

Resource Summary Report

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GENE-counter

RRID:SCR_013056

Type: Tool

Proper Citation

GENE-counter (RRID:SCR_013056)

Resource Information

URL: <http://sourceforge.net/projects/genecounter/>

Proper Citation: GENE-counter (RRID:SCR_013056)

Description: A computational pipeline for analyzing RNA-Sequencing (RNA-Seq) data for differential gene expression of eukaryotes, prokaryotes, as well as organisms with no available genome reference sequence.

Abbreviations: GENE-counter

Resource Type: software resource

Defining Citation: [PMID:21998647](#)

Keywords: bio.tools

Resource Name: GENE-counter

Resource ID: SCR_013056

Alternate IDs: OMICS_01404, biotools:gene-counter

Alternate URLs: <https://bio.tools/gene-counter>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260905T132731+0000

Ratings and Alerts

No rating or validation information has been found for GENE-counter.

No alerts have been found for GENE-counter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Filichkin SA, et al. (2015) Environmental stresses modulate abundance and timing of alternatively spliced circadian transcripts in Arabidopsis. *Molecular plant*, 8(2), 207.

Goyer A, et al. (2015) RNA-Seq analysis of resistant and susceptible potato varieties during the early stages of potato virus Y infection. *BMC genomics*, 16(1), 472.

Vicentini R, et al. (2015) Large-Scale Transcriptome Analysis of Two Sugarcane Genotypes Contrasting for Lignin Content. *PloS one*, 10(8), e0134909.

Liu S, et al. (2014) RNA-seq analysis of early hepatic response to handling and confinement stress in rainbow trout. *PloS one*, 9(2), e88492.

Bushley KE, et al. (2013) The genome of tolypocladium inflatum: evolution, organization, and expression of the cyclosporin biosynthetic gene cluster. *PLoS genetics*, 9(6), e1003496.

Filichkin SA, et al. (2012) Unproductive alternative splicing and nonsense mRNAs: a widespread phenomenon among plant circadian clock genes. *Biology direct*, 7, 20.

Cumbie JS, et al. (2011) GENE-counter: a computational pipeline for the analysis of RNA-Seq data for gene expression differences. *PloS one*, 6(10), e25279.