

Resource Summary Report

Generated by [RRID](#) on Aug 11, 2026

Meta-Prism

RRID:SCR_021836

Type: Tool

Proper Citation

Meta-Prism (RRID:SCR_021836)

Resource Information

URL: <https://github.com/HUST-NingKang-Lab/Meta-Prism-2.0>

Proper Citation: Meta-Prism (RRID:SCR_021836)

Description: Software tool as microbial community sample search method based on smart pair wise sample comparison without compromising accuracy. Used as microbial communities similarites calculation and comparison tool.

Synonyms: Meta-Prism 2.0

Resource Type: source code, software resource

Keywords: microbial community sample search, sample comparison, microbial communities similarites calculation

Availability: Free, Available for download, Freely available

Resource Name: Meta-Prism

Resource ID: SCR_021836

License: GNU General Public License v3.0

License URLs: <https://github.com/HUST-NingKang-Lab/Meta-Prism-2.0>; <http://meta-prism2.aimicrobiome.cn/Search/Introduction/>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260810T040743+0000

Ratings and Alerts

No rating or validation information has been found for Meta-Prism.

No alerts have been found for Meta-Prism.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Adella A, et al. (2026) RRAGD p.(Ser76Leu) Variant Causes Dysregulated Expression of Muscle Development and Cytoskeleton Genes in Cardiomyocytes. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(12), e72070.

Omachi S, et al. (2026) Ketone Body Supplementation Exerts Renoprotective Effects Against Adenine-Induced Kidney Injury via OXCT1-Mediated Ketolysis in Mice. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(6), e71650.

Kang K, et al. (2022) Meta-Prism 2.0: Enabling algorithm and web server for ultra-fast, memory-efficient, and accurate analysis among millions of microbial community samples. GigaScience, 11.