

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

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

Record Last Update: 20260905T133004+0000

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 190 mentions in open access literature.

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

Jain AG, et al. (2026) Mixing regimes shape microbial community composition, nutrient regimes, and plant growth attributes in Jeevamrit: metagenomics and culturomics-based insights. *Scientific reports*, 16(1), 6603.

Ravi A, et al. (2026) Cattle feces are a reservoir of diverse *Acinetobacter* species with potential to spread antibiotic resistance genes. *Animal microbiome*, 8(1).

Pavlovska M, et al. (2026) Phytoplankton dynamics shape bacterioplankton community structure and metabolism during the austral summer-autumn transition in the Western Antarctic Peninsula. *FEMS microbiology ecology*, 102(6).

Fürnwein L, et al. (2026) Uncovering transcriptional processes in microbial communities adapted to differing saline conditions in salt-weathered historic buildings. *Microbiome*, 14(1).

de Santana CO, et al. (2026) Investigating the distribution of antibiotic resistance genes in relation to bacterial, fungal, and functional diversity in a hay field. *Microbiology spectrum*, 14(5), e0323225.

Zhu XY, et al. (2026) Predicted shifts in bacterial and algal contributions to DMSP and DMS dynamics during a coastal spring-summer bloom. *The ISME journal*, 20(1).

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

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

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.

Rey Redondo E, et al. (2025) Multi-domain temporal patterns reveal stable community membership but dynamic interactions in the coastal microbiome. *Environmental microbiome*, 21(1), 8.

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.

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.

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.

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).