SMRT-Analysis
RRID:SCR_002942
Type: Tool

Proper Citation

SMRT-Analysis (RRID:SCR_002942)

Resource Information

**URL:** [https://github.com/PacificBiosciences/SMRT-Analysis/](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:** Open unspecified license

**Resource Name:** SMRT-Analysis

**Resource ID:** SCR_002942

**Alternate IDs:** OMICS_05142


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

**Record Last Update:** 20240424T182745+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 73 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](http://FDI Lab - SciCrunch.org).

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

Li X, et al. (2023) Integrated single-molecule real-time sequencing and RNA sequencing reveal the molecular mechanisms of salt tolerance in a novel synthesized polyploid genetic bridge between maize and its wild relatives. BMC genomics, 24(1), 55.


Han SR, et al. (2021) Complete genome sequence of Arthrobacter sp. PAMC25564 and its comparative genome analysis for elucidating the role of CAZymes in cold adaptation. BMC genomics, 22(1), 403.


Chen L, et al. (2020) Alternative Splicing Regulation of Anthocyanin Biosynthesis in Camellia sinensis var. assamica Unveiled by PacBio Iso-Seq. G3 (Bethesda, Md.), 10(8), 2713.