

Resource Summary Report

Generated by T1D on Aug 2, 2026

sapFinder

RRID:SCR_002685

Type: Tool

Proper Citation

sapFinder (RRID:SCR_002685)

Resource Information

URL: <http://bioconductor.org/packages/release/bioc/html/sapFinder.html>

Proper Citation: sapFinder (RRID:SCR_002685)

Description: An R software package, for detection of the variant peptides based on tandem mass spectrometry (MS/MS)-based proteomics data. It automates (1) variation-associated database construction, (2) database searching, (3) post-processing, (4) HTML-based report generation in shotgun proteomics.

Synonyms: sapFinder - A package for variant peptides detection and visualization in shotgun proteomics.

Resource Type: software resource

Defining Citation: [PMID:25053745](https://pubmed.ncbi.nlm.nih.gov/25053745/)

Keywords: standalone software, r, mass spectrometry, proteomics, rna-seq, report writing, snp, visualization, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: sapFinder

Resource ID: SCR_002685

Alternate IDs: biotools:sapfinder, OMICS_05285

Alternate URLs: <https://bio.tools/sapfinder>

License: GNU General Public License, v2

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260801T190212+0000

Ratings and Alerts

No rating or validation information has been found for sapFinder.

No alerts have been found for sapFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.