

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: 20260725T191321+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 576 mentions in open access literature.

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

Wang C, et al. (2025) Genomic-transcriptomic analysis identifies the Syrian hamster as a superior animal model for human diseases. BMC genomics, 26(1), 286.

Sheikh SI, et al. (2025) A shared gene but distinct dynamics regulate mimicry polymorphisms in closely related species. bioRxiv : the preprint server for biology.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. GigaScience, 14.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. GigaScience, 14.

Geng F, et al. (2025) Genome Assembly and Winged Fruit Gene Regulation of Chinese Wingnut: Insights from Genomic and Transcriptomic Analyses. Genomics, proteomics & bioinformatics, 22(6).

Brejon Lamartinière E, et al. (2025) A haplotype-resolved chromosomal reference genome for the porcini mushroom *Boletus edulis*. G3 (Bethesda, Md.), 15(6).

Zhang R, et al. (2025) Chromosomal level genome assembly of medicinal plant *Rosa laevigata*. Scientific data, 12(1), 716.

Liu S, et al. (2025) CgABR1-CgFAD negatively regulates the fruit neck length in citrus. Plant biotechnology journal, 23(8), 3083.

Han X, et al. (2025) The telomere-to-telomere genome assembly and annotation of the rock carp (*Procypris rabaudi*). Scientific data, 12(1), 781.

Dai Y, et al. (2025) The chromosome-scale assembly of the *Salvia plebeia* genome provides insight into the biosynthesis and regulation of rosmarinic acid. *Plant biotechnology journal*, 23(5), 1507.

Zhou C, et al. (2025) Chromosome-level genome assembly of the endangered tree species *Ormosia henryi* Prain. *Scientific data*, 12(1), 1065.

Zhang K, et al. (2025) A telomere-to-telomere gap-free genome assembly of the endangered humphead wrasse (*Cheilinus undulatus*). *Scientific data*, 12(1), 1194.

Paudel R, et al. (2025) Genome assembly and comparative analysis of *Alternaria Linariae* reveal novel genes associated with host colonization and virulence. *BMC genomics*, 26(1), 638.

Sulman M, et al. (2025) De novo Genome Assembly and Annotation of 12 Fungi Associated with Fruit Tree Decline Syndrome in ON, Canada. *Scientific data*, 12(1), 1098.

Chen P, et al. (2025) Comparative Cochlear Transcriptomics in Echolocating Bats and Mouse Reveals Hras as Protector Against Noise-Induced Hearing Loss. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(44), e08466.

Wang Y, et al. (2025) Chromosome-scale genome assembly of *Helcystogramma triannulella* (Lepidoptera: Gelechiidae). *Scientific data*, 12(1), 1525.

Bai F, et al. (2025) Genomic Insights into the Molecular Basis of Broad Host Adaptability of the Entomopathogenic Fungus *Conidiobolus coronatus* (Entomophthoromycotina). *Journal of fungi* (Basel, Switzerland), 11(8).

Zhang L, et al. (2025) Genome Analysis of *Alternaria alstroemeriae* L6 Associated with Black Spot of Strawberry: Secondary Metabolite Biosynthesis and Virulence. *Journal of fungi* (Basel, Switzerland), 11(10).

Chang M, et al. (2025) Chromosome-level genome assembly and annotation of the spottedtail morwong (*Cheilodactylus zonatus*). *Scientific data*, 12(1), 1741.

Wang C, et al. (2025) The telomere-to-telomere genome assembly of the *Triplophysa erythraea* (Nemacheilidae hypogean fishes). *Scientific data*, 12(1), 1978.