Request for Proposals

Pathogen-Agnostic Biothreat Detection

Overview

Blueprint Biosecurity is a 501(c)(3) nonprofit dedicated to strengthening society's ability to prepare for and respond to pandemics. Biosurveillance, including early warning of emerging pathogens, is a key part of pandemic prevention. Early warning helps societies respond effectively to new outbreaks, whether naturally occurring, accidental, or deliberate in origin, enabling timely action to suppress transmission and develop countermeasures.

Today, most pathogen surveillance depends on recognizable clinical signals and targeted detection methods that require knowing what molecular features to look for in advance. These systems leave us poorly prepared for novel, engineered, or otherwise unexpected pathogens — key drivers of pandemic risk.

Metagenomic sequencing (MGS) is a promising, pathogen-agnostic detection platform that addresses critical limitations of relying solely on syndromic surveillance and targeted detection methods. By sequencing all nucleic acids in a sample, MGS has the potential to detect and genomically characterize any pathogen present without prior knowledge of what to look for. Falling sequencing costs and expanding biosurveillance infrastructure have made MGS more practical as a tool for broad, pathogen-agnostic detection. A growing set of initiatives is exploring its application across wastewater, air, clinical samples, pooled nasal swabs, and the blood supply.

Through this request for proposals (RFP), we seek to accelerate the deployment and maturation of MGS as a biosurveillance platform by funding improved computational, laboratory, and modeling methods for early pathogen detection and characterization. This will serve as a foundation for establishing sequencing-based biosurveillance as a powerful, trusted, and operationally useful component of pandemic early warning.

Opportunity

We invite 2–3-page Expressions of Interest (EOI) from groups interested in investigating the following technical areas:

- Computational detection of known and novel pathogens, including zoonotic and engineered, in MGS data
- Sample processing methods for more sensitive, sequencing-based detection and rapid validation of sequences of concern
- Modeling pathogen-agnostic biosurveillance system features such as cost, sensitivity, and optimal deployment

Across all three technical areas, we are particularly interested in work targeting human pathogens with pandemic potential. Antimicrobial resistance, work primarily focused on amplicon sequencing or PCR-based technologies, and new or improved tools to predict pathogen immune evasion or pathogenicity are out of scope for this RFP.

For computational and sample processing methods development, some of our key considerations include rapid turnaround time (sample collection to bioinformatic results), ability to scale to hundreds of samples and billions of reads, and applicability to environmental or pooled-human samples such as wastewater, air, nasal swabs, saliva, and blood.

We expect computational and modeling work to incorporate real-world sequencing and other biosurveillance data, which can be complemented by synthetic or simulated data approaches. A strong consideration in evaluating proposals is their open availability and potential to accelerate maturing pathogen-agnostic biosurveillance efforts, such as the CDC Biothreat Radar, Traveler-Based Genomic Surveillance (TGS), National Wastewater Surveillance System (NWSS), CASPER, WastewaterSCAN, EU Wastewater Observatory, Zephyr, and the UK's mSCAPE, among others. Applicants are welcome to build on public datasets including but not limited to:

- Untargeted wastewater sequencing from CASPER (PRJNA1247874)
- Hybrid-capture wastewater sequencing data from Tisza et al. 2023 (PRJNA966185) and Wolfe et al. 2026 (PRJNA1438722)
- Nasal-swab sequencing data from SecureBio's Zephyr and the Broad Institute (PRJNA1052714)
- Wastewater and swab sequencing from CDC TGS (PRJNA989177) and NWSS (PRJNA747181)
- Publicly available blood sequencing datasets

Awardees are expected to make research funded by this program publicly available in a timely manner to support rapid adoption, including through publication in peer-reviewed journals, preprint servers, open-source code repositories, conferences, or other appropriate methods of dissemination. Blueprint may include publication milestones in award agreements. We recognize that certain findings may raise vulnerability-disclosure concerns, and we will work with awardees to develop responsible disclosure timelines in those cases.

Blueprint Biosecurity may engage external subject matter experts to assist with technical review of submissions. SecureBio Detection, which contributed to the development of this RFP, may provide reviewers for this purpose. All external reviewers are bound by nondisclosure agreements and subject to Blueprint's conflict-of-interest process, including recusal from review of any proposals where a conflict is identified. External reviewers do not make funding decisions; final award determinations are made solely by Blueprint Biosecurity.

Anticipated awards

We generally expect applicants to submit a proposal addressing a single technical area; however, an applicant may submit a proposal that addresses multiple technical areas as appropriate. We encourage collaboration and welcome multiple groups to form teams on related proposals.

We expect to make multiple awards across the three technical areas, with a combined total of up to $5 million across the entire RFP. There is no set maximum for individual awards. For each proposal, we ask that budgets be sized to the work proposed. Both smaller, tightly scoped efforts and larger, more ambitious proposals will be considered. It is unlikely that any single award receives a majority of the funds. Depending on proposal quality, expected impact, cost-effectiveness, and available funding, we may make several awards in some technical areas and none in others, or fund only part of a proposal. We may also choose to make no awards if no proposals meet our criteria.

Execution speed is critical. We have a strong preference for proposals that deliver results in 12 months or sooner.

Technical areas

Technical Area 1: Computational detection of known and novel, including zoonotic and engineered, pathogens in MGS data

Large-scale environmental and pooled-human-sample sequencing is a relatively new development that promises improvements in early detection and biosurveillance. But many genomic analysis approaches are designed for single-patient, high-coverage samples and are poorly suited to this kind of data. They often require individual assembly and manual interpretation, carry compute demands that can’t scale to billions of reads, and assume genomic coverage rarely seen in environmental or pooled sequencing. In practice this makes analysis slow and costly and keeps it dependent on expert review of individual samples. We’re interested in computational work that improves detection and characterization of known and novel pathogens, including zoonotic and engineered, in complex MGS samples.

We anticipate that competitive computational proposals will develop open, accessible, well-designed, documented, and user-friendly tools that emphasize speed and parallelizability, and are deployable in detection pipelines processing billions of read pairs per day. We expect

methods to be validated against well-characterized benchmarks spanning both synthetic and real-world data. Systems should be evaluated for detection performance (including false-positive and false-negative behavior), interpretability, and compute cost and scalability.

Example areas of interest include:

- **Homology-based novelty detection.** Automated, scalable, validated approaches to detecting novel pathogens by homology to known ones. Many zoonotic pandemics are caused by pathogens similar to known agents, but detecting these still requires individual assembly and interpretation. We are interested in approaches that flag dangerously diverged sequences at the read or contig level, accounting for factors like expected mutation rate and sampling frequency.

- **Taxonomic assignment in complex samples.** Reliable, efficient, sensitive, and specific reference-based assignment in complex samples like wastewater remains challenging because of incomplete or contaminated reference databases, tradeoffs between taxonomic and phylogenetic approaches, and the need to scale to large amounts of sequencing data. We welcome methodological innovation, improvement of reference databases (including through metagenomic assembly), and systematic comparison and benchmarking of existing pipelines (e.g., TaxTriage, mgs-workflow, EsViritu, nvd, ViPER, INSaFLU-TELEVIR).

- **Engineering and novelty detection.** Tools to flag signatures of genetic engineering (e.g., Chimera Detection, Synsor) or sequences that appear AI-designed (e.g., Wittmann et al. 2025), and classifiers that distinguish viral from non-viral sequences (e.g., DeepVirFinder, geNomad), with particular interest in methods that work at short read lengths and incorporate reference-free approaches.

- **Strain-level analysis and genomic epidemiology from complex samples.** Many phylogenetic and strain-level methods rely on high-coverage or assembly-based approaches (e.g., Delphy, WEPP, Freyja) that are often impractical for untargeted metagenomic data from complex samples. We believe more can be extracted from the population-level genomic information in these samples to track pathogen evolution and spread, including by methods that integrate low-coverage read-based data with traditional assembly-based approaches.

- **Assembly for complex data.** Improvements to seed-based outward assembly and more computationally efficient, reliable whole-sample assembly to recover and validate contigs from complex MGS data.

- **Indexing and anomaly detection.** Improved indexing of large sequencing datasets (e.g., Shiryev & Agarwala 2024, Mazloom et al. 2024) to support efficient lookup and anomaly detection functions, including deviations from site-specific baselines.

Technical Area 2: Sample processing methods for more sensitive, sequencing-based detection and rapid validation of sequences of concern

Sample processing, from collection through concentration, extraction, library preparation, and the molecular steps in between, has a large impact on the sensitivity and capture breadth of MGS workflows. Increasing the relative abundance of human-relevant pathogen sequences and robustly capturing their diversity can substantially improve the cost-to-sensitivity tradeoff, requiring lower sequencing depth for equivalent sensitivity or returning more genomic information per dollar. We believe significant advancements are possible here.

We anticipate that competitive proposals will apply rigorous experimental design and demonstrate familiarity with the state of the literature on wet-lab methods for the sample type they aim to optimize. We expect sequencing-based metrics, such as the relative abundance of human-relevant pathogens, captured diversity, and genome coverage breadth and depth, to form the core of validation, with measures like PCR concentration or other non-sequencing technologies used as complements rather than substitutes. Strong designs will be adequately powered and include appropriate technical replicates and negative and positive controls. To facilitate adoption, we will prioritize proposals that commit to making methods publicly available. Where a sample type is already being piloted for MGS biosurveillance, we strongly encourage applicants to partner with sample providers to run optimization experiments on real-world samples of interest and benchmark against existing approaches. We may be able to help facilitate these connections where useful, and partnerships can be developed further at the Full Proposal stage. We are especially interested in automation-friendly, high-throughput approaches with rapid turnaround (sample to prepared library in under a day).

For this technical area, we consider the following out of scope:

- Development of novel collection devices or sampling hardware as the primary deliverable
- Processing methods optimized for sample targets outside our focus on human pathogens with pandemic potential (e.g., soil)
- Optimization focused on non-sequencing-based detection platforms (e.g., CRISPR-based assays, biosensors)

We are also unlikely to fund hybrid-capture sequencing work unless it is optimized for greater sensitivity to novel or diverged pathogens, or for substantially faster turnaround than current approaches.

Example areas of interest include:

- **Depletion of abundant background.** Depleting off-target sequences can enrich rare human-relevant pathogens while remaining pathogen-agnostic. In wastewater transcriptomics, for example, bacterial ribosomal RNA often makes up more than 60% of sequences but is off-target for most detection goals. We are interested in innovative

depletion methods and benchmarking efforts across diverse sample types, particularly wastewater (e.g., improved rRNA depletion) and the removal of human nucleic acid from pooled individual samples like nasal swabs and blood (e.g., Chan et al. 2023). Approaches should be evaluated for unintended off-target depletion effects that may inadvertently reduce sensitivity to pathogens of interest.

- **Processing optimization and benchmarking.** Systematic comparison and benchmarking of processing methods for wastewater, nasal swabs, and blood, optimizing metrics such as fraction of vertebrate-infecting pathogen sequences, library complexity, genome coverage breadth and depth across human pathogens, and standard QC. We are especially interested in automation-friendly, high-throughput, rapid-turnaround approaches; optimization of low-volume reactions from residual clinical samples; improvements in scalable wastewater concentration; and single-method "total nucleic acid" extraction and prep that handles DNA and RNA viruses and other targets together.

- **Rapid verification from short flagged sequences.** Computational and wet-lab methods for rapid (<24 hours) verification and sequencing from short flagged sequences, including design of PCR-, capture-, or probe-based methods to confirm the presence of a flagged sequence and expand genomic coverage (e.g., Metsky et al. 2022).

- **Hybrid-capture sequencing evaluation and optimization.** Experiments to determine and/or improve the sensitivity of hybrid-capture probe-based sequencing to novel or diverged pathogens. Efforts to reduce the cost and turnaround time associated with pan-pathogen hybrid-capture sequencing.

Technical Area 3: Modeling pathogen-agnostic biosurveillance system features such as cost, sensitivity, and optimal deployment

Effective MGS-based surveillance requires understanding how much sequencing is needed to detect a pathogen at a given prevalence, how quickly detection can be achieved, how sensitivity and cost vary across sample types and strategies, and how systems should be deployed.

We are interested in modeling tools and statistical methods that accurately represent unique aspects of compositional metagenomic sequencing (compared to, e.g., PCR-based methods) and are directly relevant to operational deployment questions, such as: How deep should I sequence this sample? What does optimal deployment of biosurveillance sites or a layered detection network across multiple sample types look like? Systems that pair non-sequencing steps with a sequencing-based endpoint are in scope — e.g., using PCR to triage samples ahead of confirmatory sequencing. We are especially interested in ambitious system designs that can detect outbreaks significantly earlier than the current status quo and before there is widespread transmission.

We anticipate that competitive modeling proposals will be grounded in the specific characteristics of metagenomic data rather than generic epidemiological models, will be

validated or parameterized against real-world sequencing data where available, and — for tool development — will be open-source, documented, and user-friendly. Where good parameterization or validation resources do not yet exist, we are interested in efforts to address those gaps. Where appropriate, epidemiological models should consider a range of pathogens, shedding profiles, and emergence scenarios.

- **Applied modeling tools and methods.** Biostatistical and epidemiological tools and methods that accurately model or reflect the compositional dynamics of MGS sequence data and answer applied biosurveillance questions such as:

    - What is the growth rate or trajectory of a particular taxon or sequence? Are there ways to identify anomalous signatures taking into account site- and sample-level metadata?
    - What are the best ways to normalize time-series environmental MGS datasets like wastewater?
    - How can we estimate the prevalence of a pathogen from pooled sequencing data?
    - How can we optimize dynamics around sample collection and processing, sequencing depth, library diversity, and duplication rate for cost-effective, sensitive early pathogen detection?
    - What are optimal decision-making strategies and triggers to guide follow-up investigation across different biosurveillance regimes in the event of an initial detection?

    Examples of work we'd be interested to see adapted to the MGS context include EpiNow2, PooledInfRate, EpiSewer, and wwinference.

- **Cost and sensitivity across sampling strategies.** Modeling the cost and sensitivity of MGS detection across sample types and strategies, including municipal and airport or aircraft wastewater, traveler-based and public nasal swab sampling, routine clinical metagenomics, and blood supply sequencing (e.g., Sharma et al. 2023, Reddy et al. 2026, Justen et al. 2026, Jin et al. 2024). This includes improvements in methods to model sensitivity building on Grimm et al. (2025) and subsequent work which links pathogen prevalence to relative abundance (P2RA).

- **Operational deployment.** Modeling to inform deployment decisions such as the optimal number, placement, and geographic breadth of sampling sites, sampling cadence, sequencing depth, and turnaround time. This includes interactive tools to optimize and visualize system cost-effectiveness across different threat scenarios, sampling strategies, detection platforms, and budgets.

How to Apply

Submissions are encouraged, but not required, to use the Expression of Interest template available for download HERE. The template can also be copied as a Google doc with this link. Completed submissions should be sent to biosurveillance-rfp@blueprintbiosecurity.org.

For more information about the application process, please review the Application Information and Submission Guidance sections below. Additional questions may be directed to the contact email address provided in the funding opportunity.

Important dates

Posting date: Thursday, July 2, 2026

Final deadline for *Expressions of Interest*: Friday, August 21, 2026 11:59 PM ET

Expressions of Interest (EOIs) will be evaluated after the deadline. Selected EOIs will then be invited to submit a *Full Proposal* within 3 weeks after receiving a Notice of Recommendation.

Contact information

Please email all administrative, technical, and contractual questions to biosurveillance-rfp@blueprintbiosecurity.org. Questions about this program that are not sent to this email may not be replied to. All questions must be in English, and must include the name, email address, and telephone number of a point of contact.

Where Blueprint Biosecurity deems it to be helpful for all interested parties to the RFP, answers to questions (paraphrased where necessary to protect applicant information) may be posted in a public FAQ on Blueprint Biosecurity's website.

Guidelines for submission

Stage 1: *Expression of Interest*

We require applicants to submit an *Expression of Interest* with a summary of proposed work as the first stage of their application. **All submissions should be emailed to biosurveillance-rfp@blueprintbiosecurity.org.**

- This document should be **under 3 single-spaced pages**. Applicants may opt to provide links or supplemental papers for consideration as part of the evaluation, though these may not be reviewed.
- References/bibliography and supplemental papers do not contribute to the page limit.
- Please submit as a PDF or Word document, in English. Use the template if helpful. We care more about the clarity of your plan than perfect formatting or polish.
- We request that proposals do not include brochures or marketing materials; please provide only information relevant to the submission requirements or evaluation criteria.

Please include the following information in your *Expression of Interest*:

1. A simple, informative title
2. Names and affiliations of key personnel
3. A brief 2-4 sentence summary of previous experience relevant to your proposed work
4. A brief initial description of your intended approach, timeline, and deliverables
5. A rough budget including materials, personnel, and overhead costs, as well as other expenses

We understand that each of the points above may change in the process of developing a Full Proposal, including the requested budget.

We encourage creative (but rigorous) ways to accomplish the study objectives. **We have a strong preference for proposals that reasonably aim to achieve their stated deliverables within 12 months or sooner.**

Stage 2: Full Proposal

Select applicants will be invited to submit a *Full Proposal* after we review their *Expression of Interest*. A *Full Proposal* will consist of a technical section and a cost section. We will provide templates and further guidance to selected applicants after reviewing their *Expression of Interest*.

Application review

Evaluation criteria

All proposals will be evaluated based on the following criteria:

1. **Scientific and technical quality of proposed work**

Proposals will be evaluated for achievability, reasonableness, and likelihood of completion. Proposals should include a logical plan with timelines, deliverables, and a clear connection to the goals of this RFP. We will also assess whether the proposed schedule is realistic.

2. **Applicant's demonstrated capability and/or related experience**

Proposals will be evaluated for the technical team's experience and expertise relevant to the proposed work. Strong proposals will show a track record of delivering similar projects on time and within budget. Consider including any related current or past efforts, with details such as the funder, timeline, summary of progress or results, and award value, to help us assess capability.

3. **Cost-effectiveness**

Each proposal will be subject to cost analysis to ensure effective, reasonable, and realistic proposed costs for technical work and equipment, labor, and other associated program costs. Proposals will be evaluated for their cost-effectiveness, realism (the necessity of each expense to address the program objectives), and justifications.

4. **Speed of execution**

Proposals will be evaluated for the speed at which the work is initiated and completed, while not sacrificing scientific integrity. Applicants should identify how their approach will preserve scientific integrity while accelerating the experimental or development timeline.

5. **Public availability**

Proposals will be evaluated for the extent to which outputs, including tools, datasets, methods, and publications, will be made openly and freely available for adoption into biosurveillance systems in a timely manner. Proposals that produce open-source software, publicly accessible datasets, or openly published protocols will be prioritized over those that produce proprietary or restricted-access outputs.

Award administration information

Selection notices

1. **Types and delivery of notices**

The following notices will be provided as applicable:

- Notice of Disinclination (for proceeding from *Expression of Interest* to *Full Proposal*)

- Notice of Recommendation (for proceeding from *Expression of Interest* to *Full Proposal*)
- Notice of Non-Selection (for proceeding from *Full Proposal* to negotiation of an Award)
- Notice of Selection (for proceeding from *Full Proposal* to negotiation of an Award)

All notices will be sent by email to the contact information identified in the *Expression of Interest* submission.

2. **Expressions of Interest**

Blueprint Biosecurity will respond to *Expressions of Interest* with either a Notice of Recommendation or a Notice of Disinclination. All applicants may still submit a *Full Proposal*, regardless of Blueprint Biosecurity's response to the provided *Expression of Interest*. All conforming *Full Proposals* will be reviewed according to the evaluation criteria listed in the "Application Review" section; these reviews will be independent of the *Expression of Interest* reviews, though consideration may be given to the applicants' responses to feedback provided.

3. **Full Proposals**

After *Full Proposal* evaluations are complete, applicants will be notified as to whether their proposal was selected for award negotiation. For proposals that receive a Notice of Selection, the funding negotiation could be for the proposal in whole or in part. If a proposal has been selected for award negotiation, Blueprint Biosecurity will initiate those negotiations following the notification.

Application Information

Eligibility requirements

Submissions are welcome from all responsible sources, inside and outside the United States, capable of performing the work outlined in this Request for Proposals.

To avoid conflicts of interest, any individual who contributed substantive written or editorial input to drafts of this Request for Proposals within thirty (30) days prior to its public release is ineligible to serve as a principal investigator on a proposal.

Awards to non-tax-exempt entities

As a 501(c)(3) organization, we are subject to federal tax law requirements that restrict the circumstances under which grants may be awarded to entities that are not tax-exempt.

Proposals from entities that are not tax-exempt will be evaluated with particular attention to whether intellectual property generated under the award will be made broadly available for the

advancement of science and public health, and whether the proposed work produces publicly accessible outputs, such as open-source tools, open datasets, or peer-reviewed publications.

Any private benefit to the awardee must be incidental and insubstantial; proposals focused primarily on the development of proprietary products or services are unlikely to be funded.

For-profit awardees may be subject to additional terms regarding the ownership, licensing, and dissemination of intellectual property developed under the award. We reserve the right to decline awards where such awards would be inconsistent with our charitable purpose or applicable legal requirements.

We will be unable to provide awards to any individuals or entities subject to United States sanctions.

Administrative overhead policy

We maintain the following policy that limits indirect costs ("overhead") for any grant we make or recommend:

- When making or recommending grants, we restrict indirect costs to no more than 10% of direct costs.

Direct costs are defined as expenses that support and advance the project's specific goals; indirect costs are defined as general administrative and operational expenses that are not specifically identified with the funded project.

Partnering with Other Organizations

Applicants may elect to contract subcomponents of their proposed work to other groups.

We reserve the right to:

- Select for negotiation all, some, one, or none of the proposals received in response to this RFP;
- Conduct discussions with applicants where necessary;
- Select entire proposals for award, or only specific portions;
- Fund awards in increments or by milestone achievement, depending on the nature of the work proposed, the required degree of interaction between parties, and other factors;
- Offer options for continued work and additional funding following completion of the proposed work;
- Request additional documentation once the award instrument has been determined (e.g., representations and certifications)

We may stop considering a proposal for award if: all parties involved fail to reach agreement on terms (award, technical, milestones, etc.) within a reasonable time; the applicant fails to provide

requested additional information; or the application is deemed noncompliant with the requirements of the RFP at any time.

Awardees are responsible for ensuring that research is conducted in compliance with rules set forth by relevant institutional, local, and national research regulatory bodies such as Institutional Review Boards (IRBs) or Institutional Ethics Committees (IECs). Awardees shall be solely responsible for ensuring that any goods, services, or deliverables provided under this award do not infringe upon any existing patents, trademarks, or other intellectual property rights.

We retain sole discretion to select awards and to negotiate all terms and conditions with selectees.

Deliverables

We will negotiate project deliverables with individual awardees. Selected awardees may be asked to provide technical reports, virtual meetings to describe and discuss the technical progress, and a final report of funding-related activities.

Proposed project timelines should be no longer than 24 months from the award date and ideally 12 months or less.

Public dissemination of research is central to Blueprint's charitable mission. Awardees are expected to make outputs, including tools, datasets, methods, and findings, publicly available in a timely manner through peer-reviewed publication, conferences, preprint servers, open-source repositories, or other appropriate channels. We encourage awardees to publish and disseminate their findings in accordance with responsible information sharing practices in biosecurity, including awareness of information hazard and vulnerability disclosure risks.

If your proposal includes any proprietary components, please clearly identify what they are, why they need protection, and whether there is a way for us to share the information with others where we feel it may advance the scientific field.

Handling of proposal submissions and proprietary information

We treat all submissions as protected information and will only share them with authorized individuals involved in evaluation. This may include internal staff, external contractors, subject matter experts, and other collaborators (collectively, “Review Team Members”) who assist with administrative or technical review. For confidentiality and conflict of interest obligations applicable to Review Team Members, see the Proposal Evaluation Process and Conflicts of Interest section below.

Blueprint Biosecurity will retain an electronic copy of each proposal; all other copies will be destroyed. Submissions will not be returned.

Expressions of Interest should not include proprietary or confidential information unless essential for evaluation. If proprietary or confidential information must be included, it must be clearly marked as “Proprietary” or “Confidential,” as appropriate, and you must have the authority to disclose it.

Please note that Review Team Members may already possess information, methodologies, or data related to the subject matter of your submission through prior research, grantee interactions, or public sources. When marking information as "Proprietary," please ensure that you have accurately identified what is genuinely confidential and novel. If we determine that marked information is substantially similar to information we have independently obtained or already possess from other sources, we reserve the right to use that information according to the applicable rights from those sources, and such information will not be treated as confidential.

Proposal Evaluation Process and Conflicts of Interest

It is our policy to ensure fair and consistent evaluation of all submissions. The Review Team will consist of staff and a small number of external subject matter experts. All external reviewers are bound by nondisclosure agreements and subject to our conflict of interest process, including recusal from review of any proposals where a conflict is identified.

All Review Team Members are bound by confidentiality obligations at least as strict as those contained in our standard Nondisclosure Agreement, and we remain responsible for their compliance with these obligations.

External reviewers who conduct technical review of submissions are prohibited from receiving funding to conduct Blueprint-sponsored research for a period of twelve (12) months following the conclusion of the review process.

External reviewers do not make funding decisions; final award determinations are made solely by our staff. External reviewers will be acknowledged by name with the announcement of selected awardees.

Our Chief Operating Officer, who will not be part of the review team, will manage the conflict of interest process and adjudicate conflicts. Evaluation will consider potential dual-use applications of proposed work as well as vulnerability disclosure risks.

For more information about our conflict of interest process, please contact: biosurveillance-rfp@blueprintbiosecurity.org.

Applicants are required to disclose all potential, real, or perceived organizational conflicts of interest, which may include but are not limited to:

1. Financial interests or relationships with organizations involved in the sale of sample collection, processing, sequencing, bioinformatics, or related goods and services.

2. Any familial, financial, or professional connections between applicants and individuals or organizations involved in the management, review, or evaluation of proposals submitted under this RFP.

Evaluation for the Pathogen-Agnostic Biothreat Detection RFP will be led by:

- Jacob Swett, Executive Director
- Lennart Justen, Non-Resident Fellow