SIFT
RRID:SCR_012813
Type: Tool

Proper Citation

SIFT (RRID:SCR_012813)

Resource Information

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

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.

Resource Name: SIFT

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

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

Resource ID: SCR_012813

Parent Organization: Genome Institute of Singapore; Singapore; Singapore, J. Craig Venter Institute

Funding Agency: Agency for Science Technology and Research, NIGMS

References: PMID:19561590, PMID:12824425, PMID:11337480

Availability: Non-commercial
**Website Status:** Last checked up

**Alternate IDs:** nlx_154618, OMICS_00137

**Alternate URLs:** http://sift.jcvi.org/

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

**Abbreviations:** SIFT

**Mentions Count:** 5059

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**Ratings and Alerts**

No rating or validation information has been found for SIFT.

No alerts have been found for SIFT.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 5059 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](http://www.fdi-lab.org/scicrunch).


Pinnaro CT, et al. (2020) Candidate modifier genes for immune function in 22q11.2 deletion syndrome. Molecular genetics & genomic medicine, 8(1), e1057.


