Resource Summary Report

Generated by NIF on Apr 17, 2025

Krona

RRID:SCR_012785
Type: Tool

Proper Citation

Krona (RRID:SCR_012785)

Resource Information

URL: http://sourceforge.net/p/krona/home/krona/

Proper Citation: Krona (RRID:SCR_012785)

Description: Software that allows hierarchical data to be explored with zoomable pie charts.

Abbreviations: Krona

Synonyms: Krona - Hierarchical data browser

Resource Type: software resource

Defining Citation: PMID:21961884

Keywords: bio.tools

Funding:

Resource Name: Krona

Resource ID: SCR_012785

Alternate IDs: OMICS_01498, biotools:krona

Alternate URLs: https://bio.tools/krona

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250410T070305+0000

Ratings and Alerts

No rating or validation information has been found for Krona.

No alerts have been found for Krona.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 73 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Wang S, et al. (2024) Effects of mulch films with different thicknesses on the microbial community of tobacco rhizosphere soil in Yunnan laterite. Frontiers in microbiology, 15, 1458470.

Landicho DM, et al. (2024) Status of Cassava Witches' Broom Disease in the Philippines and Identification of Potential Pathogens by Metagenomic Analysis. Biology, 13(7).

Peng L, et al. (2024) Altered microbial diversity and composition of multiple mucosal organs in cervical cancer patients. BMC cancer, 24(1), 1154.

Du C, et al. (2024) Biocontrol Agents Inhibit Banana Fusarium Wilt and Alter the Rooted Soil Bacterial Community in the Field. Journal of fungi (Basel, Switzerland), 10(11).

Pinheiro LRS, et al. (2024) Identification of Viruses in Molossus Bats from the Brazilian Amazon: A Descriptive Metagenomic Analysis. Microorganisms, 12(3).

Omar KM, et al. (2024) Investigating antimicrobial resistance genes in Kenya, Uganda and Tanzania cattle using metagenomics. PeerJ, 12, e17181.

Zayakin P, et al. (2024) sRNAflow: A Tool for the Analysis of Small RNA-Seq Data. Non-coding RNA, 10(1).

Zhong S, et al. (2024) Efficacy Assessment of the Co-Administration of Vancomycin and Metronidazole in Clostridioides difficile-Infected Mice Based on Changes in Intestinal Ecology. Journal of microbiology and biotechnology, 34(4), 828.

Wang W, et al. (2023) Diversity of Fungal Communities on Diseased and Healthy Cinnamomum burmannii Fruits and Antibacterial Activity of Secondary Metabolites. Microbiology spectrum, 11(3), e0008023.

Wei N, et al. (2023) Characterization of oral bacterial and fungal microbiome in recovered COVID-19 patients. BMC microbiology, 23(1), 123.

Düsedau L, et al. (2023) Elevated Temperature-Induced Epimicrobiome Shifts in an Invasive Seaweed Gracilaria vermiculophylla. Microorganisms, 11(3).

Yang F, et al. (2023) Effects of Rhizosphere Microbial Communities on Cucumber Fusarium wilt Disease Suppression. Microorganisms, 11(6).

Ai B, et al. (2023) Uncovering the special microbiota associated with occurrence and progression of gastric cancer by using RNA-sequencing. Scientific reports, 13(1), 5722.

Feng L, et al. (2023) Altered rumen microbiome and correlations of the metabolome in heat-stressed dairy cows at different growth stages. Microbiology spectrum, 11(6), e0331223.

Sim EM, et al. (2023) Persistent Salmonella enterica serovar Typhi sub-populations within host interrogated by whole genome sequencing and metagenomics. PloS one, 18(8), e0289070.

Meyer S, et al. (2023) Bioaerosols in swine confinement buildings: A metaproteomic view. Environmental microbiology reports, 15(6), 684.

Popov IV, et al. (2023) Detection of coronaviruses in insectivorous bats of Fore-Caucasus, 2021. Scientific reports, 13(1), 2306.

Tie J, et al. (2023) Yield and Rhizosphere Soil Environment of Greenhouse Zucchini in Response to Different Planting and Breeding Waste Composts. Microorganisms, 11(4).

Zhao Z, et al. (2023) Integrated analysis of how gender and body weight affect the intestinal microbial diversity of Gymnocypris chilianensis. Scientific reports, 13(1), 8811.