

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SIFT 4G

RRID:SCR_021850

Type: Tool

Proper Citation

SIFT 4G (RRID:SCR_021850)

Resource Information

URL: <https://sift.bii.a-star.edu.sg/sift4g/AboutSIFT4G.html>

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Description: Software tool to predict whether amino acid substitution affects protein function. Faster version of SIFT that enables to scale up and provide SIFT predictions for more organisms.

Synonyms: Sorting Intolerant From Tolerant For Genomes, SIFT4G

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: sequence homology, amino acids physical properties, amino acid substitution, protein function

Availability: Free, Available for download, Freely available

Resource Name: SIFT 4G

Resource ID: SCR_021850

Alternate URLs: <https://github.com/rvaser/sift4g>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260905T133217+0000

Ratings and Alerts

No rating or validation information has been found for SIFT 4G.

No alerts have been found for SIFT 4G.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Salson M, et al. (2025) Interplay between large low-recombining regions and pseudo-overdominance in a plant genome. Nature communications, 16(1), 6458.

Shen Y, et al. (2024) Genomic insights into endangerment and conservation of the garlic-fruit tree (*Malania oleifera*), a plant species with extremely small populations. GigaScience, 13.

Kuang J, et al. (2024) PON-Tm: A Sequence-Based Method for Prediction of Missense Mutation Effects on Protein Thermal Stability Changes. International journal of molecular sciences, 25(15).

Sia BZ, et al. (2022) Prediction of the effects of the top 10 nonsynonymous variants from 30229 SARS-CoV-2 strains on their proteins. F1000Research, 11, 9.