

# Resource Summary Report

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## PePPER Prokaryote Promoter Prediction

RRID:SCR\_014740

Type: Tool

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### Proper Citation

PePPER Prokaryote Promoter Prediction (RRID:SCR\_014740)

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### Resource Information

**URL:** <http://server.molgenrug.nl/index.php/prokaryote-promoters>

**Proper Citation:** PePPER Prokaryote Promoter Prediction (RRID:SCR\_014740)

**Description:** A webserver for the prediction of prokaryote promoter elements and regulons. DNA in FASTA or plain format serve as input. A gene table can be included with the run.

**Abbreviations:** PePPER

**Resource Type:** sequence analysis software, software resource, software application, data analysis software, data processing software

**Defining Citation:** [PMID:22747501](#)

**Keywords:** promoter prediction objective, prokaryote, promoter, regulon, predict, sequence analysis software, web server

**Availability:** Free, Web application

**Resource Name:** PePPER Prokaryote Promoter Prediction

**Resource ID:** SCR\_014740

**Record Creation Time:** 20220129T080322+0000

**Record Last Update:** 20260808T190029+0000

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### Ratings and Alerts

No rating or validation information has been found for PePPER Prokaryote Promoter Prediction.

No alerts have been found for PePPER Prokaryote Promoter Prediction.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Fashedemi O, et al. (2025) Advances in human papillomavirus detection for cervical cancer screening and diagnosis: challenges of conventional methods and opportunities for emergent tools. *Analytical methods : advancing methods and applications*, 17(7), 1428.

Ananna NT, et al. (2024) Characterization of two lytic bacteriophages infecting carbapenem-resistant clinical *Klebsiella pneumoniae* in Dhaka, Bangladesh. *Virus research*, 350, 199491.

Finstrolová A, et al. (2022) Global Transcriptomic Analysis of Bacteriophage-Host Interactions between a Kayvirus Therapeutic Phage and *Staphylococcus aureus*. *Microbiology spectrum*, 10(3), e0012322.

Souto BM, et al. (2021) Functional screening of a Caatinga goat (*Capra hircus*) rumen metagenomic library reveals a novel GH3  $\beta$ -xylosidase. *PloS one*, 16(1), e0245118.

Fernández-Juárez V, et al. (2020) Differential Effects of Varying Concentrations of Phosphorus, Iron, and Nitrogen in N<sub>2</sub>-Fixing Cyanobacteria. *Frontiers in microbiology*, 11, 541558.

Dhakal S, et al. (2020) *Siccibacter turicensis* from Kangaroo Scats: Possible Implication in Cellulose Digestion. *Microorganisms*, 8(5).

Hernandez-Valdes JA, et al. (2020) Development of *Lactococcus lactis* Biosensors for Detection of Diacetyl. *Frontiers in microbiology*, 11, 1032.

Dean SN, et al. (2020) *Francisella novicida* Two-Component System Response Regulator BfpR Modulates *iglC* Gene Expression, Antimicrobial Peptide Resistance, and Biofilm Production. *Frontiers in cellular and infection microbiology*, 10, 82.

Price CE, et al. (2019) Adaption to glucose limitation is modulated by the pleiotropic regulator CcpA, independent of selection pressure strength. *BMC evolutionary biology*, 19(1), 15.

Zhong KX, et al. (2018) A New Freshwater Cyanosiphovirus Harboring Integrase. *Frontiers in microbiology*, 9, 2204.

Chen Y, et al. (2018) Novel genetically stable infectious clone for a Zika virus clinical isolate and identification of RNA elements essential for virus production. *Virus research*, 257, 14.

Coelho RV, et al. (2018) *Bacillus subtilis* promoter sequences data set for promoter prediction in Gram-positive bacteria. *Data in brief*, 19, 264.

Schilling T, et al. (2018) Genomic Analysis of the Recent Viral Isolate vB\_BthP-Goe4 Reveals Increased Diversity of  $\phi$ 29-Like Phages. *Viruses*, 10(11).

Guevara G, et al. (2017) Functional differentiation of 3-ketosteroid  $\Delta$ 1-dehydrogenase isozymes in *Rhodococcus ruber* strain Chol-4. *Microbial cell factories*, 16(1), 42.

Skowron PM, et al. (2017) The third restriction-modification system from *Thermus aquaticus* YT-1: solving the riddle of two *Taq*I specificities. *Nucleic acids research*, 45(15), 9005.

Erill I, et al. (2017) Comparative Analysis of *Ralstonia solanacearum* Methylomes. *Frontiers in plant science*, 8, 504.

Leskinen K, et al. (2017) Characterization of vB\_SauM-fRuSau02, a Twort-Like Bacteriophage Isolated from a Therapeutic Phage Cocktail. *Viruses*, 9(9).

Seong HJ, et al. (2016) Methylome Analysis of Two *Xanthomonas* spp. Using Single-Molecule Real-Time Sequencing. *The plant pathology journal*, 32(6), 500.

Sawhney N, et al. (2016) Genomic and transcriptomic analysis of carbohydrate utilization by *Paenibacillus* sp. JDR-2: systems for bioprocessing plant polysaccharides. *BMC genomics*, 17, 131.

Zhu L, et al. (2016) Precision methylome characterization of *Mycobacterium tuberculosis* complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. *Nucleic acids research*, 44(2), 730.