Resource Summary Report

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rnaSPAdes

RRID:SCR_016992
Type: Tool

Proper Citation

rnaSPAdes (RRID:SCR_016992)

Resource Information

URL: http://cab.spbu.ru/software/rnaspades/

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Description: Software tool for assembling transcripts from RNA-Seq data. Explores surprising computational parallels between assembly of transcriptomes and single cell genomes. Suitable for all kind of organisms. Part of SPAdes package since version 3.9.

Resource Type: data processing software, software application, software resource, sequence analysis software, data analysis software

Defining Citation: DOI:10.1101/420208

Keywords: assembling, transcript, RNA-Seq, data, single, cell, genome, analysis, sequence, bio.tools

Funding: Russian Science Foundation 14-50-00069

Availability: Free, Available for download, Freely available

Resource Name: rnaSPAdes

Resource ID: SCR_016992

Alternate IDs: biotools:rnaSPAdes_autogenerated

Alternate URLs: https://bio.tools/rnaSPAdes_autogenerated

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250513T061828+0000

Ratings and Alerts

No rating or validation information has been found for rnaSPAdes.

No alerts have been found for rnaSPAdes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Cho A, et al. (2024) Genomic analyses of Symbiomonas scintillans show no evidence for endosymbiotic bacteria but does reveal the presence of giant viruses. PLoS genetics, 20(4), e1011218.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Cooney EC, et al. (2024) Morphology, behavior, and phylogenomics of Oxytoxum lohmannii, Dinoflagellata. The Journal of eukaryotic microbiology, 71(6), e13050.

Erazo-Garcia MP, et al. (2024) Latent infection of an active giant endogenous virus in a unicellular green alga. bioRxiv : the preprint server for biology.

Rey Redondo E, et al. (2024) Genomic characterisation and ecological distribution of Mantoniella tinhauana: a novel Mamiellophycean green alga from the Western Pacific. Frontiers in microbiology, 15, 1358574.

Rahuman S, et al. (2024) Tidings from the Tides-De novo transcriptome assembly of the endemic estuarine bivalve Villorita cyprinoides. Scientific data, 11(1), 723.

Yebra G, et al. (2024) Bacteriophage-driven emergence and expansion of Staphylococcus aureus in rodent populations. PLoS pathogens, 20(7), e1012378.

AbuMazen N, et al. (2024) Nasopharyngeal metatranscriptomics reveals host-pathogen signatures of pediatric sinusitis. medRxiv : the preprint server for health sciences.

Gryzunov N, et al. (2024) Genomes of Alphanucleorhabdovirus Physostegiae Isolates from Two Different Cultivar Groups of Solanum melongena. Viruses, 16(10).

Andradi-Brown C, et al. (2024) A novel computational pipeline for var gene expression augments the discovery of changes in the Plasmodium falciparum transcriptome during transition from in vivo to short-term in vitro culture. eLife, 12.

Flores-Almaraz VS, et al. (2024) Foliar mycobiome remains unaltered under urban air-pollution but differentially express stress-related genes. Microbial ecology, 87(1), 72.

Mansueto L, et al. (2024) Building a community-driven bioinformatics platform to facilitate Cannabis sativa multi-omics research. GigaByte (Hong Kong, China), 2024, gigabyte137.

Juéry C, et al. (2024) Transportome remodeling of a symbiotic microalga inside a planktonic host. The ISME journal, 18(1).

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943.

Juteršek M, et al. (2024) Transcriptome-informed identification and characterization of Planococcus citri cis- and trans-isoprenyl diphosphate synthase genes. iScience, 27(4), 109441.

Ribes-Navarro A, et al. (2023) Examination of gammarid transcriptomes reveals a widespread occurrence of key metabolic genes from epibiont bdelloid rotifers in freshwater species. Open biology, 13(10), 230196.

Fromm A, et al. (2023) Homing in on the rare virosphere reveals the native host of giant viruses. bioRxiv : the preprint server for biology.

Detcharoen M, et al. (2023) Complete Genome of Rose Myrtle, Rhodomyrtus tomentosa, and Its Population Genetics in Thai Peninsula. Plants (Basel, Switzerland), 12(8).

Obiol A, et al. (2023) Gene expression dynamics of natural assemblages of heterotrophic flagellates during bacterivory. Microbiome, 11(1), 134.

Emser SV, et al. (2023) Mitochondrial polymorphism m.3017C>T of SHLP6 relates to heterothermy. Frontiers in physiology, 14, 1207620.