

# Resource Summary Report

Generated by [ASWG](#) on Aug 23, 2026

## kineticsTools

RRID:SCR\_024049

Type: Tool

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### Proper Citation

kineticsTools (RRID:SCR\_024049)

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### Resource Information

**URL:** <https://github.com/PacificBiosciences/kineticsTools>

**Proper Citation:** kineticsTools (RRID:SCR\_024049)

**Description:** Software tools for detecting DNA modifications from single molecule, real-time sequencing data. This tool implements the P\_ModificationDetection module in SMRT ? Portal, used by the RS\_Modification\_Detection and RS\_Modifications\_and\_Motif\_Detection protocol.

**Synonyms:** kineticstools

**Resource Type:** data analysis software, data processing software, software application, software resource

**Keywords:** detecting DNA modifications from single molecule, real-time sequencing data,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** kineticsTools

**Resource ID:** SCR\_024049

**Alternate IDs:** OMICS\_18309

**Alternate URLs:** <https://sources.debian.org/src/kineticstools/>

**Record Creation Time:** 20230824T050211+0000

**Record Last Update:** 20260821T194248+0000

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### Ratings and Alerts

No rating or validation information has been found for kineticsTools.

No alerts have been found for kineticsTools.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Markkanen M, et al. (2026) Sulfonamide resistance gene sul4 is hosted by common wastewater sludge bacteria and found in various newly described contexts and hosts. Microbiology spectrum, 14(1), e0085725.

Jha A, et al. (2024) DNA-m6A calling and integrated long-read epigenetic and genetic analysis with fibertools. Genome research, 34(11), 1976.

Urban JM, et al. (2021) High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, *Sciara coprophila*, using single-molecule sequencing. BMC genomics, 22(1), 643.