

# OSAC RESEARCH NEEDS ASSESSMENT FORM



**Title of research need:**

Proteomic annotation of forensically-relevant species that have published genomes but no available proteomic datasets

**Describe the need:**

Wildlife forensic proteomic species identification of degraded or processed biological evidentiary samples (e.g., hides, cooked meats, pills) can provide investigatory information when traditional DNA or morphological methods otherwise fail to yield an identification of taxonomic origin. Although publicly available genomic datasets and genome assemblies are readily accessible for many species of conservation and forensic interest, the corresponding proteomic datasets and suitable proteomic annotations are often absent [1-3]. In order to address this deficiency, proteomic sequence annotation (either whole proteome, or targeted datasets) for these species and target tissue types is necessary.

The availability of proteomes annotated in their entirety allows for the possibility of identifying peptides that are present in an evidentiary sample and that would not otherwise be identified (e.g., if the sample contains proteins from a non-target tissue type or species). The availability of relevant proteomes also allows for the bioinformatic identification of diagnostic peptide markers for a given species or taxon that can be validated with raw data. Protein annotations should be associated with relevant metadata, provide information on data acquisition, and follow guidelines provided by the Vertebrate Genomes Project [4], NCBI [5], and UniProt [6].

Targeted reference protein bioinformatic databases could be constructed based on target tissue types and relevant taxonomic coverage to differentiate legal or domestic species from illegal or wild species. These reference databases should include high-quality and complete amino acid sequences for the most abundant proteins detected in a given target tissue type. These target tissue types include, but are not limited to, fur, skin, organs, and bones. Relevant taxonomic coverage requires a knowledge of the phylogeny of the taxon of interest to ensure that sufficient representatives are included to either identify or to exclude the species of interest.

**Keyword(s):**

Proteomics, annotation, protein datasets, database, peptides

**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)?

We are not aware of any systematic or extensive efforts that focus on annotating or creating relevant proteomic databases for species of conservation or forensic interest. However, there are efforts underway to create high-quality genomic datasets that could be used for proteomic annotations such as with the California Conservation Genomics Project (CCGP) [CCGP \(ccgproject.org\)](http://ccgproject.org). Additionally, an NIJ grant was awarded for *Species Identification in Forensic Casework using Proteomics* (Research and Evaluation for the Testing and Interpretation of Physical Evidence in Publicly Funded Forensic Laboratories Award #15PNIJ-22-GG-03566-SLFO) that uses published proteomes when available, or alternately, uses bioinformatic tools to functionally annotate protein datasets when only the published genome is available.

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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5. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res*. 2016 Aug 19;44(14):6614-24. <https://doi.org/10.1093/nar/gkw569>
6. The UniProt Consortium (2017). UniProt: the universal protein knowledgebase. *Nucleic acids research*, 45(D1), D158–D169. <https://doi.org/10.1093/nar/gkw1099>

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 Toxicology, Seized Drugs, Scientific Research:** Continued advancement of practical forensic application/development of emerging or current instrumentation and software. A clear case should be made for

how new technology either may do something that current technology cannot or may be an improvement over current technology (more sensitive, faster, more cost effective, etc.).

**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?

The research results would enhance the ability to use bioinformatic and proteomics data generated for forensic investigations. Further, generation of this data would assist the standardization of proteomic data and relevant databases in forensic laboratories.

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

These research results would provide essential bioinformatic information and standardized databases that can be validated for forensic proteomic casework.

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

This research would provide the necessary bioinformatic tools to identify the taxonomic origin of biological samples that cannot currently be identified with traditional methods such as DNA or morphology. These bioinformatic tools could provide investigatory leads or exculpatory evidence that would not otherwise be known.

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

I

	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.*