**REQUEST FOR PARTNERSHIP 2023**

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THIS NATIONAL PROGRAM AIMS TO CREATE FOUNDATIONAL GENOMIC, METABOLOMIC AND PROTEOMIC DATA RESOURCES TO FAST-TRACK KNOWLEDGE AND INNOVATION OF AUSTRALIAN FUNGI

**Instructions for filling in this document:**

1. Please read the [Request for Partnership Process information](https://bioplatforms.com/fungi-rfp-2023) before completing this document.
2. Address all criteria listed.
3. Answers to all the criteria should **not exceed 6 pages**

**Deadline:** Friday 9th June 2023

**Submissions:** Please email the completed document to Sophie Mazard, smazard@bioplatforms.com, with the subject: *Functional Fungi RFP1 – [Project name summary]*

**Contact information:**

Dr Sophie Mazard, Project Manager smazard@bioplatforms.com

Dr Kelly Scarlett, Partnerships and Engagement Lead kscarlett@bioplatforms.com

**PROJECT CONTACT DETAILS**

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| Project Leader Name: |  |
| Project Name:(as brief as possible) |  |
| Institution/affiliation: |  |
| Contact details | Email: Phone:  |

**PROJECT TEAM AND COLLABORATORS**

**1. List all research and end-user industry collaborators (name, affiliation and email), and detail how each partner will participate in the project (e.g. sample provision, material extraction – DNA / RNA / protein / metabolite, bioinformatics, use of the outputs in research or applications/industry, etc.).**

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| **Name** | **Affiliation (Institution/Company etc)** | **Email** | **Intended Contribution**  |
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**2. The project team will be responsible for sample preparation and analysis of resulting genomic, metabolomic or proteomic data. Please describe the Project Teams relevant expertise;**

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| **a).** M**olecular wet lab expertise** (Note: where possible, the Australian Functional Fungi Initiative may support sample preparations (DNA extractions) in our facilities. Please indicate if your project may require sample preparation support). |
| **b). Bioinformatics expertise** (Note: The Australian Functional Fungi Initiative are able to assist in sourcing expertise and training, please indicate here if your project requires bioinformatic support).  |

**PROJECT DETAILS**

**3. What Australian Fungi is this project interesting in?**

***(\*) Note: If your project requires analysis of multiple genera, please list your fungi of interest in an appendix excel file***

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| Fungi of interest (\*) | Scientific name/s (either at genus or species level) Common name/s (if known): Estimate genome size (if known):Genome ploidy (if known):Is a pure culture(s)/isolate(s) available and accessible? |
| What sector will the utility of the data be most relevant | [ ]  Health and Medicine[ ]  Environment and Conservation[ ]  Innovation (e.g. food, biomaterials, circular economy)[ ]  Taxonomy |
| Existing Collection Specimens | Have you spoken to any relevant Collection(s) about complimentary sample availability (i.e. type specimens) and accessibility?[ ]  Yes[ ]  NoWho is your contact(s)? [please add name, contact detail and organisation] |

**4. What biomolecular resources will this project generate? Please place an *X* next to all relevant rows.**

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| **Biomolecular resource requested** | **Analysis type** | **Number of sample(s) / plate(s)** |
| Genomics | [ ]  HiFi[ ]  Nanopore ONT[ ]  short-read sequencing[ ]  transcriptomes |  |
| Metabolomics | *(please specify)* |  |
| Proteomics | *(please specify)* |  |

**5.** **Please provide some background information on your fungi of interest (genus or species level)**

*a) Explain the challenge or opportunity relevant to your project and fungi of interest.*

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*b) How would this data be used by you and your partners? What knowledge or application/s will this data bring to research and industry?*

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**6. Is there any existing relevant data for this genus or species (or a closely related species)?**

*If data exists, how will this project create additional value (e.g. the existing assembly is for a non-Australian sample, existing assembly not detailed enough for the project aims, etc.). If none, please put N/A.*

*Note: some common places to check are NCBI -* [*https://www.ncbi.nlm.nih.gov/assembly/*](https://www.ncbi.nlm.nih.gov/assembly/%20) *and JGI MycoCosm (fungi) -* [*https://mycocosm.jgi.doe.gov/mycocosm/home*](https://mycocosm.jgi.doe.gov/mycocosm/home)

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**7. How accessible are the samples required?**

*a). Do the samples already exist for the project (i.e. do you already obtain the samples)?*

*b). Is there access to a known and vouchered specimen in an Australian Collection? Outline where this is located and if the specimen has been taxonomically verified.*

*c). If no sample/s exist, please detail your approach to collect an appropriate sample/s in a timely manner.*

*Note:* Each project group is responsible for compliance with the relevant jurisdictional laws and agreements for sustainable access to Australian biodiversity including collection authority, traditional knowledge and benefit sharing. Such details will be included in relevant sample metadata fields.

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**CO-INVESTMENT**

**8. If available, please outline any other co-investment (either cash or in-kind) available to complete the project.**

*Note: The Australian Functional Fungi Initiative provides resources for sample preparation (where possible and required), sequencing costs and data management including access to high end compute resource allocation (NCI and Pawsey) through Australian BioCommons Leadership Share – ABLeS (*[*https://www.biocommons.org.au/ables*](https://www.biocommons.org.au/ables)*)* and fully subsided training and access to web-based platforms for computational research including Galaxy, Apollo, AlphaFold 2.0, Fgenesh++ delivered by the Australian BioCommons.

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**POLICY AGREEMENTS**

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| Do you agree to the Australian Functional Fungi Initiative “[collaboration and data use policy](https://bioplatforms.com/australian-fungi-data-collaboration-policy/)” terms? (<https://bioplatforms.com/australian-fungi-data-collaboration-policy/>)  | [ ]  Yes[ ]  No |
| Do you agree to provide metadata for the samples in an agreed format? *This helps to ensure reusability, utility and standards of data resources beyond the current project.* | [ ]  Yes[ ]  No |
| Do you agree to lodge any culture, collected tissues and biological material in an appropriate collection for archiving? (If not, please provide reason here) | [ ]  Yes[ ]  No |
| Do you agree that secondary data products (e.g., assembled genomes) will be made openly accessible (with full consideration for any sensitivity concerns) within 1 year of receiving sequence data, unless otherwise agreed by the project partners and Bioplatforms Australia?  | [ ]  Yes[ ]  No |