Cancer Center Shared Resources

Sanford
Burnham
Prebys

Our Mission

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The Sanford Burnham Prebys Medical Discovery Institute Cancer Center under the direction of Ze'ev Ronai, 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, molecular pathology, 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
Chemical Library Screening	Assay development, compound libraries, high-throughput screening, high-content screening, medicinal chemistry
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 http://www.spbdiscovery.org/technology/sr/Pages/Home.aspx.

Cancer Center

Shared Resources

Campus Map

Animal Facility

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Alessandra Sacco, Ph.D.
Scientific Director

The Animal Facility is a 24,000 sq ft AAALAC accredited facility that can house over 10,000 cages of mice in ventilated racks, providing full husbandry with breeding, weaning, and tail samples.

The facility also provides care for a small number of rats and has separate BSL2 mouse facilities.

Many procedures can be performed by facility staff, including injections (SC, IP, IV), tumor measurements, blood collections, and surgical assistance.

The 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
- Procedural Techniques Support
  - Blood collection
  - Injections (IP, IM, SQ, Tail Vein, Retro-orbital)
  - Oral gavage
  - Tumor measurements
  - Surgical pre- and post-op care
- Administrative & IACUC support
- Transgenic Services (including CRISPR) available at nearby Core facilities (UCSD, Salk, Scripps

EQUIPMENT & SUPPORT

- Ventilated mouse cages
- 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
  - Water maze with video camera
  - Hot plate analgesia meter
  - Stereotactic microinjection station

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Animal Imaging & Analysis

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Alessandra Sacco, Ph.D.
Scientific Director

The Animal Imaging and Analysis lab provides state-of-the-art imaging and analytical services for Sanford-Burnham investigators.

The facility can perform *in vivo* near-infrared imaging without reporter genes, as well as *in vivo* non-invasive luminescence and fluorescence imaging for xenograft tumor growth and metastasis studies.

Analytical equipment supports complete blood cell counts (CBC) and analysis of serum components revealing metabolic or organ stress from small samples of mouse blood.

SERVICES

- Imaging and analytical services can be done by trained animal facility specialists.
  - Live near-infrared imaging on animal, native cells and cell lines without reporter genes.
  - Live animal imaging - bioluminescence and fluorescence (IVIS Spectrum, Pearl Impulse)
  - Live animal imaging – ultrasound
  - Blood and serum analysis
- 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
- Vevo 770 (VisualSonics): high-resolution ultrasound & guided-injection system
- VetScan HM5 Hematology System (Zoetis) : 22-parameter blood count & clinical chemistry analyzer
- VetScan VS2 (Zoetis) for blood chemistry, electrolytes, blood gas & immunoassay
- IDEXX Catalyst One Chemistry : blood & urine
- CODA-6 (Kent Scientific): tail-cuff blood pressure system
- Faxitron MX-20 Digital Specimen Radiography
- Oxycycler (BioSpherix, Ltd.): for oxygen consumption, CO2 production & hypoxia studies.
- Stereotaxic instrument: microinjection equipment

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Tumor Analysis

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The Tumor Analysis service provides expertise in analysis of animal models of human cancers.

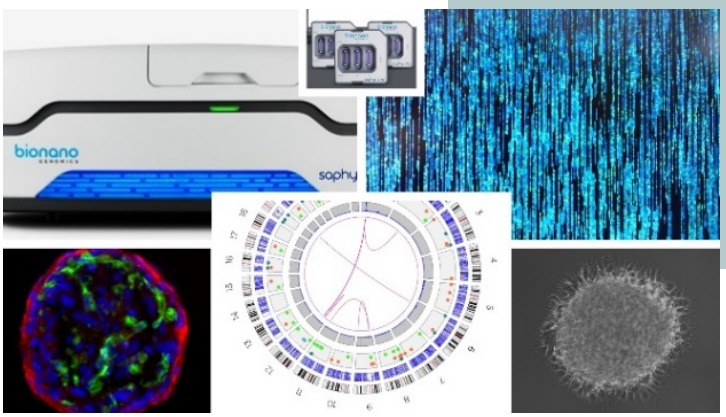
Investigators have access to a wide variety of human cancer cell lines for non-invasive xenograft studies and primary human xenograft models as well as transgenic mouse solid tumors and leukemia models.

SERVICES

- Formulation advice
- Maximum tolerated dose
- Patient-derived xenograft (PDX) model support
- Analysis of human tumors in immune deficient mice
- Analysis of mouse tumors in immune competent hosts
- Derive 2D and 3D cell cultures from xenograft tumors
- Tumor and cell line resources
- Technical Training in Animal Tumor methods

EQUIPMENT

- Bionano Saphyr Genome Mapping
- Qubit Fluorometer (Life Technologies)



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Protein Analysis

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Francesca Marassi, Ph.D.
Scientific Director

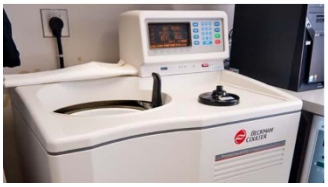
The Protein Analysis Core provides a variety of analytical services focused on biophysical characterization of structural and functional properties of proteins in solution, under native, non-denaturing conditions. The core performs quality control of protein samples (folding, stability, aggregation) 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).

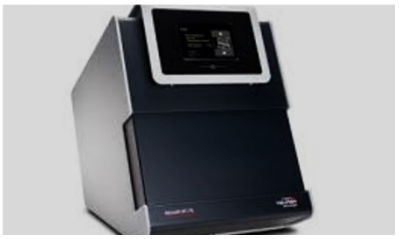
SERVICES

- 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
- Three isothermal titration calorimeters, GE Healthcare/Microcal ITC200 & VP-ITC, and TA Instr. Affinity ITC
- Stopped-flow system, BioLogic SFM-20
- Cell homogenizer EmulsiFlex-C3 (Avestin)





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Cryo-Electron Microscopy

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Jianhua Zhao, Ph.D.
Scientific Director

The newly revamped Cryo-EM core facility at the Sanford Burnham Prebys Medical Discovery Institute 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.

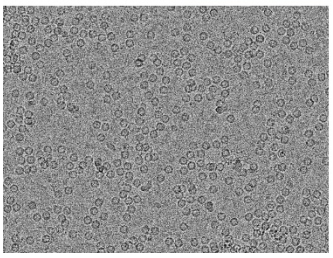
Services are currently fully subsidized for SBP-internal users. If you want to learn more about how the Cryo-EM core can help support your research project, please contact us!

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

Leslie Boyd
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Brook Emerling, Ph.D
Scientific Director

The Cell Imaging Facility broadly supports research programs by providing access to sophisticated microscopes for digital imaging.

The facility offers expertise, training, and assistance in advanced biological microscopic imaging techniques and use of complex image processing software. The facility provides well-maintained, aligned, and calibrated microscopic equipment, as well as troubleshooting for equipment and experimental problems.

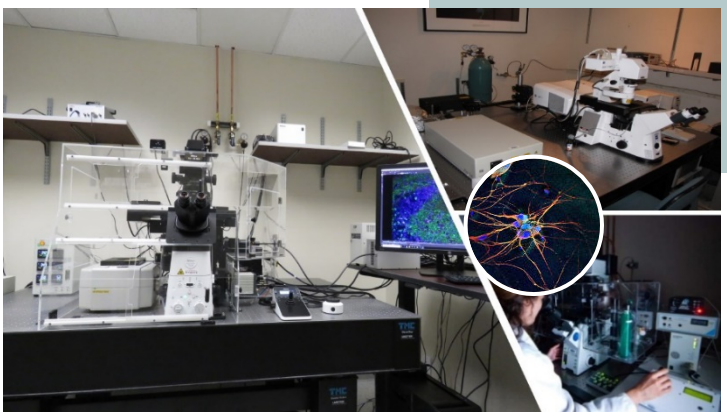
TEM and SEM are available at the nearby Salk Biophotonics facility.

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

- 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 microscope
- 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



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Histopathology

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Brook Emerling, Ph.D.
Scientific Director

The facility generates slides with frozen or fixed tissue sections and processes them with various stains and antibodies including supporting spatial transcriptomics, as well as provides 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.

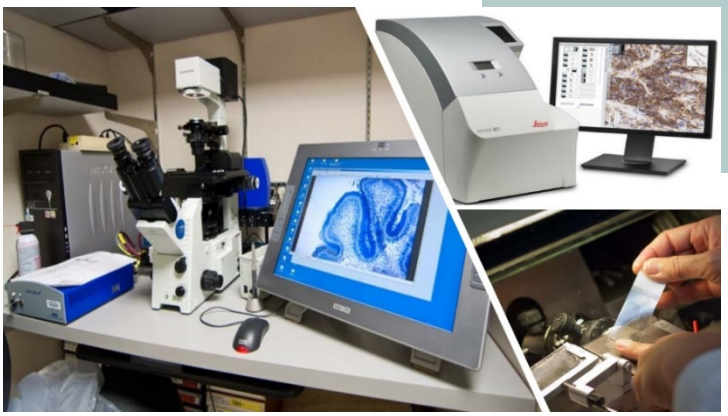
Leica/Aperio ScanScope AT2 and FL systems enable high resolution slide scanning, quantitative and morphometric analysis, digital archiving, and electronic distribution and access of standard and fluorescently stained histology slides.

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

Yoav Altman
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Maximilio D'Angelo, Ph.D.
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
  - 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 LSR Fortessa X20, 5 lasers, 18-color analyzer with HTS plate loader for 96 or 384-well plates
  - BD LSR Fortessa 4-laser, 14-color analyzer w/HTS
  - EMD Millipore Muse Cell 2-color Analyzer
  - 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

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Genomics

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Peter Adams, Ph.D.
Scientific Director

The facility provides library preparation and high throughput (next-gen) DNA sequencing using an Illumina NextSeq 500.

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

The Core supports transcriptome and exome analysis, ChIP-seq, and a variety of other NGS approaches. Single cell sequencing analysis is offered using the 10X Chromium X system for library preparation.

The Core is increasingly focused on Spatial Transcriptomics, utilizing a Nanostring GeoMx, as well as the new Nanostring CosMX instrument, which provides true single transcriptomics. STR-based cell line authentication and mycoplasma testing services are also provided.

SERVICES

- NextSeq sequencing
- Single-Cell Sequencing
- Human cell line authentication
- Quality analysis of starting RNA or DNA
- Library Preparation
- Sequencing of samples
- Basic next-generation sequencing bioinformatic analysis
- Advanced bioinformatic analysis

EQUIPMENT

- Illumina NextSeq 500 sequencer
- Eppendorf epMotion 7075 Liquid Handling system
- BioRad ddSeq single cell system
- BioRad ZOE fluorescent cell imager
- 10x Genomics Chromium Single-Cell prep system
- Mantis (Formulatrix) liquid handler

Additional analytical equipment:

- NanoString GeoMX for spatial transcriptomics
- NanoString CosMX for single transcriptomics
- Nanostring nCounter
- 2100 Bioanalyzer (Agilent)
- Qubit Fluorometer (Life Technologies)
- Nanodrop Spectrophotometer

Shared Instruments

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

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Proteomics

Svetlana Maurya, Ph.D.
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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.

Following initial digestion and sample preparation typically utilizing a robotic Bravo AssayMap system, samples are separated by 1D or 2D UHPCL (EASY nLC 1200, and 2D NanoAcquity) 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 system.

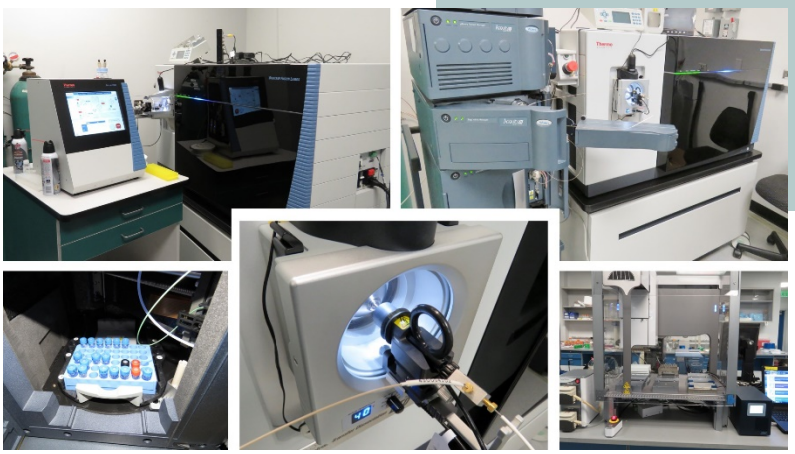
Proteomics data analysis is via a pipeline including open-source tools for protein identification, statistical and functional analyses of large proteomic datasets.

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 SP100
- Agilent AssayMap BRAVO Platform for automated protein sample preparation



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Conrad Prebys Center for Chemical Genomics

Drug Discovery Resources

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Steven Olson, Ph.D.
Medicinal Chemistry
Facility Director
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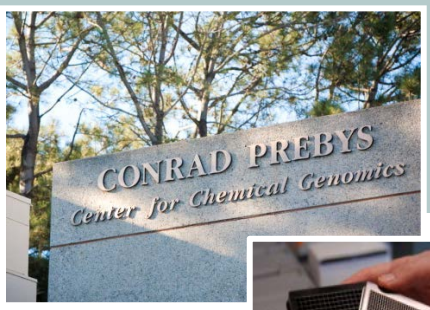
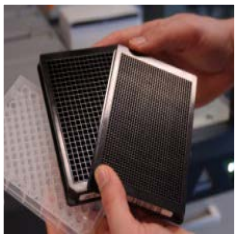
The Chemical Library Screening (CLS) Core was formerly a Cancer Center Core facility within SBP's Conrad Prebys Center for Chemical Genomics, but the CLS Core has been discontinued in light of the substantially expanded collaboration of the Cancer Center with the Prebys Center.

SERVICES and RESOURCES

- Design and development of cell-based and biochemical assays in diverse plate formats and detection platforms
- Full-scale capabilities and infrastructure providing rapid screening on a broad diversity of assays and detection platforms
- Several fully integrated industrial-scale high-throughput screening (HTS) workstations
- HTS microscopy/HCS and novel algorithm development for image analysis
- Full Hit-to-Lead chemistry and exploratory pharmacology
- Powerful NMR based Chemical Fragment Screening
- Highly integrated informatics infrastructure and efficient data mining capabilities
- Close ties with Protein production facility
- Cell production facility for scale-up tissue culture, including ES and iPSC capabilities
- Project management
- Support of projects performed by either PI laboratory or CPCCG personnel
- Full support of grant applications for available funding mechanisms





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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.

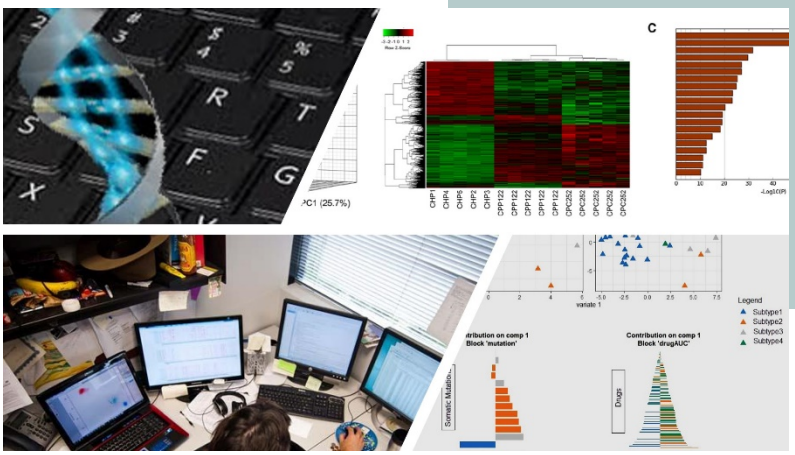
A growing area of focus is systems biology by integrating analyses across multiple data types (data generated in-house or mined), such as genomics, proteomics, and metabolomics, helping to create testable hypotheses and better understand the underlying biology.

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-level data mining, network analysis, and data integration analyses using WGCNA, DIABLO, etc.
- Dell PowerEdge R530 Linux server with 40 cores and 256G RAM



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Functional Genomics

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Ani Deshpande, Ph.D.
Scientific Director

The Core 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.

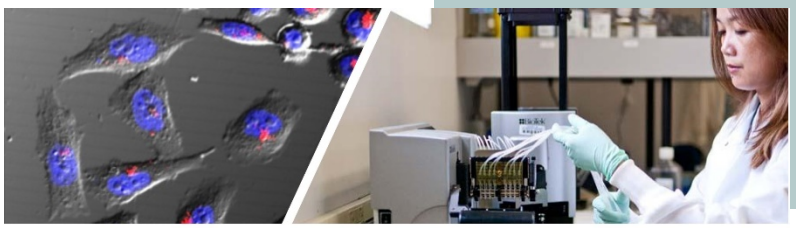
The core is equipped with high-throughput automation capable of performing DNA purification, plasmid quantification, viral vector production, clonal line creation, and many other custom assays in 96- and 384-well platforms.

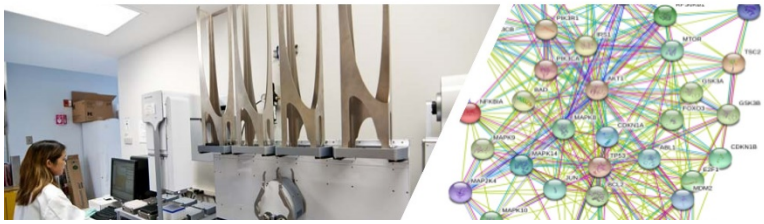
SERVICES

- Library Screening:
  - Arrayed siRNA libraries
  - Arrayed lentiviral ORF overexpression libraries
  - Pooled viral CRISPR gRNA libraries:
  - Arrayed viral CRISPR gRNA libraries
- CRISPR/Cas
  - Custom CRISPR ki, ko, a, I, on, off & base-editing
  - High activity SpCas9 & EnAsCas12a stable cell line
  - Pooled gRNA library preparation & QC'NGS-ready amplicon library preparation & QC
- Automation
  - 96-well mini-scale: plasmid DNA extraction, genomic DNA purification, lenti & retroviral production
  - 384-well micro-scale: DNA quantification & normalization; 96-384 plate conversion
- Single cell barcoding

EQUIPMENT and RESOURCES

- Benchcell & Bravo liquid handling platform (Agilent), Welllmate liquid dispenser (Matrix Tech.)
- STAR liquid handling station (Hamilton)
- Micro-plate reader Analyst HT, (Molecular Devices); Envision, (Perkin Elmer)
- High-throughput microscopes (IC100, Beckman-Coulter; INCell 1000, GE)
- Tissue culture facility
- Genome-wide siRNA libraries (Dharmacon OTP) focused libraries, miR agonists and antagonists, cDNA expression
- Developing CRISPR-CAS9 technologies for cell line editing and screening





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Viral Vectors

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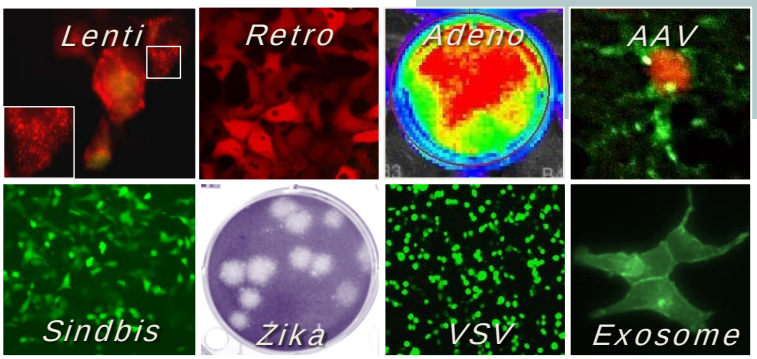
Ani Deshpande, Ph.D.
Scientific Director

The viral vector core facility provides custom packaging, concentration, and titration of lentiviral particles, as well as retrovirus, lentivirus, AAV, and VSV-based vectors. Several ready-to-use lentiviral supernatants are available to fluorescently mark cells. Vector backbones and assistance in creating effective constructs are also provided.

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 construction
- Consultation: free for core users



Sanford Burnham Prebys

Cancer Metabolism

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The scientific focus of the core is to investigate the role of metabolism in cancer at both the cellular and organismal level, combining *in vitro* and *in vivo* analysis. To that effect, the facility provides measurement of metabolites in cells, tissue samples, plasma, and media. The principal methodology used is gas chromatography-mass spectrometry (GC-MS), for broad metabolic flux analysis using stable isotope labeling.

In addition, the YSI Analyzer allows for focused analysis of specific metabolites.

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 cellular respiration and glycolysis using a Seahorse XFp.
- GC-MS and YSI analyses are mostly full service , while user training on the Seahorse analyzer is provided for SBP users

EQUIPMENT

- GCMS-QP2010 Plus for metabolite quantification and metabolic flux analysis. Includes negative chemical ionization option for highly sensitive detection
- YSI 2950 metabolite analyzer, to measure glucose, glutamine, lactate, and glutamate in media samples in 96-well format
- Seahorse XFp, XFe24 and Xfe 96 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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