

Resource Summary Report

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EvidenceModeler

RRID:SCR_014659

Type: Tool

Proper Citation

EvidenceModeler (RRID:SCR_014659)

Resource Information

URL: <https://evidencemodeler.github.io/>

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Description: Software tool for automated eukaryotic gene structure annotation that reports eukaryotic gene structures as weighted consensus of all available evidence. Used to combine ab initio gene predictions and protein and transcript alignments into weighted consensus gene structures. Inputs include genome sequence, gene predictions, and alignment data (in GFF3 format).

Abbreviations: EVM

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, software application

Defining Citation: [PMID:18190707](#)

Keywords: sequence analysis software, framework, ab initio gene, gene prediction, protein alignment, transcript alignment, consensus gene structure

Funding: NIAID N01 AI30071;
NLM R01 LM006845

Availability: Free, Available for download, Freely available

Resource Name: EvidenceModeler

Resource ID: SCR_014659

Alternate IDs: SCR_017649

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260731T042922+0000

Ratings and Alerts

No rating or validation information has been found for EVIDENCEModeler.

No alerts have been found for EVIDENCEModeler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1135 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Huang C, et al. (2025) Impacts of parental genomic divergence in non-syntenic regions on cotton heterosis. *Journal of advanced research*, 73, 15.

T??resen OK, et al. (2025) A chromosome-level genome assembly of the common eider, *Somateria mollissima* (Linnaeus, 1758). *The Journal of heredity*, 116(3), 363.

Fan Z, et al. (2025) Chromosome-level genome assembly and annotation of *Spinibarbus caldwelli*. *Scientific data*, 12(1), 1138.

Yue D, et al. (2025) Chromosome-level genome assembly of *Ampulex clypeocomplana* Chen & Li (Hymenoptera: Ampulicidae). *Scientific data*, 12(1), 1328.

Zhu W, et al. (2025) Chromosome-level genome assembly of Marco Polo Blister Beetle (*Hycleus marcipoli*). *Scientific data*, 12(1), 1396.

Choi S, et al. (2025) Chromosome-level genome assembly of *Salvia sclarea*. *Scientific data*, 12(1), 14.

Ding R, et al. (2025) Chromosome-Level Genome Assembly and Whole-Genome Resequencing Revealed Contrasting Population Genetic Differentiation of Black Bream (*Megalobrama skolkovii*) (Teleostei: Cyprinidae) Allopatric and Sympatric to Its Kin Species. *Ecology and evolution*, 15(1), e70874.

Liang Z, et al. (2025) A chromosomal-scale reference genome for *Rosa hugonis*. *Scientific data*, 12(1), 272.

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

Lv Y, et al. (2025) Genomic insights into evolution of parthenogenesis and triploidy in the flowerpot snake. *Science advances*, 11(14), eadt6477.

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

Huang C, et al. (2025) A comparative genomic analysis at the chromosomal-level reveals evolutionary patterns of aphid chromosomes. *Communications biology*, 8(1), 427.

Liu HL, et al. (2025) Chromosome-level genome assembly of the Adonis ladybird *Hippodamia variegata*. *Scientific data*, 12(1), 558.

Gong X, et al. (2025) Chromosome-level genome assembly of *Iodes seguinii* and its metabonomic implications for rheumatoid arthritis treatment. *The plant genome*, 18(1), e20534.

Zhang L, et al. (2025) Chromosome-level genome assembly and annotation of the gynogenetic large-scale loach (*Paramisgurnus dabryanus*). *Scientific data*, 12(1), 155.

Du H, et al. (2025) Pangenome Reveals Gene Content Variations and Structural Variants Contributing to Pig Characteristics. *Genomics, proteomics & bioinformatics*, 22(6).

Gong X, et al. (2025) Chromosome-level genome assembly of flathead asp (*Pseudaspius leptocephalus*). *Scientific data*, 12(1), 321.

Shi Y, et al. (2025) Chromosome-level genome assembly of the traditional medicinal plant *Lindera aggregata*. *Scientific data*, 12(1), 565.

Chen D, et al. (2025) Largest genome assembly in Brassicaceae: retrotransposon-driven genome expansion and karyotype evolution in *Matthiola incana*. *Plant biotechnology journal*, 23(9), 4109.