# **Resource Summary Report**

Generated by <u>dkNET</u> on Apr 30, 2025

# **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

Funding:

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: 20250420T014316+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 <u>dkNET</u>.

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.