# Resource Summary Report

Generated by NIF on May 25, 2025

## 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:** core facility, service resource, access service resource

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

**Funding:**

**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:** 20250525T032844+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 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

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

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.