## **Resource Summary Report**

Generated by NIF on May 16, 2025

# 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

**Funding:** 

Availability: GNU General Public License, v2

Resource Name: sapFinder

Resource ID: SCR 002685

Alternate IDs: biotools:sapfinder, OMICS\_05285

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

**Record Creation Time:** 20220129T080214+0000

Record Last Update: 20250420T014116+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.