

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

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

Availability: Free, Freely available

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: 20260905T132456+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 [PRECISE-TBI](#) .

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).

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.

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

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).