Biomedical Advanced Research and Development Authority (BARDA)

Administration for Strategic Preparedness & Response (ASPR)
U.S. Department of Health and Human Services (HHS)

Request for Information (RFI) for

"AI-Enabled Discovery of Broad-Spectrum Small-Molecule Inhibitors for Filoviruses"

Issued: 18 May 2026

Responses Due: 1pm EDT, 17 June 2026

Biomedical Advanced Research and Development Authority (BARDA)
Contracts Management & Acquisition (CMA)
400 7th Street, SW, Washington, DC 20024

MedicalCountermeasures.gov

Request for Information (RFI)

AI-Enabled Discovery of Broad-Spectrum Small-Molecule Inhibitors for Filoviruses

Purpose:

The purpose of this Request for Information (RFI) is to conduct market research to identify organizations with capabilities in artificial intelligence (AI) for application in the discovery and advancement of broad-spectrum, small-molecule therapeutics targeting filoviruses (e.g., Ebola virus (EBOV), Sudan virus (SUDV), Marburg virus (MARV)).

This RFI seeks information on technical capabilities, infrastructure, prior experience, and recommended approaches. Areas of interest include: AI-driven design, *in vitro* verification of hits, and early preclinical proof-of-concept evaluation. Information obtained through this RFI will inform acquisition planning and may shape the scope and structure of a future solicitation.

Respondents may propose teaming arrangements or partnerships to address the full scope of capabilities described in this RFI.

Request for Information

Respondents do not have to be a member of the RRPV consortium to submit a response for this RFI; however, they must be a member of the consortium to respond to any future request for project proposals (RPP) for this requirement.

Please submit responses by email to rrpv@ati.org no later than

1pm EDT June 17th, 2026

Late responses will not be considered.

This RFI is for information gathering purposes only. It does not constitute a Request for Project Proposal (RPP) nor does it imply any obligation to issue a future solicitation, make any award, or pay any costs associated with responding to this RFI. Submission is voluntary and does not commit the responder to respond to any subsequent opportunities (if any) related to this topic. The RRPV will not return or provide feedback on any submissions, however, BARDA reserves the right to further engage with respondents in a Market Research Call to clarify understanding of submitted information. All responses to this RFI will be treated as sensitive information and confidentiality will be protected accordingly.

Background:

Filoviruses are high-consequence pathogens requiring BSL-4 containment and represent ongoing biodefense and global health threats. The current small-molecule antiviral pipeline remains limited, and no small-molecule therapeutics have been approved for treatment of filovirus infection. Advances in AI, structure-based modeling, molecular dynamics, and

computational chemistry provide opportunities to modernize antiviral discovery and enable the identification of small-molecule therapeutics that target conserved viral functions critical to filovirus replication and pathogenesis.

Technical Focus:

The potential funding effort is expected to span AI-enabled discovery through lead selection and preclinical *in vitro* and *in vivo* testing in small animal models. Preference is for direct-acting antiviral treatment approaches; however, host-targeted approaches relevant to viral replication may also be considered. Approaches targeting host dysregulation or disease state are out of scope, as are nucleic acid-based therapeutics and candidates being developed for a prophylactic indication.

Broad-spectrum activity across EBOV, SUDV, and MARV will be required, with preference for candidates also demonstrating efficacy against other negative-sense RNA viruses.

Through this RFI, BARDA seeks input on approaches to discover and advance potent, safe, broad-spectrum, small-molecule therapeutics targeting filoviruses using advanced analytics, including AI-enabled and other in silico methods.

Specific Questions for Respondents:

Respondents are requested to address BARDA's interest in the discovery and advancement of potent, safe, broad spectrum, small molecule inhibitors of filoviruses.

A. Strategic Scope

1) What are the risks and benefits of releasing a potential future funding initiative focused on a specific viral target (e.g., a defined protein or stage of the viral life cycle) as opposed to a broader approach for anti-filovirus activity without a prescribed target? Describe how your approach would differ under each scenario (target-specific vs. virus family–level development).

2) Nucleoside analog RNA-dependent RNA polymerase (RdRp) inhibitors have demonstrated effective antiviral activity against filoviruses but have faced limitations in safety/toxicity, pharmacokinetics, and/or potency.
    a. How could your approach improve upon this specific class of compounds for filoviruses?
    b. What are the key benefits and risks/challenges of a program focused on nucleoside/nucleotide analogs for filoviruses?

Provide concise technical rationale addressing risk, feasibility, timelines, and expected impact.

B. Technical Capabilities

3) BARDA is considering a funding initiative focused on small molecule therapeutics targeting filoviruses, which could include novel chemical structures, peptides, and other synthetic molecules.
    a. What types of small molecule modalities does your organization produce? Describe the benefits and risks of your approach.
    b. Is your approach focused on viral or host targets involved in pathogenesis? Describe the benefits and risks of your approach.
4) Describe your AI and in silico drug discovery capabilities relevant to antiviral small-molecule design, particularly for RNA virus targets. As applicable, include:
    a. Platform overview, including key components and end-to-end workflow
    b. Data assets (types, scale, diversity) and general approaches to data quality and validation)
    c. Molecular design and optimization approaches (e.g., generative methods, chemical space exploration, and multiparameter optimization, including but not limited to SAR-informed refinement).
    d. Modeling and simulation capabilities (e.g., docking, binding prediction), including use of AI/machine learning (ML).
    e. Approaches to synthetic feasibility and developability, including retrosynthesis, synthetic accessibility, and in silico ADME-Tox/safety.
    f. Strategies to identify and mitigate potential viral resistance mechanisms during the design phase.
5) Describe how your organization evaluates and optimizes molecular designs and integrates AI-driven design with medicinal chemistry, ADME/Tox prediction, and experimental verification. It is highly desirable to understand how you assess antiviral activity, safety, selectivity, and off-target risk; balance potency and toxicity; and use experimental data (*in vitro/in vivo*) to inform decisions.
6) Describe your approach to model improvement/optimization, including how experimental data (e.g., *in vitro* assays) are incorporated into model retraining and iterative design cycles, and provide examples of model performance, benchmarking, or historical results demonstrating predictive accuracy or reliability, if available.
7) Briefly describe any experience and/or partnerships with small animal models and early preclinical development for viral pathogens.

C. End-to-End Example, Timeline and Feasibility

8) Provide information addressing the following:
    a. Progression from computational design to *in vitro* assessment and, where applicable, *in vivo* proof-of-concept, preferably for antiviral or related RNA virus targets. If available, please provide an example of prior relevant work through *in vitro* and/or *in vivo* evaluation.

b. Based on this or similar efforts, provide high-level estimates for timelines and rough-order-of-magnitude (ROM) costs to progress from in silico design to *in vivo* proof-of-concept. Detailed cost proposals are not requested.

c. Key challenges associated with executing this type of effort (e.g., computational design, compound synthesis, execution of *in vitro/in vivo* characterization).

D. Broad-Spectrum Strategy

9) Describe your strategy for achieving activity across multiple filovirus species and, where applicable, related RNA virus families. Include how you identify and leverage conserved structural motifs as well as representative potency and selectivity benchmarks used to define broad-spectrum activity.

E. Intellectual Property

10) Describe your approach to intellectual property and freedom-to-operate for AI-assisted drug design.

F. General

11) Would your organization be interested in participating in partner-matching mechanisms (e.g., an interested parties portal or partnering events) to identify collaborators? Please briefly describe any capability gaps (e.g., preclinical or *in vivo* development) and the types of partnerships that would be beneficial?

12) If a Request for Project Proposals (RPP) is released which includes work ranging from lead generation to *in vivo* testing, how much time would your organization require to prepare a response?

Submission Instructions:

Interested parties should respond to this RFI with a written response consisting of a cover page and a technical response (PDF or Word; no smaller than 10-point font). The cover page should provide administrative and contact Information (contact name, title, email address, phone number) and organizational information of the responder (entity name, headquarters, mailing address). **The technical response should be no longer than five (5) pages**.

- BARDA requests concise, technically focused responses intended to inform planning and potential future program development.
- Detailed cost proposals, full development plans, or proprietary data are not requested at this stage.

Responses should include:

- Brief description of relevant capabilities

- Description of potential teaming arrangements (if/where applicable)

Add references as necessary but be sure to include all relevant information in the response. Cited publications or attachments may not be read.

Respondents must clearly mark all copyrighted information, data, and materials with appropriate restrictive legends (e.g., confidential, privileged, proprietary, trade secret). DO NOT SUBMIT ANY CLASSIFIED INFORMATION.