

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: data analysis software, web application, software application, software resource, sequence 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: 20260801T190331+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 [kravitz2](#) .

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.

Law STS, et al. (2025) Genome of tropical bed bug *Cimex hemipterus* (Cimicidae, Hemiptera) reveals tetraspanin expanded in bed bug ancestor. *Insect science*, 32(1), 42.

Cao S, et al. (2025) *Lactuca* super-pangenome provides insights into lettuce genome evolution and domestication. *Nature communications*, 16(1), 7257.

Zhao K, et al. (2025) Pangenome analysis reveals structural variation associated with seed size and weight traits in peanut. *Nature genetics*, 57(5), 1250.

Pu YL, et al. (2025) The first chromosome-level genome of the lappet moth *Trabala vishnou* (Lepidoptera: Lasiocampidae). *Scientific data*, 12(1), 1154.

Paudel R, et al. (2025) Genome assembly and comparative analysis of *Alternaria Linariae* reveal novel genes associated with host colonization and virulence. *BMC genomics*, 26(1), 638.

Gong W, et al. (2025) A chromosome-level genome assembly and annotation of *Cercis chuniana* (Fabaceae). *Scientific data*, 12(1), 1163.

Wang Y, et al. (2025) Comparative genomic analyses reveal different genetic basis of two types of fruit in Maloideae. *Nature communications*, 16(1), 7463.

Chen X, et al. (2025) Chromosome-level genome assembly of the vegetable leafminer *Liriomyza sativae* (Diptera: Agromyzidae). *Scientific data*, 12(1), 1393.

Shen R, et al. (2025) Chromosome-level genome of the shining chafer *Kibakoganea tamdaoensis* (Coleoptera: Scarabaeidae: Rutelinae). *Scientific data*, 12(1), 1345.

Zhang M, et al. (2025) Telomere-to-telomere genome assembly uncovers Wolbachia-driven recurrent male bottleneck effect and selection in a sawfly. *Communications biology*, 8(1), 1211.

Liu JN, et al. (2025) Pan-genome analyses of 11 *Fraxinus* species provide insights into salt adaptation in ash trees. *Plant communications*, 6(1), 101137.

MacNish TR, et al. (2025) Brassica Panache: A multi-species graph pangenome representing presence absence variation across forty-one Brassica genomes. *The plant genome*, 18(1), e20535.

Geng F, et al. (2025) Genome Assembly and Winged Fruit Gene Regulation of Chinese Wingnut: Insights from Genomic and Transcriptomic Analyses. *Genomics, proteomics & bioinformatics*, 22(6).

Lai E, et al. (2025) Genome of root celery and population genomic analysis reveal the complex breeding history of celery. *Plant biotechnology journal*, 23(3), 946.

Ledoux JB, et al. (2025) Chromosome-Level Genome Assembly and Annotation of *Corallium rubrum*: A Mediterranean Coral Threatened by Overharvesting and Climate Change. *Genome biology and evolution*, 17(2).

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.