

Core Facility Name SKCCC Experimental and Computational Genomics Core
Last Name Wheelan
First Name Sarah
Email swheelan@jhmi.edu
Phone 4105027754
Amount of Funding Requested \$25,000

Briefly describe the core services you offer: The Experimental and Computational Genomics Core (ECGC) is a newly integrated core, fusing microarray, next-generation sequencing, bioinformatics and biostatistics analysis, and genomics education capacities in the SKCCC. Our focus is on start-to-finish support for complex and custom applications, starting with experimental design and including laboratory methods, analysis, and training. Our most popular packages are RNAseq, whole exome sequencing, whole genome sequencing, and ChIPseq, though we are seeing an increase in interest in microbiome applications, single cell sequencing, amplicon sequencing, and specialized methods. We also support custom standalone analyses for data produced outside the core. We are particularly well suited for providing highly integrated analysis of different types of experiments, using data generated in the core as well as publicly available data, and we wish to highlight that capacity through these grants.

Users are faculty members from throughout the Johns Hopkins University, including clinical, translational, and basic science labs. The ECGC is situated in the Cancer Center, but nearly half of users are from outside the cancer center and projects are quite diverse.

Briefly describe your current material or resources. We also hope to expand the breadth and user base and how the depth of questions asked by users, by encouraging more rigorous current proposal will expand research questions using public data and multiple methodologies. that base? This will stimulate investigators to think more creatively about their experimental design and will likely broaden our user base to include people who think they do not have the resources to ask rigorous questions using next generation sequencing. Also, recent NIH RFAs have focused on utilizing already available datasets, and we hope to encourage investigators to incorporate these into their proposals so that they may be eligible for such external awards, to support followup projects.

What specific services do you plan to offer as part of this RFA? We plan to support projects that integrate measurements across different sequencing modalities, either by collecting multiple data types or using publicly available data to supplement data generated by the ECGC. Typical projects include 4-12 samples and involve

one type of measurement on all samples; for example, a person might be interested in gene expression and would ask for RNAseq data from all samples. This grant would support additional measurements, such as ChIPseq, whole exome or whole genome sequencing, or methylation assessment, on those samples, and would prioritize support for adding publicly available datasets into the analysis. The additional experiments and analyses could cost up to \$8K-\$12K, depending on the scope of the experiment and the samples available.

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

While any investigator would benefit from this service, new investigators, who are just beginning to fully characterize their systems, would benefit from performing a broader and deeper set of analyses or experiments to establish a richer dataset that they can explore for years. We have found, in our consultations, that these investigators often believe that if they don't have large numbers of replicates, that they are relegated to more preliminary, explorative experiments; in fact, by adding publicly available data and data from complementary modalities, they can attain statistically and biologically significant results. While the amount awarded to an individual investigator is not large, it is enough to cover sequencing and library prep costs for several samples or to include multiple publicly available datasets in the analysis.

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

After advertising the RFA on our iLabs home page and our website, we would evaluate applications monthly until funds are allocated. Applications will be evaluated for scientific content and appropriateness of the experiments proposed, and must identify one or more publicly available datasets to include in analysis. The application must describe a set of experiments and analyses that will truly enhance the value of their dataset, asking questions that could not be addressed with only one sequencing modality. New users, junior faculty, and faculty needing preliminary data for grants will be prioritized.

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

Each investigator would be eligible for up to \$12,500 in funding, aiming for 2 or 3 grants allocated from the \$25,000 award. Investigators meeting the criteria would typically be awarded what they request, unless an experiment or analysis is deemed unnecessary or out of scope of the project.