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

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

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

Funding Agency: Wellcome Trust, Alexander von Humboldt Stiftung/Foundation, Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: Bio-tradis

Resource ID: SCR_015993

Alternate IDs: OMICS_11083, biotools:bio-tradis
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 35 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


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

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.


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.

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


Larivière D, et al. (2021) Reproducible and accessible analysis of transposon insertion sequencing in Galaxy for qualitative essentiality analyses. BMC microbiology, 21(1), 168.


