

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

GenoBase

RRID:SCR_007682

Type: Tool

Proper Citation

GenoBase (RRID:SCR_007682)

Resource Information

URL: <http://ecoli.naist.jp/GB8/>

Proper Citation: GenoBase (RRID:SCR_007682)

Description: A database of high-throughput data being collected to understand comprehensively the living E. coli K-12 model cell. GenoBase is a public repository for sequence information, proteome, transcription, and metabolome data. The GenoBase contains columns labeled Gene, Synonym, ECK, Genome, ID, Left, Right, Direction, Description, Comment, and Status. The table displays two rows for each gene: one row shows data for the E. coli K-12 MG1655 genome; the other shows data for the E. coli K-12 W3110 genome. Left, Right, and direction give the coordinates and orientation of the gene. Search/Clip allows the user to find information in GenoBase based on gene, position, or DNA sequence. References is currently not fully operational. Other search allows execution of an SQL query., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: GenoBase

Resource Type: database, data or information resource

Keywords: e. coli, e coli k-12 model cell, escheria coli, k-12, metabolome, proteome, transcription, model

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GenoBase

Resource ID: SCR_007682

Alternate IDs: nif-0000-02894

Old URLs: <http://sal.cs.purdue.edu:8097/GB7/index.jsp>

Record Creation Time: 20220129T080243+0000

Ratings and Alerts

No rating or validation information has been found for GenoBase.

No alerts have been found for GenoBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Parada CM, et al. (2025) Growth-dependent concentration gradient of the oscillating Min system in Escherichia coli. The Journal of cell biology, 224(2).

Collins J, et al. (2024) Sequence-function mapping of proline-rich antimicrobial peptides. bioRxiv : the preprint server for biology.

Muta M, et al. (2020) Nascent SecM chain interacts with outer ribosomal surface to stabilize translation arrest. The Biochemical journal, 477(2), 557.

Niwa T, et al. (2015) Comprehensive study of liposome-assisted synthesis of membrane proteins using a reconstituted cell-free translation system. Scientific reports, 5, 18025.

Murakami Y, et al. (2015) Global coordination in adaptation to gene rewiring. Nucleic acids research, 43(2), 1304.

Niwa T, et al. (2015) Large-scale analysis of macromolecular crowding effects on protein aggregation using a reconstituted cell-free translation system. Frontiers in microbiology, 6, 1113.

Ying BW, et al. (2015) Bacterial transcriptome reorganization in thermal adaptive evolution. BMC genomics, 16, 802.

Takeuchi R, et al. (2014) Colony-live--a high-throughput method for measuring microbial colony growth kinetics--reveals diverse growth effects of gene knockouts in Escherichia coli. BMC microbiology, 14, 171.