Resource Summary Report

Generated by dkNET on May 20, 2025

STRBase

RRID:SCR_013465
Type: Tool

Proper Citation

STRBase (RRID:SCR_013465)

Resource Information

URL: http://www.cstl.nist.gov/div831/strbase/

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Description: A database of information on short tandem repeat systems. It contains facts and sequence information on each STR system, population data, commonly used multiplex STR systems, PCR primers and conditions, and a review of various technologies for analysis of STR alleles. STRBase consolidates and organizes the abundant literature on this subject to facilitate on-going efforts in DNA typing. Observed alleles and annotated sequence for each STR locus are described along with a review of STR analysis technologies. Additionally, commercially available STR multiplex kits are described, published polymerase chain reaction (PCR) primer sequences are reported, and validation studies conducted by a number of forensic laboratories are listed. To supplement the technical information, addresses for scientists and hyperlinks to organizations working in this area are available, along with the comprehensive reference list of over 1300 publications on STRs used for DNA typing purposes.

Synonyms: STRBase

Resource Type: database, data or information resource

Defining Citation: PMID:11125125

Keywords: dna typing, short tandem repeat, str, str allele, str loci, str locus

Funding:

Resource Name: STRBase

Resource ID: SCR_013465

Alternate IDs: nif-0000-03501

Record Creation Time: 20220129T080316+0000

Record Last Update: 20250519T204818+0000

Ratings and Alerts

No rating or validation information has been found for STRBase.

No alerts have been found for STRBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Lim L, et al. (2023) Human profiling from STR and SNP analysis of tropical bed bug, Cimex hemipterus, for forensic science. Scientific reports, 13(1), 1506.

Chen YH, et al. (2023) Short tandem repeat profiling via next-generation sequencing for cell line authentication. Disease models & mechanisms, 16(10).

Bañuelos MM, et al. (2022) Associations between forensic loci and expression levels of neighboring genes may compromise medical privacy. Proceedings of the National Academy of Sciences of the United States of America, 119(40), e2121024119.

Moon MH, et al. (2022) Sequence Variations of 31 ?-Chromosomal Short Tandem Repeats Analyzed by Massively Parallel Sequencing in Three U.S. Population Groups and Korean Population. Journal of Korean medical science, 37(6), e40.

Kwon YL, et al. (2021) Massively parallel sequencing of 25 autosomal STRs including SE33 in four population groups for forensic applications. Scientific reports, 11(1), 4701.

Peng D, et al. (2020) Identification of sequence polymorphisms at 58 STRs and 94 iiSNPs in a Tibetan population using massively parallel sequencing. Scientific reports, 10(1), 12225.

Miao X, et al. (2020) Development and Verification of an Economical Method of Custom Target Library Construction. ACS omega, 5(22), 13087.

Grugni V, et al. (2019) Y-chromosome and Surname Analyses for Reconstructing Past Population Structures: The Sardinian Population as a Test Case. International journal of molecular sciences, 20(22).

Hussing C, et al. (2018) Sequencing of 231 forensic genetic markers using the MiSeq FGx™ forensic genomics system - an evaluation of the assay and software. Forensic sciences research, 3(2), 111.

Mautner ME, et al. (2017) Using long ssDNA polynucleotides to amplify STRs loci in degraded DNA samples. PloS one, 12(11), e0187190.

Zhang S, et al. (2017) Massively parallel sequencing of 231 autosomal SNPs with a custom panel: a SNP typing assay developed for human identification with Ion Torrent PGM. Forensic sciences research, 2(1), 26.

Yen YC, et al. (2015) Insulin-like growth factor-independent insulin-like growth factor binding protein 3 promotes cell migration and lymph node metastasis of oral squamous cell carcinoma cells by requirement of integrin ?1. Oncotarget, 6(39), 41837.

Warshauer DH, et al. (2015) Novel Y-chromosome Short Tandem Repeat Variants Detected Through the Use of Massively Parallel Sequencing. Genomics, proteomics & bioinformatics, 13(4), 250.

Benn Torres J, et al. (2015) Genetic Diversity in the Lesser Antilles and Its Implications for the Settlement of the Caribbean Basin. PloS one, 10(10), e0139192.

Gymrek M, et al. (2012) lobSTR: A short tandem repeat profiler for personal genomes. Genome research, 22(6), 1154.

Baca M, et al. (2012) Ancient DNA reveals kinship burial patterns of a pre-Columbian Andean community. BMC genetics, 13, 30.

da Costa Francez PA, et al. (2011) Allelic frequencies and statistical data obtained from 12 codis STR loci in an admixed population of the Brazilian Amazon. Genetics and molecular biology, 34(1), 35.

Deng YJ, et al. (2005) Preliminary DNA identification for the tsunami victims in Thailand. Genomics, proteomics & bioinformatics, 3(3), 143.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.