

Resource Summary Report

Generated by [NIF](#) on Aug 19, 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: 20260819T044329+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 [NIF](#) .

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.