Resource Summary Report

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Stanford Geomicrobiology Shared Laboratories Core Facility

RRID:SCR_025000
Type: Tool

Proper Citation

Stanford Geomicrobiology Shared Laboratories Core Facility (RRID:SCR_025000)

Resource Information

URL: https://geomicrobiologylabs.stanford.edu/

Proper Citation: Stanford Geomicrobiology Shared Laboratories Core Facility (RRID:SCR_025000)

Description: Geomicrobiology analytical facilities consist of four different labs in the Green Earth Sciences Building. Main areas of study are: molecular, bio(geo)chemical, and ecological aspects of microbial cycling of nitrogen, carbon, and metals in environment diversity, distribution, and activity of microorganisms driving greenhouse gas cycling in ocean and beyond molecular biomarkers in modern organisms to refine our interpretations of microbial fossil record.

Synonyms: https://geomicrobiologylabs.stanford.edu/

Resource Type: access service resource, service resource, core facility

Keywords: ABRF, geomicrobiology analytical facilities,

Resource Name: Stanford Geomicrobiology Shared Laboratories Core Facility

Resource ID: SCR_025000

Alternate IDs: ABRF_2630

Alternate URLs: https://coremarketplace.org/?FacilityID=2630&citation=1

Record Creation Time: 20240210T050231+0000

Record Last Update: 20260729T044615+0000

Ratings and Alerts

No rating or validation information has been found for Stanford Geomicrobiology Shared Laboratories Core Facility.

No alerts have been found for Stanford Geomicrobiology Shared Laboratories Core Facility.

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 nidm-terms .

McShea HS, et al. (2025) The evolutionary history and modern diversity of triterpenoid cyclases. bioRxiv : the preprint server for biology.

McShea HS, et al. (2025) The Evolutionary History and Modern Diversity of Triterpenoid Cyclases. Molecular biology and evolution, 42(9).

Jaffe AL, et al. (2025) Abundant and metabolically flexible bacterial lineages underlie a vast potential for rubisco-mediated carbon fixation in the dark ocean. Genome biology, 26(1), 167.