Resource Summary Report

Generated by RRID on Aug 4, 2026

MaAsLin2

RRID:SCR_023241
Type: Tool

Proper Citation

MaAsLin2 (RRID:SCR_023241)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/Maaslin2.html

Proper Citation: MaAsLin2 (RRID:SCR_023241)

Description: SoftwareR package that identifies microbial taxa correlated with factors of interest using generalized linear models and mixed models.Used for efficiently determining multivariable association between clinical metadata and microbial meta'omic features.

Resource Type: software toolkit, software resource

Defining Citation: DOI:10.1371/journal.pcbi.1009442

Keywords: Microbiome Multivariable Associations with Linear Models,

Funding: NSF DEB-2028280;
NIAID U19AI110820;
NHGRI R01HG005220;
NIDDK R24DK110499;
NIDDK U54DK102557

Availability: Free, Available for download, Freely available

Resource Name: MaAsLin2

Resource ID: SCR_023241

Alternate URLs: https://huttenhower.sph.harvard.edu/maaslin/

License: MIT license

Record Creation Time: 20230207T050158+0000

Record Last Update: 20260803T040854+0000

Ratings and Alerts

No rating or validation information has been found for MaAsLin2.

No alerts have been found for MaAsLin2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 170 mentions in open access literature.

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

de Albuquerque Lemos DE, et al. (2026) Synbiotic Nutraceutical Mitigates Gestational Diabetes Effects and Cardiovascular Dysfunction in Rat Offspring. Molecular nutrition & food research, 70(1), e70340.

An L, et al. (2025) Gut microbiota modulation via fecal microbiota transplantation mitigates hyperoxaluria and calcium oxalate crystal depositions induced by high oxalate diet. Gut microbes, 17(1), 2457490.

Zhang X, et al. (2025) Intestinal TM6SF2 protects against metabolic dysfunction-associated steatohepatitis through the gut-liver axis. Nature metabolism, 7(1), 102.

Yunusbayev B, et al. (2025) Gut dysbiosis narrative in psoriasis: matched-pair approach identifies only subtle shifts correlated with elevated fecal calprotectin. Microbiology spectrum, 13(1), e0138224.

Charlesson B, et al. (2025) Training load influences gut microbiome of highly trained rowing athletes. Journal of the International Society of Sports Nutrition, 22(1), 2507952.

Ji S, et al. (2025) Engrafting gut bacteriophages have potential to modulate microbial metabolism in fecal microbiota transplantation. Microbiome, 13(1), 149.

Jardon KM, et al. (2025) Distinct gut microbiota and metabolome features of tissue-specific insulin resistance in overweight and obesity. Gut microbes, 17(1), 2501185.

Peng Q, et al. (2025) In vivo systematic analysis of microbiota-prebiotic crosstalk reveals a synbiotic that effectively ameliorates DSS-induced colitis in mice. Gut microbes, 17(1), 2541028.

Yu S, et al. (2025) Identification of a 10-species microbial signature of inflammatory bowel disease by machine learning and external validation. Cell regeneration (London, England), 14(1), 32.

Temmermans J, et al. (2025) Agricultural practices and pollinators modulate the anthosphere microbiome. ISME communications, 5(1), ycaf026.

Prajapati SK, et al. (2025) Protection of Alzheimer's disease progression by a human-origin probiotics cocktail. Scientific reports, 15(1), 1589.

Fan J, et al. (2025) Potential roles of cigarette smoking on gut microbiota profile among Chinese men. BMC medicine, 23(1), 25.

Pirola CJ, et al. (2025) Metabolic dysfunction-associated steatotic liver disease exhibits sex-specific microbial heterogeneity within intestinal compartments. Clinical and molecular hepatology, 31(1), 179.

Wong MK, et al. (2025) Microbial Ecosystem Therapeutics 4 (MET4) elicits treatment-specific IgG responses associated with changes in gut microbiota in immune checkpoint inhibitor recipients with advanced solid tumors. Journal for immunotherapy of cancer, 13(3).

Ravelo AD, et al. (2025) Associations between hyperketonemia and the rumen metagenome and metabolome in Holstein cows during the first 2 weeks postpartum. Animal microbiome, 7(1), 59.

Schmidt JE, et al. (2025) Optimizing Cocoa Productivity Through Soil Health and Microbiome Enhancement: Insights from Organic Amendments and a Locally Derived Biofertilizer. Microorganisms, 13(6).

Soto-L??pez JD, et al. (2025) Taxonomic and functional profiling of bat guano microbiota from hiking trail-associated tunnels: a potential risk for human health? Environmental microbiome, 20(1), 123.

Sommer F, et al. (2025) Life-long microbiome rejuvenation improves intestinal barrier function and inflammaging in mice. Microbiome, 13(1), 91.

Leech SM, et al. (2025) Consensus approach to differential abundance analysis detects few differences in the oral microbiome of pregnant women due to pre-existing type 2 diabetes mellitus. Microbial genomics, 11(4).

Wagner J, et al. (2025) Early-life gut microbiome associates with positive vaccine take and shedding in neonatal schedule of the human neonatal rotavirus vaccine RV3-BB. Nature communications, 16(1), 3432.