OSAC RESEARCH NEEDS ASSESSMENT FORM

Title of research need:	Concurrent forensic proteomic and nucleic acid workflows to maximize the probative value of sample-limited evidence during consumptive testing
Describe the need:	Genetic profiling seeks to identify evidence but often relies on additional tests to determine the biological source of the genetic material, crucial for accurate scenario-specific interpretation. This additional testing may include identifying the fluid of origin in sexual assault cases or the species of origin in wildlife forensics, where forensic proteomics plays a key role in establishing contextual information about the sample that DNA testing cannot provide. Due to its high probative value, current workflows typically focus on protecting DNA analysis and can sacrifice proteomic information. In cases with limited sample material, one biological assay may be prioritized. Research is still needed for the co-extraction of both genetic and proteomic markers from the same evidentiary material through alternative enzymes, novel purification techniques, and other automated solutions. Research in this area may benefit from assessing how current automated DNA workflow waste fractions may be recycled for proteomic analysis, or the impact of automated proteomic sample preparation on DNA recovery.
Keyword(s):	Proteomics, serology, mass spectrometry, consumptive testing, concurrent workflow, waste fractions

Submitting subcommittee(s):	Forensic Proteomics Task Group	**Date Approved:**	4/2/2026

Background Information:

1. Does this research need address a gap(s) in a current or planned standard? (ex.: Field identification system for on scene opioid detection and confirmation)

Drafting of relevant standards to address this gap are in progress.

2. Are you aware of any ongoing research that may address this research need that has not yet been published (e.g., research presented in conference proceedings, studies that you or a colleague have participated in but have yet to be published)?

Ongoing research using non-specific proteases is underway to ensure compatibility between DNA and protein extraction workflows as well as studies using waste fractions from sexual assault materials for proteomic analysis. However, validated or standardized concurrent workflow methodologies are needed for forensic casework applications.

3. Key bibliographic references relating to this research need: (ex.: Toll, L., Standifer, K. M., Massotte, D., eds. (2019). Current Topics in Opioid Research. Lausanne: Frontiers Media SA. doi: 10.3389/978-2-88963-180-3)

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4. Review the annual operational/research needs published by the National Institute of Justice (NIJ) at https://nij.ojp.gov/topics/articles/forensic-science-research-and-development-technology-working-group-operational#latest? Is your research need identified by NIJ?

This research need would be included under the following Operational Requirements published by the NIJ in February 2024:
Forensic Biology, Scientific Research: Foundational research related to the discriminatory power and sensitivity of alternate biological analyses (e.g., proteomics, microbiome, plants, animals) to associate individuals with crime scene evidence.

5. In what ways would the research results improve current laboratory capabilities?

Protocols for differential/co-extraction of proteins and genetic components address the limitations of serological testing and species identification when low sample levels would otherwise force prioritization of either DNA or protein.

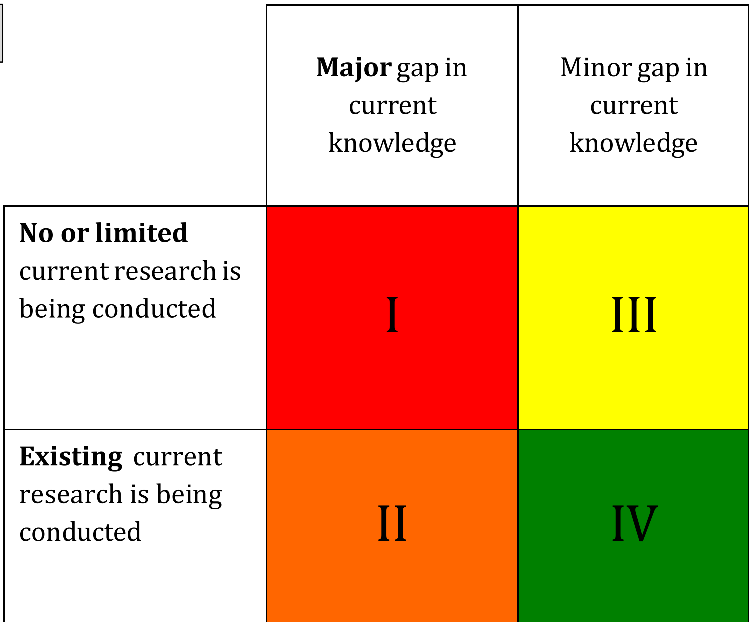
6. In what ways would the research results improve understanding of the scientific basis for the subcommittee(s)?

This research would provide the greater proteomics community with novel chemistries, automation tools, and alternate enzymes that are compatible with nucleic acid workflows.

7. In what ways would the research results improve services to the criminal justice system?

Developing preparation protocols will allow for the forensic and criminal justice communities in the United States communities to overcome limitations in challenging evidence types where a single biological sample is prioritized. This protocol development would enable both DNA identification and source determination through proteomics or mass spectrometry-based serology.

8. Status assessment (I, II, III, or IV): II



	Major gap in current knowledge	Minor gap in current knowledge
No or limited current research is being conducted	I	III
Existing current research is being conducted	II	IV

This research need has been identified by one or more subcommittees of OSAC and is being provided as an informational resource to the community.