## **Resource Summary Report**

Generated by ASWG on Apr 28, 2025

# **SiPhy**

RRID:SCR\_000564

Type: Tool

## **Proper Citation**

SiPhy (RRID:SCR\_000564)

#### **Resource Information**

URL: http://www.broadinstitute.org/genome\_bio/siphy/

**Proper Citation:** SiPhy (RRID:SCR\_000564)

**Description:** Software that implements rigorous statistical tests to detect bases under selection from a multiple alignment data. It takes full advantage of deeply sequenced phylogenies to estimate both unlikely substitution patterns as well as slowdowns or accelerations in mutation rates. It can be applied as an Hidden Markov Model (HMM), in sliding windows, or to specific regions.

Abbreviations: SiPhy

Resource Type: sequence analysis resource

**Defining Citation: PMID:19478016** 

**Keywords:** java, mutation, phylogeny, substitution pattern, mutation rate

Funding: NHGRI;

NSF

Availability: Acknowledgement requested, Free, Public

Resource Name: SiPhy

Resource ID: SCR 000564

Alternate IDs: OMICS\_00183

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20250420T013955+0000

## **Ratings and Alerts**

No rating or validation information has been found for SiPhy.

No alerts have been found for SiPhy.

#### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 6 mentions in open access literature.

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

Zhang X, et al. (2024) Clinical phenotype and genetic characteristics of SZT2 related diseases: A case report and literature review. Seizure, 114, 111.

Zhang X, et al. (2023) A novel heterozygous ATP1A2 pathogenic variant in a Chinese child with MELAS-like alternating hemiplegia. Molecular genetics & genomic medicine, 11(5), e2146.

Liu J, et al. (2023) Loss-of-function variants in KCTD19 cause non-obstructive azoospermia in humans. iScience, 26(7), 107193.

Barbosa P, et al. (2022) Computational prediction of human deep intronic variation. GigaScience, 12.

Wu J, et al. (2016) dbWGFP: a database and web server of human whole-genome single nucleotide variants and their functional predictions. Database: the journal of biological databases and curation, 2016.

Li Q, et al. (2014) Gene-specific function prediction for non-synonymous mutations in monogenic diabetes genes. PloS one, 9(8), e104452.