

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 analysis software, data processing 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: 20260729T044545+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 450 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anelli*). *G3 (Bethesda, Md.)*, 16(1).

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Patel HR, et al. (2025) A near telomere-to-telomere phased genome assembly and annotation for the Australian central bearded dragon *Pogona vitticeps*. *GigaScience*, 14.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae: Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Nebenführ M, et al. (2025) Chromosome-level genome assembly of the lemon sole, *Microstomus kitt* (*Pleuronectiformes: Pleuronectidae*). *GigaByte (Hong Kong, China)*, 2025, gigabyte156.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of *Cypriniformes*. *GigaScience*, 14.

Feiner N, et al. (2025) The genome sequence of the Dalmatian wall lizard, *Podarcis melisellensis* (Braun, 1877). *Wellcome open research*, 10, 247.

Davison NJ, et al. (2025) The genome sequence of long-finned pilot whale, *Globicephala melas* (Traill, 1809). *Wellcome open research*, 10, 180.

Feiner N, et al. (2025) The genome sequence of Bocage's wall lizard, *Podarcis bocagei* (Lopez-Seoane, 1885). *Wellcome open research*, 10, 246.

Sivell O, et al. (2025) The genome sequence of the solitary wasp, *Cerceris ruficornis* (Fabricius, 1793). *Wellcome open research*, 10, 276.

Chittaro Y, et al. (2025) The genome sequence of the Dusky Meadow Brown, *Cercyonis lycaon* (*Lepidoptera: Nymphalidae*). *Wellcome open research*, 10, 395.

Boyes D, et al. (2025) The genome sequence of the Large Birch Bell moth, Large Birch Roller, *Epinotia brunnichana* (Linnaeus, 1767). Wellcome open research, 10, 101.

Christenhusz MJM, et al. (2025) The genome sequence of the common hop, *Humulus lupulus* L. Wellcome open research, 10, 210.

Barclay MVL, et al. (2025) The genome sequence of a longhorn beetle, *Rhagium mordax* (Degeer, 1775). Wellcome open research, 10, 51.

Adkins P, et al. (2025) The genome sequence of the amphioxus, *Branchiostoma lanceolatum* (Pallas, 1774). Wellcome open research, 10, 95.

Power D, et al. (2025) The genome sequence of Greek sea-spurrey, *Spergularia bocconeii* (Scheele) Graebn. (Caryophyllaceae). Wellcome open research, 10, 34.

Booth R, et al. (2025) The genome sequence of a leaf beetle, *Galerucella nymphaeae* (Linnaeus, 1758). Wellcome open research, 10, 57.

Barclay MVL, et al. (2025) The genome sequence of a pallopterid fly, *Toxonevra muliebris* (Harris, 1780). Wellcome open research, 10, 55.

Boyes D, et al. (2025) The genome sequence of Red Underwing, *Catocala nupta* Linnaeus, 1767. Wellcome open research, 10, 36.