Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

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

Funding:

Resource Name: Rnnotator

Resource ID: SCR_011897

Alternate IDs: OMICS_01323

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250410T070218+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 23 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

Kjærbølling 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.

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.

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.

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.

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

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.

Onda Y, et al. (2015) Transcriptome analysis of thermogenic Arum concinnatum reveals the molecular components of floral scent production. Scientific reports, 5, 8753.