Resource Summary Report

Generated by NIF on Apr 18, 2025

Database Enabled Code for Ideal Probe Hybridization Employing R

RRID:SCR_000581
Type: Tool

Proper Citation

Database Enabled Code for Ideal Probe Hybridization Employing R (RRID:SCR_000581)

Resource Information

URL: http://decipher.cee.wisc.edu/index.html

Proper Citation: Database Enabled Code for Ideal Probe Hybridization Employing R (RRID:SCR_000581)

Description: A software toolset that can be used for deciphering and managing DNA sequences efficiently using the R statistical programming language.

Abbreviations: DECIPHER

Resource Type: software toolkit, software resource

Defining Citation: PMID:22101057

Keywords: 16s rrna sequence, chimera, primer, probe, array, 16s oligo, dna sequence, r

Funding:

Availability: Free

Resource Name: Database Enabled Code for Ideal Probe Hybridization Employing R

Resource ID: SCR_000581

Alternate IDs: OMICS_01114

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250412T054553+0000

Ratings and Alerts

No rating or validation information has been found for Database Enabled Code for Ideal Probe Hybridization Employing R.

No alerts have been found for Database Enabled Code for Ideal Probe Hybridization Employing R.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Hanajima D, et al. (2015) Survival of free-living Acholeplasma in aerated pig manure slurry revealed by (13)C-labeled bacterial biomass probing. Frontiers in microbiology, 6, 1206.

Zaborin A, et al. (2014) Membership and behavior of ultra-low-diversity pathogen communities present in the gut of humans during prolonged critical illness. mBio, 5(5), e01361.