

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Augustus

RRID:SCR_008417

Type: Tool

Proper Citation

Augustus (RRID:SCR_008417)

Resource Information

URL: <http://bioinf.uni-greifswald.de/augustus/>

Proper Citation: Augustus (RRID:SCR_008417)

Description: Software for gene prediction in eukaryotic genomic sequences. Serves as a basis for further steps in the analysis of sequenced and assembled eukaryotic genomes.

Synonyms: Augustus: Gene Prediction, WebAUGUSTUS, Augustus, Augustus [gene prediction]

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, web application

Defining Citation: [PMID:23700307](#), [DOI:10.1093/bioinformatics/btw494](#)

Keywords: software, gene, prediction, eucaryotic, genomic, sequence

Funding: Deutsche Forschungsgemeinschaft (DFG) HO4545/1-1;; STA1009/6-1 ;

Institute for Mathematics and Computer Science ;

Ernst Moritz Arndt University of Greifswald

Availability: Free, Available for download, Freely available

Resource Name: Augustus

Resource ID: SCR_008417

Alternate IDs: SCR_015981, OMICS_07777, nif-0000-30133

Alternate URLs: <https://sources.debian.org/src/autodock-vina/>

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260905T132622+0000

Ratings and Alerts

No rating or validation information has been found for Augustus.

No alerts have been found for Augustus.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3886 mentions in open access literature.

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

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Guan DL, et al. (2026) A chromosome-level genome assembly for the mulberry thrips *Pseudodendrothrips mori* (Thysanoptera: Thripidae). *Scientific data*, 13(1).

Nie Y, et al. (2026) Identification of sex chromosome, sex-biased gene expression and dosage compensation in the pygmy mole cricket *Xya riparia* (Orthoptera: Tridactyloidea). *BMC genomics*, 27(1).

Doe D, et al. (2026) Insights into the Phylogeny of *Ustilago maydis* Strains via Comparative Analysis of Their Respective Mitogenomes. *Journal of fungi* (Basel, Switzerland), 12(3).

Pevsner R, et al. (2026) Telomere-to-telomere genome assembly of *Microsporidia* sp. MB, a microsporidian symbiont of *Anopheles coluzzii* isolated from Burkina Faso. *BMC genomics*, 27(1).

Thatchanamoorthy N, et al. (2026) Emergence and Genomic Profiling of Multidrug-Resistant *Candida auris* Isolated from Intensive Care Unit Patients in a Malaysian Teaching Hospital. *Mycopathologia*, 191(3).

Zhang J, et al. (2026) Polymorphism and evolutionary origins of accessory chromosomes in the basidiomycete *Tremella fuciformis*. *Nature communications*, 17(1).

Yao B, et al. (2026) Cascaded regulatory network composed of small RNAs involves in the symbiosis of *Panax notoginseng* and fungus *Acremonium* sp. D212. *Scientific reports*, 16(1).

Xin G, et al. (2026) The chromosome-scale genome assembly, annotation of *Bischofia polycarpa* (H. L??v.) Airy Shaw, *Phyllanthaceae*. *Scientific data*, 13(1).

Kawaguchi YW, et al. (2026) Improved genome assembly of whale shark, the world's biggest fish: revealing intragenomic heterogeneity in molecular evolution. *GigaScience*, 15.

Zhang D, et al. (2026) The *Microtus fortis* chromosome-level genome: illuminating adaptive evolution and natural parasite immunity. *BMC genomics*, 27(1).

Han D, et al. (2026) Pan-genome assembly of vine tea (*Nekemias grossedentata*) reveals structural variation in its dihydromyricetin biosynthesis diversity. *Horticulture research*, 13(2), uhaf307.

Alabady M, et al. (2026) A chromosome-scale genome of *Sarracenia purpurea* reveals a significant expansion of plant defense and stress response gene families following paleopolyploidization. *The plant genome*, 19(1), e70221.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Marin-Carvajal S, et al. (2026) Whole-genome sequencing, phenotypic characterization, and antifungal susceptibility profiles of three *Aspergillus hortae* clinical isolates from Colombia. *PloS one*, 21(2), e0342479.

Wu Y, et al. (2026) Telomere-to-telomere gapless genome assembly of *Siniperca scherzeri*. *Scientific data*, 13(1).

Hong L, et al. (2026) Chromosome-Level Genome Assembly of *Morchella sextelata* Reveals Its Early Divergence and Adaptive Evolution. *Journal of fungi (Basel, Switzerland)*, 12(5).

Han Y, et al. (2026) Comparative functional genomics of *Saccharomyces cerevisiae* reveals genetic determinants of stress tolerance and ethanol fermentation. *Microbiology spectrum*, 14(6), e0363225.

Revel-Muroz AZ, et al. (2026) Gut Hi-C metagenomes of severe COVID-19 patients: bacteria and yeast involved in gut-lung axis. *mSphere*, 11(6), e0013926.

Heraghty SD, et al. (2026) Sequencing, annotation and analysis of the genome of *Oxycarenus hyalinipennis*, the cotton seed bug. *Life science alliance*, 9(8).