

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

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: 20260904T000057+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 [kravitz2](#).

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*.