

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

## Fitness Browser

RRID:SCR\_018981

Type: Tool

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### Proper Citation

Fitness Browser (RRID:SCR\_018981)

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### 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 access protocol, data or information resource, 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:** 20260803T040803+0000

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### Ratings and Alerts

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

No alerts have been found for Fitness Browser.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [ASWG](#).

Pearson AN, et al. (2025) RB-TnSeq elucidates dicarboxylic-acid-specific catabolism in ??-proteobacteria for improved plastic monomer upcycling. *Applied and environmental microbiology*, 91(10), e0092425.

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.

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*.

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).

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.

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.