

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## GIIRA

RRID:SCR\_015507

Type: Tool

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### Proper Citation

GIIRA (RRID:SCR\_015507)

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### 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 analysis software, software application, software resource, sequence analysis software, data processing software

**Defining Citation:** [DOI:10.1093/bioinformatics/btt577](https://doi.org/10.1093/bioinformatics/btt577)

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

**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:** 20260801T190515+0000

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### Ratings and Alerts

No rating or validation information has been found for GIIRA.

No alerts have been found for GIIRA.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

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.