

Resource Summary Report

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LACHESIS

RRID:SCR_017644

Type: Tool

Proper Citation

LACHESIS (RRID:SCR_017644)

Resource Information

URL: <https://github.com/shendurelab/LACHESIS>

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Description: Software tool for chromosome scale scaffolding of de novo genome assemblies based on chromatin interactions. Method exploits signal of genomic proximity in Hi-C datasets for ultra long range scaffolding of de novo genome assemblies.

Synonyms: Ligating Adjacent Chromatin Enables Scaffolding In Situ

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

Defining Citation: [PMID:24185095](#)

Keywords: Chromosome, scale, scaffolding, de novo, genome, assembly, chromatin, Hi-C, data, clustering, contig

Funding: NHGRI HG006283;
National Science Foundation ;
NHGRI T32 HG000035

Availability: Free, Available for download, Freely available

Resource Name: LACHESIS

Resource ID: SCR_017644

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260727T040706+0000

Ratings and Alerts

No rating or validation information has been found for LACHESIS.

No alerts have been found for LACHESIS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#).

Deng C, et al. (2025) A high-quality chromosome-scale genome assembly of Xingan mandarin (*Citrus reticulata* 'Xingan'), a primitive Mandarin type. *Scientific data*, 12(1), 1257.

Wen X, et al. (2025) The genome of giant waterlily provides insights into the origin of angiosperms, leaf gigantism, and stamen function innovation. *Plant communications*, 6(6), 101342.

Song Y, et al. (2025) Haplotype-Phased Chromosome-Level Genome Assembly of *Cryptoporus qinlingensis*, a Typical Traditional Chinese Medicine Fungus. *Journal of fungi* (Basel, Switzerland), 11(2).

Wang C, et al. (2025) Genomic-transcriptomic analysis identifies the Syrian hamster as a superior animal model for human diseases. *BMC genomics*, 26(1), 286.

Xia H, et al. (2025) Chromosome-level genome assembly of the *Rhizoctonia solani*. *Scientific data*, 12(1), 1053.

Du H, et al. (2025) Pangenome Reveals Gene Content Variations and Structural Variants Contributing to Pig Characteristics. *Genomics, proteomics & bioinformatics*, 22(6).

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Hong L, et al. (2024) Construction and analysis of telomere-to-telomere genomes for 2 sweet oranges: Longhuihong and Newhall (*Citrus sinensis*). *GigaScience*, 13.

Hu Z, et al. (2024) Genomics insights into flowering and floral pattern formation: regional duplication and seasonal pattern of gene expression in *Camellia*. *BMC biology*, 22(1), 50.

Fu X, et al. (2024) Key homeobox transcription factors regulate the development of the firefly's adult light organ and bioluminescence. *Nature communications*, 15(1), 1736.

Xia W, et al. (2024) Chromosome-level genome provides new insight into the overwintering process of Korla pear (*Pyrus sinkiangensis* Yu). *BMC plant biology*, 24(1),

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex communication. *GigaScience*, 13.

Du H, et al. (2024) Chromosome-level genome assembly of Huai pig (*Sus scrofa*). *Scientific data*, 11(1), 1072.

Zhang J, et al. (2024) Chromosome-Level Assembly and Comparative Genomic Analysis of *Suillus bovinus* Provides Insights into the Mechanism of Mycorrhizal Symbiosis. *Journal of fungi* (Basel, Switzerland), 10(3).

Zou M, et al. (2024) The chromosome-level genome assembly of the giant dobsonfly *Acanthacorydalis orientalis* (McLachlan, 1899). *Scientific data*, 11(1), 351.

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

Yang YX, et al. (2024) The chromosome-level genome assembly of an endangered herb *Bergenia scopulosa* provides insights into local adaptation and genomic vulnerability under climate change. *GigaScience*, 13.

Fu L, et al. (2024) Chromosome-level genome assembly of predatory *Arma chinensis*. *Scientific data*, 11(1), 962.

Shen C, et al. (2024) Genome-wide identification analysis in wild-type *Solanum pinnatisectum* reveals some genes defending against *Phytophthora infestans*. *Frontiers in genetics*, 15, 1379784.

Fu X, et al. (2024) An Improved Chromosome-Level Genome Assembly of the Firefly *Pyrocoelia pectoralis*. *Insects*, 15(1).