

Resource Summary Report

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Massachusetts Institute of Technology MIT BioMicro Center Core Facility

RRID:SCR_026413

Type: Tool

Proper Citation

Massachusetts Institute of Technology MIT BioMicro Center Core Facility
(RRID:SCR_026413)

Resource Information

URL: <http://biomicro.mit.edu>

Proper Citation: Massachusetts Institute of Technology MIT BioMicro Center Core Facility (RRID:SCR_026413)

Description: Integrated genomics/bioinformatics facility located at MIT. Provides Illumina HiSeq2000, NextSeq500 and MiSeq sequencing instruments as well as PacBio Sequel and Oxford Minion. Provides services in preparing Illumina libraries for high-throughput sequencing samples using several different methods, supports technologies including Agilent BioAnalyzer, AATI Fragment Analyzer, AATI FemtoPulse, Roche LC480 qPCR machines, automated liquid handling through Tecan Evo150s, TTP Labtech Mosquito HV. Supports 10X Chromium and single cell work using NamoCell single cell dispenser and custom oligo synthesis using Dr.Oligo 192. Supports informatics and bioIT tools. Core administers ~2PB of data storage on several platforms, including 600TB Isilon server. Hosts 400 processor Dell cluster and Dell Quad Core 2950 application server for Illumina sequencing and bioinformatic applications. All application servers and storage servers are interconnected by 1gigabyte private networks or by fiber optic lines and are administered by IT staff that are part of the BioMicro Center. Servers are configurable to provide secure data storage for clinical data if required.

Synonyms: , Massachusetts Institute of Technology MIT BioMicro Center, MIT BioMicro Center

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

Keywords: ABRF, integrated genomics services, bioinformatics services, servers, storage servers, secure data storage,

Availability: Restricted

Resource Name: Massachusetts Institute of Technology MIT BioMicro Center Core Facility

Resource ID: SCR_026413

Alternate IDs: ABRF_506

Alternate URLs: <https://coremarketplace.org/?FacilityID=506&citation=1>

Record Creation Time: 20250212T060343+0000

Record Last Update: 20260905T133521+0000

Ratings and Alerts

No rating or validation information has been found for Massachusetts Institute of Technology MIT BioMicro Center Core Facility.

No alerts have been found for Massachusetts Institute of Technology MIT BioMicro Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Jiang Z, et al. (2019) Arsenic mobilization in a high arsenic groundwater revealed by metagenomic and Geochip analyses. Scientific reports, 9(1), 12972.

Qi Q, et al. (2017) The Biogeographic Pattern of Microbial Functional Genes along an Altitudinal Gradient of the Tibetan Pasture. Frontiers in microbiology, 8, 976.

Bai R, et al. (2017) Microbial Community and Functional Structure Significantly Varied among Distinct Types of Paddy Soils But Responded Differently along Gradients of Soil Depth Layers. Frontiers in microbiology, 8, 945.

Bouskill NJ, et al. (2016) Belowground Response to Drought in a Tropical Forest Soil. I. Changes in Microbial Functional Potential and Metabolism. Frontiers in microbiology, 7, 525.

Zhang B, et al. (2016) The Composition and Spatial Patterns of Bacterial Virulence Factors and Antibiotic Resistance Genes in 19 Wastewater Treatment Plants. PloS one, 11(12), e0167422.

Xia Y, et al. (2016) Diversity and interactions of microbial functional genes under differing environmental conditions: insights from a membrane bioreactor and an oxidation ditch. *Scientific reports*, 6, 18509.

Wood SA, et al. (2015) Farm management, not soil microbial diversity, controls nutrient loss from smallholder tropical agriculture. *Frontiers in microbiology*, 6, 90.

Yue H, et al. (2015) The microbe-mediated mechanisms affecting topsoil carbon stock in Tibetan grasslands. *The ISME journal*, 9(9), 2012.

Cai M, et al. (2015) Crude oil as a microbial seed bank with unexpected functional potentials. *Scientific reports*, 5, 16057.

Chu H, et al. (2014) Contrasting soil microbial community functional structures in two major landscapes of the Tibetan alpine meadow. *MicrobiologyOpen*, 3(5), 585.

Wang X, et al. (2014) Microbial community functional structures in wastewater treatment plants as characterized by GeoChip. *PloS one*, 9(3), e93422.

Wohlbach DJ, et al. (2014) Comparative genomics of *Saccharomyces cerevisiae* natural isolates for bioenergy production. *Genome biology and evolution*, 6(9), 2557.

Nam M, et al. (2014) Development of the large-scale oligonucleotide chip for the diagnosis of plant viruses and its practical use. *The plant pathology journal*, 30(1), 51.

Tsvetanova NG, et al. (2014) Spatial encoding of cyclic AMP signaling specificity by GPCR endocytosis. *Nature chemical biology*, 10(12), 1061.

Vimolmangkang S, et al. (2014) Transcriptome analysis of the exocarp of apple fruit identifies light-induced genes involved in red color pigmentation. *Gene*, 534(1), 78.

Jung SH, et al. (2013) De novo copy number variations in cloned dogs from the same nuclear donor. *BMC genomics*, 14, 863.

Yang Y, et al. (2013) Microbial electricity generation enhances decabromodiphenyl ether (BDE-209) degradation. *PloS one*, 8(8), e70686.

Holmes KJ, et al. (2013) Whi3, an *S. cerevisiae* RNA-binding protein, is a component of stress granules that regulates levels of its target mRNAs. *PloS one*, 8(12), e84060.

Willmund F, et al. (2013) The cotranslational function of ribosome-associated Hsp70 in eukaryotic protein homeostasis. *Cell*, 152(1-2), 196.

Jung SH, et al. (2012) Simultaneous copy number gains of NUPR1 and ERBB2 predicting poor prognosis in early-stage breast cancer. *BMC cancer*, 12, 382.