Resource Summary Report

MHCPEP

RRID:SCR_007786
Type: Tool

Proper Citation

MHCPEP (RRID:SCR_007786)

Resource Information

URL: http://bio.dfci.harvard.edu/DFRMLI/

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Description: This repository contains full data from MHCPEP database, and selected data including independent data sets of proteins and protein fragments, non-binding peptides, lists of T-cell epitopes, and recommendations for scaling and comparison of performance of prediction systems. It can be used in conjunction with IEDB data sets for the development of advanced machine learning and pattern recognition solutions.

Synonyms: MHCPEP

Resource Type: database, data or information resource

Funding:

Resource Name: MHCPEP

Resource ID: SCR_007786

Alternate IDs: nif-0000-03124

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250412T055213+0000

Ratings and Alerts

No rating or validation information has been found for MHCPEP.

No alerts have been found for MHCPEP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Charoentong P, et al. (2012) Bioinformatics for cancer immunology and immunotherapy. Cancer immunology, immunotherapy : CII, 61(11), 1885.

Zhang GL, et al. (2011) Dana-Farber repository for machine learning in immunology. Journal of immunological methods, 374(1-2), 18.

Hu X, et al. (2011) Ensemble approaches for improving HLA class I-peptide binding prediction. Journal of immunological methods, 374(1-2), 47.

Bordner AJ, et al. (2010) MultiRTA: a simple yet reliable method for predicting peptide binding affinities for multiple class II MHC allotypes. BMC bioinformatics, 11, 482.

Singh SP, et al. (2008) Prediction of MHC binding peptide using Gibbs motif sampler, weight matrix and artificial neural network. Bioinformation, 3(4), 150.