Resource Summary Report

Generated by dkNET on Sep 18, 2026

Beth Israel Deaconess Medical Center Mass Spectrometry Core Facility

RRID:SCR_017735
Type: Tool

Proper Citation

Beth Israel Deaconess Medical Center Mass Spectrometry Core Facility (RRID:SCR_017735)

Resource Information

URL: http://www.bidmcmassspec.org/

Proper Citation: Beth Israel Deaconess Medical Center Mass Spectrometry Core Facility (RRID:SCR_017735)

Description: Provides servies in mass spectrometry, proteomics, metabolomics and lipidomics. Services include Thermo Orbitrap Elite and Thermo QExactive HF Orbitrap microcapillary LC-MS/MS:Protein identification, Post-translational modification site mapping,Relative quantification: Label-free, SILAC, TMT, etc.;AB/SCIEX 5500 QTRAP LC-MS/MS:Polar metabolomics profiling,13C/15N metabolic flux analysis;Thermo QExactive Plus/HF Orbitrap LC-MS/MS:Untargeted Lipidomics profiling, Untargeted Metabolomics Profiling.

Synonyms: BIDMC Mass Spectrometry

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

Keywords: Protein identification, post translational, modification, site, mapping, quantification, polar, metabolomic, profiling, metabolic, flux, analysis, untargeted, lipidomics, metabolomic, profiling, service, cores

Availability: Open

Resource Name: Beth Israel Deaconess Medical Center Mass Spectrometry Core Facility

Resource ID: SCR_017735

Alternate IDs: ABRF_193

Alternate URLs: https://coremarketplace.org/?FacilityID=193&citation=1

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260912T200400+0000

Ratings and Alerts

No rating or validation information has been found for Beth Israel Deaconess Medical Center Mass Spectrometry Core Facility.

No alerts have been found for Beth Israel Deaconess Medical Center Mass Spectrometry 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 dkNET .

Jiang D, et al. (2022) Post-GWAS functional analysis identifies CUX1 as a regulator of p16INK4a and cellular senescence. Nature aging, 2(2), 140.

Scherlinger M, et al. (2022) Phosphofructokinase P fine-tunes T regulatory cell metabolism, function, and stability in systemic autoimmunity. Science advances, 8(48), eadc9657.

Zhao Y, et al. (2020) A sequential methodology for the rapid identification and characterization of breast cancer-associated functional SNPs. Nature communications, 11(1), 3340.