

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

MicrobiomeDB

RRID:SCR_022766

Type: Tool

Proper Citation

MicrobiomeDB (RRID:SCR_022766)

Resource Information

URL: <https://microbiomedb.org/>

Proper Citation: MicrobiomeDB (RRID:SCR_022766)

Description: Systems biology platform for integrating, mining and analyzing microbiome experiments. Data discovery and analysis web based resource that empowers researchers to fully leverage experimental variables to interrogate microbiome datasets. Used to mine complex microbiome and metagenome studies.

Synonyms: MicrobiomeDB.org

Resource Type: data or information resource

Defining Citation: [DOI:10.1093/nar/gkx1027](https://doi.org/10.1093/nar/gkx1027)

Keywords: Data discovery and analysis, microbiome datasets, microbiome and metagenome studies mining, integrating, mining and analyzing microbiome experiments

Availability: Free, Freely available

Resource Name: MicrobiomeDB

Resource ID: SCR_022766

Record Creation Time: 20220921T050149+0000

Record Last Update: 20260725T191024+0000

Ratings and Alerts

No rating or validation information has been found for MicrobiomeDB.

No alerts have been found for MicrobiomeDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Wang L, et al. (2025) A systematic longitudinal study of microbiome: integrating temporal-spatial dimensions with causal and deep learning models. BMC genomics, 26(1), 1068.

Basenko EY, et al. (2024) What is new in FungiDB: a web-based bioinformatics platform for omics-scale data analysis for fungal and oomycete species. Genetics, 227(1).

Taylor KD, et al. (2024) Metagenomic Study of the MESA: Detection of Gemella Morbillorum and Association With Coronary Heart Disease. Journal of the American Heart Association, 13(19), e035693.

Cui W, et al. (2023) The gut microbiome changes in wild type and IL-18 knockout mice after 9.0??Gy total body irradiation. Animal microbiome, 5(1), 42.