

# Resource Summary Report

Generated by T1D on Sep 5, 2026

## Immune Epitope Database and Analysis Resource (IEDB)

RRID:SCR\_006604

Type: Tool

### Proper Citation

Immune Epitope Database and Analysis Resource (IEDB) (RRID:SCR\_006604)

### Resource Information

**URL:** <https://www.iedb.org/>

**Proper Citation:** Immune Epitope Database and Analysis Resource (IEDB) (RRID:SCR\_006604)

**Description:** Repository contains antibody/B cell and T cell epitope information and epitope prediction and analysis tools. Immune epitopes are defined as molecular structures recognized by specific antigen receptors of the immune system, namely antibodies, B cell receptors, and T cell receptors. Immune epitopes from infectious diseases, excluding HIV, and immune-mediated diseases and the accompanying biological information are included.

**Abbreviations:** IEDB

**Synonyms:** Immune Epitope Database and Analysis Resource, , IEDB

**Resource Type:** analysis service resource, data analysis service, data repository, production service resource, service resource, storage service resource

**Defining Citation:** [PMID:39558162](#)

**Keywords:** human, non-human primate, rodent, pig, cat, non-human animal, t cell, b cell, epitope, infectious disease, major histocompatibility complex, bio.tools, FASEB list

**Funding:** niad

**Availability:** open

**Resource Name:** Immune Epitope Database and Analysis Resource (IEDB)

**Resource ID:** SCR\_006604

**Alternate IDs:** nif-0000-03017, biotools:iedb, r3d100012702

**Alternate URLs:** <https://nextgen-tools.iedb.org/>, <https://doi.org/10.17616/R3X217>

**License URLs:** [https://www.iedb.org/terms\\_of\\_use\\_v3.php](https://www.iedb.org/terms_of_use_v3.php)

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20260903T234834+0000

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## Ratings and Alerts

No rating or validation information has been found for Immune Epitope Database and Analysis Resource (IEDB).

No alerts have been found for Immune Epitope Database and Analysis Resource (IEDB).

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 622 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Naveed M, et al. (2026) In silico design and immunoinformatics assessment of a multiepitope vaccine targeting borealpoX virus. Scientific reports, 16(1), 3885.

Lee KH, et al. (2026) NeoPrecis: enhancing immunotherapy response prediction through integration of qualified immunogenicity and clonality-aware neoantigen landscapes. Nature communications, 17(1).

Zhu H, et al. (2026) Single-cell and proteomic profiling unveil aberrant immune phenotypes in gestational diabetes following assisted reproductive technology. Communications biology, 9(1).

Chourir A, et al. (2026) Design of a multiepitope immunotherapy for fish allergy. Scientific reports, 16(1).

Richardson E, et al. (2026) Curation at Scale with EPITOME: Extraction Pipeline for Immunological Texts and Open-Source Multimodal Enquiry. bioRxiv : the preprint server for biology.

Nishioka K, et al. (2026) Lack of molecular mimicry between HPV vaccine L1 antigen and human proteins by a computational analysis. International journal of clinical oncology, 31(3), 494.

Lorenz P, et al. (2026) Patients Suffering From Post-COVID-19 Syndrome Feature Enhanced Antibody Reactivity Towards Specific Linear Epitopes Within EBV EBNA1. *Scandinavian journal of immunology*, 103(1), e70088.

Islam S, et al. (2026) Bioinformatics-Guided structural characterization and immunogenicity assessment of multi-epitope vaccine candidates against Zika virus. *Journal, genetic engineering & biotechnology*, 24(1), 100641.

Rahimi-Farsi N, et al. (2026) Immunoinformatic-driven design of a multi-epitope vaccine against *Helicobacter pylori*. *Biochemistry and biophysics reports*, 45, 102498.

Mecklenbräuker S, et al. (2026) Identification of MHC Ligands Through Allele-Guided Isolation Combined With Machine Learning for Improved MHC Assignment Using ARDisplay-I. *Molecular & cellular proteomics : MCP*, 25(5), 101560.

Sholokhova A, et al. (2026) Neoantigen evolution and response to checkpoint inhibitor immunotherapy in colorectal cancer. *Nature communications*, 17(1).

Raj N, et al. (2026) Non-Coding DNA-Derived Mimotopes of A??? as Novel Candidates for Alzheimer's Peptide Vaccine Design. *International journal of medical sciences*, 23(4), 1320.

Teimoori P, et al. (2026) Computational Design of an mRNA Vaccine Targeting LRP6 for Triple-Negative Breast Cancer Therapy. *Cancer reports (Hoboken, N.J.)*, 9(5), e70567.

Zong X, et al. (2026) Immune Protection Effect of an OmpC-Recombinant T4 Bacteriophage Vaccine Against Infection Caused by Extraintestinal Pathogenic *Escherichia coli* in Mice. *Vaccines*, 14(5).

Schober K, et al. (2026) The T Cell Receptor: Molecular Sensor, Therapeutic Mediator and Probabilistic Driver of Adaptive Immunity. *Immunological reviews*, 340(1), e70136.

Abebe MA, et al. (2026) In silico Design and Analysis of Engineered Proteins Containing Multi-Epitope and Immunodominant Domains Derived From *Rickettsia prowazekii* Antigens. *Bioinformatics and biology insights*, 20, 11779322261461934.

Dutta S, et al. (2026) Prediction of potential NS3-based T cell epitopes of hepatitis C virus by in-silico and in-vitro approach. *Scientific reports*, 16(1).

Ramadan MA, et al. (2026) A protocol for computational design of mRNA vaccines with high functionality and specificity. *Biology direct*, 21(1).

Naveed M, et al. (2026) Multi-epitope vaccine against nucleoprotein and envelopment polyprotein of Batai orthobunyavirus using molecular docking and molecular dynamics studies. *Scientific reports*, 16(1).

Nguyen TC, et al. (2026) Subtle Genetic Shifts of African Swine Fever Virus Among Vietnamese Domestic Swine Following Live-Attenuated Vaccine Commercialization. *Transboundary and emerging diseases*, 2026, 8776906.