BioImage Analysis	Service Name	Description
Judith Drazba, Ph.D. Staff, Core Director Location: NB1-46 Phone: 216-445-3760 Email: drazbaj@ccf.org Ajay Zalavadia, Ph.D. Location: NB1 Imaging Core Email: zalavaa@ccf.org	Image Processing and Analysis	The use of commercial and open-source software to extract quantitative data and meaningful insights from biological images obtained through light microscopy, electron microscopy (TEM and SEM), computed tomography (CT), and magnetic resonance imaging (MRI). This process leverages advanced computational techniques—including machine learning—to enable the automated analysis of large and complex image datasets. Processes include segmentation, pixel/object classification, morphometric analysis, colocalization, spatial analysis, 3D reconstruction, object tracking, high content imaging, and cell behavior analysis. Training is available.
Cell Culture	**Service Name**	**Description**
Carmel M. Burns Core Manager Location: NB1-25 Phone: 216-444-5814 Email: burnsc@ccf.org RRID# SCR_026664	Cell Culture Training	The Core provides training on good lab practice for new researchers. The training can be tailored to individual needs and includes aseptic technique and culturing and maintaining cell lines.
	Cryogenic Storage	The core can accommodate the storage of cryovials. The core offers this service to Cleveland Clinic researchers for back-up storage of precious cell lines.
	Mycoplasma Testing - Direct	This method uses an enriched agar to support the growth of colonies. Cells and supernatant are swabbed onto agar and incubated in a modular incubator chamber. Samples are viewed microscopically every other day for 2 weeks. Mycoplasma contamination is detected by the appearance of a "fried egg" - like growth.
	Mycoplasma Testing - Indirect	The Core uses a quick method to detect mycoplasma. This kit detects the four most common types of mycoplasmas to contaminate cells. This is useful in determining the type of mycoplasma present.
	Preparing Samples for Mycoplasma Testing	The cells should be grown without antibiotics for 3-4 days. Collect ~5mls of cell supernatant for adherent cells. For suspension cells, grow without antibiotics and supply ~ 5 mL for testing.

	Roller Bottle Cultures	The Core has the capability of producing large scale adherent cells cultured in either 850 cm2 or 1750 cm2 roller bottles grown on a roller apparatus in a 37C warm room. This is a very suitable method when large amounts of cells are required. This method also works well with suspension cells.
	Spinner Cultures Cells	It is useful to produce large volumes of suspension cells. Vessels come in various sizes that are used in conjunction with a magnetic stirrer spinner base. The core can provide volumes from 100 mLs-10L.
	Sterility Testing	The Core offers sterility services using in-house prepared broths along with regular mycoplasma and endotoxin testing. Quarterly testing results are available on request.
	Cell Line Authentication	The Core provides convenient and cost-effective cell authentication services in partnership with LabCorp. Researchers request the service in iLab and receive guidance on test selection and sample preparation. Completed forms and samples can be dropped off to NB1-15. Samples are sent out on a weekly basis. For additional information please contact the lab.
Clinical Research Unit	Service Name	Description
Rebecca Algeri Administrative Director Location: JJN3 Phone: 216-445-3157 Email: algerir@ccf.org	Clinical Research	Facilities and personnel to conduct clinical research studies. Seven-bed nursing unit and pre-analytic lab are located on M51 at Main Campus. Pre-proposal consultations, protocol-specific nursing, pre-analytic lab, research coordination services, recruitment specialist consultation of special populations and project management.
Electron Microscopy	Service Name	Description
Judith Drazba, Ph.D. Staff, Core Director Location: NB1-46 Phone: 216-445-3760 Email: drazbaj@ccf.org RRID# SCR_027161	Electron Microscopy (Transmission)	A microscopy technique in which a beam of electrons (rather than photons) is transmitted through an ultrathin section to investigate the ultrastructure. Resolution < 1 nm (TEM).
	Electron Microscopy (Scanning)	A microscopy technique in which a beam of electrons is used to investigate the surface structure of a whole-mount sample. Resolution down to ~2 nm (SEM).
	Electron Microscopy (2D-EM Section Scanning)	A microscopy technique that uses a scanning electron beam to generate a large TEM-like image of an entire section from a sample. Images are usually generated by stitching together many small, high resolution, tiles. Resolution down to ~4 nm.

	Elemental Analysis (with SEM, EDAX)	Determination of the elemental composition of a sample prepared for EM observation.
EM Sample Prep:	**Service Name**	**Description**
Judith Drazba, Ph.D. Staff, Core Director Location: NB1-46 Phone: 216-445-3760 Email: drazbaj@ccf.org RRID# SCR_027161	Transmission EM Sample Preparation	Samples are fixed, stained, dehydrated, and embedded into a plastic resin that will allow it to be observed in a transmission electron microscope.
	Thin Sectioning (for TEM)	Samples embedded in plastic are cut with a diamond knife into ultrathin, 50-100 nm slices and picked up onto grids for viewing in the electron microscope.
	Thick Sectioning (for TEM)	Samples embedded in plastic are cut into 0.5-2 um thick sections and picked up on a glass slide. Following staining, typically with Toluidine Blue, they are viewed in light microscope.
	Glow Discharge (for TEM)	Removal of the positive charge from an electron microscope grid to prevent dispersion of the sample.
	Immuno EM/ Immunogold Labeling (for TEM)	Labeling with gold-tagged antibodies for ultrastructural localization of proteins in cells and tissues using TEM.
	Negative Staining (for TEM)	Particles of a suspension are adsorbed onto the surface of a specimen support, stabilized, and contrasted usually by heavy metal stains. By this approach, particles can be visualized down to sub-nanometer size and categorized based on their morphology.
	Scanning EM Sample Preparation (Critical Point Drying)	Process for drying a sample for scanning electron microscopy in a way that does not cause surface deformation.
	Sputter Coating	Samples for scanning electron microscopy are first prepared by depositing an ultra-thin layer of gold on the surface.
Flow Cytometry Core	**Service Name**	**Description**
Kewal Asosingh, Ph.D. Staff, Core Director Location: NB2-28a Phone: 216-444-0891 Email: asosink@ccf.org RRID# SCR_026460	10x or Single Cell RNAseq	Single cell gene transcriptome analyses using 10x Chromium Controller.

	Flow Cytometry Consultation	Assistance with panel design, controls, troubleshooting, data analysis and interpretation, grant writing, budget, generation of publication quality figure according to the current standards of the International Society for Advancement of Cytometry (ISAC).
	Immunophenotyping and/ or Enumeration of Extracellular Vesicles	Volumetric quantification of extracellular vesicles (micro-particles and exosomes) in biological fluids or cell culture supernatant using Zetaview QUATT nanoparticle tracking analyzer.
	Immunophenotyping of Cells	Analysis of cell surface and or intracellular expression of markers (cytokines, CD proteins, phosphoproteins, etc.) using flow cytometry.
	Single Cell Suspension Preparation	Assistance, guidance with the preparation of high-quality single cell suspension for various assays.
	Quantification and or Detection of Expressible Fluorescent Proteins	Analysis of fluorescent proteins using flow cytometry.
	Quantification and or Detection of Fluorescent Probes of Cell Function	Analysis of fluorescent cell function specific probes using flow cytometry.
	Sterile and BLS2 Single-Cell, Bulk and Plate Sorting	Purification of specific cell subsets using electrostatic cell sorting.
Genomics Core	Service Name	Description
Min Hui Lim, Ph.D. Core Manager Location: R4-058 Phone: 216-346-3348 Email: limm3@ccf.org RRID# SCR_027093	Nucleic Acid Quality/ Quantity Assessment	Assessment of RNA and DNA sample integrity using the Agilent Bioanalyzer, TapeStation, or Qiagen QIAxcel systems. Samples may be intended for downstream applications including microarray analysis, genotyping, and next-generation sequencing (NGS) library preparation and sequencing. Fluorometric quantification using Qubit is also available.
	Nucleic Acid Shearing Covaris Services	Nucleic acid fragmentation is a crucial first step in NGS sequencing workflow. Covaris S220 shears DNA without GC bias or thermal damage. The Adaptive Focused Acoustics™ (AFA) technology is firmly established as the fragmentation method of choice for NGS library generation.
	Single Cell Sequencing	Single-cell mRNA libraries are prepared and sequenced using the 10x Genomics Chromium platform, either in collaboration with the Flow Cytometry Core when cell sorting is needed or directly through the Genomics Core.

	RNA sequencing	Extracted RNA libraries submitted to the Genomics Core can be prepared for RNAseq using either poly-A tail selection or rRNA reduction methods. Additional specialty services are also offered for challenging samples, including FFPE, low concentration, or degraded samples.
	Whole Genome Sequencing (WGS)	The Genomics Core offers a PCR-free WGS workflow which can prepare high quality DNA samples for sequencing on our Novaseq system.
	Walk-up Sequencing	For experienced users, the Genomics Core offers a walk-up sequencing service for all our sequencing platforms. Users can purchase an entire flow cell dedicated to their prepared libraries, and data can be returned to the investigator rapidly.
	Spatial Transcriptomics	Spatial transcriptomics projects are supported on a case-by-case basis. The Genomics Core collaborates with investigators on experimental design, sample preparation, library construction, and sequencing, with workflows tailored to project needs.
Glassware Core	**Service Name**	**Description**
Carmel M. Burns Core Manager Location: NB1-20 Phone: 216-444-5814 Email: burnsc@ccf.org RRID# SCR_026665	Biohazard Waste Processing	Live or contagious waste can be decontaminated by the autoclave process before disposal; this service is available through the glassware core.
	Glassware Services	Collection of glassware from labs and storage of sterile glassware. Daily delivery and stocking of glassware in all lab areas. Special glassware services available upon request.
	Quarterly Testing of DI Water	DI water from the Cleveland campus is tested for Endotoxins on a quarterly basis. Results available upon request.
	Sterilization and Autoclaving	Washing and sterilization of all types of glassware, sterile pipettes and Pasteur's, autoclaving of liquids and dry materials, washing and sterilization of special glassware, sterile tips and custom tips available, and sterile DI water.

Hematology Analysis	Service Name	Description
Kimberly Peterson Core Manager Location: NE3-256 Phone: 216-444-5447 Email: petersk6@ccf.org RRID# SCR_027128	Analysis of Whole Blood CBCs	Absolute and percent Reticulocyte (Retic), CBC plus white cell differential counts (CBC/diff), CBC/Diff plus retic (CBC/diff/retic), CBC/retic, Complete Blood Count (CBC).
Histology Core	**Service Name**	**Description**
Judith Drazba, Ph.D. Staff, Core Director Location: NB1-46 Phone: 216-445-3760 Email: drazbaj@ccf.org	Cryosectioning	Frozen tissue is cut into sections and placed on slides using a cryostat.
	Frozen Sectioning	Frozen tissue is cut into sections and placed on slides using a cryostat.
	Histology	The processing, wax embedding, cutting and staining of tissue for observation in a microscope.
	Paraffin Embedding	Placement of processed samples into wax blocks for sectioning onto slides.
	Sectioning	The cutting of embedded tissue onto slides. If the tissue is frozen it is called "cryosectioning."
	Tissue Processing	The preparation of tissue for cutting and staining that involves dehydration and infiltration with paraffin or plastic.
	Tissue Staining	Use of various dyes to render tissue visible and to mark particular features.
Hybridoma Core	**Service Name**	**Description**
Melanie Hoffner Shared Lab Resource Specialist Location: NB1-25 Phone: 216-445-6635 Email: hoffnem@ccf.org RRID# SCR_026666	Large-Scale Antibody Production	Uses static cell culture system - the Integra Flask - to produce high concentration (>.5mg/mL) monoclonal antibodies. This can be done in serum free or using ultra-low 1gG/1gM serum. Yields can be as high as 100mg/month/flask.
	Large-Scale Antibody Purification	Purify monoclonal or polyclonal antibodies using Protein G or an epitope specific affinity column. Can purify up to 80 mg of 1gG from one sample using a Protein G column.
	Liquid Nitrogen Storage of Cells	Storage for cloned cell lines. The stored cell lines must be mycoplasma free.
Imaging Core	**Service Name**	**Description**
Judith Drazba, Ph.D. Staff, Core Director Location: NB1-46 Phone: 216-445-3760 Email: drazbaj@ccf.org	3-D Microscope Imaging	"Optical sections" or "Z Stacks" of samples can be obtained on confocal microscopes. The stacks can be reconstructed with software that allows 3-D visualization and analysis.

	Confocal Microscope	Laser-based confocal microscopes generate a thin "optical section" within a sample, thus removing the out of focus light that comes from other layers of the sample. This offers not just a clearer image but clarifies the location of the signal within a cell or tissue. Both samples on slides and live samples can be examined.
	Fluorescence Microscope	Microscopes with specialized illumination and detection that allow the imaging of fluorescently tagged specimens - both on slides and in wells, dishes and flasks.
	Image Analysis/ Quantitation	Various software programs allow microscope images to be examined for data such as area, intensity, volume, velocity, trajectory, etc. as required for 2-D, 3-D, and time-lapse experiments.
	Infrared Scanner (Odyssey)	Infrared scanning of gels, membranes, or slides on a LI-COR Odyssey instrument.
	Laser Capture Microdissection	Use of a specialized microscope equipped with lasers to cut and collect individual cells or small sections of tissues or cultured cells.
	Light Microscope	Samples can be viewed on a microscope using visible light for brightfield on fluorescence observation.
	Live Cell Imaging	Inverted microscopes allow the imaging of live cells in culture acquiring either still photos or time-lapse movies.
	Multi-Photon Microscope	A multi-photon microscope allows deeper penetration of light into a sample (up to 500um rather than the 100um of standard confocal) and can be used for tissue slices or pre-clinical research models.
	Slide Scanning	A large region of interest - or even the whole surface of a slide - can be imaged in brightfield or fluorescence mode using a special scanning microscope.
	Stereomicroscope	A dissecting microscope with a color digital camera that allows the imaging of large, unmounted samples with brightfield and/or fluorescence illumination.
	Time-Lapse Imaging	Inverted microscopes allow the imaging of live cells in culture over a determined period of time and at set intervals, producing time-lapse movies.

	TIRF Microscope	Total Internal Reflection Fluorescence with a microscope using a laser and specifically designed optics to view a thin region of a sample (less than 200 nm) attached to glass.
	Two-Photon Microscope	A multi-photon microscope allows deeper penetration of light into a sample (up to 500um rather than the 100um of standard confocal) and can be used for tissue slices or preclinical research models.
	Whole Slide Scanner	A large region of interest - or even the whole surface of a slide can be imaged with a special scanner.
	Multiplex Whole Slide Scanning	Imaging whole formalin fixed paraffin embedded (FFPE) tissue sections and TMAs that have been stained with antibodies (up to 9 colors) for the purpose of visualizing, analyzing, quantifying, and phenotyping cells in situ. (See Multiplex IHC below for tissue staining.)
Immunohistochemistry	Service Name	Description
Judith Drazba, Ph.D. Staff, Core Director Location: NB1-46 Phone: 216-445-3760 Email: drazbaj@ccf.org	Antibody Titration	Experimental determination of appropriate antibody concentration for optimal protein localization.
	Immunohistochemistry	Staining tissues with antibodies to visualize the expression levels and distribution of specific proteins within cells and tissues.
	In situ Hybridization (ISH/FISH)	Chromogenic or Fluorescent in Situ Hybridization for localizing DNA or RNA in cells and tissue.
	Multiplex IHC	Labeling tissues with 3-8 fluorescent antibodies to localize multiple proteins simultaneously in a single tissue section.
	RNA Scope/HCR	Chromogenic or Fluorescent in situ Hybridization for localizing RNA in tissue.
Laboratory Diagnostics	Service Name	Description
Kimberly Peterson Core Manager Location: NE3-256 Phone: 216-444-5447 Email: petersk6@ccf.org RRID# SCR_027128	Laboratory Testing	Automated clinical chemistry assays, Drugs of Abuse/Toxicology/Specific Proteins/ Metabolic Special Chemistry/ Fertility/ Pregnancy/ Therapeutic Drug/ Monitoring/ ELISA based testing
	Phlebotomy	Limited phlebotomy services provided for consented research study subjects.

Media Preparation	Service Name	Description
Carmel M. Burns Core Manager Location: NB1-15 Phone: 216-444-5814 Email: burnsc@ccf.org RRID# SCR_026667	Bacteriological Media	Media used for the growth of bacteria.
	Solutions/Buffers	A buffer is an aqueous solution that has a highly stable pH (i.e. Phosphate and Tris Buffered Saline)
	Cell Culture Media	A growth medium to support the growth of cells (i.e. RPMI 1640 and DMEM).
	Endotoxin Testing	The Endoscan V software system uses Kinetic Turbidimetrics to provide quantitative Endotoxin results for in-process and end product samples. The assay sensitivity available for use is 0.06EU/mL using a standard curve of 5-0.05 EU/mL. The second method uses an Endosafe-PTS - A rapid, point of use test system that utilizes Limulus Amebocyte Lysate (LAL) reagents in a test cartridge with a handheld spectrophotometer. The PTS can effectively be used to obtain fast, quantitative LAL results in about 15 minutes.
	FBS - Heat Inactivated or Regular	Fetal Bovine Serum, the most widely used serum supplement due to its very low levels of antibodies and the fact that it contains more growth factors, allowing for versatility in many different cell culture applications.
	LB Agar Plates	Luria Broth agar plates are typically used as a growth substrate for the culture of bacteria. Selective growth compounds may also be added to the media, such as antibiotics. (i.e. Ampicillin and Kanamycin) Custom plates are also available.
	LB Broth	Luria Broth, a nutritionally rich medium used for the growth of bacteria.
	Specialty and Custom Media	A custom recipe prepared according to researchers' instructions or guidelines.
	Sterility Testing	Verifying the sterility of our products or yours through QC broths, endotoxin and Mycoplasma testing.

Microbial Sequencing & Analytics Core	Service Name	Description
Naseer Sangwan, Ph.D. Assistant Staff, Core Director Location: NE5 Phone: 216-445-4030 Email: sangwan@ccf.org RRID# SCR_026609	Nucleic Acid Isolation	The isolation of microbial DNA/RNA from various sample types (e.g. stool, tissue, saliva, urine, blood).
	Sequencing Library Prep. for Amplicon Based Sequencing	The amplification and sequencing of microbial biomarker genes. For example, the variable region of the 16S rRNA (e.g. V4), 18S rRNA gene, or the ITS region of fungi.
	Sequencing Library Prep for Whole Genome Microbial Sequencing. (i.e. shotgun genomics and metagenomics)	Library preparation that targets the total microbial gDNA. Basically, attaching appropriate sequence adapters and indexes to total community DNA fragments for de-multiplexing on an Illumina platform.
	Library Prep for Microbial Transcriptomic Sequencing	Converts microbial community mRNA into sequencing libraries compatible with Illumina's MiSeq. Notably, this library prep focuses on depleting rRNA from the sample before converting it to cDNA.
	NextGen Sequencing	High-throughput sequencing using Illumina's Iseq and/or MiSeq platform.
	BioInformatics	State of the art bioinformatics analysis and publication-ready visualization of microbial genomics and metagenomics data. 1. Amplicon sequence data (e.g. 16s rRNA gene, 18S rRNA amplicon), (Qiime, DADA2, Deblur, FAPROTAX, PiCRUST, pyloseq, microbiomeSeq, ggplot2 etc.) 2. Microbial genomics data a. QC and adapter trimming, De novo (e.g. Spades) and reference-based (e.g. Unicycler) assembly, and validation b. De novo and reference-based genome annotation 3. Shotgun metagenomics data a. Quality filtering and adapter trimming and de novo assembly b. Taxonomy and functional analysis using raw sequencing and/or assembly data. c. De novo microbial genome reconstruction from shotgun metagenomics libraries (i.e. MAGs) 4. Meta-transcriptomics data a. Quality trimming and adapter trimming. b. Reference genome/s mapping

		c. Statistical analysis and visualization d. Pathway and GSEA analysis
	Dual-RNAseq	Extraction, sequencing and multi-omics analysis of the host (human or pre-clinical models) and microbial RNA from the same tissue (e.g. cecum). It offers: 1. Host mRNA expression (pathways or enzymes) 2. Microbial taxonomy and expression (pathways or enzymes) 3. Correlation of 1 and 2 4. Immune cell profiling (RNASeq deconvolution) 5. Correlation of 4, 2 and 1
Molecular Biotechnology Core	**Service Name**	**Description**
Smarajit Bandyopadhyay, Ph.D. Project Staff, Core Director Location: NE5-214 Phone: 216-212-2947 (Cell) Email: bandyos1@ccf.org RRID# SCR_012600	Circular Dichroism (CD) Spectroscopy	A Circular Dichroisms (CD) Spectropolarimeter (Model J-815 from Jasco) is a type of light absorption spectroscopy that can provide information on the structure of optically active biological macromolecules. CD spectra of proteins between 250 and 185 nm can be analyzed for different secondary structural types such as, alpha helix, parallel and antiparallel beta sheet, turn other random structures.
	Isothermal Titration Calorimetry (ITC)	ITC is a thermodynamic technique that directly measures the heat released or absorbed during a biomolecular binding event and determines binding parameters. The Core model MicroCal ITC 200 simultaneously determines all binding parameters, including the binding constant (KD), reaction stoichiometry (n), enthalpy (δH) and entropy (δS), thus providing a complete thermodynamic profile of the molecular interaction in a single experiment. Interactions between any two molecules can be studied with ITC, including, protein-small molecule, protein-protein, target-drug, enzyme-inhibitor, antibody-antigen, protein-DNA, protein-lipid, and small molecule-small molecule.
	Microscale Thermophoresis (MST)	The Microscale Thermophoresis (MST) technology allows measuring of every interaction type, including huge protein complexes to the binding of single metal ions. In a typical MST experiment, a microscopic temperature gradient is induced by an infrared laser, and the directed movement of molecules is detected by intrinsic fluorescence (Monolith NT. Label Free) or fluorescence of only one of the interacting molecules with attached fluorophore (Monolith NT.115) and quantified

		to determine the affinity constant (KD). This technology permits studying of the interaction of small molecules and proteins, or membrane proteins stabilized in buffers of choice. Thus, its high adaptability over other techniques renders it unique and unparalleled.
	Nuclear Magnetic Resonance (NMR) Spectroscopy	NMR is a versatile technology for the characterization of structure and dynamics of small molecules as well as biological macromolecules in solution (even as part of mixtures and in cells). The CCF facility houses state of the art Bruker-BioSpin Avance ICE 600MHz Spectrometer primarily for solution NMR. It is recently updated with superior sensitivity and capability to do direct 13C detect as well as 19F experiments.
	Surface Plasma Resonance (SPR) Spectroscopy	SPR has been used to monitor macromolecular interactions in real time. The core houses the Biacore model S200 which uses SPR technology for measuring the interactions of macromolecules with each other, and with small molecule ligands. It can be used for measuring the binding parameters, such as on-rate, off-rate, affinity constant etc., of biomolecular interactions (protein-protein, nucleic acids - protein, protein-lipids, protein-small molecule/fragments etc.). Biacore S200 is a label-free interaction analysis system designed to meet the requirements of high sensitivity and short time to results and analysis for kinetics and affinity, rapid screening of small molecules (96\384-well format), competition assays, epitope mapping, ranking affinities, and thermodynamics.
Proteomics and Metabolomics	Service Name	Description
Belinda Willard, Ph.D. Associate Staff, Core Director Location: NE1-251 Phone: 216-444-7170 Email: willarb@ccf.org RRID# SCR_026563	Method Development	It is essential to provide accurate, reliable and consistent data in analytical services. Based on the need of investigators, we provide services for developing analytical methods using either LC-MS/MS or GC-MS/MS for analysis of endogenous compounds in biological matrices like plasma, urine and tissues.
	Molecular Weight Analysis	Determination of the molecular weight of a small molecule, peptide or protein.

	Post-translational Modification analysis: Global	Identification and quantitation of global post-translational modification sites from complex samples such as cell lysates or tissue homogenates. These experiments are performed using modification specific enrichment. The post translational modifications that can be identified include phosphorylation, acetylation, and, ubiquitination.
	Untargeted Metabolomics	The unbiased analysis of small molecules (100-800 Daltons) derived from a variety of biological matrices such as plasma, urine, and cell extracts. These experiments involve the extraction of the small molecule metabolites, LC-MS/MS analysis, chromatographic alignment of the LC-MS data, and quantitative comparison of these metabolites across groups. This analysis results in the identification of 1000's metabolites. The identification of compounds of interest can be validated by follow up LC-MS/MS experiments.
	Protein Identification and Quantitation	These experiments are performed from proteins fractionated on a gel, affinity enriched on agarose or magnetic beads, or proteins in-solution. Protein identification is performed using bottom-up proteomics which involved tryptic digestion followed by LC-MS/MS analysis. Proteins are identified by searching the LC-MS/MS data against a protein database. Bottom-up proteomics can also be used to determine the relative abundance of proteins across a series samples. These quantitation experiments can be performed using label free methods, isobaric tagging, or SILAC. For complex samples such as cell lysates or tissue homogenates, the samples can be pre-fractionated prior to LC-MS/MS to increase proteome coverage.
	Targeted Metabolomics	Targeted LC-MS/MS or GC-MS/MS analysis of small molecule metabolites in biological matrices. Several metabolite panels are available including amino acids, TCA metabolites, short chain fatty acids, fatty acids, oxidized fatty acids, along with others. Please contact the core to see if methods are in place for any metabolites of interest. The Metabolomics core will also perform method development for metabolites not currently available in a targeted panel.

Pre-Clinical Imaging Core	Service Name	Description
Charlie Androjna, D.Eng. Assistant Staff, Core Director Phone: 216-287-1738 Email: androjc2@ccf.org	Biospec 70/20 USR MRI	The Bruker Biospec 70/20USR is a 7T horizontal bore magnet that operates at 400 MHz and runs ParaVision™ 7.0.1 software. This micro-MRI system is designed for high-resolution MR spectroscopy and imaging of pre-clinical specimens. The 20 cm diameter bore, and extra-long table offers imaging capabilities on various research sized models/in situ specimens. The facility has several different coil systems allowing for high resolution scanning at < 100 um voxel size. BioSpec 70/20 and 94/20 | Bruker
	GE CT120 Micro-CT GE CT120 Micro-CT	The GE eXplore CT 120 scanner is a research CT scanner that has x-ray source technology derived from clinical systems and is a high-throughput micro-CT for in vivo imaging of pre-clinical models in a variety of applications. Standard features of the scanner include: - High energy (70-120 kVp) - High throughput (1-15 minutes per scan) - High resolution (25-100 µm) - Large field of view (85 mm in diameter, 55 mm to 275 mm in length) - Prospective gating (up to 600 bpm) for up to 12 phases per scan - Low dose in vivo imaging for pre-clinical models Applications include: (1) small pre-clinical model in vivo at 45 or 93 µm voxel size (2) specific regions in vivo at 20 µm voxel size and (2) in vitro specimens at 20 µm voxel size.
	Mediso nanoScan PET/CT	The Mediso nanoScan PET/CT acquires high resolution PET/CT or CT scans of small and large research models and 'ultra-zoom' CT scans of specimens. Its transverse field of view is up to 12 cm, and its bore diameter is 16 cm. Pre-clinical imaging is supported using chambers of various sizes; a "hotel system" is also available for scanning up to four research models at once. Mediso - nanoScan® PET/CT

	PerkinElmer IVIS Lumina III XRMS	The IVIS Lumina XR Series III system provides an expandable, sensitive imaging system that is easy to use for fluorescent, bioluminescent, radio-isotopic and X-Ray imaging with multiple research models imaging at one time. Ideal for researchers in oncology, infectious disease, drug discovery, efficacy and/or toxicology research.
	PerkinElmer IVIS Spectrum CT	The IVIS Lumina XR Series III provides an expandable, sensitive imaging system that is easy to use for fluorescent, bioluminescent, radio-isotopic and micro-CT imaging with multiple research models imaging at one time. Ideal for researchers in oncology, infectious disease, drug discovery, efficacy and/or toxicology research.
	Precision X-Ray Irradiator SmART+	The (SmART+) is a highly sophisticated, expandable platform system that mimics clinical radiotherapy imaging and treatments in a preclinical research setting. The easy-to-use software and an advanced set of imaging modalities, including Cone-Beam CT, µCT and Bioluminescence (BLI), is the perfect tool for image-guided radiation research. The system can also be used for standard pre-clinical model cell ablation studies. **Key Features** - Rotational gantry, mimicking clinical radiotherapy imaging and treatment - Cone-Beam CT, µCT, and bioluminescent imaging modalities - Fully integrated treatment planning and delivery software with multi-modality image guidance - Dynamic collimator and X-Y-Z stage to deliver precise and accurate focal irradiation XRad320 I X-Ray Irradiation I Imaging | Precision X-Ray

	Precision X-Ray Irradiator X-Rad320	The X-Rad320, a state-of-the-art x-ray irradiation system, delivers a precise and full range radiation dose to specimens. It is a shielded cabinet that includes an adjustable specimen shelf, sample viewing window and beam hardening filter holder. The system also includes an OptiMAX imaging module that facilitates rapid switching between imaging modalities (e.g. BLI and x-ray imaging) and ensures accurate dose targeting if needed. **Key Features** - High throughput capability for pre-clinical model Irradiation - Planetary turntable and motorized shelf allows up to 33 specimens per cycle - Full screen, real-time specimen viewing XRad320 I X-Ray Irradiation I Imaging | Precision X-Ray
All imaging spaces contain bench top procedure areas for preparation of pre-clinical models or specimens for MRI, PET/CT, IVIS, or multi-modal imaging experiments.		
Pre-Clinical Behavior Core	**Service Name**	**Description**
Tom Jaramillo, Ph.D. Project Staff, Core Director Phone: 216-938-1548 Email: jaramit@ccf.org	Cognitive Testing	Morris Water Maze, Associative Learning, Novel Object Recognition, Y-Maze, Barnes Maze
	Anxiety Testing	Elevated Plus Maze, Dark/Light, Open Field
	Motor Testing	Rotarod, Grip Strength, Gait Analysis, Locomotor Activity, Treadmill
	Social Interaction Testing	3-Box Social Interaction, Sex & Genotype-matched Social Interaction
	Innate Behavior Testing	Olfactory discrimination, Nesting, Visual Acuity and Contrast Sensitivity, Vocalization, Taste Discrimination, Circadian Rhythm
	Repetitive Behavior Testing	Grooming, Marble Burying, Rearing Activity
	Sensorimotor Testing	Temperature and tactile perception, Pre-pulse Inhibition
	Psychological Testing	Swim, Sucrose Preference
	Circadian Rhythm Testing	Running Wheel.
	Metabolic and Weight Testing	CLAMS, Oxymax, EchoMRI.

FRIC Flow Core	Service Name	Description
James Thomas, Ph.D. Assistant Staff, Core Director Location: FRIC room 209G Phone: 772-345-8116 Email: thomasj86@ccf.org RRID# SCR_021844	Flow Cytometry Consultation	Expert guidance on panel design, controls, troubleshooting, data analysis, figure generation, and grant support.
	Immunophenotyping	High resolution analysis of cell surface and intracellular markers, including cytokines, CD markers, and phosphoproteins.
	Fluorescent Protein Detection & Quantification	Sensitive detection of fluorescent reporters and probes in live or fixed cells.
	Sterile Cell Sorting (BSL2+)	Single-cell, bulk, and plate sorting using a spectral cell sorter with simultaneous isolation of up to **6 distinct populations**.
	Sterile Cell Sorting (BSL3)	Single-cell, bulk, and plate sorting using a conventional cytometer with up to **4 distinct populations**.
	Flow Cytometric Analysis (BSL2)	Spectral analysis using a 5-laser system supporting **45+ fluorescent markers**.
	Flow Cytometric Analysis (BSL3)	Conventional 4-laser cytometry with up to **16 fluorescent parameters**.
FRIC High Containment Core	**Service Name**	**Description**
Kun Li, Ph.D. Project Scientist, Core Director Location: FRIC room 201G Phone: 772-419-2239 Email: lik11@ccf.org	BSL-3/ABSL-3 Experimental Services	The High Containment Core provides comprehensive support for research projects requiring BSL-3 and ABSL-3 containment. Services span the entire project lifecycle, from initial study design and protocol development to execution and data analysis. We offer consultation, hands-on assistance, and full-service project management to help researchers safely and effectively achieve their research goals in a high-containment environment.
FRIC Imaging Core	**Service Name**	**Description**
Ruofan Cao, Ph.D. Assistant Staff, Core Director Location: FRIC room 107 Phone:772-345-8124 Email: caor@ccf.org RRID# SCR_021852	Image Processing and Analysis	The use of commercial and open-source software enables the extraction of quantitative data and meaningful insights from microscopy-based biological images. This service uses advanced computational techniques—including machine learning—for the automated analysis of large, complex image datasets. Key workflows include image segmentation, object classification, morphometric analysis, colocalization, molecular interactions, 3D reconstruction, object tracking and the study of cell behavior. Training is available for widely used platforms such as ImageJ and IMARIS.
	Cryosectioning	Frozen tissue is cut into sections and placed on slides using a cryostat.

	3-D Microscope Imaging	"Optical sections" or "Z Stacks" of samples can be obtained on confocal microscopes. The stacks can be reconstructed with software that allows 3-D visualization and analysis.
	Confocal Microscope	Laser- based confocal microscopes generate a thin "optical section" within a sample, thus removing the out of focus light that comes from other layers of the sample. This offers not just a clearer image, but clarifies the location of the signal within a cell or tissue. Both samples on slides and live samples can be examined.
	Fluorescence Microscope	Microscopes with specialized illumination and detection that allow the imaging of fluorescently tagged specimens - both on slides and in wells, dishes and flasks.
	Light Microscope	Samples can be viewed on a microscope using visible light for brightfield on fluorescence observation.
	Live Cell Imaging	Inverted microscopes and a microscope incubator allow the imaging of live cells in culture acquiring either still photos or time-lapse movies.
	Slide Scanning	A large region of interest - or even the whole surface of a slide - can be imaged in brightfield or fluorescence mode using a special scanning microscope.
	Stereomicroscope	A dissecting microscope with a color digital camera that allows the imaging of large, unmounted samples with brightfield and/or fluorescence illumination.
	Time-lapse Imaging	Inverted microscopes allow the imaging of live cells in culture over a determined period of time and at set intervals, producing time-lapse movies.
	Mosaic and Position Retrieval Imaging	The motorized stage with nanometer-scale resolution allows tiling and stitching imaging for a larger field of view, position retrieval with time-lapse imaging
	Fluorescence Lifetime Imaging	The fluorescence lifetime imaging measures the time it takes for a fluorophore to emit light after being excited, providing information about the fluorophore's environment. Unlike traditional intensity-based microscopy, FLIM is independent of fluorophore concentration and offers insights into molecular interactions and biochemical processes.

	GeoMx Spatial Profiler	GeoMx allows for the spatial analysis of RNA and protein in a tissue sample, combining imaging with next-generation sequencing (NGS) or nCounter analysis. It enables researchers to select specific regions of interest (ROIs) within a tissue section and quantify the RNA or protein expression within those regions.
	Deconvolution Imaging	Deconvolution imaging is a computational technique to reverse image blurring caused by optical limitations, such as those in a microscope, to improve image contrast and resolution. This technique is available in both confocal and widefield microscope
	Widefield Imaging BSL3	Widefield microscope with deconvolution, time lapse and motorized stage.
	Pre-clinical Imaging in ABSL2 and ABSL3	IVIS system allows pre-clinical model bioluminescence imaging (BLI), fluorescence imaging and X-ray imaging. It's widely used in pre-clinical research to track tumors, monitor drug distribution, study cell trafficking, and investigate biological processes like protein-protein interactions and viral infections in real-time.
	AKTA Pure Protein Purification/Analysis	The AKTA pure is an automated, modular liquid chromatography system used for fast and reliable purification and analysis of proteins, peptides, and nucleic acids.
	Histology	The processing, wax embedding, cutting and staining of tissue for observation in a microscope.
	Paraffin Embedding	Placement of processed samples into wax blocks for sectioning onto slides.
	Sectioning	The cutting of embedded tissue onto slides. If the tissue is frozen it is called "cryosectioning."
FRIC Bioinformatics and Protein Engineering Core	**Service Name**	**Description**
Manjeet Kumar, Ph.D. Assistant Staff, Core Director Location: FRIC room 201J Phone: 772-345-8227 Email: kumarm18@ccf.org	Bioinformatics and Protein Engineering Consultation	Assistance with the data analyses and contextual interpretation of insights from studies. Support in grant/proposal writing for bioinformatics/protein engineering aspects, generation of publication quality figures.
	Bulk RNASeq Data Analyses	Differential gene expression analysis. Differential exon usage and splice variant analysis. Functional interrogation of gene sets using enrichment (GSEA, GO, KEGG, REACTOME, Wiki Pathways etc.) Biological pathway integration and interpretation.

	Multiomics Data Integration	Integration of data from different Omic modalities (focus on transcriptome, proteome, and metabolome). Network-based integration/analyses with in-depth visualization of different data insights. We use Cytoscape for building high-quality networks to support system-level studies
	Protein-Protein/Protein-Small Molecule/Protein-Peptide Interactions	Modeling protein interactions with diverse partner types (drug/metabolite/protein/RNA/DNA) at scale using AI-based methods (for instance:AlphaFold2/AlphaFold3/RoseTTAFold/Boltz/Boltzgen/ESMFold) and the classical physics methods. Prediction and analysis of protein-protein interactions (PPIs) in health and disease contexts. Predicting the interaction interface and ranking of the interacting residues for mutation analyses. Providing impact analyses of the variants on protein structure and function.
	Intrinsically Disordered Proteins (IDPs)/Short Linear Motifs (SLiMs)	Analysis and prediction of IDPs and SLiMs in biological systems. Deployment of SLiM based pipelines to find novel functions as well as annotate protein datasets with unknown functions. Check our existing toolkit for examples: http://elm.eu.org
	Host-Pathogen Interactions (Infection Biology)	Predicting the mechanistics of host-pathogen protein-protein interactions at systems as well at the molecular levels (for examples, check: http://camkipedia.embl.de/search/SARS_CoV_2/GID1762).
	Kinase Specificity	Revealing the kinase-substrate relationships while utilizing contextual knowledge. The predicted phosphosite would have support with sequence motifs as well as with the structural models (For examples, check: http://camkinet.embl.de/v2/search/kinase_ksnetwork/GID1268).
	Protein Design	Rational design of proteins for enhanced stability, activity, solubility, binding affinity, or novel functions. De novo protein design for synthetic biology and therapeutic applications.
	Molecular Modeling	Docking and MD simulations.
	Evolutionary Analyses	Deployment of Phylogeny based pipelines to find out evolutionary linkages. Generate phylogenetic trees and annotate them to present the evolutionary data.
	Therapeutics Development	Engineering of therapeutic enzymes and antibodies, including denovo discovery of high affinity nanobodies, PROTACs development

		and tight binders (peptides, small molecules, miniproteins).
	Visualizations/Figures for Publication	Generate high quality figures to reveal data insights, for instance - heatmaps, volcano plots, PCA, t-SNE, UMAP, circos and UpSet plots, networks (CytoScape), Multiple Sequence Alignment (MSA), Protein structure (3D) models, graphs, etc.
Immunomonitoring Laboratory	**Service Name**	**Description**
C. Marcela Diaz Assistant Staff, Scientific Director Location: NA2-019 Phone: 216-386-5929 Email: Diazc2@ccf.org	Tissue procurement, processing, and biobanking	Isolation of PBMCs is performed by density gradient centrifugation followed by cryopreservation in freezing media compatible with cell viability. Tumor tissue is subjected to enzymatic digestion using the gentleMACS™ tissue dissociation platform from Miltenyi Biotech. Both blood and tumor tissue processing takes place under sterile conditions. Specimens are entered into LabVantage for cataloguing and tracking.
	High Parameter Flow Cytometry and cell sorting	The IML has a dedicated FACSymphony A5 Special Order Cell Analyzer. The system is equipped with 5 lasers (UV, Violet, Blue, Green and Red), tube photomultiplier tubes (PMTs) in decagon arrays and FACSDiva v9.1 software.
	Single Cell Transcriptomics	The IML offers 10x genomics and Parse Biosciences platforms for single cell whole transcriptome and TCR analysis.
	Proteomics	Plasma proteomic signatures will be generated using Proximity Extension Assay (PEA) technology by Olink®. The assay involves a pair of oligonucleotide-labeled antibodies which are allowed to pair-wise bind to the target protein present in the sample. When the two probes are in close proximity, a new PCR target sequence is formed by a proximity-dependent DNA polymerization event, and the resulting sequence is subsequently detected and quantified using standard real-time PCR. The dual recognition, DNA-coupled method is thought to enhance specificity by excluding read-outs from anti-body cross-reactivity.
	Liquid Biopsy	The IML offers PGDx elio plasma complete, a comprehensive, liquid biopsy next-generation sequencing (NGS) assay designed to analyze circulating cell-free DNA (cfDNA) from blood samples to detect tumor alterations. It covers 521 genes, identifying SNVs, indels, copy number alterations, translocation, MSI, and bTMB in solid tumors

	Multiplex IHCC	Advanced phenoptics involves multiomic integration of spatial and single-cell data from FFPE tissue slides. Targeted proteomic data will be obtained using the PhenoCycler-Fusion instrument from Akoya which is available in our department. The PhenoCycler-Fusion workflow consists of iterative cycles of labelling, imaging and removing fluorescent reporters. In each imaging cycle, three fluorescent reporters are attached to their corresponding DNA-tagged antibodies and imaged via standard fluorescent optics. Thereafter, the three reporters are removed, and a new cycle images additional reporters. The process is fully automated, and data are acquired across whole slides at single-cell resolution. This technology combines antibody specificity with molecular barcodes allowing them to simultaneously detect 100+ targets while preserving tissue integrity.