

Resource Summary Report

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NetMHC

RRID:SCR_021651

Type: Tool

Proper Citation

NetMHC (RRID:SCR_021651)

Resource Information

URL: <https://services.healthtech.dtu.dk/service.php?NetMHC-4.0>

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Description: Web tool for binding prediction of peptides to MHC class I molecules. The newest version NetMHC- 4.0 is used for prediction of peptide MHC class I binding affinity using gapped sequence alignment that allows insertions and deletions in alignment.

Synonyms: NetMHC- 3.0, NetMHC- 2.1, NetMHC- 2.0, NetMHC- 1.0, NetMHC- 3.2, NetMHC- 4.0, NetMHC-3.4

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

Defining Citation: [PMID:18463140](#), [PMID:26515819](#)

Keywords: Gapped sequence alignment, peptide-MHC, artificial neural networks, MHC class I system, histocompatibility complex, peptide binding, binding prediction

Availability: Free, Freely available

Resource Name: NetMHC

Resource ID: SCR_021651

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260821T194201+0000

Ratings and Alerts

No rating or validation information has been found for NetMHC.

No alerts have been found for NetMHC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Rongchuan X, et al. (2026) Identification and bioinformatics analysis of a novel member of the lumbrokinase gene family in earthworms. *Frontiers in bioinformatics*, 6, 1736746.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Lennerz V, et al. (2025) T-cell receptors identified by a personalized antigen-agnostic screening approach target shared neoantigen KRAS Q61H. *Frontiers in immunology*, 16, 1509855.

Lara-Ramírez D, et al. (2025) In silico design of Ebola virus Glycoprotein antigenic peptides as vaccine candidates. *PloS one*, 20(3), e0319496.

Schoufour TAW, et al. (2024) CRISPR-Cas9 screening reveals a distinct class of MHC-I binders with precise HLA-peptide recognition. *iScience*, 27(6), 110120.

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

Giannakopoulou E, et al. (2023) A T cell receptor targeting a recurrent driver mutation in FLT3 mediates elimination of primary human acute myeloid leukemia in vivo. *Nature cancer*, 4(10), 1474.

Mariano IHM, et al. (2023) Analysis of LruC lipoprotein and identification of peptides candidates for vaccine development and diagnosis of leptospirosis. *PloS one*, 18(2), e0281344.

Zahedipour F, et al. (2023) Nanoliposomal VEGF-R2 peptide vaccine acts as an effective therapeutic vaccine in a murine B16F10 model of melanoma. *Cancer nanotechnology*, 14(1), 62.

van den Bulk J, et al. (2023) Neoantigen Targetability in Progressive Advanced Melanoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(20), 4278.

Garcia-Del Rio DF, et al. (2023) Protocol to identify human subcellular alternative protein interactions using cross-linking mass spectrometry. *STAR protocols*, 4(3), 102380.

Wang Y, et al. (2023) Structural Analyses of a Dominant *Cryptosporidium parvum* Epitope Presented by H-2Kb Offer New Options To Combat Cryptosporidiosis. *mBio*, 14(1), e0266622.

Meyer S, et al. (2023) Prevalent and immunodominant CD8 T cell epitopes are conserved in SARS-CoV-2 variants. *Cell reports*, 42(1), 111995.

Garcia-Del Rio DF, et al. (2023) Employing non-targeted interactomics approach and subcellular fractionation to increase our understanding of the ghost proteome. *iScience*, 26(2), 105943.

Pandey K, et al. (2023) A combined immunopeptidomics, proteomics, and cell surface proteomics approach to identify immunotherapy targets for diffuse intrinsic pontine glioma. *Frontiers in oncology*, 13, 1192448.

Cheng M, et al. (2023) Transcriptomics integrated with metabolomics provides a new strategy for mining key genes in response to low temperature stress in *Helictotrichon virescens*. *International journal of biological macromolecules*, 242(Pt 3), 125070.

Gupta S, et al. (2022) Design of an Epitope-Based Peptide Vaccine Against Dengue Virus Isolate from Eastern Uttar Pradesh, India. *International journal of peptide research and therapeutics*, 28(3), 91.

Bonté PE, et al. (2022) Single-cell RNA-seq-based proteogenomics identifies glioblastoma-specific transposable elements encoding HLA-I-presented peptides. *Cell reports*, 39(10), 110916.

Baumgaertner P, et al. (2022) CD8 T cell function and cross-reactivity explored by stepwise increased peptide-HLA versus TCR affinity. *Frontiers in immunology*, 13, 973986.

Alshammari A, et al. (2022) Computer-Aided Multi-Epitope Vaccine Design against *Enterobacter xiangfangensis*. *International journal of environmental research and public health*, 19(13).