

The Immune Epitope Database Analysis Resource:

Epitope prediction benchmark references and datasets
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Contributing tools to the Analysis Resource

Bjoern Peters
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Tool downloads

IEDB Tools Downloads

Complete Download: IEDB Analysis Resource Virtual Machine Image

For users that would like to run the entire analysis resource locally, a virtual machine image file is available with a paid commercial license. The image is kept in sync with the current version of the IEDB Analysis Resource and is updated on a six month cycle. Please [contact us](#) for details on licensing options.

Standalone Downloads

Many of the tools hosted on the IEDB-AR are available as command-line tools. They are freely available to academic users through an open source license. Please [contact us](#) to inquire about a commercial license or if you have any questions in general. For a complete list of standalone tools, including previous versions, please click [here](#).

Linear B cell epitope predictor

This allows for scoring of amino acid residues using the 6 scale-based methods of the linear B cell epitope prediction tool.

- [Linear B cell epitope predictor](#)

MHC class I & II epitope predictors

For users with batch processing needs, the MHC class I and II binding prediction tools are available as standalone scripts for download. These command line tools are kept in sync with the web tools and should therefore produce the same results as clicking through the web interface.

- [MHC Class I](#)
- [MHC Class II](#)

ElliPro

This will produce the same output as the web version of the tool but does not include the initial template finding functionality. It accepts either a PDB ID or a path to a PDB file as input. Usage instructions are printed by calling the program without any parameters.

- [ElliPro](#)

Epitope Cluster Analysis

This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

- [Epitope Cluster Analysis](#)

Class I Immunogenicity

This tool uses amino acid properties as well as their position within the peptide to predict the immunogenicity of a peptide MHC (pMHC) complex.

- [Class I Immunogenicity](#)

Proteasomal Cleavage Prediction

The distributions 'IEDB_NetChop-1.0.tar.gz' contains methods for NetChop, NetCTL and NetCTLpan.

NetChop is a predictor of proteasomal processing based upon a neural network. NetCTL is a predictor of T cell epitopes along a protein sequence. It also employs a neural network architecture. NetCTLpan is an update to the original NetCTL server that allows for prediction of CTL epitope with restriction to any MHC molecules of known protein sequence.

- [Proteasomal Cleavage Prediction](#)

Population Coverage

This tool calculates the fraction of individuals predicted to respond to a given epitope set on the basis of HLA genotypic frequencies and on the basis of MHC binding and/or T cell restriction data. HLA allele genotypic frequencies were obtained from [Allele Frequency database](#).

- [Population Coverage](#)

Benchmark Datasets

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Download](#) **[Datasets](#)** [Contribute Tools](#) [References](#)

IEDB Analysis Resource benchmark references and datasets

For convenience, references and datasets related to benchmarking results of the IEDB Analysis Resource are listed here.

- ▶ [MHC class I binding prediction](#)
- ▶ [MHC class II binding prediction](#)
- ▶ [B-cell epitope prediction](#)

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This site is best viewed with current versions of [Mozilla Firefox](#) or [Google Chrome](#).

For convenience, references and datasets related to benchmarking results of the IEDB Analysis Resource predictive tools are collected here.

▼ MHC class I binding prediction

- [Automated benchmarking of peptide-MHC class I binding predictions](#)

Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M.

Bioinformatics

- **Description:**

Numerous in silico methods predicting peptide binding to major histocompatibility complex (MHC) class I molecules have been developed over the last decades. However, the multitude of available prediction tools makes it non-trivial for the end-user to select which tool to use for a given task. To provide a solid basis on which to compare different prediction tools, we here describe a framework for the automated benchmarking of peptide-MHC class I binding prediction tools. The framework runs weekly benchmarks on data that are newly entered into the Immune Epitope Database (IEDB), giving the public access to frequent, up-to-date performance evaluations of all participating tools. To overcome potential selection bias in the data included in the IEDB, a strategy was implemented that suggests a set of peptides for which different prediction methods give divergent predictions as to their binding capability. Upon experimental binding validation, these peptides entered the benchmark study.

- **Links:**

[Weekly results](#)

[Participate](#)

- [Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions.](#)

Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B.

BMC Bioinformatics

- **Description of the dataset:**

1) All binding data used in the paper: BD2009, BD2013, and Blind.

Contributing tools to the IEDB

Contribute tools to the IEDB-AR

One of the overarching goals of the IEDB is to be the central repository for tools that are of general use to the Immunology communities. As such, we encourage developers of such tools to contact us to inquire about hosting your tool at the IEDB-AR with the developers to create a web portal and keep it up and running indefinitely. We believe this arrangement benefits the Immunology community as a whole. The process for submitting your tool for inclusion at the IEDB-AR is outlined below.

Tool contribution process

1. Send an email to help@iedb.org and include the following information:
 - A summary of the problem that is addressed by your tool and why it is of general interest.
 - The publication status of your tool.
 - If there is a web server that currently hosts your tool, please provide the URL.
 - The time frame in which you will be ready to hand off your tool to IEDB developers.
2. Submissions will be evaluated by IEDB staff to determine whether the tool fits within the scope of the IEDB-AR capability (hardware, personnel, etc.) to implement it.
3. You will receive a reply within 2 weeks with either a decision or a request for further information.
4. Once your tool is approved for inclusion, you will work with IEDB developers to hand off code and create a web portal.
5. The tool will be thoroughly tested for bugs and the load it exerts on the IEDB servers.
6. After you give the go-ahead, links will be made public and it will be officially announced in the IEDB Nucleic Acids Research (AR) release notes. It will also be referenced in any future publication on the general capabilities of the IEDB-AR (webserver issue).
7. Finally, any updates you make to the tool can be applied, tested, and released in our 6-month development cycle.

Thanks!