

Resource Summary Report

Generated by [dkNET](#) on Sep 2, 2026

funannotate

RRID:SCR_023039

Type: Tool

Proper Citation

funannotate (RRID:SCR_023039)

Resource Information

URL: <https://github.com/nextgenusfs/funannotate>

Proper Citation: funannotate (RRID:SCR_023039)

Description: Software package for genome annotation. Built specifically for fungi, but will also work with higher eukaryotes. Used for genome prediction, annotation, and comparison.

Resource Type: analysis service resource, data analysis service, data analytics software, production service resource, service resource, software application, software resource

Keywords: GeneMark, Eukaryotic Genome Annotation, genome annotation

Availability: Free, Available for download, Freely available

Resource Name: funannotate

Resource ID: SCR_023039

Alternate URLs: <https://funannotate.readthedocs.io/en/latest/>

License: BSD-2-Clause license

Record Creation Time: 20221208T050157+0000

Record Last Update: 20260829T182814+0000

Ratings and Alerts

No rating or validation information has been found for funannotate.

No alerts have been found for funannotate.

Data and Source Information

Usage and Citation Metrics

We found 89 mentions in open access literature.

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

Wei G, et al. (2026) Metagenomic sequencing reveals the dynamic changes of pig gut fungal composition following the ages and identifies fungal species associated with diarrhea in piglets. *Animal microbiome*, 8(1).

Osorio-Navarro Y, et al. (2026) Whole Genome Sequence of *Xylaria chamelensis* (Xylariales, Ascomycota), A New Species Associated with Fabaceae Pods. *Mycobiology*, 54(3), 384.

Sarhan MS, et al. (2026) The Iceman's microbiome: unveiling millennia of microbial diversity and continuity. *Microbiome*, 14(1).

Dettman JR, et al. (2026) Evolution of genomic architecture of the plant-pathogenic fungus *Alternaria* revealed by comparative analyses of 12 chromosome-level assemblies. *Microbial genomics*, 12(4).

Ren Y, et al. (2026) Insights into cephalochordate genome and gene evolution from the early-diverging amphioxus *Asymmetron lucayanum*. *Proceedings of the National Academy of Sciences of the United States of America*, 123(12), e2521280123.

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte (Hong Kong, China)*, 2026, gigabyte174.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Tam R, et al. (2025) Long-read genomics reveal extensive nuclear-specific evolution and allele-specific expression in a dikaryotic fungus. *Genome research*, 35(6), 1364.

Toker IA, et al. (2025) Divergence in neuronal signaling pathways despite conserved neuronal identity among *Caenorhabditis* species. *Current biology : CB*, 35(12), 2927.

Shen Y, et al. (2025) Chromosome-level genome assembly of the clam, *Xishi tongue Coelomactra antiquata*. *Scientific data*, 12(1), 422.

D'Angelo D, et al. (2025) ???IMA GENOME - F20 A draft genome assembly of *Agroatheliarolfii*, *Ceratobasidium papillatum*, *Pyrenopeziza brassicae*, *Neopestalotiopsis macadamiae*, *Sphaerellopsis filum* and genomic resources for *Colletotrichum spaethianum* and *Colletotrichum fructicola*. *IMA fungus*, 16, e141732.

Abu-Helu R, et al. (2025) Whole-genome sequencing of the first *Candida auris* clinical isolate from a patient with sepsis in Palestine. *Microbiology resource announcements*, 14(5), e0123924.

Xing TF, et al. (2025) Extensive Recombination Suppression and Genetic Degeneration of a Young ZW Sex Chromosome System in Halfbeak Fish. *Molecular biology and evolution*, 42(7).

Valencia-Pesqueira LM, et al. (2025) Chromosome-level de novo genome assembly of wild, anoxia-tolerant crucian carp, *Carassius carassius*. *Scientific data*, 12(1), 491.

Coelho MA, et al. (2025) Tracing the evolution and genomic dynamics of mating-type loci in *Cryptococcus* pathogens and closely related species. *bioRxiv : the preprint server for biology*.

Liu F, et al. (2025) Pan-genome analysis reveals genomic variations during enoki mushroom domestication, with emphasis on genetic signatures of cap color and stipe length. *Journal of advanced research*, 75, 199.

Bennis NX, et al. (2025) Chromosome level genome assembly and annotation of *Hanseniaspora mollemarum* CBS 18055 strain. *Microbiology resource announcements*, 14(3), e0100524.

Wang Y, et al. (2025) Whole-genome sequencing and comparative genomic analysis of *Irpex lacteus* isolated from the female reproductive tract. *Microbial genomics*, 11(6).

Coelho MA, et al. (2025) Genomic and phenotypic insights into the expanding phylogenetic landscape of the *Cryptococcus* genus. *PLoS genetics*, 21(11), e1011945.

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.