

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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](#)

**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:** 20260725T190532+0000

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## Ratings and Alerts

No rating or validation information has been found for sapFinder.

No alerts have been found for sapFinder.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.