

Resource Summary Report

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Prokaryotic Genomes Automatic Annotation Pipeline

RRID:SCR_021329

Type: Tool

Proper Citation

Prokaryotic Genomes Automatic Annotation Pipeline (RRID:SCR_021329)

Resource Information

URL: <https://github.com/ncbi/pgap>

Proper Citation: Prokaryotic Genomes Automatic Annotation Pipeline (RRID:SCR_021329)

Description: Software tool as NCBI prokaryotic genome annotation pipeline. Used to annotate both complete genomes and draft genomes comprising multiple contigs. Integrated into NCBI infrastructure and processes, and uses modular software framework, GPipe, developed at NCBI for execution of all annotation tasks, from fetching of raw and curated data from public repositories through sequence alignment and model based gene prediction, to submission of annotated genomic data to public NCBI databases.

Abbreviations: PGAP

Synonyms: Prokaryotic Genomes Automatic Annotation Pipeline (PGAP)

Resource Type: software resource, software toolkit

Keywords: NCBI, prokaryotic genome, annotation pipeline, annotate complete genomes, annotate draft genomes, genomes comprising multiple contigs, FASEB list

Availability: Free, Freely available

Resource Name: Prokaryotic Genomes Automatic Annotation Pipeline

Resource ID: SCR_021329

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Ratings and Alerts

No rating or validation information has been found for Prokaryotic Genomes Automatic Annotation Pipeline.

No alerts have been found for Prokaryotic Genomes Automatic Annotation Pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 214 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Jin YW, et al. (2026) Bile Salt Tolerance Determines Intestinal Colonization Efficacy of *Heyndrickxia coagulans*: A Phenotypic and Genomic Study. *International journal of molecular sciences*, 27(4).

Frazão MR, et al. (2026) *Campylobacter jejuni* strains isolated in Brazil have important virulence related genes and survive to different stress conditions. *Brazilian journal of microbiology : [publication of the Brazilian Society for Microbiology]*, 57(1).

Petrushin IS, et al. (2026) Genomic Features of the Micropredator *Lysobacter* sp. Hz25 Isolated from the Rhizosphere of *Hedysarum zundukii*. *International journal of molecular sciences*, 27(9).

Assis RAB, et al. (2026) Unlocking the genetic arsenal of *Xanthomonas arboricola*: new insights into taxonomic classification, pathogenicity and adaptation beyond the effectorome. *BMC genomics*, 27(1).

Tanabe G, et al. (2026) Complete genomes of *Phascolarctobacterium faecium* isolates obtained from pediatric mucosal-luminal interface aspirate samples. *Microbiology resource announcements*, 15(2), e0078925.

Valença CAS, et al. (2026) Genome-guided antimicrobial potential of *Bacillus stercoris* from coastal sand with activity against multidrug-resistant bacteria, including MRSA. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(5), 713.

Rahim N, et al. (2026) A case of yogurt central line-associated bloodstream infection in a child with intestinal failure. *Nutrition in clinical practice : official publication of the American Society for Parenteral and Enteral Nutrition*, 41(3), 968.

Spahr Y, et al. (2026) The veterinary clinic backyard lawn used for relief walks of hospitalized dogs is a hotspot for OXA-type carbapenemases in multiple *Enterobacterales*. *The Journal of antimicrobial chemotherapy*, 81(5).

Liu X, et al. (2025) Comparative genomics of *Brucella* species reveals key determinants of secondary metabolism, antimicrobial resistance, and virulence. *Scientific reports*, 16(1), 3765.

Spahr Y, et al. (2025) Genomic comparative analysis of *Enterobacter asburiae* harbouring a conjugative bla_{IMI-6}-plasmid isolated from a public garden in Switzerland. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 44(7), 1739.

Trejo-Alarcon LM, et al. (2025) Integrative metabolo-genomics suggests a biosynthetic pathway for tetrangulol in *Streptomyces* sp. KL110A. *World journal of microbiology & biotechnology*, 41(3), 101.

Ang WSL, et al. (2025) Genome sequences of two cyanobacteria strains isolated from hornworts. *Microbiology resource announcements*, 14(5), e0111824.

Han Y, et al. (2025) Antibiotic-associated changes in *Akkermansia muciniphila* alter its effects on host metabolic health. *Microbiome*, 13(1), 48.

Javier-López R, et al. (2025) Transcriptomic and proteomic insights into feather keratin degradation by *Fervidobacterium*. *Frontiers in microbiology*, 16, 1509937.

Boff D, et al. (2025) *Staphylococcus aureus* LukMF' targets neutrophils to promote skin and soft tissue infection. *Science advances*, 11(27), eadr5240.

Rossi GAM, et al. (2025) Antimicrobial-Resistant Enteric Gram-Negative Bacteria Isolated from a Fatal Diarrhea in a Horse: Genomic Characterization of CTX-M-2-Producing *Escherichia coli*. *Antibiotics (Basel, Switzerland)*, 14(12).

Kim HY, et al. (2025) Molecular basis of the hepatobiliary tropism of typhoid toxin promoting *Salmonella* pathogenicity. *Science advances*, 11(23), eadt2040.

Guerrero Garzón JF, et al. (2025) Genome mining of *Streptomyces bambergiensis* AC-800 unravels the biosynthetic gene cluster for inhibitors of prolyl hydroxylase fibrostatins. *Scientific reports*, 15(1), 32142.

Zaman SAU, et al. (2025) Whole genome of petroleum hydrocarbon degrading *Rhodococcus indonesiensis* isolated from Nacharam, Hyderabad, India. *Scientific reports*, 16(1), 165.

Pe?ka K, et al. (2025) Probiotic potential of *Bacillus* Isolates from Polish Bee Pollen and Bee Bread. *Probiotics and antimicrobial proteins*, 17(1), 364.