Research Development Fund – Fall 2023 Application Template
Submission Deadline: ***12:00PM CDT Monday – October 23, 2023,*** **to** rdf@tamu.edu

*****Applications exceeding page limits for any section or do not follow the template will not be reviewed*****

Application Title: Enhancing Genomic Research Capabilities: Modernizing DNA Sequencing Infrastructure and Introducing Advanced Long-Read Sequencing at the Molecular Genomics Core

Lead contact for RDF Application:
Name: John C Blazier
Department: Texas A&M Institute for Genome Sciences and Society (TIGSS)
Email address: jcb244@tamu.edu
Phone number: 512-820-0046

Key Participating Units: Molecular Genomics Core (MGC)

RDF Amount Requested ($): $ 1,274,617.16

Executive Summary

This application addresses the need to **replace and upgrade existing critical equipment** as well as to **expand state-of-the-art DNA sequencing capabilities** for the Molecular Genomics Core (MGC). We will replace the MGC's deprecated thermal cyclers, used in library preparation for both short- and long-read DNA/RNA sequencing libraries, upgrade the Illumina iScan imager for capture and analysis of data on Infinium genotyping arrays, purchase a microscope with camera for imaging and optimization of single-cell gene expression libraries, and procure a state-of-the-art Pacific Biosciences (PacBio) Revio sequencing platform, not available anywhere at TAMU, but already widely used by the TAMU community through outsourcing. A large community of TAMU researchers currently use innovative genomics-based approaches to understand the biology of model and non-model organisms, improve understanding of host organism interactions with other organisms and their environment, and facilitate translation of research findings related to diseases that impact human and animal wellbeing. The PacBio Revio platform has emerged as the gold standard for genome assembly and full-length mRNA sequencing. PacBio data allows researchers to more easily and cost-effectively sequence genomes telomere-to-telomere. The Revio's lower costs and 15x higher data output compared to the previous generation PacBio sequencer bring human or other vertebrate genomes under $1,000. However, the new sequencers and their predecessors are currently limited in distribution at core facilities nationwide, and **timely access to long-read sequencing impacts TAMU's competitiveness.** Having a machine onsite will provide rapid sequence turnaround time for campus investigators and their collaborators statewide, a major shortcoming of outsourcing to core labs where project queues may be months, particularly for this improved, high-demand technology and bring home to TAMU an existing local user base that is outsourcing. This investment will quickly facilitate the development of novel research and associated outcomes at TAMU based on long-read sequence data for: 1) the rapid and nearly complete assembly of targeted genomes of biomedical, agricultural, and basic research interest; 2) the generation of full-length RNA transcript discovery; and 3) identification of the structure and locations of epigenetic modifications genome-wide. The four requested investments will also ensure TAMU's ability to produce cutting-edge single-cell and spatial transcriptomics data sets from 10X Genomics, already a high-volume business for MGC, as these technologies migrate from short-read Illumina platforms to PacBio. Replacing the MGC's aging fleet of thermal cyclers provides critical infrastructure for these current and future services. Lastly, the upgraded microscope works synergistically with the PacBio Revio to ensure that MGC can provide the highest quality single-cell gene expression data sets to TAMU researchers now and in the coming decade.