

Resource Summary Report

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A Classification of Mobile genetic Elements

RRID:SCR_001694

Type: Tool

Proper Citation

A Classification of Mobile genetic Elements (RRID:SCR_001694)

Resource Information

URL: <http://aclame.ulb.ac.be/>

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Description: A database dedicated to the collection and classification of mobile genetic elements (MGEs) from various sources, comprising all known phage genomes, plasmids and transposons. In addition to provide information on the full genomes and genetic entities, it aims at building a comprehensive classification of the functional modules of MGE's at the protein, gene, and higher levels. Prophinder, a tool dedicated to the detection of prophages in sequenced bacterial genomes, is available on ACLAME.

Abbreviations: ACLAME

Synonyms: ACLAME: A CLAssification of Mobile genetic Elements

Resource Type: data or information resource, database

Defining Citation: [PMID:19933762](#), [PMID:14681355](#)

Keywords: mobile genetic element, phage genome, plasmid, virus, prophage, transposon, protein, gene, classification, data analysis service, prophage prediction, bio.tools, FASEB list

Funding: ESTEC contract ESTEC 16370/02/NL/CK

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: A Classification of Mobile genetic Elements

Resource ID: SCR_001694

Alternate IDs: nif-0000-02533, OMICS_01528, biotools:aclame

Alternate URLs: <https://bio.tools/aclame>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260804T043131+0000

Ratings and Alerts

No rating or validation information has been found for A Classification of Mobile genetic Elements.

No alerts have been found for A Classification of Mobile genetic Elements.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Pan T, et al. (2025) Mobile genetic elements in *Klebsiella pneumoniae*. *Journal of bacteriology*, 207(5), e0001225.

Bravo JE, et al. (2024) The TELCoMB Protocol for High-Sensitivity Detection of ARG-MGE Colocalizations in Complex Microbial Communities. *Current protocols*, 4(10), e70031.

Pal S, et al. (2021) Complete genome sequence and identification of polyunsaturated fatty acid biosynthesis genes of the myxobacterium *Minicystis rosea* DSM 24000T. *BMC genomics*, 22(1), 655.

Kazi TA, et al. (2021) Characterization of a novel theta-type plasmid pSM409 of *Enterococcus faecium* RME isolated from raw milk. *Gene*, 777, 145459.

Jones GH, et al. (2021) Acquisition of *pcnB* [poly(A) polymerase I] genes via horizontal transfer from the γ -Proteobacteria. *Microbial genomics*, 7(2).

Smyshlyaev G, et al. (2021) Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. *Molecular systems biology*, 17(5), e9880.

Guo W, et al. (2019) Comparative Study of Gut Microbiota in Wild and Captive Giant Pandas (*Ailuropoda melanoleuca*). *Genes*, 10(10).

Yano H, et al. (2019) Reconsidering plasmid maintenance factors for computational plasmid design. *Computational and structural biotechnology journal*, 17, 70.

Chu BTT, et al. (2018) Metagenomics Reveals the Impact of Wastewater Treatment Plants on the Dispersal of Microorganisms and Genes in Aquatic Sediments. *Applied and*

environmental microbiology, 84(5).

Thirugnanasambandam R, et al. (2017) De novo assembly and annotation of the whole genomic analysis of *Vibrio campbellii* RT-1 strain, from infected shrimp: *Litopenaeus vannamei*. *Microbial pathogenesis*, 113, 372.

Carding SR, et al. (2017) Review article: the human intestinal virome in health and disease. *Alimentary pharmacology & therapeutics*, 46(9), 800.

Sorokin DY, et al. (2017) Discovery of anaerobic lithoheterotrophic haloarchaea, ubiquitous in hypersaline habitats. *The ISME journal*, 11(5), 1245.

Park C, et al. (2017) Metabolic and stress responses of *Acinetobacter oleivorans* DR1 during long-chain alkane degradation. *Microbial biotechnology*, 10(6), 1809.

Delattre H, et al. (2016) Phagonaute: A web-based interface for phage synteny browsing and protein function prediction. *Virology*, 496, 42.

Ullrich SR, et al. (2016) Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile "Ferrovum". *Frontiers in microbiology*, 7, 797.

Zolfaghari Emameh R, et al. (2016) Horizontal transfer of α -carbonic anhydrase genes from prokaryotes to protozoans, insects, and nematodes. *Parasites & vectors*, 9, 152.

Ullrich SR, et al. (2016) Genome Analysis of the Biotechnologically Relevant Acidophilic Iron Oxidising Strain JA12 Indicates Phylogenetic and Metabolic Diversity within the Novel Genus "Ferrovum". *PloS one*, 11(1), e0146832.

Rombouts S, et al. (2016) Characterization of Novel Bacteriophages for Biocontrol of Bacterial Blight in Leek Caused by *Pseudomonas syringae* pv. *porri*. *Frontiers in microbiology*, 7, 279.

Arango-Argoty G, et al. (2016) MetaStorm: A Public Resource for Customizable Metagenomics Annotation. *PloS one*, 11(9), e0162442.

Hulo C, et al. (2015) A structured annotation frame for the transposable phages: a new proposed family "Saltoviridae" within the Caudovirales. *Virology*, 477, 155.