

Resource Summary Report

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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 analysis software, software application, software resource, data processing software, sequence analysis 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: 20260812T044310+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.