

Resource Summary Report

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PePPER Prokaryote Promoter Prediction

RRID:SCR_014740

Type: Tool

Proper Citation

PePPER Prokaryote Promoter Prediction (RRID:SCR_014740)

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: data analysis software, data processing software, sequence analysis software, software application, software resource

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: 20260903T235248+0000

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 [dkNET](#).

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 β -xylosidase. *PloS one*, 16(1), e0245118.

Fernández-Juárez V, et al. (2020) Differential Effects of Varying Concentrations of Phosphorus, Iron, and Nitrogen in N₂-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 ϕ 29-Like Phages. *Viruses*, 10(11).

Guevara G, et al. (2017) Functional differentiation of 3-ketosteroid ϕ 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.