Resource Summary Report

Generated by RRID on Apr 28, 2025

SSAKE

RRID:SCR_010753
Type: Tool

Proper Citation

SSAKE (RRID:SCR_010753)

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

Keywords: bio.tools

Funding:

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: 20250420T014508+0000

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 RRID.

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.

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.

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).

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.