# **Resource Summary Report**

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# 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: software resource, software application, simulation software

Defining Citation: PMID:32273506

Keywords: proteogenomics analysis

Funding:

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: 20250522T061521+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 2 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.