

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

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: 20260725T190707+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 424 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Mazny BE, et al. (2026) Evolved formate assimilation in phototrophic *Rhodopseudomonas palustris* indicates the need for a CO₂-concentrating mechanism. *Current biology : CB*, 36(1), 110.

Jain R, et al. (2025) Fatty acid metabolism and the oxidative stress response support bacterial predation. *Proceedings of the National Academy of Sciences of the United States of America*, 122(5), e2420875122.

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*.

Cao L, et al. (2025) Quorum sensing inhibits phage infection by regulating biofilm formation of *P. aeruginosa* PAO1. *Journal of virology*, 99(2), e0187224.

Widney KA, et al. (2025) Mutations Elevate an Underground Pathway to a Physiologically Relevant Protopathway. *Molecular biology and evolution*, 42(8).

Wessel AJ, et al. (2025) DNA repair is essential for *Vibrio cholerae* growth on thiosulfate-citrate-bile salts-sucrose (TCBS) medium. *Journal of bacteriology*, 207(4), e0000425.

Rosenberg M, et al. (2025) Experimental evolution of *Escherichia coli* on semi-dry silver, copper, stainless steel, and glass surfaces. *Microbiology spectrum*, 13(4), e0217324.

Wright G, et al. (2025) A Natural Depsipeptide Antibiotic that Targets the E site of the Bacterial Ribosome. *Research square*.

Rokes AB, et al. (2025) History shapes regulatory and evolutionary responses to tigecycline in two reference strains of *Acinetobacter baumannii*. *Microbiology (Reading, England)*, 171(6).

Bubnov DM, et al. (2025) Multiple routes for non-physiological l-threonine uptake in *Escherichia coli* K-12. *Frontiers in microbiology*, 16, 1579813.

Sane M, et al. (2025) Mutation bias alters the distribution of fitness effects of mutations. *PLoS biology*, 23(7), e3003282.

Royer G, et al. (2025) Antibiotics and phages drive region-specific diversity of OmpK36 in *Klebsiella pneumoniae*. *mBio*, 16(9), e0134325.

Shook JC, et al. (2025) Diabetes potentiates the emergence and expansion of antibiotic resistance. *Science advances*, 11(7), eads1591.

Chadwick GL, et al. (2025) Methanogenesis marker 16 metalloprotein is the primary coenzyme M synthase in *Methanosarcina acetivorans*. *PLoS genetics*, 21(5), e1011695.

Xu Z, et al. (2025) Engineering broad-spectrum phage-resistant *Escherichia coli* via adaptive and programmable defense strategies. *Applied and environmental microbiology*, 91(11), e0159625.

Delaby M, et al. (2025) Phenotypic plasticity in cell elongation among closely related bacterial species. *Nature communications*, 16(1), 5099.

Fung BL, et al. (2025) A single point mutation is sufficient to drive syp-dependent biofilm formation and promote colonization by *Vibrio fischeri*. *Journal of bacteriology*, 207(8), e0013125.

de Zwaan R, et al. (2025) Verification of emerging genomic mutations in *Mycobacterium tuberculosis* allows transmission chains to be distinguished in an epidemiological typing cluster extending over thirty years. *PloS one*, 20(6), e0319630.

McCausland JW, et al. (2025) Bacterial and host enzymes modulate the pro-inflammatory response elicited by the peptidoglycan of Lyme disease agent *Borrelia burgdorferi*. *PLoS pathogens*, 21(7), e1013324.

Gencel M, et al. (2025) Quantifying the intra- and inter-species community interactions in microbiomes by dynamic covariance mapping. *Nature communications*, 16(1), 6314.