

Resource Summary Report

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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: 20260725T190540+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 529 mentions in open access literature.

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

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.

Steinsdóttir HGR, et al. (2026) Microbial dynamics in coral reef waters: Diel cycles in contrasting seasons. Science advances, 12(1), eady9534.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. Microbiome, 13(1), 200.

Rodiles A, et al. (2025) Supplementation of a new combination of prebiotic and postbiotic shapes fecal microbiota of old dogs while influencing immune parameters. Scientific reports, 15(1), 28447.

Chao H, et al. (2025) Litter quality modulates changes in bacterial and fungal communities during the gut transit of earthworm species of different ecological groups. ISME communications, 5(1), ycae171.

Brunet M, et al. (2025) Year-Round Quantification, Structure and Dynamics of Epibacterial Communities From Diverse Macroalgae Reveal a Persistent Core Microbiota and Strong Host Specificities. Environmental microbiology reports, 17(2), e70077.

Otani S, et al. (2025) Genomic and functional co-diversification imprint African Hominidae microbiomes to signal dietary and lifestyle adaptations. Gut microbes, 17(1), 2484385.

Dufresne K, et al. (2025) TSST-1 promotes colonization of Staphylococcus aureus within the vaginal tract by activation of CD8+ T cells. Infection and immunity, 93(2), e0043924.

Welham Z, et al. (2025) Gut Mucosal Microbiome of Patients With Low-Grade Adenomatous Bowel Polyps. Gastro hep advances, 4(8), 100687.

García-Sánchez JC, et al. (2025) Differences in composition and potential function of the bacterial communities of cave- and surface-dwelling Mexican salamanders. Animal microbiome, 7(1), 56.

McGovern KC, et al. (2025) Replacing normalizations with interval assumptions enhances differential expression and differential abundance analyses. *BMC bioinformatics*, 26(1), 164.

Fernández-González AJ, et al. (2025) Unveiling essential host genes and keystone microorganisms of the olive tree holobiont linked to *Verticillium* wilt tolerance. *Microbiome*, 13(1), 239.

Philippe C, et al. (2025) Diversity of the *Ixodes ricinus* Microbiome Across Belgian Ecoregions and Its Association with Pathogen and Symbiont Presence. *Microbial ecology*, 88(1), 73.

Foley MH, et al. (2025) Differential modulation of post-antibiotic colonization resistance to *Clostridioides difficile* by two probiotic *Lactobacillus* strains. *mBio*, 16(8), e0146825.

Pivrcova E, et al. (2025) Viable bacterial communities in freshly pumped human milk and their changes during cold storage conditions. *International breastfeeding journal*, 20(1), 44.

Matijašić M, et al. (2025) Serum proteins and faecal microbiota as potential biomarkers in newly diagnosed, treatment-naïve inflammatory bowel disease and irritable bowel syndrome patients. *Journal of molecular medicine (Berlin, Germany)*, 103(8), 963.

Bartosik T, et al. (2025) Dupilumab treatment has no effect on the nasal microbiome in patients with NSAID-exacerbated respiratory disease: a longitudinal pilot study. *Frontiers in immunology*, 16, 1508500.

Andersen S, et al. (2025) Prebiotic fiber enteral supplementation after allogeneic transplantation: feasibility and impact on the microbiome. *Blood advances*, 9(16), 4167.

Liu H, et al. (2025) Unexplored diversity and potential functions of extra-chromosomal elements. *mSystems*, 10(9), e0017525.

Cortez-Martínez M, et al. (2025) Seasonal and spatial dynamics of the intestinal microbiome in tropical freshwater fish: insights from *Astyanax aeneus* and *Brycon costaricensis* in the Peñas Blancas river basin, Costa Rica. *BMC microbiology*, 25(1), 595.