### **Resource Summary Report**

Generated by dkNET on Apr 28, 2025

# **DSGseq**

RRID:SCR\_001104

Type: Tool

### **Proper Citation**

DSGseq (RRID:SCR\_001104)

#### **Resource Information**

**URL:** <a href="http://bioinfo.au.tsinghua.edu.cn/software/DSGseq/">http://bioinfo.au.tsinghua.edu.cn/software/DSGseq/</a>

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

**Description:** 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.

Abbreviations: DSGseq

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

**Defining Citation: PMID:23228854** 

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

Funding:

Availability: Open source

Resource Name: DSGseq

Resource ID: SCR\_001104

Alternate IDs: OMICS\_01331

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

**Record Last Update:** 20250428T052849+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.