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 Agency: NIH, Lucille P. Markey Foundation, NIGMS
Availability: Acknowledgement requested, Open source

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Resource ID: SCR_002437

Alternate IDs: nif-0000-02784


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 53 mentions in open access literature.

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


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.


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


