

# Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

## Mercury

RRID:SCR\_022964

Type: Tool

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### Proper Citation

Mercury (RRID:SCR\_022964)

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### Resource Information

**URL:** <https://github.com/marbl/mercury>

**Proper Citation:** Mercury (RRID:SCR\_022964)

**Description:** Software toolkit for reference free quality, completeness, and phasing assessment for genome assemblies. Genome assembly quality evaluation based on k-mers.

**Resource Type:** software toolkit, software resource

**Defining Citation:** [PMID:32928274](#)

**Keywords:** reference free quality, completeness, phasing assessment, genome assemblies, quality evaluation based on k-mers

**Funding:** NHGRI

**Availability:** Free, Available for download, Freely available

**Resource Name:** Mercury

**Resource ID:** SCR\_022964

**License URLs:** <https://github.com/marbl/mercury/blob/master/LICENSE>

**Record Creation Time:** 20221115T050204+0000

**Record Last Update:** 20260815T183008+0000

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### Ratings and Alerts

No rating or validation information has been found for Mercury.

No alerts have been found for Mercury.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 72 mentions in open access literature.

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

Möllmann JS, et al. (2026) A Chromosome-Level Genome Assembly and Resequencing Data Reveal Low DNA Methylation and Reduced Diversity in the Solitary Bee Pollinator *Osmia cornuta*. *Genome biology and evolution*, 18(1).

Xie X, et al. (2026) Chromosome-level genome assembly of mud snail *Bullacta exarata*. *Scientific data*, 13(1).

Doré G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte (Hong Kong, China)*, 2026, gigabyte176.

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. *GigaScience*, 15.

Huang Y, et al. (2026) The near-complete genome assembly of allotetraploid *Pennisetum purpureum* 'Purple' reveals the genetic and epigenetic landscape of centromeres. *Horticulture research*, 13(2), uhaf301.

Peng G, et al. (2025) The high-quality telomere-to-telomere genome assembly of the earthworm (*Amyntas aspergillum*). *Scientific data*, 12(1), 931.

Bian C, et al. (2025) A complete telomere-to-telomere chromosome-level genome assembly of X-ray tetra (*Pristella maxillaris*). *Scientific data*, 12(1), 496.

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.

Xia W, et al. (2025) Chromosome-level genome assembly and annotation of *Pterygoplichthys pardalis*. *Scientific data*, 12(1), 1091.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Bian C, et al. (2025) A telomere-to-telomere chromosome-scale genome assembly of glass catfish (*Kryptopterus vitreolus*). *Scientific data*, 12(1), 483.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Li Z, et al. (2025) Phased high-quality genome of the gymnosperm Himalayan Yew assists in paclitaxel pathway exploration. *GigaScience*, 14.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

Simmons NB, et al. (2025) The genome sequence of *Glossophaga mutica* (Chiroptera, Phyllostomidae, Glossophaginae; Merriam, 1898). *Wellcome open research*, 10, 174.

Wang F, et al. (2025) Analysis of the *Rehmannia chingii* genome identifies RcCYP72H7 as an epoxidase in iridoid glycoside biosynthesis. *Nature communications*, 16(1), 6035.

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.

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.