

Resource Summary Report

Generated by [NIF](#) on Aug 9, 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: web application, sequence analysis software, software resource, software application, data analysis software, data processing software

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: 20260808T185901+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 [NIF](#) .

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.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Dexter E, et al. (2026) Rapid evolution of a large structural polymorphism during a bacterial epidemic. *Heredity*, 135(1), 1.

Wong ELY, et al. (2026) Historical comparative genomics to track the evolution of fungal pathogens: a proof of concept. *BMC genomics*, 27(1), 164.

Brown A, et al. (2026) Brownotate, a Comprehensive Solution to Generate Protein Sequence Databases for Any Species. *Proteomics*, 26(5), 13.

Lei FL, et al. (2026) Chromosome-level genome assembly of *Nemipterus japonicus* based on PacBio sequencing and Hi-C technology. *Scientific data*, 13(1), 218.

Zaccaron AZ, et al. (2026) The poplar pathogen *Sphaerulina musiva* has a dynamic genome architecture marked by chromosomal inversions and changes in transposable element abundance. *Microbial genomics*, 12(1).

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

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

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

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

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.

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.

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).

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).

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.