Resource Summary Report

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breseq

RRID:SCR_010810

Type: Tool

Proper Citation

breseq (RRID:SCR_010810)

Resource Information

URL: https://code.google.com/p/breseq/

Proper Citation: breseq (RRID:SCR_010810)

Description: A computational pipeline for finding mutations relative to a reference sequence

in short-read DNA re-sequencing data intended for haploid microbial genomes.

Abbreviations: breseq

Synonyms: breseq - Determine mutations in evolved microbes from next-generation

sequencing data

Resource Type: software resource

Keywords: windows, genomics, sequencing, bio.tools

Availability: GNU General Public License, v2

Resource Name: breseq

Resource ID: SCR_010810

Alternate IDs: OMICS_00298, biotools:breseq

Alternate URLs:

https://barricklab.org/twiki/bin/view/Lab/ToolsBacterialGenomeResequencing,

https://bio.tools/breseq

Ratings and Alerts

No rating or validation information has been found for breseq.

No alerts have been found for breseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 265 mentions in open access literature.

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

Ghoshal M, et al. (2024) Transcriptomic analysis using RNA sequencing and phenotypic analysis of Salmonella enterica after acid exposure for different time durations using adaptive laboratory evolution. Frontiers in microbiology, 15, 1348063.

Rader TS, et al. (2024) The utility of whole-genome sequencing to inform epidemiologic investigations of SARS-CoV-2 clusters in acute-care hospitals. Infection control and hospital epidemiology, 45(2), 144.

Martinez Pastor M, et al. (2024) TroR is the primary regulator of the iron homeostasis transcription network in the halophilic archaeon Haloferax volcanii. Nucleic acids research, 52(1), 125.

Abdul-Mutakabbir JC, et al. (2024) Determining Susceptibility and Potential Mediators of Resistance for the Novel Polymyxin Derivative, SPR206, in Acinetobacter baumannii. Antibiotics (Basel, Switzerland), 13(1).

Watson BNJ, et al. (2024) CRISPR-Cas in Pseudomonas aeruginosa provides transient population-level immunity against high phage exposures. The ISME journal, 18(1).

Poret AJ, et al. (2024) De novo mutations mediate phenotypic switching in an opportunistic human lung pathogen. bioRxiv: the preprint server for biology.

Harris RA, et al. (2024) Complete genomes of Clostridium botulinum type B(F) isolates associated with a 1995 foodborne botulism outbreak from commercial pâté reveals a recombination event disrupting the ntnh gene. Microbial genomics, 10(1).

Foxall RL, et al. (2024) Inoviridae prophage and bacterial host dynamics during diversification, succession, and Atlantic invasion of Pacific-native Vibrio parahaemolyticus. mBio, 15(1), e0285123.

Lai H-Y, et al. (2024) Interaction with a phage gene underlie costs of a ?-lactamase. mBio, 15(2), e0277623.

Würstle S, et al. (2024) Optimized preparation pipeline for emergency phage therapy against Pseudomonas aeruginosa at Yale University. Scientific reports, 14(1), 2657.

Ghoshal M, et al. (2023) Adaptive laboratory evolution of Salmonella enterica in acid stress. Frontiers in microbiology, 14, 1285421.

Katz S, et al. (2023) Metabolic adaptation to consume butyrate under prolonged resource exhaustion. PLoS genetics, 19(6), e1010812.

Benz F, et al. (2023) Host-specific plasmid evolution explains the variable spread of clinical antibiotic-resistance plasmids. Proceedings of the National Academy of Sciences of the United States of America, 120(15), e2212147120.

Boyd CM, et al. (2023) A Vibrio cholerae viral satellite maximizes its spread and inhibits phage by remodeling hijacked phage coat proteins into small capsids. bioRxiv: the preprint server for biology.

Carrilero L, et al. (2023) Evolutionary Responses to Acquiring a Multidrug Resistance Plasmid Are Dominated by Metabolic Functions across Diverse Escherichia coli Lineages. mSystems, 8(1), e0071322.

Cutugno L, et al. (2023) The Vibrio vulnificus stressosome is dispensable in nutrient-rich media. Access microbiology, 5(7).

Sayin S, et al. (2023) Evolved bacterial resistance to the chemotherapy gemcitabine modulates its efficacy in co-cultured cancer cells. eLife, 12.

Vinchhi R, et al. (2023) Pervasive gene deregulation underlies adaptation and maladaptation in trimethoprim-resistant E. coli. mBio, 14(6), e0211923.

Toida K, et al. (2023) The GGDEF protein Dgc2 suppresses both motility and biofilm formation in the filamentous cyanobacterium Leptolyngbya boryana. Microbiology spectrum, 11(5), e0483722.

Hurley KE, et al. (2023) The contribution of DNA repair pathways to Staphylococcus aureus fitness and fidelity during nitric oxide stress. mBio, 14(6), e0215623.