Resource Summary Report

Generated by NIF on Apr 25, 2025

ARB project

RRID:SCR_000515
Type: Tool

Proper Citation

ARB project (RRID:SCR_000515)

Resource Information

URL: http://www.arb-home.de/

Proper Citation: ARB project (RRID:SCR_000515)

Description: Software environment for maintaining databases of molecular sequences and additional information, and for analyzing the sequence data, with emphasis on phylogeny reconstruction. Programs have primarily been developed for ribosomal ribonucleic acid (rRNA) sequences and, therefore, contain special tools for alignment and analysis of these structures. However, other molecular sequence data can also be handled. Protein gene sequences and predicted protein primary structures as well as protein secondary structures can be stored in the same database. ARB package is designed for graphical user interface. Program control and data display are available in a hierarchical set of windows and subwindows. Majority of operations can be controlled using mouse for moving pointer and the left mouse button for initiating and performing operations.

Abbreviations: ARB

Synonyms: The ARB project

Resource Type: software resource

Defining Citation: PMID:14985472

Keywords: rrna sequence, rrna, phylogeny, alignment, analysis, protein, gene

Funding:

Availability: Free, Freely available

Resource Name: ARB project

Resource ID: SCR_000515

Alternate IDs: OMICS_01515

Alternate URLs: https://sources.debian.org/src/arb/

License URLs: Http://help.arb-home.de/copyright.html

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250420T013952+0000

Ratings and Alerts

No rating or validation information has been found for ARB project.

No alerts have been found for ARB project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Prem EM, et al. (2023) Effects of phenyl acids on different degradation phases during thermophilic anaerobic digestion. Frontiers in microbiology, 14, 1087043.

Peng J, et al. (2018) Metatranscriptomics reveals a differential temperature effect on the structural and functional organization of the anaerobic food web in rice field soil. Microbiome, 6(1), 169.

Lehours AC, et al. (2018) Biogeographic patterns of aerobic anoxygenic phototrophic bacteria reveal an ecological consistency of phylogenetic clades in different oceanic biomes. Scientific reports, 8(1), 4105.

Maixner F, et al. (2018) The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. Current biology : CB, 28(14), 2348.

Garate L, et al. (2017) Endosymbiotic calcifying bacteria across sponge species and oceans. Scientific reports, 7, 43674.

Mohr KI, et al. (2017) Myxobacteria in high moor and fen: An astonishing diversity in a neglected extreme habitat. MicrobiologyOpen, 6(4).

Chesneau T, et al. (2017) Sequevar Diversity and Virulence of Ralstonia solanacearum Phylotype I on Mayotte Island (Indian Ocean). Frontiers in plant science, 8, 2209.

Dowell F, et al. (2016) Microbial Communities in Methane- and Short Chain Alkane-Rich Hydrothermal Sediments of Guaymas Basin. Frontiers in microbiology, 7, 17.

Fradet DT, et al. (2016) Members of the methanotrophic genus Methylomarinum inhabit inland mud pots. PeerJ, 4, e2116.

Leite J, et al. (2016) Cowpea Nodules Harbor Non-rhizobial Bacterial Communities that Are Shaped by Soil Type Rather than Plant Genotype. Frontiers in plant science, 7, 2064.

Mohr KI, et al. (2016) Comparison of myxobacterial diversity and evaluation of isolation success in two niches: Kiritimati Island and German compost. MicrobiologyOpen, 5(2), 268.

Raes EJ, et al. (2016) Reduction of the Powerful Greenhouse Gas N2O in the South-Eastern Indian Ocean. PloS one, 11(1), e0145996.

Han Y, et al. (2015) The globally widespread genus Sulfurimonas: versatile energy metabolisms and adaptations to redox clines. Frontiers in microbiology, 6, 989.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 4, 38.

Frindte K, et al. (2015) Microbial Response to Experimentally Controlled Redox Transitions at the Sediment Water Interface. PloS one, 10(11), e0143428.

Zaraî Jaouadi N, et al. (2015) A novel keratinase from Bacillus tequilensis strain Q7 with promising potential for the leather bating process. International journal of biological macromolecules, 79, 952.

Mhuantong W, et al. (2015) Survey of Microbial Diversity in Flood Areas during Thailand 2011 Flood Crisis Using High-Throughput Tagged Amplicon Pyrosequencing. PloS one, 10(5), e0128043.

Essinger SD, et al. (2015) A toolkit for ARB to integrate custom databases and externally built phylogenies. PloS one, 10(1), e0109277.

Silva PE, et al. (2015) Leprous lesion presents enrichment of opportunistic pathogenic bacteria. SpringerPlus, 4, 187.

Hori T, et al. (2015) Isolation of microorganisms involved in reduction of crystalline iron(III) oxides in natural environments. Frontiers in microbiology, 6, 386.