

Resource Summary Report

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NetMHCpan Server

RRID:SCR_018182

Type: Tool

Proper Citation

NetMHCpan Server (RRID:SCR_018182)

Resource Information

URL: <http://www.cbs.dtu.dk/services/NetMHCpan/>

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Description: Web server for quantitative prediction of peptide binding to any MHC molecule of known sequence using artificial neural networks. Characterizes binding specificity of given major histocompatibility complex molecule and predicts peptide length profile and peptide binding affinity. NetMHCpan 3.0 is improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length data sets. NetMHCpan 4.0 is trained on naturally eluted ligands and on peptide binding affinity data. NetMHCpan-4.1 server predicts binding of peptides to any MHC molecule of known sequence using artificial neural networks (ANNs).

Synonyms: NetMHCpan 1.0, NetMHCpan 3.0, NetMHCpan 2.0, NetMHCpan 4.1, NetMHCpan 4.0, NetMHCpan

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:19002680](#), [PMID:28978689](#)

Keywords: Quantitative prediction, peptide binding, MHC molecule, artificial neural network, Major Histocompatibility Complex, peptide length, peptide binding affinity, data, bio.tools

Funding: Agencia Nacional de Promoción Científica y Tecnológica ; Argentina ; NIAID

Availability: Free, Available for download, Freely Available

Resource Name: NetMHCpan Server

Resource ID: SCR_018182

Alternate IDs: biotools:netmhcpa

Alternate URLs: <https://bio.tools/netmhcpa>,
<https://services.healthtech.dtu.dk/services/NetMHCpan-4.1/>

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260919T195348+0000

Ratings and Alerts

No rating or validation information has been found for NetMHCpan Server.

No alerts have been found for NetMHCpan Server.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 169 mentions in open access literature.

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

Laurenson AJ, et al. (2026) TEpiNom: A computational framework integrating population data to prioritize Plasmodium falciparum T cell epitopes. Vaccine, 77, 128388.

Venafr V, et al. (2026) Kinase inhibition rewires the HLA-I immunopeptidome in chronic myeloid leukemia. iScience, 29(6), 115944.

Montellier E, et al. (2026) Neoantigenic properties of TP53 variants influence cancer risk in individuals with Li-Fraumeni syndrome. EBioMedicine, 123, 106065.

Rahimnahal S, et al. (2026) Designing a novel vaccine against COVID-19 based on spike SARS-Cov-2 notable mutations using immunoinformatics approaches. PloS one, 21(2), e0334662.

Guleed S, et al. (2026) CD8+ T cell responses recognizing immunodominant Chlamydia antigens fail to protect against infection. iScience, 29(4), 115242.

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

Lehikoinen J, et al. (2026) EBV genome analysis in multiple sclerosis shows extensive viral diversity and links to autoimmunity. NAR molecular medicine, 3(2), ugag019.

Zeng Q, et al. (2026) Intratumoral Tertiary Lymphoid Structures Characterized by a B Cell-Related Signature Elicit Antitumor Effect through HAPLN3 in Hepatocellular Carcinoma. Cancer immunology research, 14(5), 771.

Jwo SH, et al. (2025) Dual prophylactic and therapeutic potential of iPSC-based vaccines and neoantigen discovery in colorectal cancer. *Theranostics*, 15(12), 5890.

Goswami S, et al. (2025) Immune checkpoint inhibitors plus debulking surgery for patients with metastatic renal cell carcinoma: clinical outcomes and immunological correlates of a prospective pilot trial. *Nature communications*, 16(1), 1846.

Peng X, et al. (2025) Bioinformatics-based screening and prediction of compounds and antigen epitopes for immune targets with point mutations in colitis-associated colorectal cancer. *Discover oncology*, 17(1), 189.

Wan X, et al. (2025) Therapeutic T cells with 3-in-1 strategy for the treatment of biliary tract cancer. *Cell reports. Medicine*, 102349.

Sahoo S, et al. (2025) An integrated structural and immunoinformatic approach to design a multi-epitope based vaccine against the foot-and-mouth disease virus. *Scientific reports*, 15(1), 35911.

Eggebo MS, et al. (2025) TCR-engineered T cells targeting a shared β -catenin mutation eradicate solid tumors. *Nature immunology*.

Lopez M, et al. (2025) Exploring the role of ESR1 mutations in metastatic hormone receptor-positive breast cancer T cell immune surveillance disruption. *Breast cancer research : BCR*, 27(1), 19.

Abdul-Zahra HH, et al. (2025) Molecular Analysis and Bioinformatics Assessment of Full-Length L1 Gene of Bovine Papillomavirus Type-1 as a Potential DNA Vaccine Study. *Veterinary medicine international*, 2025, 6785087.

Estephan H, et al. (2025) Immunopeptidomics Workflow for Isolation and LC-MS/MS Analysis of MHC Class I-Bound Peptides Under Hypoxic Conditions. *Bio-protocol*, 15(22), e5505.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. *Heliyon*, 11(1), e41714.

Li C, et al. (2025) Engineered *Lactococcus lactis* biovaccine containing NY-ESO-1 long peptides as potent immunotherapeutics. *Materials today. Bio*, 35, 102440.

Mashrur MN, et al. (2025) In silico design of novel multi-epitope peptide vaccine against *Neospora caninum* induced cattle abortion targeting extracellular GRA2 and Nc-p43 protein. *Scientific reports*, 15(1), 42169.