

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 1519 mentions in open access literature.

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

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.

Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.

Zhang Y, et al. (2026) Multi-omics and functional analyses in *Aesculus wilsonii* elucidate the biosynthetic pathways of moretane- and oleanane-type triterpenoids. *Plant communications*, 7(4), 101715.

Saldamando CI, et al. (2026) Genomic and phylogenetic insights for three species of thrips (Thysanoptera: Terebrantia) associated with Colombian avocado. *Journal of insect science (Online)*, 26(1).

Shan X, et al. (2026) Chromosome-level genome assembly of Siberian kale (*Brassica napus* subsp. *pabularia*). *Scientific data*, 13(1).

Li M, et al. (2026) De Novo Chromosome-Level Genome Assembly of 'Qing Zhou Mi' Landrace Peach and Analysis of Late Maturity and Fruit Weight Traits in Peach. *Plants (Basel, Switzerland)*, 15(7).

Cr??peault O, et al. (2026) Genomic and transcriptomic basis of morphological and life cycle diversity in the prasinophyte alga *Pseudoscurfieldia marina*. *Communications biology*, 9(1).

Han J, et al. (2026) A comprehensive analysis of two Chinese cucumber genomes and a mutant population as resources for precision breeding. *Horticulture research*, 13(2), uhaf284.

Li X, et al. (2026) A chromosome-level genome assembly of two-spotted cricket, *Gryllus bimaculatus* (Orthoptera: Grylloidea). *Scientific data*, 13(1).

Li L, et al. (2026) Genomic features and the transcriptional regulation of secondary metabolite biosynthesis of endophytic fungus *Xylaria* sp. VDL4 isolated from *Vaccinium dunalianum*. *Microbial genomics*, 12(4).

Shi X, et al. (2026) Chromosome-level genome assembly of *Sinodiscula camellicola* strain Scam5. *Scientific data*, 13(1).

Li F, et al. (2026) Transition From Land to Sea: Comparative Genomics Illuminates the Adaptive Evolution of the Intertidal Spider. *Molecular ecology resources*, 26(4), e70147.

Han ZR, et al. (2026) Chromosome-level genome assembly of *Neoseiulus longispinosus* (Phytoseiidae). *Scientific data*, 13(1).

Liu S, et al. (2026) The Genetically Homogeneous Population Structure of *Evynnis cardinalis* Along the Chinese Coast Revealed by Whole Genome Sequencing. *Evolutionary applications*, 19(5), e70272.

Shao H, et al. (2026) Decoding the Pine Wood Nematode's survival mystery: Gene family expansion drives adaptation revealed by dual-omics. *PLoS pathogens*, 22(3), e1014033.

Zhao Y, et al. (2026) Chromosome-level genome assembly and annotation of the *Rhinogobio ventralis*, an endangered endemic fish from the Yangtze River. *Scientific data*, 13(1).

Huang X, et al. (2026) An Improved Chromosome-Level Genome Assembly and Comprehensive Annotation of the Model Ascidian *Ciona savignyi*. *Scientific data*, 13(1).

Wolf M, et al. (2026) The genome of the relict earless monitor lizard, *Lanthanotus borneensis*, and the *Toxicofera* hypothesis. *BMC biology*, 24(1).

Wu W, et al. (2026) Telomere-to-telomere genome assembly and multiomics analyses illustrate the high accumulation of quercetin glucosides in tetraploid *Descurainia sophia*. *Horticulture research*, 13(3), uhaf335.

Sotiropoulos AG, et al. (2026) Combining pangenomics and population genetics finds chromosomal re-arrangements, diversified chromosome segments, copy number variations and transposon polymorphisms in wheat and rye powdery mildew. *PLoS pathogens*, 22(4), e1013196.