

Resource Summary Report

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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: 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/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: 20260804T043617+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 82 mentions in open access literature.

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

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).

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

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

Grewal S, et al. (2025) Chromosome-level haplotype-resolved genome assembly of bread wheat's wild relative *Aegilops mutica*. *Scientific data*, 12(1), 438.

Benoit M, et al. (2025) *Solanum* pan-genetics reveals paralogues as contingencies in crop engineering. *Nature*, 640(8057), 135.

Feng JW, et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. *Nature*, 645(8080), 429.

Piovani L, et al. (2025) The genomic origin of the unique chaetognath body plan. *Nature*, 645(8082), 964.

Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. *GigaScience*, 14.

Lind AL, et al. (2025) Contiguous and complete assemblies of *Blastocystis* gut microbiome-associated protists reveal evolutionary diversification to host ecology. *Genome research*, 35(6), 1377.

Godec T, et al. (2025) Haplotype-resolved genome assembly of the tetraploid potato cultivar Désirée. *Scientific data*, 12(1), 1044.

Romero Charria P, et al. (2025) Adenine DNA methylation associated with transcriptionally permissive chromatin is widespread across eukaryotes. *Nature genetics*, 57(12), 3126.

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late embryogenesis abundant genes. *BMC genomics*, 26(1), 1125.

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.

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

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.

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.

Beier S, et al. (2025) Chromosome-level genome assemblies of Thai cassava ecotypes (*Manihot esculenta* & *Manihot glaziovii*). *Scientific data*, 12(1), 1591.

Seong K, et al. (2025) The Annotated Blueprint: Integrated Functional Genomic Resources for a model Tetraploid Wheat *Triticum turgidum* cv. Kronos. *bioRxiv* : the preprint server for biology.

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.