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IEDB-AR: immune epitope database—analysis resource in 2019

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ABSTRACT

The Immune Epitope Database (IEDB) captures experiments that identify and characterize epitopes and epitope specific immune receptors along with various other details such as host organism, immune exposures, and induced immune responses (1). A companion site, IEDB-Analysis Resource (IEDB-AR), hosts various B and T cell epitope prediction tools based on algorithms trained and validated on the IEDB data along with epitope analysis tools. Since the last update, the number of monthly users visiting the IEDB-AR has more than tripled from under 1,500 in 2012 to over 4,500 in 2018 (Supplementary Figure S1). New epitope prediction and analysis tools are regularly added in the IEDB-AR with features to advance epitope-based therapeutics and vaccine development (2). For example, a tool to reduce undesired immunogenicity of therapeutic proteins was implemented recently (3). Here, we describe the newly implemented tools (Table 1), updates to the previously existing tools, and novel functionalities that have been added since the last report in the 2012 NAR webserver edition (4).

INTRODUCTION

The adaptive immune system in vertebrates can recognize a large repertoire of antigens from a broad spectrum of pathogens. B and T cell receptors are responsible for recognizing these diverse set of antigens and triggering immune responses. The specific regions recognized by these receptors are termed as epitopes. Thus, understanding the mechanism of immune receptor:epitope interactions is important in developing diagnostics, therapeutics, and vaccines against infectious and autoimmune diseases, cancers and allergies.

The authors wish it to be known that, in their opinion, the first three authors should be regarded as Joint First Authors.

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Table 1. New and updated tools in the IEDB-AR

<table>
<thead>
<tr>
<th>Category</th>
<th>Name</th>
<th>Update type</th>
<th>Key features</th>
<th>Purpose</th>
</tr>
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<tbody>
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<td>T cell</td>
<td>TepiTool</td>
<td>New tool</td>
<td>Interactive and easy to use tool for immunologists</td>
<td>Prediction of T cell epitopes</td>
</tr>
<tr>
<td></td>
<td>MHC-NP</td>
<td>New tool</td>
<td>Uses binding and ligand elution data to train the model.</td>
<td>Prediction of naturally processed ligands for MHC class I.</td>
</tr>
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<td></td>
<td>MHCII-NP</td>
<td>New tool</td>
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</tr>
<tr>
<td></td>
<td>Immunogenicity</td>
<td>New tool</td>
<td>Uses properties and position of amino acids to predict immunogenicity</td>
<td>Predicting immunogenicity for MHC-class I epitopes.</td>
</tr>
<tr>
<td></td>
<td>CD4EpiScore</td>
<td>New tool</td>
<td>Combines the prediction from immunogenicity and MHC binding algorithms</td>
<td>Predicting CD4 T cell reactivity in human population.</td>
</tr>
<tr>
<td></td>
<td>Deimmunization</td>
<td>New tool</td>
<td>Predicts non-immunogenic regions based on reduced binding to a set of reference MHC II alleles</td>
<td>Identification of immunogenic regions and suggested amino acid substitutions to reduce immunogenicity.</td>
</tr>
<tr>
<td>B cell / T cell</td>
<td>LYRA</td>
<td>New tool</td>
<td>Easy to use and fast antibody and TCR structure prediction.</td>
<td>Template-based 3D structure modeling of B- and T-cell receptors.</td>
</tr>
<tr>
<td>B cell</td>
<td>BepiPred2.0</td>
<td>New version</td>
<td>Training on conformational epitope dataset using random forest algorithm</td>
<td>Prediction of linear B-cell epitopes.</td>
</tr>
<tr>
<td></td>
<td>DiscoTope2.0</td>
<td>New version</td>
<td>Novel spatial neighborhood and surface exposure definitions.</td>
<td>Prediction of discontinuous B-cell epitopes.</td>
</tr>
<tr>
<td>Analysis tools</td>
<td>RATE</td>
<td>New tool</td>
<td>Infers HLA restriction by generating a matrix of subjects and given immune response</td>
<td>Inferring allele restriction for epitopes based on immune response data from HLA-typed subjects.</td>
</tr>
<tr>
<td></td>
<td>ImmunomeBrowser</td>
<td>New tool</td>
<td>User specified epitopes and source proteins.</td>
<td>Aggregating and mapping the immune response from heterogeneous epitope data to source proteins.</td>
</tr>
<tr>
<td></td>
<td>Cluster2.0</td>
<td>Re-engineered</td>
<td>Multiple clustering methods and visualization.</td>
<td>Grouping and visualizing peptides similar in sequence.</td>
</tr>
</tbody>
</table>

Table 2. Methods and versions available in the IEDB T cell epitope prediction tools

<table>
<thead>
<tr>
<th>MHC class</th>
<th>Prediction method</th>
<th>Versions available</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>MHC class I</td>
<td>IEDB consensus (Recommended*)</td>
<td>2.18 (default)</td>
<td>Moutafis et al. (22)</td>
</tr>
<tr>
<td></td>
<td>NetMHCpan</td>
<td>4.0 (default), 3.0, 2.8</td>
<td>Jurtz et al. (23)</td>
</tr>
<tr>
<td></td>
<td>NetMHC (also called ANN)</td>
<td>4.0 (default), 3.4</td>
<td>Andreattia and Nielsen (24)</td>
</tr>
<tr>
<td></td>
<td>SMMPMEC</td>
<td>1.0</td>
<td>Kim et al. (25)</td>
</tr>
<tr>
<td></td>
<td>SMM</td>
<td>1.0</td>
<td>Peters and Sette (26)</td>
</tr>
<tr>
<td></td>
<td>Combib_hajdany2008</td>
<td>1.0</td>
<td>Sidney et al. (27)</td>
</tr>
<tr>
<td></td>
<td>PickPocket</td>
<td>1.1</td>
<td>Zhang et al. (28)</td>
</tr>
<tr>
<td></td>
<td>NetMHCcons</td>
<td>1.1</td>
<td>Karosene et al. (29)</td>
</tr>
<tr>
<td></td>
<td>netMHCstabpan</td>
<td>1.0</td>
<td>Rasmussen et al. (30)</td>
</tr>
<tr>
<td>MHC II</td>
<td>IEDB consensus (Recommended*)</td>
<td>2.17</td>
<td>Wang et al. (31)</td>
</tr>
<tr>
<td></td>
<td>NetMHCPan</td>
<td>3.1</td>
<td>Andreattia et al. (32)</td>
</tr>
<tr>
<td></td>
<td>NN-align</td>
<td>2.2</td>
<td>Nielsen and Lund (33)</td>
</tr>
<tr>
<td></td>
<td>SMM-align</td>
<td>1.1</td>
<td>Nielsen et al. (34)</td>
</tr>
<tr>
<td></td>
<td>Combinatorial Library</td>
<td>1.0</td>
<td>Sidney et al. (27)</td>
</tr>
<tr>
<td></td>
<td>Sturniolo</td>
<td>1.0</td>
<td>Sturniolo et al. (35)</td>
</tr>
</tbody>
</table>

*Recommended methods can change based on regular benchmarking evaluations.

**TepiTool**

TepiTool (http://tools.iedb.org/tepitool) (5) is a new interface for IEDB T cell epitope predictions and is designed as a step-by-step wizard combining both MHC class I and class II prediction methods. The tool provides recommended default values at each step for the prediction and selection of an optimal set of peptides for a given application. TepiTool also offers additional functionalities that go beyond binding predictions. For example, conservancy analysis of peptides among the input sequences and different options for selecting the top-predicted peptides. Once the prediction task is finished, the user is provided with a concise set of top-predicted peptides and links to download the complete prediction results and conservancy estimates. The prediction results and links are also emailed to the user, if an email address is provided.

**Prediction of naturally processed ligands for MHC class I and class II**

MHC-NP (http://tools.iedb.org/mhcnp) (6) is a tool for predicting peptides that are naturally processed by the MHC class I pathway and bind to MHC class I molecules. The tool can predict MHC I ligands for six human and two mouse MHC alleles. Similarly, MHCII-NP (http://tools.iedb.org/mhcnp) (7) is a tool for predicting naturally processed MHC II ligands. These tools were developed by training on the naturally processed peptides eluted from MHC molecules.

**Immunogenicity**

This new tool (http://tools.iedb.org/immunogenicity) is intended to classify peptides that bind to MHC class I (pMHC) into two categories: epitopes and non-epitopes (8). It is based on an analysis of amino acid composition of the peptide at non-anchor positions, where the side chains of amino acids are likely to be in contact with the TCR.

**CD4EpiScore**

CD4EpiScore (http://tools.iedb.org/cd4episcore) is a new tool for predicting the immunogenicity of CD4-restricted peptides in human populations that utilizes a neural network to identify patterns associated with immunogenicity.
(9). It has been validated on a series of independent datasets reported in the literature for different ethnicities and diverse antigens using a variety of experimental approaches.

**Deimmunization**

The Deimmunization tool ([http://tools.iedb.org/deimmunization](http://tools.iedb.org/deimmunization)) was added to IEDB-AR to address the issue of undesired immune reactivity to therapeutically important proteins. In a stepwise wizard, this tool makes use of the class II peptide:MHC binding prediction tools to predict potentially immunogenic regions in protein sequences and suggest amino acid substitutions to reduce their immunogenicity (3). As a proof-of-concept, the tool has been validated experimentally on recombinant factor VIIa (Vatrepacog alpha), which was discontinued from clinical trials due to immunogenicity issues (10).

**B CELL EPITOPE PREDICTION TOOLS**

The IEDB-AR hosts linear B cell epitope prediction tools, such as BepiPred (11), various amino acid physicochemical property based scales ([http://tools.iedb.org/bcell/](http://tools.iedb.org/bcell/)), and discontinuous B cell epitope prediction tools, such as DiscoTope ([http://tools.iedb.org/discotope/](http://tools.iedb.org/discotope/)) (12) and ElliPro ([http://tools.iedb.org/ellipro/](http://tools.iedb.org/ellipro/)) (13). Since the last update of IEDB-AR, the recommended B cell epitope prediction methods, BepiPred (14) and DiscoTope (15), were updated to their 2.0 versions.

**LYRA**

A new tool named LYRA (Lymphocyte Receptor Automated Modelling) was added to model the 3D structures of B and T cell receptors (16). The LYRA tool ([http://tools.iedb.org/lyra/](http://tools.iedb.org/lyra/)) predicts the structure of B- and T-cell receptors from their amino acid sequence. Using homology modelling, it selects the best framework templates and, if necessary, models the complementary determining regions (CDRs) based on the predicted canonical structure (17) of each loop, which are then grafted onto the framework templates. The results page shows the aligned sequence and a visualization of the structure allowing for quick inspection of the CDRs in both sequence and structure.

**ANALYSIS TOOLS**

The analysis section of IEDB-AR contains tools that automate common tasks when working with sets of epitopes or epitope-candidates. Updates to this section include a revised version of epitope clustering along with a new tool to map epitopes to source proteins, and a tool to infer allele restrictions of epitopes from immune response data on HLA-typed subjects.

**Cluster2.0**

The epitope clustering tool ([http://tools.iedb.org/cluster2](http://tools.iedb.org/cluster2)) has been completely re-engineered to group peptidic epitopes based on their sequence similarity. In addition to providing three different clustering approaches, this new version also supports interactive graphical visualizations of the clusters to show connectivity among peptides (18).

**ImmunomeBrowser**

The ImmunomeBrowser tool in the IEDB website maps epitopes to their source antigen and provides a visualization of the observed immune responses across all tested regions of the protein. In a new customizable version of this tool ([http://tools.iedb.org/immunomebrowser/](http://tools.iedb.org/immunomebrowser/)), we have extended this application to perform a similar analysis for user-provided datasets of epitopes and source antigens (19).

**Restrictor Analysis Tool for Epitopes (RATE)**

RATE ([http://tools.iedb.org/rate](http://tools.iedb.org/rate)) (20) is an automated method that can computationally infer the HLA restrictions of epitopes, given large datasets of T cell responses in HLA typed subjects. The tool takes two inputs, the alleles expressed by the subjects and the immune response of the peptides in the subjects. It then calculates the odds ratios for each allele being the restricting allele for a specific peptide and estimates significance using Fisher’s exact test. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

**NEW FEATURES IN THE IEDB-AR**

In addition to implementing new tools, IEDB-AR development since 2012 has also targeted improvements that address how users want to interact with the tools. Two of the most readily apparent and prevalent new features are the ability to submit prediction jobs for processing in the background and the architectural changes made at the hardware and software levels to improve stability and support parallelization.

**Background batch job processing**

With the release of version 2.17 of the IEDB-AR in June 2017, users were given the ability to provide an email address upon submission of a class I or class II peptide binding prediction job. This enhancement has allowed users to run larger prediction jobs (in terms of the number of input sequences and predicted alleles) than would be possible directly through the web interface. Upon completion of the job, results are sent as an email attachment to the user. Since the initial implementation, this feature has been added to TepiTool and the Deimmunization tool - both of which are computationally intensive and could timeout with a reasonable-sized request through the web interface. For tools that support batch processing, it is available through the web interface as well as the API.

**Hardware & software architectural changes to improve stability and support parallelization**

Several architectural changes have been made to the hardware and software in order to decouple the front-end from the back-end, improve stability, and support parallelization of several tools. At the hardware level, a separate job-processing cluster was created to run all CPU-intensive tasks, such as binding predictions. These machines are physically separated from the web server so that heavy processing has little effect on web site performance. To make use
of the redesigned server architecture, the backend software was completely reengineered in Python and Django with special attention to make use of a message queuing system (RabbitMQ) and task manager (Celery). With this integrated system in place, it has allowed parallelization of jobs for several of the resource tools with speedups as great as 15-fold over the single-threaded version. It has also enabled efficient use of resources and prioritization of jobs based upon their origins. As an example, a separate resource queue has been configured in collaboration with the Griffith lab to support the CPU-intensive requests of their pVAC-Seq pipeline (21) while keeping the IEDB systems responsive to requests from other users.

**AVAILABILITY OF THE TOOLS**

IEDB application programming interface (IEDB-API)

In addition to the main web interface, public-facing APIs are made available for several of the tools hosted at the IEDB-AR. Included among these tools are the MHC class I and class II binding and processing predictions, MHC-NP, and the B cell linear epitope predictor. To provide a consistent experience, each of the APIs adhere to a similar interface, with parameter names shared among them where possible. All of the APIs work via HTTP POST requests and return responses in plain text. The MHC class I and II binding prediction APIs are very heavily utilized, accounting for over 300,000 predictions each month and upward of 90% of the jobs run through the IEDB-AR.

Software distribution packages

While the goal of the public IEDB-AR server is to accommodate as many prediction jobs as reasonably possible, resources can be limiting for extremely large requests. This is one of the many reasons that the IEDB-AR team provides downloadable packages to run the predictions locally on the user hardware. Currently, 8 different standalone packages are available, covering the most widely used tools, and new packages are developed based upon user demand and available resources. Additionally, a complete virtual machine image of the IEDB-AR is made available to external entities through license agreements. These two modes of distribution cover a broad range of use cases, enabling users to run many of the IEDB-AR tools on their own hardware and in complete privacy.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

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