Version 3



Search engine for genes in large single-cell sequencing collections <u>https://scfind.sanger.ac.uk/</u> (User Guide)

The User interface of Scfind

International Search-by-genes, or we find you the genes The text search fuels versarily Automicia disease or or/164404 Dp4	C Biters 4	1 Search box: Users can input a list of genes, SNPs ID, MeSH ID or medical/biological/chemical terms
		2 Dataset check box: Where the user can find all the datasets in the index and limit the search result by dataset / tissue
scfind		Parameters: Where the user can adjust the parameters for each search
		4 Home button: To the home page of our index collection
2 Tabula Muris - FACS 12/12 datasets	3 Parameters	

4 Steps : From your a query to your target cell type

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Step I: Input your query

- The bar chart **1** is a summary of the number of cells in the index expressing the gene
- User can always amend the initial gene list by clicking on

Step *II*: select one of our recommended sub-query on table 2 according to TF-IDF score

- subqueries are ranked by TF-IDF score (Highest = likely the best)
- click on TF-IDF to sort TF-IDF score in order

Step III: Select the enriched cell types on table

- Cells expressing all genes in the query are grouped by cell type. The user can rank them based on enrichment by clicking on p-value
- User can limit the dataset by clicking on 🗹 in 🧃
- User can adjust the degree of greediness in 4 to get the best gene set for each term in the query. The higher the degree, the more gene (but less relevancy) will return.

Step IV: Check the best representing genes

- Click on any cell type you are interested in 3
- 5 allows you to view the cells in a *UMAP*, compare *precision* / *recall / f1 scores* of each gene corresponding to each cell type and generate a *Word Cloud* relevant to your query.
- User can click on Copy CSV Excel to export the tables as raw text, csv file or .xlsx file

