

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: sequence analysis software, software resource, software application, data 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: 20260808T190230+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 1283 mentions in open access literature.

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

T??rresen OK, et al. (2026) Chromosome-level genome assembly of Norwegian wild alpine reindeer (*Rangifer tarandus tarandus*). *The Journal of heredity*, 117(3), 557.

Teixeira MdM, et al. (2026) Morphological and genetic characterization of novel *Sarocladium spinificis* strains in association with *Coccidioides posadasii*. *Microbiology spectrum*, 14(2), e0068925.

Xu M, et al. (2026) Telomere to telomere level genome assembly of the Yarkand hare (*Lepus yarkandensis*). *Scientific data*, 13(1).

Zhang D, et al. (2026) Assembling a chromosome-level genome for the *Microtus fortis* using PacBio HiFi and Hi-C technologies. *Scientific data*, 13(1).

Wang A, et al. (2026) Cross-species dissection of saline-related genes by genetically deciphering a euryhaline microalga *Chlorella* sp. *Nature communications*, 17(1), 1577.

Han L, et al. (2026) Chromosome-level genome provides new insights into the fatty acid biosynthesis and metabolism of the sea urchin *Strongylocentrotus intermedius*. *BMC genomics*, 27(1).

Strand MA, et al. (2026) The origin of the octoploid cloudberry (*Rubus chamaemorus*) genome is the result of multiple and complex polyploidization events. *The Journal of heredity*, 117(4), 822.

Feng X, et al. (2026) Chromosomal-scale and haplotype-resolved genome assembly of the first Trinitario hybrid cacao ICS 1. *Scientific data*, 13(1).

Lan L, et al. (2026) Comparative Genomics Provide Insights Into Karyotype Evolution in Vespertilionid Bats (Vespertilionidae, Chiroptera). *Molecular ecology resources*, 26(3), e70129.

Dong W, et al. (2026) PHR-Mediated Pi Starvation Response Mobile Messenger RNAs Represent Noncoding Transcripts in Recipient Tissues. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e02911.

Wang W, et al. (2026) Comparative genomics reveals evolutionary signatures of genes associated with jumping in beetles. *Zoological research*, 47(1), 88.

Chen X, et al. (2026) A de novo assembled chromosome-level genome of *Ainsliaea gracilis* Franch. (Pertyeae, Asteraceae) and its comparative phylogenomics within Asteraceae. *BMC plant biology*, 26(1).

Mohindra V, et al. (2026) Genome sequencing and assembly of *Neolissochilus pnar*, the largest cavefish species of Mahseer. *Scientific data*, 13(1).

Chen D, et al. (2026) The Neijiang pig T2T genome reveals domestication history and germplasm traits of Southwest Chinese local breeds. *Communications biology*, 9(1), 278.

Wang Y, et al. (2026) Recurrent sex chromosome turnover mediated by distinct *ARR17* and *PISTILLATA* duplications in willows. *Genome biology*, 27(1).

Jiang XL, et al. (2026) Population genomics of *Quercus gilva* provides insights into the conservation of fengshui forests. *Communications biology*, 9(1).

Li H, et al. (2026) Evolutionary genomic basis of mimicry diversity of *Epicopeiidae* moths. *Molecular biology and evolution*, 43(3).

Xie H, et al. (2026) Large-scale multi-omics profiling reveals environmental and evolutionary drivers of fungal phylogeographic and metabolic diversity. *Nature communications*, 17(1).

Hua Z, et al. (2026) Chromosome-level genome assembly and population genomics unveil strigolactone-regulated growth adaptation in the mycoheterotrophic orchid *Gastrodia elata*. *Horticulture research*, 13(7), uhag099.

Peng W, et al. (2026) The Genome of the Rice Variety Mowanggu Provides Insight Into Resistance to *Magnaporthe oryzae*. *Molecular plant pathology*, 27(3), e70223.