

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 [nidm-terms](#) .

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.