Resource Summary Report

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North Carolina University at Chapel Hill School of Medicine High Throughput Peptide Synthesis and Array Core Facility

RRID:SCR_017837
Type: Tool

Proper Citation

North Carolina University at Chapel Hill School of Medicine High Throughput Peptide Synthesis and Array Core Facility (RRID:SCR_017837)

Resource Information

URL: http://www.med.unc.edu/csb/unc-peptides

Proper Citation: North Carolina University at Chapel Hill School of Medicine High Throughput Peptide Synthesis and Array Core Facility (RRID:SCR_017837)

Description: Core offers services for: High quality synthetic peptides, stable isotope labeled peptides, peptides with PTM and fluorescent and affinity tags, synthesis of peptide libraries. Analysis of synthetic peptides. Purification, lyophilization and aliquoting of synthetic peptides.

Synonyms: UNC High-Throughput Peptide Synthesis and Array Facility

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

Keywords: Synthetic, peptide, stable, isotope, labeled, library, analysis, purification, lyophilization, aliquoting, service, core, ABRF

Funding: NCI P30 CA016086

Availability: Open

Resource Name: North Carolina University at Chapel Hill School of Medicine High Throughput Peptide Synthesis and Array Core Facility

Resource ID: SCR_017837

Alternate IDs: ABRF_626

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260810T040731+0000

Ratings and Alerts

No rating or validation information has been found for North Carolina University at Chapel Hill School of Medicine High Throughput Peptide Synthesis and Array Core Facility.

No alerts have been found for North Carolina University at Chapel Hill School of Medicine High Throughput Peptide Synthesis and Array Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Shelby C, et al. (2026) Enhancing Enzymatic Bioconjugation Efficiency via Computer-Based Installation of a Substrate Recruitment Domain. Bioconjugate chemistry, 37(4), 699.

Zhao Y, et al. (2025) Post-translational modification of H2B C-terminal helix regulates nucleosome interactions and chromatin signaling. Nucleic acids research, 53(17).

Jain K, et al. (2025) Histone H3 N-terminal recognition by the PHD finger of PHRF1 is required for proper DNA damage response. Nucleic acids research, 53(13).

Jain K, et al. (2024) Histone H3 N-terminal recognition by the PHD finger of PHRF1 is required for proper DNA damage response. bioRxiv : the preprint server for biology.

Düzgüne? N, et al. (2024) Peptides Derived from the SARS-CoV-2 S2-Protein Heptad-Repeat-2 Inhibit Pseudoviral Fusion at Micromolar Concentrations: The Role of Palmitic Acid Conjugation. International journal of molecular sciences, 25(12).

Day EC, et al. (2024) Insights into conformational ensembles of compositionally identical disordered peptidomimetics. Polymer chemistry, 15(29), 2970.

Jain K, et al. (2023) An acetylation-mediated chromatin switch governs H3K4 methylation read-write capability. eLife, 12.

Wick ET, et al. (2022) Insight into Viral Hijacking of CRL4 Ubiquitin Ligase through Structural Analysis of the pUL145-DDB1 Complex. Journal of virology, 96(17), e0082622.