

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

JR-Assembler

RRID:SCR_010681

Type: Tool

Proper Citation

JR-Assembler (RRID:SCR_010681)

Resource Information

URL: <http://jr-assembler.iis.sinica.edu.tw/>

Proper Citation: JR-Assembler (RRID:SCR_010681)

Description: An assembler for the de novo assembly of large genomes using short sequence reads via jumping extension and read remapping.

Abbreviations: JR-Assembler

Resource Type: software resource

Defining Citation: [PMID:23966565](#)

Resource Name: JR-Assembler

Resource ID: SCR_010681

Alternate IDs: OMICS_00018

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260725T190701+0000

Ratings and Alerts

No rating or validation information has been found for JR-Assembler.

No alerts have been found for JR-Assembler.

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 [kravitz2](#) .

Wagner JT, et al. (2018) The genome of *Austrofundulus limnaeus* offers insights into extreme vertebrate stress tolerance and embryonic development. *BMC genomics*, 19(1), 155.

Hou Y, et al. (2016) Comparative Genomics of Pathogens Causing Brown Spot Disease of Tobacco: *Alternaria longipes* and *Alternaria alternata*. *PloS one*, 11(5), e0155258.

M??bius P, et al. (2015) Comprehensive insights in the *Mycobacterium avium* subsp. *paratuberculosis* genome using new WGS data of sheep strain JIII-386 from Germany. *Genome biology and evolution*, 7(9), 2585.

Campana MG, et al. (2015) America's red gold: multiple lineages of cultivated cochineal in Mexico. *Ecology and evolution*, 5(3), 607.