

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 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 toolkit, software resource

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: 20260803T040248+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 101 mentions in open access literature.

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

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.

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

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.

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

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

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.

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*.

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

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.

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.

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