

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

sva package

RRID:SCR_012836

Type: Tool

Proper Citation

sva package (RRID:SCR_012836)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/sva.html>

Proper Citation: sva package (RRID:SCR_012836)

Description: Contains functions for removing batch effects and other unwanted variation in high-throughput experiment.

Abbreviations: sva package

Synonyms: Surrogate Variable Analysis

Resource Type: software resource

Resource Name: sva package

Resource ID: SCR_012836

Alternate IDs: OMICS_00861

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260801T190440+0000

Ratings and Alerts

No rating or validation information has been found for sva package.

No alerts have been found for sva package.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. *Cell reports*, 45(1), 116835.

Mokhtari A, et al. (2025) Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study. *EBioMedicine*, 113, 105569.

Ayabe H, et al. (2025) Cellular crosstalk mediated by TGF- β drives epithelial-mesenchymal transition in patient-derived multi-compartment biliary organoids. *Nature communications*, 16(1), 6575.

Rohan P, et al. (2025) High expression of THY1 is a prognostic marker for gastric Cancer: Deciphering its transcriptional regulation as a component of the Epithelial-mesenchymal transition. *Biochemistry and biophysics reports*, 42, 102050.

Tan C, et al. (2025) A Machine Learning-Based Diagnostic Nomogram for Moyamoya Disease: The Validation of Hypoxia-Immune Gene Signatures. *Bioengineering (Basel, Switzerland)*, 12(6).

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. *Cancer discovery*, 15(8), 1630.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. *medRxiv : the preprint server for health sciences*.

Duan H, et al. (2025) FAR1 as a ferroptosis-related biomarker and potential therapeutic target in acute kidney injury: integrated bioinformatics and experimental validation. *Renal failure*, 47(1), 2547260.

Huang P, et al. (2025) Identification of aberrantly expressed genes during aging in the mouse heart via integrated bioinformatics analysis. *Medicine*, 104(13), e41972.

Huang S, et al. (2025) Identification of Ferroptosis-Related Hub Genes as Diagnosis Biomarkers and Therapeutic Monitoring for Major Depressive Disorder Diagnosis. *IET systems biology*, 19(1), e70045.

Mal A, et al. (2025) HIF-2-Dependent Regulation of PTHrP and Paraneoplastic Hypercalcemia in Aggressive Clear-Cell Renal Cell Carcinoma. *Cancer discovery*, 15(12), 2485.

Keele GR, et al. (2025) Genetic architecture of the murine red blood cell proteome reveals central role of hemoglobin beta cysteine 93 in maintaining redox balance. *Cell genomics*, 101069.

Alfaro-García JP, et al. (2025) Characterization of the Temporal Dynamics of the Endothelial-Mesenchymal-like Transition Induced by Soluble Factors from Dengue Virus Infection in Microvascular Endothelial Cells. *International journal of molecular sciences*, 26(5).

Ali M, et al. (2025) Multi-cohort cerebrospinal fluid proteomics identifies robust molecular signatures across the Alzheimer disease continuum. *Neuron*, 113(9), 1363.

Araya P, et al. (2025) Interferon signaling modulates Down syndrome-associated Alzheimer's disease pathology in a mouse model. *iScience*, 28(8), 113130.

Wang X, et al. (2025) Integrative machine learning and transcriptomic analysis identifies key molecular targets in MNPN-associated oral squamous cell carcinoma pathogenesis. *Frontiers in bioinformatics*, 5, 1664576.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. *bioRxiv : the preprint server for biology*.

Liao Y, et al. (2024) Protocol to analyze immune cells in the tumor microenvironment by transcriptome using machine learning. *STAR protocols*, 5(1), 102684.

Lu Y, et al. (2024) Development and experimental validation of an energy metabolism-related gene signature for diagnosing of osteoporosis. *Scientific reports*, 14(1), 8153.