

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>

Proper Citation: Blobtools (RRID:SCR_017618)

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

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

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: 20260905T132827+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 225 mentions in open access literature.

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

Davis DD, et al. (2026) Whole-genome assembly and annotation of the acorn weevil, *Curculio nanulus* (Coleoptera: Curculionidae). *G3* (Bethesda, Md.), 16(2).

Panossian B, et al. (2026) Phage toxin variants are linked to protection specificity in a defensive symbiont. *Molecular biology and evolution*, 43(5).

Kim S, et al. (2026) Chromosome-Scale Reference Genome Assemblies for Two Anoplophora Longhorned Beetle Species (Coleoptera: Cerambycidae). *Genome biology and evolution*, 18(3).

Al-Hasan BA, et al. (2026) Complete genome sequence and functional characterization of *Bacillus amyloliquefaciens* NJF-55: a sheep-derived probiotic candidate. *Scientific reports*, 16(1), 6408.

Boulain H, et al. (2026) Ancient but dynamic: structural expansion, massive gene duplication, and transposable element colonization in a supergene controlling ant social organization. *Molecular biology and evolution*, 43(6).

Davies BE, et al. (2026) A Chromosome-level Assembly and Functional Genomic Resources for the Model Annelid *Capitella teleta*. *Genome biology and evolution*, 18(3).

Franchini P, et al. (2026) Highly contiguous chromosome-level assembly of the rock goby (*Gobius paganellus*) genome. *Scientific data*, 13(1).

Chakraborty A, et al. (2026) Chromosome-level genome assemblies of *Nicotiana attenuata* (coyote tobacco) and *Nicotiana obtusifolia* (desert tobacco). *Scientific data*, 13(1).

Perkin LC, et al. (2026) A chromosome level reference genome for the pecan weevil, *Curculio caryae*. *Scientific data*, 13(1).

Law STS, et al. (2026) The first chromosome-level cubozoan genome differentiates unique and common features in different cnidarian lineages. *BMC biology*, 24(1).

Heraghty SD, et al. (2026) Sequencing, annotation and analysis of the genome of *Oxycarenus hyalinipennis*, the cotton seed bug. *Life science alliance*, 9(8).

Kr??semer R, et al. (2026) Experimental *Sodalis* infection eliminates ancient insect symbiont. *Nature communications*, 17(1).

Marcheschi AK, et al. (2026) Chromosome-level genome assembly of the Australian *Chenopodium trigonon* reveals a new subgenome type. *Frontiers in plant science*, 17, 1841078.

Kataoka K, et al. (2026) Temporal orchestration of transcriptional and epigenomic programming underlying maternal embryonic diapause in a cricket model. *Communications biology*, 9(1).

Latrofa MS, et al. (2026) Nuclear, mitochondrial, and *Wolbachia* endosymbiont genomes of *Onchocerca lupi*, Portugal. *mSphere*, 11(2), e0062525.

Law STS, et al. (2026) Chromosome-level genomes of hard clams *Meretrix lamarckii* (Deshayes, 1853) and *Meretrix meretrix* (Linnaeus, 1758). *Scientific data*, 13(1).

Paris JR, et al. (2026) A High-quality Reference Genome and Tissue Expression Atlas for the European Lobster (*Homarus gammarus*). *Genome biology and evolution*, 18(6).

Samano A, et al. (2026) Structural variants are enriched in deleterious visible phenotypes in *Drosophila*. *Genome research*, 36(7), 1369.

Li Y, et al. (2026) Single-cell analyses of tissue regeneration in two true jellyfish. *Molecular biology and evolution*, 43(6).

Quintanilla-Mena M, et al. (2026) De novo Genome Assembly, Annotation, and Comparative Analysis of the Lined Sole *Achirus lineatus* as a Resource for Evolutionary and Environmental Genomics. *Marine biotechnology* (New York, N.Y.), 28(4).