

# Resource Summary Report

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

## [ARACHNE](#)

RRID:SCR\_000351

Type: Tool

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### Proper Citation

ARACHNE (RRID:SCR\_000351)

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### Resource Information

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

**Proper Citation:** ARACHNE (RRID:SCR\_000351)

**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

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**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:** 20260801T190111+0000

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### Ratings and Alerts

No rating or validation information has been found for ARACHNE.

No alerts have been found for ARACHNE.

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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](#) .

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.