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, transponson, 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: 20260912T195833+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 SPARC SAWG .

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.

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

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

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).

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

Rooke JL, et al. (2024) Genome-wide fitness analysis of Salmonella enterica reveals aroA mutants are attenuated due to iron restriction in vitro. mBio, 15(10), e0331923.