

Resource Summary Report

Generated by SPARC SAWG on Aug 10, 2026

Mikado

RRID:SCR_016159

Type: Tool

Proper Citation

Mikado (RRID:SCR_016159)

Resource Information

URL: <https://github.com/lucventurini/mikado/>

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Description: Mikado is a lightweight Python3 pipeline whose purpose is to facilitate the identification of expressed loci from RNA-Seq data * and to select the best models in each locus.

Resource Type: source code, software resource

Defining Citation: [DOI:10.1101/216994](https://doi.org/10.1101/216994)

Keywords: annotation, rna-seq, genomics, transcriptomics

Funding: BBSRC BB/J004669/1;
BBSRC BB/J010375/1;
BBSRC BB/CSP17270/1;
BBSRC BB/CCG1720/1

Availability: Free, Available for download

Resource Name: Mikado

Resource ID: SCR_016159

Alternate URLs: <http://mikado.readthedocs.io/>

License: LGPL 3, gnu lesser general public license

License URLs: <https://github.com/lucventurini/mikado/blob/master/LICENSE.txt>

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260810T040659+0000

Ratings and Alerts

No rating or validation information has been found for Mikado.

No alerts have been found for Mikado.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 93 mentions in open access literature.

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

Santos LBD, et al. (2026) Pangenome analysis of nine soybean cyst nematode genomes reveals hidden variation contributing to diversity and adaptation. BMC genomics, 27(1), 177.

De Vega JJ, et al. (2026) A haplotype-complete chromosome-level assembly of octoploid *Urochloa humidicola* cv. Tully reveals multiple genomic compositions and evolutionary histories in the species. G3 (Bethesda, Md.), 16(4).

Shipova AA, et al. (2026) From Adam's rib: the Siberian moth's female W chromosome is derived from its Z counterpart. Molecular biology and evolution, 43(3).

Ord J, et al. (2026) Single-cell analysis of a salmonid immune system (river brown trout *Salmo trutta fario*) reveals evolutionary divergence and hatchery-induced transcriptional reprogramming. BMC biology, 24(1).

Zadesenets KS, et al. (2026) Mining Differentially Expressed Genes in the Marine Free-Living Flatworm *Macrostomum lignano* Under Aneuploidy-Driven Ploidy Changes. Cells, 15(3).

Kale SM, et al. (2026) Extensive variation between chromosomes of North American and European hop. Nature communications, 17(1).

van Rengs WMJ, et al. (2026) Wild tomato genome assemblies reveal structural variants and repeat content act as recombination barriers. Nature communications, 17(1).

Tan K, et al. (2026) Near-complete genome assembly of a transformation-efficient elite inbred line LH244 and its comparison with B73. Journal of integrative plant biology, 68(2), 366.

Hoff SNK, et al. (2026) Rapid genome modifications including chromosomal fusions and large-scale inversions are key features in Arctic codfish species. Genome biology, 27(1).

Schoonmaker AN, et al. (2026) A whole-genome assembly of St. Augustinegrass and visualizing diversity within the species. The plant genome, 19(1), e70144.

Sanchez G, et al. (2026) Rapid mid-Cretaceous diversification of squid and cuttlefish preceded radiation into coastal niches. *Nature ecology & evolution*, 10(4), 662.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Ryan C, et al. (2025) A haplotype-resolved chromosome-level genome assembly of *Urochloa decumbens* cv. Basilisk resolves its allopolyploid ancestry and composition. *G3* (Bethesda, Md.), 15(4).

McMullan M, et al. (2025) Developing a crop- wild-reservoir pathogen system to understand pathogen evolution and emergence. *eLife*, 14.

Hill R, et al. (2025) Evolutionary genomics reveals variation in structure and genetic content implicated in virulence and lifestyle in the genus *Gaeumannomyces*. *BMC genomics*, 26(1), 239.

Riquier S, et al. (2025) RNA-Seq analysis reveals the long noncoding RNAs associated with immunity in wild *Myotis myotis* bats. *BMC genomics*, 26(1), 345.

Cheng L, et al. (2025) Leveraging a phased pangenome for haplotype design of hybrid potato. *Nature*, 640(8058), 408.

Feng H, et al. (2025) Genome and Tissue-Specific Transcriptome of the Tropical Milkweed (*Asclepias curassavica*). *Plant direct*, 9(3), e70031.

Gavriouchkina D, et al. (2025) A single-cell atlas of the bobtail squid visual and nervous system highlights molecular principles of convergent evolution. *Nature ecology & evolution*, 9(7), 1245.

Kim IV, et al. (2025) Chromatin loops are an ancestral hallmark of the animal regulatory genome. *Nature*, 642(8069), 1097.