

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 2026

lobSTR

RRID:SCR_008030

Type: Tool

Proper Citation

lobSTR (RRID:SCR_008030)

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](https://pubmed.ncbi.nlm.nih.gov/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: 20260808T185903+0000

Ratings and Alerts

No rating or validation information has been found for lobSTR.

No alerts have been found for lobSTR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

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.

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.

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

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.

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.

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.

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.

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.

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).

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