

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

## DSS

RRID:SCR\_002754

Type: Tool

---

### Proper Citation

DSS (RRID:SCR\_002754)

---

### Resource Information

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

**Proper Citation:** DSS (RRID:SCR\_002754)

**Description:** Software R library performing differential analysis for count-based sequencing data. It detects differentially expressed genes (DEGs) from RNA-seq, and differentially methylated loci or regions (DML/DMRs) from bisulfite sequencing (BS-seq). The core of DSS is a new dispersion shrinkage method for estimating the dispersion parameter from Gamma-Poisson or Beta-Binomial distributions.

**Synonyms:** Dispersion Shrinkage for Sequencing data, DSS - Dispersion shrinkage for sequencing data

**Resource Type:** software library, software resource, software toolkit

**Defining Citation:** [PMID:24561809](#)

**Keywords:** standalone software, unix/linux, mac os x, windows, r, differential expression, rna-seq, chip-seq, dna methylation, differential expression, sequencing

**Availability:** Free, Freely available, Available for download

**Resource Name:** DSS

**Resource ID:** SCR\_002754

**Alternate IDs:** OMICS\_03273

**License:** GNU General Public License

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260912T195546+0000

---

### Ratings and Alerts

No rating or validation information has been found for DSS.

No alerts have been found for DSS.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Zhang Q, et al. (2026) Integrated analysis of DNA methylation and transcriptome profiles in broiler heart and lung tissues reveals epigenetic regulatory mechanisms underlying ascites syndrome. Poultry science, 105(1), 106034.

Karwaciak I, et al. (2025) Staphylococcus aureus ??-hemolysin induces DNA methylation changes in human Th1 cells. Immunologic research, 73(1), 95.

Akbulut S, et al. (2024) Role of Epigenetic Factors in Determining the Biological Behavior and Prognosis of Hepatocellular Carcinoma. Diagnostics (Basel, Switzerland), 14(17).

Graham MK, et al. (2024) The TERT Promoter is Polycomb-Repressed in Neuroblastoma Cells with Long Telomeres. Cancer research communications, 4(6), 1533.

O'Neill K, et al. (2024) Long-read sequencing of an advanced cancer cohort resolves rearrangements, unravels haplotypes, and reveals methylation landscapes. Cell genomics, 4(11), 100674.

Ewing AD, et al. (2020) Nanopore Sequencing Enables Comprehensive Transposable Element Epigenomic Profiling. Molecular cell, 80(5), 915.

Luo C, et al. (2019) Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. eLife, 8.

Ziller MJ, et al. (2018) Dissecting the Functional Consequences of De Novo DNA Methylation Dynamics in Human Motor Neuron Differentiation and Physiology. Cell stem cell, 22(4), 559.

Gaspar JM, et al. (2017) DMRfinder: efficiently identifying differentially methylated regions from MethylC-seq data. BMC bioinformatics, 18(1), 528.