Shared Resources

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Our Mission

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The Sanford Burnham Prebys Medical Discovery Institute Cancer Center has an extensive Core system , with the primary mission of the 9 Shared Resources (cores) to provide advanced technology, expertise, and instrumentation to cancer researchers that may not be easily acquired by individual laboratories.
The cores, staffed by technical experts, offer high quality interactive services that provide not only cost-effective sample analysis, but also assistance in experimental design, data analysis, and grant or manuscript preparation. Many of the cores offer a choice of full service, or investigator training on their advanced instrumentation for independent use. Most cores facilities can also provide expert services for outside non-profit and for-profit investigators.

Core Facilities

Animal Resources	Animal husbandry, mouse genetics, *in vivo* imaging, tumor analysis
Structural Biology	Protein analysis; cryo-electron microscopy
Cell Analysis & Histology	Microscopy, histology, tissue procurement
Flow Cytometry	Analytical flow cytometry, high speed cell sorting
Genomics	ChiP-Seq, NGS, single –cell seq, spatial transcriptomics
Proteomics	Protein separation, mass spectrometry, protein and post-translational modification ID, proteome-wide analysis
Bioinformatics	Bioinformatics, biostatistics, data analysis and integration
Functional Genomics	siRNA, shRNA, miRNA & cDNA libraries, assay development, high-throughput screening, viral vectors
Cancer Metabolism	Metabolites, metabolic flux, cellular respiration

Additional information such as pricing, are available at the Sanford-Burnham Shared Resource site Shared Resources | Sanford Burnham Prebys (sbpdiscovery.org)

Cancer Center

Shared Resources

Campus Map

Animal Facility

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Alessandra Sacco, Ph.D.
Scientific Director

The Animal Facility's mission is to provide a comprehensive animal care and use program for SBP investigators utilizing animals in their cancer research projects. The facility strives to maximize scientific benefits of animal experimentation while maintaining an emphasis on animal welfare.

The 24,000 sq. ft. AAALAC accredited facility can house 8,000 cages of mice in ventilated racks. Services include cage washing and prep, husbandry, daily animal health checks and breeding colony maintenance. The Facility also maintains a small number of rats and has a separate dedicated BSL2 containment mouse facility in Bldg. 12.

Many procedures can be performed by the *In vivo* Procedures Team, including injections (SQ, IM, IP, IV, TV, RO), compound/drug dosing, tumor measurements, blood collection, tissue harvest, pre- and post-op surgical assistance, live animal imaging and X-Ray irradiations.

Creation of knockout or transgenic mice, as well as re-derivation and cryopreservation are being done under special agreement at the UCSD Moores Cancer Center Transgenic Core and at the Salk Institute Transgenic Core.

SERVICES

- Husbandry and cage washing
- Breeding Colony Maintenance
- Veterinary Services
  - Animal transfers and quarantine
  - Animal health screening
- *In vivo* Procedures
  - Blood and tissue collection
  - Injections (IP, IM, SQ, Tail Vein, Retro-orbital)
  - Oral gavage, dosing
  - Time point blood collections
  - Tumor palpation and measurement
  - Surgical pre- and post-op care
- Administrative & IACUC support

EQUIPMENT & SUPPORT

- Ventilated mouse cages (IVCs)
- Centralized cage washing facilities
- Autoclaves
- Anesthesia machines
- Procedure rooms
- Biosafety cabinets and changing hoods
- X-Ray Irradiator (cell and animal)
- Motor and sensory equipment
  - Treadmill
  - 5-Station Rota-Rod
  - Grip strength device
  - Water maze with video camera
  - Hot plate analgesia meter
  - Stereotactic microinjection station

Animal Imaging & Analysis

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Alessandra Sacco, Ph.D.
Scientific Director

Live animal imaging tools include the IVIS Spectrum (Xenogen) for bioluminescence and fluorescence imaging; Pearl Impulse Imager (Li Cor) for *in vivo* near-infrared fluorescence optical imaging; Vevo 770 high frequency ultrasound (VisualSonics);

Bone density radiography: X-Ray (Trident)

RS 2000 X-Ray Irradiator (RadSource), for animals or cells.

PET/SPECT/CT and MRI imaging capabilities are available at the nearby Sanford Consortium for Regenerative Medicine.

A variety of widely used tumor cell lines labeled with luciferase are available for xenograft tumor growth and metastasis studies.

Analytical services support complete blood cell counts (CBCs) and chemistry analysis of serum components revealing metabolic or organ stress, using small samples of mouse blood.

SERVICES

- Imaging and analytical services can be done by trained animal facility specialists.
  - Live animal near-infrared fluorescence optical imaging on animal, native cells and cell lines without reporter genes (Pearl Impulse, Li Cor).
  - Live animal imaging - bioluminescence and fluorescence (IVIS Spectrum, Xenogen)
  - Live animal imaging - ultrasound (Vevo 770, VisualSonics)
  - Blood and serum analysis (Zoetis Vetscan HM5, Zoetis Vetscan VS2, IDEXX Catalyst One)
- Training on the various instruments can also be provided for SBP regular users.
- Luciferin and luciferase-labeled cell lines.

EQUIPMENT

- Pearl Impulse Imager (Li-Cor): near IR imaging
- IVIS Spectrum: bioluminescence & fluorescence imaging
- VetScan HM5 Hematology System (Zoetis) : CBCs, 22-parameter blood count & clinical chemistry analyzer
- VetScan VS2 (Zoetis) for blood chemistry, electrolytes, blood gas & immunoassay
- IDEXX Catalyst One: blood & urine chemistries
- CODA-6 (Kent Scientific): tail-cuff blood pressure system
- Trident Digital Specimen Radiography, bone density
- RS 2000 X-Ray Small Animal or Cell Irradiator
- Oxycycler (BioSpherix, Ltd.): for oxygen consumption, CO2 production & hypoxia studies.
- Stereotaxic instrument: microinjection equipment

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Protein Analysis

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Jianhua Zhao, Ph.D.
Scientific Director

The Protein Analysis Core provides a variety of analytical services focused on biophysical characterization of structural and functional properties of proteins in solution, under native, non-denaturing conditions.

The core performs quality control of protein samples (folding, stability, aggregation) and measure molecular weight of proteins, protein complexes, oligomers and assemblies. It also can characterize protein conformation and shape in solution; determine oligomeric state of protein (including stoichiometry and Kd for self-association) as well as measure protein binding to proteins, peptides, small molecules, compounds, metal ions, lipids, carbohydrates, nucleotides and other ligands (including determination of equilibrium (Kd) and kinetic rate (k_{on}, k_{off}) constants, stoichiometry, binding enthalpy and entropy).

SERVICES

- Analytical ultracentrifugation (AUC)
- Differential scanning calorimetry (DSC)
- Fluorescence spectroscopy/Fast Kinetics
- Grating-Coupled Interferometry (GCI)
- Isothermal titration calorimetry (ITC)
- Microscale thermopheresis

EQUIPMENT & RESOURCES

- Creoptix WAVE Delta for microfluidics
- NanoTemper Monolith 115 for measuring any interaction from ion to particles by thermopheresis
- Analytical ultracentrifuge,BeckmanCoulter XL-I
- Differential scanning calorimeter Malvern VP-Capillary DSC
- Fluorescence spectrometer, BioLogic MOS-250
- Isothermal titration calorimeter, TA Instrument. Affinity ITC
- Stopped-flow system, BioLogic SFM-20
- Cell homogenizer EmulsiFlex-C3 (Avestin)

Cryo-Electron Microscopy

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Jianhua Zhao, Ph.D.
Scientific Director

The Cryo-EM core facility offers high-resolution Cryo-EM imaging services and instrumentation.

The facility is optimized for single particle analysis (SPA) workflows and offers Cryo-EM solutions for a wide range of research including drug discovery in collaboration with the Conrad Prebys Center. Cryo-EM SPA data can be used to generate high resolution maps and atomic models of proteins and other macromolecules. Additionally, this data can capture different conformational states of the macromolecule in the sample, potentially offering additional insight into their function.

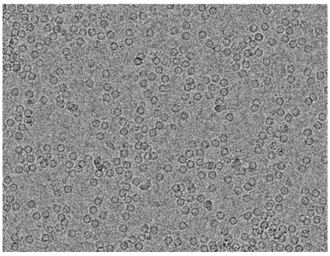
Services are heavily subsidized for SBP-internal users, making our services highly accessible. If you want to learn more about how the Cryo-EM core can help support your research project, please contact us!

SERVICES

- Cryo-EM sample preparation, screening and high-resolution data collection
- Preparation of negative stained samples, screening and data collection
- Service options: full services from start to finish, assisted use, or do-it-yourself are available
- Training on the different instruments
- Consultation: evaluating Cryo-EM feasibility, experimental design, data analysis and interpretation

EQUIPMENT & RESOURCES

- **Titan Krios with Gatan K3 direct electron detector** - 300kV cryo-electron microscope with a 3-condenser lens system primarily used to collect high-resolution single particle analysis data.
- **Tecnai T12 with Eagle 4K CCD** - 120kV electron microscope, primarily used for imaging negative stained samples.
- **Vitrobot Mark IV** - Semi-automated vitrification system for Cryo-EM samples. Control of process parameters (humidity & temperature) for preparing reproducible and consistent sample grids.
- **EasyGlow Glow Discharger** - Prepares grids for the application of the sample solution.



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Cell Imaging

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Maximiliano D'Angelo, Ph.D
Scientific Director

The core houses a wide variety of microscopes, and provides investigator training and use of the instruments, as well as full-service imaging.

Facility microscopes include a Miltenyi Blaze Light Sheet ultramicroscope, a Zeiss AiryScan laser scanning confocal microscope, a Nikon N-SIM super resolution/A1ER confocal microscope, three additional confocal systems (a multiphoton Zeiss LSM-710 NLO system, an Olympus FluoView 1000, and a Yokagawa Spinning Disk system), and six advanced fluorescence microscopes.

Sophisticated systems for FRET, Calcium imaging, and laser TIRF are also available. The microscopes are integrated with advanced image capture systems and analytical software, and a number are equipped with environmental chambers for extended live cell confocal analysis.

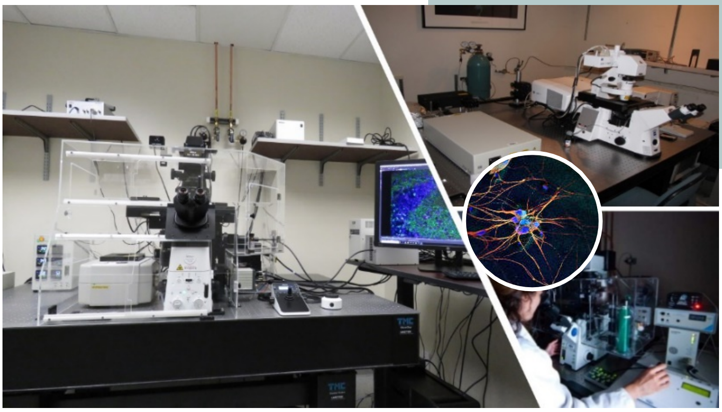
TEM and SEM are available at the nearby Salk Biophotonics facility.

SERVICES

- Wide-field microscopy, phase and differential interference (Nomarski) contrasts, multi-spectral epi-fluorescence microscopy
- Single and multi-photon laser point scanning confocal microscopy
- High-speed spinning disk confocal microscopy.
- Time-lapse imaging in CO_2 and temperature-controlled environment.
- Recording dynamics of single molecule interactions within single cells .Foster Resonance Energy Transfer (FRET), Fluorescence Recovery After Photobleaching (FRAP), calcium flux imaging and Total Internal Reflection (TIRF).
- 3D & 4D Image rendering & morphometric analysis.
- Training and consultation

EQUIPMENT

- Miltenyi Blaze Light Sheet ultramicroscope
- Zeiss LSM 980 AiryScan Super-resolution system
- Nikon N-SIM super resolution/A1ER confocal system
- Three confocal systems:
  1. Zeiss LSM 710 NLO multiphoton laser point scanning confocal microscope
  2. Olympus FluoView-1000; laser point scanning confocal microscope
  3. Yokogawa Spinning Disk Laser confocal system
- Six wide-field fluorescence microscopes with cooled CCD cameras , some with automated XYZ stage, microinjection attachment, CO_2/Temp. controlled chambers
- EVOS FL Auto Imaging system
- Multiple image processing software packages



Histology

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Maximiliano D’Angelo, Ph.D.
Scientific Director

The Histology core facility generates slides with frozen or fixed tissue sections and processes them with various stains and antibodies including supporting spatial transcriptomics, as well as providing expertise in pathology and tissue microarray analysis.

Leica equipment (ST5010 and BOND-RX) support automated H&E and IHC staining. Additional support for spatial analysis includes RNAScope analysis and preparing slides for the NanoString GeoMx.

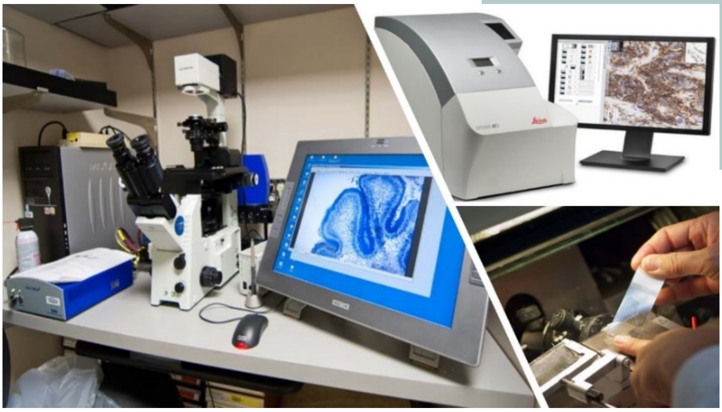
Leica/Aperio ScanScope AT2 and FL systems enable high resolution slide scanning, quantitative and morphometric analysis, digital archiving, and electronic distribution and access of standard and fluorescently stained histology slides.

SERVICES

- Traditional Histology: Conventional and research-specific custom sectioning and staining.
- Immunohistochemistry: Development of custom protocols (overlay assays, competition assays).
- Laser Capture Micro Dissection (MMI CellCut): Sample Preparation for DNA and RNA extraction, training and assistance.
- Digital Pathology: Electronic data acquisition, data analysis, web based data sharing and archiving of histology results. Network of consulting pathologists.
- Custom Image Analysis and development of novel algorithm-based scoring methods to quantify immunohistochemical and histological parameters
- Assistance with all aspects of tissue acquisition.

EQUIPMENT

- Aperio Scanscope AT2 and FL systems
- Leica CM 3050 cryostat
- Leica RM 2125 paraffin microtome
- Leica BOND-RX automated system for IHC/ISH
- Leica Autostainer ST5010 for H&E
- Shandon Cytospin 3
- Sakura Tissue Tek vacuum infiltration tissue processor
- Leica EG 1160 paraffin embedding station
- MMI Cell Cut Laser Microdissection system



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Flow Cytometry

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Scientific Director

The facility provides access to high-speed cell sorting and analytical flow cytometry in two locations on the Sanford-Burnham campus. Trained investigators have 24-hour access to a variety of analytical flow cytometers available for independent use. Core staff provide technical expertise, hardware and software training, operate the facility's cell sorters and are available to assist with analysis experiments for those who prefer to have their samples run by an expert cytometrist.

Scientists planning a flow cytometry experiment are encouraged to consult facility staff for assistance with protocols, fluorochrome selection or other aspects of experiment design.

SERVICES

- High speed cell sorting done by facility personnel
    - Single-cell (clone) sorting into 96 or 384-well plates
    - Simultaneous sorting of up to 4 populations
- Analytical flow cytometry: do-it-yourself 24hr/day, or assisted by appointment
- Imaging Flow Cytometry operated by core staff or do-it-yourself
- Hardware and software training
- Consultation
    - Experiment design
    - Data analysis and interpretation
    - Pre-publication manuscript review

EQUIPMENT

- Analyzers & Sorters
    - Cytek Aurora Full Spectrum Analyzer with 5 lasers and 64 fluorescent detectors
    - Amnis ImageStreamX MarkII imaging flow cytometer, 12 channels, 3 lasers, 3 magnifications & plate loader
    - ACEA Novocyte 3000, 3 lasers, 13-color analyzer with 96-well plate loader
    - BD LSRFortessa X20, 5 lasers, 18-color analyzer with HTS plate loader for 96 or 384-well plates
    - BD LSRFortessa 4-laser, 14-color analyzer w/HTS
    - BD FACSAria IIu 16-color and BD FACSAriaIIu 15-color high-speed cell sorters in biosafety enclosures
- FlowJo site license
- Computer Workstations with FlowJo and ModFit LT

Genomics

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Peter Adams, Ph.D.
Scientific Director

The facility provides library preparation and high throughput (next-gen) sequencing using an Element Biosciences AVITI sequencer.

RNA/DNA quality analysis is performed utilizing Agilent TapeStation, NanoDrop, and Qubit instruments, with automated sample preparation using an Eppendorf epMotion.

The Core supports transcriptome and genome analysis, and a variety of other NGS approaches. Single cell sequencing analysis is offered using the 10X Chromium X system and Illumina PIP-seq system.

The Core is increasingly focused on Spatial Transcriptomics, utilizing a Nanostring GeoMx DSP, as well as the 10x Genomics CytAssist instrument for whole transcriptome spatial profiling.

STR-based cell line authentication services are also provided.

SERVICES

- AVITI sequencing
- Single-Cell Sequencing
- Spatial Transcriptomics
- Human cell line authentication
- Quality analysis of starting RNA or DNA
- Library Preparation

EQUIPMENT

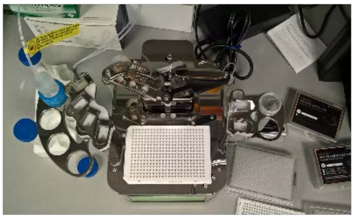
- Element Biosciences AVITI sequencer
- Eppendorf epMotion 7075 Liquid Handling system
- 10x Genomics Chromium X
- 10x Genomics CytAssist
- NanoString GeoMX Digital Spatial Profiler
- Illumina PIP-seq system
- BioRad ddSeq single cell system
- BioRad ZOE fluorescent cell imager
- Revvity Cellometer K2 Fluorescent Cell Counter
- Mantis (Formulatrix) liquid handler

Additional analytical equipment:

- Nanostring nCounter
- TapeStation (Agilent)
- Qubit Fluorometer (Life Technologies)
- Nanodrop Spectrophotometer

Shared Instruments

- 1 Roche LC480 (96 or 384-wells) & 4 LC96 QPCR
- ABI7900HT QPCR (96 & 384-wells)



Proteomics

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Elena Pasquale, Ph.D.
Scientific Director

The facility provides services ranging from protein identification in IP enriched material, to global analysis of proteins and their post-translational modifications. The Core supports comparative proteomics using mass tagging (e.g., TMT) or label-free analysis in both DIA and DDA mode.

Following initial digestion and sample preparation typically utilizing a robotic Bravo AssayMap system, samples are separated by EASY nLC 1200 and then analyzed by mass spectrometry.

Advanced mass spectrometry instruments include two Thermo Orbitrap Fusion Lumos Tribrid systems and a Thermo Q-Exactive Plus. Global serum proteomic analysis (thousands of proteins) is supported with the Seer Proteograph SP100 system.

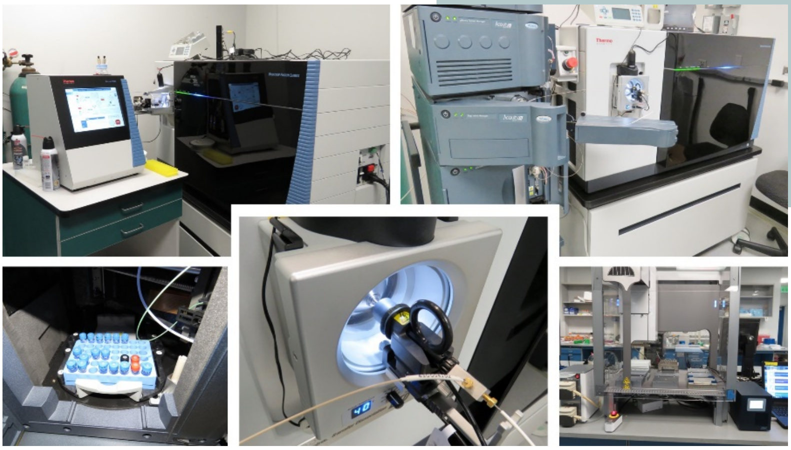
Proteomics data analysis is via a pipeline including open-source tools for protein identification, statistical and functional analyses of large proteomic datasets.

SERVICES

- Protein/Peptide Identification
- Identification and Localization of Post-Translational Modifications (e.g., phosphorylation, ubiquitinylation, acetylation, methylation, nitrosylation)
- Quantitative comparison of protein abundances in complex mixtures using label-free or label-based techniques (e.g., SILAC, TMT)
- Identification of protein-protein interactions by Affinity Purification followed by Mass Spectrometry (APMS) analysis
- Targeted protein identification and quantification

EQUIPMENT

- Thermo Orbitrap Fusion Lumos with ETD coupled to NanoEASY 1200
- Thermo Orbitrap Fusion Lumos coupled to NanoEASY 1200
- Thermo Q-Exactive Plus coupled to NanoEASY 1200
- SEER Proteograph XT
- Agilent AssayMap BRAVO Platform for automated protein sample preparation



Bioinformatics

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Kevin Yip, Ph.D.
Scientific Director

The Bioinformatics Core provides computational and systems biology support, specializing in omics data analysis, multi-omics data integration, network and pathway analysis, statistical analysis, and machine learning. The Core has built automated computational pipelines using state-of-the-art software packages to QC, align, summarize, statistically analyze, and visualize NGS data sets. Analysis includes multi-omics data integration and customized pathway and network analysis.

The Core has licensed commercial software packages for advanced genomic studies.

Regular trainings and tutorials are given on using these software packages and other publicly available bioinformatics software and databases.

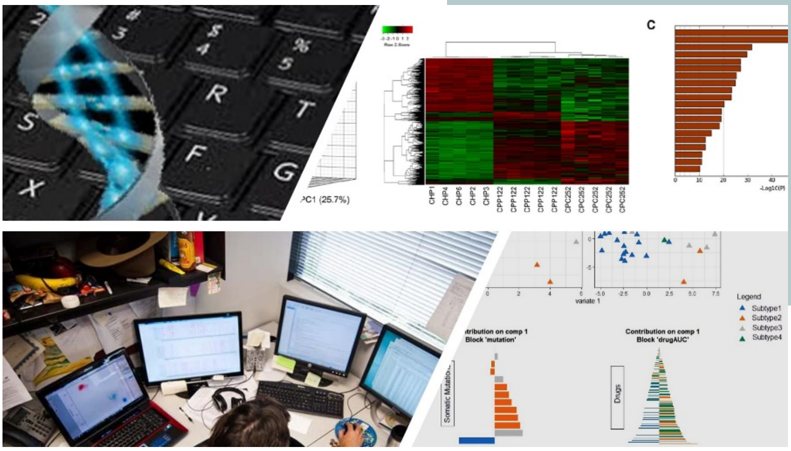
A growing area of focus is systems biology by integrating analyses across multiple data types (data generated in-house or mined), such as genomics, proteomics, and metabolomics, helping to create testable hypotheses and better understand the underlying biology.

SERVICES

- Data mining of Next Generation Sequencing (NGS) data sets, including RNA-seq, ChIP-seq, ATAC-seq, single cell sequencing, spatial omics, etc.
- Data mining of Next Generation Sequencing (NGS) data sets, including RNA-seq, ChIP-seq, ATAC-seq, single cell sequencing, spatial omics, etc.
- Data integration of transcriptomics, genomics, proteomics, and epigenomics data sets
- Network analysis and pathway analysis using customized algorithms and commercially available software, including Ingenuity Pathway Analysis, Transfac, GSEA, Metascape etc.
- Machine learning application
- Biomarker identification
- Biostatistics
- Training and consultation on bioinformatics
- Grant writing and letter of support

EQUIPMENT & RESOURCES

- Automated NGS analyses pipelines for RNA-seq, ATAC-seq, ChIP-seq etc.
- Licensed Systems Biology software, Ingenuity Pathway Analysis (IPA), TRANSFAC.
- High_Performance Cluster: 100 cores, 512 GB memory, 96 TB network attached storage for computationally intensive analyses & access to cloud–based resources



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Functional Genomics

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Ani Deshpande, Ph.D.
Scientific Director

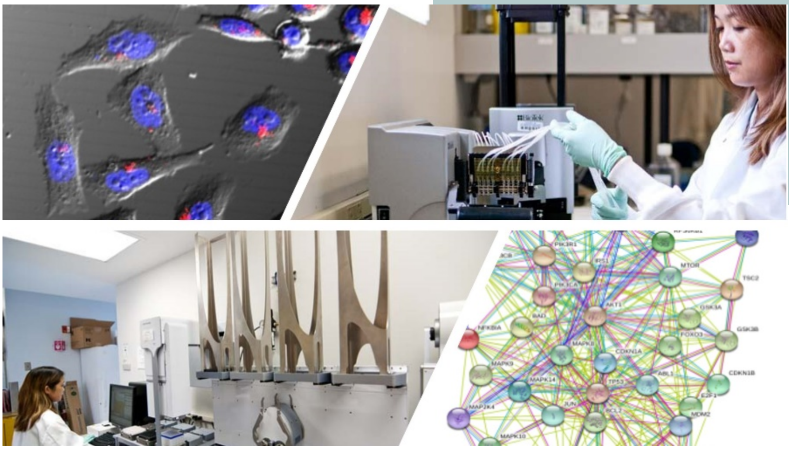
The Functional Genomics Core Facility provides the infrastructure for cell-based gain-of-function (ORF, CRISPRa and CRISPRon) and loss-of-function (siRNA, miRNA mimics, shRNA, CRISPRko, CRISPRi and CRISPRoff) libraries screening services, starting with reporter knock-in cell line engineering, assay development and carrying all the way through verification of identified targets. Assorted genome-wide and pathway-specific libraries with choice of arrayed or pooled formats are ready-to-screen. CRISPR tiling screen is achieved through different nucleotide base editors to interrogate drug-target interaction and identify functional genetic variants. The core is equipped with high-throughput automation capable of performing DNA purification, plasmid quantification, viral vector production, clonal line creation, and many other custom assays in 96- and 384-well platforms.

SERVICES

- Library Screening:
    - Arrayed siRNA libraries (384- & 1516-well formats)
    - Arrayed miRNA mimic and antagonist libraries
    - Arrayed lentiviral ORF overexpression libraries
    - Arrayed/Pooled lentiviral CRISPR gRNA libraries
- CRISPR/Cas
    - Custom CRISPR/Cas9 ki, ko, a, i, on, off & base-editing
    - Custom CRISPR/Cas12 ko
    - Custom CRISPR/Cas13 RNAi
    - High-activity SpCas9 & EnAsCas12a stable cell line enrichment
    - Pooled gRNA library preparation & QC
    - NGS-ready amplicon library preparation & QC
- Automation
    - 96-well mini-scale: plasmid DNA extraction, gDNA purification, lenti & retro-viral production
    - 384-well micro-scale: DNA quantification & normalization, 96-384 plate conversion
- Single cell barcoding

EQUIPMENT and RESOURCES

- Biomek i7 Hybrid Automated Workstation (Beckman Coulter), funded by S10 OD036254
- CloneSelect Imager (Molecular Devices)
- Benchcell & Bravo liquid handling platform (Agilent)
- Wellmate liquid dispenser (Matrix Tech.)
- STAR liquid handling station (Hamilton)
- ELx 405 Plate Washer (BioTek)
- Micro-plate reader Analyst HT (Molecular Devices)
- EVOS fluorescence microscope (Life Tech.)
- Tissue culture facility



Viral Vectors

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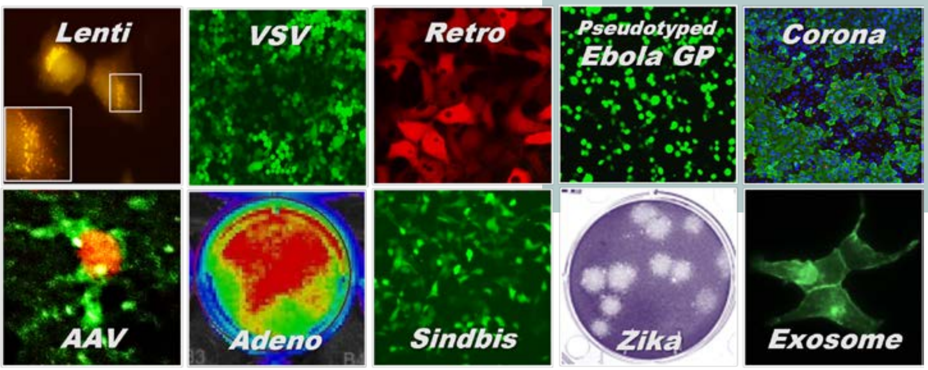
Scientific Director

The Viral Vector Core Facility provides state-of-the-art viral vector-based gene / shRNA delivery technology. Its portfolio ranges from lentivirus, retrovirus, adenovirus, adeno-associated virus, zika virus, coronavirus, sindbis virus and vesicular stomatitis virus products as well as customized "The Works" viral vector construction and swapping service packages. There are over 50 ready-to-transduce reporter viruses available for live cell imaging and 2D/3D cell-based assays. For custom virus production, we can achieve high-titer, top quality viral particles suitable for in vitro and in vivo studies. The automated mini-scale preparations of vector plasmids and viruses in 96-well format can immediately allow downstream viral array screening. The core also extends technical expertise in non-viral nanoparticles which includes large extracellular vesicles and exosome purification, analysis and engineering.

SERVICES

- Viral vector construction and production:
    - Lentivirus (HIV-1 and FIV)
    - Integrase defective lentivirus (IDLV)
    - Retrovirus (MSCV and MMLV)
    - Adenovirus (Ad5)
    - AAV (serotype 1-9, DJ, DJ/8, PHP.B)
    - Sindbis virus (SinRep5)
    - Zika virus (African, Asian, and Brazilian strain)
    - VSV (Ebola virus glycoprotein
    - Coronavirus (OC43)
- Ready-to-transduce viral preps:
    - Fluorescence reporters
    - Bioluminescence reporters
    - Secreted bioluminescence reporters
    - Cell cycle reporters
    - Autophagy reporters
- siRNA to lentiviral shRNA conversion
    - Doxy inducible H1 or constitutive U6 promoter
    - Puromycin or neomycin selection marker
- Exosome purification and engineering:
    - Exosome isolation
    - SBI XPACK and XMIRs exosome loading
- Large scale DNA plasmid preparation & QC
- Single, dual (Cas9), triple (Cas12) & quadruple-gRNAs (3 Cas12 & 1 Cas9) vector constructions
- Consultation: free for core users



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Cancer Metabolism

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Brooke Emerling, Ph.D.
Scientific Director

The Cancer Metabolism Core provides expert advice and analytical services for research in metabolism, both in cancer and other systems. The principal methodology used is gas chromatography-mass spectrometry (GC-MS), for the sensitive quantification of amino acids/ TCA cycle and glycolysis metabolites, fatty acids/cholesterol, short-chain fatty acids, sugars or sugar-phosphates. Other metabolites that are amenable to GC-MS analysis may also be measurable, in consultation with the Facility Director. We also are specialists in stable isotope-based metabolic tracer (13C, 15N, 2H) methods, which allow determination of cellular metabolic fluxes. Metabolites in cells, tissue samples, plasma/ serum and media can be assayed by GC-MS.

In addition, the YSI analyzer allows a rapid and inexpensive analysis of metabolic function in cells via comparative glucose, lactate and glutamine measurement. Relative oxidative and glycolytic activity of cells can be measured using Seahorse analyzers.

SERVICES

- GC-MS-based quantification or stable-isotope-labeling analysis of metabolites including amino acids, keto acids, fatty acids, cholesterol, short-chain fatty acids, sugars, sugar phosphates.
- Rapid measurement of major metabolites (glucose, glutamine, lactate, glutamate) in medium samples using the YSI 2950 analyzer.
- Measurement of mitochondrial respiration and glycolysis in cells using Seahorse analyzers (this is mostly self-service, but with training, advice and supplies of consumables available).

EQUIPMENT

- GCMS-QP2010 Plus and GC-MS/MS TSQ 9610 for metabolite quantification and metabolic flux analysis. Negative chemical ionization and MS/MS options allow for highly sensitive detection in complex mixtures.
- YSI 2950 metabolite analyzer, to measure glucose, glutamine, lactate, and glutamate in media samples in 96-well format
- Seahorse XFp, XFe24 and XF96 to measure the two major energy producing pathways of the cell – mitochondrial respiration and glycolysis - in real-time, with automated injection of metabolic substrates or inhibitors.
- Shimadzu Prominence HPLC for bioenergetics and other small molecules analyses.

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