

# Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

## DAFGA

RRID:SCR\_003319

Type: Tool

### Proper Citation

DAFGA (RRID:SCR\_003319)

### Resource Information

**URL:** <https://github.com/outbig/DAFGA>

**Proper Citation:** DAFGA (RRID:SCR\_003319)

**Description:** A python script package which estimates the evolutionary rate of a particular functional gene in a standardized manner by relating its sequence divergence to that of the 16S rRNA gene. It provides gene-specific parameter sets for OTU clustering and taxonomic assignment at desired rank, and it can be implemented into the diversity measurements offered by QIIME or Mothur.

**Synonyms:** DAFGA: Diversity Analysis of Functional Gene Amplicons, Diversity analysis of Functional Gene Amplicons

**Resource Type:** software resource

**Defining Citation:** [PMID:24939150](#)

**Keywords:** standalone software, python

**Availability:** Free, Available for download, Freely available

**Resource Name:** DAFGA

**Resource ID:** SCR\_003319

**Alternate IDs:** OMICS\_04654

**Record Creation Time:** 20220129T080218+0000

**Record Last Update:** 20260912T195556+0000

### Ratings and Alerts

No rating or validation information has been found for DAFGA.

No alerts have been found for DAFGA.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [Kravitz](#) .

Z??niga-Gonzalez CA, et al. (2022) Diversity of functional edaphic macrofauna in Musa acuminata x Musa balbisiana (AAB) agroecosystems. F1000Research, 11, 1300.