SPAdes
RRID:SCR_000131
Type: Tool

Proper Citation

SPAdes (RRID:SCR_000131)

Resource Information

URL: http://bioinf.spbau.ru/spades/

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.

Resource Name: SPAdes

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

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

Resource ID: SCR_000131

Parent Organization: Saint Petersburg Academic University; Saint Petersburg; Russia

Funding Agency: Government of the Russian Federation, NCRR

Related resources: rnaSPAdes, rnaQUAST

References: PMID:24093227, PMID:22506599

Availability: Free, Available for download, Freely available
Website Status: Last checked up

Alternate IDs: OMICS_01502

Abbreviations: SPAdes

Mentions Count: 55

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 55 mentions in open access literature.

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


Greig DR, et al. (2019) Comparison of single-nucleotide variants identified by Illumina and Oxford Nanopore technologies in the context of a potential outbreak of Shiga toxin-producing
Escherichia coli. GigaScience, 8(8).


