

Resource Summary Report

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Bio-tradis

RRID:SCR_015993

Type: Tool

Proper Citation

Bio-tradis (RRID:SCR_015993)

Resource Information

URL: <https://github.com/sanger-pathogens/Bio-Tradis>

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Description: Analysis software for the output from TraDIS (Transposon Directed Insertion Sequencing) analyses of dense transposon mutant libraries. The Bio-Tradis analysis pipeline is implemented as an extensible Perl library which can either be used as is, or as a basis for the development of more advanced analysis tools.

Abbreviations: TraDIS:Transposon Directed Insertion Sequencing

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

Defining Citation: [PMID:26794317](#), [DOI:10.1093/bioinformatics/btw022](#)

Keywords: software, tool, analysis, data, sequencing, insertion, transposon, direct, mutant, library, perl, bio.tools

Funding: Alexander von Humboldt Stiftung/Foundation ;
Medical Research Council G1100100/1;
Wellcome Trust WT098051

Availability: Free, Available for download, Freely available

Resource Name: Bio-tradis

Resource ID: SCR_015993

Alternate IDs: OMICS_11083, biotools:bio-tradis

Alternate URLs: <https://bio.tools/bio-tradis>, <https://sources.debian.org/src/bio-tradis/>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260821T194032+0000

Ratings and Alerts

No rating or validation information has been found for Bio-tradis.

No alerts have been found for Bio-tradis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Yousief SW, et al. (2026) Genome-wide identification of tissue-specific fitness genes in murine models of *Staphylococcus aureus* infection. *iScience*, 29(1), 114261.

Matanza XM, et al. (2026) Genome-wide analysis exploring mechanisms used by *Shigella sonnei* to survive long-term nutrient starvation. *mSystems*, 11(4), e0008826.

Hanke M, et al. (2026) ConNIS and labeling instability: New statistical methods for improving the detection of essential genes in TraDIS libraries. *PLoS computational biology*, 22(3), e1013428.

Katsburg M, et al. (2026) What makes them stick? A genetic analysis of biofilm formation of an infective endocarditis-causing *Streptococcus canis* strain using transposon directed insertion-site sequencing. *Frontiers in cellular and infection microbiology*, 16, 1777632.

Champie A, et al. (2026) Comparative analysis of gene importance in *Escherichia coli* across growth conditions. *mSystems*, 11(5), e0142525.

Di Martino ML, et al. (2025) A scalable gut epithelial organoid model reveals the genome-wide colonization landscape of a human-adapted pathogen. *Nature genetics*, 57(7), 1730.

Morris FC, et al. (2025) Gene dependence during mammalian *Acinetobacter baumannii* pneumonia and septicaemia infections. *Microbial genomics*, 11(11).

Harding KR, et al. (2025) Genome-wide identification of bacterial genes contributing to nucleus-forming jumbo phage infection. *Nucleic acids research*, 53(3).

Smallman TR, et al. (2025) Comparative analysis of shared and unique mechanisms important for diverse strains of *Pasteurella multocida* to cause systemic infection in mice. *PLoS pathogens*, 21(12), e1013398.

Krause AL, et al. (2025) Transposon-directed insertion-site sequencing (TraDIS) analysis of *Enterococcus faecium* using nanopore sequencing and a WebAssembly analysis platform. *Microbiology spectrum*, 13(7), e0062825.

Yang Z, et al. (2025) Loss of cardiolipin and porins bypasses the essentiality of the sigma E cell envelope stress response in *Escherichia coli*. *mBio*, 16(9), e0161325.

Ma Y, et al. (2025) Chromosomal genes modulating fosfomycin susceptibility in uropathogenic *Escherichia coli*: a genome-wide analysis. *Antimicrobial agents and chemotherapy*, 69(4), e0141724.

Padilla JJ, et al. (2025) Characterization of the Antibiotic and Copper Resistance of Emergent Species of Onion-Pathogenic *Burkholderia* Through Genome Sequence Analysis and High-Throughput Sequencing of Differentially Enriched Random Transposon Mutants. *Pathogens (Basel, Switzerland)*, 14(3).

A Ghomi F, et al. (2024) High-throughput transposon mutagenesis in the family *Enterobacteriaceae* reveals core essential genes and rapid turnover of essentiality. *mBio*, 15(10), e0179824.

Ma Y, et al. (2024) The intrinsic macrolide resistome of *Escherichia coli*. *Antimicrobial agents and chemotherapy*, 68(8), e0045224.

Alobaidallah MSA, et al. (2024) Enhancing the Efficacy of Chloramphenicol Therapy for *Escherichia coli* by Targeting the Secondary Resistome. *Antibiotics (Basel, Switzerland)*, 13(1).

Wellner SM, et al. (2024) Genome-wide identification of fitness-genes in aminoglycoside-resistant *Escherichia coli* during antibiotic stress. *Scientific reports*, 14(1), 4163.

Fabian BK, et al. (2024) Identifying the suite of genes central to swimming in the biocontrol bacterium *Pseudomonas protegens* Pf-5. *Microbial genomics*, 10(3).

Yousief SW, et al. (2024) Optimizing phage-based mutant recovery and minimizing heat effect in the construction of transposon libraries in *Staphylococcus aureus*. *Scientific reports*, 14(1), 22831.

Mediati DG, et al. (2024) Genetic requirements for uropathogenic *E. coli* proliferation in the bladder cell infection cycle. *mSystems*, 9(10), e0038724.