

Resource Summary Report

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Rnnotator

RRID:SCR_011897

Type: Tool

Proper Citation

Rnnotator (RRID:SCR_011897)

Resource Information

URL: <https://sites.google.com/a/brown.edu/bioinformatics-in-biomed/rnnotator>

Proper Citation: Rnnotator (RRID:SCR_011897)

Description: Software designed to assemble Illumina single or paired-end reads.

Abbreviations: Rnnotator

Resource Type: software resource

Resource Name: Rnnotator

Resource ID: SCR_011897

Alternate IDs: OMICS_01323

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260905T132715+0000

Ratings and Alerts

No rating or validation information has been found for Rnnotator.

No alerts have been found for Rnnotator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Mondo SJ, et al. (2025) Consecutive low-frequency shifts in A/T content denote nucleosome positions across microeukaryotes. *iScience*, 28(5), 112472.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in *Colletotrichum* fungi. *GigaScience*, 13.

Wang Y, et al. (2023) Divergent Evolution of Early Terrestrial Fungi Reveals the Evolution of Mucormycosis Pathogenicity Factors. *Genome biology and evolution*, 15(4).

Dorrell RG, et al. (2023) Convergent evolution and horizontal gene transfer in Arctic Ocean microalgae. *Life science alliance*, 6(3).

Martin K, et al. (2021) The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. *Nature communications*, 12(1), 5483.

Koch RA, et al. (2021) Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. *Current biology : CB*, 31(17), 3905.

Kjærboelling I, et al. (2020) A comparative genomics study of 23 *Aspergillus* species from section *Flavi*. *Nature communications*, 11(1), 1106.

Pederson ERA, et al. (2019) Genome Sequencing of *Pleurozium schreberi*: The Assembled and Annotated Draft Genome of a Pleurocarpous Feather Moss. *G3 (Bethesda, Md.)*, 9(9), 2791.

Varga T, et al. (2019) Megaphylogeny resolves global patterns of mushroom evolution. *Nature ecology & evolution*, 3(4), 668.

Druzhinina IS, et al. (2018) Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus *Trichoderma* from its plant-associated hosts. *PLoS genetics*, 14(4), e1007322.

Huang X, et al. (2018) Transcriptome Comparison Reveals Distinct Selection Patterns in Domesticated and Wild Agave Species, the Important CAM Plants. *International journal of genomics*, 2018, 5716518.

Lopez D, et al. (2018) Genome-Wide Analysis of *Corynespora cassiicola* Leaf Fall Disease Putative Effectors. *Frontiers in microbiology*, 9, 276.

Knapp DG, et al. (2018) Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. *Scientific reports*, 8(1), 6321.

Miyauchi S, et al. (2018) Integrative visual omics of the white-rot fungus *Polyporus brumalis* exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. *Biotechnology for biofuels*, 11, 201.

Ungaro A, et al. (2017) Challenges and advances for transcriptome assembly in non-model species. *PloS one*, 12(9), e0185020.

Mujic AB, et al. (2017) Comparative Genomics of the Ectomycorrhizal Sister Species *Rhizopogon vinicolor* and *Rhizopogon vesiculosus* (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type B Locus. *G3* (Bethesda, Md.), 7(6), 1775.

de Vries RP, et al. (2017) Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus *Aspergillus*. *Genome biology*, 18(1), 28.

Okada T, et al. (2016) Comparative analysis of transcriptomes in aerial stems and roots of *Ephedra sinica* based on high-throughput mRNA sequencing. *Genomics data*, 10, 4.

Peter M, et al. (2016) Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus *Cenococcum geophilum*. *Nature communications*, 7, 12662.

Kourist R, et al. (2015) Genomics and Transcriptomics Analyses of the Oil-Accumulating Basidiomycete Yeast *Trichosporon oleaginosus*: Insights into Substrate Utilization and Alternative Evolutionary Trajectories of Fungal Mating Systems. *mBio*, 6(4), e00918.