Resource Summary Report

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Minimum Information about Biosynthetic Gene cluster

RRID:SCR_023660
Type: Tool

Proper Citation

Minimum Information about Biosynthetic Gene cluster (RRID:SCR_023660)

Resource Information

URL: https://mibig.secondarymetabolites.org/

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Description: MIBiG is genomic standards consortium project and biosynthetic gene cluster database used as reference dataset. Provides community standard for annotations and metadata on biosynthetic gene clusters and their molecular products. Standardised data format that describes minimally required information to uniquely characterise biosynthetic gene clusters. MIBiG 2.0 is expended repository for biosynthetic gene clusters of known function. MIBiG 3.0 is database update comprising large scale validation and re-annotation of existing entries and new entries. Community driven effort to annotate experimentally validated biosynthetic gene clusters.

Abbreviations: MIBiG

Synonyms: MIBiG 3.0, MIBiG 2.0

Resource Type: portal, data or information resource, database, project portal

Defining Citation: PMID:36399496, DOI:10.1093/nar/gkz882

Keywords: Genomic standards consortium project, community standard, annotations and metadata standards, biosynthetic gene clusters, sequence framework, biosynthetic gene cluster data,

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UK government Department for Environment ;
Food and Rural Affairs ;
German Chemical Industry ;
Natural Sciences and Engineering Council of Canada

Availability: Free, Freely available

Resource Name: Minimum Information about Biosynthetic Gene cluster

Resource ID: SCR_023660

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Record Creation Time: 20230607T050210+0000

Record Last Update: 20260801T042911+0000

Ratings and Alerts

No rating or validation information has been found for Minimum Information about Biosynthetic Gene cluster.

No alerts have been found for Minimum Information about Biosynthetic Gene cluster.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 55 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Meijer D, et al. (2025) Empowering natural product science with AI: leveraging multimodal data and knowledge graphs. Natural product reports, 42(4), 654.

Islam MS, et al. (2025) Characterization of Congregicoccus parvus gen. nov., sp. nov., a novel slow-growing ultramicrobacterium of the phylum Verrucomicrobiota. PloS one, 20(6), e0326734.

Steffen K, et al. (2025) An integrative genomic and chemical similarity approach linking fungal secondary metabolites and biosynthetic gene clusters. bioRxiv : the preprint server for biology.

Cediel-Becerra JDD, et al. (2025) Targeted genome mining with GATOR-GC maps the evolutionary landscape of biosynthetic diversity. Nucleic acids research, 53(13).

Ragozzino C, et al. (2025) Last Decade Insights in Exploiting Marine Microorganisms as Sources of New Bioactive Natural Products. Marine drugs, 23(3).

Cediel-Becerra JDD, et al. (2025) Targeted genome mining with GATOR-GC maps the evolutionary landscape of biosynthetic diversity. bioRxiv : the preprint server for biology.

Lai Q, et al. (2025) Deciphering the biosynthetic potential of microbial genomes using a BGC language processing neural network model. Nucleic acids research, 53(7).

Zdouc MM, et al. (2025) MIBiG 4.0: advancing biosynthetic gene cluster curation through global collaboration. Nucleic acids research, 53(D1), D678.

Augustijn HE, et al. (2025) Regulatory Genes as Beacons for Discovery and Prioritization of Biosynthetic Gene Clusters in Streptomyces. Biochemistry, 64(13), 2877.

Singh G, et al. (2025) Breaking into nature's secret medicine cabinet: lichens - a biochemical goldmine ready for discovery. The New phytologist, 246(2), 437.

Byers AK, et al. (2025) Whole genome sequencing of Penicillium and Burkholderia strains antagonistic to the causal agent of kauri dieback disease (Phytophthora agathidicida) reveals biosynthetic gene clusters related to antimicrobial secondary metabolites. Molecular ecology resources, 25(2), e13810.

Pasinato A, et al. (2025) Bioinformatic exploration of RiPP biosynthetic gene clusters in lichens. Fungal biology and biotechnology, 12(1), 6.

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

Piedl K, et al. (2024) The Microbiota of Moon Snail Egg Collars is Shaped by Host-Specific Factors. bioRxiv : the preprint server for biology.

Han KI, et al. (2024) Characterization of Bacillus velezensis TJS119 and its biocontrol potential against insect pathogens. Frontiers in microbiology, 15, 1361961.

Piedl K, et al. (2024) The microbiota of moon snail egg collars is shaped by host-specific factors. Microbiology spectrum, 12(11), e0180424.

Sweeney D, et al. (2024) Pattern-based genome mining guides discovery of the antibiotic indanopyrrole A from a marine streptomycetef. bioRxiv : the preprint server for biology.

Alas I, et al. (2024) Micromonosporaceae biosynthetic gene cluster diversity highlights the need for broad-spectrum investigations. Microbial genomics, 10(1).

Yang H, et al. (2024) Unraveling the metabolic potential of biocontrol fungi through omics data: a key to enhancing large-scaleapplication strategies. Acta biochimica et biophysica Sinica, 56(6), 825.