

Resource Summary Report

Generated by [NIF](#) on Sep 5, 2026

AutoRT

RRID:SCR_024513

Type: Tool

Proper Citation

AutoRT (RRID:SCR_024513)

Resource Information

URL: <https://github.com/bzhanglab/AutoRT/>

Proper Citation: AutoRT (RRID:SCR_024513)

Description: Software tool for peptide retention time prediction using deep learning. Supports peptide retention prediction for tryptic peptides, MHC bound peptides and PTM peptides.

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:32273506](#)

Keywords: proteogenomics analysis

Availability: Free, Available for download, Freely available

Resource Name: AutoRT

Resource ID: SCR_024513

License: GNU GPL v3.0

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260903T235923+0000

Ratings and Alerts

No rating or validation information has been found for AutoRT.

No alerts have been found for AutoRT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Mahmud A, et al. (2026) Assessing the Performance of Mass Spectrometry Search Strategies in Identifying Translational Errors Using PDX Proteomics Data. Molecular & cellular proteomics : MCP, 25(2), 101500.

Yi X, et al. (2024) Deep Learning Prediction Boosts Phosphoproteomics-Based Discoveries Through Improved Phosphopeptide Identification. Molecular & cellular proteomics : MCP, 23(2), 100707.

Jiang W, et al. (2021) Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. Molecular & cellular proteomics : MCP, 20, 100171.