Resource Summary Report

Generated by NIF on Sep 3, 2026

SIFT

RRID:SCR_012813
Type: Tool

Proper Citation

SIFT (RRID:SCR_012813)

Resource Information

URL: http://sift.bii.a-star.edu.sg/

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Description: Data analysis service to predict whether an amino acid substitution affects protein function based on sequence homology and the physical properties of amino acids. SIFT can be applied to naturally occurring nonsynonymous polymorphisms and laboratory-induced missense mutations. (entry from Genetic Analysis Software) Web service is also available.

Abbreviations: SIFT

Synonyms: Sorting Intolerant From Tolerant

Resource Type: analysis service resource, data access protocol, data analysis service, production service resource, service resource, software resource, source code, web service

Defining Citation: PMID:19561590, PMID:12824425, PMID:11337480, DOI:10.1038/nprot.2009.86

Keywords: gene, genetic, genomic, amino acid, substitution, protein function, coding region, single nucleotide variant, coding indel, deletion, insertion, sequence, protein, bio.tools

Funding: Agency for Science Technology and Research ;
NIGMS GM29009

Availability: Non-commercial

Resource Name: SIFT

Resource ID: SCR_012813

Alternate IDs: biotools:sift, OMICS_00137, nlx_154618

Alternate URLs: http://sift.jcvi.org/, https://bio.tools/sift, https://sources.debian.org/src/sift/

Old URLs: http://sift.bii.a-star.edu.sg/SIFT.html

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260829T182422+0000

Ratings and Alerts

No rating or validation information has been found for SIFT.

No alerts have been found for SIFT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10996 mentions in open access literature.

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

Hollis RL, et al. (2026) Molecular Profiling and Tumor Biomarker Analysis of GOG281/LOGS: A Positive Late-Phase Trial of Trametinib for Recurrent/Persistent Low-Grade Serous Ovarian Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 724.

Roush SM, et al. (2026) Mutational profiling of HIV+ diffuse large B-cell lymphoma reveals distinct mutational features with evidence of genomic instability. AIDS (London, England), 40(6), 719.

Park MS, et al. (2026) Unique TTR Variants D38A and M13dup Among Korean Patients with Hereditary Transthyretin Amyloidosis: A Retrospective Single-Center Cohort Study. Annals of laboratory medicine, 46(3), 309.

Owrang D, et al. (2026) Uncovering dual molecular diagnoses in families with complex phenotypes through structural and clinical studies of novel COL4A6 variants. QJM : monthly journal of the Association of Physicians, 119(3), 187.

Jiang Y, et al. (2026) Prenatal Exome Sequencing Analysis in Fetuses With Structural Anomalies: A Multicenter Prospective Cohort Study With Practical Implications. Prenatal diagnosis, 46(1), 46.

Showpnil IA, et al. (2026) De Novo Heterozygous ZFX Frameshift Variant in a Female With an X-Linked Neurodevelopmental Disorder. American journal of medical genetics. Part A, 200(2), 521.

Jiang Q, et al. (2026) Beyond the genome: clinical challenges in diagnosing LONP1-related mitochondrial disorders. Frontiers in cell and developmental biology, 14, 1779332.

Rey F, et al. (2026) Study of POLR3A variants in a family trio suggests mutation-specific pathogenetic mechanisms: insights from integrative OMIC approaches. Cell communication and signaling : CCS, 24(1).

Babur Güler G, et al. (2026) Phenotypic, Epidemiologic, and Imaging Features of Hypertrophic Cardiomyopathy: A Single-Center Experience. Anatolian journal of cardiology, 30(5), 321.

Ullah MF, et al. (2026) Whole-exome sequencing in obstructive coronary artery disease identifies rare and novel variants in cardiac arrhythmia and pulmonary arterial hypertension-associated genes. Biomolecules & biomedicine, 26(8), 1344.

Boone PM, et al. (2026) Clinical, in vitro, and in vivo evidence of WAPL as a novel cohesinopathy gene and phenotypic driver of 10q22.3q23.2 genomic disorder. medRxiv : the preprint server for health sciences.

Lee WH, et al. (2026) Prognostic implications of genetic and transcriptomic abnormalities in MDS according to IPSS-R, IPSS-M, and the International Consensus Classification. Blood cancer journal, 16(1).

López-López L, et al. (2026) Accurate and cost-effective workflow integrating trio pooled-WES for novel gene discovery in neurodevelopmental disorders. European journal of human genetics : EJHG, 34(5), 675.

Kim HI, et al. (2026) Exome sequencing and analysis of 44,028 British South Asians enriched for high autozygosity. Nature genetics, 58(4), 821.

Wan J, et al. (2026) The genetic spectrum of LRRK2 variants in Parkinson's disease: findings from a large Chinese cohort. NPJ Parkinson's disease, 12(1).

Armengol-Alsina M, et al. (2026) Placental insufficiency markers to assess the risk of non-chromosomal genetic conditions in early-onset fetal growth restriction. Ultrasound in obstetrics & gynecology : the official journal of the International Society of Ultrasound in Obstetrics and Gynecology, 67(4), 492.

Afkari M, et al. (2026) A Compound Heterozygous Missense Variant in The DNAH5 Gene Could Be A Significant Factor in Unexplained Male Infertility: A Case Study. International journal of fertility & sterility, 20(2), 159.

Jaggers TN, et al. (2026) Rhesus macaques with an OPA1 mutation demonstrate features of autosomal dominant optic atrophy. Proceedings of the National Academy of Sciences of the United States of America, 123(16), e2509165123.

Zhou Z, et al. (2026) Somatic mosaicism in ALS and FTD identifies focal mutations associated with widespread degeneration. Nature genetics, 58(5), 1019.

Wei X, et al. (2026) A Novel CRYBB2 Splicing Mutation Is Associated With Lens Extracellular Matrix Remodeling and Vascular Alterations in Congenital Cataract. Investigative ophthalmology & visual science, 67(4), 36.