Resource Summary Report

Generated by NIF on Aug 26, 2026

SIFT

RRID:SCR_012813
Type: Tool

Proper Citation

SIFT (RRID:SCR_012813)

Resource Information

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

Proper Citation: SIFT (RRID:SCR_012813)

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: 20260821T193938+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.

Lipi?ski P, et al. (2026) Riboflavin treatment in L-2-hydroxyglutaric aciduria: report on a pediatric patient and literature review. Journal of applied genetics, 67(2), 443.

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.

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.

Lensing K, et al. (2026) A generic pipeline for CADD score generation: chickenCADD and turkeyCADD. G3 (Bethesda, Md.), 16(1).

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.

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.

Krantz S, et al. (2026) Dissection of G?s and Hedgehog Signaling Cross-talk Reveals Therapeutic Opportunities to Target Hedgehog-Dependent Tumors. Cancer research, 86(4), 940.

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.

Wang M, et al. (2026) Exploration of the Pathogenic Mechanism of the Factor XIII A Subunit in a Patient With Congenital Factor XIII Deficiency. Molecular genetics & genomic medicine, 14(1), e70193.

Ou S, et al. (2026) Clinical and Genetic Analysis of SMARCC2-Related Diseases in Three Chinese Patients. Molecular genetics & genomic medicine, 14(1), e70198.

Malovitski K, et al. (2026) Defective Function of Inhibitor of ?B Kinase Subunit Beta Associated With Multiple Immune-Mediated Disorders. Experimental dermatology, 35(1), e70206.

Floriot S, et al. (2026) An autosomal recessive nonsense variant in the EGFR gene induces perinatal lethality in "Blonde d'Aquitaine" calves. BMC veterinary research, 22(1), 89.

Hasani E, et al. (2026) A novel frameshift deletion in SLC25A38 and its role in mitochondrial dysfunction: A case study of sideroblastic anemia in a child from Iran. Annals of hematology, 105(4), 128.

Jenni R, et al. (2026) Novel genetic variants identification and immune profiling in ataxia telangiectasia patients. Journal of translational medicine, 24(1).

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.

Hlongwa L, et al. (2026) Uncovering genetic variation in humoral inborn errors of immunity in African populations: insights from the African genome variation database. Scientific reports, 16(1).

Kikuchi S, et al. (2026) Compound heterozygous CHAT gene mutations, a missense and a splice site variant, in two siblings with congenital myasthenic syndrome. Scientific reports, 16(1).