Label	Value
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 next-gen sequencing and, new this year, single cell genomics. Overall, our goal is to provide high quality, economical services to the Hopkins community.
What specific services do you plan to offer as part of this RFA?	Three years ago the GRCF introduced a new service offering genomic analysis of single cells, including RNA-seq, gene expression profiling by qPCR and DNA amplification for whole-genome or targeted (exome or PCR-based analysis). To this end, in the spring of 2016, the GRCF acquired a 10x Genomics Single-Cell system, a new technology allowing for cell capture rates not available through commercial alternatives. This system offers a high throughput molecular barcoding and analysis suite that delivers cell-by-cell 3' counting of mRNA transcripts for many tens of thousands of cells per run. The platform supports a broad range of applications, including cancer-cell transcriptomics and cell-type identification and discovery. More recently, 10x Genomics released the V(D)J solution aimed at being a scalable tool for profiling full-length paired V(D)J transcripts from hundreds to millions of lymphocytes. The solution enables assembly of full-length V(D)J sequences on a cell-by-cell basis, providing high resolution insights into the adaptive immune system. Because the 10x Genomics Single-Cell platform works with short read sequencers, it integrates easily into the existing GRCF RNAseq workflow in which data is provided to investigators via MARCC. Last year the GRCF was awarded $25,000 for studies in single cell genomics and received an overwhelming response to the RFA. Due to limited funds, many worthy projects could not be supported. Within the last year, in combination with the Core Coins awardees, the GRCF has performed nearly 75 single cell captures, with no shortage of interest in the technology. Results from these captures have been presented at international / national meetings and within the Johns Hopkins community through the annual GRCF symposium. The GRCF would like to reissue the RFA and encourage further use of this powerful technology in 2017. As part of the RFA, the GRCF would offer awards for the capture and library preparation of **8** specimens. These awards would be divided, based on the received applications, to award a single investigator funds for one or two samples (**awarding a total of 4-8 investigator projects**) of up to 10,000 cells each using the 10x platform. The cost of downstream RNA sequencing and first-pass analysis through the 10x Genomics pipeline would be the responsibility of the awardee. A single sample with a cell capture rate of ~6000 cells could be sequenced and entered into the pipeline for a cost of $3,400 (targeting 100,000 reads per cell).

How do these services address the goals of the pilot program?	Awarding of these services to Hopkins investigators would connect investigators to the GRCF core facility for equipment and expertise typically unattainable to an individual laboratory, helping to accelerate research. Utilization of the single cell genomics systems offered by the GRCF would generate large amounts of data that can help in deciphering the heterogeneity of cellular populations, discovery of novel populations/ processes of cells or providing supporting material for defining cellular populations. Additionally, because this is a relatively new service to the GRCF core facility, this award would help to familiarize investigators with both novel and our currently offered services.
How would you select recipients to receive core services? Please describe the process and criteria you might use.	A recipient of the Core Coins award 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 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 **8** potential captures /single cell library preparations. Each awardee would receive funding for the capture of one to two specimens. Depending on applications, this would account for a total of **4-8** Core Coins single cell genomic project awards. Awardees would then be responsible for the remaining experimental cost of sequencing the single cell libraries.