

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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: simulation software, software resource, software application

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: 20260731T042842+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 [kravitz2](#) .

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.

Shahed K, et al. (2025) Benchmarking pangenome dynamics and horizontal gene transfer in Mycobacterium marinum evolution. Frontiers in microbiology, 16, 1537826.

Paterson JR, et al. (2025) Enhanced resistance of metal sequestering agents by reconfiguration of the Staphylococcus aureus cell wall. npj antimicrobials and resistance, 3(1), 61.

Zhang L, et al. (2025) The dysbiosis of gut microbiota and dysregulation of metabolites in IgA nephropathy and membranous nephropathy. Frontiers in medicine, 12, 1618947.

Villette R, et al. (2025) Human gut microbiome gene co-expression network reveals a loss in taxonomic and functional diversity in Parkinson's disease. NPJ biofilms and microbiomes, 11(1), 142.

Winder JC, et al. (2025) Environmental adaptations in metagenomes revealed by deep learning. BMC biology, 23(1), 252.

Gajigan AP, et al. (2025) A dinoflagellate-infecting giant virus with a micron-length tail. bioRxiv : the preprint server for biology.

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.

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

Gulyaeva A, et al. (2025) Identification and characterization of *Faecalibacterium* prophages rich in diversity-generating retroelements. Microbiology spectrum, 13(2), e0106624.

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.

Tian C, et al. (2025) Industrialization drives the gut microbiome and resistome of the Chinese populations. mSystems, 10(3), e0137224.