

Resource Summary Report

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HMS Taplin Mass Spectrometry Core Facility

RRID:SCR_009813

Type: Tool

Proper Citation

HMS Taplin Mass Spectrometry Core Facility (RRID:SCR_009813)

Resource Information

URL: <http://harvard.eagle-i.net/i/0000012b-00c3-414f-db6e-7a3f80000000>

Proper Citation: HMS Taplin Mass Spectrometry Core Facility (RRID:SCR_009813)

Description: Core facility that provides the following services: Protein identification from SDS-PAGE gel bands/spots (Coomassie stained level of protein), Protein phosphorylation service, TCA samples service. The Taplin Biological Mass Spectrometry Facility opened in February 2001 as a core facility for the analysis of proteins and peptides by mass spectrometry. The facility is focused on serving the needs of investigators at Harvard Medical School (HMS) and all the Harvard affiliated Institutions.

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

Keywords: protein identification, mass spectrometry assay

Resource Name: HMS Taplin Mass Spectrometry Core Facility

Resource ID: SCR_009813

Alternate IDs: nlx_156280

Alternate URLs: <https://taplin.med.harvard.edu/>

Record Creation Time: 20220129T080255+0000

Record Last Update: 20260805T044228+0000

Ratings and Alerts

No rating or validation information has been found for HMS Taplin Mass Spectrometry Core Facility.

No alerts have been found for HMS Taplin 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](#) .

Gupta D, et al. (2025) COP9 signalosome and PRMT5 methylosome complexes are essential regulators of Lis1-dynein-based transport. Cell reports, 45(1), 116736.

Gupta D, et al. (2025) A LisH-domain protein interaction map reveals a Lis1-ARIH2-dynein regulatory axis. iScience, 28(11), 113912.