

# Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

## MHCPEP

RRID:SCR\_007786

Type: Tool

### Proper Citation

MHCPEP (RRID:SCR\_007786)

### Resource Information

**URL:** <http://bio.dfci.harvard.edu/DFRMLI/>

**Proper Citation:** MHCPEP (RRID:SCR\_007786)

**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:** data or information resource, database

**Resource Name:** MHCPEP

**Resource ID:** SCR\_007786

**Alternate IDs:** nif-0000-03124

**Record Creation Time:** 20220129T080243+0000

**Record Last Update:** 20260801T190944+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 [ASWG](#) .

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.