Resource Summary Report

Generated by NIF on Apr 26, 2025

SMRT-Analysis

RRID:SCR_002942
Type: Tool

Proper Citation

SMRT-Analysis (RRID:SCR_002942)

Resource Information

URL: https://github.com/PacificBiosciences/SMRT-Analysis/

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Description: Open-source bioinformatics software suite for analyzing single molecule, real-time DNA sequencing data. Users can choose from a variety of analysis protocols that utilize PacBio and third-party tools. Analysis protocols include de novo genome assembly, cDNA mapping, DNA base-modification detection, and long-amplicon analysis to determine phased consensus sequences.

Synonyms: SMRT Analysis

Resource Type: software resource

Keywords: software suite

Funding:

Availability: Open unspecified license

Resource Name: SMRT-Analysis

Resource ID: SCR_002942

Alternate IDs: OMICS_05142

Alternate URLs: http://www.pacb.com/devnet/, https://sources.debian.org/src/smrtanalysis/

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250420T014131+0000

Ratings and Alerts

No rating or validation information has been found for SMRT-Analysis.

No alerts have been found for SMRT-Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 75 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Du X, et al. (2024) Proximity-based defensive mutualism between Streptomyces and Mesorhizobium by sharing and sequestering iron. The ISME journal, 18(1).

Masson F, et al. (2024) Pathogen-specific social immunity is associated with erosion of individual immune function in an ant. Nature communications, 15(1), 9260.

Ma W, et al. (2024) A Novel Strain of Bacillus cereus with a Strong Antagonistic Effect Specific to Sclerotinia and Its Genomic and Transcriptomic Analysis. Microorganisms, 12(3).

Li X, et al. (2023) Integrated single-molecule real-time sequencing and RNA sequencing reveal the molecular mechanisms of salt tolerance in a novel synthesized polyploid genetic bridge between maize and its wild relatives. BMC genomics, 24(1), 55.

Gao Y, et al. (2023) A pangenome reference of 36 Chinese populations. Nature, 619(7968), 112.

Kim B, et al. (2023) Comparative Genomic Analysis of Biofilm-Forming Polar Microbacterium sp. Strains PAMC22086 and PAMC21962 Isolated from Extreme Habitats. Microorganisms, 11(7).

Kang M, et al. (2023) The pan-genome and local adaptation of Arabidopsis thaliana. Nature communications, 14(1), 6259.

Paudel L, et al. (2022) Complete genome of Nakamurella sp. PAMC28650: genomic insights into its environmental adaptation and biotechnological potential. Functional & integrative genomics, 23(1), 18.

Liu H, et al. (2022) Chromosome-level genome of the globe skimmer dragonfly (Pantala

flavescens). GigaScience, 11.

Qi W, et al. (2022) The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. GigaScience, 11.

Bossé JT, et al. (2021) Complete genome for Actinobacillus pleuropneumoniae serovar 8 reference strain 405: comparative analysis with draft genomes for different laboratory stock cultures indicates little genetic variation. Microbial genomics, 7(11).

von Mentzer A, et al. (2021) Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic Escherichia coli (ETEC) circulating in modern time. Scientific reports, 11(1), 9256.

Mao L, et al. (2021) Functional identification of the terpene synthase family involved in diterpenoid alkaloids biosynthesis in Aconitum carmichaelii. Acta pharmaceutica Sinica. B, 11(10), 3310.

Han SR, et al. (2021) Complete genome sequence of Arthrobacter sp. PAMC25564 and its comparative genome analysis for elucidating the role of CAZymes in cold adaptation. BMC genomics, 22(1), 403.

Xiao Q, et al. (2021) Molecular Analysis Uncovers the Mechanism of Fertility Restoration in Temperature-Sensitive Polima Cytoplasmic Male-Sterile Brassica napus. International journal of molecular sciences, 22(22).

Ma T, et al. (2021) Genome-Wide Analysis of Light-Regulated Alternative Splicing in Artemisia annua L. Frontiers in plant science, 12, 733505.

Yang J, et al. (2021) Transcriptome-Based WGCNA Analysis Reveals Regulated Metabolite Fluxes between Floral Color and Scent in Narcissus tazetta Flower. International journal of molecular sciences, 22(15).

Peñaloza C, et al. (2021) A chromosome-level genome assembly for the Pacific oyster Crassostrea gigas. GigaScience, 10(3).

Landínez-Macías M, et al. (2021) The RNA-binding protein Musashi controls axon compartment-specific synaptic connectivity through ptp69D mRNA poly(A)-tailing. Cell reports, 36(11), 109713.

Sharma P, et al. (2021) Improvements in the sequencing and assembly of plant genomes. GigaByte (Hong Kong, China), 2021, gigabyte24.