

Resource Summary Report

Generated by PRECISE-TBI on Sep 1, 2026

Mikado

RRID:SCR_016159

Type: Tool

Proper Citation

Mikado (RRID:SCR_016159)

Resource Information

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

Proper Citation: Mikado (RRID:SCR_016159)

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: software resource, source code

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

Keywords: annotation, rna-seq, genomics, transcriptomics

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

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: 20260829T183256+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 [PRECISE-TBI](#) .

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.

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

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.

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.

Liu Q, et al. (2025) Genome assembly of the maize B chromosome provides insight into its epigenetic characteristics and effects on the host genome. *Genome biology*, 26(1), 47.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.