## **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:** software resource, service resource, production service resource, analysis service resource, web service, data access protocol

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

Funding:

Availability: Free, Freely available

Resource Name: NetMHC

Resource ID: SCR\_021651

Record Creation Time: 20220129T080356+0000

Record Last Update: 20250501T081551+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 32 mentions in open access literature.

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

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.

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.

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.

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

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.

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.

Hammer Q, et al. (2022) SARS-CoV-2 Nsp13 encodes for an HLA-E-stabilizing peptide that abrogates inhibition of NKG2A-expressing NK cells. Cell reports, 38(10), 110503.

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

Jahangirian E, et al. (2021) A reverse vaccinology and immunoinformatics approach for designing a multiepitope vaccine against SARS-CoV-2. Immunogenetics, 73(6), 459.

Tarrahimofrad H, et al. (2021) Designing a multi-epitope vaccine to provoke the robust immune response against influenza A H7N9. Scientific reports, 11(1), 24485.

Kischkel B, et al. (2021) Immunoproteomic and Immunopeptidomic Analyses of Histoplasma capsulatum Reveal Promiscuous and Conserved Epitopes Among Fungi With Vaccine Potential. Frontiers in immunology, 12, 764501.

Cui C, et al. (2021) Neoantigen-driven B cell and CD4 T follicular helper cell collaboration promotes anti-tumor CD8 T cell responses. Cell, 184(25), 6101.

Kaaijk P, et al. (2021) Novel mumps virus epitopes reveal robust cytotoxic T cell responses after natural infection but not after vaccination. Scientific reports, 11(1), 13664.

Chand Y, et al. (2021) Prioritization of potential vaccine candidates and designing a multiepitope-based subunit vaccine against multidrug-resistant Salmonella Typhi str. CT18: A subtractive proteomics and immunoinformatics approach. Microbial pathogenesis, 159, 105150.