

# Resource Summary Report

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## Meraculous

RRID:SCR\_010700

Type: Tool

### Proper Citation

Meraculous (RRID:SCR\_010700)

### Resource Information

**URL:** <http://www.plosone.org/article/info:doi%2F10.1371%2Fjournal.pone.0023501>

**Proper Citation:** Meraculous (RRID:SCR\_010700)

**Description:** An algorithm for de novo genome assembly with short paired-end reads.

**Abbreviations:** Meraculous

**Synonyms:** Meraculous: De Novo Genome Assembly with Short Paired-End Reads

**Resource Type:** software resource

**Resource Name:** Meraculous

**Resource ID:** SCR\_010700

**Alternate IDs:** OMICS\_00021

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260801T190355+0000

### Ratings and Alerts

No rating or validation information has been found for Meraculous.

No alerts have been found for Meraculous.

### Data and Source Information

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

### Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Araya-Donoso R, et al. (2025) Structural Rearrangements and Selection Promote Phenotypic Evolution in Anolis Lizards. *Genome biology and evolution*, 17(11).

Ho DV, et al. (2024) Post-meiotic mechanism of facultative parthenogenesis in gonochoristic whiptail lizard species. *eLife*, 13.

Marlétaz F, et al. (2024) The hagfish genome and the evolution of vertebrates. *Nature*, 627(8005), 811.

Schultz DT, et al. (2024) Acceleration of genome rearrangement in clitellate annelids. *bioRxiv : the preprint server for biology*.

Gaspar J, et al. (2024) De-novo assembly of four rail (Aves: Rallidae) genomes: A resource for comparative genomics. *Ecology and evolution*, 14(7), e11694.

Elizondo EC, et al. (2023) A high-quality de novo genome assembly for clapper rail (*Rallus crepitans*). *G3 (Bethesda, Md.)*, 13(8).

Chen C, et al. (2023) A pathogen-induced putative NAC transcription factor mediates leaf rust resistance in barley. *Nature communications*, 14(1), 5468.

Chávez Montes RA, et al. (2022) A comparative genomics examination of desiccation tolerance and sensitivity in two sister grass species. *Proceedings of the National Academy of Sciences of the United States of America*, 119(5).

Rayamajhi N, et al. (2022) Evaluating Illumina-, Nanopore-, and PacBio-based genome assembly strategies with the bald notothen, *Trematomus borchgrevinki*. *G3 (Bethesda, Md.)*, 12(11).

Zee A, et al. (2022) Sequencing Illumina libraries at high accuracy on the ONT MinION using R2C2. *Genome research*, 32(11-12), 2092.

Magid M, et al. (2022) Leveraging an existing whole-genome resequencing population data set to characterize toll-like receptor gene diversity in a threatened bird. *Molecular ecology resources*, 22(7), 2810.

Koochekian N, et al. (2022) A chromosome-level genome assembly and annotation of the desert horned lizard, *Phrynosoma platyrhinos*, provides insight into chromosomal rearrangements among reptiles. *GigaScience*, 11.

Yu H, et al. (2022) Palaeogenomic analysis of black rat (*Rattus rattus*) reveals multiple European introductions associated with human economic history. *Nature communications*, 13(1), 2399.

Friis G, et al. (2022) A high-quality genome assembly and annotation of the dark-eyed junco *Junco hyemalis*, a recently diversified songbird. *G3 (Bethesda, Md.)*, 12(6).

Gomes-Dos-Santos A, et al. (2021) The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel *Margaritifera margaritifera* (Linnaeus, 1758). *DNA research : an international journal for rapid publication of reports on genes and genomes*, 28(2).

Burley JT, et al. (2021) Genome assemblies for two Neotropical trees: *Jacaranda copaia* and *Handroanthus guayacan*. *G3 (Bethesda, Md.)*, 11(2).

Raszick TJ, et al. (2021) Population genomics and phylogeography of the boll weevil, *Anthonomus grandis* Boheman (Coleoptera: Curculionidae), in the United States, northern Mexico, and Argentina. *Evolutionary applications*, 14(7), 1778.

Thompson AW, et al. (2021) The bowfin genome illuminates the developmental evolution of ray-finned fishes. *Nature genetics*, 53(9), 1373.

Said M, et al. (2021) Development of DNA Markers From Physically Mapped Loci in *Aegilops comosa* and *Aegilops umbellulata* Using Single-Gene FISH and Chromosome Sequences. *Frontiers in plant science*, 12, 689031.

Catanach A, et al. (2021) The genome of New Zealand trevally (Carangidae: *Pseudocaranx georgianus*) uncovers a XY sex determination locus. *BMC genomics*, 22(1), 785.