

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

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 [FDI Lab - SciCrunch.org](#).

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 European 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 division-site 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 diacylglycerol 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 β -lactam resistance in *Enterococcus faecalis* strains. *mBio*, 15(12), e0289724.