CB BAA HDTRA122S0002 CALL 7

THE PROPOSAL SUBMISSION DEADLINE FOR THE FOLLOWING TOPICS IS SEPTEMBER 2, 2026 AT 2:00PM EASTERN DAYLIGHT TIME (EDT).

THE DEADLINE TO SUBMIT QUESTIONS RELATED TO THE FOLLOWING TOPICS IS JULY 22, 2026.

CBPD-01: Advanced Triggers for Autonomous Biological Aerosol Collection

Background: Warfighters are often deployed to austere environments with potential exposure to biological pathogens. To provide Integrated Layered Defense and Integrated Early Warning, there is a need for autonomous sensors that can detect the presence of an aerosolized biothreat, confirm if it is a hazard, and inform the Warfighter. Current triggers primarily rely on Laser-Induced Fluorescence (LIF) however this technology is not without flaws. The objective of this topic is to move beyond LIF to develop and demonstrate next-generation trigger technologies that overcome the limitations of current systems. This new system will focus on reduced Size, Weight, Power and Cost (SWaP-C), improved sensitivity and selectivity, and a lower false alarm rate in complex operational environments.

Current biosurveillance architectures often employ a "trigger-then-collect" paradigm, where a low-power, continuously operating sensor detects a potential threat and activates a higher-fidelity, but more consumptive, collection and analysis system. For decades, Laser-Induced Fluorescence (LIF) has been the state-of-the-art trigger technology. While effective to a degree, LIF-based triggers suffer from significant operational drawbacks, including:

- High False Positive Rates: Common battlefield and urban interferents such as diesel exhaust, dust, pollen, and smoke can mimic the fluorescence signature of biological agents, leading to unnecessary collection events that waste consumables and tax analytical resources.
- Significant SWaP-C: LIF systems require lasers, optics, and sensitive detectors that contribute to a considerable size, weight, power, and cost footprint, limiting their use in dismounted or unattended ground sensor applications.

- Limited Discrimination: LIF provides little to no information to differentiate between threat categories (e.g., virus vs. bacteria) or to screen out near-neighbor non-pathogenic organisms.

JSTO seeks innovative solutions for autonomous biological aerosol collection systems that can reliably differentiate biological aerosols from background clutter to initiate a collection/sampling event. This effort is part of a larger goal to develop an all-in-one fieldable biosensing capability that can operate autonomously to monitor for threats, collect samples, analyze, and report results to the end user.

Objective: Develop non-LIF trigger technologies capable of discriminating against biological and non-biological aerosols in real-time. The goal is to mature a technology that can serve as a "smart" front-end for a modular, potentially all-in-one biosurveillance system. The trigger should be able to analyze particles with biological characteristics in ambient air. The resulting output should be sent in a contested and limited network environment to activate a downstream collector for subsequent identification. The prototype system must be agile, man-portable, robust, and low SWaP-C, with the ability to perform multiple analysis cycles between human interaction.

JSTO is interested in a wide range of innovative physical, chemical, and computational approaches. Proposals should clearly articulate a scientific basis for their proposed technology. While not an exhaustive list, areas of interest include, but are not limited to:

- Micro-scale Fluidics and Particle Dynamics: Technologies that differentiate particles based on physical properties like density, morphology, and momentum in air or microfluidic channels (1).
- Advanced Spectroscopic Methods (Non-Fluorescence): Techniques such as Raman spectroscopy, elastic or multi-angle light scattering (MALS), and particle-mass spectrometry that can provide structural or chemical information about individual particles in real-time (1).
- Electromagnetic and Electrostatic Approaches: Systems that measure a particle's dielectric properties, charge state, or response to specific electromagnetic fields to infer its composition (1).
- Artificial Intelligence and Machine Learning (AI/ML)-Enhanced Sensing: The use of machine learning algorithms to process complex data from one or more low-power sensors (e.g., optical particle counters, environmental sensors) to create a composite signature for bioaerosols and distinguish them from clutter. This could

include a network of low-fidelity sensors whose fused data provides a high-fidelity trigger decision (2, 3).

- Biochemical Interaction Triggers: Novel concepts where low-power interactions with broadly specific biochemical probes (e.g., engineered peptides, aptamers) on a sensor surface generate a rapid, detectable signal.

TECHNICAL REQUIREMENTS & DESIRED METRICS

Proposals will be evaluated on their plan to achieve, at a minimum, the following performance characteristics by the end of the effort. Offerors should propose a clear path to demonstrating these metrics.

Metric	Threshold (Minimum Acceptable)	Objective (Desired)
Probability of Detection - Biological	≥ 90% for relevant agents (e.g., *Bacillus* spores, viral simulants) at threat-relevant concentrations.	≥ 99%
Probability of False Alarm	≤ 1 false alarm per 24 hours in a complex background environment.	≤ 1 false alarm per 72 hours
Response Time	≤ 10 seconds from particle introduction to trigger signal.	≤ 1 second
Size	< 0.25 ft^3 (approx. 7 liters)	< 0.1 ft^3 (approx. 2.8 liters)
Weight	< 10 lbs (4.5 kg)	< 3 lbs (1.4 kg)
Interferent Rejection	Demonstrated rejection of at least three common interferents (e.g., diesel soot, Arizona road dust, pollen).	Demonstrated rejection of a complex mixture of at least five interferents.
Data Fusion & Integration	System demonstrates networking/integration of data sources to reduce false reporting.	System architecture utilizes advanced computing to process data at the source, with the ability to layer in ML/AI algorithms for advanced data/measurement analysis and improved reporting accuracy.

Impact: This topic will advance sensing technology to ultimately support the Warfighter with a man-portable, autonomous early warning system for biological threats. Such a capability is critically important for providing Integrated Layered Defense and early warning in austere environments where Warfighters face potential exposure to aerosolized biological agents. The envisioned trigger technology will enable the development of a potential all-in-one biosurveillance system that can be deployed with far forward units or as an unattended ground sensor, alerting personnel to the presence of a biothreat with high confidence and low false alarm rates. These individual and small-unit protective benefits will add up to a broader impact on force protection, survivability, and mission assurance in contested environments.

References:

1. Gao, T., Wang, K., Shen, X., Cao, Y., & Xue, B. (2025). Collection and characterization of aerosol particles. *Materials Research Express*, *12*(4), 042002. https://doi.org/10.1088/2053-1591/adc4c2
2. Fontal, A., Borràs, S., Cañas, L., Pozdniakova, S., & Rodó, X. (2025). Laser-Induced Fluorescence coupled with Machine Learning as an effective approach for real-time identification of bacteria in bioaerosols. *Atmospheric Measurement Techniques, 18*, 7297–7313. https://doi.org/10.5194/amt-18-7297-2025
3. Lee, J. Y. Y., Miao, Y., Chau, R. L. T., Hernandez, M., & Lee, P. K. H. (2023). Artificial intelligence-based prediction of indoor bioaerosol concentrations from indoor air quality sensor data. *Environment International*, *174*, 107900. https://doi.org/10.1016/j.envint.2023.107900

CBPD-02: Second Wave

Background: The goal of the Second Wave program is to develop a novel, robust, and scalable bioinformatics software suite capable of rapidly identifying and characterizing genetically modified organisms (GMOs), including viruses, bacteria, and fungi, from complex metagenomic sequence data. The accelerating pace and accessibility of synthetic biology and gene-editing technologies, such as CRISPR-Cas systems, present a dual-use dilemma. While offering immense benefits, these tools also lower the barrier for the potential creation of engineered biological threats. Current methods for identifying such threats are often slow, require a prior knowledge of the engineered sequences, and fail to keep pace with the novelty of modern engineering techniques.

JSTO seeks proposals to fundamentally shift the paradigm from reactive, signature-based detection to proactive, heuristic-based identification. The program will fund the development of innovative computational tools that can detect the subtle, intrinsic "scars" and "fingerprints" of the engineering process itself, even in the absence of known inserted genes or markers. The program will embrace artificial intelligence and machine learning (AI/ML) to move beyond traditional methods and develop proactive, next-generation biodefense capabilities. The ultimate vision is a platform that can automatically flag a sequence as "potentially engineered" with a high degree of confidence and provide actionable intelligence to an analyst.

Objectives: The Second Wave program is structured into two primary Technical Areas (TAs). Proposers must address TA1 and should consider the additional capabilities identified in TA2 to develop the most attractive proposal.

Technical Area 1 (TA1): Core Algorithm and Platform Development
This Technical Area focuses on the development of the core software engine for identifying engineered sequences. The desired capabilities of this platform must include, but are not limited to:

- Signature-Agnostic Detection: The ability to identify genetic modifications without relying on a pre-defined library of known "cargo" genes, and to confirm the syntenic colocalization of the discovered gene cassette within a specific target genome (e.g., GFP, antibiotic resistance markers) (1).

- Engineering Scar Identification (2): The ability to detect subtle artifacts of the engineering process, such as:
    - Remnants of plasmid backbones, vector sequences, or reverse genetics systems.
    - Unnatural densities or patterns of restriction enzyme sites.
    - Anomalous codon usage patterns inconsistent with the host organism's genome.
    - Statistical deviations in sequence complexity or composition indicative of synthetic DNA insertion.
    - Evidence of "seamless" edits or homology-directed repair (HDR) by identifying unusually perfect sequence homology at non-recombinogenic loci.
- Chimeric and Hybrid Organism Detection: Robust algorithms to identify genomes constructed from segments of two or more distinct natural organisms (e.g., viral reassortments that do not occur in nature) (3).
- Probabilistic Scoring: The platform must generate a quantitative, statistically grounded "Engineered Probability Score" (EPS) for any given contig or genome, rather than a simple binary "yes/no" output.
- Scalability and Performance: The software must be capable of processing large, complex metagenomic datasets (Terabytes) in a computationally efficient manner. Ideally, algorithms will be implementable on edge compute capabilities (64 cores / 128 threads, 384GB of memory, and 32TB auxiliary storage)

Technical Area 2 (TA2) (Optional): Threat Characterization and Attribution
This Technical Area focuses on adding layers of context and intelligence to the core detection engine from TA1. The goal is to provide an analyst with immediate, actionable information about a flagged sequence (4). Desired capabilities include:

- Functional Impact Assessment: Automatically predict the likely functional consequence of an insertion or modification (e.g., "gain-of-function in protein binding," "knockout of immune modulator") (5).
- Toolmark and Technique Identification: Attempt to identify the likely engineering tool or technique used (e.g., "CRISPR-Cas9 signature," "Gibson Assembly scar," "Type IIs assembly remnant") (6).
- Lab-of-Origin Attribution (Stretch Goal): A high-risk, high-payoff goal to explore whether specific labs, plasmid series, or synthetic DNA providers have unique, subtle sequence "fingerprints" that could be used to provide probabilistic hints about the origin of an engineered sequence.

Impact: This program will advance the science of computational biology to ultimately support the Warfighter with a threat detection capability that can be used for force protection, environmental surveillance, and biodefense. Such a detection capability is critically important in providing early warning and actionable intelligence against the use of a novel or engineered biological agent. The envisioned software suite will help direct the Warfighter to the most critical threats in complex data, alerting decision makers to the nature of a potential biological attack. These analytical benefits will add up to a broader impact on improved situational awareness, early warning, force protection, and strategic advantage against biological threats.

References:

1. Alfonsi, T., Bernasconi, A., Chiara, M., & Ceri, S. (2025). Multi-scale early warning system for influenza A spillovers. *bioRxiv*. https://doi.org/10.1101/2025.05.24.655955
2. Deatherage, D. E., & Barrick, J. E. (2014). Identification of mutations in laboratory-evolved microbes from next-generation sequencing data using breseq. *Methods in molecular biology (Clifton, N.J.)*, *1151*, 165–188. https://doi.org/10.1007/978-1-4939-0554-6_12
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4. Lee, J. Y., et al. (2022). Deep learning for regulatory genomics. *Cell*, *185*(21), 3925-3945.
5. Adzhubei, I. A., Schmidt, S., Peshkin, L., Ramensky, V. E., Gerasimova, A., Bork, P., ... & Sunyaev, S. R. (2010). A method and server for predicting damaging missense mutations. *Nature methods*, *7*(4), 248–249. https://doi.org/10.1038/nmeth0410-248
6. Brinkman, E. K., Chen, T., Amendola, M., & van Steensel, B. (2014). Easy quantification of template-directed CRISPR/Cas9 editing. *Nucleic acids research*, *42*(22), e168. https://doi.org/10.1093/nar/gku936