Resource Summary Report

Generated by NIF on Apr 26, 2025

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

Defining Citation: PMID:26794317, DOI:10.1093/bioinformatics/btw022

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

Funding: Wellcome Trust WT098051;
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Medical Research Council G1100100/1

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

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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 42 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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.

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).

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.

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.

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).

Gray J, et al. (2024) Transposon mutagenesis screen in Klebsiella pneumoniae identifies genetic determinants required for growth in human urine and serum. eLife, 12.

Wang M, et al. (2023) Uncovering the determinants of model Escherichia coli strain C600 susceptibility and resistance to lytic T4-like and T7-like phage. Virus research, 325, 199048.

Yee WX, et al. (2023) Evolution, persistence, and host adaption of a gonococcal AMR plasmid that emerged in the pre-antibiotic era. PLoS genetics, 19(5), e1010743.

Fong WY, et al. (2023) Genome-wide fitness analysis identifies genes required for in vitro growth and macrophage infection by African and global epidemic pathovariants of Salmonella enterica Enteritidis. Microbial genomics, 9(5).

Ba X, et al. (2023) High-Throughput Mutagenesis Reveals a Role for Antimicrobial Resistance- and Virulence-Associated Mobile Genetic Elements in Staphylococcus aureus Host Adaptation. Microbiology spectrum, 11(2), e0421322.

Yasir M, et al. (2022) Long-read sequencing for identification of insertion sites in large transposon mutant libraries. Scientific reports, 12(1), 3546.

Sullivan MJ, et al. (2022) Regulatory cross-talk supports resistance to Zn intoxication in Streptococcus. PLoS pathogens, 18(7), e1010607.

Smallman TR, et al. (2022) Genome-Wide Investigation of Pasteurella multocida Identifies the Stringent Response as a Negative Regulator of Hyaluronic Acid Capsule Production. Microbiology spectrum, 10(2), e0019522.

Rhodes KA, et al. (2022) Neisseria genes required for persistence identified via in vivo screening of a transposon mutant library. PLoS pathogens, 18(5), e1010497.

Yasir M, et al. (2022) Genome-Wide Analysis of Innate Susceptibility Mechanisms of Escherichia coli to Colistin. Antibiotics (Basel, Switzerland), 11(11).

Georgoulis SJ, et al. (2021) Genome-Wide Identification of Tomato Xylem Sap Fitness Factors for Three Plant-Pathogenic Ralstonia Species. mSystems, 6(6), e0122921.

García V, et al. (2021) Genome-wide analysis of fitness-factors in uropathogenic Escherichia coli during growth in laboratory media and during urinary tract infections. Microbial genomics, 7(12).