

Resource Summary Report

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YaHS

RRID:SCR_022965

Type: Tool

Proper Citation

YaHS (RRID:SCR_022965)

Resource Information

URL: <https://github.com/c-zhou/yahs>

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Description: Software command line tool for construction of chromosome scale scaffolds from Hi-C data. Scaffolding tool using Hi-C or Omni-C data. Used to scaffold contig level assemblies into chromosome scale scaffolded assemblies.

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

Defining Citation: [DOI:10.1101/2022.06.09.495093](https://doi.org/10.1101/2022.06.09.495093)

Keywords: construction of chromosome scale scaffolds, Hi-C data, Omni-C data, scaffold contig level assemblies, chromosome scale scaffolded assemblies

Funding: Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: YaHS

Resource ID: SCR_022965

License: MIT License

Record Creation Time: 20221115T050204+0000

Record Last Update: 20260820T055007+0000

Ratings and Alerts

No rating or validation information has been found for YaHS.

No alerts have been found for YaHS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 806 mentions in open access literature.

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

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Sanchez A, et al. (2026) The genome sequence of the Osiris Blue, *Cupido osiris* (Meigen, 1830) (Lepidoptera: Lycaenidae). *Wellcome open research*, 11, 71.

Coleman D, et al. (2026) The genome sequence of the Bicolour Sedge, *Triaenodes bicolor* (Curtis, 1834) (Trichoptera: Leptoceridae). *Wellcome open research*, 11, 26.

Pérez T, et al. (2026) The chromosomal genome sequence of the carnivorous sponge, *Lycopodina hypogea* (Vacelet & Boury-Esnault, 1996) (Poecilosclerida: Cladorhizidae) and its associated microbial metagenome sequences. *Wellcome open research*, 11, 130.

Iankoshvili G, et al. (2026) The genome sequence of Menetries' Clouded Yellow, *Colias thisoa* Ménétriers, 1832 (Lepidoptera: Pieridae). *Wellcome open research*, 11, 64.

Menchetti M, et al. (2026) The genome sequence of the Portuguese Dappled White, *Euchloe tagis* (Hübner, 1804) (Lepidoptera: Pieridae). *Wellcome open research*, 11, 100.

Brownlow A, et al. (2026) The genome sequence of the Atlantic white-sided dolphin, *Leucopleurus acutus* (Gray, 1828) (Artiodactyla: Delphinidae). *Wellcome open research*, 11, 2.

Langdon WBV, et al. (2026) The genome sequence of the Suspected, *Parastichtis suspecta* (Hübner, 1809) (Lepidoptera: Noctuidae). *Wellcome open research*, 11, 288.

Ruedi M, et al. (2026) The genome sequence of Nathusius' pipistrelle, *Pipistrellus nathusii* (Keyserling & Blasius, 1839) (Chiroptera: Vespertilionidae). *Wellcome open research*, 11, 234.

Prabhudas SK, et al. (2026) Chromosome level genome and full length transcriptome of long whiskers catfish, *Mystus gulio* (Hamilton, 1822). *Scientific data*, 13(1).

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Jones ARC, et al. (2026) *Cryptocercus* Genomes Expand Knowledge of Adaptations to Xylophagy and Termite Sociality. *Genome biology and evolution*, 18(2).

Huang Y, et al. (2026) *Digitaria* genome analyses indicate introgression may drive local adaptation and herbicide resistance. *Nature communications*, 17(1).

de Souza Araujo N, et al. (2026) Retroelement expansions underlie genome evolution in stingless bees. *BMC genomics*, 27(1), 160.

Crowley LM, et al. (2026) The genome sequence of the soldier beetle, *Malthodes minimus* (Linnaeus, 1758) (Coleoptera: Cantharidae). *Wellcome open research*, 11, 16.

Baalsrud HT, et al. (2026) Chromosomal fusions shaped the genome of the greater hornwrack bryozoan (*Flustra foliacea*) (Linnaeus, 1758). *The Journal of heredity*, 117(4), 750.

Dinc? V, et al. (2026) The genome sequence of the Eastern Pale Clouded Yellow, *Colias erate* (Esper, 1805) (Lepidoptera: Pieridae). *Wellcome open research*, 11, 102.

Crowley LM, et al. (2026) The genome sequence of the Cramp-ball Fungus Weevil, *Platyrhinus resinosus* (Scopoli, 1763) (Coleoptera: Anthribidae). *Wellcome open research*, 11, 327.