

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

MeGX

RRID:SCR_000738

Type: Tool

Proper Citation

MeGX (RRID:SCR_000738)

Resource Information

URL: <http://www.megx.net>

Proper Citation: MeGX (RRID:SCR_000738)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 12,2023. Set of databases and tools that handle genomic and metagenomic sequences in their environmental contexts.Includes geographic information system to systematically store and analyse marine genomic and metagenomic data in conjunction with contextual information; environmental genome browser with fast search functionalities; database with precomputed analyses for selected complete genomes; database and tool to classify metagenomic fragments based on oligonucleotide signatures.

Synonyms: Marine Ecological GenomiX, megx: marine ecological genomics, Megx.net

Resource Type: data access protocol, software resource, web service, data or information resource, database

Defining Citation: [PMID:16381894](#)

Keywords: functioning of marine ecosystems, marine bacterial, archaeal, phage, metagenome, marine microbe, megdb, analysis

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MeGX

Resource ID: SCR_000738

Alternate IDs: nif-0000-03109, nif-0000-21260, SCR_008204, r3d100011324

Alternate URLs: <https://doi.org/10.17616/R3B05S>

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260731T042601+0000

Ratings and Alerts

No rating or validation information has been found for MeGX.

No alerts have been found for MeGX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kostadinov I, et al. (2011) Quantifying the effect of environment stability on the transcription factor repertoire of marine microbes. Microbial informatics and experimentation, 1(1), 9.

Hankeln W, et al. (2010) MetaBar - a tool for consistent contextual data acquisition and standards compliant submission. BMC bioinformatics, 11, 358.