

# Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

## lobSTR

RRID:SCR\_008030

Type: Tool

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### Proper Citation

lobSTR (RRID:SCR\_008030)

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### Resource Information

**URL:** <http://erlichlab.wi.mit.edu/lobSTR/>

**Proper Citation:** lobSTR (RRID:SCR\_008030)

**Description:** A software tool for profiling Short Tandem Repeats (STRs) from high throughput sequencing data., THIS RESOURCE IS NO LONGER IN SERVICE.  
Documented on September 16,2025.

**Abbreviations:** lobSTR

**Synonyms:** lobSTR - Profiling STRs in personal genomes

**Resource Type:** software resource

**Defining Citation:** [PMID:22522390](#)

**Keywords:** bio.tools

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** lobSTR

**Resource ID:** SCR\_008030

**Alternate IDs:** OMICS\_00109, biotools:lobstr

**Alternate URLs:** <https://bio.tools/lobstr>

**Record Creation Time:** 20220129T080245+0000

**Record Last Update:** 20260801T190343+0000

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### Ratings and Alerts

No rating or validation information has been found for lobSTR.

No alerts have been found for lobSTR.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Palacio M, et al. (2025) Real-time visualization of reconstituted transcription reveals RNA polymerase II activation mechanisms at single promoters. *bioRxiv : the preprint server for biology*.

Kinney N, et al. (2025) Short tandem repeat variants are possibly associated with RNA secondary structure and gene expression. *PloS one*, 20(6), e0326355.

Hansen SB, et al. (2024) A conserved juxtamembrane motif in plant NFR5 receptors is essential for root nodule symbiosis. *Proceedings of the National Academy of Sciences of the United States of America*, 121(46), e2405671121.

Whedon SD, et al. (2024) Circular Engineered Sortase for Interrogating Histone H3 in Chromatin. *Journal of the American Chemical Society*, 146(49), 33914.

de Witt J, et al. (2024) Biodegradation of poly(ester-urethane) coatings by *Halopseudomonas formosensis*. *Microbial biotechnology*, 17(1), e14362.

Haasl RJ, et al. (2024) Fitness landscapes of human microsatellites. *PLoS genetics*, 20(12), e1011524.

Das A, et al. (2023) Efficacy of Nivolumab in Pediatric Cancers with High Mutation Burden and Mismatch Repair Deficiency. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(23), 4770.

Susvirkar V, et al. (2023) Shieldin complex assembly kinetics and DNA binding by SHLD3. *Communications biology*, 6(1), 384.

Scholz S, et al. (2022) One-Pot Chemoenzymatic Synthesis of Microviridin Analogs Containing Functional Tags. *Chembiochem : a European journal of chemical biology*, 23(20), e202200345.

Akopian D, et al. (2022) Co-adaptor driven assembly of a CUL3 E3 ligase complex. *Molecular cell*, 82(3), 585.

Quinones-Valdez G, et al. (2022) scAllele: A versatile tool for the detection and analysis of variants in scRNA-seq. *Science advances*, 8(35), eabn6398.

Gasilina A, et al. (2022) A lysine-rich cluster in the N-BAR domain of ARF GTPase-activating protein ASAP1 is necessary for binding and bundling actin filaments. *The Journal of biological chemistry*, 298(3), 101700.

Das A, et al. (2022) Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency. *Nature medicine*, 28(1), 125.

Kinney N, et al. (2021) Ethnically biased microsatellites contribute to differential gene expression and glutathione metabolism in Africans and Europeans. *PloS one*, 16(3), e0249148.

Wu Z, et al. (2021) A worldwide map of swine short tandem repeats and their associations with evolutionary and environmental adaptations. *Genetics, selection, evolution : GSE*, 53(1), 39.

Rajan-Babu IS, et al. (2021) Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. *Genome medicine*, 13(1), 126.

Baeumers M, et al. (2020) Lethal (2) giant discs (Lgd)/CC2D1 is required for the full activity of the ESCRT machinery. *BMC biology*, 18(1), 200.

Metrick CM, et al. (2020) Conserved Outer Tegument Component UL11 from Herpes Simplex Virus 1 Is an Intrinsically Disordered, RNA-Binding Protein. *mBio*, 11(3).

Cai Y, et al. (2020) Genome-wide screening of microsatellites in golden snub-nosed monkey (*Rhinopithecus roxellana*), for the development of a standardized genetic marker system. *Scientific reports*, 10(1), 10614.

Halman A, et al. (2020) Accuracy of short tandem repeats genotyping tools in whole exome sequencing data. *F1000Research*, 9, 200.