

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

## SSAKE

RRID:SCR\_010753

Type: Tool

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### Proper Citation

SSAKE (RRID:SCR\_010753)

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### Resource Information

**URL:** <http://www.bcgsc.ca/platform/bioinfo/software/ssake>

**Proper Citation:** SSAKE (RRID:SCR\_010753)

**Description:** Software designed to help leverage the information from short sequences reads by stringently clustering them into contigs that can be used to characterize novel sequencing targets.

**Abbreviations:** SSAKE

**Resource Type:** software resource

**Defining Citation:** [DOI:10.1093/bioinformatics/btl629](https://doi.org/10.1093/bioinformatics/btl629)

**Keywords:** bio.tools

**Resource Name:** SSAKE

**Resource ID:** SCR\_010753

**Alternate IDs:** biotools:ssake, OMICS\_00033

**Alternate URLs:** <https://bio.tools/ssake>, <https://sources.debian.org/src/ssake/>

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260808T185935+0000

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### Ratings and Alerts

No rating or validation information has been found for SSAKE.

No alerts have been found for SSAKE.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Reddy B, et al. (2022) Structured Framework and Genome Analysis of Magnaporthe grisea Inciting Pearl Millet Blast Disease Reveals Versatile Metabolic Pathways, Protein Families, and Virulence Factors. Journal of fungi (Basel, Switzerland), 8(6).

Owen JR, et al. (2021) One-step generation of a targeted knock-in calf using the CRISPR-Cas9 system in bovine zygotes. BMC genomics, 22(1), 118.

Ye H, et al. (2021) SCIGA: Software for large-scale, single-cell immunoglobulin repertoire analysis. GigaScience, 10(9).

Yao W, et al. (2020) Features of sRNA biogenesis in rice revealed by genetic dissection of sRNA expression level. Computational and structural biotechnology journal, 18, 3207.

Kong J, et al. (2019) GAAP: A Genome Assembly + Annotation Pipeline. BioMed research international, 2019, 4767354.

Zhao J, et al. (2019) Characterizing the Biology of Lytic Bacteriophage vB\_EaeM\_??Eap-3 Infecting Multidrug-Resistant Enterobacter aerogenes. Frontiers in microbiology, 10, 420.

Bowen CD, et al. (2019) Comparison of Herpes Simplex Virus 1 Strains Circulating in Finland Demonstrates the Uncoupling of Whole-Genome Relatedness and Phenotypic Outcomes of Viral Infection. Journal of virology, 93(8).

Goldstein LD, et al. (2019) Massively parallel single-cell B-cell receptor sequencing enables rapid discovery of diverse antigen-reactive antibodies. Communications biology, 2, 304.

Li E, et al. (2016) Isolation and characterization of a bacteriophage phiEap-2 infecting multidrug resistant Enterobacter aerogenes. Scientific reports, 6, 28338.

Di Tommaso P, et al. (2015) The impact of Docker containers on the performance of genomic pipelines. PeerJ, 3, e1273.

Gui J, et al. (2011) Recent advances in molecular technologies and their application in pathogen detection in foods with particular reference to yersinia. Journal of pathogens, 2011, 310135.