Resource Summary Report

Generated by NIF on May 21, 2025

Fitness Browser

RRID:SCR_018981
Type: Tool

Proper Citation

Fitness Browser (RRID:SCR_018981)

Resource Information

URL: http://fit.genomics.lbl.gov/cgi-bin/myFrontPage.cgi

Proper Citation: Fitness Browser (RRID:SCR_018981)

Description: Web tool for browsing genome wide fitness experiments for diverse bacteria from Deutschbauer lab, the Arkin lab, and collaborators. Collection of mutant phenotypes for bacterial genes of unknown function.

Resource Type: data or information resource, data access protocol, web service, software resource

Defining Citation: PMID:29769716

Keywords: Genome browser, bacteria, mutant phenotype, bacterial genes, unknown function, data

Funding: NCRR S10 RR029668;
NCRR S10 RR027303;
NIH Office of the Director OD018174;
Office of Science of the US Department of Energy

Availability: Free, Freely available

Resource Name: Fitness Browser

Resource ID: SCR_018981

Record Creation Time: 20220129T080342+0000

Record Last Update: 20250521T061801+0000

Ratings and Alerts

No rating or validation information has been found for Fitness Browser.

No alerts have been found for Fitness Browser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Bouillet S, et al. (2024) A negative feedback loop is critical for recovery of RpoS after stress in Escherichia coli. PLoS genetics, 20(3), e1011059.

Borchert AJ, et al. (2024) Machine learning analysis of RB-TnSeq fitness data predicts functional gene modules in Pseudomonas putida KT2440. mSystems, 9(3), e0094223.

Villalobos-Escobedo JM, et al. (2023) Genome-wide fitness profiling reveals molecular mechanisms that bacteria use to interact with Trichoderma atroviride exometabolites. PLoS genetics, 19(8), e1010909.

Denise R, et al. (2023) Pyridoxal 5'-phosphate synthesis and salvage in Bacteria and Archaea: predicting pathway variant distributions and holes. Microbial genomics, 9(2).

Bouillet S, et al. (2023) A negative feedback loop is critical for recovery of RpoS after stress in Escherichia coli. bioRxiv : the preprint server for biology.

Suban S, et al. (2022) Impairment of a cyanobacterial glycosyltransferase that modifies a pilin results in biofilm development. Environmental microbiology reports, 14(2), 218.

Prahlad J, et al. (2020) The DUF328 family member YaaA is a DNA-binding protein with a novel fold. The Journal of biological chemistry, 295(41), 14236.