Resource Summary Report

Generated by NIF on Apr 9, 2025

ARACHNE

RRID:SCR_000351
Type: Tool

Proper Citation

ARACHNE (RRID:SCR_000351)

Resource Information

URL: http://www.broadinstitute.org/science/programs/genome-biology/computational-rd/computational-research-and-development

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Description: A software for genome assembly, and is specifically designed to analyze long Sanger-chemistry reads.

Abbreviations: ARACHNE

Synonyms: ARACHNE: a whole-genome shotgun assembler, ARACHNE (Unsupported)

Resource Type: software resource

Defining Citation: PMID:11779843

Keywords: genome, sequencing, analysis, sanger, chemistry, bio.tools

Funding:

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Resource Name: ARACHNE

Resource ID: SCR_000351

Alternate IDs: OMICS_01812, biotools:arachne

Alternate URLs: https://bio.tools/arachne

Record Creation Time: 20220129T080201+0000

Record Last Update: 20250214T182916+0000

Ratings and Alerts

No rating or validation information has been found for ARACHNE.

No alerts have been found for ARACHNE.

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.

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. Briefings in bioinformatics, 17(1), 154.

Bedognetti D, et al. (2011) SITC/iSBTc Cancer Immunotherapy Biomarkers Resource Document: online resources and useful tools - a compass in the land of biomarker discovery. Journal of translational medicine, 9, 155.

Batzoglou S, et al. (2002) ARACHNE: a whole-genome shotgun assembler. Genome research, 12(1), 177.