Questions and Answers in Response to RFA-DK-21-034

Data Management/Tools/Integration

1. **What data are the (Re)Building A Kidney (RBK) and GenitoUrinary Development Molecular Anatomy Project (GUDMAP) consortia generating, and what data already reside in the RBK and GUDMAP databases?**

   The RBK and GUDMAP consortia are generating and hosting a variety of high-throughput molecular data that include (a) molecular data, such as bulk RNA-seq, single-cell and single-nucleus RNA-seq, single-cell ATAC-seq, and 10X spatial transcriptomics; (b) imaging data, such as CODEX, merFISH/RNAScope, nanoCT imaging, and light-sheet microscopy; and (c) additional community resources, such as protocols, cell lines, induced pluripotent stem cell (iPSC) reporter lines, and archival data (microarrays, *in situ* hybridization [ISH]).

   The RBK consortium is a network of research projects focused on the expansion of tools, resources, and knowledge that will guide studies to either stimulate productive kidney repair and/or regeneration *in vivo* or generate functional kidney tissue *ex vivo* for transplantation. The RBK database contains more than 213 whole-mount or section imaging samples (183 ISH and 30 immunohistochemistry images) representing 102 genes. Transcriptional profile datasets include 272 bulk RNA-seq samples and 31 single-cell or single-nuclei RNA-seq samples (with visualization images covering 17,913 genes). RBK resources also include 7 parental and 15 reporter iPSC lines, 70 metabolomic samples, 201 antibody tests, and 26 protocols.

   The GUDMAP consortium has generated a murine molecular atlas of the urogenital tract in the developing embryo and a human molecular atlas of the cell types found in the kidney. The GUDMAP website allows access to a database of gene expression data for the developing urogenital tract. The database contains more than 460 microarray CEL files and more than 13,027 whole-mount or section imaging samples (11,454 ISH images, 1,176 immunohistochemistry images, 380 histology slide images, and 17 nanoCT scans) representing 22,971 genes. The database includes transcriptional profile datasets, which include 375 bulk RNA-seq datasets collected from renal sub-compartments captured by laser and from the use of translating ribosome affinity purification (TRAP); and 218 single-cell or single-nuclei RNA-seq datasets with visualization images covering 19,515 genes. All data are annotated in detail against a standard anatomical ontology developed by the GUDMAP consortium that is updated as data reveals new genetic sub-compartments. In addition, the database houses data sheets on 150 characterized transgenic lines and 80 antibodies and supports 81 protocols.

   Further information about actively funded projects within the RBK and GUDMAP consortia can be found at the following links:

   - RBK: https://reporter.nih.gov/search/P1CK680kqk67N8kwED7YhA/projects?shared=true
   - GUDMAP: https://reporter.nih.gov/search/lmxdoxDhokSSdOZtgW8MLA/projects?shared=true

2. **How will the Analysis, Technology, Leadership, Administration, and Science (ATLAS) Center integrate with the existing RBK–GUDMAP infrastructure?**

   The ATLAS Center's central role will be to implement and improve upon state-of-the-art computational and systems-level approaches to integrate the molecular, spatial, and imaging data from GUDMAP and RBK consortia to generate 2D and 3D molecular atlases and reference maps. One major expectation of the ATLAS Center is to develop tools that allow users of various bioinformatics skill levels to interrogate, explore, and effectively analyze and visualize the data that are generated by the GUDMAP and RBK consortia.

3. **Can tools such as knowledge graphs or linked open data be used and developed?**

   Yes, applicants will provide scientific vision and leadership for an interactive knowledgebase that integrates multiple datasets and datatypes and provides tools for analysis and visualization as the "go-to" open-access resource for the research community regarding mouse and human renal and genitourinary development and disease. The RFA does not prescribe the approaches for tools, data integration, and data visualization but encourages the use of existing software and tools when available and appropriate.

Eligibility

4. **Are industry or foundation collaborations allowed?**

   Yes, for-profit organizations, such as small businesses, and nonprofit organizations other than institutions of higher education are eligible to apply. Please see RFA-DK-21-034, Section III. Eligibility Information, for a full list of all eligible organizations.

5. **Are foreign components allowed?**

   Yes, foreign components, as defined in the *NIH Grants Policy Statement*, **are** allowed. However, foreign institutions may not be the applicant organization. Please see RFA-DK-21-034, Section III. Eligibility Information, for a full list of all eligible organizations and additional details on foreign institutions.

Budget

6. **How will iPSCs be incorporated in terms of distribution and budget?**

   Applicants will be expected to advertise and develop a system for the distribution of iPSC reporter lines through a contract with a third party. The budget should request $50,000 to support the cost of distributing and advertising the iPSC reporter lines through a third party.

7. **Do you expect the Opportunity Pool projects to span one year or multiple years?**

   It is anticipated that the Opportunity Pool will support about 30 subawards over the 5-year project period (with each subaward being about $50,000 total costs per year), however the amount and duration for each Opportunity Pool project will be flexible and dependent on the specific gap and/or scientific opportunity.