

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

SCEVAN

RRID:SCR_028766

Type: Tool

Proper Citation

SCEVAN (RRID:SCR_028766)

Resource Information

URL: <https://github.com/AntonioDeFalco/SCEVAN>

Proper Citation: SCEVAN (RRID:SCR_028766)

Description: Software R package that automatically classifies the cells in the scRNA data by segregating non-malignant cells of tumor microenvironment from the malignant cells. It also infers the copy number profile of malignant cells, identifies subclonal structures and analyses the specific and shared alterations of each subpopulation.

Synonyms: Single CELL Variational ANeuploidy

Resource Type: software toolkit, software resource, source code

Defining Citation: [PMID:36841879](#)

Keywords: automatically classify cells, scRNA data, segregating non-malignant cells of tumor microenvironment, malignant cells, copy number profile of malignant cells, identify subclonal structures,

Funding: Italian Ministry of Research Grant

Availability: Free, Available for download, Freely available

Resource Name: SCEVAN

Resource ID: SCR_028766

License: GNU GPL v3

Record Creation Time: 20260728T043813+0000

Record Last Update: 20260813T055422+0000

Ratings and Alerts

No rating or validation information has been found for SCEVAN.

No alerts have been found for SCEVAN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.