Resource Summary Report

Generated by NIF on Apr 30, 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 NIF.

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.