

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

Defining Citation: [DOI:10.1101/420208](https://doi.org/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: 20260803T040725+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 53 mentions in open access literature.

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

Paris JR, et al. (2025) Gene Expression Shifts in Emperor Penguin Adaptation to the Extreme Antarctic Environment. *Molecular ecology*, 34(15), e17552.

Lüddecke T, et al. (2025) Comparative venomomics suggests an evolutionary adaption of spider venom from predation to defense. *Communications biology*, 8(1), 1496.

Kusová A, et al. (2025) TRB proteins in moss reveal their evolutionarily conserved roles in plant development and telomere maintenance. *The Plant journal : for cell and molecular biology*, 124(3), e70574.

Kim S, et al. (2025) Chromosome-level genome assembly of the white-spotted sawyer *Monochamus scutellatus* (Coleoptera: Cerambycidae). *Scientific data*, 12(1), 2009.

Ortiz R, et al. (2025) Skin transcriptomics of invasive Coqui frogs: stress responses, parasite signatures, and antimicrobial peptides. *PloS one*, 20(7), e0328623.

Bilcke G, et al. (2025) Conserved genetic markers reveal widespread diatom sexual reproduction in the global ocean. *Nature communications*, 16(1), 10029.

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.

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

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*.

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.

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

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

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.

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.

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

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

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

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