Resource Summary Report

Generated by dkNET on May 21, 2025

EcoGene

RRID:SCR_002437
Type: Tool

Proper Citation

EcoGene (RRID:SCR_002437)

Resource Information

URL: http://ecogene.org/

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Description: Database that contains updated information about the Escherichia coli K-12 genome and proteome sequences, including extensive gene bibliographies. Users are able to download customized tables, perform Boolean query comparisons, generate sets of paired DNA sequences, and download any E. coli K-12 genomic DNA sub-sequence. BLAST functions, microarray data, an alphabetical index of genes, and gene overlap queries are also available. The Database Table Downloads Page provides a full list of EG numbers cross-referenced to the new cross-database ECK numbers and other common accession numbers, as well as gene names and synonyms. Monthly release archival downloads are available, but the live, daily updated version of EcoGene is the default mysql database for download queries.

Abbreviations: ECK, ECOGENE, ECOGENE G

Synonyms: EcoGene Database of Escherichia coli Sequence and Function

Resource Type: data or information resource, database

Defining Citation: PMID:23197660, PMID:10592181

Keywords: life sciences, genomics, proteomics, gene, gene expression, genetics, protein, protein binding, protein-protein interaction, membrane, rna, dna, structure, function, functional annotation, annotation, blast, FASEB list

Funding: NIH ;
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NIGMS 5-R01-GM58560-05

Availability: Acknowledgement requested, Open source

Resource Name: EcoGene

Resource ID: SCR_002437

Alternate IDs: nif-0000-02784

Old URLs: http://bmb.med.miami.edu/ http://bmb.med.miami.edu/EcoGene/EcoWeb/ http://www.ecogene.org/old/

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250521T060842+0000

Ratings and Alerts

No rating or validation information has been found for EcoGene.

No alerts have been found for EcoGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 56 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

A Ghomi F, et al. (2024) High-throughput transposon mutagenesis in the family Enterobacteriaceae reveals core essential genes and rapid turnover of essentiality. mBio, 15(10), e0179824.

Yao Y, et al. (2023) A DnaA-dependent riboswitch for transcription attenuation of the his operon. mLife, 2(2), 126.

Nagao A, et al. (2023) Quality control of protein synthesis in the early elongation stage. Nature communications, 14(1), 2704.

Pollo-Oliveira L, et al. (2022) The absence of the queuosine tRNA modification leads to

pleiotropic phenotypes revealing perturbations of metal and oxidative stress homeostasis in Escherichia coli K12. Metallomics : integrated biometal science, 14(9).

DeBenedictis EA, et al. (2022) Measuring the tolerance of the genetic code to altered codon size. eLife, 11.

Gant Kanegusuku A, et al. (2021) A Shift to Human Body Temperature (37°C) Rapidly Reprograms Multiple Adaptive Responses in Escherichia coli That Would Facilitate Niche Survival and Colonization. Journal of bacteriology, 203(22), e0036321.

Orench-Rivera N, et al. (2021) Differential Packaging Into Outer Membrane Vesicles Upon Oxidative Stress Reveals a General Mechanism for Cargo Selectivity. Frontiers in microbiology, 12, 561863.

Stenum TS, et al. (2021) Three Ribosomal Operons of Escherichia coli Contain Genes Encoding Small RNAs That Interact With Hfq and CsrA in vitro. Frontiers in microbiology, 12, 625585.

Yahashiri A, et al. (2020) DrpB (YedR) Is a Nonessential Cell Division Protein in Escherichia coli. Journal of bacteriology, 202(23).

Heo J, et al. (2020) Genome-wide high-throughput screening of interactive bacterial metabolite in the algal population using Escherichia coli K-12 Keio collection. Scientific reports, 10(1), 10647.

Acar Kirit H, et al. (2020) Experimental determination of evolutionary barriers to horizontal gene transfer. BMC microbiology, 20(1), 326.

Ahmad M, et al. (2020) Real-time monitoring of glutathione in living cells using genetically encoded FRET-based ratiometric nanosensor. Scientific reports, 10(1), 992.

Hsiao FS, et al. (2019) Protein interactome analysis of iduronic acid-containing glycosaminoglycans reveals a novel flagellar invasion factor MbhA. Journal of proteomics, 208, 103485.

Brameyer S, et al. (2019) DNA-binding directs the localization of a membrane-integrated receptor of the ToxR family. Communications biology, 2, 4.

Carija A, et al. (2019) Computational Assessment of Bacterial Protein Structures Indicates a Selection Against Aggregation. Cells, 8(8).

Mao Z, et al. (2019) iMTBGO: An Algorithm for Integrating Metabolic Networks with Transcriptomes Based on Gene Ontology Analysis. Current genomics, 20(4), 252.

Kintses B, et al. (2019) Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. Nature communications, 10(1), 5731.

Ghatak S, et al. (2019) The y-ome defines the 35% of Escherichia coli genes that lack experimental evidence of function. Nucleic acids research, 47(5), 2446.

Hou Q, et al. (2018) Computational analysis of the amino acid interactions that promote or decrease protein solubility. Scientific reports, 8(1), 14661.

Tello M, et al. (2018) Codon usage and modular interactions between messenger RNA coding regions and small RNAs in Escherichia coli. BMC genomics, 19(1), 657.