

Resource Summary Report

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EukRep

RRID:SCR_024985

Type: Tool

Proper Citation

EukRep (RRID:SCR_024985)

Resource Information

URL: <https://github.com/patrickwest/EukRep>

Proper Citation: EukRep (RRID:SCR_024985)

Description: Software tool as classifier that utilizes k-mer composition of assembled sequences to identify eukaryotic genome fragments prior to gene prediction. Used for eukaryotic sequence identification. Classification of Eukaryotic and Prokaryotic sequences from metagenomic datasets.

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

Defining Citation: [PMID:29496730](#)

Keywords: Classification of Eukaryotic and Prokaryotic sequences, metagenomic datasets, identify genome fragments, sequence identification,

Funding: National Science Foundation Graduate Research Fellowship ;
Sloan Foundation ;
NSF Sustainable Chemistry ;
Office of Science of the US Department of Energy ;
German Science Foundation

Availability: Free, Available for download, Freely available

Resource Name: EukRep

Resource ID: SCR_024985

License: MIT license

Record Creation Time: 20240202T050227+0000

Record Last Update: 20260815T042854+0000

Ratings and Alerts

No rating or validation information has been found for EukRep.

No alerts have been found for EukRep.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Lin D, et al. (2026) Nutrient balance regulates soil microbial health under long-term fertilization. Cell reports, 45(4), 117274.

Li D, et al. (2026) The Anna Karenina principle in the assembly of plant microbiome under pathogen stress. NPJ biofilms and microbiomes, 12(1).

Freyria NJ, et al. (2025) Shotgun metagenomics reveals the flexibility and diversity of Arctic marine microbiomes. ISME communications, 5(1), ycaf007.

Kim H, et al. (2025) Genome Evolution of Two Intertidal Sargassum Species (*S. fusiforme* and *S. thunbergii*) and Their Response to Abiotic Stressors. Genome biology and evolution, 17(5).

G??mez-Consarnau L, et al. (2025) Unexpected microbial rhodopsin dynamics in sync with phytoplankton blooms. Nature communications, 17(1), 790.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Sun C, et al. (2024) Integrated analysis of facial microbiome and skin physio-optical properties unveils cutotype-dependent aging effects. Microbiome, 12(1), 163.

Yang JX, et al. (2024) Gene horizontal transfers and functional diversity negatively correlated with bacterial taxonomic diversity along a nitrogen gradient. NPJ biofilms and microbiomes, 10(1), 128.

Huang L, et al. (2024) A multi-kingdom collection of 33,804 reference genomes for the human vaginal microbiome. Nature microbiology, 9(8), 2185.

Schimpl VC, et al. (2024) Microbial consortia driving (ligno)cellulose transformation in agricultural woodchip bioreactors. Applied and environmental microbiology, 90(12), e0174224.

Wang C, et al. (2023) Bacterial genome size and gene functional diversity negatively correlate with taxonomic diversity along a pH gradient. Nature communications, 14(1),

7437.

Ngugi DK, et al. (2023) Abiotic selection of microbial genome size in the global ocean. *Nature communications*, 14(1), 1384.

Zhang ZF, et al. (2023) Long-read assembled metagenomic approaches improve our understanding on metabolic potentials of microbial community in mangrove sediments. *Microbiome*, 11(1), 188.

Weissman JL, et al. (2022) Benchmarking Community-Wide Estimates of Growth Potential from Metagenomes Using Codon Usage Statistics. *mSystems*, 7(5), e0074522.

Zorrilla F, et al. (2021) metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. *Nucleic acids research*, 49(21), e126.