

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 2, 2026

TRANSIT

RRID:SCR_024389

Type: Tool

Proper Citation

TRANSIT (RRID:SCR_024389)

Resource Information

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

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Description: Software tool for Himar1 TnSeq analysis. Provides graphical interface to three different statistical methods for analyzing TnSeq data. Used for identifying essential genes in individual datasets as well as comparative analysis between conditions.

Synonyms: tnseq-transit

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

Defining Citation: [PMID:26447887](#)

Keywords: Himar1 TnSeq data analysis, identifying essential genes in individual datasets, comparative analysis between conditions,

Availability: Free, Available for download, Freely available,

Resource Name: TRANSIT

Resource ID: SCR_024389

Alternate IDs: OMICS_10215

Alternate URLs: <https://sources.debian.org/src/tnseq-transit/>

Record Creation Time: 20230830T050218+0000

Record Last Update: 20260801T190816+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 1 mentions in open access literature.

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

Joyce LR, et al. (2025) Global genome analysis identifies glycolipids and lipoteichoic acid alanylation as contributors to group B streptococcal diabetic wound infection. Cell reports, 44(11), 116510.