

Resource Summary Report

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Blobtools

RRID:SCR_017618

Type: Tool

Proper Citation

Blobtools (RRID:SCR_017618)

Resource Information

URL: <https://blobtools.readme.io/docs>

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Description: Software tool as modular command line solution for visualisation, quality control and taxonomic partitioning of genome datasets. Used for interrogation of genome assemblies. Assists in primary partitioning of data, leading to improved assemblies, and screening of final assemblies for potential contaminants.

Synonyms: BlobTools

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

Defining Citation: [DOI:10.12688/f1000research.12232.1](https://doi.org/10.12688/f1000research.12232.1)

Keywords: Modular, command, line, solution, visualisation, quality, control, taxonomic, partitioning, genome, dataset, genome assembly, screening, contaminant, bio.tools

Funding: James Hutton Institute/Edinburgh University School of Biological Sciences fellowship ;
BBSRC

Availability: Free, Available for download, Freely available

Resource Name: Blobtools

Resource ID: SCR_017618

Alternate IDs: biotools:blobtools

Alternate URLs: <https://github.com/DRL/blobtools>, <https://bio.tools/blobtools>

License: GNU General Public License v3.0

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Ratings and Alerts

No rating or validation information has been found for Blobtools.

No alerts have been found for Blobtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 199 mentions in open access literature.

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

Choi J, et al. (2025) Accelerated Pseudogenization in the Ancient Endosymbionts of Giant Scale Insects. *Molecular biology and evolution*, 42(6).

Iwai H, et al. (2025) Genome assembly of the temporary socially parasitic spiny ant *Polyrhachis lamellidens* and its host *Camponotus japonicus*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(2).

Chen X, et al. (2025) High-quality genome assembly of the azooxanthellate coral *Tubastraea coccinea* (Lesson, 1829). *Scientific data*, 12(1), 507.

Liesenfelt T, et al. (2025) Genome report: genome sequence of the hibiscus mealybug, *Nipaecoccus viridis* (Newstead), an invasive pest of citrus. *G3 (Bethesda, Md.)*, 15(11).

Domínguez M, et al. (2025) Long read genome unravels MHC I genomic architecture, evolution, and diversity loss in *Gubernatrix cristata*. *iScience*, 28(5), 112301.

Dittmer J, et al. (2025) The Endosymbiont Consortia of Two Cixiidae Planthoppers Reveal an Ancient Symbiosis With 'Candidatus Mirabilia Symbiotica'. *Environmental microbiology reports*, 17(5), e70204.

García-Muñoz A, et al. (2025) Evaluating the Assembly Strategy of a Fungal Genome from Metagenomic Data: *Solorina crocea* (Peltigerales, Ascomycota) as a Case Study. *Journal of fungi (Basel, Switzerland)*, 11(8).

Chang X, et al. (2025) Re-annotation improved large-scale assembly of the reef-building coral *Acropora intermedia*. *Scientific data*, 12(1), 1504.

Radice VZ, et al. (2025) First reference genomes for two mesophotic, reef-building coral species: *Leptoseris* cf. *scabra* and *Montipora* cf. *grisea*. *The Journal of heredity*, 116(4), 488.

Kirbis A, et al. (2025) Comparative analysis using a chromosome-scale genome assembly for *Funaria hygrometrica* suggests greater collinearity in mosses than in seed plants. *Communications biology*, 8(1), 330.

Fujiwara K, et al. (2025) Chromosome-scale genomes of two wild flowering cherries (*Cerasus itosakura* and *Cerasus jamasakura*) provide insights into structural evolution in *Cerasus*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).

Cunha VAS, et al. (2025) Genome of the Myiasis-Causing Fly *Chrysomya bezziana*, the Old-World Screwworm. *Genome biology and evolution*, 17(8).

Borisenko I, et al. (2025) First draft genome assembly of sponge *Halisarca dujardinii* reveals key components of basement membrane and broad repertoire of aggregation factors. *Scientific reports*, 15(1), 44778.

Jarvis DE, et al. (2025) Whole-genome assembly and annotation of the firecracker penstemon (*Penstemon eatonii*). *The Journal of heredity*, 116(3), 373.

Canitz J, et al. (2025) Reference genome of the leopard seal (*Hydrurga leptonyx*), a Southern Ocean apex predator. *Frontiers in genetics*, 16, 1561273.

Masui M, et al. (2025) Loss of the starvation-and-light fruitbody formation trigger in the myxomycete *Physarum roseum*. *Biology letters*, 21(7), 20250215.

Hill R, et al. (2025) Evolutionary genomics reveals variation in structure and genetic content implicated in virulence and lifestyle in the genus *Gaeumannomyces*. *BMC genomics*, 26(1), 239.

Mahillon M, et al. (2025) From insect endosymbiont to phloem colonizer: comparative genomics unveils the lifestyle transition of phytopathogenic *Arsenophonus* strains. *mSystems*, 10(5), e0149624.

McMullan M, et al. (2025) Developing a crop- wild-reservoir pathogen system to understand pathogen evolution and emergence. *eLife*, 14.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.