

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

Grinder

RRID:SCR_000168

Type: Tool

Proper Citation

Grinder (RRID:SCR_000168)

Resource Information

URL: <http://sourceforge.net/projects/biogrinder/>

Proper Citation: Grinder (RRID:SCR_000168)

Description: An open-source bioinformatic tool to create simulated omic shotgun and amplicon sequence libraries for all main sequencing platforms. The tool is available through multiple interfaces like GUI, CLI and API. It is useful for simulating clinical or environmental microbial communities and complements the use of in vitro mock communities.

Abbreviations: Grinder

Resource Type: software resource

Defining Citation: [PMID:22434876](#), [DOI:10.1093/nar/gks251](#)

Keywords: simulation, amplicon, shotgun, genomic sequencing, clinical, metagenomic, transcriptomic and metatranscriptomic

Availability: Free, Available for download, Freely available

Resource Name: Grinder

Resource ID: SCR_000168

Alternate IDs: OMICS_01508

Alternate URLs: <https://sources.debian.org/src/grinder/>

License: GNU General Public License version 2.0 (GPLv2) Features

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260808T185715+0000

Ratings and Alerts

No rating or validation information has been found for Grinder.

No alerts have been found for Grinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Leung RK, et al. (2015) Circulating microbial RNA and health. Scientific reports, 5, 16814.

Angly FE, et al. (2012) Grinder: a versatile amplicon and shotgun sequence simulator. Nucleic acids research, 40(12), e94.

Angly FE, et al. (2009) The GAAS metagenomic tool and its estimations of viral and microbial average genome size in four major biomes. PLoS computational biology, 5(12), e1000593.