

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

SysCall

RRID:SCR_005307

Type: Tool

Proper Citation

SysCall (RRID:SCR_005307)

Resource Information

URL: <http://bio.math.berkeley.edu/SysCall/>

Proper Citation: SysCall (RRID:SCR_005307)

Description: A logistic regression based classifier distinguishing heterozygous sites from systematic errors. Given a list of candidate heterozygous genomic locations and a sam file of sequenced reads SysCall classifies each genomic location as either a heterozygous site or a systematic error and outputs according lists, along with the assigned posterior probabilities.

Abbreviations: SysCall

Synonyms: SysCall - Distinguishing heterozygous sites from systematic errors

Resource Type: software resource

Defining Citation: [PMID:22099972](#)

Keywords: high-throughput sequencing

Availability: Acknowledgement requested, Registration required

Resource Name: SysCall

Resource ID: SCR_005307

Alternate IDs: OMICS_01080

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260829T182218+0000

Ratings and Alerts

No rating or validation information has been found for SysCall.

No alerts have been found for SysCall.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. Briefings in bioinformatics, 17(1), 154.

Meacham F, et al. (2011) Identification and correction of systematic error in high-throughput sequence data. BMC bioinformatics, 12, 451.