

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

FCROS

RRID:SCR_006195

Type: Tool

Proper Citation

FCROS (RRID:SCR_006195)

Resource Information

URL: <http://cran.r-project.org/web/packages/fcros/>

Proper Citation: FCROS (RRID:SCR_006195)

Description: A fold change ranks ordering statistics based software for detecting differentially expressed genes.

Abbreviations: FCROS

Synonyms: fold change rank ordering statistics, fcros: FCROS for detecting differentially expressed genes

Resource Type: software resource

Defining Citation: [PMID:24423217](#)

Keywords: differentially expressed, gene, fold, statistics, windows, os x, microarray

Availability: GNU General Public License, v2, v3

Resource Name: FCROS

Resource ID: SCR_006195

Alternate IDs: OMICS_02234

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260912T195636+0000

Ratings and Alerts

No rating or validation information has been found for FCROS.

No alerts have been found for FCROS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Burkard M, et al. (2020) Common Gene Expression Patterns in Environmental Model Organisms Exposed to Engineered Nanomaterials: A Meta-Analysis. Environmental science & technology, 54(1), 335.

Agrawal P, et al. (2019) Enabling cell-type-specific behavioral epigenetics in Drosophila: a modified high-yield INTACT method reveals the impact of social environment on the epigenetic landscape in dopaminergic neurons. BMC biology, 17(1), 30.

Bonito G, et al. (2019) Fungal-Bacterial Networks in the Populus Rhizobiome Are Impacted by Soil Properties and Host Genotype. Frontiers in microbiology, 10, 481.

Kamenova I, et al. (2019) Co-translational assembly of mammalian nuclear multisubunit complexes. Nature communications, 10(1), 1740.

Makhijani RK, et al. (2018) Fold change based approach for identification of significant network markers in breast, lung and prostate cancer. IET systems biology, 12(5), 213.