

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

Parallel-META

RRID:SCR_000121

Type: Tool

Proper Citation

Parallel-META (RRID:SCR_000121)

Resource Information

URL: <http://www.computationalbioenergy.org/parallel-meta.html>

Proper Citation: Parallel-META (RRID:SCR_000121)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 30,2023. Open source pipeline for metagenomic data analysis, which enables efficient and parallel analysis of multiple metagenomic datasets and visualization of results for multiple samples. Can perform rapid data mining among microbial community data for comparative taxonomic and functional analysis.

Synonyms: Parallel META, Parallel Meta

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: [PMID:23046922](#)

Keywords: data mining, microbial community data, comparative taxonomics, metagenomic analysis, parallel algorithms

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Parallel-META

Resource ID: SCR_000121

Alternate IDs: OMICS_01519

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260729T043957+0000

Ratings and Alerts

No rating or validation information has been found for Parallel-META.

No alerts have been found for Parallel-META.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Escobar-Zepeda A, et al. (2015) The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. *Frontiers in genetics*, 6, 348.

Su X, et al. (2014) Parallel-META 2.0: enhanced metagenomic data analysis with functional annotation, high performance computing and advanced visualization. *PloS one*, 9(3), e89323.

Wang Y, et al. (2012) A culture-independent approach to unravel uncultured bacteria and functional genes in a complex microbial community. *PloS one*, 7(10), e47530.

Su X, et al. (2012) Parallel-META: efficient metagenomic data analysis based on high-performance computation. *BMC systems biology*, 6 Suppl 1(Suppl 1), S16.