Step I: FDA ARGOS Sample Submission Application

**Application Guidelines**

1. *The application should be submitted electronically per requirements via the [web site](https://argos.igs.umaryland.edu/).*
2. *There are no submission deadlines; applications can be submitted at anytime.*
3. *IGS and FDA personnel can assist / guide you in preparing the application.*
4. *In the application, please respond to the following:*
	1. *State the relevance to infectious disease for the organism(s) to be studied; for example the public health significance, model system etc.*
	2. *Are there genome data for organisms in the same phylum / class / family / genus? What is the status of other sequencing / genotyping projects on the same organism? Provide information on other characteristics (genome size, GC content, repetitive DNA, pre- existing arrays etc.) relevant to the proposed study.*
	3. *Provide the rationale behind the selection of strains and the number of strains proposed in the study. Are the strains listed on the FDA ARGOS Preferred Organism List?*
	4. *For bacterial, fungal, and parasite organisms, are you able to provide >10ug of high-molecular weight genomic DNA for each isolate? For viral isolates, what genomic material will be provided?*
	5. *Can the resulting genome sequence data be promptly released to public archives (NCBI SRA, Genbank, etc.)?*
5. *Investigators can expect to receive a response within 4-6 weeks after submission.*

FDA ARGOS Sample Submission Application

 Project Title:

Authors:

**Primary Investigator Contact:**

|  |  |
| --- | --- |
| Name |  |
| Position |  |
| Institution |  |
| Address |  |
| State |  |
| ZIP Code |  |
| Telephone |  |
| Fax |  |
| E-Mail |  |

1. Executive Summary

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2. Justification

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**3.** **Rationale for Strain Selection**

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4. Availability & Information of Strains:

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| 1. *Indicate availability of relevant laboratory strains and clinical isolates. Are the strains/isolates of interest retrospectively collected, prepared and ready to ship?*
2. *Attach relevant information, if available in an excel spreadsheet for multiple samples: e.g*

*• Name**• Identifier**• Material type (DNA/RNA/Strain)**• Genus**• Species**• Specimen / Strain**• Identification method**• Isolation source**• Isolated from/host**• Collected by**• Taxonomy\_ID**• Select agent status**• International permit requirement**• BEIR/ATCC repository accession number**• Other public repository location**• Other public repository identifier**• Sample provider’s name**• Sample provider’s contact*1. *What supporting metadata and clinical data have been collected or are planned on being collected that could be made available for community use?*
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 5. Public Data Release:

*Please confirm that resulting genome sequence data, genome assemblies & annotation, and related metadata will be promptly released to public archives, including but not limited to NCBI SRA and Genbank.*

 Accept [x]  Decline [ ]

 5a. Public Data Access:

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| 1. *State any comments or concerns about rapid public genome data release.*
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Investigator Signature:

Investigator Name: Date