

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/>

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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: 20260821T193643+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 511 mentions in open access literature.

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

Elhai J, et al. (2026) Genomes of N₂-fixing endosymbionts of unicellular eukaryotes and host-independence. *BMC genomics*, 27(1), 189.

Han H, et al. (2026) Systematic Metabolic Engineering and Model-Guided Optimization for High-Level Production of L-Theanine from Xylose in *Escherichia coli*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(17), e21440.

Champie A, et al. (2026) Comparative analysis of gene importance in *Escherichia coli* across growth conditions. *mSystems*, 11(5), e0142525.

Pick K, et al. (2026) Transcriptomic profiling of a commensal *Escherichia coli* lysogen in simulated intestinal fluid reveals broad changes in both core and accessory regions of the genome. *BMC genomics*, 27(1), 223.

Gawel D, et al. (2026) Abrogation of SOS mutagenesis by the *E. coli* OxyR oxidative stress response. *mSystems*, 11(4), e0000326.

Royer G, et al. (2026) Identification of specific metabolic capacities associated with major extraintestinal pathogenic *Escherichia coli* lineages. *Journal of bacteriology*, 208(3), e0042125.

Zhang T, et al. (2026) ZmTH1 Is Vital for Healthy Plant Growth and Promotes Cold/Drought Tolerance by Regulating Thiamin Diphosphate-Dependent Metabolisms in Maize. *Plant biotechnology journal*, 24(3), 1234.

Mackrell EJ, et al. (2026) Global analysis of protein degradation reveals instability of diverse regulators in *Escherichia coli*. *Proceedings of the National Academy of Sciences of the United States of America*, 123(10), e2515265123.

- Kamei KF, et al. (2026) Revealing global stoichiometry conservation architecture in cells from Raman spectral patterns. *eLife*, 14.
- Afinanisa Q, et al. (2026) Microbial Primer: Bacterial energy metabolism. *Microbiology* (Reading, England), 172(4).
- Kalapis D, et al. (2026) Gene loss and compensatory evolution as a source of metabolic preadaptations. *Molecular biology and evolution*, 43(6).
- Dehner CA, et al. (2026) Human body temperature cues widespread changes in virulence gene expression in uropathogenic *Escherichia coli*. *Infection and immunity*, 94(2), e0042225.
- Yadav D, et al. (2026) Chaperone dependency during biogenesis does not correlate with chaperone dependency during refolding. *Molecular systems biology*, 22(1), 139.
- Stone CJ, et al. (2026) Bayesian analysis of longitudinal RB-TnSeq resolves the fitness seascape in fluctuating environments. *bioRxiv : the preprint server for biology*.
- Tawfiq R, et al. (2026) Evaluating completeness, coherence, and consistency of genome-scale function annotations. *Briefings in bioinformatics*, 27(3).
- 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).
- 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.
- Trofimova E, et al. (2025) Improved in silico and in vitro methods for *Escherichia coli* LPS outer core typing. *Microbial genomics*, 11(9).
- 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.
- Lu J, et al. (2025) Rhomboid protease GlpG regulates type 1 pili quality control and virulence in pathogenic *E. coli*. *Nature communications*.