

Core Facility Name Genetic Resources Core Facility
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Amount of Funding Requested 25,000

Briefly describe the core services you offer:

The Genetic Resources Core Facility (GRCF), a member of Johns Hopkins Genomics, is a service center at the leading edge of technology that includes support in both research and clinical services. The GRCF's expertise and sophisticated equipment is available to Johns Hopkins investigators performing studies in genetics, genomics, clinical science, cell biology, molecular biology, and translational medicine. The GRCF strives to streamline services by helping in project design, sample collection, blood isolation, cell line establishment, cell line authentication, cryogenic preservation and storage, DNA isolation, oligo and gene synthesis, methylation testing, custom array design and development, both Sanger and high throughput sequencing, single cell genomics, and new this year, true single molecule long read sequencing. Overall, our goal is to provide high quality, economical services to meet the Hopkins community needs. This particular application requests support for nanopore sequencing, a new long-read DNA/RNA technology that we recently acquired.

Briefly describe your current user base and how the current proposal will expand that base?

The GRCF service center user base includes hundreds of JHU investigators on all campuses. For more than 20 years the service center has offered support and guidance in sequencing efforts across many disciplines. Given the wide range of applications and complexity of individual project needs, the GRCF has expanded on our servicing options by now offering a long-read, high-fidelity DNA and RNA sequencing with the GridION. This is a new and exciting technology that offers the utility of long reads to the broader community at an affordable rate. For the GRCF, the long-read sequencing service would benefit from Core Coins supported collaboration with a broad group of users, varying in expertise and familiarity with the data generated through this technology. As experience and confidence in this new technology grows, the GRCF will be better equipped to guide direction and appropriate applications for this new service. This exposure and growing expertise will help expand the GRCF user base into the JHU community need for long-read, high fidelity sequencing.

What specific services do you plan to offer as part of this RFA?

We will offer single molecule sequencing on the Oxford Nanopore GridION platform, with a focus on rapid sequence identification, utilizing long reads for improved genome assembly, analysis of full length RNA transcripts from cDNA, direct sequencing of RNA

molecules, metagenomic analysis, structural variant detection, copy Number detection in complex regions, and any experiment where short reads are insufficient.

How do these services address the goals of the pilot program?

The Oxford Nanopore sequencing service is new to the GRCF core facility. This award would not only offer a new and exciting technology to the JHU community, but it would help to familiarize investigators with other services and expertise offered through the GRCF. Given the relatively inexpensive cost of an individual experiment, these funds would have an impact on a high number of users.

How would you select recipients to receive core services? Please describe the process and criteria you might use.

As with our previous Core Coins awards, recipients would be selected based on project, need, time to completion, agreement to recognize the Core Coins program and the GRCF in any publications generated as a result of the funding and, depending on the stage of research, presentation of results at the annual GRCF research symposium. In order to apply, a brief questionnaire and one-page statement of research, and how awarding of the coins would help bridge gaps currently not funded by other sources, would be required. Preferences will be made for junior faculty lacking full support, data needed to strengthen a grant application, new faculty with specific needs or supporting data needed for publication. Applicants will be reviewed by a GRCF panel and promptly notified of an award and timetable for utilization.

How do you plan to allocate the amounts available to individual investigators?

The Core Coins award will be divided into 20-30 experiments, which would include library preparation, sequencing, and analysis. Depending on application, and given the flexibility of the platform, multiple libraries and sequencing runs may be necessary (for example, de novo genome studies may need more sequencing data than a metagenomic experiment).