

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 2026

ALDEx2

RRID:SCR_003364

Type: Tool

Proper Citation

ALDEx2 (RRID:SCR_003364)

Resource Information

URL: <https://github.com/ggloor/ALDEx2>

Proper Citation: ALDEx2 (RRID:SCR_003364)

Description: Software tool to examine compositional high-throughput sequence data with Welch's t-test. A differential relative count abundance analysis for the comparison of two conditions. For example, single-organism and meta-rna-seq high-throughput sequencing assays, or of selected and unselected values from in-vitro sequence selections. Uses a Dirichlet-multinomial model to infer abundance from counts, that has been optimized for three or more experimental replicates. Infers sampling variation and calculates the expected Benjamini-Hochberg false discovery rate given the biological and sampling variation using several parametric and non-parametric tests. Can to glm and Kruskal-Wallace tests on one-way ANOVA style designs.

Resource Type: software resource

Defining Citation: [PMID:24910773](#)

Keywords: standalone software, r, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: ALDEx2

Resource ID: SCR_003364

Alternate IDs: biotools:aldex2, OMICS_04634

Alternate URLs: <https://bio.tools/aldex2>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260912T195557+0000

Ratings and Alerts

No rating or validation information has been found for ALDEx2.

No alerts have been found for ALDEx2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 609 mentions in open access literature.

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

Jensen EEB, et al. (2026) Tanzanian goat gut microbiomes adapt to roadside pollutants and environmental stressors. Microbiology spectrum, 14(2), e0203625.

Dowrick JM, et al. (2026) Integrated multi-omic and symptom clustering reveals lower-gastrointestinal disorders of gut-brain interaction heterogeneity. Gut microbes, 18(1), 2604871.

Serrano GA, et al. (2026) Environmental gradients and habitat specificity structure benthic microbial assemblages in a temperate seagrass ecosystem. bioRxiv : the preprint server for biology.

Weber C, et al. (2026) Dysbiotic shift in the oral microbiota of patients with Alzheimer's disease compared to their healthy life partners-a combinatorial approach and a paired study design. Alzheimer's research & therapy, 18(1), 23.

Odendaal J, et al. (2026) CD138 expression in the endometrium associates with endometrial timing and inflammatory status but not microbiota composition. Human reproduction (Oxford, England), 41(5), 699.

Wang R, et al. (2026) Mikania micrantha invasion restructures rhizosphere nitrogen cycling through enzyme activation, microbial recruitment, and allelopathic regulation. Microbiome, 14(1).

Sangermani M, et al. (2026) Effects of repeated freeze and thaw cycles on the stability of faecal microbiome composition. Scientific reports, 16(1).

Gu Y, et al. (2026) Structurally distinct yeast-derived β -glucans modulate intestinal morphology and microbial metabolism in broiler chickens differentially. Poultry science, 105(5), 106689.

Krupa-Kozak U, et al. (2026) INulin-type β -fructans supplementation to modulate gut microbiota and assessment of its effects on health status and GUT-SKIN axis parameters in patients with psoriasis (INGUTSKIN): the 8-week, randomised, double-blind, placebo-controlled clinical study protocol. Nutrition journal, 25(1).

Silvaraju S, et al. (2026) Transgenerational dynamics of gut microbiota in black soldier fly larvae (*Hermetia illucens*) reared on a novel substrate. *Microbiology spectrum*, 14(5), e0190325.

de Freitas AS, et al. (2026) Boosting tree growth in the Amazon rainforest using Amazonian Dark Earths. *BMC ecology and evolution*, 26(1), 15.

Shan Y, et al. (2026) Sex-biased intratumoral microbiome influences tumor molecular and immune landscape and disease outcomes. *Cell reports. Medicine*, 7(5), 102757.

Zhang P, et al. (2026) Gut microbiota and SCFA biomarkers for early diagnosis of PD patients and differentiation of its motor subtypes. *NPJ Parkinson's disease*, 12(1).

Ji X, et al. (2026) ResMicroDb: a comprehensive database and analysis platform for the human respiratory microbiome. *Nucleic acids research*, 54(D1), D858.

Magistrado D, et al. (2026) The *Aedes aegypti* bacterial microbiota is robust to infection with the obligate microsporidian parasite *Edhazardia aedis*. *bioRxiv : the preprint server for biology*.

Kim YC, et al. (2026) Identification of an altered gut microbiome and the protective effect of microbiome changer in prion diseases. *Veterinary research*, 57(1), 31.

Dellisanti W, et al. (2026) Interactive effects of warming and iron supplementation on O₂ dynamics, trace metal content, and microbial diversity within different compartments of two Mediterranean corals. *Biology open*, 15(1).

Holdaway CM, et al. (2026) Dietary Ethanolamine Increases Hepatic Lipid Accumulation in Mice Fed a High Fat Diet. *The Journal of nutrition*, 101348.

Ndlovu KS, et al. (2026) The vaginal microbiome of pregnant people living with HIV on antiretroviral therapy in the Democratic Republic of Congo: a pilot study and global meta-analysis. *mSphere*, 11(2), e0059725.

Valdez-Palomares F, et al. (2026) Human fecal transplantation from stunted children promotes metabolic dysfunction in mice fed with a high-fat and high-fructose corn syrup diet. *Gut microbes*, 18(1), 2651984.