

Resource Summary Report

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GlimmerHMM

RRID:SCR_002654

Type: Tool

Proper Citation

GlimmerHMM (RRID:SCR_002654)

Resource Information

URL: <http://ccb.jhu.edu/software/glimmerhmm/>

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Description: A gene finder based on a Generalized Hidden Markov Model (GHMM). Although the gene finder conforms to the overall mathematical framework of a GHMM, additionally it incorporates splice site models adapted from the GeneSplicer program and a decision tree adapted from GlimmerM. It also utilizes Interpolated Markov Models for the coding and noncoding models. Currently, GlimmerHMM's GHMM structure includes introns of each phase, intergenic regions, and four types of exons (initial, internal, final, and single).

Abbreviations: GlimmerHMM

Synonyms: GlimmerHMM - Eukaryotic Gene-Finding System

Resource Type: software resource, source code

Defining Citation: [PMID:15145805](#)

Keywords: gene, hidden markov model

Funding: NIH ;
NLM R01-LM06845;
NLM R01-LM007938

Availability: Free, Available for download, Freely available

Resource Name: GlimmerHMM

Resource ID: SCR_002654

Alternate IDs: nlx_156092

License: Open unspecified license, OSI certified

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260905T133323+0000

Ratings and Alerts

No rating or validation information has been found for GlimmerHMM.

No alerts have been found for GlimmerHMM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 643 mentions in open access literature.

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

Liu T, et al. (2026) Chromosome-level genome assembly and annotation of the endangered plant *Primula kwangtungensis* (Primulaceae). *Scientific data*, 13(1), 212.

Wang W, et al. (2026) Integrating pan-genome analysis, GWAS, and interpretable machine learning to prioritize trait-associated structural variations in *Setaria italica*. *Plant communications*, 7(3), 101626.

Huang X, et al. (2026) Pangenome Analysis Reveals Structural Variations Associated With Citric Acid Accumulation in *Prunus mume*. *Plant biotechnology journal*, 24(4), 2623.

Ding S, et al. (2026) Chromosome-level genome assembly of a Chinese evergreen sweetgum (*Liquidambar gracilipes*, Altingiaceae). *Scientific data*, 13(1), 66.

Iizuka R, et al. (2026) First high-quality genome assembly of *Umbelopsis nana* isolated from forest soil. *G3 (Bethesda, Md.)*, 16(4).

Zhao Q, et al. (2026) Multi-omics analyses of *Dracocephalum moldavica* L. reveal two flavonoid glycosyltransferases in tilianin biosynthesis. *BMC genomics*, 27(1), 208.

You Q, et al. (2026) Sub-pangenome analysis reveals structural variants associated with fruit color and bacterial wilt resistance in eggplant. *Nature communications*, 17(1).

Liu Y, et al. (2026) A high-quality chromosome-level genome assembly of the endangered species *Magnolia amoena*. *Scientific data*, 13(1).

Niu Y, et al. (2026) Chromosome-level genome assembly of the blackchin tilapia (*Sarotherodon melanotheron*). *Scientific data*, 13(1).

- Cheng X, et al. (2026) Haplotype-resolved genome assembly provides insights into the unique floral scent of *Rosa rugosa* originated in China. *Molecular horticulture*, 6(1).
- Sun Y, et al. (2026) Chromosome level genome assembly of taro (*Colocasia esculenta*). *Scientific data*, 13(1).
- Coleine C, et al. (2026) Genomic and Ecological Flexibility Shape the Global Distribution of a Black Fungus. *Environmental microbiology*, 28(4), e70301.
- Wang ZL, et al. (2026) Centromeric tandem repeats expansions in plateau zokor enhance chromosome stability for high-altitude adaptation. *Genome biology*, 27(1).
- Lu Z, et al. (2026) The *Rhus chinensis* Genome Provides Insights Into Tannin, Flavonoid Biosynthesis, and Glandular Trichome Development. *Plant biotechnology journal*, 24(3), 988.
- Liu S, et al. (2026) Chromosome-level genome assembly of the casuarina moth, *Lymantria xyli* Swinhoe (1903). *Scientific data*, 13(1).
- Zhao S, et al. (2026) Multi-Omics Insights Into Anthraquinone Biosynthesis in *Rheum tanguticum*. *Plant biotechnology journal*, 24(6), 3953.
- Yang M, et al. (2026) Chromosome-level genome assemblies of the pink snow mold pathogens *Microdochium majus* and *Microdochium nivale*. *Scientific data*, 13(1).
- Xie Z, et al. (2026) High quality chromosome-level genome assembly of *Psammosilene tunicoides* (Caryophyllaceae), an endangered medicinal plant. *Scientific data*, 13(1).
- Ma Q, et al. (2026) The pan-genome provides insights into evolutionary dynamics and fatty acid metabolism in *Aceraceae* family. *Genome biology*, 27(1).
- Zhao L, et al. (2026) Chromosome-level Genome Assembly and Annotation of the bighead beaked sandfish (*Gonorynchus abbreviatus*). *Scientific data*, 13(1).