

# Resource Summary Report

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

## Tn-seq explorer

RRID:SCR\_024387

Type: Tool

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### Proper Citation

Tn-seq explorer (RRID:SCR\_024387)

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### Resource Information

**URL:** <https://github.com/sina-cb/Tn-seqExplorer>

**Proper Citation:** Tn-seq explorer (RRID:SCR\_024387)

**Description:** Software package written in Java for analysis of high-throughput sequencing data of transposon mutant libraries. Reads the alignment and the gene annotation, and provides the user with set of tools to investigate data and identify possibly essential or advantageous genes as those that contain significantly low counts of transposon insertions.

**Synonyms:** , Tn-seq Explorer, tn-seqexplorer

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

**Defining Citation:** [PMID:25938432](#)

**Keywords:** high-throughput sequencing data analysis, transposon mutant libraries, read alignment and gene annotation, identify genes, low counts of transposon insertions genes,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** Tn-seq explorer

**Resource ID:** SCR\_024387

**Old URLs:** <https://sources.debian.org/src/tn-seqexplorer/>

**Record Creation Time:** 20230830T050217+0000

**Record Last Update:** 20260801T190826+0000

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### Ratings and Alerts

No rating or validation information has been found for Tn-seq explorer.

No alerts have been found for Tn-seq explorer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Bell??s-Sancho P, et al. (2024) Tn-seq profiling reveals that NodS of the beta-rhizobium Paraburkholderia phymatum is detrimental for nodulating soybean. Communications biology, 7(1), 1706.

Patel Y, et al. (2020) A regulatory pathway that selectively up-regulates elongasome function in the absence of class A PBPs. eLife, 9.

Zhang C, et al. (2018) The essential genome of the crenarchaeal model Sulfolobus islandicus. Nature communications, 9(1), 4908.