Resource Summary Report

Generated by NIF on May 25, 2025

Prodigal

RRID:SCR_011936
Type: Tool

Proper Citation

Prodigal (RRID:SCR_011936)

Resource Information

URL: https://github.com/hyattpd/Prodigal

Proper Citation: Prodigal (RRID:SCR_011936)

Description: Software tool for protein coding gene prediction for prokaryotic genomes.

Abbreviations: Prodigal

Synonyms: , PROkaryotic DYnamic programming Gene-finding ALgorithm, Prokaryotic Dynamic Programming Genefinding Algorithm

Resource Type: software resource, simulation software, software application

Defining Citation: PMID:20211023

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Prodigal

Resource ID: SCR_011936

Alternate IDs: SCR_021246, OMICS_01493

Alternate URLs: https://sources.debian.org/src/prodigal/

Old URLs: http://prodigal.ornl.gov/

License: GNU GPL v3.0

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250524T060424+0000

Ratings and Alerts

No rating or validation information has been found for Prodigal.

No alerts have been found for Prodigal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2496 mentions in open access literature.

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

Zeng X, et al. (2025) Effects of Different Nitrogen Fertilizer Application Rates on Soil Microbial Structure in Paddy Soil When Combined with Rice Straw Return. Microorganisms, 13(1).

Tang G, et al. (2025) Metagenomic estimation of absolute bacterial biomass in the mammalian gut through host-derived read normalization. bioRxiv : the preprint server for biology.

Hameed A, et al. (2025) Neobacillus driksii sp. nov. isolated from a Mars 2020 spacecraft assembly facility and genomic potential for lasso peptide production in Neobacillus. Microbiology spectrum, 13(1), e0137624.

Gabor CE, et al. (2025) Characterization of Shigella flexneri serotype 6 strains from geographically diverse low- and middle-income countries. mBio, 16(1), e0221024.

Yang Y, et al. (2025) Systematic identification of secondary bile acid production genes in global microbiome. mSystems, 10(1), e0081724.

Unzueta-Martínez A, et al. (2025) Taxonomic diversity and functional potential of microbial communities in oyster calcifying fluid. Applied and environmental microbiology, 91(1), e0109424.

Santoro EP, et al. (2025) Inherent differential microbial assemblages and functions associated with corals exhibiting different thermal phenotypes. Science advances, 11(3), eadq2583.

Wang F, et al. (2025) The impact of straw and its post-pyrolysis incorporation on functional microbes and mineralization of organic carbon in yellow paddy soil. PloS one, 20(1), e0314984.

Kamilari E, et al. (2025) Bacillus safensis APC 4099 has broad-spectrum antimicrobial activity against both bacteria and fungi and produces several antimicrobial peptides, including the novel circular bacteriocin safencin E. Applied and environmental microbiology, 91(1), e0194224.

Neumann CJ, et al. (2025) First-year dynamics of the anaerobic microbiome and archaeome in infants' oral and gastrointestinal systems. mSystems, 10(1), e0107124.

Facimoto CT, et al. (2025) Hindguts of Kyphosus sydneyanus harbor phylogenetically and genomically distinct Alistipes capable of degrading algal polysaccharides and diazotrophy. mSystems, 10(1), e0100724.

Schechter MS, et al. (2025) Ribosomal protein phylogeography offers quantitative insights into the efficacy of genome-resolved surveys of microbial communities. bioRxiv : the preprint server for biology.

Lam HYP, et al. (2025) A Novel Bacteriophage with the Potential to Inhibit Fusobacterium nucleatum-Induced Proliferation of Colorectal Cancer Cells. Antibiotics (Basel, Switzerland), 14(1).

Ghiotto G, et al. (2025) Impact of trace metal supplementation on anaerobic biological methanation under hydrogen and carbon dioxide starvation. NPJ biofilms and microbiomes, 11(1), 7.

Low SJ, et al. (2025) PathoGD: an integrative genomics approach to primer and guide RNA design for CRISPR-based diagnostics. Communications biology, 8(1), 147.

Xu T, et al. (2025) Discovery and characterization of complete genomes of 38 head-tailed proviruses in four predominant phyla of archaea. Microbiology spectrum, 13(1), e0049224.

Midot F, et al. (2025) Temporal dynamics of soil microbial C and N cycles with GHG fluxes in the transition from tropical peatland forest to oil palm plantation. Applied and environmental microbiology, 91(1), e0198624.

Takita K, et al. (2025) Distribution and functional analysis of two types of quorum sensing gene pairs, glaI1/glaR1 and glaI2/glaR2, in Burkholderia gladioli. FEMS microbiology letters, 372.

Wagatsuma R, et al. (2025) vClean: assessing virus sequence contamination in viral genomes. NAR genomics and bioinformatics, 7(1), lqae185.

Chuckran PF, et al. (2025) Codon bias, nucleotide selection, and genome size predict in situ bacterial growth rate and transcription in rewetted soil. Proceedings of the National Academy of Sciences of the United States of America, 122(3), e2413032122.