

Resource Summary Report

Generated by T1D on Sep 20, 2026

MetaGeneAnnotator

RRID:SCR_011934

Type: Tool

Proper Citation

MetaGeneAnnotator (RRID:SCR_011934)

Resource Information

URL: <http://whale.bio.titech.ac.jp/metagene/>

Proper Citation: MetaGeneAnnotator (RRID:SCR_011934)

Description: A gene-finding software program for prokaryote and phage., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: MetaGeneAnnotator

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MetaGeneAnnotator

Resource ID: SCR_011934

Alternate IDs: OMICS_01490

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260919T195221+0000

Ratings and Alerts

No rating or validation information has been found for MetaGeneAnnotator.

No alerts have been found for MetaGeneAnnotator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 88 mentions in open access literature.

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

Gittrich MR, et al. (2025) Isolation and characterization of 24 phages infecting the plant growth-promoting rhizobacterium *Klebsiella* sp. M5al. *PloS one*, 20(2), e0313947.

Schmitz MA, et al. (2025) Lineage-specific microbial protein prediction enables large-scale exploration of protein ecology within the human gut. *Nature communications*, 16(1), 3204.

Alseth EO, et al. (2025) Mystique, a broad host range *Acinetobacter* phage, reveals the impact of culturing conditions on phage isolation and infectivity. *PLoS pathogens*, 21(4), e1012986.

Negrete-Méndez H, et al. (2025) Genomic and proteomic analyses of Nus-dependent non-lambdoid phages reveal a novel coliphage group prevalent in gut: mEpimml. *Frontiers in microbiology*, 16, 1480411.

Yamada Y, et al. (2024) Identification of plasmids from thermophilic *Streptomyces* strains and development of a gene cloning system for thermophilic *Streptomyces* species. *Journal of industrial microbiology & biotechnology*, 51.

Sato S, et al. (2024) Genomic properties of a *Bartonella quintana* strain from Japanese macaque (*Macaca fuscata*) revealed by genome comparison with human and rhesus macaque strains. *Scientific reports*, 14(1), 10941.

Martinez-Soto CE, et al. (2024) Multireceptor phage cocktail against *Salmonella enterica* to circumvent phage resistance. *microLife*, 5, uqae003.

Oshiki M, et al. (2024) Collaborative metabolisms of urea and cyanate degradation in marine anammox bacterial culture. *ISME communications*, 4(1), ycad007.

Würstle S, et al. (2024) Optimized preparation pipeline for emergency phage therapy against *Pseudomonas aeruginosa* at Yale University. *Scientific reports*, 14(1), 2657.

Alburkat H, et al. (2024) Evolution and genetic characterization of Seoul virus in wild rats *Rattus norvegicus* from an urban park in Lyon, France 2020-2022. *PLoS neglected tropical diseases*, 18(5), e0012142.

Gambino M, et al. (2024) Diversity and phage sensitivity to phages of porcine enterotoxigenic *Escherichia coli*. *Applied and environmental microbiology*, 90(7), e0080724.

Vik D, et al. (2023) MArVD2: a machine learning enhanced tool to discriminate between archaeal and bacterial viruses in viral datasets. *ISME communications*, 3(1), 87.

Moraru C, et al. (2023) VirClust-A Tool for Hierarchical Clustering, Core Protein Detection and Annotation of (Prokaryotic) Viruses. *Viruses*, 15(4).

Morohoshi T, et al. (2023) Genomic Reclassification and Phenotypic Characterization of *Pseudomonas putida* Strains Deposited in Japanese Culture Collections. *Microbes and environments*, 38(2).

Hosseini N, et al. (2023) MQM1, a bacteriophage infecting strains of *Aeromonas salmonicida* subspecies *salmonicida* carrying Prophage 3. *Virus research*, 334, 199165.

Thapa S, et al. (2023) Exploring the microbial diversity and characterization of cellulase and hemicellulase genes in goat rumen: a metagenomic approach. *BMC biotechnology*, 23(1), 51.

Yanagisawa M, et al. (2022) Effects of carbon ion beam-induced mutagenesis for the screening of RED production-deficient mutants of *Streptomyces coelicolor* JCM4020. *PLoS one*, 17(7), e0270379.

Uchiyama J, et al. (2022) Phylogenetic analysis of new viral cluster of large phages with unusual DNA genomes containing uracil in place of thymine in gene-sharing network, using phages S6 and PBS1 and relevant uncultured phages derived from sewage metagenomics. *Virus research*, 319, 198881.

Dimonaco NJ, et al. (2022) No one tool to rule them all: prokaryotic gene prediction tool annotations are highly dependent on the organism of study. *Bioinformatics (Oxford, England)*, 38(5), 1198.

Demina TA, et al. (2022) Virus-Host Interactions and Genetic Diversity of Antarctic Sea Ice Bacteriophages. *mBio*, 13(3), e0065122.