

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 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: software application, data analysis software, sequence analysis software, software resource, data processing software

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: 20260729T044008+0000

Ratings and Alerts

No rating or validation information has been found for DSGseq.

No alerts have been found for DSGseq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.