

Resource Summary Report

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metagenomeseq

RRID:SCR_024246

Type: Tool

Proper Citation

metagenomeseq (RRID:SCR_024246)

Resource Information

URL: <https://bioconductor.org/packages/metagenomeSeq/>

Proper Citation: metagenomeseq (RRID:SCR_024246)

Description: Software R package to determine features that are differentially abundant between two or more groups of multiple samples. Used to address the effects of both normalization and under-sampling of microbial communities on disease association detection and testing of feature correlations.

Resource Type: software resource, software toolkit

Keywords: determine features that are differentially abundant, two or more groups of multiple samples, disease association detection, testing of feature correlations,

Resource Name: metagenomeseq

Resource ID: SCR_024246

Alternate IDs: OMICS_07813

Alternate URLs: <https://sources.debian.org/src/r-bioc-metagenomeseq/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260904T000043+0000

Ratings and Alerts

No rating or validation information has been found for metagenomeseq.

No alerts have been found for metagenomeseq.

Data and Source Information

Usage and Citation Metrics

We found 243 mentions in open access literature.

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

He Z, et al. (2026) Gut microbiota remodeling by Astragalus membranaceus stems and leaves correlates dual modulation of arachidonic acid and tryptophan metabolism to counteract perinatal stress-induced hemometabolic dysregulation in sows. *Animal microbiome*, 8(1), 21.

Holman DB, et al. (2026) Multi-omic characterization of the sow colostrum and milk microbiome and proteome. *Microbial genomics*, 12(6).

Drovetski SV, et al. (2026) Cotton farming affects ileal virome in a sedentary wild passerine. *Animal microbiome*, 8(1), 8.

Castaldi V, et al. (2026) Prosystemin-derived signals: bridging leaf microbiome dynamics and defense activation. *Environmental microbiome*, 21(1).

Han N, et al. (2026) Formulation-dependent kinetics of *Lactocaseibacillus paracasei* Zhang in mice. *Microbiology spectrum*, 14(6), e0363725.

Godoy-Lozano EE, et al. (2026) Enrichment hydrocarbon-degrading bacterial communities from the southern Gulf of Mexico in long-term stored sediments. *Biodegradation*, 37(2).

Consuegra-Asprilla JM, et al. (2026) Characterization of the vaginal microbiome and its metabolic potential in Colombian patients with recurrent vulvovaginal candidiasis. *Medical mycology*, 64(4).

Wu CE, et al. (2026) Effects of *Ligilactobacillus salivarius* on the control of pullorum disease and cecal microbiota in red-feathered native chickens. *Poultry science*, 105(3), 106384.

Lin F, et al. (2026) An engineered *Escherichia coli*-ClyA-NetB outer membrane vesicle delivery system modulates jejunal microbiota in broiler chickens with necrotic enteritis. *Poultry science*, 105(8), 107062.

Chen Y, et al. (2026) Dietary *Bacillus subtilis* Group Reduces the General Infection of *Salmonella Pullorum* in Broiler Chicken. *Antibiotics (Basel, Switzerland)*, 15(4).

Aldeia C, et al. (2026) A commercial bacteriophage cocktail failed to decolonize *Zophobas morio* larvae and promoted overgrowth of an OXA-48-producing *Salmonella enterica*. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 45(2), 363.

Liu Y, et al. (2026) Acute High-Intensity Noise Exposure Induces Cognitive Impairment and Arachidonic Acid Metabolism-Related Molecular Alterations in Rats: A Multi-Omics

Study. *Metabolites*, 16(2).

Alexandre PA, et al. (2026) Harnessing gastrointestinal microbial co-association networks to predict feed efficiency and methane emissions across beef and dairy cattle. *Microbial genomics*, 12(4).

Chen YJ, et al. (2026) *Akkermansia Muciniphila* Ameliorates Imiquimod-Induced Skin Thickening, Colitis, and Gut Microbiota Alterations: A Metagenome Association Study. *Inflammation*, 49(1), 78.

Mei Z, et al. (2026) Traditional Chinese medicine improves performance and intestinal health in laying hens under acute and chronic heat stress by modulating ileal metabolic functions. *Poultry science*, 105(8), 107056.

Castonguay-Paradis S, et al. (2025) The Human Fecal Endocannabinoidome Mediator Profile Is Mainly Defined by the Fecal Microbiota and Diet. *The Journal of clinical endocrinology and metabolism*, 110(3), 739.

Gao CY, et al. (2025) Abdominal ultrasound stimulation alleviates DSS-induced colitis and behavioral disorders in mice by mediating the microbiota-gut-brain axis balance. *Neurotherapeutics : the journal of the American Society for Experimental NeuroTherapeutics*, 22(2), e00494.

Hao W, et al. (2025) Intestinal epithelial *Dicer1* regulates gut microbiome and Alzheimer's pathology in App-knock-in mice. *Alzheimer's research & therapy*, 17(1), 202.

Liu X, et al. (2025) Comprehensive metabolomic and microbial analysis of tobacco rhizosphere soil responses to crop rotation and fertilization. *Frontiers in plant science*, 16, 1595870.

Ahn JS, et al. (2025) Comparison of metagenomic analysis of fecal and gastrointestinal tract samples for identifying beneficial gut microorganisms. *Frontiers in microbiology*, 16, 1533580.