OSAC RESEARCH NEEDS ASSESSMENT FORM

Title of research need:	Establishing performance metrics and population statistics for robust sets of single amino acid polymorphisms (SAPs) in the human population
Describe the need:	Single amino acid polymorphisms (SAPs) in protein are the result of non-synonymous single nucleotide polymorphisms (nsSNPs) in DNA. Germline SAPs are inherited and can be used to infer human identity and ancestry. SAPs can occur in many contexts. When a SAP occurs in the context of an observable peptide, that peptide is termed a genetically variant peptide (GVP). Work has recently been conducted to establish SAP-containing peptide panels to assist in human identification when nuclear DNA is either not present or is significantly degraded. Preliminary work on tissues such as hair, skin, and bone exemplify the utility and breadth of coverage for peptides. However, this area is still lacking in an in-depth characterization of informative SAPs, determination of robustness, validation strategies, and standardized protocols for performing relevant population statistical calculations such as random match probability or likelihood ratio. Here, robustness is referring to the detectability and true positive identification of a peptide while challenged under different real-world scenarios and degradative conditions using laboratory standard operating procedures. Further research is needed to (1) identify robust sets of SAP-containing peptides in forensically relevant body fluids and tissues (i.e., robust panels); (2) verify that observed SAP frequencies are similar to that of nsSNP frequencies from DNA databases; (3) establish true positive and false positive rates for SAP identification and their corresponding sources of false assignment (e.g., chemical, bioinformatic, homology); (4) compare methods of calculation for random match probability and likelihood ratio as derived from DNA databases; and (5) conduct formal linkage analyses for current SAP datasets using information from DNA databases.
Keyword(s):	Single amino acid polymorphisms (SAPs), non-synonymous single nucleotide polymorphisms (nsSNPs), genetically variant peptide (GVP), robust panels, peptide performance, population statistics

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)?

Research is currently being conducted at NIST and UC Davis to identify robust sets of peptides that contain germline SAPs. Controlled degradation experiments are being conducted from both environmental and biological perspectives.

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?

Currently, there are limited works reported for determining robustness of SAPs detected in bottom-up proteomics used for human identification. There are also no standardized laboratory strategies for selecting or defining the parameters of a good quality SAP, or the characterization of SAP robustness that would allow for reliable SAP peptides to be validated for use in a crime laboratory setting. Additionally, there is no consensus on the calculation of random match probability or likelihood ratios from observed SAP frequencies. There are a number of research manuscripts that handle the problem in different ways, but not in an intuitive and report-centric approach. Curating a list of robust SAPs with associated DNA-based population statistics and recommended calculations would help meet requirements for standardization and implementation in forensic science laboratories.

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

This task group could benefit from the information obtained in such studies for developing written standards relevant to SAP characterization and for the creation of data interpretation guidelines. Analysis pipelines resulting from such work could also advise best practice strategies for the identification of SAPs and validation of their presence. These types of projects could also expand the field of human identification using proteomics and lead to alternative methods and approaches in other OSAC groups such as the Wildlife Forensic Biology or Forensic Toxicology Subcommittees.

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

Characterization of SAPs in peptides is currently limited to a research setting due to gaps in knowledge such as how to validate peptide identifications, how to define and identify robustness of SAP-containing peptides, and how to perform forensically-relevant calculations such as random match probability or likelihood ratio. If these gaps are filled with the above mentioned research, this would help strengthen the scientific fortitude of forensic proteomics for use in human identification.

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.