Resource Summary Report

Generated by nidm-terms on Jul 28, 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: 20260725T190725+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 nidm-terms .

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: mEpimmI. Frontiers in microbiology, 16, 1480411.

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.

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.

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.

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

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.

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

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.

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

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.

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.

Uchiyama J, et al. (2022) Phylogenic 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.