

# Resource Summary Report

Generated by T1D on Sep 5, 2026

## 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 [T1D](#) .

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.

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

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

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.

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).

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).

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

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

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).

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.

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.

Spiegelhauer MR, et al. (2025) Protection against experimental necrotizing enterocolitis by fecal filtrate transfer requires an active donor virome. *Gut microbes*, 17(1), 2486517.

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.

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.