Resource Summary Report

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New York University School of Medicine Langone Health Proteomics Laboratory Core Facility

RRID:SCR_017926
Type: Tool

Proper Citation

New York University School of Medicine Langone Health Proteomics Laboratory Core Facility (RRID:SCR_017926)

Resource Information

URL: https://med.nyu.edu/research/scientific-cores-shared-resources/proteomics-laboratory

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Description: Core offers specialized expertise for analysis of proteins and peptides using mass spectrometry. Develops new methods and customized approaches for proteomic analysis and suggests experimental strategies and sample preparation prior to mass spectrometry analysis. Services include:comprehensive protein identification ,analysis of affinity purified complexes,characterizing protein post-translational modifications,de novo sequencing,label and label-free quantitation ,multiplexed quantitation global phosphorylation and ubiquitin analysis,analysis of laser-capture microdissected formalin-fixed paraffin-embedded tissue,secretome analysis,crosslinking analysis,disulfide mapping.

Synonyms: New York University School of Medicine Langone Health Proteomics Laboratory, Proteomics Laboratory

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

Keywords: Analysis, protein, peptide, mass, spectrometry, proteomics, sample, preparation, de novo sequencing, quantitation, serice, core, ABRF, USEDit

Funding: NCI P30 CA016087

Resource Name: New York University School of Medicine Langone Health Proteomics Laboratory Core Facility

Resource ID: SCR_017926

Alternate IDs: ABRF_820

Alternate URLs: https://coremarketplace.org/?FacilityID=820&citation=1

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260806T054659+0000

Ratings and Alerts

No rating or validation information has been found for New York University School of Medicine Langone Health Proteomics Laboratory Core Facility.

No alerts have been found for New York University School of Medicine Langone Health Proteomics Laboratory Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Ulrich RJ, et al. (2025) Prophage-encoded methyltransferase drives adaptation of community-acquired methicillin-resistant Staphylococcus aureus. The Journal of clinical investigation, 135(18).

Coleman KE, et al. (2025) SLFN11 counteracts the RFWD3-PRIMPOL DNA damage tolerance axis to restrain gapped DNA synthesis in response to replication stress. Nature communications, 16(1), 11029.

Wang L, et al. (2025) CLNS1A regulates genome stability and cell cycle progression to control CD4 T cell function and autoimmunity. Science immunology, 10(108), eadq8860.

Ulrich RJ, et al. (2024) Prophage-encoded methyltransferase drives adaptation of community-acquired methicillin-resistant Staphylococcus aureus. bioRxiv : the preprint server for biology.

Gasser MT, et al. (2024) Membrane vesicles can contribute to cellulose degradation by Teredinibacter turnerae, a cultivable intracellular endosymbiont of shipworms. bioRxiv : the preprint server for biology.

Brady M, et al. (2023) Ratiometric Fluorescent Sensors Illuminate Cellular Magnesium Imbalance in a Model of Acetaminophen-Induced Liver Injury. Journal of the American Chemical Society, 145(40), 21841.

Churchill MJ, et al. (2022) Infection-induced lymphatic zippering restricts fluid transport and viral dissemination from skin. The Journal of experimental medicine, 219(5).

Wang YH, et al. (2022) Distinct roles of ORAI1 in T cell-mediated allergic airway inflammation and immunity to influenza A virus infection. Science advances, 8(40), eabn6552.

Cheng P, et al. (2022) Proteogenomic analysis of cancer aneuploidy and normal tissues reveals divergent modes of gene regulation across cellular pathways. eLife, 11.