

The Immune Epitope Database Analysis Resource:

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

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Tool downloads

IEDB Analysis Resource

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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 upon request with the current version of the IEDB Analysis Resource and is updated on a six month cycle. This is freely available under an open-source license. Commercial licenses are also available. Please [contact us](#) for details on either license.

Standalone Downloads

Many of the tools hosted on the IEDB-AR are available as command-line tools. They are freely available to academic users under an open-source license. Please [contact us](#) to inquire about a commercial license or if you have any questions in general.

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 command line tools. 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](#)

Benchmark Datasets

IEDB Analysis Resource

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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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IEDB Analysis Resource benchmark references and datasets

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▼ MHC class I binding prediction

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

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

BMC Bioinformatics (submitted)

- **Description of the dataset:**

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

- 2) For BD2009 data set, three cross-validation data partitions were generated: cv_rnd, cv_sr, and cv_gs.

- 3) FILE_S1: Prediction performances for SMMPMBEC, NetMHC, and NetMHCpan. An R script that constructs log-likelihood models of deviations (i.e. |cv - blind|) is also included.

- **Date of the dataset generation:** 2014

Contributing tools to the IEDB

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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!