

Resource Summary Report

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

RepeatSeq

RRID:SCR_013235

Type: Tool

Proper Citation

RepeatSeq (RRID:SCR_013235)

Resource Information

URL: <https://github.com/adaptivegenome/repeatseq>

Proper Citation: RepeatSeq (RRID:SCR_013235)

Description: Software that determines genotypes for microsatellite repeats in high-throughput sequencing data.

Abbreviations: RepeatSeq

Resource Type: software resource

Defining Citation: [PMID:23090981](#)

Resource Name: RepeatSeq

Resource ID: SCR_013235

Alternate IDs: OMICS_00112

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260801T190446+0000

Ratings and Alerts

No rating or validation information has been found for RepeatSeq.

No alerts have been found for RepeatSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

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

McComish BJ, et al. (2024) Ancient and Modern Genomes Reveal Microsatellites Maintain a Dynamic Equilibrium Through Deep Time. *Genome biology and evolution*, 16(3).

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.

Boluda CG, et al. (2021) Species Delimitation and Conservation in Taxonomically Challenging Lineages: The Case of Two Clades of *Capurodendron* (Sapotaceae) in Madagascar. *Plants (Basel, Switzerland)*, 10(8).

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.

Pimentel JDSM, et al. (2020) Genetic evaluation of migratory fish: Implications for conservation and stocking programs. *Ecology and evolution*, 10(19), 10314.

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

Li Z, et al. (2019) Effects of marker type and filtering criteria on Q ST-F ST comparisons. *Royal Society open science*, 6(11), 190666.

Kinney N, et al. (2019) Abundance of ethnically biased microsatellites in human gene regions. *PloS one*, 14(12), e0225216.

Kinney N, et al. (2019) CAGm: a repository of germline microsatellite variations in the 1000 genomes project. *Nucleic acids research*, 47(D1), D39.

Pimentel JSM, et al. (2018) High-Throughput Sequencing Strategy for Microsatellite Genotyping Using Neotropical Fish as a Model. *Frontiers in genetics*, 9, 73.

Engelbrecht J, et al. (2017) New microsatellite markers for population studies of *Phytophthora cinnamomi*, an important global pathogen. *Scientific reports*, 7(1), 17631.

Fang H, et al. (2017) Whole genome sequencing of one complex pedigree illustrates challenges with genomic medicine. *BMC medical genomics*, 10(1), 10.

Kinney N, et al. (2017) ZDHHC3 as a Risk and Mortality Marker for Breast Cancer in African American Women. *Cancer informatics*, 16, 1176935117746644.

Quilez J, et al. (2016) Polymorphic tandem repeats within gene promoters act as modifiers of gene expression and DNA methylation in humans. *Nucleic acids research*, 44(8), 3750.

Amambua-Ngwa A, et al. (2016) Exceptionally long-range haplotypes in *Plasmodium falciparum* chromosome 6 maintained in an endemic African population. *Malaria journal*, 15(1), 515.

Bilgin Sonay T, et al. (2015) Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. *Genome research*, 25(11), 1591.

Willems T, et al. (2014) The landscape of human STR variation. *Genome research*, 24(11), 1894.