Resource Summary Report

Generated by NIF on Apr 18, 2025

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

Funding:

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: 20250410T070328+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 NIF.

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

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

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.

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.