## **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

**Funding:** 

Availability: Free, Freely available

Resource Name: Prokaryotic Genomes Automatic Annotation Pipeline

Resource ID: SCR\_021329

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**Record Creation Time:** 20220129T080354+0000

**Record Last Update:** 20250513T062142+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 191 mentions in open access literature.

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

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. lzh-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.

lyer 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.

Naknaen A, et al. (2024) Virulent properties and genomic diversity of Vibrio vulnificus isolated from environment, human, diseased fish. Microbiology spectrum, 12(7), e0007924.

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).

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.

Manzulli V, et al. (2024) Psychrobacter raelei sp. nov., isolated from a dog with peritonitis. International journal of systematic and evolutionary microbiology, 74(4).

Lee GY, et al. (2024) Single missense mutations in Vi capsule synthesis genes confer hypervirulence to Salmonella Typhi. bioRxiv: the preprint server for biology.

Otto SB, et al. (2024) Interactions between pili affect the outcome of bacterial competition driven by the type VI secretion system. Current biology: CB, 34(11), 2403.

Mendoza RM, et al. (2023) Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. Food science and biotechnology, 32(4), 389.

Avendaño-Herrera R, et al. (2023) Draft Genome Sequence of Tenacibaculum haliotis Strain RA3-2T, Isolated from Korean Wild Abalone (Haliotis discus hannai). Microbiology resource announcements, 12(3), e0102522.

Singh RP, et al. (2023) Genome Sequence of Environmental Isolate Staphylococcus aureus OS-6, Isolated from a Soil Sample. Microbiology resource announcements, 12(6), e0023823.

Wu Y, et al. (2023) Global Phylogeography and Genomic Epidemiology of Carbapenem-Resistant blaOXA-232-Carrying Klebsiella pneumoniae Sequence Type 15 Lineage. Emerging infectious diseases, 29(11), 2246.

Nishida AH, et al. (2023) Origins and Evolution of Novel Bacteroides in Captive Apes. bioRxiv: the preprint server for biology.

Tisza MJ, et al. (2023) Roving methyltransferases generate a mosaic epigenetic landscape and influence evolution in Bacteroides fragilis group. Nature communications, 14(1), 4082.

Hafeez AB, et al. (2023) Whole-genome sequencing and antimicrobial potential of bacteria isolated from Polish honey. Applied microbiology and biotechnology, 107(20), 6389.

Wang S, et al. (2023) Disproportionation of Inorganic Sulfur Compounds by Mesophilic Chemolithoautotrophic Campylobacterota. mSystems, 8(1), e0095422.