

Resource Summary Report

Generated by RRID on Aug 5, 2026

The Rockefeller University Proteomics Resource Center Core Facility

RRID:SCR_017797

Type: Tool

Proper Citation

The Rockefeller University Proteomics Resource Center Core Facility
(RRID:SCR_017797)

Resource Information

URL: <http://proteomics.rockefeller.edu/>

Proper Citation: The Rockefeller University Proteomics Resource Center Core Facility
(RRID:SCR_017797)

Description: Core provides analysis of proteins, peptides, lipids, polar metabolites and small molecules by high resolution/high mass spectrometry. Targeted and hypothesis free analysis are offered combined with relative quantitation based on either label free, tandem mass tags or metabolic labelling. Acquisition tools include Data Dependent (DDA) and Data Independent (DIA).

Synonyms: , Rockefeller University Proteomics Resource Center, Rockefeller University Proteomics Resource Center Core Facility, Proteomics Resource Center

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

Keywords: Analysis, biomolecule, protein, peptide, mass, spectrometry, proteomics, parallel, reaction, monitoring, selected, ion, stable, isotope, labeled, service, core, PRM, SIM, Metabolomics, Lipidomics

Availability: Open

Resource Name: The Rockefeller University Proteomics Resource Center Core Facility

Resource ID: SCR_017797

Alternate IDs: ABRF_443

Alternate URLs: <https://coremarketplace.org/?FacilityID=443&citation=1>

Record Creation Time: 20220129T080337+0000

Ratings and Alerts

No rating or validation information has been found for The Rockefeller University Proteomics Resource Center Core Facility.

No alerts have been found for The Rockefeller University Proteomics Resource Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Notti RQ, et al. (2025) The resting and ligand-bound states of the membrane-embedded human T-cell receptor-CD3 complex. Nature communications, 16(1), 10996.

Buzovetsky O, et al. (2025) Helicase-mediated mechanism of SSU processome maturation and disassembly. Nature, 648(8094), 746.

Buzovetsky O, et al. (2025) Helicase-mediated mechanism of SSU processome maturation and disassembly. bioRxiv : the preprint server for biology.

Clark JF, et al. (2024) Diverse Fgfr1 signaling pathways and endocytic trafficking regulate early mesoderm development. bioRxiv : the preprint server for biology.

Clark JF, et al. (2024) Diverse Fgfr1 signaling pathways and endocytic trafficking regulate mesoderm development. Genes & development, 38(9-10), 393.

Hossain AA, et al. (2024) DNA glycosylases provide antiviral defence in prokaryotes. Nature, 629(8011), 410.

Aydin B, et al. (2024) Gut bacteria-derived succinate induces enteric nervous system regeneration. bioRxiv : the preprint server for biology.

Soula M, et al. (2024) Glycosphingolipid synthesis mediates immune evasion in KRAS-driven cancer. Nature, 633(8029), 451.

Conti BA, et al. (2024) RTF2 controls replication repriming and ribonucleotide excision at the replisome. Nature communications, 15(1), 1943.

Zhang S, et al. (2024) Resistance of estrogen receptor function to BET bromodomain inhibition is mediated by transcriptional coactivator cooperativity. bioRxiv : the preprint server for biology.

Zhao H, et al. (2024) An IDR-dependent mechanism for nuclear receptor control of Mediator interaction with RNA polymerase II. *Molecular cell*, 84(14), 2648.

Harper NJ, et al. (2023) Principles of mitoribosomal small subunit assembly in eukaryotes. *Nature*, 614(7946), 175.

Berman AY, et al. (2023) A nucleotide binding-independent role for γ -tubulin in microtubule capping and cell division. *The Journal of cell biology*, 222(3).

Hsu DJ, et al. (2023) Arginine limitation drives a directed codon-dependent DNA sequence evolution response in colorectal cancer cells. *Science advances*, 9(1), eade9120.

Sanghai ZA, et al. (2023) A co-transcriptional ribosome assembly checkpoint controls nascent large ribosomal subunit maturation. *Nature structural & molecular biology*, 30(5), 594.

Kenny TC, et al. (2023) Integrative genetic analysis identifies FLVCR1 as a plasma-membrane choline transporter in mammals. *Cell metabolism*, 35(6), 1057.

Notti RQ, et al. (2023) The resting state of the human T-cell receptor. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2023) Autoregulatory control of mitochondrial glutathione homeostasis. *Science (New York, N.Y.)*, 382(6672), 820.

Choi CHJ, et al. (2022) LRG1 is an adipokine that promotes insulin sensitivity and suppresses inflammation. *eLife*, 11.