

# Resource Summary Report

Generated by [ASWG](#) on Aug 5, 2026

## DSGseq

RRID:SCR\_001104

Type: Tool

### Proper Citation

DSGseq (RRID:SCR\_001104)

### Resource Information

**URL:** <http://bioinfo.au.tsinghua.edu.cn/software/DSGseq/>

**Proper Citation:** DSGseq (RRID:SCR\_001104)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 15,2025. R software program for identifying differentially spliced genes from two groups of RNA-seq samples. It reads the count file and outputs the differences in the relative abundance of the isoforms of each gene in the annotation., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** DSGseq

**Resource Type:** data processing software, data analysis software, software resource, sequence analysis software, software application

**Defining Citation:** [PMID:23228854](#)

**Keywords:** rna seq, isoform, genes, spliced genes, r, genomics, sequence analysis software

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** DSGseq

**Resource ID:** SCR\_001104

**Alternate IDs:** OMICS\_01331

**Record Creation Time:** 20220129T080205+0000

**Record Last Update:** 20260805T044018+0000

### Ratings and Alerts

No rating or validation information has been found for DSGseq.

No alerts have been found for DSGseq.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.