

Resource Summary Report

Generated by ASWG on Aug 12, 2026

MHCBN: A comprehensive database of MHC binding and non-binding peptides

RRID:SCR_007785

Type: Tool

Proper Citation

MHCBN: A comprehensive database of MHC binding and non-binding peptides
(RRID:SCR_007785)

Resource Information

URL: <http://www.imtech.res.in/raghava/mhcbn/>

Proper Citation: MHCBN: A comprehensive database of MHC binding and non-binding peptides (RRID:SCR_007785)

Description: The MHCBN is a curated database consisting of detailed information about Major Histocompatibility Complex (MHC) Binding, Non-binding peptides and T-cell epitopes. The version 4.0 of database provides information about peptides interacting with TAP and MHC linked autoimmune diseases.

Synonyms: MHCBN

Resource Type: data or information resource, database

Resource Name: MHCBN: A comprehensive database of MHC binding and non-binding peptides

Resource ID: SCR_007785

Alternate IDs: nif-0000-03123

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260811T043317+0000

Ratings and Alerts

No rating or validation information has been found for MHCBN: A comprehensive database of MHC binding and non-binding peptides.

No alerts have been found for MHCBN: A comprehensive database of MHC binding and non-binding peptides.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Kawakita S, et al. (2024) An integrated database of experimentally validated major histocompatibility complex epitopes for antigen-specific cancer therapy. *Antibody therapeutics*, 7(2), 177.

Sharma A, et al. (2021) Advanced strategies for development of vaccines against human bacterial pathogens. *World journal of microbiology & biotechnology*, 37(4), 67.

Liu G, et al. (2017) PSSMHCPan: a novel PSSM-based software for predicting class I peptide-HLA binding affinity. *GigaScience*, 6(5), 1.

Kelly A, et al. (2017) Introduction: MHC/KIR and governance of specificity. *Immunogenetics*, 69(8-9), 481.

Khan AM, et al. (2017) Analysis of viral diversity for vaccine target discovery. *BMC medical genomics*, 10(Suppl 4), 78.

Backert L, et al. (2015) Immunoinformatics and epitope prediction in the age of genomic medicine. *Genome medicine*, 7, 119.

Luo H, et al. (2015) Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. *BMC bioinformatics*, 16 Suppl 13(Suppl 13), S9.

Zhang XW, et al. (2013) A combination of epitope prediction and molecular docking allows for good identification of MHC class I restricted T-cell epitopes. *Computational biology and chemistry*, 45, 30.

Tong JC, et al. (2011) Understanding infectious agents from an in silico perspective. *Drug discovery today*, 16(1-2), 42.

Lundegaard C, et al. (2010) Major histocompatibility complex class I binding predictions as a tool in epitope discovery. *Immunology*, 130(3), 309.

Tong JC, et al. (2009) Immunoinformatics: current trends and future directions. *Drug discovery today*, 14(13-14), 684.

Lata S, et al. (2009) MHCBN 4.0: A database of MHC/TAP binding peptides and T-cell epitopes. *BMC research notes*, 2, 61.

Chaudhary N, et al. (2009) Prophylactic and Therapeutic Potential of Asp f1 Epitopes in Na⁺ve and Sensitized BALB/c Mice. *Immune network*, 9(5), 179.

Cui J, et al. (2007) Prediction of MHC-binding peptides of flexible lengths from sequence-derived structural and physicochemical properties. *Molecular immunology*, 44(5), 866.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.

Toseland CP, et al. (2005) AntiJen: a quantitative immunology database integrating functional, thermodynamic, kinetic, biophysical, and cellular data. *Immunome research*, 1(1), 4.