

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 3, 2026

LEfSe

RRID:SCR_014609

Type: Tool

Proper Citation

LEfSe (RRID:SCR_014609)

Resource Information

URL: <http://huttenhower.sph.harvard.edu/galaxy>

Proper Citation: LEfSe (RRID:SCR_014609)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Algorithm for high-dimensional biomarker discovery and explanation that identifies genes, pathways, or taxa characterizing the differences between two or more biological conditions. The algorithm identifies features that are statistically different among biological classes, then performs additional tests to assess whether these differences are consistent with respect to expected biological behavior. Statistical significance and biological relevance are emphasized., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: LDA Effect Size

Resource Type: algorithm resource, software resource

Defining Citation: [DOI:10.1186/gb-2011-12-6-r60](https://doi.org/10.1186/gb-2011-12-6-r60)

Keywords: microbiome, algorithm, biomarker, genomic feature, web application

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: LEfSe

Resource ID: SCR_014609

Alternate IDs: OMICS_07818

Alternate URLs: <https://sources.debian.org/src/lefse/>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260803T040639+0000

Ratings and Alerts

No rating or validation information has been found for LEfSe.

No alerts have been found for LEfSe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7008 mentions in open access literature.

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

Zhang L, et al. (2026) Identification of key gut microbiota and microbial QTL in contributing to the significant differences in body weight between two Chinese local chicken breeds. *Animal genetics*, 57(1), e70060.

Kim CW, et al. (2025) Gut dysbiosis from high-salt diet promotes glioma via propionate-mediated TGF- β activation. *The Journal of experimental medicine*, 222(8).

Beckers KF, et al. (2025) Pregnancy-specific shifts in the maternal microbiome and metabolome in the BPH/5 mouse model of superimposed preeclampsia. *Physiological genomics*, 57(3), 115.

Jin S, et al. (2025) Disruption of the transsulfuration pathway by acute kidney injury causes intestinal damage. *iScience*, 28(10), 113511.

Abukhiran IM, et al. (2025) Mucosal Microbiome Markers of Complete Pathologic Response to Neoadjuvant Therapy in Rectal Carcinoma. *Cancer research communications*, 5(5), 756.

Zhang T, et al. (2025) Intratumoral *Fusobacterium nucleatum* Recruits Tumor-Associated Neutrophils to Promote Gastric Cancer Progression and Immune Evasion. *Cancer research*, 85(10), 1819.

Pu Y, et al. (2025) Gut metagenome and plasma metabolome profiles in older adults suggest pyruvate metabolism as a link between sleep quality and frailty. *Cell reports*, 44(10), 116297.

Wu JJ, et al. (2025) Melatonin alleviates high temperature exposure induced fetal growth restriction via the gut-placenta-fetus axis in pregnant mice. *Journal of advanced research*, 68, 131.

Chero-Sandoval L, et al. (2025) Comparative assessment of phenotypic markers in patients with chronic inflammation: Differences on *Bifidobacterium* concerning liver status. *European journal of clinical investigation*, 55(2), e14339.

Lin H, et al. (2025) Metagenome-based diversity and functional analysis of culturable microbes in sugarcane. *Microbiology spectrum*, 13(1), e0198224.

Xi Y, et al. (2025) Stability of gut microbiota in non-small cell lung cancer patients during chemoradiotherapy and its association with radiation pneumonitis. *iScience*, 28(8), 113163.

Dong J, et al. (2025) Extraction of anthocyanins from purple sweet potato: evaluation of anti-inflammatory effects in a rheumatoid arthritis animal model, mechanistic studies on inflammatory cells, and development of exosome-based delivery for enhanced targeting. *Frontiers in immunology*, 16, 1559874.

Dang Y, et al. (2025) Gut microbiome signatures predict 5-ASA efficacy in ulcerative colitis. *iScience*, 28(6), 112568.

Lee JG, et al. (2025) Loss of *Cutibacterium* is responsible for chronic kidney disease-associated pruritus in patients on dialysis. *Kidney research and clinical practice*, 44(1), 176.

Hicks C, et al. (2025) Oral, Vaginal, and Stool Microbial Signatures in Patients With Endometriosis as Potential Diagnostic Non-Invasive Biomarkers: A Prospective Cohort Study. *BJOG : an international journal of obstetrics and gynaecology*, 132(3), 326.

Zhang X, et al. (2025) Gut microbiota signatures in food allergy children without and with malnutrition: a cross-sectional study. *BMC pediatrics*, 25(1), 220.

Jiamin X, et al. (2025) The distribution of aerobic bacteria in Chinese cropland is linked to the soil texture. *Frontiers in microbiology*, 16, 1541460.

Mai Z, et al. (2025) Intra-tumoral sphingobacterium multivorum promotes triple-negative breast cancer progression by suppressing tumor immunosurveillance. *Molecular cancer*, 24(1), 6.

Sundararajan P, et al. (2025) The impact of spray-induced gene silencing on cereal phyllosphere microbiota. *Environmental microbiome*, 20(1), 1.

Zhu H, et al. (2025) The gut microbiota-SCFA-inflammation axis in patients with AECOPD. *PloS one*, 20(1), e0312606.