

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: data or information resource, database, portal, 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 Biotechnology and Biological Sciences Research Council ;
UK government Department for Environment ;
Food and Rural Affairs

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: 20260912T200112+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 85 mentions in open access literature.

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

Fan X, et al. (2026) Targeted identification of new phaterpenes and elucidation of the relevant biosynthetic pathway in *Streptomyces phaeochromogenes* OSK-123. Synthetic

and systems biotechnology, 13, 73.

Zhang X, et al. (2026) A hybrid assembly mechanism employs nonreducing polyketide synthase-like logic for partially reduced polyketide formation. *Marine life science & technology*, 8(1), 180.

Boldt J, et al. (2026) Phylogeny-Aware Metabologenomics Accurately Assigns Natural Products to Biosynthetic Gene Clusters. *Microbial biotechnology*, 19(1), e70298.

Tocino-Márquez I, et al. (2026) Unveiling the genomes and secondary metabolomes of *Streptomyces* spp. from freshwater sediments. *Frontiers in microbiology*, 17, 1793713.

Belhadj MSE, et al. (2026) Comparative genome mining and metabolomics reveal divergent NRPS-derived fengycin biosynthetic gene clusters in *Bacillus halotolerans*. *FEMS microbes*, 7, xtag037.

Rosas-Becerra LR, et al. (2026) Functional shifts of the dual-substrate phosphoribosyl isomerase PriA from primary to specialized metabolism in rare Actinomycetota. *Microbial genomics*, 12(4).

Draisma A, et al. (2026) BiG-SCAPE 2.0 and BiG-SLiCE 2.0: scalable, accurate and interactive sequence clustering of metabolic gene clusters. *Nature communications*, 17(1).

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. *Microbial genomics*, 12(4).

Yancey CE, et al. (2026) Secondary metabolism of *Microcystis*: current understanding and recent advances in unlocking genomic and chemical diversity. *Applied and environmental microbiology*, 92(1), e0163425.

Jackson SA, et al. (2026) New insights into the microbiome of the deep-sea sponge *Inflatella pellicula* and the secondary metabolic potential of metagenome-assembled genomes and the wider microbiome. *Microbial genomics*, 12(1).

Wiederkehr F, et al. (2026) Coral microbiomes as reservoirs of unknown genomic and biosynthetic diversity. *Nature*, 652(8110), 686.

Dias GR, et al. (2026) Gems From the Caves: Genomic Insights Into the Biosynthetic Potential of Antimicrobial-Producing Bacteria Associated With Tropical Cave-Dwelling Sponges. *Environmental microbiology*, 28(1), e70244.

Hemmati R, et al. (2026) Draft genome sequence of *Talaromyces trachyspermus*, a biocontrol fungus isolated from broomrape. *G3 (Bethesda, Md.)*, 16(4).

Lu J, et al. (2026) Genomic and chemical analyses of 713 marine biofilm-derived bacterial strains. *Applied and environmental microbiology*, 92(4), e0259325.

Li K, et al. (2026) Telomere-to-Telomere Genomes Reveal that Multiscale Evolution Shapes the Largest Metabolic Arsenal of Diaporthe Fungi. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(27), e13287.

Dobryakov MY, et al. (2026) Genomic and Phenotypic Characterization of *Streptomyces marxii* sp. nov., Producer of Kinanthraquinone B. *Microorganisms*, 14(6).

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

Mesquita FA, et al. (2025) Genome Mining Reveals Pathways for Terpene Production in Aerobic Endospore-Forming Bacteria Isolated from Brazilian Soils. *Microorganisms*, 13(11).

Calvo-Peña C, et al. (2025) Rapamycin Plays a Pivotal Role in the Potent Antifungal Activity Exhibited Against *Verticillium dahliae* by *Streptomyces iranensis* OE54 and *Streptomyces lacaronensis* sp. nov. Isolated from Olive Roots. *Microorganisms*, 13(7).

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.