# **Resource Summary Report**

Generated by NIF on Apr 19, 2025

# **GlimmerHMM**

RRID:SCR\_002654

Type: Tool

## **Proper Citation**

GlimmerHMM (RRID:SCR\_002654)

#### **Resource Information**

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

**Proper Citation:** GlimmerHMM (RRID:SCR\_002654)

**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:** 20250420T015914+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 lodes 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.

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

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.

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).

Cheng Y, et al. (2024) A chromosome-level genome assembly of the Echiura Urechis unicinctus. Scientific data, 11(1), 90.

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

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.

Hao Y, et al. (2024) Genomic and phenotypic signatures provide insights into the wide adaptation of a global plant invader. Plant communications, 5(4), 100820.

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

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