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, data visualization software, data analytics software, data processing software, software resource

Defining Citation: DOI: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

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250417T065623+0000

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 158 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Poullet M, et al. (2025) High-fidelity annotated triploid genome of the quarantine root-knot nematode, Meloidogyne enterolobii. Scientific data, 12(1), 184.

Wu J, et al. (2025) A chromosome-level genome assembly of the cabbage aphid Brevicoryne brassicae. Scientific data, 12(1), 167.

Toubiana W, et al. (2025) Functional monocentricity with holocentric characteristics and chromosome-specific centromeres in a stick insect. Science advances, 11(1), eads6459.

Bett VK, et al. (2024) Chromosome-Level Assembly of Artemia franciscana Sheds Light on Sex Chromosome Differentiation. Genome biology and evolution, 16(1).

Burns JA, et al. (2024) An in situ digital synthesis strategy for the discovery and description of ocean life. Science advances, 10(3), eadj4960.

Busoms S, et al. (2024) Local cryptic diversity in salinity adaptation mechanisms in the wild outcrossing Brassica fruticulosa. Proceedings of the National Academy of Sciences of the United States of America, 121(40), e2407821121.

Singh RP, et al. (2024) Genome assembly of a nocturnal butterfly (Macrosoma

leucophasiata) reveals convergent adaptation of visual genes. Communications biology, 7(1), 1664.

Haidar R, et al. (2024) Two Paenibacillus spp. strains promote grapevine wood degradation by the fungus Fomitiporia mediterranea: from degradation experiments to genome analyses. Scientific reports, 14(1), 15779.

Sacchi B, et al. (2024) Phased Assembly of Neo-Sex Chromosomes Reveals Extensive Y Degeneration and Rapid Genome Evolution in Rumex hastatulus. Molecular biology and evolution, 41(4).

Cho A, et al. (2024) Genomic analyses of Symbiomonas scintillans show no evidence for endosymbiotic bacteria but does reveal the presence of giant viruses. PLoS genetics, 20(4), e1011218.

Markee A, et al. (2024) De Novo Long-Read Genome Assembly and Annotation of the Luna Moth (Actias luna) Fully Resolves Repeat-Rich Silk Genes. Genome biology and evolution, 16(7).

Fuchs LIR, et al. (2024) A draft genome of the neritid snail Theodoxus fluviatilis. G3 (Bethesda, Md.), 14(3).

Weng YM, et al. (2024) Evolutionary genomics of three agricultural pest moths reveals rapid evolution of host adaptation and immune-related genes. GigaScience, 13.

McElroy KE, et al. (2024) A chromosome-level genome assembly of the disco clam, Ctenoides ales. G3 (Bethesda, Md.), 14(9).

, et al. (2024) Genome assembly of the rare and endangered Grantham's camellia, Camellia granthamiana. GigaByte (Hong Kong, China), 2024, gigabyte124.

Reatini B, et al. (2024) Chromosome-scale Reference Genome and RAD-based Genetic Map of Yellow Starthistle (Centaurea solstitialis) Reveal Putative Structural Variation and QTL Associated With Invader Traits. Genome biology and evolution, 16(12).

Nash WJ, et al. (2024) The genome sequence of the Violet Carpenter Bee, Xylocopa violacea (Linnaeus, 1785): a hymenopteran species undergoing range expansion. Heredity, 133(6), 381.

Maciszewski K, et al. (2024) Reduced plastid genomes of colorless facultative pathogens Prototheca (Chlorophyta) are retained for membrane transport genes. BMC biology, 22(1), 294.

Marcet-Houben M, et al. (2024) Genomics of the expanding pine pathogen Lecanosticta acicola reveals patterns of ongoing genetic admixture. mSystems, 9(3), e0092823.

Skojec C, et al. (2024) Long read genome assembly of Automeris io (Lepidoptera: Saturniidae) an emerging model for the evolution of deimatic displays. G3 (Bethesda, Md.), 14(3).