

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/>

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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

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: 20260815T182222+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 148 mentions in open access literature.

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

Li Y, et al. (2026) Biocontrol Efficacy and Mechanisms of *Bacillus velezensis* AP6 Against Brown Rot in Yam by *Fusarium solani*. *Journal of fungi* (Basel, Switzerland), 12(5).

Xue L, et al. (2026) Near telomere-to-telomere diploid genome assembly of *Acrossocheilus wenchowensis*. *Scientific data*, 13(1).

Silva RMB, et al. (2026) A single viral enzyme drives tRNA-dependent hypermodification of DNA at adenine. *Nature communications*, 17(1).

Taheri N, et al. (2026) Genomic characterization of Enterotoxigenic *Escherichia coli* lineage 2 (CS2 + CS3) by long-read sequencing reveals distinct lineage-specific genome organization. *Scientific reports*, 16(1).

Ge F, et al. (2026) The chromosome-level genome of Chinese indicine cattle breed provides insights into bovine adaptation and immunity. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Fagundes WC, et al. (2026) Interspecies hybridization as a route of accessory chromosome origin in fungal pathogens. *mBio*, 17(4), e0346825.

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

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).

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

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.

Du L, et al. (2025) High-quality chromosome-level genome assembly of the snake *Pseudoxenodon stejnegeri* (Squamata: Colubridae). Scientific data, 13(1), 93.

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

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.

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

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

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

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.

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.