# Resource Summary Report

Generated by NIF on May 19, 2025

# Glimmer-MG

RRID:SCR_011932
Type: Tool

## Proper Citation

Glimmer-MG (RRID:SCR_011932)

## Resource Information

**URL:** http://www.cbcb.umd.edu/software/glimmer-mg/

**Proper Citation:** Glimmer-MG (RRID:SCR_011932)

**Description:** A software system for finding genes in environmental shotgun DNA sequences.

**Abbreviations:** Glimmer-MG

**Synonyms:** Glimmer-MG: Metagenomics Gene-Finding System, Gene Locator and Interpolated Markov ModelER - MetaGenomics

**Resource Type:** software resource

**Keywords:** metagenomics, gene

**Funding:**

**Availability:** Open unspecified license, OSI certified

**Resource Name:** Glimmer-MG

**Resource ID:** SCR_011932

**Alternate IDs:** OMICS_01487

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20250420T014602+0000

## Ratings and Alerts

No rating or validation information has been found for Glimmer-MG.

No alerts have been found for Glimmer-MG.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Marcos-Zambrano LJ, et al. (2021) Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. Frontiers in microbiology, 12, 634511.

Sarkar A, et al. (2019) Altered Integrative and Conjugative Elements (ICEs) in Recent Vibrio cholerae O1 Isolated From Cholera Cases, Kolkata, India. Frontiers in microbiology, 10, 2072.

Malla MA, et al. (2018) Exploring the Human Microbiome: The Potential Future Role of Next-Generation Sequencing in Disease Diagnosis and Treatment. Frontiers in immunology, 9, 2868.

Escobar-Zepeda A, et al. (2015) The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. Frontiers in genetics, 6, 348.

Sarkar A, et al. (2015) Attributes of carbapenemase encoding conjugative plasmid pNDM-SAL from an extensively drug-resistant Salmonella enterica Serovar Senftenberg. Frontiers in microbiology, 6, 969.

Gupta A, et al. (2014) Whole genome sequencing and analysis of plant growth promoting bacteria isolated from the rhizosphere of plantation crops coconut, cocoa and arecanut. PloS one, 9(8), e104259.

Yoshida M, et al. (2013) Metagenomic analysis of viral communities in (hado)pelagic sediments. PloS one, 8(2), e57271.