

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

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 uncultivable 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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260904T000019+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 108 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Withatanung P, et al. (2026) Genomic diversity and clade clustering of Burkholderia pseudomallei and B. thailandensis prophages with soil-derived phages. *iScience*, 29(2), 114658.

Charlier C, et al. (2026) Specificities of pediatric listeriosis beyond the neonatal period: A national prospective study. *Med (New York, N.Y.)*, 7(2), 100933.

Delgado-Suarez EJ, et al. (2026) Emergence of multidrug-resistant blaCTX-M-65/gyrA_D87Y clones among the circulating Salmonella Infantis population in Mexico. *Microbial genomics*, 12(2).

Begnel ER, et al. (2026) Comparison of gut virome in Kenyan infants born to women with and without HIV. *iScience*, 29(3), 114900.

Shen F, et al. (2026) Capsule modulation enhances immunity and delays resistance in MDR Acinetobacter baumannii. *iScience*, 29(6), 115761.

Tran M, et al. (2025) Bacteriophage infection drives loss of ??-lactam resistance in methicillin-resistant Staphylococcus aureus. *eLife*, 13.

Terpis KX, et al. (2025) Multiple plastid losses within photosynthetic stramenopiles revealed by comprehensive phylogenomics. *Current biology : CB*, 35(3), 483.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Unitt A, et al. (2025) *Neisseria gonorrhoeae* LIN codes provide a robust, multi-resolution lineage nomenclature. *eLife*, 14.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. *GigaByte (Hong Kong, China)*, 2025, gigabyte154.

Peng D, et al. (2024) The telomere-to-telomere (T2T) genome provides insights into the evolution of specialized centromere sequences in sandalwood. *GigaScience*, 13.

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.

Koncz M, et al. (2024) Genomic surveillance as a scalable framework for precision phage therapy against antibiotic-resistant pathogens. *Cell*, 187(21), 5901.

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

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.

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*.