

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

PacmonSTR

RRID:SCR_002796

Type: Tool

Proper Citation

PacmonSTR (RRID:SCR_002796)

Resource Information

URL: <https://github.com/alibashir/pacmonstr>

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Description: Software that implements a reference-based probabilistic approach to identify the Tandem Repeat (TR) region and estimate the number of these TR elements in long DNA reads.

Synonyms: PacmonsTR - Tandem Repeat Detection for Long Read Sequence Data

Resource Type: software resource

Defining Citation: [PMID:25028725](#)

Keywords: standalone software, pacific biosciences

Availability: Free, Freely available, Available for download

Resource Name: PacmonSTR

Resource ID: SCR_002796

Alternate IDs: OMICS_05208

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260725T190531+0000

Ratings and Alerts

No rating or validation information has been found for PacmonSTR.

No alerts have been found for PacmonSTR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Kosugi S, et al. (2025) TRsv: simultaneous detection of tandem repeat variations, structural variations, and short indels using long read sequencing data. *Genome biology*, 26(1), 246.

Walker K, et al. (2022) The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. *F1000Research*, 11, 530.

Garg P, et al. (2021) Pervasive cis effects of variation in copy number of large tandem repeats on local DNA methylation and gene expression. *American journal of human genetics*, 108(5), 809.

Mitsuhashi S, et al. (2019) Tandem-genotypes: robust detection of tandem repeat expansions from long DNA reads. *Genome biology*, 20(1), 58.