ExFAB Fall 2026 Call for External User Proposals: Proposal Guidelines

The NSF ExFAB BioFoundry is pleased to announce its 2026 Fall Call for External User Proposals. This document outlines both project scope and proposal format.
Two submission tracks are available:

Track 1: Activation
This track is for external users that are interested in leveraging the following protocols and capabilities. ExFAB anticipates approving 5-10 Track 1 project proposals.

- **PhenoTypic**. PhenoTypic is a novel analysis platform developed by ExFAB that automates and standardizes bioimage analysis. Combined with ExFAB's automated microbial array and image acquisition capabilities, it constitutes an automated pipeline for high-throughput phenotyping of extreme or exceptional microbes grown on solid media across various growth conditions. PhenoTypic delivers quantitative measures of microbial phenotypes, including growth rates, colony morphology, and color/pigmentation, and has been successfully applied to collections of bacteria, yeast, and filamentous fungi. See an example here.

    - *Eligible microbes:* Bacteria, yeast, or filamentous fungi with medium-high growth rates (12-240 hrs to full growth). Preferably, microbes are amenable to growth in liquid, but accommodations can be made.
    - *Maximum sample set:* Microbial libraries of up to 2000 isolates.
    - *Other constraints:* Please note that there is a trade-off between number of strains and number of conditions. With >750 strains up to two conditions can be tested across all strains. More conditions can be tested with smaller libraries.

- **High-Throughput Microbial Chemotyping**: GNPS2go is an agentic AI platform that transforms raw mass spectrometry data into potential molecular identifications within minutes. LC-MS/MS data is first processed through the Global Natural Products Social Molecular Networking platform (GNPS2) using an automated identification and quantitation pipeline. The results are then delivered via an agentic AI portal designed for tailored queries - including comparative metabolomics, differential abundance analysis (up- and down-regulated metabolites), and pathway-level comparisons across samples.

  Coupled with high-throughput LC-MS/MS, GNPS2go accelerates untargeted metabolomics discovery to an unprecedented scale and speed. For ExFAB proposals, projects focusing on metabolites from extreme and exceptional microbes are strongly encouraged. Learn more about our workflows here.

    - *Suggested sample format:*
        - Cleared, filtered lysates or culture supernatants from any cultivated microbe or microbial community
        - 0.2 - 1ml culture volume, target OD of 1.0
        - Frozen or lyophilized
    - *Maximum sample set:* 500 samples

- *Other constraints:* Meant for comprehensive global analyses of microbial metabolomes, rather than targeted characterization or quantification of a small number of compounds.

- **Functional Enrichment Within Anaerobic Microbial Communities.** Anaerobes are difficult to isolate, cultivate, and phenotype due to the need to manipulate these microbes without oxygen. ExFAB houses all the infrastructure necessary to cultivate and phenotype anaerobes and anaerobic communities in a chamber that integrates liquid handlers and robotics to manipulate anaerobes at scale. This bespoke automation platform can easily be used to enrich functions within anaerobic communities - especially when that function can be coupled to a colorimetric, fluorogenic, or optical readout. Examples include the enrichment or isolation of anaerobes that degrade PFAS, components of plant biomass, or other organic substrates. Learn more here.

    - *Suggested sample types:* Source microbiome (e.g. from soil, rumen, digestor, compost) ideally with some prior amplicon sequencing characterization.
    - *Maximum sample set:* One source microbiome, must meet BSL-1 or BSL-2 categorization.
    - *Other constraints:* Source microbiome can be grown in liquid culture (e.g. non-biofilm forming) and media must be amenable to liquid handling. Users must have a pre-determined selection method for the function they seek, which may include cleavage of a target colorimetric/fluorogenic compound or growth of microbes against a certain substrate with serial dilutions.

Track 2: Ignition

This track is for large scale projects aligned with ExFAB's strategic research priorities. These projects leverage ExFAB facilities to address a Grand Scientific Challenge. ExFAB anticipates approving 1-3 Track 2 project proposals.

ExFAB Grand Scientific Challenges:

- **AI-driven design and editing of anaerobic microbial communities from bioproduction to biomedical applications**
    - ExFAB is particularly well suited to phenotype and enrich functions within human and animal-sourced microbiomes.

- **Cell-free production & screening of redox-sensitive & bioremediation pathways at scale**
    - Of particular interest for this call are oxygen-sensitive pathways and proteins using iron-sulfur clusters (e.g. ferredoxins), especially those for which there are established methods for tracking pathway performance (e.g. colorimetric assays or established LC-MS workflows).

- **MPG: Integrating Metabolomes, Phenotypes, and Genomes for Discovery of Extreme Traits at Scale**
    - Seeking users with interests in integrating metabolomic and genomic data

- **High-Throughput Functional Genomics in Extreme Microbes for Fungal Biotechnology**
    - We are especially interested in advancing yeast and fungal transformation in high-throughput.

- **Rewriting our understanding of compartmentalization to control microbial resilience**
    - We especially seek partners with access to large culture collections that can be imaged and phenotyped (e.g. cyanobacteria, large sulfur bacteria, etc.)

Please note: ExFAB and its in-house research team has a particular interest in growing our community and fostering strong, long-term collaborations with external academics. ExFAB will help applicants identify potential collaborations with its in-house researchers as part of the Track 2 proposal submission process.

Proposal Instructions

All project proposals for Track 1 and Track 2 must include the following sections. You may also include supplementary materials such as images, charts, tables, and references. All proposals should be 1-6 pages in length and submitted in PDF format through our web portal.

1. **Identifying details**. Include the project title, authors and affiliation(s), and the submission date.
    - For Track 2 proposals, please also indicate the ExFAB Grand Challenge most relevant to your project, and list at least one ExFAB-affiliated researcher with whose work the proposed project most closely aligns.
2. **Objective**. Provide a 2-3 sentence objective that includes both your general motive and specific experimental goal(s).
3. **Background and justification**. Discuss the proposed work's connection to extreme/exceptional microbes. Explain how the work will advance knowledge in microbial Biosynthesis, Bioremediation, or Rules of Life.
4. **Methods**. Describe the proposed experiments to be conducted at ExFAB. Include details such as sample numbers, required equipment, and special reagents or consumables. Be sure to call out any methods or protocols that are new to you or that must be adapted or scaled for use in our facilities. Specify a project timeline, including any preparatory steps to be conducted outside of ExFAB, and indicate the earliest possible start date for this work.
    - For Track 2 proposals, include details about your planned or proposed collaboration with an ExFAB-affiliated researcher.
5. **Personnel**. If you or a member of your lab intend(s) to conduct work at ExFAB, please: list the lab personnel involved and state their general level of lab experience, their experience with the proposed techniques, and what degree of training they will require from ExFAB staff.
6. **Anticipated outcomes**. Highlight any new protocols or workflows that will be developed during your project. Explain how the proposed work will benefit the ExFAB community (e.g. through the creation of knowledge, data, or tools).