Resource Summary Report

Generated by dkNET on Apr 26, 2025

breseq

RRID:SCR_010810 Type: Tool

Proper Citation

breseq (RRID:SCR_010810)

Resource Information

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

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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

Funding:

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

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014510+0000

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 333 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Lu Z, et al. (2025) Coevolution of marine phytoplankton and Alteromonas bacteria in response to pCO2 and coculture. The ISME journal, 19(1).

Wessel AJ, et al. (2025) DNA repair is essential for Vibrio cholerae growth on Thiosulfate-Citrate-Bile Salts-Sucrose (TCBS) Medium. bioRxiv : the preprint server for biology.

Wright G, et al. (2025) A microbial natural product fractionation library screen with HRMS/MS dereplication identifies new lipopeptaibiotics against Candida auris. Research square.

Longmire P, et al. (2025) Complex roles for proliferating cell nuclear antigen in restricting human cytomegalovirus replication. bioRxiv : the preprint server for biology.

Coll F, et al. (2025) The mutational landscape of Staphylococcus aureus during colonisation. Nature communications, 16(1), 302.

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.

Amoura A, et al. (2024) Variability in cell division among anatomical sites shapes Escherichia coli antibiotic survival in a urinary tract infection mouse model. Cell host & microbe, 32(6), 900.

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.

de Neeling AJ, et al. (2024) Characteristic SNPs defining the major multidrug-resistant Mycobacterium tuberculosis clusters identified by EuSeqMyTB to support routine surveillance, EU/EEA, 2017 to 2019. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 29(12).

Choe D, et al. (2024) Advancing the scale of synthetic biology via cross-species transfer of cellular functions enabled by iModulon engraftment. Nature communications, 15(1), 2356.

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.

Boyd CM, et al. (2024) A phage satellite manipulates the viral DNA packaging motor to inhibit phage and promote satellite spread. Nucleic acids research, 52(17), 10431.

Bartlett TM, et al. (2024) FacZ is a GpsB-interacting protein that prevents aberrant divisionsite placement in Staphylococcus aureus. Nature microbiology, 9(3), 801.

Rachwalski K, et al. (2024) A screen for cell envelope stress uncovers an inhibitor of prolipoprotein diacylglyceryl transferase, Lgt, in Escherichia coli. iScience, 27(10), 110894.

Sun C, et al. (2024) A panel of genotypically and phenotypically diverse clinical Acinetobacter baumannii strains for novel antibiotic development. Microbiology spectrum, 12(8), e0008624.

Harris RA, et al. (2024) Prevalence of Clostridium botulinum in Retail Peanut Butters from a 2007 Survey in Ottawa, Canada. Current microbiology, 81(10), 322.

Sulaiman JE, et al. (2024) Human gut microbiota interactions shape the long-term growth dynamics and evolutionary adaptations of Clostridioides difficile. bioRxiv : the preprint server for biology.

Hall RJ, et al. (2024) Multidrug resistance plasmids commonly reprogram the expression of metabolic genes in Escherichia coli. mSystems, 9(3), e0119323.

Ulrich NJ, et al. (2024) Integration of horizontally acquired light-harvesting genes into an ancestral regulatory network in the cyanobacterium Acaryochloris marina MBIC11017. mBio, 15(12), e0242324.

Ugalde Silva P, et al. (2024) Evolutionary trajectories of ?-lactam resistance in Enterococcus faecalis strains. mBio, 15(12), e0289724.