***\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_***

***New User or New Project Introductory Questionnaire***

***\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_***

Thank you for your interest in our core. For new users or new project requests, we ask that you please create a Power Point slide or two addressing the following questions and send the attachment to SingleCell@bwh.harvard.edu:

**Customer Information**

* **User/Principle Investigator Name**: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
* **Goal of Project**: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
* **Funding**: [ ]  Internal MGB Peoplesoft Fund [ ] External non-MGB Source

**Project Information**

1. Please state basic experimental design, questions, and project goals. *(Note: when designing experiment, take into account batch effects which can often confound biological signal.*[*Here is a blog post with best practices.*](https://hbctraining.github.io/Intro-to-rnaseq-hpc-salmon/lessons/experimental_planning_considerations.html)*)*
2. If you plan to submit multiple samples, what is the total number of samples you expect to submit in the next 3 months?
3. What is the species of origin & cell type you wish to submit?
4. When was your sample collected?
5. If isolating cells from tissue, has the tissue dis-aggregation/digestion protocol been optimized?
6. What is the cell yield and viability of your sample?
7. What is your method of cell isolation: Flow Sorting, MACS, etc? (Note: If requesting CITE-seq service and using flow sorting as isolation method, please provide list of antibodies used in each panel)

Note: we require the viability to be at least 85% for optimal sequencing results. In most cases, some form of live cell purification, either by FACS or MACS column, is required. We therefore request that prior to scheduling a consult with us, you undertake necessary optimization to ensure adequate cell yield and viability. If applicable, we can offer to perform a QC check of your technique on our automated cell counter.

1. For Nuc-Seq/ATAC-Seq projects, has cell lysis protocol for nuclei isolation from your cells of interest been optimized? [See the cell lysis protocols here.](https://support.10xgenomics.com/single-cell-atac/sample-prep)
2. What is the expected size of your cells? (Note: According to 10X, the microfluidics chip used to capture cells has a cell size maximum of ~ 60um)
3. How many different condition(s) are you interested in comparing?
4. Does your lab have experience with bulk- or single-cell RNAseq of these cells?
5. What is your bioinformatic capacity?
6. For billing purposes, do you plan to use an internal MGB Peoplesoft Fund or an external non-MGB source of funding? *(Note: if external, please provide more details)*