

Resource Summary Report

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MAKER

RRID:SCR_005309

Type: Tool

Proper Citation

MAKER (RRID:SCR_005309)

Resource Information

URL: <http://www.yandell-lab.org/software/maker.html>

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Description: Software genome annotation pipeline. Portable and easily configurable genome annotation pipeline. Used to allow smaller eukaryotic and prokaryotic genome projects to independently annotate their genomes and to create genome databases. MAKER identifies repeats, aligns ESTs and proteins to genome, produces ab-initio gene predictions and automatically synthesizes these data into gene annotations having evidence based quality values.

Synonyms: Maker2, maker

Resource Type: software toolkit, software resource

Defining Citation: [PMID:25501943](#)

Keywords: gene prediction, genome annotation, identifies repeats, aligns ESTs and proteins to genome, data management, genome annotation, annotation, curation, bio.tools, FASEB list

Resource Name: MAKER

Resource ID: SCR_005309

Alternate IDs: SCR_023883, nlx_144363, biotools:maker

Alternate URLs: <https://bio.tools/maker>, <https://github.com/Yandell-Lab/maker>

License: GNU GPL

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260803T040417+0000

Ratings and Alerts

No rating or validation information has been found for MAKER.

No alerts have been found for MAKER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1422 mentions in open access literature.

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

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Chen W, et al. (2025) Graph pangenome reveals the regulation of malate content in blood-fleshed peach by NAC transcription factors. *Genome biology*, 26(1), 7.

Yin M, et al. (2025) The haplotype-resolved genome assembly of an ancient citrus variety provides insights into the domestication history and fruit trait formation of loose-skin mandarins. *Genome biology*, 26(1), 61.

Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.

Tu M, et al. (2025) Integrative omics reveals mechanisms of biosynthesis and regulation of floral scent in *Cymbidium tracyanum*. *Plant biotechnology journal*, 23(6), 2162.

Raiyemo DA, et al. (2025) Chromosome-level assemblies of *Amaranthus palmeri*, *Amaranthus retroflexus*, and *Amaranthus hybridus* allow for genomic comparisons and identification of a sex-determining region. *The Plant journal : for cell and molecular biology*, 121(4), e70027.

Lu J, et al. (2025) Haplotype-resolved chromosome-level genome assembly of *Fragaria × ananassa* Duch. cv. 'Yuexin'. *Scientific data*, 12(1), 974.

Lu Z, et al. (2025) Construction of a Multi-Omics database for *Paeonia lactiflora*: A resource for comprehensive data integration and analysis. *BMC plant biology*, 25(1), 1047.

Chimed-Ochir O, et al. (2025) Assessing Data Completeness in Emergency Medical Team Reports: Analysis of the Response to Cyclone Idai in Mozambique using the WHO Minimum Data Set. *Archives of academic emergency medicine*, 13(1), e63.

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

Ibrahim A, et al. (2025) Low Heterozygosity and Historical Bottleneck Effect Depicted From the Genome Assembly of the Indus River Dolphin (*Platanista minor*). *Ecology and evolution*, 15(5), e71462.

Freedman AH, et al. (2025) Building better genome annotations across the tree of life. *Genome research*, 35(5), 1261.

Kreiner JM, et al. (2025) The evolution of separate sexes in waterhemp is associated with surprising chromosomal diversity and complexity. *PLoS biology*, 23(6), e3003254.

Zheng W, et al. (2025) Chromosome-level genome assembly of starry flounder (*Platichthys stellatus*). *Scientific data*, 12(1), 1215.

Turmel M, et al. (2025) Comparative Genomics of *Chloropicon primus* and *Chloropicon roscoffensis* Provide Insights into the Evolutionary Dynamics and Ecological Success of These Tiny Green Algae in Marine Environments. *Genome biology and evolution*, 17(7).

Luo Y, et al. (2025) Regulatory changes in the fatty acid elongase *eloF* underlie the evolution of sex-specific pheromone profiles in *Drosophila prolongata*. *BMC biology*, 23(1), 117.

Wu Y, et al. (2025) Chromosome-scale genome assembly and annotation of *Xenocypris argentea*. *Scientific data*, 12(1), 573.

Ding Y, et al. (2025) High-quality assembly of the chromosomal genome for *Flemingia macrophylla* reveals genomic structural characteristics. *BMC genomics*, 26(1), 535.

Bisht MS, et al. (2025) A high-quality genome assembly of *Annona squamosa* (custard apple) provides functional insights into an emerging fruit crop. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(3).

Wang Y, et al. (2025) A chromosome-level genome assembly of *Electrophorus voltai*, a species of electric eel. *Scientific data*, 12(1), 1367.