

Resource Summary Report

Generated by [kravitz2](#) on Sep 19, 2026

ALDEx2

RRID:SCR_003364

Type: Tool

Proper Citation

ALDEx2 (RRID:SCR_003364)

Resource Information

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

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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 [kravitz2](#) .

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.

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

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

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).

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.

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.

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

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

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*.

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

Krupa-Kozak U, et al. (2026) INulin-type γ -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).

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.

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.