Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 9, 2025

HiRise

RRID:SCR_023037

Type: Tool

Proper Citation

HiRise (RRID:SCR_023037)

Resource Information

URL: https://github.com/DovetailGenomics/HiRise_July2015_GR

Proper Citation: HiRise (RRID:SCR_023037)

Description: Software pipeline to identify poor quality joins and produce accurate, long

range sequence scaffolds.

Synonyms: Omni-C Scuffolder

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

processing software

Defining Citation: PMID:26848124

Keywords: Omni-C, Hi-C, Scaffolder, identify poor quality joins, produce accurate sequence

scaffolds, long range sequence scaffolds,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: HiRise

Resource ID: SCR_023037

Record Creation Time: 20221208T050157+0000

Record Last Update: 20250509T060427+0000

Ratings and Alerts

No rating or validation information has been found for HiRise .

No alerts have been found for HiRise.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Li T, et al. (2024) The American Cherimoya Genome Reveals Insights into the Intra-Specific Divergence, the Evolution of Magnoliales, and a Putative Gene Cluster for Acetogenin Biosynthesis. Plants (Basel, Switzerland), 13(5).

Jiang L, et al. (2024) The Bioinformatic Applications of Hi-C and Linked Reads. Genomics, proteomics & bioinformatics, 22(4).

Gumangan MA, et al. (2024) Chromosome-level genome assembly and annotation of the crested gecko, Correlophus ciliatus, a lizard incapable of tail regeneration. GigaByte (Hong Kong, China), 2024, gigabyte140.

De Silva NP, et al. (2022) Genome assembly of an Australian native grass species reveals a recent whole-genome duplication and biased gene retention of genes involved in stress response. GigaScience, 12.