

Resource Summary Report

Generated by T1D on Aug 9, 2026

Pseudomonas Genome Database

RRID:SCR_006590

Type: Tool

Proper Citation

Pseudomonas Genome Database (RRID:SCR_006590)

Resource Information

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

Proper Citation: Pseudomonas Genome Database (RRID:SCR_006590)

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: data or information resource, production service resource, data analysis service, database, analysis service resource, 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: 20260808T185839+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 543 mentions in open access literature.

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

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

Nerke P, et al. (2026) Engineering *Pseudomonas taiwanensis* VLB120 for regio- and stereospecific hydroxylation of L-lysine fueled by the Weimberg pathway. *Microbial cell factories*, 25(1).

Yang R, et al. (2026) Parallel microevolution of multidrug resistance and hypermucoviscosity in two carbapenem-resistant *Pseudomonas aeruginosa* clinical isolates with strikingly divergent virulence outcomes. *BMC microbiology*, 26(1).

Xu Z, et al. (2026) The nucleoid-associated protein subunit HupA positively regulates the Pqs system and pyocyanin production in *Pseudomonas aeruginosa*. *Applied and environmental microbiology*, 92(4), e0242525.

Paracuellos P, et al. (2026) Molecular basis of type VI secretion system effector loading. *Nature microbiology*, 11(7), 1982.

Ru Y, et al. (2026) Thermoregulation of functional amyloid Fap-dependent biofilm formation via cyclic diguanosine monophosphate signaling in *Pseudomonas fluorescens*. *Applied and environmental microbiology*, 92(4), e0238725.

Novakova K, et al. (2026) High-risk lineages shape the resistome and virulome of multidrug-resistant *Pseudomonas aeruginosa*. *Frontiers in cellular and infection microbiology*, 16, 1843668.

Sposato D, et al. (2026) Activation of the envelope stress-responsive two-component system AmgRS compensates for depletion of the essential lipoprotein signal peptidase LspA in *Pseudomonas aeruginosa*. *Current research in microbial sciences*, 10, 100565.

García-Reyes S, et al. (2026) A decade of insight into ExlA toxin research and the biotechnological potential of non-virulent *Pseudomonas aeruginosa* strains. *Journal of bacteriology*, 208(3), e0049625.

Hessami A, et al. (2026) Design of a novel proteome-derived scaffold presenting epitopes of *Pseudomonas aeruginosa* in native conformation. *Scientific reports*, 16(1).

Wauters M, et al. (2026) Identification of DksA as a novel pro-inflammatory mediator of *Pseudomonas aeruginosa* under conditions mimicking chronic cystic fibrosis lung infection. *Virulence*, 17(1), 2670050.

Bai Y, et al. (2026) Direct interaction between phosphotransferase LpxT and ArnT modulates polymyxin B resistance in *Pseudomonas aeruginosa*. *Microbiology spectrum*, 14(5), e0185225.

Heredia-Ponce Z, et al. (2026) High-resolution visualization of biofilm matrix development in space and time using fluorescent stains for cellulose. *NPJ biofilms and microbiomes*, 12(1), 26.

Puiggené Ò, et al. (2026) Functional organization and regulatory logic of the ped gene cluster in *Pseudomonas* species. *Applied and environmental microbiology*, 92(3), e0004626.

Baltrus DA, et al. (2026) Independent, ongoing clade-specific expansions of IS5 elements in *Pseudomonas syringae*. *Microbial genomics*, 12(1).

Pu QY, et al. (2026) Discovery and Biosynthesis of Farnesyl Pyrophosphate-Derived Noncanonical C17 Terpenes from *Pseudomonas* Species. *Journal of the American Chemical Society*, 148(11), 11939.

García-Reyes S, et al. (2026) Role of PsrA in physiology and virulence regulation in *Pseudomonas aeruginosa* and other bacterial species. *Journal of bacteriology*, 208(4), e0047025.

Mohamed SH, et al. (2026) Integrative Systems-Level Transcriptomic Network Analysis Identifies Candidate Genes Associated with Biofilm Formation and Virulence in *Pseudomonas aeruginosa*. *International journal of molecular sciences*, 27(12).

Yuan L, et al. (2026) Enhanced rhamnolipid production in *Pseudomonas aeruginosa* 8D by systematic genetic engineering. *Microbial cell factories*, 25(1), 48.

Shen C, et al. (2026) *Pseudomonas aeruginosa* tRNA nucleotidyltransferase Cca controls resistance and tolerance to aminoglycoside antibiotics by regulating the MexXY multidrug efflux pump. *Antimicrobial agents and chemotherapy*, 70(4), e0165325.