

Resource Summary Report

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Iowa State University Office of Biotechnology Protein Core Facility

RRID:SCR_017780

Type: Tool

Proper Citation

Iowa State University Office of Biotechnology Protein Core Facility (RRID:SCR_017780)

Resource Information

URL: <http://www.protein.iastate.edu>

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Description: Core offers protein/peptide sequencing, large and small scale peptide synthesis (Fmoc), matrix assisted laser desorption/ionization (MALDI) mass spectrometry, SDS-PAGE/electroblotting, 2-D gel electrophoresis, isoelectric focusing (IEF), in-gel and solution digestion, tandem mass spectrometry (LC-MS/MS), ion mobility mass spectrometry (IM-MS), digital image acquisition and analysis using Typhoon imaging system and 2D gel documentation/analysis system, and semi-preparative, analytical and micro-analytical high performance liquid chromatography (HPLC). MALDI, HPLC, SDS-PAGE/blotting, IEF, 2D gel electrophoresis, 2D gel documentation/analysis and Typhoon imaging system are all available for user operation after appropriate training.

Synonyms: Protein Facility of the Iowa State University Office of Biotechnology

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

Keywords: Protein, peptide, sequencing, synthesis, laser, desorption, ionization, mass, spectrometry, SDS-PAGE, gel, electrophoresis, liquid, chromatography, imaging, system, training, service, core

Availability: Open

Resource Name: Iowa State University Office of Biotechnology Protein Core Facility

Resource ID: SCR_017780

Alternate IDs: ABRF_359

Record Creation Time: 20220129T080336+0000

Ratings and Alerts

No rating or validation information has been found for Iowa State University Office of Biotechnology Protein Core Facility.

No alerts have been found for Iowa State University Office of Biotechnology Protein 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 [T1D](#).

Luo D, et al. (2024) Transcriptome- and proteome-wide effects of a circular RNA encompassing four early exons of the spinal muscular atrophy genes. Scientific reports, 14(1), 10442.

Luo D, et al. (2024) Transcriptome- and proteome-wide effects of a circular RNA encompassing four early exons of the spinal muscular atrophy genes. Research square.