

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

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 toolkit, software resource

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

License: Creative Commons Attribution-ShareAlike 4.0

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260803T040808+0000

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 202 mentions in open access literature.

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

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.

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.

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

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.

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

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.
- Chen Q, et al. (2025) Systems-level immunomonitoring in children with solid tumors to enable precision medicine. *Cell*, 188(5), 1425.
- Lee GY, et al. (2024) Single missense mutations in Vi capsule synthesis genes confer hypervirulence to *Salmonella* Typhi. *Nature communications*, 15(1), 5258.
- Iduu NV, et al. (2024) Mutation in Wzz(fepE) Linked to Altered O-Antigen Biosynthesis and Attenuated Virulence in Rough *Salmonella* Infantis Variant. *Veterinary sciences*, 11(12).
- Li E, et al. (2024) Analysis of the complete genome sequence of *Paenibacillus* sp. Izh-N1 reveals its antagonistic ability. *BMC genomics*, 25(1), 276.
- Javier-López R, et al. (2024) Comparative genomics of *Fervidobacterium*: a new phylogenomic landscape of these wide-spread thermophilic anaerobes. *BMC genomics*, 25(1), 1248.
- Wang JH, et al. (2024) Characterization of CRISPR-Cas Systems in *Shewanella* algae and *Shewanella* haliotis: Insights into the Adaptation and Survival of Marine Pathogens. *Pathogens (Basel, Switzerland)*, 13(6).
- Naknaen A, et al. (2024) Virulent properties and genomic diversity of *Vibrio vulnificus* isolated from environment, human, diseased fish. *Microbiology spectrum*, 12(7), e0007924.
- Iyer R, et al. (2024) Whole genome sequencing data of *Acinetobacter venetianus* JKSF06 collected from Houston ship channel sediment in La Porte, Texas. *Data in brief*, 53, 110117.
- Huang YT, et al. (2024) Emergence of carbapenem resistance in persistent *Shewanella* algae bacteremia: the role of pdsS G547W mutation in adaptive subpopulation dynamics. *Annals of clinical microbiology and antimicrobials*, 23(1), 102.
- Dahar GY, et al. (2024) Comparative genomic analysis of *Bacillus atrophaeus* HAB-5 reveals genes associated with antimicrobial and plant growth-promoting activities. *Frontiers in microbiology*, 15, 1384691.