NGS-Based Pilot Projects – Sequencing, Bioinformatics, and Analysis
Request for Applications

Purpose and Overview

To advance precision oncology and the molecular understanding of cancer, the MCW Cancer Center (CC), in partnership with the Genomic Sciences and Precision Medicine Center (GSPMC), is inviting proposals for small-scale research projects that utilize any combination of the genomic, transcriptomic or epigenomic technologies and bioinformatics platforms available in the GSPMC. Responsive proposals will describe projects that either improve our understanding of cancer initiation, progression or therapeutic resistance or show promise to improve cancer prevention, early detection, diagnosis or treatment.

Priority Areas of Funding for the Current Funding Cycle

Cancer relevant research from all areas of science are invited to apply to this RFA. Priority will be given to collaborations between basic/translational science and population science researchers who propose to study topics related to understanding or addressing cancer disparities, as well as projects that will support grant submissions or publications before December 1, 2021.

Eligibility

- Tenure track faculty that has a cancer-relevant project involving NGS-based methodologies (see GSPMC Technology & Bioinformatics Platforms below).
    - For sequencing applications, NGS will be performed at GSPMC.
    - For bioinformatics-only applications, sequencing data should meet minimum QC metrics appropriate for each NGS technology.
- Projects should lead to the identification of novel markers for tumor classification, diagnosis, prevention or therapeutics or provide insight into novel mechanisms of cancer initiation, progression and metastasis.
- To ensure appropriate allocation of resources, we recommend consulting with the GSPMC technology and bioinformatics team. 30-minute consultation slots will be available by appointment in both mid-October and mid-November. To schedule, please contact Chris Bauer at chbauer@mcw.edu. General questions can be sent to GSPMCInfo@mcw.edu.

Sample and Data Ready Requirement

To be eligible for funding, applicants must indicate the ability to either a) submit samples within three months for sequencing applications (with appropriate IRB/IACUC approvals) or b) transfer NGS ‘omics data within four weeks of award for bioinformatics-only applications. If samples or data are not submitted within these time frames following award notification, the award will be void.

Number of Awards and Budget

CC Leadership expects to fund up to 10 awards across the following categories in 2021:

- Sequencing through bioinformatics projects will receive up to $15K for GSPMC services.
- Bioinformatics-only projects will receive up to $5K for GSPMC services.

Application Instructions - Please see the MCW Cancer Center website here for additional information and forms.

Application Format: Use standard 11-point font, single space, and half-inch margins throughout the application. Consecutively number all pages.

- **Cover Page:** To initiate, please click here. This will take you to the Faculty Collaboration Database to sign in so that certain fields can be auto populated. Include project title, investigators and affiliations.
- **Scientific Abstract:** Provide a summary of the project. (250-word limit).
- **Lay Abstract:** Provide a brief summary of the proposed research project in layman's terms. If funded, this abstract will be distributed to the funding source and can be used in written correspondence with donors and interested parties. (200-word limit).
- **Research plan:** Provide specific aims, background, significance and rationale for the use of NGS-based methodologies and analysis. Describe (as available or applicable) sample availability, data set(s) to be analyzed, impact of proposed study, preliminary results and the experimental approach. (3-page limit).
- **Future Plans:** Provide clear information on how the award will lead to external grant funding. (1/2 page limit).
- **Facilities.** Briefly describe where the work will be done and what special resources are available to you.
- **Budget:** Use budget template found on the Cancer Center webpage followed by a Budget Justification.
- **Form B: Non-Supplanting Form.** Use separate forms for each Principal and Co-investigator.
- **Form D: Return on Investment.** Previous Cancer Center Pilot Grant recipients must complete.
- **Letter of Support from the GSPMC.** Letter of support should summarize the statement of work, quality control assessment, preparation of sample(s), and bioinformatic analysis of the NGS data.
- **References.** List references cited (not counted in page limit).
- **Biographical sketches.** Provide a NIH-format biosketch for each PI and co-investigator.

Evaluation Criteria and Reporting

Grants will be reviewed by a specially assembled review panel, and decisions for funding made one month following the RFA deadline. Proposals showing promise to support submission of a high-impact paper or a larger proposal for extramural funding before December 1, 2021 will be prioritized. Awardees will be required to submit a summary report (2-page limit) at the conclusion of the project and to present their data at the 2021 annual **Cancer Genomics Mini-retreat.**

Timelines

- Full applications are due by 5:00 pm on Tuesday, December 1, 2020.
- Please email one PDF file of the application to Nicole Davis (nmdavis@mcw.edu)
- Notifications of award will be made after peer review, by February 8, 2021.
- The start date will be dependent on the status of any required human and animal studies protocol approvals, with the requirement that the study must begin within nine months of award notice for sequencing applications or within six months of award notice for bioinformatics-only applications.
- Contact Nicole Davis (nmdavis@mcw.edu) with any questions.

GSPMC Technology & Bioinformatics Platforms

- **Molecular profiling of cancer** (testing based on multiple analytes)
  - Myeloid (blood or Bone Marrow) and solid tumor panels (pediatric and adult, on FFPE)
  - Detection of SNV, MNV, INDEL, CNV, and fusions
- **DNA-Based testing**
  - Tumor and/or somatic variant calling and analysis

    - Germline variant calling and analysis for cancer patients to investigate etiology or predisposition
    - Differences in variant (SNV, MNV, INDEL, CNV) frequencies between cases and controls
    - Analysis of specific inheritance patterns among duos, trios, or quads
- **RNA-Seq differential expression analysis**
    - Sample types include frozen cell pellets, flash-frozen tissue, or isolated total RNA (from 10pg to 1ug)
    - Differential expression by pairwise conditions or among groups of conditions/phenotypes
    - Results summary *via* PCA (dimensionality reduction), volcano plot, heatmaps, and pathway analysis
- **DNA CpG Methylation *via* RRBS** (reduced representation bisulfite sequencing)
    - Sample types include frozen cell pellets, flash-frozen tissue, isolated DNA (150ng - 1ug)
    - Report on genome-wide patterns of methylation changes
    - Summary on genes and their proximal regulatory regions
- **Histone-based ChIP-Seq and/or cut-and-run**
    - Actively growing tissue culture cells or fixed cell pellet (consultation available regarding method of fixation and total numbers needed)
    - Report on genome-wide patterns of peak position and intensity differences
    - Summary on genes and their proximal regulatory regions