

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, web service, software resource

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:netmhcpn

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

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260803T040741+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 138 mentions in open access literature.

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

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

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.

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

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.

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.

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

He S, et al. (2025) Comprehensive assessment of computational methods for cancer immunoediting. Cell reports methods, 5(3), 101006.

Rahman E, et al. (2025) Computational Immunogenetic Analysis of Botulinum Toxin A Immunogenicity and HLA Gene Haplotypes: New Insights. *Toxins*, 17(4).

Goto Y, et al. (2025) Molecular basis of potent antiviral HLA-C-restricted CD8⁺ T cell response to an immunodominant SARS-CoV-2 nucleocapsid epitope. *Nature communications*, 16(1), 8062.

Luo JR, et al. (2025) Design of a multi-Epitope mRNA vaccine against Brucella type IV secretion system using reverse vaccinology and immunogenicity approaches. *Scientific reports*, 15(1), 30698.

Barbosa AAS, et al. (2025) A Multi-Epitope Recombinant Vaccine Candidate Against Bovine Alpha herpesvirus 1 and 5 Elicits Robust Immune Responses in Mice and Rabbits. *Vaccines*, 13(11).

Li C, et al. (2025) Design of a multi-epitope recombinant BCG vaccine targeting Brucella OMP31, LptE and VirB2 in immunoinformatics approaches. *PloS one*, 20(11), e0334843.

Ri MT, et al. (2025) Protocol for hybrid mass spectrometry-AI mapping of proteasome-generated HLA class I epitopes. *STAR protocols*, 6(4), 104154.

He M, et al. (2025) B Cells Can Trigger the T-Cell-Mediated Autoimmune Response Against Melanocytes in Psoriasis. *Cells*, 14(24).

Tai W, et al. (2025) An mRNA vaccine against monkeypox virus inhibits infection by co-activation of humoral and cellular immune responses. *Nature communications*, 16(1), 2971.

Sadeghi SA, et al. (2025) Immunoinformatics study of CD40 ligand-targeting vaccine constructs: a novel immunotherapeutic approach. *Osong public health and research perspectives*, 16(4), 311.

Altadill M, et al. (2025) Human Cytomegalovirus Antigen Presentation by HLA-G in Infected Cells. *HLA*, 105(5), e70089.

Chai ZL, et al. (2025) Reverse vaccinology-driven construction and bioinformatics validation of a multi-epitope vaccine against Brucella spp. *Scientific reports*, 15(1), 36663.

Shi Q, et al. (2025) Massively parallel immunopeptidome by DNA sequencing provides insights into cancer antigen presentation. *Nature genetics*, 57(8), 2062.

Siwek JC, et al. (2025) Sliding Window Interaction Grammar (SWING): a generalized interaction language model for peptide and protein interactions. *Nature methods*, 22(8), 1707.