Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 2026

Mutation Surveyor

RRID:SCR_001247
Type: Tool

Proper Citation

Mutation Surveyor (RRID:SCR_001247)

Resource Information

URL: http://www.softgenetics.com/mutationSurveyor.php

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Software for DNA sequencing analysis that integates with Sanger Sequencing files generated by Applied Biosystems Genetic Analyzers, MegaBACE, and Beckman CEQ electrophoresis systems. It can be used to find single nucleotide polymorphisms (SNPs), insertions and deletions (INDELS), and somatic mutations in direct sequencing, PCR sequencing, mitochondrial DNA sequencing, and resequencing projects.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: PMID:21780000, PMID:20938837

Keywords: dna, sequencing, dna-seq, sanger sequencing, sequence analysis software

Availability: Restricted

Resource Name: Mutation Surveyor

Resource ID: SCR_001247

Alternate IDs: OMICS_01816

Alternate URLs: Mutation Surveyor software version 5.0

Old URLs: http://www.softgenetics.com/mutationSurveyor.html

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195522+0000

Ratings and Alerts

No rating or validation information has been found for Mutation Surveyor.

No alerts have been found for Mutation Surveyor.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 668 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Arenillas C, et al. (2025) Convergent Genetic Adaptation in Human Tumors Developed Under Systemic Hypoxia and in Populations Living at High Altitudes. Cancer discovery, 15(5), 1037.

Al-Hamed MH, et al. (2025) Genetics of Primary Adrenal Insufficiency Beyond CAH in Saudi Arabian Population. Molecular genetics & genomic medicine, 13(1), e70052.

Wang RJ, et al. (2025) Unprecedented female mutation bias in the aye-aye, a highly unusual lemur from Madagascar. PLoS biology, 23(2), e3003015.

Cif L, et al. (2025) KMT2B-related disorders: expansion of the phenotypic spectrum and long-term efficacy of deep brain stimulation. ArXiv.

Hamadamin PS, et al. (2024) Exploring the anticancer potential of hydrogen sulfide and BAY?876 on clear cell renal cell carcinoma cells: Uncovering novel mutations in VHL and KDR genes among ccRCC patients. Molecular and clinical oncology, 20(3), 21.

Li M, et al. (2024) Clinical features of a novel compound heterozygous genotype of the BBS2 gene: a case report. The Journal of international medical research, 52(8), 3000605241274239.

Lee Y, et al. (2024) Diagnostic Approaches to Investigate JAK2-Unmutated Erythrocytosis Based on a Single Tertiary Center Experience. Molecular diagnosis & therapy, 28(3), 311.

Alasmar A, et al. (2024) Novel Mutations in AKT1 Gene in Prostate Cancer Patients in Jordan. Current issues in molecular biology, 46(9), 9856.

Parvathareddy SK, et al. (2024) Radioactive iodine refractoriness in Middle Eastern differentiated thyroid cancer: clinical outcome and risk factor analysis. Frontiers in endocrinology, 15, 1326976.

Al-Hamed MH, et al. (2024) Use of Whole-Exome Sequencing and Pedigree Analysis to Identify X-linked Hypophosphatemia in Saudi Arabian Families. Journal of the Endocrine Society, 9(1), bvae203.

Saber BA, et al. (2024) Mutations in Genes Producing Nitric Oxide and Hydrogen Sulfide and Their Connection With Apoptotic Genes in Chronic Myeloid Leukemia. Cureus, 16(6), e61570.

Nazarova A, et al. (2024) Leeches Baicalobdella torquata feed on hemolymph but have a low effect on the cellular immune response of amphipod Eulimnogammarus verrucosus from Lake Baikal. PeerJ, 12, e17348.

Khalil SS, et al. (2024) Mutations in the TP53, VEGFA, and CTH Genes as Key Molecular Markers for the Diagnosis of Glioblastoma. Cureus, 16(5), e61165.

Holthöfer L, et al. (2024) A case of an Angelman-syndrome caused by an intragenic duplication of UBE3A uncovered by adaptive nanopore sequencing. Clinical epigenetics, 16(1), 101.

Zhang B, et al. (2024) SMC3 contributes to heart development by regulating super-enhancer associated genes. Experimental & molecular medicine, 56(8), 1826.

Saadeh NA, et al. (2024) The Ser434Phe Androgen Receptor Gene Mutation Does Not Affect Fertility but is Associated with Increased Prolactin. The application of clinical genetics, 17, 143.

Yu C, et al. (2024) MEF2B C-terminal mutations enhance transcriptional activity and stability to drive B cell lymphomagenesis. Nature communications, 15(1), 7195.

Franke M, et al. (2024) A MYH7 variant in a five-generation-family with hypertrophic cardiomyopathy. Frontiers in genetics, 15, 1306333.

van der Velden JJAJ, et al. (2024) Variants in the L12 linker domain of KRT10 are causal to atypical epidermolytic ichthyosis. The Journal of dermatology, 51(9), 1180.

Keefer-Jacques E, et al. (2024) Investigation of cryptic JAG1 splice variants as a cause of Alagille syndrome and performance evaluation of splice predictor tools. HGG advances, 5(4), 100351.