Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 13, 2025

SMRT View

RRID:SCR_003029
Type: Tool

Proper Citation

SMRT View (RRID:SCR_003029)

Resource Information

URL: https://github.com/PacificBiosciences/DevNet/wiki/SMRT-View

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Description: An open source Genome Browser that visualizes data generated by PacBio Sequencing Systems. * Users can explore and interact with all types of analysis results, including resequencing, De novo, cDNA, and barcoding. * Users can also visualize base modifications, base identification and motifs analysis results.

Synonyms: SMRT-View

Resource Type: software resource

Keywords: standalone software, unix/linux, mac os x, windows, bio.tools

Funding:

Availability: Open unspecified license

Resource Name: SMRT View

Resource ID: SCR_003029

Alternate IDs: biotools:smrt_view, OMICS_05137

Alternate URLs: https://bio.tools/smrt_view

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250410T064937+0000

Ratings and Alerts

No rating or validation information has been found for SMRT View.

No alerts have been found for SMRT View.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Fan X, et al. (2023) Tandem gene duplications contributed to high-level azole resistance in a rapidly expanding Candida tropicalis population. Nature communications, 14(1), 8369.

Fan R, et al. (2023) Gut microbiota composition is associated with disease severity and host immune responses in COVID-19. Frontiers in cellular and infection microbiology, 13, 1274690.

Hu X, et al. (2021) The Mycobacterial DNA Methyltransferase HsdM Decreases Intrinsic Isoniazid Susceptibility. Antibiotics (Basel, Switzerland), 10(11).

Jin CZ, et al. (2020) Genomic and Metabolic Insights into Denitrification, Sulfur Oxidation, and Multidrug Efflux Pump Mechanisms in the Bacterium Rhodoferax sediminis sp. nov. Microorganisms, 8(2).

Gutiérrez-Escobar AJ, et al. (2020) Identification of New Helicobacter pylori Subpopulations in Native Americans and Mestizos From Peru. Frontiers in microbiology, 11, 601839.

Han B, et al. (2020) A Chromosome-Level Genome Assembly of Dendrobium Huoshanense Using Long Reads and Hi-C Data. Genome biology and evolution, 12(12), 2486.

Li J, et al. (2020) Complete genome sequencing and comparative genomic analyses of Bacillus sp. S3, a novel hyper Sb(III)-oxidizing bacterium. BMC microbiology, 20(1), 106.

Lebeurre J, et al. (2019) Comparative Genome Analysis of Staphylococcus lugdunensis Shows Clonal Complex-Dependent Diversity of the Putative Virulence Factor, ess/Type VII Locus. Frontiers in microbiology, 10, 2479.

Lu FH, et al. (2018) Independent assessment and improvement of wheat genome sequence assemblies using Fosill jumping libraries. GigaScience, 7(5).