Resource Summary Report

Generated by NIF on May 18, 2025

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: Open unspecified license, OSI certified

Resource Name: GlimmerHMM

Resource ID: SCR_002654

Alternate IDs: nlx_156092

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250514T061230+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 465 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier Arhopalus unicolor. Scientific data, 12(1), 111.

Medrano JF, et al. (2025) De novo whole-genome assembly and annotation of Coffea arabica var. Geisha, a high-quality coffee variety from the primary origin of coffee. G3 (Bethesda, Md.), 15(1).

Bende G, et al. (2025) The Neosartorya (Aspergillus) fischeri antifungal protein NFAP2 has low potential to trigger resistance development in Candida albicans in vitro. Microbiology spectrum, 13(1), e0127324.

Tenger-Trolander A, et al. (2025) Genomic Resources for the Scuttle Fly Megaselia abdita: A Model Organism for Comparative Developmental Studies in Flies. bioRxiv : the preprint server for biology.

Clancy SM, et al. (2025) The Calicophoron daubneyi genome provides new insight into mechanisms of feeding, eggshell synthesis and parasite-microbe interactions. BMC biology, 23(1), 11.

Kariba R, et al. (2025) Draft genome sequence of Kei apple, an underutilized African tree crop. Scientific data, 12(1), 70.

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

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.

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 W, et al. (2025) Chromosome-level genome assembly of tetraploid Chinese cherry (Prunus pseudocerasus). Scientific data, 12(1), 136.

Akdeniz Z, et al. (2025) The expanded genome of Hexamita inflata, a free-living diplomonad. Scientific data, 12(1), 192.

Sun S, et al. (2024) Chromosomal-scale genome assembly and annotation of the land slug (Meghimatium bilineatum). Scientific data, 11(1), 35.

Klug K, et al. (2024) Genome Comparisons between Botrytis fabae and the Closely Related Gray Mold Fungus Botrytis cinerea Reveal Possible Explanations for Their Contrasting Host Ranges. Journal of fungi (Basel, Switzerland), 10(3).

Hu R, et al. (2024) A Chromosomal-Level Genome of Dermatophagoides farinae, a Common Allergenic Mite Species. International journal of genomics, 2024, 3779688.

Tournayre J, et al. (2024) MicroAnnot: A Dedicated Workflow for Accurate Microsporidian Genome Annotation. International journal of molecular sciences, 25(2).

Wang J, et al. (2024) A fully haplotype-resolved and nearly gap-free genome assembly of wheat stripe rust fungus. Scientific data, 11(1), 508.

Zhang G, et al. (2024) Chromosome-level genome assembly of Hippophae tibetana provides insights into high-altitude adaptation and flavonoid biosynthesis. BMC biology, 22(1), 82.

Ding K, et al. (2024) Chromosome-level genome provides insights into environmental adaptability and innate immunity in the common dolphin (delphinus delphis). BMC genomics, 25(1), 373.

Xu S, et al. (2024) Genome sequencing and comparative genome analysis of Rhizoctonia solani AG-3. Frontiers in microbiology, 15, 1360524.

Chen N, et al. (2024) Chromosome-scale genome assembly reveals insights into the evolution and ecology of the harmful algal bloom species Phaeocystis globosa Scherffel. iScience, 27(8), 110575.