Innovations in Low-Cost and Simplified Pathogen Sequencing Workflows

Grand Challenges

Request for Proposals

Applications are due no later than September 29, 2026, 11:30 a.m. U.S. Pacific Time

Before applying, applicants should review the supporting documents for this Grand Challenge, including the rules and guidelines, application instructions, and frequently asked questions.

If you are planning to apply to this RFP, we will be hosting a dedicated webinar on September 1, 2026, from 5:30-6:30 AM Pacific Time. This session will provide a comprehensive overview of the RFP details and an opportunity to answer your questions. To participate in the webinar, please register and submit your questions in advance. If you cannot attend live, the webinar will be recorded and available on this challenge page after the session.

Catalyzing Innovation through Partnerships

At its core, Grand Challenges catalyzes bold innovation through partnership—bringing together funders, researchers, implementers, and public health leaders to solve complex global challenges. This multi-partner initiative reflects the Grand Challenges ethos, leveraging complementary expertise and investments to accelerate accessible genomic sequencing solutions for low- and middle-income Countries.

About this Challenge

This Grand Challenge is co-funded by the Gates Foundation, and the Temasek Foundation, and will be managed by the United Nations Foundation. This Grand Challenge is implemented in collaboration with a network of global and regional partners, including International Pathogen Surveillance Network (IPSN), hosted by the WHO Hub for Pandemic and Epidemic Intelligence, the Africa Pathogen Genomics Initiative (Africa PGI), and the Asia Pathogen Genomics Initiative (Asia PGI) as regional technical and public-health partners. This RFP aims to accelerate the development of affordable, scalable, and operationally simple sequencing solutions, enabling routine use of genomics for public health in low- and middle-income countries (LMICs).

Background and Problem Statement

Pathogen genomic sequencing is a foundational capability for modern public health surveillance. It enables the detection of outbreaks and emerging variants, characterization of transmission dynamics, monitoring of diagnostic and drug resistance, informing clinical decisions, and evaluation of intervention impact. During the COVID-19 pandemic, unprecedented investments expanded sequencing infrastructure across many LMICs. However, that capacity is largely confined to outbreak response, donor-supported pilots, and research projects. End-to-end workflows are often costly, technically complex, and dependent on fragile supply chains, cold-chain logistics, and specialized expertise. As a result, only a small fraction of clinically detected or environmentally sampled pathogens are ever sequenced, limiting the public health value of existing capacity.

Over the past decade, the cost of sequencing has decreased significantly; however, these advancements have not yet been fully translated into accessible diagnostic and population-level surveillance and routine programmatic use. Sequencing a single pathogen - viral, bacterial, or parasitic - can still exceed several hundred dollars per sample once all reagents, consumables, and logistical overhead are included. Emerging advances in protocol design, reagent chemistry, workflow simplification, and platform interoperability suggest that a fundamentally different cost and operational paradigm is now within reach.

This Grand Challenge initiative seeks to accelerate the development of low-cost, streamlined, and operationally simple targeted pathogen sequencing workflows designed for routine public health use in LMICs. We invite researchers and innovators to propose bold, scalable solutions that lower sequencing costs, simplify protocols, and democratize access to genomics.

The Challenge

We are seeking ideas that substantially lower the cost and complexity of pathogen sequencing for at least one priority pathogen or use case in **Table 1**. The primary objective is to drive the total sample-to-sequence cost to approximately US$1–10 per sample, while remaining fit for public-health use.

Rather than developing new sequencing hardware, this call prioritizes sequencing methodology and workflow that enables existing sequencing platforms (including, but not limited to, Illumina, Oxford Nanopore Technology, MGI/BGI, and other sequencers) to be used more affordably, reliably, and at scale. Proposed solutions should be adaptable across pathogens and platforms and explicitly designed for routine deployment in LMIC public-health laboratories (see **Table 2**).

We are especially interested in transformative approaches that rethink the sequencing workflow itself. At a minimum, a competitive workflow should be built on a shared laboratory backbone, complemented by interchangeable primer panels or assay modules that can be adapted quickly to different pathogens, programs, or surveillance objectives. Strong proposals will set out a clear roadmap showing how the workflow reduces protocol heterogeneity and lets laboratories pivot between pathogens without substantial retooling, retraining, or redesign.

Proposals should address the following objectives, calibrated to the maturity of the proposed solution.

- **Cost reduction**: Demonstrate a credible pathway to achieving per-sample costs (from sample to sequencing data) of approximately US$1–10, inclusive of reagents and consumables. Cost reductions should arise primarily from workflow and protocol-level innovation. While increased volume may contribute to incremental savings, this RFP prioritizes approaches that reduce per-sample costs through improved methods, streamlined workflows, and technical efficiencies independent of scale. Proposals should clearly articulate the assumptions underlying cost projections, including target coverage, sequencing depth, multiplexing, assay performance, and operational context, and demonstrate that affordability is achieved without compromising data quality or public-health utility. Approaches that rely primarily on increased multiplexing or throughput to reduce costs will not be prioritized. Guidance on minimum coverage and depth is provided in **Table 1**.

- **Workflow simplification**: Replace complex, multi-step, pathogen-specific protocols with streamlined, modular workflows suitable for routine public-health use. Priority areas include low-cost amplicon-based or other targeted sequencing assays; direct-from-sample amplification that reduces or eliminates dependence on culture and/or nucleic-acid extraction where technically and biologically appropriate; and integrated or "one-pot" reaction designs that consolidate processing steps and reduce hands-on time. Shelf-stable or lyophilized reagent formats are of interest where they simplify workflows, improve robustness, or reduce logistical complexity (e.g., cold-chain dependence), even if they do not by themselves lower reagent costs. Proposals should make their technical assumptions, constraints, and trade-offs explicit, including specimen requirements and performance implications.

- **Platform compatibility and scalability**: Proposed methods should be compatible with widely deployed sequencing platforms (including, but not limited to, Illumina, Oxford Nanopore, and MGI/BGI). Preference will be given to workflows that are compatible with multiple sequencing platforms at the assay-design level, or that clearly explain how they can be adapted across platforms with minimal modification.

- **Reduced turnaround time**: Proposals should clearly specify expected turnaround times for core laboratory processing steps (e.g., sample preparation, library construction, and sequencing) and describe how workflow design choices reduce turnaround time without compromising data quality.
- **Demonstration of efficacy and performance**: Proposals should include a clear plan to demonstrate efficacy for priority pathogens and/or use-cases (see **Table 1**). Applicants may submit preliminary proof-of-concept data where available; however, the primary expectation is that funded projects will generate and validate proof-of-concept evidence during the award period. Resulting data should demonstrate that the proposed low-cost sequencing approach maintains accuracy, reliability, and public-health utility comparable to current reference or gold-standard methods, appropriate to the intended pathogen and use case.

Achieving the above objectives will likely require expertise from multiple disciplines and a strong understanding of on-the-ground needs. We encourage partnerships across academic, public-health, and private-sector.

We are looking for proposals that:

- Present a credible pathway to low-cost sequencing, supported by a preliminary cost model and grounded in realistic technical assumptions.
- Emphasize simplicity of protocols and workflows-reduced steps, limited protocol variants, minimal specialized training, and designs suitable for routine use by public-health laboratory staff.
- Clearly articulate a sequencing workflow innovation aligned with the in-scope pathogens and use cases described in **Table 1**.
- Prioritize technical and methodological innovation over operational fixes, focusing on assay-, workflow-, or protocol- level redesign rather than cost reductions driven primarily by bulk procurement, price negotiations, or throughput-based protocols.

- Describe operational feasibility for LMIC public-health laboratory settings (see **Table 2**), including explicit consideration of limited automation, reagent shelf-life, constrained cold-chain access, and staff with standard molecular-biology training. Where relevant, describe suitability for low-to-moderate-throughput surveillance and justify programmatic use.
- Include a feasible workplan and milestones appropriate to the maturity of the proposed solution, with a clear 18-month plan and proof-of-concept data generated within the first 12 months of the award.
- Provide justification for the requested funding level, demonstrating alignment between scope of work, technical maturity, milestones, and budget.
- Describe adaptability across pathogens, including a clear roadmap for extending the proposed workflow to additional pathogens or surveillance use cases.
- Describe a credible pathway toward mainstreaming and sustainability - how a validated workflow could transition into routine national surveillance, remain affordable and supported beyond the award period.

The following types of proposals are out of scope and will not be considered:

- Proposals that offer only modest refinements or incremental modifications to established workflows that lack a plausible step-change in cost and operational simplicity toward the US$1–10 sample-to-sequence target.
- Approaches focused primarily on bulk procurement, price negotiations, service delivery models, or throughput-driven and/or multiplexing-driven cost reduction. This RFP targets technological and methodological innovation, not procurement strategies.
- Approaches that compromise accuracy, coverage, and depth to the point of being unactionable for public health decision-making as per the indicative minimum requirement provided on **Table 1**.
- Proposals that do not involve sequencing-based assays
- Theoretical concepts: early-stage ideas that lack practical research and development plan for testing or validating the concept within the proposed timeframe.
- Requests for funding that are not supported by commensurate technical maturity, feasibility evidence, or a credible plan to generate and validate proof-of-concept data within the proposed timeframe.
- Proposals that are unwilling to support independent evaluation or appropriate sharing of protocols, reagents, or data under suitable governance arrangements.

Eligibility Criteria

This opportunity is open to research institutes, nonprofit organizations, for-profit companies, international organizations, government agencies, and academic institutions. Please note that all applicants will be expected to comply with the Gates Foundation's global access requirements. We encourage projects and/or consortia applications led by applicants from LMICs. Individuals and organizations classified as individuals for U.S. tax purposes are not eligible to receive an award under this RFP.

Eligible entities must not be subject to United Nations sanction or have committed serious violations of United States or UN sanctions. Eligible entities must not have derived revenue from

the production of controversial weapons (such as antipersonnel landmines, cluster bombs, or nuclear bombs) or the production or manufacture of tobacco.

Award Structure and Funding Level

To accommodate different stages of innovation maturity, this RFP supports a tiered award structure, with funding levels and expectations aligned to the readiness and scope of the proposed work. Indicative award categories are:

Tier 1: Early-stage feasibility awards: up to US$300,000 (grant term up to 24 months). For technically ambitious or higher-risk, earlier-stage concepts focused on feasibility testing, assay or workflow prototyping, and initial cost-reduction validation. Intended approaches that require focused development to demonstrate viability.

Tier 2: Mid-stage development awards: up to US$600,000 (grant term up to 24 months). For concepts with preliminary feasibility evidence that are ready to advance from prototype toward an integrated workflow-optimizing performance, broadening assay or pathogen coverage, and generating more robust cost-reduction and performance data.

Tier 3: Advanced development and validation awards: up to US$800,000 (grant term up to 36 months). For more mature concepts aimed at workflow refinement, performance optimization, and generation of proof-of-concept and validation data in relevant public-health use cases in LMICs.

We anticipate making approximately 15 awards across the three tiers. The final award amounts, number of awards, and funding mix will depend on proposal quality, technical maturity, funding availability, and strategic fit. Applicants should request funding commensurate with the scope and readiness of their proposed work and include a clear, milestone-based plan appropriate to the requested budget.

Table 1: In-Scope Pathogens and Use Cases: Applicants may propose solutions addressing one or more of the following categories. We are open to a range of approaches, including targeted assays, amplicon sequencing, and untargeted or enrichment-based whole-genome sequencing, as well as other innovative methods, provided that proposed solutions meet the performance requirements and cost objectives outlined in this RFP.

Pathogen / Pathogen Group	Target	Technical Comments / Minimum Requirements
Viral genomes including Polio, Measles, Arboviruses, rotavirus, viral hemorrhagic fevers (VHFs), mpox, and other public health relevant viruses	Whole-genome sequencing (WGS) target-enrichment or amplicon sequencing where WGS is not feasible. This could also include Metagenomic sequencing (mNGS) for detection and characterization of novel or unexpected pathogens	- Sample source: clinical specimens and/or environmental samples (e.g., wastewater). - Depth and coverage as appropriate to sample complexity and use-case - Protocols should support both routine genotyping and higher-resolution transmission analysis.
Malaria (*Plasmodium* spp.)	Drug and diagnostic resistance markers for Plasmodium *falciparum* and *Plasmodium vivax*	– Drug resistance and *hrp2/3* deletion from dried blood spots (DBS) or used RDTs – Turnaround time: less than 48h from clinical samples to results

		– Depth and coverage as appropriate to sample complexity and use-case
Tuberculosis (*Mycobacterium tuberculosis*)	tNGS-based drug resistance testing as per the WHO catalogue of drug resistance mutations in Mycobacterium tuberculosis complex (ref: https://www.who.int/publications/i/item/9789240089488) or WGS	– As per WHO guidance for tNGS-based drug resistance testing – Culture-free sequencing preferred – Clinical specimens and/or environmental samples (e.g., wastewater). – Depth and coverage as appropriate to sample complexity and use-case – Turnaround time: less than 48h from clinical samples to results
Bacterial / microbial pathogens	Antimicrobial resistance (AMR) and transmission dynamics profiling or lineage-specific SNPs or WGS	– Clinical specimens and/or wastewater samples – Priority AMR markers or WGS

		– High-resolution transmission dynamics – Depth and coverage as appropriate to sample complexity and use-case

Table 2: Cross-cutting design expectations for low-cost pathogen sequencing workflows

Criterion	Expectation
Affordability	Credible pathway to US $1-10 per sample, end-to-end (from sample to sequence)
Simplicity	Minimal steps; reduced protocol diversity
LMIC robustness	Operates reliably with limited infrastructure, and variable supply chains
Modularity	Unified wet-lab backbone with interchangeable assay components
Scalability	Suitable for high-volume, routine surveillance
Data quality	Generates sequencing outputs suitable for outbreak detection, surveillance, monitoring, and decision-making as described on Table 1
Cold-chain independence	Preference for workflows that are based on reagents that are lyophilized or stable at ambient temperature in settings of use
Platform agnostic	Preference for solutions that are compatible with multiple sequencing platforms, or that clearly articulates how the proposed solutions can be adapted across multiple sequencing platforms with minimal modification