**MetaPhlAn**  
RRID:SCR_004915  
Type: Tool

**Proper Citation**  
MetaPhlAn (RRID:SCR_004915)

**Resource Information**

**URL:** [http://huttenhower.sph.harvard.edu/metaphlan2](http://huttenhower.sph.harvard.edu/metaphlan2)

**Description:** Computational tool for profiling the composition of microbial communities from metagenomic shotgun sequencing data. It relies on unique clade-specific marker genes identified from reference genomes.

**Resource Name:** MetaPhlAn  
**Proper Citation:** MetaPhlAn (RRID:SCR_004915)

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

**Keywords:** microbial community, microbial composition, microbial genome, microbial sequence

**Resource ID:** SCR_004915

**Parent Organization:** Bitbucket, Harvard T.H. Chan School of Public Health

**References:** PMID:22688413

**Availability:** Free, Public, Acknowledgement requested

**Website Status:** Last checked up

**Alternate IDs:** OMICS_02286
Ratings and Alerts

No rating or validation information has been found for MetaPhlAn.

No alerts have been found for MetaPhlAn.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 158 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Shi X, et al. (2019) Microfluidics-Based Enrichment and Whole-Genome Amplification Enable
Strain-Level Resolution for Airway Metagenomics. mSystems, 4(4).


