**Bioanalytics and Single-Cell Core (BASiC):**

Located in the South Texas Research Facility, BASiC provides services to the research community at the NCI-designated Cancer Center, and is directed by Dr. Nameer Kirma since 2017. The four objectives of the BASiC are to provide: 1) clinical sample processing for single-cell isolation and banking; 2) high-throughput platforms for single-cell identification and characterization; 3) robust single-cell based informatics and statistical analyses for data integration and interpretation; and 4) outreach and pilot project programs to enhance the BASiC user base, seed collaborations and support early-stage investigators. Current single-cell isolation platforms include three combined immunofluorescence-micromanipulator workstations and the C1 single-cell capture and processing station, capable of automated single-cell cDNA preparation for PCR and RNA-seq. For single-cell PCR expression analysis, the C1 single-cell auto prep system (Fluidigm) and the BioMark (Fluidigm) high-throughput microfluidic chip system are available for running 48x48 (2,304 PCR data points in one chip) and 96x96 (9,216 PCR data points), among other types of microfluidic PCR chips. The Visium spatial transcriptomic profiling system (10X Genomics) has been established at BASiC for the integration of spatial imaging of tissue sections and RNA-seq (in collaboration with the Next-Generation Sequencing Core). Atomic force microscopy (AFM) is also at hand for examining nanomechanical features of individual cells (e.g., cell elasticity, adhesiveness, and deformability) and chemobiologic detection/distribution of cell surface markers. The BASiC core also incorporates the Helios CyTOF platform for single-cell proteomics. The core has a wide range of CyTOF-validated metal-conjugated antibody panels as well as the capacity to generate custom metal-conjugated antibody panels. Additional instrumentation include the FlexMAp Luminex multiplexing system, capillary automated Western Blot system, and the Disgenode SX-8G IP-Star robotic for automated ChIP-seq, MBDCAp-seq and other sequencing library construction. The pyrosequencing unit, PyroMark Q48 (Qiagen), is also available for high-throughput genetic and epigenetic analyses of candidate genes. In-house bioinformaticians specialized in single-cell analysis are available to help with study design, data analysis, and generation of publication-ready figures.