

# Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

## EchoBASE

RRID:SCR\_002430

Type: Tool

### Proper Citation

EchoBASE (RRID:SCR\_002430)

### Resource Information

**URL:** <http://www.ecoli-york.org/>

**Proper Citation:** EchoBASE (RRID:SCR\_002430)

**Description:** A database that curates new experimental and bioinformatic information about the genes and gene products of the model bacterium *Escherichia coli* K-12 strain MG1655. It has been created to integrate information from post-genomic experiments into a single resource with the aim of providing functional predictions for the 1500 or so gene products for which we have no knowledge of their physiological function. While EchoBASE provides a basic annotation of the genome, taken from other databases, its novelty is in the curation of post-genomic experiments and their linkage to genes of unknown function. Experiments published on *E. coli* are curated to one of two levels. Papers dealing with the determination of function of a single gene are briefly described, while larger dataset are actually included in the database and can be searched and manipulated. This includes data for proteomics studies, protein-protein interaction studies, microarray data, functional genomic approaches (looking at multiple deletion strains for novel phenotypes) and a wide range of predictions that come out of in silico bioinformatic approaches. The aim of the database is to provide hypothesis for the functions of uncharacterized gene products that may be used by the *E. coli* research community to further our knowledge of this model bacterium.

**Abbreviations:** EchoBASE

**Synonyms:** EchoBASE: an integrated post-genomic database for *Escherichia coli*

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:15608209](#)

**Keywords:** gene, bio.tools

**Funding:** GlaxoSmithKline ;  
BBSRC

**Resource Name:** EchoBASE

**Resource ID:** SCR\_002430

**Alternate IDs:** nif-0000-02781, biotools:echobase, r3d100011646

**Alternate URLs:** <https://bio.tools/echobase>, <https://doi.org/10.17616/R38W6H>

**Record Creation Time:** 20220129T080213+0000

**Record Last Update:** 20260912T200125+0000

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## Ratings and Alerts

No rating or validation information has been found for EchoBASE.

No alerts have been found for EchoBASE.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Badaczewska-Dawid AE, et al. (2024) A3D Model Organism Database (A3D-MODB): a database for proteome aggregation predictions in model organisms. Nucleic acids research, 52(D1), D360.

Amin SA, et al. (2019) Towards creating an extended metabolic model (EMM) for E. coli using enzyme promiscuity prediction and metabolomics data. Microbial cell factories, 18(1), 109.

Eydallin G, et al. (2010) Genome-wide screening of genes whose enhanced expression affects glycogen accumulation in Escherichia coli. DNA research : an international journal for rapid publication of reports on genes and genomes, 17(2), 61.

Eydallin G, et al. (2007) Genome-wide screening of genes affecting glycogen metabolism in Escherichia coli K-12. FEBS letters, 581(16), 2947.

Riley M, et al. (2006) Escherichia coli K-12: a cooperatively developed annotation snapshot--2005. Nucleic acids research, 34(1), 1.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.