

Resource Summary Report

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

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: 20260804T043406+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 3542 mentions in open access literature.

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

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.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Li X, et al. (2025) Chromosome-level genome assembly for the ecologically and economically important alga *Saccharina japonica*. *Scientific data*, 12(1), 290.

Radice VZ, et al. (2025) First reference genomes for two mesophotic, reef-building coral species: *Leptoseris* cf. *scabra* and *Montipora* cf. *grisea*. *The Journal of heredity*, 116(4), 488.

Bigey F, et al. (2025) Insights into the genomic and phenotypic diversity of *Monosporozyma unispora* strains isolated from anthropic environments. *FEMS yeast research*, 25.

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*.

Adaskaveg JA, et al. (2025) In a nutshell: pistachio genome and kernel development. *The New phytologist*, 246(3), 1032.

Shi R, et al. (2025) Chromosome-Level Genome Assembly of the Leafcutter Bee *Megachile rotundata* Reveals Its Ecological Adaptation and Pollination Biology. *Advanced*

science (Weinheim, Baden-Wurttemberg, Germany), 12(23), e2417054.

Roy F, et al. (2025) Illuminating ecology and distribution of the rare fungus *Phellinidium pouzarii* in the Bavarian Forest National Park. *Scientific reports*, 15(1), 8604.

Feng DD, et al. (2025) Chromosome-level genome assembly of a specialist walnut pest *Atrijuglans aristata*. *Scientific data*, 12(1), 434.

Guan C, et al. (2025) Haplotype-resolved and chromosome-level reference genome assembly of *Diospyros deyangensis* provides insights into the evolution and juvenile growth of persimmon. *Horticulture research*, 12(4), uhaf001.

Feng Y, et al. (2025) Unveiling the Genomic Features and Biocontrol Potential of *Trichoderma hamatum* Against Root Rot Pathogens. *Journal of fungi (Basel, Switzerland)*, 11(2).

Jaggi KE, et al. (2025) A pangenome reveals LTR repeat dynamics as a major driver of genome evolution in *Chenopodium*. *The plant genome*, 18(1), e70010.

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

Shen C, et al. (2025) A chromosome-level genome assembly of *Mylabris sibirica* Fischer von Waldheim, 1823 (Coleoptera, Meloidae). *Scientific data*, 12(1), 269.

Ametrano CG, et al. (2025) UnFATE: A Comprehensive Probe Set and Bioinformatics Pipeline for Phylogeny Reconstruction and Multilocus Barcoding of Filamentous Ascomycetes (Ascomycota, Pezizomycotina). *Systematic biology*, 74(5), 740.

Cao J, et al. (2025) Chromosome-level genome assembly of Jaguar guapote (*Parachromis manguensis*) by massive parallel sequencing. *Scientific data*, 12(1), 411.

Jiang L, et al. (2025) Chromosome-level genome assembly and annotation of pawak croaker (*Pennahia pawak*). *Scientific data*, 12(1), 412.