

# Resource Summary Report

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## SMRT-Analysis

RRID:SCR\_002942

Type: Tool

### Proper Citation

SMRT-Analysis (RRID:SCR\_002942)

### Resource Information

**URL:** <https://github.com/PacificBiosciences/SMRT-Analysis/>

**Proper Citation:** SMRT-Analysis (RRID:SCR\_002942)

**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

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**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/>

**License:** Open unspecified license

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

**Record Last Update:** 20260801T190158+0000

### Ratings and Alerts

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

No alerts have been found for SMRT-Analysis.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 134 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#).

Hu Q, et al. (2025) Assembly and analysis of the complete mitochondrial genome of *Leonurus japonicus* (Lamiaceae). *Scientific reports*, 15(1), 13372.

Yoshida S, et al. (2025) Towards molecular evolutionary epigenomics with an expanded nucleotide code involving methylated bases. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).

Jin GD, et al. (2025) Complete genome sequence of the probiotic candidate strain *Lacticaseibacillus rhamnosus* B3421 isolated from *Panax ginseng* C. A. Meyer in South Korea. *BMC genomic data*, 26(1), 61.

Lau NS, et al. (2025) Comparative genomics and multiomics analyses reveal the evolution and physiological basis of rubber biosynthesis in *Hevea* species. *GigaScience*, 14.

Wang Q, et al. (2025) Chromosome-level genome assembly of a critically endangered species *Leuciscus chuanchicus*. *Scientific data*, 12(1), 441.

Li Z, et al. (2025) The chromosomal-level genome assembly and annotation of pen shell *Atrina pectinata*. *Scientific data*, 12(1), 617.

Yang J, et al. (2025) The telomere-to-telomere genome assembly of the wild mulberry, *Morus mongolica*. *Scientific data*, 12(1), 694.

Nguyen TB, et al. (2025) Aberrant splicing in Huntington's disease accompanies disrupted TDP-43 activity and altered m6A RNA modification. *Nature neuroscience*, 28(2), 280.

Ren L, et al. (2025) Chromosome-level genome assembly of the synanthropic fly *Chrysomya megacephala*: insights into oviposition location. *BMC genomics*, 26(1), 442.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Teng G, et al. (2025) The *wzc* mutation mediates virulence changes in K1-type *Klebsiella pneumoniae* within the same patient. *Frontiers in microbiology*, 16, 1577629.

Jin GD, et al. (2025) Complete genome of *Leuconostoc mesenteroides* B22051 from *Panax ginseng* Meyer C. A. in South Korea. *BMC genomic data*, 26(1), 75.

Yin Y, et al. (2025) Genomic and stress resistance characterization of *Lactiplantibacillus plantarum* GX17, a potential probiotic for animal feed applications. *Microbiology spectrum*, 13(10), e0124325.

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

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).

Zhang L, et al. (2024) Reconstruction and analyses of genome-scale *Halomonas* metabolic network yield a highly efficient PHA production. *Metabolic engineering communications*, 19, e00251.

Teng G, et al. (2024) Adaptive attenuation of virulence in hypervirulent carbapenem-resistant *Klebsiella pneumoniae*. *mSystems*, 9(6), e0136323.

Xiao X, et al. (2024) Characterization of pKPN945B, a novel transferable IncR plasmid from hypervirulent carbapenem-resistant *Klebsiella pneumoniae*, harboring blaIMP-4 and qnrS1. *Microbiology spectrum*, 12(11), e0049124.

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.

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).