blythe M, Bui HH, Cachau RE, Crowe J, Davies M, Kolaskar AS, Lund O, Morrison S, Mumey B, Ofra Y, Pellequer JL, Pinilla C, Ponomarenko JV, Raghava GP, van Regenmortel MH, Roggen EL, Sette A, Schlessinger A, Sollner J, Zand M, Peters B

A B-cell epitope is the three-dimensional structure within an antigen that can be bound to the variable region of an antibody. The prediction of B-cell epitopes is highly desirable for various immunological applications, but has presented a set of unique challenges to the bioinformatics and immunology communities. Improving the accuracy of B-cell epitope prediction methods depends on a community consensus on the data and metrics utilized to develop and evaluate such tools. A workshop, sponsored by the National Institute of Allergy and Infectious Disease (NIAID), was recently held in Washington, DC to discuss the current state of the B-cell epitope prediction field. Many of the currently available tools were surveyed and a set of recommendations was devised to facilitate improvements in the currently existing tools and to expedite future tool development. An underlying theme of the recommendations put forth by the panel is increased collaboration among research groups. By developing common datasets, standardized data formats, and the means with which to consolidate information, we hope to greatly enhance the development of B-cell epitope prediction tools. Copyright (c) 2007 John Wiley & Sons, Ltd.

PMID: 17205610 [PubMed - as supplied by publisher]

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In the coming year, as we complete more curation in a wider variety of areas and pathogens, we expect the pace of discussions to pick up substantially. If you haven't taken a look at the forums, please do. When you're there, please post a question or comment... we look forward to hearing from you online.

[Home](#) » [IEDB Discussion Forum](#)

Welcome to the Immune Epitope Database and Analysis Resource discussion forum.





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|  Queries / Reporting | 246 | 3 / 6 | Jan 22, 2007 4:53 PM by: swilson » |
|  Analysis Tools | 183 | 1 / 1 | Nov 7, 2006 7:26 PM by: swilson » |
|  NIAID B cell epitope prediction tools workshop | 38 | 1 / 1 | Jan 10, 2007 5:16 PM by: iqbaum » |

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Last message posted at:
Jan 22, 2007 4:53 PM


 New content since your last visit



You can search the forums or browse by category and thread (topic). Once registered, you can set your profile to watch any number of threads or create new ones.

The Emergence of the Biocurator

With bioinformatics becoming a growing field and the wonder of the internet, data are made readily available to people all over the world. The ability to share and collaborate regardless of physical boundaries has caused the emergence of a new profession in the field of science, Biocuration.

Day after day, a biocurator will devote their time to analyze, understand and interpret published articles, and re-gurgitate information from scientific literature. They must do this with the utmost attention to detail to ensure that only the highest quality of data are incorporated into their databases. These biocurators are highly trained with masters and doctoral degrees because the information captured within the pages to be curated are highly detailed and include complex experiments.

Databases and other types of repositories cannot exist without the deposition of data, and the biocurators are the ones to thank. To further appreciate those who are in this field of work, please explore the following published articles:

Biocurators: Contributors to the World of Science - Bourne PE, McEntyre J [CLICK HERE](#)

A Biocurator Perspective: Annotation at the Research Collaboratory for Structural Bioinformatics Protein Data Bank - Burkhardt K, Schneider B, Ory J [CLICK HERE](#)

The Biocurator: Connecting and Enhancing Scientific Data - Salimi N, Vita R [CLICK HERE](#)

enough to be a target for a new vaccine.

Of all 600 epitopes studied, only one appears to be ideal for a vaccine that would be effective against multiple strains, the scientists said.

Several areas of research have not received enough attention, the scientists found.

Most influenza research is based on flu strains maintained in the lab, rather than wild influenza strains.

“Since we know the virus mutates, research needs to be done using influenza strains currently circulating in the population,” said Stephen Wilson, chief technology officer for the La Jolla Institute for Allergy and Immunology.

Furthermore, most influenza epitope studies have been conducted in mice. Only one of the antibody epitopes detailed in studies around the world is a site that the human immune system targets.

Experimenting with the flu virus in humans poses ethical problems, but scientists said they need more information about how the human immune system responds to the virus – not just how the immune systems of animals respond.

During the analysis, the scientists also found that few of the 600 epitopes studied around the world are sites found on the avian flu virus, H5N1.

“To develop vaccines against avian flu, we need all the information we can get,” Wilson said.

The information that the flu study examined was part of a database constructed by the La Jolla Institute for Allergy and Immunology. The database, funded in 2004 by a \$25 million contract with the National Institutes of Health, is intended to catalog everything that’s known about epitopes for all infectious diseases – not just influenza.

Called the Immune Epitope Database and Analysis Resources Program, the project places particular emphasis on emerging infectious diseases, such as West Nile virus, and diseases the government considers potential terrorist threats.

The NIH directed the La Jolla institute to study the influenza virus first, given the global health concerns about avian flu.

“This study is interesting for what it shows we know and do not know,” said Anthony S. Fauci, director of the National Institute of Allergy and Infectious Diseases, the NIH division that awarded the 2004 grant.

“It reveals many gaps in our knowledge . . . and where we need to focus our attention.”

Contact Information

The Immune Epitope Database is supported by a contract from the National Institute of Allergy & Infectious Disease, NIH, DHHS (Contract #HHSN266200400006C). 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 contact project staff, send your email information to the email address below.

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