

# Immune Epitope Database

## NEWSLETTER

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### Data Submission Tool Wizard Now Available for B Cell Assays

Another new feature in the data submission tool (DST) was released in June 2011. The DST Wizard provides submitters with an on screen field-by-field guided submission experience. The user will be asked questions about the nature of their B cell data and their answers will be used to fill out the data fields required for a valid data submission. The Wizard is recommended for first-time submitters, and for smaller data submissions consisting of fewer than 10 epitopes and 10 assays. This second release of the Wizard accommodates B cell assays for both linear and discontinuous antibody epitopes. The wizard will continue to be expanded in the next several months to also handle MHC binding and MHC ligand elution assays.

The DST is designed to be used by researchers to facilitate submission of data to the IEDB without an in-depth knowledge of curation rules. The DST provides submitters with three methods to submit data: spreadsheet-style files, a newly developed data submission wizard, and XML file. At present, the spreadsheet-style submission is the method of choice by almost all submitters. With this method, the submitter is provided with tab-delimited template files corresponding to the various types of data that can be submitted (MHC binding, MHC Ligand Elution, T cell, and/or B cell), as well as a submission file where important submission details are reported. These files serve as data entry forms where the submitter formats the data according to guidelines. All the preformatted template files can be downloaded from the “download template files” link. Upon completion, the submitter then submits the validated files to the IEDB, where IEDB personnel review and transfer the data to the IEDB website where it will be publicly accessible.

The DST Wizard provides the user with the option to export all data into these preformatted spreadsheets. This function is available in the lower left hand corner of the Wizard interface, and is called “download as spreadsheet files.” This enables the user to manipulate or augment the data submission more efficiently. The finalized spreadsheets can then be directly submitted via the spreadsheet submission option available in the user center. The case of discontinuous antibody epitopes, however, is an exception. While a spreadsheet template has existed for linear antibody epitopes for some time, a template for the discontinuous case currently does not exist.

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## IEDB Version 2.7 Features a New T Cell Assay Finder

A new version of the IEDB was released to the public on July 25, 2011. One of the major new features is a new Assay Finder on the advanced T Cell Search page, which can be accessed from the “Search” pull-down menu. T Cell assays are displayed in a tree structure. Users can also search for assays by their method/technique and by the starting characters of the assay’s name (Figure 1). This new format will be implemented for the other types of Assay Finders with the next IEDB release. The performance of the Molecule Finder was also significantly improved. The Molecule Finder now only loads data as needed for display in the tree structure. As the tree is expanded by the user, the required new data are loaded. Previously, the data for the entire tree were loaded before the user started to expand the tree. While this method worked well before implemented, it became very cumbersome as the amount of data increased by an order of magnitude.

**Assay Finder**

**Current Selection**  
IL-10 release by ELISA  
Clear All Remove Apply

**Find**  
Method/Technique: ELISA  
Name: IL-1  
Search Reset

8 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)  
« previous 1 2 next » Go To » 1 Items per page: 5

Name	Obi Id	Method/Technique
IL-10 release by ELISA [Highlight in Tree] [Select]	<a href="http://purl.obolibrary.org/obo/OBI_1110156">http://purl.obolibrary.org/obo/OBI_1110156</a>	ELISA
IL-12 release by ELISA [Highlight in Tree] [Select]	<a href="http://purl.obolibrary.org/obo/OBI_1110160">http://purl.obolibrary.org/obo/OBI_1110160</a>	ELISA
IL-13 release by ELISA [Highlight in Tree] [Select]	<a href="http://purl.obolibrary.org/obo/OBI_1110159">http://purl.obolibrary.org/obo/OBI_1110159</a>	ELISA
IL-15 release by ELISA [Highlight in Tree] [Select]	<a href="http://purl.obolibrary.org/obo/OBI_0001283">http://purl.obolibrary.org/obo/OBI_0001283</a>	ELISA
IL 17 release by ELISA [Highlight in Tree] [Select]	<a href="http://purl.obolibrary.org/obo/OBI_1110162">http://purl.obolibrary.org/obo/OBI_1110162</a>	ELISA

**Tcell Assay Tree**

- T cell epitope assay
  - cytokine release
    - chemokine (C-C motif) ligand 1 (TCA-3) release
    - chemokine (C-C motif) ligand 4 (MIP-1b) release
    - chemokine (C-X-C motif) ligand 9 (MIC) release
    - GM-CSF release
    - IFN $\beta$  release
    - IFN $\gamma$  release
    - IL-10 release
      - IL-10 release by bioassay
      - IL-10 release by cytometric bead array
      - IL-10 release by ELISA**
      - IL-10 release by ELISPOT
      - IL-10 release by ICS

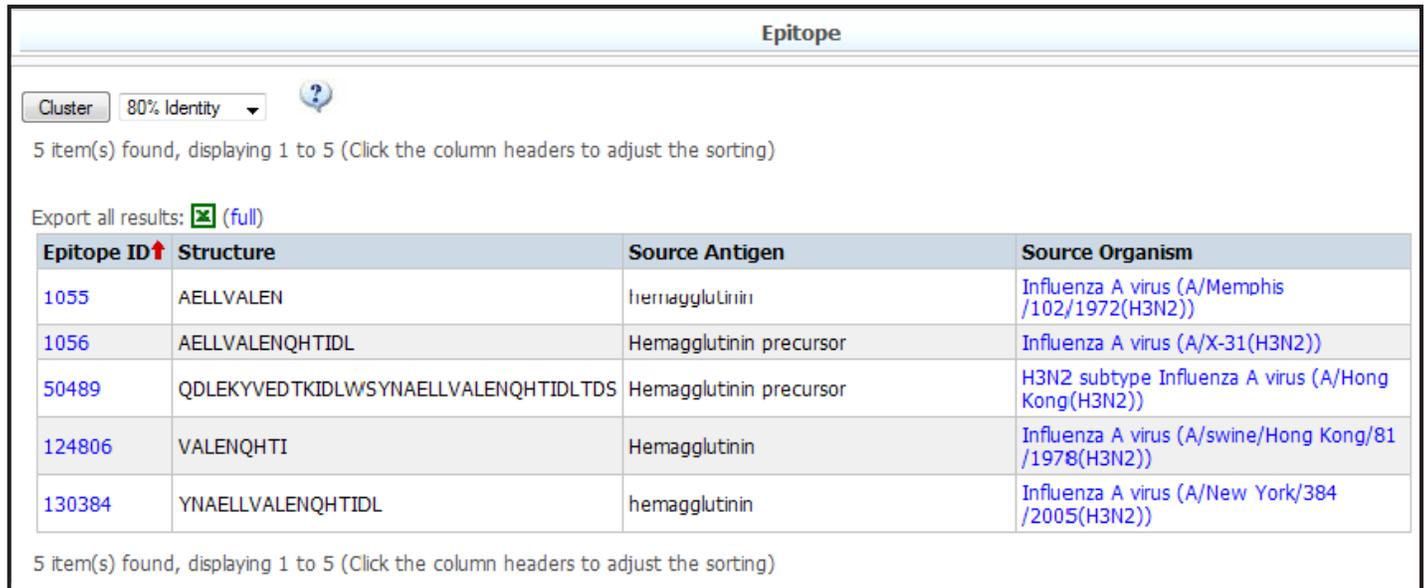
**Figure 1.** The latest release of the IEDB website features a new Assay Finder for the advanced T Cell Search, located on the Search pull-down menu. Assays are displayed in a tree structure and users can find assays by their method/technique and by the characters with which the assay name starts.

The functionality of the linear peptide substring search found in the upper left portion of the IEDB home page was augmented. In addition to finding peptides in the database that contain the specified amino acid sequence, the updated substring search also finds epitopes within the input sequence itself. For example, when the sequence AELLVALENQHTIDL is submitted for a substring search, the query results, shown in Figure 2, yields

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five peptide sequences. Three of them (the second, third, and fifth) contain the input sequence. The two others (the first and fourth) are substrings of the input sequence that are also epitopes contained in the IEDB.

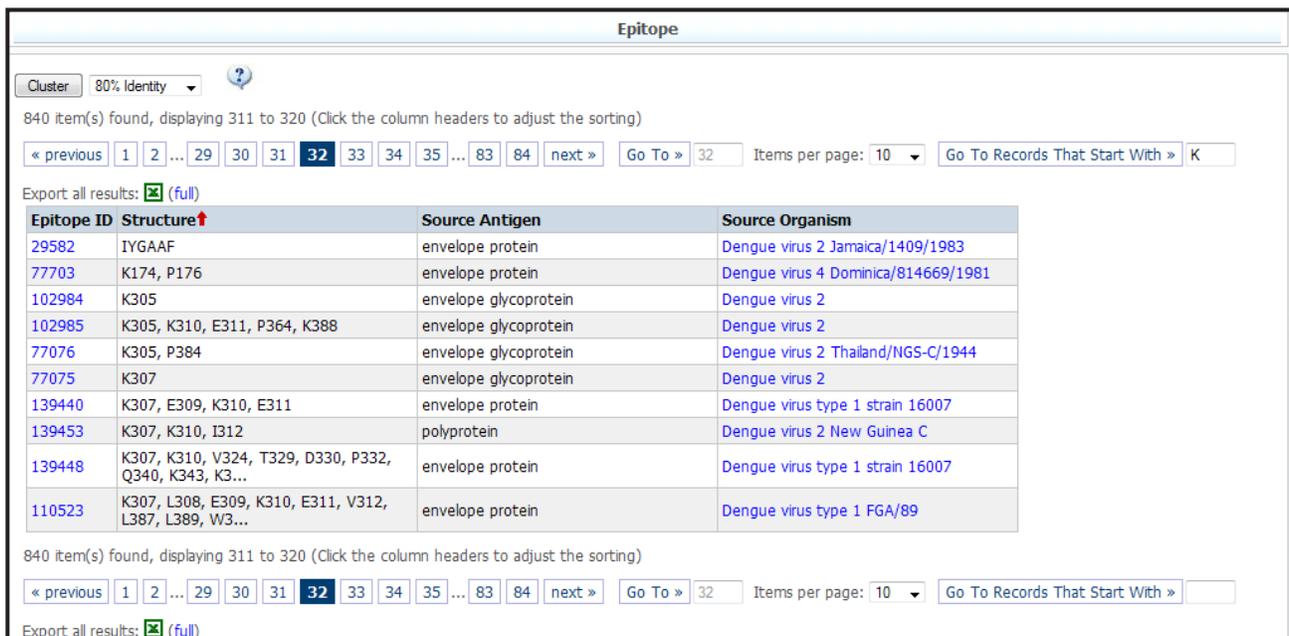


The screenshot shows the IEDB Epitope search results page. At the top, it says "Epitope" and "Cluster 80% Identity". Below that, it states "5 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)". There is an "Export all results" button with a green icon and the text "(full)". The main table has four columns: "Epitope ID", "Structure", "Source Antigen", and "Source Organism". The table contains five rows of results. Below the table, it says "5 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)".

Epitope ID	Structure	Source Antigen	Source Organism
1055	AELLVALEN	hemagglutinin	Influenza A virus (A/Memphis/102/1972(H3N2))
1056	AELLVALENQHTIDL	Hemagglutinin precursor	Influenza A virus (A/X-31(H3N2))
50489	QDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDS	Hemagglutinin precursor	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))
124806	VALENQHTI	Hemagglutinin	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))
130384	YNAELLVALENQHTIDL	hemagglutinin	Influenza A virus (A/New York/384/2005(H3N2))

**Figure 2.** Query results for a substring search performed on the input sequence AELLVALENQHTIDL.

The results pages for the home page search and the advanced searches were enhanced with two useful display options. A user can now specify the number of items or rows to display on the results page from a list of four values (10, 25, 50, and 100). Previously this value was set at 25 for all cases. Figure 3 shows an Epitope results page that displays 10 items per page. If the user then selects a column on which to sort results, a “Go To Records That Start With” button and input field appears, as shown in the figure. In this example, page 1 of the results displayed sequences starting with the letter “A” until a “K” was used as input and the page in the figure appeared. This latter feature will be added to the keyword query results in the next IEDB website release.



The screenshot shows the IEDB Epitope search results page. At the top, it says "Epitope" and "Cluster 80% Identity". Below that, it states "840 item(s) found, displaying 311 to 320 (Click the column headers to adjust the sorting)". There is a pagination bar with "previous", "1", "2", "29", "30", "31", "32", "33", "34", "35", "83", "84", "next", "Go To", "32", "Items per page: 10", and "Go To Records That Start With" followed by an input field containing "K". There is an "Export all results" button with a green icon and the text "(full)". The main table has four columns: "Epitope ID", "Structure", "Source Antigen", and "Source Organism". The table contains ten rows of results. Below the table, it says "840 item(s) found, displaying 311 to 320 (Click the column headers to adjust the sorting)". There is another pagination bar and an "Export all results" button with a green icon and the text "(full)".

Epitope ID	Structure	Source Antigen	Source Organism
29582	IYGAAF	envelope protein	Dengue virus 2 Jamaica/1409/1983
77703	K174, P176	envelope protein	Dengue virus 4 Dominica/814669/1981
102984	K305	envelope glycoprotein	Dengue virus 2
102985	K305, K310, E311, P364, K388	envelope glycoprotein	Dengue virus 2
77076	K305, P384	envelope glycoprotein	Dengue virus 2 Thailand/NGS-C/1944
77075	K307	envelope glycoprotein	Dengue virus 2
139440	K307, E309, K310, E311	envelope protein	Dengue virus type 1 strain 16007
139453	K307, K310, I312	polyprotein	Dengue virus 2 New Guinea C
139448	K307, K310, V324, T329, D330, P332, Q340, K343, K3...	envelope protein	Dengue virus type 1 strain 16007
110523	K307, L308, E309, K310, E311, V312, L387, L389, W3...	envelope protein	Dengue virus type 1 FGA/89

**Figure 3.** The user can now select the number of items/rows to be displayed and jump to pages that contain items starting with a specified letter (top right).

## The IEDB at AAI and FOCIS

The IEDB exhibit booth returned to the Annual Meeting of the American Association of Immunologists, May 14 – 16, at the Moscone Center in San Francisco, after skipping the 2010 meeting. The exhibit booth was staffed for the three day period by Senior Curators Nima Salimi and Randi Vita, and by Bioinformatics Post-doctoral Fellow Yohan Kim. The booth experienced good traffic with over 50 conference attendees stopping to ask questions about the IEDB. In addition, an exhibitor’s workshop was presented by Salimi on Saturday, May 14, 11:00 – 12:00. Approximately 25 people not related to the IEDB were in attendance.

The booth appeared again several weeks later at the Federation of Clinical Immunology Societies (FOCIS) conference at the Marriott Wardman Park in Washington, D.C., June 23 – 26. The booth was staffed by Senior Curators Ken Chan and Jennifer Floyd. The FOCIS conference was specifically chosen to highlight the large quantity of autoimmune epitopes curated since last year. Prior to the conference, the IEDB team re-designed the booth background to emphasize “Epitope” and “Free”, two concepts that were not always clear to some of the AAI attendees, based on their feedback. The redesigned booth can be seen in Figure 5. Booth traffic was better than 2010. Most people who stopped by had not previously heard of the IEDB and were curious about it. There was a lot of interest about the epitope prediction tools. Several people were very excited to learn about the resource. As hoped, there was a lot of interest in the IEDB’s autoimmune disease data. In fact, for those who stopped to ask questions, autoimmune was the category that received the most inquiries.



**Figure 4. Senior Curators Randi Vita and Nima Salimi, along with bioinformatics postdoc Yohan Kim (not shown), staffed the IEDB exhibit booth at this year’s AAI Annual Meeting. A variety of IEDB handouts are shown in the foreground.**



**Figure 5. Senior Curators Ken Chan and Jennifer Floyd staffed the IEDB exhibit booth at the 2011 FOCIS meeting. The backdrop was revised between the AAI and FOCIS meetings.**

## Recent Publications

### A Model for Collaborative Curation, The IEDB and ChEBI Curation of Non-peptidic Epitopes

Randi Vita, Bjoern Peters, Zara Josephs, Paula de Matos, Marcus Ennis, Steve Turner, Christoph Steinbeck, Emily Seymour, Laura Zarebski, and Alessandro Sette

Immunome Research, Volume 7, No. 1 (2011)

The Immune Epitope Database (IEDB) recently expanded and enhanced its non-peptidic epitope related data utilizing a collaboration with Chemical Entities of Biological Interest (ChEBI), resulting in the first resource that brings together published immunological data with the expertise of the ChEBI database. This procedure took advantage of the distinct expertise of the IEDB and ChEBI databases to improve content and enhance interoperability of both databases. This project has resulted in the comprehensive inventory and curation of immune epitope data related to non-peptidic structures and serves as a model for successful collaborative curation between established resources.

## Curation Update

Curation of data relating to peptidic epitopes for all infectious diseases, allergens, and autoimmune diseases, and non-peptidic epitopes for allergens and autoimmune diseases is current for references appearing in PubMed as of the end of 8 July 2011. A query for new potentially relevant epitope references, which had been run quarterly to update the database, is now being run monthly. Curation of non-peptidic epitopes for infectious diseases is over 80% complete and will be completed by the end of this summer. The curation of transplant and alloantigen references for both peptidic and non-peptidic epitopes is over 93% complete. As of the end July 2011, data from approximately 13,000 references have been incorporated into the IEDB. The IEDB contains data for over 84,000 epitopes, 2,740 epitope source organisms, and 584 restricting MHC alleles. **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 NIAID-directed priorities (Category A-C priority pathogens, emerging and re-emerging infectious diseases, other infectious diseases, allergies, autoimmune diseases, and transplantation). The IEDB does not curate cancer and HIV references. Citations should be sent to [help@iedb.org](mailto:help@iedb.org).

## Contact Information

The Immune Epitope Database and Analysis Resource is supported by a contract from the National Institute of Allergy and 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 to contact project staff, send your email information to the email address below.

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