

# Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

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

RRID:SCR\_007785

Type: Tool

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### Proper Citation

MHCBN: A comprehensive database of MHC binding and non-binding peptides  
(RRID:SCR\_007785)

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### 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:** 20260804T043331+0000

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### 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.

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## Data and Source Information

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

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## 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.

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.

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

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<sup>+</sup>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.