# **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.

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

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