Resource Summary Report

Generated by ASWG on Aug 2, 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: data analysis service, data access protocol, service resource, source code, production service resource, software resource, analysis service resource, 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: 20260801T190451+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 10223 mentions in open access literature.

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

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.

Quarello P, et al. (2026) DNA Methylation Episignature as a Novel Diagnostic Tool for Diamond-Blackfan Anemia Syndrome. American journal of hematology, 101(2), 228.

Xiangwen W, et al. (2026) A De Novo Splicing Mutation of SRP72 in Bone Marrow Failure Syndrome Type 1: Case Report and Review of the Literature. Molecular genetics & genomic medicine, 14(1), e70168.

Wei Y, et al. (2026) Transformer-based InsightGWAS improves GERD genetic discovery via pretraining on GWAS for major depressive disorder. Communications biology, 9(1), 2.

Guo W, et al. (2026) Pathogenicity of novel GLA gene missense mutations in Fabry disease and the therapeutic impact of migalastat. Journal of advanced research, 79, 549.

Watanabe T, et al. (2026) Whole exome sequencing in Japanese spinocerebellar ataxia identifies novel variants. Journal of human genetics, 71(1), 35.

Eising E, et al. (2026) De novo protein-coding gene variants in developmental stuttering. Molecular psychiatry, 31(1), 104.

Ncir WB, et al. (2026) First LDLRAP1 and Recurrent LDLR Mutations in Tunisian Families With Familial Hypercholesterolemia. Journal of cellular and molecular medicine, 30(1),

e70997.

Treger TD, et al. (2025) Predisposition Footprints in the Somatic Genome of Wilms Tumors. Cancer discovery, 15(2), 286.

Schoenrock SA, et al. (2025) Genetic mapping in collaborative cross mouse strains identifies loci that affect initial sensitivity to cocaine. Psychopharmacology.

Lucaciu SA, et al. (2025) Skin disease-associated GJB4 variants differentially influence connexin stability, cell viability and channel function. The Journal of physiology, 603(15), 4383.

Roush SM, et al. (2025) Shared genomic features of HIV+???diffuse large B-cell lymphoma in two African cohorts. Scientific reports, 15(1), 24599.

van Ravensteijn SG, et al. (2025) Cemiplimab in Locally Advanced or Metastatic Secondary Angiosarcomas (CEMangio): A Phase II Clinical Trial and Biomarker Analyses. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(17), 3678.

Fiorica PN, et al. (2025) Germline Pathogenic DROSHA Variants Are Linked to Pineoblastoma and Wilms Tumor Predisposition. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(8), 1491.

Gaikwad AS, et al. (2025) Functional and clinical insights into nuclear receptor variants for advancing precision diagnostics in male infertility. EBioMedicine, 119, 105899.

Goshayeshi L, et al. (2025) Germline variants in patients from the Iranian hereditary colorectal cancer registry. Cancer cell international, 25(1), 140.

Mohamed W, et al. (2025) 3D reconstruction from 2D multi-view dental 2D images based on EfficientNetB0 model. Scientific reports, 15(1), 28775.

Peng SQ, et al. (2025) A gain-of-function mutation in ATP6V0A4 drives primary distal renal tubular alkalosis with enhanced V-ATPase activity. The Journal of clinical investigation, 135(13).

Babu Sait MR, et al. (2025) Genome-wide identification of modulators of Chlamydia trachomatis parasitophorous vacuole stability highlights an important role for sphingolipid supply. PLoS biology, 23(8), e3003297.

Yao M, et al. (2025) A case report of SPONASTRIME dysplasia with novel TONSL mutation: genetic analysis, clinical manifestations, and the effect of growth hormone treatment. Human molecular genetics, 34(19), 1665.