Resource Summary Report

Generated by <u>dkNET</u> on May 20, 2025

SPAdes

RRID:SCR_000131 Type: Tool

Proper Citation

SPAdes (RRID:SCR_000131)

Resource Information

URL: https://cab.spbu.ru/software/spades/

Proper Citation: SPAdes (RRID:SCR_000131)

Description: Software package for assembling single cell genomes and mini metagenomes. Uses short read sets as input. Used for genomes of uncultivatable bacteria that vastly exceeds what may be obtained via traditional metagenomics studies. Works with Illumina or IonTorrent reads and can provide hybrid assemblies using PacBio, Oxford Nanopore and Sanger reads. Intended for small genomes like bacterial or fungal.

Abbreviations: SPAdes

Synonyms: SPAdes Genome Assembler

Resource Type: software resource, software toolkit

Defining Citation: PMID:24093227, PMID:22506599, DOI:10.1089/cmb.2012.0021

Keywords: assembler, single, cell, small, genome, short, read, data

Funding: Government of the Russian Federation ; NCRR P41 RR024851

Availability: Free, Available for download, Freely available

Resource Name: SPAdes

Resource ID: SCR_000131

Alternate IDs: OMICS_01502

Alternate URLs: https://sources.debian.org/src/spades/

Old URLs: http://bioinf.spbau.ru/spades/

License: GNU General Public License, v2

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250519T204449+0000

Ratings and Alerts

No rating or validation information has been found for SPAdes.

No alerts have been found for SPAdes.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 94 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Knickmann J, et al. (2024) A simple method for rapid cloning of complete herpesvirus genomes. Cell reports methods, 4(2), 100696.

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

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

Ghoshal M, et al. (2024) Transcriptomic analysis using RNA sequencing and phenotypic analysis of Salmonella enterica after acid exposure for different time durations using adaptive laboratory evolution. Frontiers in microbiology, 15, 1348063.

Yin H, et al. (2024) IPEV: identification of prokaryotic and eukaryotic virus-derived sequences in virome using deep learning. GigaScience, 13.

Welgemoed T, et al. (2023) Population genomic analyses suggest recent dispersal events of the pathogen Cercospora zeina into East and Southern African maize cropping systems. G3

(Bethesda, Md.), 13(11).

Pei X, et al. (2023) Genome resource of Streptomyces atratus PY-1, a broad-spectrum antimicrobial strain in particular antagonistic against Plasmopara viticola. Plant disease.

Gilroy R, et al. (2023) An initial genomic blueprint of the healthy human oesophageal microbiome. Access microbiology, 5(6).

Nguyen DT, et al. (2023) Characterization of Shigella flexneri in northern Vietnam in 2012-2016. Access microbiology, 5(6).

Cadena-Caballero CE, et al. (2023) APGW/AKH Precursor from Rotifer Brachionus plicatilis and the DNA Loss Model Explain Evolutionary Trends of the Neuropeptide LWamide, APGWamide, RPCH, AKH, ACP, CRZ, and GnRH Families. Journal of molecular evolution, 91(6), 882.

Ghoshal M, et al. (2023) Adaptive laboratory evolution of Salmonella enterica in acid stress. Frontiers in microbiology, 14, 1285421.

Hefetz I, et al. (2023) A reversible mutation in a genomic hotspot saves bacterial swarms from extinction. iScience, 26(2), 106043.

Clilverd H, et al. (2023) Infection dynamics, transmission, and evolution after an outbreak of porcine reproductive and respiratory syndrome virus. Frontiers in microbiology, 14, 1109881.

D'Adamo GL, et al. (2023) Bacterial clade-specific analysis identifies distinct epithelial responses in inflammatory bowel disease. Cell reports. Medicine, 4(7), 101124.

Charlier C, et al. (2023) Fatal neonatal listeriosis following L. monocytogenes horizontal transmission highlights neonatal susceptibility to orally acquired listeriosis. Cell reports. Medicine, 4(7), 101094.

Gattoni G, et al. (2023) Biosynthetic gene profiling and genomic potential of the novel photosynthetic marine bacterium Roseibaca domitiana. Frontiers in microbiology, 14, 1238779.

Mizzi R, et al. (2022) Global Phylogeny of Mycobacterium avium and Identification of Mutation Hotspots During Niche Adaptation. Frontiers in microbiology, 13, 892333.

Ewers C, et al. (2022) Occurrence of mcr-1 and mcr-2 colistin resistance genes in porcine Escherichia coli isolates (2010-2020) and genomic characterization of mcr-2-positive E. coli. Frontiers in microbiology, 13, 1076315.

Majeske AJ, et al. (2022) The first complete mitochondrial genome of Diadema antillarum (Diadematoida, Diadematidae). GigaByte (Hong Kong, China), 2022, gigabyte73.

Heckenhauer J, et al. (2022) Genome size evolution in the diverse insect order Trichoptera. GigaScience, 11.