# **Resource Summary Report**

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# **Scfind**

RRID:SCR\_017339 Type: Tool

**Proper Citation** 

Scfind (RRID:SCR\_017339)

#### **Resource Information**

URL: https://scfind.sanger.ac.uk/

Proper Citation: Scfind (RRID:SCR\_017339)

**Description:** Software R package as search tool for single cell RNA-seq data by gene lists. Builds index from scRNA-seq datasets which organizes information in suitable and compact manner so that datasets can be very efficiently searched for either cells or cell types in which given list of genes is expressed.

**Resource Type:** software application, software resource, data or information resource, data processing software

Keywords: Single, cell, RNA-seq, data, gene, list, build, index, organize

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Scfind

Resource ID: SCR\_017339

Alternate URLs: https://genat.uk/post/scfind/, http://bioconductor.org/packages/scfind/, https://github.com/hemberg-lab/scfind

License: GNU GPLv3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250517T060319+0000

### **Ratings and Alerts**

No rating or validation information has been found for Scfind.

No alerts have been found for Scfind.

### Data and Source Information

Source: SciCrunch Registry

## Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Townes FW, et al. (2023) Nonnegative spatial factorization applied to spatial genomics. Nature methods, 20(2), 229.