Resource Summary Report

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Pseudomonas Genome Database

RRID:SCR_006590
Type: Tool

Proper Citation

Pseudomonas Genome Database (RRID:SCR_006590)

Resource Information

URL: http://www.pseudomonas.com/

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Description: Database of peer-reviewed, continually updated annotation for the Pseudomonas aeruginosa PAO1 reference strain genome expanded to include all Pseudomonas species to facilitate cross-strain and cross-species genome comparisons with high quality comparative genomics. The database contains robust assessment of orthologs, a novel ortholog clustering method, and incorporates five views of the data at the sequence and annotation levels (Gbrowse, Mauve and custom views) to facilitate genome comparisons. Other features include more accurate protein subcellular localization predictions and a user-friendly, Boolean searchable log file of updates for the reference strain PAO1. The current annotation is updated using recent research literature and peer-reviewed submissions by a worldwide community of PseudoCAP (Pseudomonas aeruginosa Community Annotation Project) participating researchers. If you are interested in participating, you are invited to get involved. Many annotations, DNA sequences, Orthologs, Intergenic DNA, and Protein sequences are available for download.

Abbreviations: PseudoCAP

Synonyms: Pseudomonas Genome Database - Improving Disease Treatment Through Genome Research

Resource Type: service resource, data analysis service, data or information resource, database, production service resource, analysis service resource

Defining Citation: PMID:18978025

Keywords: gene, genome, annotation, localization, prokaryote, pseudomonas aeruginosa, sequence, subcellular, cystic fibrosis, ortholog, annotation, dna sequence, intergenic dna, protein sequence, bio.tools, FASEB list

Funding: Cystic Fibrosis Foundation Therapeutics Inc

Resource Name: Pseudomonas Genome Database

Resource ID: SCR_006590

Alternate IDs: nif-0000-03369, biotools:pseudomonas_genome_database

Alternate URLs: https://bio.tools/pseudomonas_genome_database

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250426T055859+0000

Ratings and Alerts

No rating or validation information has been found for Pseudomonas Genome Database.

No alerts have been found for Pseudomonas Genome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 448 mentions in open access literature.

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

Meyer AC, et al. (2025) Proteomic profiling of zinc homeostasis mechanisms in Pseudomonas aeruginosa through data-dependent and data-independent acquisition mass spectrometry. bioRxiv : the preprint server for biology.

Yang Y, et al. (2025) High level non-carbapenemase carbapenem resistance by overlaying mutations of mexR, oprD, and ftsI in Pseudomonas aeruginosa. Microbiology spectrum, 13(1), e0139824.

Choe D, et al. (2024) Advancing the scale of synthetic biology via cross-species transfer of cellular functions enabled by iModulon engraftment. Nature communications, 15(1), 2356.

Lee CY, et al. (2024) Investigating the biosynthesis and roles of the auxin phenylacetic acid during Pseudomonas syringae-Arabidopsis thaliana pathogenesis. Frontiers in plant science, 15, 1408833.

Zhou Y, et al. (2024) Recombinase-aided amplification assay for rapid detection of imipenem-resistant Pseudomonas aeruginosa and rifampin-resistant Pseudomonas aeruginosa. Frontiers in cellular and infection microbiology, 14, 1428827.

Köbbing S, et al. (2024) Reliable Genomic Integration Sites in Pseudomonas putida Identified by Two-Dimensional Transcriptome Analysis. ACS synthetic biology, 13(7), 2060.

Kok LC, et al. (2024) Roles of transcriptional factor PsrA in the regulation of quorum sensing in Pseudomonas aeruginosa PAO1. Frontiers in microbiology, 15, 1424330.

Leinweber A, et al. (2024) RNA-Seq reveals that Pseudomonas aeruginosa mounts growth medium-dependent competitive responses when sensing diffusible cues from Burkholderia cenocepacia. Communications biology, 7(1), 995.

Sanchez CA, et al. (2024) Highly Effective Biocides against Pseudomonas aeruginosa Reveal New Mechanistic Insights Across Gram-Negative Bacteria. ACS infectious diseases, 10(11), 3868.

Mulet M, et al. (2024) Genome-Based Taxonomy of Species in the Pseudomonas syringae and Pseudomonas lutea Phylogenetic Groups and Proposal of Pseudomonas maioricensis sp. nov., Isolated from Agricultural Soil. Microorganisms, 12(3).

Mandler MD, et al. (2024) The modification landscape of P. aeruginosa tRNAs. bioRxiv : the preprint server for biology.

Deery J, et al. (2024) Comparative genomics reveals distinct diversification patterns among LysR-type transcriptional regulators in the ESKAPE pathogen Pseudomonas aeruginosa. Microbial genomics, 10(2).

Kristensen R, et al. (2024) Inhibition of Pseudomonas aeruginosa quorum sensing by chemical induction of the MexEF-oprN efflux pump. Antimicrobial agents and chemotherapy, 68(2), e0138723.

Elsen S, et al. (2024) Cross-regulation and cross-talk of conserved and accessory two-component regulatory systems orchestrate Pseudomonas copper resistance. PLoS genetics, 20(6), e1011325.

Numata S, et al. (2024) Novel humanized anti-PcrV monoclonal antibody COT-143 protects mice from lethal Pseudomonas aeruginosa infection via inhibition of toxin translocation by the type III secretion system. Antimicrobial agents and chemotherapy, 68(10), e0069424.

Yaeger LN, et al. (2024) A genetic screen identifies a role for oprF in Pseudomonas aeruginosa biofilm stimulation by subinhibitory antibiotics. NPJ biofilms and microbiomes, 10(1), 30.

Li R, et al. (2024) Ser/Thr protein kinase Stk1 phosphorylates the key transcriptional regulator AlgR to modulate virulence and resistance in Pseudomonas aeruginosa. Virulence, 15(1), 2367649.

Miles J, et al. (2024) Massively parallel mutant selection identifies genetic determinants of Pseudomonas aeruginosa colonization of Drosophila melanogaster. mSystems, 9(3), e0131723.

Lechtenberg T, et al. (2024) Improving 5-(hydroxymethyl)furfural (HMF) tolerance of Pseudomonas taiwanensis VLB120 by automated adaptive laboratory evolution (ALE). Metabolic engineering communications, 18, e00235.

Ezeduru V, et al. (2024) Defining the functional properties of cyclopropane fatty acid synthase from Pseudomonas aeruginosa PAO1. The Journal of biological chemistry, 300(9), 107618.