

Resource Summary Report

Generated by T1D on Aug 2, 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](https://pubmed.ncbi.nlm.nih.gov/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: 20260801T190217+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 [T1D](#) .

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.