Resource Summary Report

Generated by NIF on Apr 26, 2025

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.

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

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

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:netmhcpan

Alternate URLs: https://bio.tools/netmhcpan

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250425T060304+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 114 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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

Zhou S, et al. (2024) Identification of Enhanced Vaccine Mimotopes for the p15E Murine Cancer Antigen. Cancer research communications, 4(4), 958.

Luo T, et al. (2024) Potential SLA Hp-4.0 haplotype-restricted CTL epitopes identified from the membrane protein of PRRSV induce cell immune responses. Frontiers in microbiology, 15, 1404558.

Kortleve D, et al. (2024) TCR-Engineered T Cells Directed against Ropporin-1 Constitute a Safe and Effective Treatment for Triple-Negative Breast Cancer. Cancer discovery, 14(12), 2450.

Naully PG, et al. (2024) Design of multi-epitope-based therapeutic vaccine candidates from HBc and HBx proteins of hepatitis B virus using reverse vaccinology and immunoinformatics approaches. PloS one, 19(12), e0313269.

Yuan F, et al. (2024) Selection, Design and Immunogenicity Studies of ASFV Antigens for Subunit mRNA Cocktail Vaccines with Specific Immune Response Profiles. bioRxiv : the

preprint server for biology.

Wang Y, et al. (2024) Immunotherapies targeting the oncogenic fusion gene CLDN18-ARHGAP in gastric cancer. EMBO molecular medicine, 16(9), 2170.

Cen L, et al. (2024) Efficacy of MAGE-A4 long peptide as a universal immunoprevention cancer vaccine. Cancer cell international, 24(1), 232.

Choi S, et al. (2024) pXg: Comprehensive Identification of Noncanonical MHC-I-Associated Peptides From De Novo Peptide Sequencing Using RNA-Seq Reads. Molecular & cellular proteomics : MCP, 23(4), 100743.

Hamza H, et al. (2024) Identification and relative abundance of naturally presented and cross-reactive influenza A virus MHC class I-restricted T cell epitopes. Emerging microbes & infections, 13(1), 2306959.

Boyne C, et al. (2024) Characterising the HLA-I immunopeptidome of plasma-derived extracellular vesicles in patients with melanoma. Journal of extracellular biology, 3(3), e146.

Hasan MZ, et al. (2024) SARS-CoV-2 infection induces adaptive NK cell responses by spike protein-mediated induction of HLA-E expression. Emerging microbes & infections, 13(1), 2361019.

Mösch A, et al. (2024) NeoAgDT: optimization of personal neoantigen vaccine composition by digital twin simulation of a cancer cell population. Bioinformatics (Oxford, England), 40(5).

Qin L, et al. (2024) Intratumor injection of BCG Ag85A high-affinity peptides enhanced antitumor efficacy in PPD-positive melanoma. Cancer immunology, immunotherapy : CII, 73(6), 103.

Vecchio F, et al. (2024) Coxsackievirus infection induces direct pancreatic ? cell killing but poor antiviral CD8+ T cell responses. Science advances, 10(10), eadl1122.

Nguyen TL, et al. (2024) Immunoinformatics and computational approaches driven designing a novel vaccine candidate against Powassan virus. Scientific reports, 14(1), 5999.

Shivarov V, et al. (2024) Differential modulation of mutant CALR and JAK2 V617F-driven oncogenesis by HLA genotype in myeloproliferative neoplasms. Frontiers in immunology, 15, 1427810.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. Cancer cell, 42(1), 135.

Dey J, et al. (2023) Designing of multi-epitope peptide vaccine against Acinetobacter baumannii through combined immunoinformatics and protein interaction-based approaches. Immunologic research, 1.

Chiaro J, et al. (2023) Development of mesothelioma-specific oncolytic immunotherapy enabled by immunopeptidomics of murine and human mesothelioma tumors. Nature communications, 14(1), 7056.