

Resource Summary Report

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Database of prOkaryotic OpeRons

RRID:SCR_007593

Type: Tool

Proper Citation

Database of prOkaryotic OpeRons (RRID:SCR_007593)

Resource Information

URL: <http://csbl1.bmb.uga.edu/OperonDB/>

Proper Citation: Database of prOkaryotic OpeRons (RRID:SCR_007593)

Description: DOOR (Database of prOkaryotic OpeRons) is an operon database. The operons in the database are based on prediction. The database provides an organism view, gene search, operon search, and operon prediction tools. Currently DOOR has operons for 675 prokaryotic genomes.

Synonyms: DOOR

Resource Type: data or information resource, database

Keywords: operon, operon prediction, prokaryote, prokaryotic genome

Resource Name: Database of prOkaryotic OpeRons

Resource ID: SCR_007593

Alternate IDs: nif-0000-02762

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260729T044151+0000

Ratings and Alerts

No rating or validation information has been found for Database of prOkaryotic OpeRons.

No alerts have been found for Database of prOkaryotic OpeRons.

Data and Source Information

Usage and Citation Metrics

We found 64 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Banerjee R, et al. (2025) Study protocol for a multicenter, multinational prospective randomized controlled trial comparing outcomes in subjects with Gram-negative bacteremia who have blood culture evaluation using Fast Antibiotic Susceptibility Testing vs. standard of care testing: the FAST trial. *Trials*, 26(1), 500.

VanBuren JM, et al. (2025) Evaluating the desirability of outcome ranking and response adjusted for duration of antibiotic risk for clinical trials of antibiotics in pediatric pneumonia. *American journal of epidemiology*, 194(4), 1090.

Johns BP, et al. (2025) Comparison of surgical treatments for hip and knee periprosthetic joint infections using the desirability of outcome ranking in a prospective multicentre study. *Journal of bone and joint infection*, 10(2), 73.

Yogendrakumar V, et al. (2024) Evaluating the Safety and Efficacy of Telemedicine Physician Assessments on a Mobile Stroke Unit: Protocol for a Prospective Open-Label Blinded End-Point Randomized Controlled Trial. *Journal of the American Heart Association*, 13(21), e036856.

Vivash L, et al. (2023) The adaptation of the desirability of outcome ranking for interventional clinical trials in epilepsy: A novel consumer-led outcome measure. *Epilepsia open*, 8(4), 1608.

Lee AJ, et al. (2023) Compendium-Wide Analysis of *Pseudomonas aeruginosa* Core and Accessory Genes Reveals Transcriptional Patterns across Strains PAO1 and PA14. *mSystems*, 8(1), e0034222.

Gao Y, et al. (2023) The *Escherichia coli* Fur pan-regulon has few conserved but many unique regulatory targets. *Nucleic acids research*, 51(8), 3618.

Gupta N, et al. (2022) A comprehensive approach to discover Toxin-Antitoxin systems from human pathogen *Helicobacter pylori*: A poison and its antidote encapsulated in the genome. *Life sciences*, 288, 120149.

Merchante N, et al. (2022) Early Use of Sarilumab in Patients Hospitalized with COVID-19 Pneumonia and Features of Systemic Inflammation: the SARICOR Randomized Clinical Trial. *Antimicrobial agents and chemotherapy*, 66(2), e0210721.

Howard-Anderson JR, et al. (2022) Poor outcomes in both infection and colonization with carbapenem-resistant Enterobacterales. *Infection control and hospital epidemiology*, 43(12), 1840.

Tagini F, et al. (2021) Pathogenic Determinants of the *Mycobacterium kansasii* Complex: An Unsuspected Role for Distributive Conjugal Transfer. *Microorganisms*, 9(2).

Poudel S, et al. (2021) Identification and characterization of proteins of unknown function (PUFs) in *Clostridium thermocellum* DSM 1313 strains as potential genetic engineering targets. *Biotechnology for biofuels*, 14(1), 116.

Barlow A, et al. (2021) Using an Ordinal Approach to Compare Outcomes Between Vancomycin Versus Ceftaroline or Daptomycin in MRSA Bloodstream Infection. *Infectious diseases and therapy*, 10(1), 605.

Brenner T, et al. (2021) Optimization of sepsis therapy based on patient-specific digital precision diagnostics using next generation sequencing (DigiSep-Trial)-study protocol for a randomized, controlled, interventional, open-label, multicenter trial. *Trials*, 22(1), 714.

Liu T, et al. (2021) Position preference of essential genes in prokaryotic operons. *PloS one*, 16(4), e0250380.

Luo X, et al. (2020) High-Throughput Screen for Cell Wall Synthesis Network Module in *Mycobacterium tuberculosis* Based on Integrated Bioinformatics Strategy. *Frontiers in bioengineering and biotechnology*, 8, 607.

Pawliszak T, et al. (2020) Operon-based approach for the inference of rRNA and tRNA evolutionary histories in bacteria. *BMC genomics*, 21(Suppl 2), 252.

Daroz BB, et al. (2020) In Silico Structural and Functional Characterization of HtrA Proteins of *Leptospira* spp.: Possible Implications in Pathogenesis. *Tropical medicine and infectious disease*, 5(4).

Bathke J, et al. (2020) iCLIP analysis of RNA substrates of the archaeal exosome. *BMC genomics*, 21(1), 797.

Ara KZG, et al. (2020) Characterization and diversity of the complete set of GH family 3 enzymes from *Rhodothermus marinus* DSM 4253. *Scientific reports*, 10(1), 1329.