

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 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: 20260815T182443+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 3398 mentions in open access literature.

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

Lazzari G, et al. (2026) Gempipe: a tool for drafting, curating, and analyzing pan and multi-strain genome-scale metabolic models. *mSystems*, 11(1), e0100725.

Kwon Y, et al. (2026) Rice *gs3* allele and low-nitrogen conditions enrich rhizosphere microbiota that mitigate methane emissions and promote beneficial crop traits. *The ISME journal*, 20(1).

Ricci F, et al. (2026) Chemosynthesis enables microbial communities to flourish in a marine cave ecosystem. *The ISME journal*, 20(1).

Merchant AT, et al. (2026) Semantic design of functional de novo genes from a genomic language model. *Nature*, 649(8097), 749.

Harrass S, et al. (2026) Lactobacilli Probiotics Prevent Amyloid-Beta Fibril Formation In Vitro. *Probiotics and antimicrobial proteins*, 18(3), 4640.

Dell M, et al. (2026) Chemical richness and diversity of uncultivated 'Entotheonella' symbionts in marine sponges. *Nature chemical biology*, 22(2), 217.

Maynard RH, et al. (2026) Hidden genetic diversity among *Blochmanniella* endosymbionts of closely related carpenter ant populations. *Journal of evolutionary biology*, 39(1), 158.

Feng N, et al. (2026) Controlled release of coated antioxidants inhibits *Citrobacter rodentium* colonization in the colon of rats by reducing gut redox potential. *Redox biology*, 89, 104005.

Li M, et al. (2026) Manipulating root-associated microbiomes to boost drought resistance in dryland winter wheat with *Streptomyces pactum* Act12. *BMC microbiology*, 26(1).

Ye L, et al. (2026) Fecal metagenome and plasma metabolome analyses reveal changes in gut microbiota composition and plasma metabolites in rats with abemaciclib-induced diarrhea. *BMC gastroenterology*, 26(1).

Wang P, et al. (2026) The *Medicago* SPX1/3-PHR2 network relays phosphate signaling to orchestrate root nodulation-dependent nitrogen acquisition by controlling flavonoid biosynthesis. *Plant communications*, 7(4), 101695.

Kerek ??, et al. (2026) Integrated Phenotypic and Genomic Profiling of Antimicrobial Resistance and Virulence-Associated Determinants in Poultry-Derived Enterococcus spp. from Hungary. Veterinary sciences, 13(2).

Yang J, et al. (2026) The impact of rumen and hindgut microbiomes on the persistent productivity of long-lived dairy cows. Microbiome, 14(1), 60.

Guo Z, et al. (2026) MetaRanker: precise profiling of antibiotic resistome risk in metagenomes by integrating abundance and genetic co-occurrence. Applied and environmental microbiology, 92(3), e0242225.

Su JW, et al. (2026) Metagenomic analysis of antimicrobial resistance, virulence, and mobile genetic elements in the gut microbiota of Caprinae species. Communications biology, 9(1).

Zheng H, et al. (2026) Plasmids as persistent genetic reservoirs of bacterial defense systems in wastewater treatment. Microbiome, 14(1), 50.

Yu S, et al. (2026) Keystone bacterial taxa drive denitrification and N₂O emission via adaptive genomic and metabolic strategies in contrasting agricultural soils. Environmental microbiome, 21(1).

Zhen D, et al. (2026) Intratumoral delivery of probiotic *Ligilactobacillus salivarius* H22A013 modulates the melanoma microenvironment and enhances trametinib efficacy. BMC microbiology, 26(1).

Feng L, et al. (2026) Comprehensive analysis of the complete chloroplast genome of white pomegranate and phylogenetic relationships within Myrtales. BMC genomics, 27(1), 220.

Michelioudakis V, et al. (2026) Comparative Genomic and Transcriptomic Analysis Reveals Why *Paenarthrobacter* Strains Are Specialists in the Degradation of the Fungicide Iprodione. Microbial biotechnology, 19(2), e70319.