

Resource Summary Report

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University of Kansas Mass Spectrometry and Analytical Proteomics Core Facility

RRID:SCR_021857

Type: Tool

Proper Citation

University of Kansas Mass Spectrometry and Analytical Proteomics Core Facility
(RRID:SCR_021857)

Resource Information

URL: <https://mass-spec.ku.edu/>

Proper Citation: University of Kansas Mass Spectrometry and Analytical Proteomics Core Facility (RRID:SCR_021857)

Description: Provides range of mass spectrometry based services including small molecule analysis and quantitation, peptide and protein MW determination; MS based proteomics services and associated bioinformatics including: global proteome IDs and targeted proteomics, post-translational modification mapping, quantitative proteomics, consultation for designing proteomics experiments, thermal protein profiling and cellular thermal shift assay analysis.

Abbreviations: MSAPL

Synonyms: Lawrence KU Mass Spec & Proteomics Core, University of Kansas Mass Spec and Proteomics Core Laboratory, KU Mass Spec & Proteomics Core

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

Keywords: USEdit, ABRF, mass spectrometry based services, proteomics services

Resource Name: University of Kansas Mass Spectrometry and Analytical Proteomics Core Facility

Resource ID: SCR_021857

Alternate IDs: ABRF_1254

Alternate URLs: <https://coremarketplace.org/?FacilityID=1254>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260905T133422+0000

Ratings and Alerts

No rating or validation information has been found for University of Kansas Mass Spectrometry and Analytical Proteomics Core Facility.

No alerts have been found for University of Kansas Mass Spectrometry and Analytical Proteomics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ishino T, et al. (2025) Immunopectidomics combined with full-length transcriptomics uncovers diverse neoantigens. Cell reports, 45(1), 116781.