Resource Summary Report

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Wistar Proteomics and Metabolomics Core Facility

RRID:SCR_010211
Type: Tool

Proper Citation

Wistar Proteomics and Metabolomics Core Facility (RRID:SCR_010211)

Resource Information

URL: https://www.wistar.org/resources/proteomics-metabolomics-facility/

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Description: Core facility that provides the following services: In-gel protease digestion service, LC-MS/MS protein identification service, Gel/LC-MS/MS Comprehensive analysis of a subproteome or proteome, MudPIT (LC/LC-MS/MS) analyis?comprehensive analysis of a subproteome or proteome, Reverse phase microbore HPLC peptide mapping service, MALDI mass spectrometry, ESI of intact proteins, Post-translational modification identifications, Custom proteomics database creation, Custom proteomics data analysis, Proteomics methods development. The Wistar Proteomics Facility provides mass spectrometry (MS) and sequence analysis of proteins and peptides at maximum sensitivity using state-of-the-art instruments and methods. The most commonly used services are identifications of either purified proteins or complex protein mixtures, such as sub-proteomes or complete proteomes, using electrospray ionization tandem mass spectrometry (ESI MS/MS). Typically, either individual bands are excised from 1-D SDS gels, or the entire gel lane is analyzed by slicing it into uniform fractions followed by trypsin digestion and nanocapillary HPLC interfaced directly with hybrid ion trap mass spectrometry (Gel/LC-MS/MS). Data is analyzed and filtered to produce low false-positive rates. Several options are available for quantitatively comparing protein changes in related samples, and additional options will be implemented in the future. Complementary services include reverse-phase microbore HPLC peptide mapping with UV detection and mass measurements of intact peptides and proteins using MALDI MS or ESI MS. Posttranslational modification (PTM) analyses including identifications of specific modified residues also are provided, although investigators should recognize that in most cases these studies are quite complex and require substantial effort. These studies, as well as analyses of complex protein mixtures, usually require preparation of custom sequence databases and/or custom data analyses, which can be provided by the facility as needed.

Synonyms: Wistar Proteomics Facility

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

Keywords: trypsination, liquid chromatography?tandem mass spectrometry, protein identification, mass spectrometry data analysis, protein expression profiling, ion chromatography, high performance liquid chromatography, post translational modification identification by mass spectrometry, matrix-assisted laser desorption ionization time-of-flight mass spectrometry, electrospray ionization mass spectrometry, data analysis

Funding:

Resource Name: Wistar Proteomics and Metabolomics Core Facility

Resource ID: SCR_010211

Alternate IDs: nlx_156689, ABRF_2804

Alternate URLs: https://coremarketplace.org/?FacilityID=2804&citation=1

Old URLs: http://eagle-i.itmat.upenn.edu/i/0000013f-67e1-2fdc-a468-831a80000000

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Ratings and Alerts

No rating or validation information has been found for Wistar Proteomics and Metabolomics Core Facility.

No alerts have been found for Wistar Proteomics and Metabolomics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.