Resource Summary Report

Generated by NIF on Sep 15, 2026

TRANSIT

RRID:SCR_016492
Type: Tool

Proper Citation

TRANSIT (RRID:SCR_016492)

Resource Information

URL: http://saclab.tamu.edu/essentiality/transit/

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Description: Software tool Python based and open source for statistical analysis of TnSeq data. Provides a graphical interface to three different statistical methods for analyzing TnSeq data capable of identifying essential genes in individual datasets as well as comparative analysis between conditions.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: PMID:26447887

Keywords: statistical, analysis, TnSeq, data, identify, gene, dataset, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: TRANSIT

Resource ID: SCR_016492

Alternate IDs: biotools:transit

Alternate URLs: https://github.com/mad-lab/transit, https://bio.tools/transit

License: GNU GPL v3

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260912T195840+0000

Ratings and Alerts

No rating or validation information has been found for TRANSIT.

No alerts have been found for TRANSIT.

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 NIF .

Lyon LM, et al. (2025) Genome-wide mutagenesis identifies factors involved in MRSA vaginal colonization. Cell reports, 44(3), 115421.

Fiebig A, et al. (2024) Bile acid fitness determinants of a Bacteroides fragilis isolate from a human pouchitis patient. mBio, 15(1), e0283023.

Peterson EJR, et al. (2023) MtrA modulates Mycobacterium tuberculosis cell division in host microenvironments to mediate intrinsic resistance and drug tolerance. Cell reports, 42(8), 112875.

Baranowski C, et al. (2018) Maturing Mycobacterium smegmatis peptidoglycan requires non-canonical crosslinks to maintain shape. eLife, 7.