

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[isva](#)

RRID:SCR_008772

Type: Tool

Proper Citation

isva (RRID:SCR_008772)

Resource Information

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

Proper Citation: isva (RRID:SCR_008772)

Description: An algorithm for feature selection in the presence of potential confounding factors.

Abbreviations: isva

Synonyms: Independent Surrogate Variable Analysis, isva: Independent Surrogate Variable Analysis

Resource Type: software resource

Resource Name: isva

Resource ID: SCR_008772

Alternate IDs: OMICS_00860

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260801T190337+0000

Ratings and Alerts

No rating or validation information has been found for isva.

No alerts have been found for isva.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Campos-Martin R, et al. (2023) Epigenome-wide analysis identifies methylome profiles linked to obsessive-compulsive disorder, disease severity, and treatment response. *Molecular psychiatry*, 28(10), 4321.

Guevara EE, et al. (2021) Comparative analysis reveals distinctive epigenetic features of the human cerebellum. *PLoS genetics*, 17(5), e1009506.

Br??gelmann J, et al. (2019) A comparative analysis of cell-type adjustment methods for epigenome-wide association studies based on simulated and real data sets. *Briefings in bioinformatics*, 20(6), 2055.