

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, r3d100012086, biotools:pseudomonas_genome_database

Alternate URLs: https://bio.tools/pseudomonas_genome_database,
<https://doi.org/10.17616/R3935H>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260731T042725+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 489 mentions in open access literature.

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

Marted?? R, et al. (2026) De novo cysteine biosynthesis in *Pseudomonas aeruginosa*: Characterization of the two main cysteine synthase isoforms. *iScience*, 29(1), 114304.

Dupont CA, et al. (2025) The GacS/GacA two-component system strongly regulates antimicrobial competition mechanisms of *Pseudomonas fluorescens* MFE01 strain. *Journal of bacteriology*, 207(2), e0038824.

Zhang N, et al. (2025) Interspecies signaling modulates the biosynthesis of antimicrobial secondary metabolites related to biological control activities of *Pseudomonas fluorescens* 2P24. *Microbiology spectrum*, 13(3), e0188624.

Simon V, et al. (2025) Functional and Pangenomic Exploration of Roc Two-Component Regulatory Systems Identifies Novel Players Across *Pseudomonas* Species. *Molecular microbiology*, 123(5), 439.

Chen F, et al. (2025) VimR is a conserved master transcription regulator controlling virulence and metabolism in *Pseudomonas*. *Nucleic acids research*, 53(11).

Guo W, et al. (2025) Identification and characterization of alternative homologs of histidinol-phosphate phosphatase in *Pseudomonas aeruginosa*. *BMC microbiology*, 25(1), 377.

Bellamoroso KR, et al. (2025) Inactivation of MexT in *Pseudomonas aeruginosa* destabilizes cooperation and favors the emergence of a unique quorum sensing variant. *bioRxiv : the preprint server for biology*.

Salpadoru T, et al. (2025) A novel non-catalytic function of PA2803-encoded PcrP contributes to polymyxin B resistance in *P. aeruginosa* and redefines the functional role of the PA2803 subfamily. *bioRxiv : the preprint server for biology*.

Bernal-Vicente A, et al. (2025) ABP-B9, a new strain of *Pseudomonas seleniipraecipitans* with biostimulant activity. *Frontiers in plant science*, 16, 1561298.

Gao W, et al. (2025) Comparative Analysis of Signature Sequences from Adenylation Domains Situated within Bacterial-Origin Nonribosomal Peptide Synthetase Modules. *Journal of microbiology and biotechnology*, 35, e2502030.

Liu YS, et al. (2025) Dual-species proteomics and targeted intervention of animal-pathogen interactions. *Journal of advanced research*, 73, 397.

Martino RA, et al. (2025) Genetic Dissection of Cyclic di-GMP Signalling in *Pseudomonas aeruginosa* via Systematic Diguanylate Cyclase Disruption. *Microbial biotechnology*, 18(4), e70137.

Mallery CP, et al. (2025) Evolution of PqsE as a *Pseudomonas aeruginosa*-specific regulator of LuxR-type receptors: insights from *Pseudomonas* and *Burkholderia*. *mBio*, 16(5), e0064625.

Van Loon JC, et al. (2025) Structural and functional analysis of *Pseudomonas aeruginosa* PelA provides insight into the modification of the Pel exopolysaccharide. *The Journal of biological chemistry*, 301(5), 108432.

Ben-David Y, et al. (2025) SadB, a mediator of AmrZ proteolysis and biofilm development in *Pseudomonas aeruginosa*. *NPJ biofilms and microbiomes*, 11(1), 77.

Salpadoru T, et al. (2025) The PA2803-encoded PcrP exhibits a novel non-catalytic function and contributes to polymyxin B resistance in *P. aeruginosa*. *Journal of bacteriology*, 207(11), e0018925.

Foik IP, et al. (2025) Bacteria detect neutrophils via a system that responds to hypochlorous acid and flow. *bioRxiv : the preprint server for biology*.

Neetu , et al. (2025) *Cellulophaga algicola* alginate lyase and *Pseudomonas aeruginosa* Psl glycoside hydrolase inhibit biofilm formation by *Pseudomonas aeruginosa* CF2843 on three-dimensional aggregates of lung epithelial cells. *Biofilm*, 9, 100265.

Olana MD, et al. (2025) Molecular characterization of serotype and virulence genes of *Pseudomonas aeruginosa* isolated from patients admitted at two hospitals in Addis Ababa, Ethiopia. *Journal of medical microbiology*, 74(6).

Qu M, et al. (2025) Molecular Characterization of a Transcriptional Regulator GntR for Gluconate Metabolism in Industrial 2-Ketogluconate Producer *Pseudomonas plecoglossicida* JUIM01. *Microorganisms*, 13(6).