

Resource Summary Report

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FragGeneScan

RRID:SCR_011929

Type: Tool

Proper Citation

FragGeneScan (RRID:SCR_011929)

Resource Information

URL: <https://sourceforge.net/projects/fraggenescan/>

Proper Citation: FragGeneScan (RRID:SCR_011929)

Description: A software application for finding fragmented genes in short reads and may be applied to predict prokaryotic genes in incomplete assemblies or complete genomes.

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

Keywords: microbiome, sequence analysis, fragment, gene, short read, bio.tools

Availability: Acknowledgement requested, Available for download

Resource Name: FragGeneScan

Resource ID: SCR_011929

Alternate IDs: OMICS_01484, biotools:fraggenescan

Alternate URLs: <http://omics.informatics.indiana.edu/FragGeneScan/>,
<https://bio.tools/fraggenescan>

Record Creation Time: 20220129T080307+0000

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Ratings and Alerts

No rating or validation information has been found for FragGeneScan.

No alerts have been found for FragGeneScan.

Data and Source Information

Usage and Citation Metrics

We found 183 mentions in open access literature.

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

Lema NK, et al. (2025) Secondary metabolite biosynthetic gene clusters and microbial diversity as predicted by shotgun metagenomic sequencing approach in hospitals and pharmaceutical industry wastes. *Scientific reports*, 15(1), 25500.

Grießhammer A, et al. (2025) Non-antibiotics disrupt colonization resistance against enteropathogens. *Nature*, 644(8076), 497.

Füßy Z, et al. (2025) Genome-resolved biogeography of Phaeocystales, cosmopolitan bloom-forming algae. *Nature communications*, 16(1), 8559.

Wang M, et al. (2025) Targeted assembly recovers high ammonia monooxygenase diversity in mudflat intertidal. *mSystems*, 10(10), e0062025.

Wulf B, et al. (2025) ReadSeeker: A DNABERT based de-novo read-level gene predictor. *PloS one*, 20(11), e0335732.

Tanca A, et al. (2025) Critical Assessment of MetaProteome Investigation 2 (CAMPI-2): multi-laboratory assessment of sample processing methods to stabilize fecal microbiome for functional analysis. *Microbiome*, 13(1), 245.

Lustermans JJM, et al. (2025) Extracellular electron transfer genes expressed by candidate flocking bacteria in cable bacteria sediment. *mSystems*, 10(1), e0125924.

Priest T, et al. (2025) Seasonal recurrence and modular assembly of an Arctic pelagic marine microbiome. *Nature communications*, 16(1), 1326.

Wallbank JA, et al. (2025) Plastic Type and Condition Have Minimal Impact on Associated Marine Biofilm Communities. *Environmental microbiology*, 27(12), e70214.

Martínez-Nava GA, et al. (2025) Metatranscriptomic analysis reveals gut microbiome bacterial genes in pyruvate and amino acid metabolism associated with hyperuricemia and gout in humans. *Scientific reports*, 15(1), 9981.

Kim JW, et al. (2025) Standardizing the approach to clinical-based human microbiome research: from clinical information collection to microbiome profiling and human resource utilization. *Osong public health and research perspectives*, 16(3), 300.

Rahman MS, et al. (2024) Comprehensive analysis of genomic variation, pan-genome and biosynthetic potential of *Corynebacterium glutamicum* strains. *PloS one*, 19(5), e0299588.

Oggerin M, et al. (2024) Niche differentiation within bacterial key-taxa in stratified surface waters of the Southern Pacific Gyre. *The ISME journal*, 18(1).

Kifle BA, et al. (2024) Shotgun metagenomic insights into secondary metabolite biosynthetic gene clusters reveal taxonomic and functional profiles of microbiomes in natural farmland soil. *Scientific reports*, 14(1), 15096.

Aguilar C, et al. (2024) Actinomycetota bioprospecting from ore-forming environments. *Microbial genomics*, 10(5).

Wang FQ, et al. (2024) Particle-attached bacteria act as gatekeepers in the decomposition of complex phytoplankton polysaccharides. *Microbiome*, 12(1), 32.

Rigkos K, et al. (2024) Biomimetic CO₂ Capture Unlocked through Enzyme Mining: Discovery of a Highly Thermo- and Alkali-Stable Carbonic Anhydrase. *Environmental science & technology*, 58(40), 17732.

Miao Y, et al. (2024) DeePhafier: a phage lifestyle classifier using a multilayer self-attention neural network combining protein information. *Briefings in bioinformatics*, 25(5).

Richy E, et al. (2024) Long-read sequencing sheds light on key bacteria contributing to deadwood decomposition processes. *Environmental microbiome*, 19(1), 99.

Wongkuna S, et al. (2024) Identification of a microbial sub-community from the feral chicken gut that reduces *Salmonella* colonization and improves gut health in a gnotobiotic chicken model. *Microbiology spectrum*, 12(3), e0162123.