

# Resource Summary Report

Generated by T1D on Aug 2, 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](https://bio.tools/smrt_view)

**Record Creation Time:** 20220129T080216+0000

**Record Last Update:** 20260801T190224+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 [T1D](#).

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).

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.

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

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).