

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

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 application, simulation software, software resource

Defining Citation: [PMID:20211023](#)

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: 20260728T043359+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 2985 mentions in open access literature.

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

Munyoki SK, et al. (2025) The microbiota extends the reproductive lifespan of mice by safeguarding the ovarian reserve. Cell host & microbe.

Gao Y, et al. (2025) Benchmarking short-read metagenomics tools for removing host contamination. GigaScience, 14.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. GigaByte (Hong Kong, China), 2025, gigabyte154.

Li W, et al. (2025) Benchmarking and optimizing qualitative and quantitative pipelines in environmental metatranscriptomics using mixture controlling experiments. ISME communications, 5(1), ycaf090.

Xu CCY, et al. (2025) Pre-exposure to stress reduces loss of community and genetic diversity following severe environmental disturbance. Current biology : CB, 35(5), 1061.

Tran M, et al. (2025) Bacteriophage infection drives loss of ??-lactam resistance in methicillin-resistant Staphylococcus aureus. eLife, 13.

Pan S, et al. (2025) A holistic genome dataset of bacteria and archaea of mangrove sediments. GigaScience, 14.

Wang S, et al. (2025) Deterministic succession patterns in the rumen and fecal microbiome associate with host metabolic shifts in peripartum dairy cattle. GigaScience, 14.

Li T, et al. (2025) Turning antagonists into allies: Bacterial-fungal interactions enhance the efficacy of controlling Fusarium wilt disease. Science advances, 11(7), eads5089.

Zhu Y, et al. (2025) In-depth analysis of 17,115 rice transcriptomes reveals extensive viral diversity in rice plants. Nature communications, 16(1), 1559.

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).

Wang L, et al. (2025) PhyloFunc: phylogeny-informed functional distance as a new ecological metric for metaproteomic data analysis. *Microbiome*, 13(1), 50.

Abdel-Glil MY, et al. (2025) High intra-laboratory reproducibility of nanopore sequencing in bacterial species underscores advances in its accuracy. *Microbial genomics*, 11(3).

Orellana E, et al. (2025) Sustainable Food Waste Management in Anaerobic Digesters: Prediction of the Organic Load Impact by Metagenome-Scale Metabolic Modeling. *Environmental science & technology*, 59(13), 6659.

Zhu J, et al. (2025) Asgard Arf GTPases can act as membrane-associating molecular switches with the potential to function in organelle biogenesis. *Nature communications*, 16(1), 2622.

Yan W, et al. (2025) Microbiota-reprogrammed phosphatidylcholine inactivates cytotoxic CD8 T cells through UFMylation via exosomal SerpinB9 in multiple myeloma. *Nature communications*, 16(1), 2863.

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

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.

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.