Resource Summary Report

Generated by NIF on Apr 27, 2025

GIIRA

RRID:SCR_015507
Type: Tool

Proper Citation

GIIRA (RRID:SCR_015507)

Resource Information

URL: https://sourceforge.net/projects/giira/

Proper Citation: GIIRA (RRID:SCR_015507)

Description: Gene prediction method that identifies potential coding regions based on the mapping of reads from an RNA-Seq experiment.

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

Defining Citation: DOI:10.1093/bioinformatics/btt577

Keywords: gene prediction, rna seq, coding region, potential coding region

Funding:

Availability: Available for download

Resource Name: GIIRA

Resource ID: SCR_015507

Alternate IDs: OMICS_07360

Alternate URLs:
http://www.rki.de/EN/Content/Institute/DepartmentsUnits/JuniorGroups/JRG4.html,
https://sources.debian.org/src/giira/

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250426T060500+0000

Ratings and Alerts

No rating or validation information has been found for GIIRA.

No alerts have been found for GIIRA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zickmann F, et al. (2015) MSProGene: integrative proteogenomics beyond six-frames and single nucleotide polymorphisms. Bioinformatics (Oxford, England), 31(12), i106.

Spies D, et al. (2015) Dynamics in Transcriptomics: Advancements in RNA-seq Time Course and Downstream Analysis. Computational and structural biotechnology journal, 13, 469.

Zickmann F, et al. (2015) IPred - integrating ab initio and evidence based gene predictions to improve prediction accuracy. BMC genomics, 16(1), 134.