

Resource Summary Report

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Blobtoolkit

RRID:SCR_025882

Type: Tool

Proper Citation

Blobtoolkit (RRID:SCR_025882)

Resource Information

URL: <https://github.com/blobtoolkit/blobtoolkit>

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Description: Software suite based on BlobTools to aid researchers in identifying and isolating non-target data in draft and publicly available genome assemblies. Used for genome assembly QC and contaminant cobiont detection and filtering. Can be used to process assembly, read and analysis files for fully reproducible interactive exploration in the browser-based Viewer. Can be used during assembly to filter non-target DNA. BlobToolKit is comprised of four distinct components: BlobTools2 (command line tools to create and filter datasets), Specification (a formal specification and validator for the JSON-based data format), Viewer (interactive dataset visualization), and INSDC-pipeline (a Snakemake pipeline to run the BlobToolKit workflow on publicly available datasets).

Synonyms: BlobToolKit

Resource Type: source code, software toolkit, software resource

Defining Citation: [PMID:32071071](#)

Keywords: genome assemblies, identifying and isolating non-target data, non-target DNA, genome assembly QC,

Funding: BBSRC Bioinformatics and Biological Resources award

Availability: Free, Available for download, Freely available

Resource Name: Blobtoolkit

Resource ID: SCR_025882

License: MIT license

Record Creation Time: 20241015T053249+0000

Ratings and Alerts

No rating or validation information has been found for Blobtoolkit.

No alerts have been found for Blobtoolkit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte* (Hong Kong, China), 2025, gigabyte150.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (*Strix uralensis*) enables investigations of cell cultures as a genomic resource for endangered species. *GigaScience*, 14.

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

Starcevic A, et al. (2025) Long-read metagenomic sequencing negates inferred loss of cytosine methylation in *Myxosporea* (Cnidaria: Myxozoa). *GigaScience*, 14.

Ryan H, et al. (2024) The genome sequence of the whiskered bat, *Myotis mystacinus* (Kuhl, 1817). *Wellcome open research*, 9, 684.

Brennan M, et al. (2024) The genome sequence of the Atlantic mackerel, *Scomber scombrus* Linnaeus, 1758. *Wellcome open research*, 9, 610.

Lopez Colom R, et al. (2024) The genome sequence of the black-headed gull, *Chroicocephalus ridibundus* (Linnaeus, 1766). *Wellcome open research*, 9, 399.

Boyes D, et al. (2024) The genome sequence of the Poplar Grey moth, *Subacronicta megacephala* (Denis & Schiffermüller, 1775). *Wellcome open research*, 9, 696.