

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 analysis software, software application, software resource, sequence analysis software, data processing software

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: 20260801T190738+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 [NIF](#) .

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.

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.

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

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

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

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

Zhao X, et al. (2025) Chromosome-level genome assembly of an endoparasitoid *Cotesia ruficrus*. *Scientific data*, 12(1), 508.

Cheng G, et al. (2025) Genomic Insights into Cobweb Disease Resistance in *Agaricus bisporus*: A Comparative Analysis of Resistant and Susceptible Strains. *Journal of fungi (Basel, Switzerland)*, 11(3).

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.

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.
- Gong X, et al. (2025) Chromosome-level genome assembly of flathead asp (*Pseudaspius leptocephalus*). *Scientific data*, 12(1), 321.
- Huang C, et al. (2025) Impacts of parental genomic divergence in non-syntenic regions on cotton heterosis. *Journal of advanced research*, 73, 15.
- Liu X, et al. (2025) Positive selection and relaxed purifying selection contribute to rapid evolution of sex-biased genes in green seaweed *Ulva*. *BMC ecology and evolution*, 25(1), 44.
- Liu B, et al. (2025) Chromosome-level genome assembly and annotation of Chinese herring (*Ilisha elongata*). *Scientific data*, 12(1), 668.
- 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.
- Zhu W, et al. (2025) Chromosome-level genome assembly of Marco Polo Blister Beetle (*Hycleus marcipoli*). *Scientific data*, 12(1), 1396.
- Becker DJ, et al. (2025) Proteomic Signatures of SARS-CoV-2 Susceptibility in Mexican Free-tailed Bats and Their Application to Viral Surveillance. *Integrative and comparative biology*, 65(6), 1884.
- Lv Z, et al. (2025) Near telomere-to-telomere genome assembly of *Camellia pitardii*. *Scientific data*, 12(1), 1422.
- Liu Y, et al. (2025) Two haplotype-resolved telomere-to-telomere genome assemblies of *Xanthoceras sorbifolium*. *Scientific data*, 12(1), 791.