# Resource Summary Report

Generated by dkNET on Apr 29, 2025

## 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

**Funding:**

**Resource Name:** isva

**Resource ID:** SCR_008772

**Alternate IDs:** OMICS_00860

**Record Creation Time:** 20220129T080249+0000

**Record Last Update:** 20250420T014439+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 dkNET.

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.

Brägelmann 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.