

Resource Summary Report

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EcoCyc

RRID:SCR_002433

Type: Tool

Proper Citation

EcoCyc (RRID:SCR_002433)

Resource Information

URL: <http://ecocyc.org/>

Proper Citation: EcoCyc (RRID:SCR_002433)

Description: Database for the bacterium Escherichia coli K-12 MG1655, the EcoCyc project performs literature-based curation of the entire genome, and of transcriptional regulation, transporters, and metabolic pathways. The long-term goal of the project is to describe the molecular catalog of the E. coli cell, as well as the functions of each of its molecular parts, to facilitate a system-level understanding of E. coli. EcoCyc is an electronic reference source for E. coli biologists, and for biologists who work with related microorganisms.

Abbreviations: EcoCyc, EcoCyc REF

Synonyms: EcoCyc REF

Resource Type: data or information resource, database

Defining Citation: [PMID:23143106](#), [PMID:21097882](#)

Keywords: genome, metabolic pathway, transcription, transporters, escherichia coli, transcriptional regulation, metabolism, pathway, FASEB list

Funding: NCRR ;
NIGMS GM077678;
NIGMS GM71962

Availability: Free, Freely available

Resource Name: EcoCyc

Resource ID: SCR_002433

Alternate IDs: OMICS_01645, nif-0000-02783, r3d100011277

Alternate URLs: <https://doi.org/10.17616/R34K99>

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260804T043150+0000

Ratings and Alerts

No rating or validation information has been found for EcoCyc.

No alerts have been found for EcoCyc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 482 mentions in open access literature.

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

Yadav D, et al. (2026) Chaperone dependency during biogenesis does not correlate with chaperone dependency during refolding. *Molecular systems biology*, 22(1), 139.

Chawla M, et al. (2025) (p)ppGpp and DksA play a crucial role in reducing the efficacy of β -lactam antibiotics by modulating bacterial membrane permeability. *Microbiology spectrum*, 13(4), e0116924.

Hasenauer FC, et al. (2025) Genome-wide mapping of spontaneous DNA replication error-hotspots using mismatch repair proteins in rapidly proliferating *Escherichia coli*. *Nucleic acids research*, 53(2).

Boada Y, et al. (2025) Synthetic biology design principles enable efficient bioproduction of Heparosan with low molecular weight and low polydispersion index for the biomedical industry. *Synthetic biology (Oxford, England)*, 10(1), ysaf006.

Murashko ON, et al. (2025) Comprehensive analysis of repetitive extragenic palindrome sequences identified in bacteria and archaea using a new web-based tool, RepRanger. *mSphere*, 10(7), e0012425.

Lindback MM, et al. (2025) Virocell resource manipulation under nutrient limitation. *mSystems*, 10(7), e0052125.

Cuesta-Morrondo S, et al. (2025) Unraveling the genomic complexity of secretion systems in the most virulent *Xanthomonas arboricola* pathovars. *PloS one*, 20(9), e0332834.

Bush NG, et al. (2025) Insights into antibiotic resistance promoted by quinolone exposure. *Antimicrobial agents and chemotherapy*, 69(1), e0099724.

Zhou X, et al. (2025) A phylogeny-based method in detecting the species-specialized genes in microbes and its application to a marine symbiont bacterium. *mBio*, 16(12), e0356624.

Luo X, et al. (2025) RNA-RNA Interactome Approaches Provide in vivo Evidence for a Critical Role of the Hfq Rim Face in sRNA-mRNA Pairing. *bioRxiv : the preprint server for biology*.

Carrera-Reyna M, et al. (2025) Analysis and comparison of the bacterial σ^{54} regulon: Evidence of phylogenetic trends in gene regulation. *PloS one*, 20(8), e0327805.

Yu J, et al. (2025) In Vivo Ribosome-Amplified MetaBOLism, RAMBO, Effect Observed by Real Time Pulse Chase, RTPC, NMR Spectroscopy. *Biochemistry*, 64(12), 2660.

Wu DG, et al. (2025) Comparative metagenomics of tropical reef fishes show conserved core gut functions across hosts and diets with diet-related functional gene enrichments. *Applied and environmental microbiology*, 91(2), e0222924.

Hamm CW, et al. (2025) Inorganic polyphosphate and the stringent response coordinately control cell division and cell morphology in *Escherichia coli*. *mBio*, 16(2), e0351124.

Bryant JC, et al. (2025) The DigH glycosyl hydrolase is conditionally required for daughter cell separation in *Escherichia coli*. *Journal of bacteriology*, 207(7), e0006825.

Sidor LM, et al. (2025) Tunable light-focusing behavior of engineered bacterial microlenses with controllable shapes. *bioRxiv : the preprint server for biology*.

Hernandez-Benitez EM, et al. (2025) Computational inference of *Rhizobium phaseoli* transcriptional regulatory network predicts Transcription Factors involved in nodulation. *Briefings in functional genomics*, 24.

Lee J, et al. (2025) Efflux pump knockout minimizes crosstalk and boosts response in transcription factor-based biosensors. *Journal of biological engineering*, 19(1), 101.

Daruka L, et al. (2025) ESKAPE pathogens rapidly develop resistance against antibiotics in development in vitro. *Nature microbiology*, 10(2), 313.

Röschinger T, et al. (2025) The Environment-Dependent Regulatory Landscape of the *E. coli* Genome. *ArXiv*.