



Shared Resources Handbook 2022-2023

BARBARA ANN
 **Karmanos**
CANCER INSTITUTE
Wayne State University

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 **Comprehensive
Cancer Center**
A Cancer Center Designated by the
National Cancer Institute

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INTRODUCTION

Cancer. It's the word that changes everything, for patients and those who love them. At the Barbara Ann Karmanos Cancer Institute, we are exclusively focused on providing our patients with every resource to give them their best chance at a favorable outcome. At Karmanos, we're doing things to fight cancer that didn't exist as far back as yesterday. While every hospital will do all that they can, we can do things other hospitals just can't. From groundbreaking research to the most up-to-date therapies and individualized treatment plans, Karmanos is truly leading the fight against cancer.

Karmanos Cancer Institute, headquartered in Detroit, understands that beating cancer means bringing together the best. Cancer is a complex disease that demands complex care. With 16 locations throughout Michigan and Ohio and proudly a part of McLaren Health Care, Karmanos is the largest provider of cancer care and research in Michigan. Cancer patients have increased access to advanced cancer care in communities throughout the state and northern Ohio. This provides an extra level of comfort and peace of mind to patients and their families, knowing they can receive the best care locally.

Caring for approximately 12,000 new patients annually and conducting more than 800 cancer-specific scientific investigation programs and clinical trials, Karmanos is among the nation's best cancer centers. Karmanos offers one of the largest clinical trials program in the nation, giving patients access to more than 250 promising new treatments often not found at other hospitals or health organizations.

Through the commitment of 1,000 staff, including nearly 300 faculty members, and supported by thousands of volunteer and financial donors, Karmanos strives to lead in transformative cancer care, research and education through courage, commitment and compassion. Our long-term partnership with the Wayne State University School of Medicine enhances the collaboration of critical research and academics related to cancer care.

"A world free of cancer."

SHARED RESOURCES AND NIH PUBLIC ACCESS

The Shared Resources (Cores) at the Karmanos Cancer Institute, in partnership with Wayne State University, provide access to specialized technologies, services, and expertise that enhance scientific interaction and productivity. These Cores are supported, in part, through a NIH/NCI Cancer Center Support Grant (CCSG), P30 CA022453 (PI: Uberti). *As such, any peer-reviewed manuscript that includes results from these Cores must adhere to the NIH Public Access Policy, which states:*

The NIH Public Access Policy (<https://publicaccess.nih.gov/policy.htm>) applies to any manuscript that:

- Is peer-reviewed;
- And, is accepted for publication in a journal on or after April 7, 2008;
- And, arises from:
 - Any direct funding from an NIH grant or cooperative agreement active in Fiscal Year 2008 or beyond, or;
 - Any direct funding from an NIH contract signed on or after April 7, 2008, or;
 - Any direct funding from the NIH Intramural Program, or;
 - An NIH employee.

Compliance is evidenced by the presence of a PubMed Central ID (PMCID) number. You are required to provide the PMCID number when citing your papers in biosketches, NIH applications, proposals, and reports.

Some journals automatically deposit all NIH-funded final published articles in PubMed Central, to be made publicly available within 12 months of publication, without author involvement. Alternatively, articles can be submitted by the author or designee through the NIHMS system (<https://www.nihms.nih.gov>). KCI Research Administration acts as the designee on behalf of KCI members.

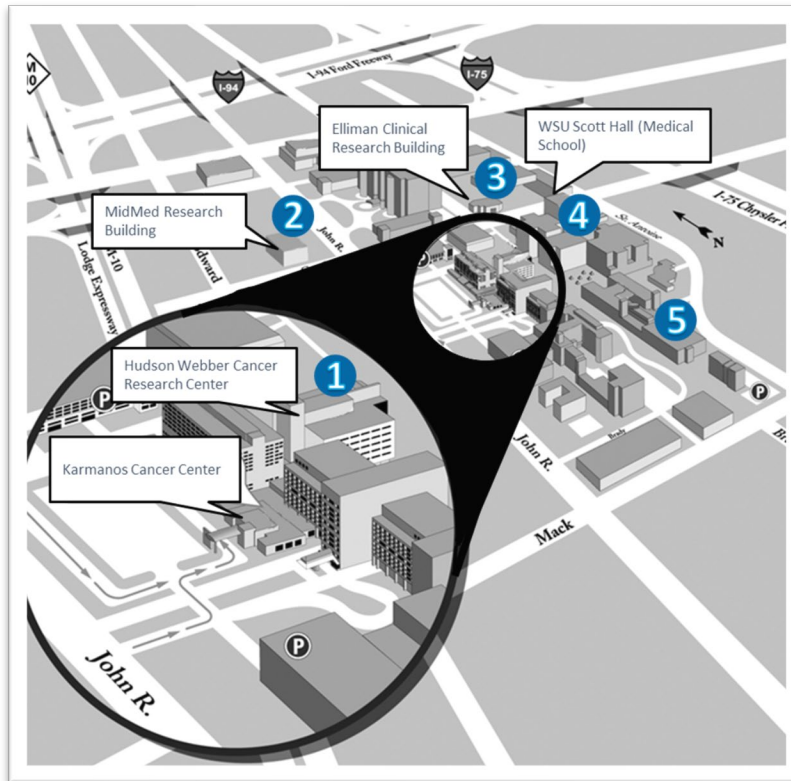
The NIH Public Access Policy applies to all publications that are funded directly through the P30 Cancer Center Support Grant (CCSG) via CCSG-supported Shared Resources, Developmental Funds, or Early Phase Clinical Research Support (EPCRS) funds.

Additionally, when a publication results from use of a KCI Shared Resource, it is essential that the CCSG be listed in the funding acknowledgements section of the published article. This helps identify research supported by the NIH. Specifically,

“The (Insert Name) Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

Questions? researchadmin@karmanos.org

LOCATION OF SHARED RESOURCES



1 Hudson Webber Cancer Research Center

- Biobanking and Correlative Sciences (BCS) Core
- Microscopy, Imaging, and Cytometry Resources (MICR) Core-Cytometry Division
- Pharmacology and Metabolomics Core (PMC)

2 Mid Med Research Building

- Biostatistics and Bioinformatics Core (BBC)
- Clinical Trials Office
- Epidemiology Research Core (ERC)

3 Elliman Clinical Research Building

- Animal Model and Therapeutics Evaluation Core (AMTEC)
- Microscopy, Imaging, and Cytometry Resources (MICR) Core-Imaging Division

4 Scott Hall - WSU School of Medicine

- Microscopy, Imaging, and Cytometry Resources (MICR) Core-Imaging Division
- Proteomics Core

5 Children's Hospital of Michigan

- Cyclotron & Radiochemistry (C&R) Core

DIRECTORY OF SHARED RESOURCES



Animal Model and Therapeutics Evaluation Core (AMTEC)

Director: Lisa Polin, PhD (313) 578-4270

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Biobanking and Correlative Sciences (BCS) Core

Director: Julie Boerner, PhD (313) 576-8351

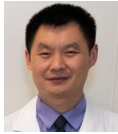
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Cyclotron & Radiochemistry (C&R) Core

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Mission of the Core:

The purpose of the Animal Model and Therapeutics Evaluation Core (AMTEC) is to enhance the peer reviewed funded research activities of KCI members whose research needs involve the use of animal models. Our goal is to provide expert scientific consultation, technical expertise and access to a wide breadth of relevant tumor models and associated animal-related services.

Core Services Available:

- Animal Study Technical Support
- Tumor Models and Cell Lines (Mouse and Human - Syngeneic, Transgenic, GEMM, Xenograft and PDX)
- In Vivo Orthotopic Tumor and Metastasis Models
- In Vivo Therapeutic Evaluation: Consultation, Study Design, Implementation and Analysis
- In Vivo Training/Teaching for researchers, staff and students
- Consultation and Assistance: Grant, manuscript and IACUC submissions
- In Vivo Study Sampling: pK analysis treatment and time point collections; treatment and harvest of tumor and/or tissue specimens at endpoint or during Rx regimens for further analyses (e.g. to BCS, Proteomics, Pharmacology Cores as well as for genomics, metabolomics and veterinary pathological examination).

Resources:

- Two ultracold units (-80°C & -150°C) connected to the Public Safety monitoring system
- New dedicated cell culture room w/BSL2 laminar flow hood
- Table top refrigerated centrifuge
- Two Panasonic incubators equipped with germicidal & UV sterilization
- New BSL2 flow hood (animal suite)
- Eight liquid nitrogen dewars
- Somno suite and SurgiSuite surgical platforms for surgical procedures
- Techniplast environmental chamber
- Excelsior AS Tissue Processor and HistoStar Instrument Embedding Center

Research:

Patient Derived Xenograft (PDX) In House Development

Metastatic hormone resistant prostate PDX: 3 models (KCI-PR022 (shown in right panel, established from patient bone biopsy), KCI-PR035 and 18-016 in current development):

Metastatic lung PDX:

20 metastatic lung models established and undergoing characterization: Utilization: Part of an R01 submission to assess USP10's role in platinum response in NSCLC patients. Drs. Bepler (MT) and Zhang (MT)

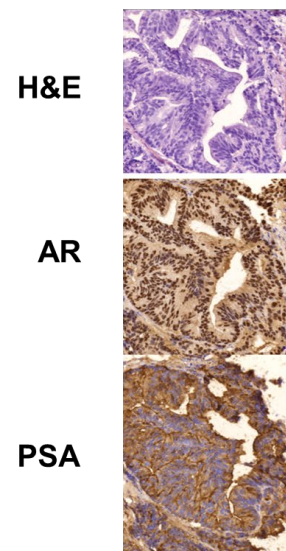
samples	Date*	Lab ID	USP10 level	p53 status
1	12/9/2014	14-049 M2	0.12	wt
2	12/18/2014	14-055 M7	0.23	mut
3	2/10/2015	14-065 M7	0.43	wt
4	2/10/2015	14-068 M12	2.25	mut
5	6/23/2015	14-012 M8	1.51	wt
6	6/3/2015	14-113 M6	3.37	mut
7	6/23/2015	14-023 M8	7.91	wt
8	7/2/2015	15-002 M7	0.22	wt
9	10/13/2015	15-009 M7	0.94	mut
10	8/27/2015	14-110 M3	0.97	mut
11	8/27/2015	15-030 M3	2.66	wt
12	10/9/2015	15-028 M8	2.06	mut
13	10/20/2015	15-001 M5	0.96	mut
14	10/27/2015	14-097 M4	1.93	mut
15	11/11/2015	14-114 M4	1.52	wt
16	10/20/2015	15-033 M3	0.07	wt
17	3/22/2016	14-112S M6	0.65	mut
18	3/31/2016	15-016 M8	1.34	wt
19	9/20/2016	15-022 M7	0.13	wt
20	10/25/2016	15-018 M5	1.44	mut

*dates on which tumors were harvested

Legend:

- WT-p53 USP10-Low
- WT-p53 USP10-High
- Mut-p53 USP10-Low
- Mut-p53 USP10-High

KCI-PR-022 PDX



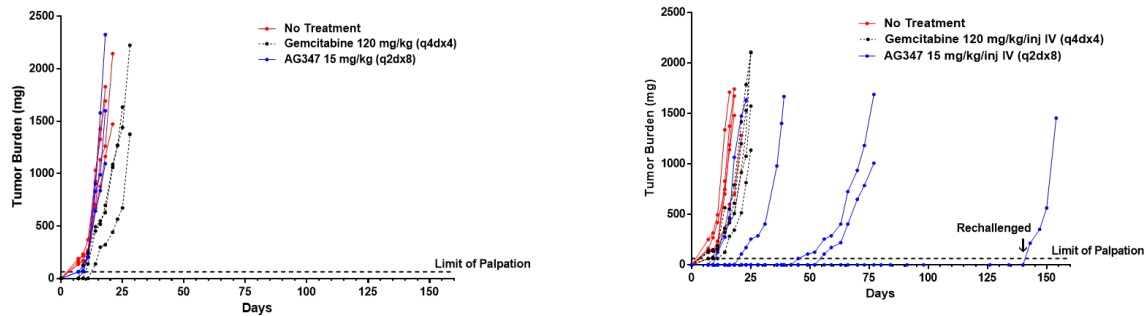
Prostate PDX:
AMTEC with Drs. Elisabeth Heath (MT) and Julie Boerner (MT)

Metastatic Lung PDX:
AMTEC with Drs. Sandeep Mittal (MT) and Sharon Michelhaugh

AGF-347 - A Novel Therapy for Pancreatic Cancer: In Vivo Study with MiaPaCa-2 in SCID Mice

Goal: Develop a new class of antifolates: Multi-targeted cytosolic and mitochondrial C1 metabolism inhibitors that are efficacious against lung, colon and pancreatic cancer.

Genes encoding one-carbon (C1) metabolism enzymes in the mitochondria and cytosol are consistently upregulated across multiple cancer types. Dr Matherly and collaborators have designed and evaluated AGF-347 as one such prototype multi-targeted small molecule inhibitor of mitochondrial C1 metabolism at serine hydroxymethyltransferase (SHMT) 2, and cytosolic C1-dependent purine biosynthesis (β -glycinamide ribonucleotide formyltransferase and 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase). *In vivo* proof of principle study shown below: MiaPaCa-2 xenografts with WT multi C1 targets: Left panel (standard diet) vs Right panel (folate depleted diet):



Supported in part by R01 CA53535 and R44 221543 from the National Institutes of Health. The Animal Model and Therapeutics Evaluation Core was supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute and Wayne State University.

Acknowledgement Text:

Publications that result from Core involvement should include following statement:

“The Animal Model and Therapeutics Evaluation Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

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Mission of the Core:

The purpose of the Biobanking and Correlative Sciences (BCS) Core is three-fold: 1) the Biobank pillar facilitates peer reviewed, funded research activities requiring IRB-approved access to patient tissue, 2) the Clinical Correlates pillar facilitates clinical studies by reviewing protocols, managing tissue specimens and linking radiology and study biopsies back to CTO, and 3) the Correlative Sciences pillar assists Physicians, Epidemiologists and Basic Scientists with Preclinical Assays and study development.

Core Services Available:

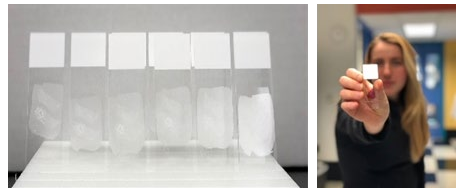
Biobanking

- Consenting patient for biobanking protocols
- Biospecimen acquisition and processing
- Biospecimen storage and quality control
- Consulting
 - Assistance with IRB protocol requirements and submission
 - Letters of support for grants
 - Annotation of biospecimens (ex. Race, ER/PR status, chemotherapy, etc.)



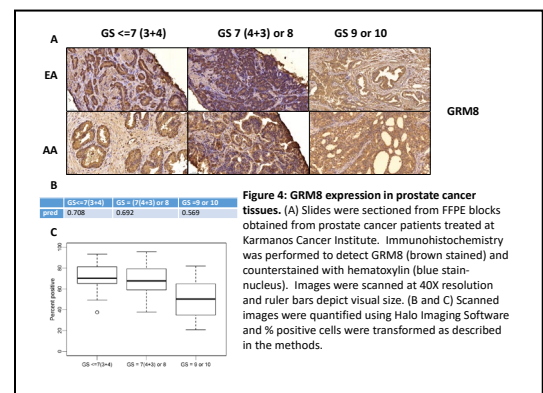
Clinical Correlates

- Protocol specific tissue retrieval for clinical trials
- Processing of tissue for clinical trials
- Pathologic verification and diagnosis of tissue
- IATA approved shipping of biospecimens
- Consulting
 - Assistance with the development of IITs
 - Flowsheet and laboratory manual (for IITs) construction based on clinical trial protocol

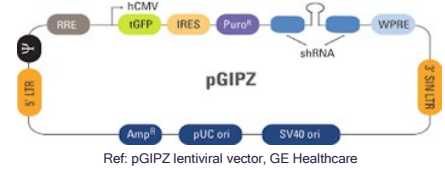
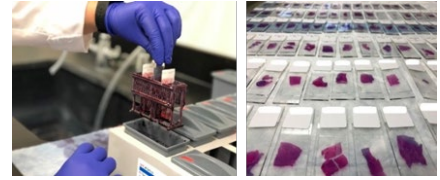


Correlative Sciences

- Authentication of cell lines and xenografts models using STR profile analysis
- Signed authentication reports for journal publications and grant reviews
- Protein expression and activation assays
 - Standard viability drug treatment assays
 - Cell survival and tumorigenesis assays
 - Detection of proteins in tissues (Westerns, immunohistochemistry)



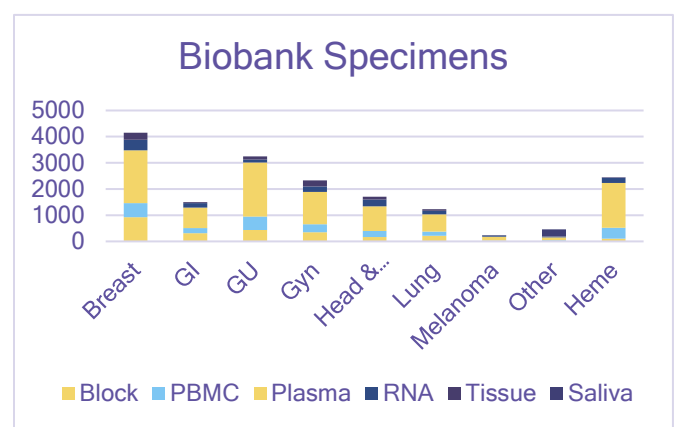
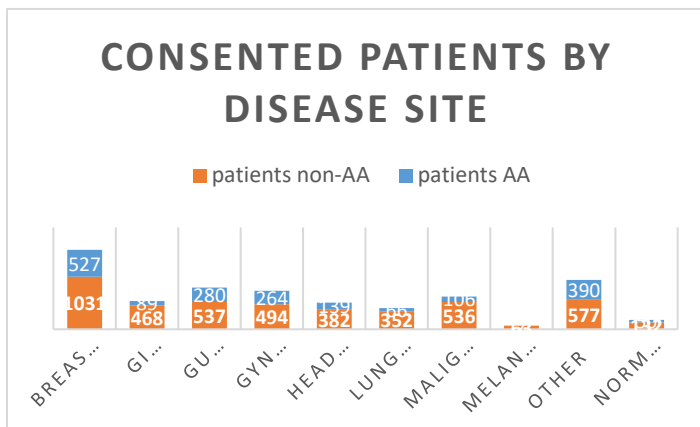
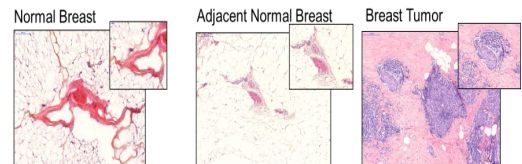
- Histology
 - Human and animal tissue processing
 - FFPE and frozen tissue sectioning
 - H&E and specialty stains
 - Immunohistochemistry
 - Tissue microarray construction
 - Slide scanning and IHC quantification
- Distribution of shRNA clones GIPZTM lentiviral shRNA (OpenBiosystem)
- Consulting
 - Assistance with protocol development
 - Letters of support of grants



Resources:

The BCS employs the following resources and instrumentation to provide quality services to KCI investigators and its affiliates:

- Growing inventory of biospecimens for research- tissue, blood, saliva, urine
 - Each specimen QC for tumor or normal tissue
 - <https://biobank.karmanos.org/> Biobank website with searchable interface and how to guides for requesting specimen tissue
- Leica DM5500B microscopy
- Syngene PXi imaging system
- Gel Count colony analysis
- Bio-Rad and Invitrogen SDS-PAGE systems
- Perkin-Elmer TMA Master
- Aperio slide scanner and HALO imaging software
- Reichert-Jung 2040 Autocut Microtome, Microm Hm 505E Cryostat, Fisher 166MP Automated Tissue Processor, Shannon Cytospin 2 Centrifuge
- The OpenBiosystems (Thermo-Fisher) human GIPZTM lentiviral shRNA library (maintained in *E.coli*), comprised of ~ 130,000 individual RNAi vectors that include 3-5 clones targeted for each human gene



Acknowledgement Text:

Publications that result from Core involvement should include following statement:

“The Biobanking and Correlative Sciences Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

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Mission of the Core:

The Biostatistics and Bioinformatics Core is a resource for KCI members in basic (*in vitro* and *in vivo*), clinical, population and translational sciences. Biostatistics is important in the design of cancer research studies to ensure that the scientific questions are framed so that they can be answered precisely and efficiently and in the analysis of these studies to ensure that the conclusions are accurate and valid. Bioinformatics is important to ensure computationally efficient and informative analyses.

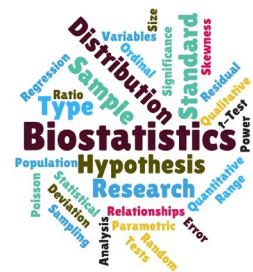
Core Services Available:

The work of the Core falls into four major categories: 1) development of grant proposals for peer reviewed, external funding, 2) design and protocol development of investigator-initiated clinical trials, 3) analysis of pilot studies, and 4) statistical analysis of data for publication. Specifically, members of the Core:

- Develop experimental designs for clinical, laboratory, intervention, and observational studies
- Conduct statistical and bioinformatic analyses and collaborate on interpretation of results
- Process raw genomic data (e.g., RNA-seq, exome sequencing) for use in statistical analyses
- Conduct downstream bioinformatics analyses, including pathway, differential expression, and network analyses
- Conduct statistical analyses of *in vivo*, clinical and epidemiologic data
- Write statistical reports and make statistical presentations
- Write statistical and bioinformatic sections for grant proposals and manuscripts in collaboration with investigators
- Provide instruction in biostatistics to cancer researchers in journal clubs, seminar series and grand rounds presentations
- Evaluate new and conventional statistical and bioinformatic methodology for applicability to cancer research projects and for application or adaptation of methods as required
- When current methods are inadequate, develop biostatistics and bioinformatics methods for specific cancer research projects

Resources:

Bioinformatics software includes ANNOVAR (annovar.openbioinformatics.org/), Bioconductor (www.bioconductor.org), GATK (gatk.broadinstitute.org), iPathwayGuide (www.advaitabio.com), iVariantGuide (www.advaitabio.com), Ingenuity (www.qiagen.com/us/) and Oncomine (oncomine.com), among others. The Core continuously reviews and updates processes to follow and maintain best practices when designing custom computational pipelines for all stages of bioinformatics analysis from data pre-processing to variant discovery. Statistical applications include general-purpose software R, SAS and Stata/MP. Software for calculating statistical power includes PASS and nQuery Advisor.



MS Windows based application software resides on a Dell PowerEdge 2950 III, which has two quad core Intel Xeon 5460 3.16 MHz processors, each with 2x6 MB cache, 32GB memory and two 300 GB disk drives and a Dell R820 with 4 Xeon E5-4650 2.70GHz processors, each with eight cores, 128GB memory, four 600GB and two 146GB disk drives. The backup unit is a 4 DAT drive running Veritas Backup Exec. Incremental backup of data files is performed nightly.

Full back-ups are performed weekly and the data tapes are maintained off-site in a secure, fireproof storage facility. Access to the server is restricted to members of the Biostatistics Core and authorized guests.

Linux based application software may be run on the Wayne State University high-performance grid system. The Wayne State University Grid is a tightly networked system of 400+ nodes and over 8000 processing cores.

Integrated into the Wayne State University high-performance grid computing facility are two PowerEdge R710 computers, each with 48GB RAM; dual 6 core Intel Xeon X5680 3.33 GHz processors and 1TB hard drives that run under the Linux operating system. Those computers were purchased by Karmanos for the use of Core members, but are accessible to other authorized Karmanos members whose research requires high performance computing capabilities.

The Core uses the Google Cloud Platform for computationally intensive analyses, analyses that require large memory, are highly distributed or CPU intensive, particularly pre-processing raw sequence data. Cloud resources will also be utilized for medium and long-term storage of raw data, processed data and associated procedures and pipelines. All third-party resources are HIPAA compliant.



Google Cloud Platform

Core Service Eligibility

- All KCI members
- Clinical fellows, post-doctoral fellows, residents and graduate students who conduct cancer research under the supervision of a mentor who is a KCI member

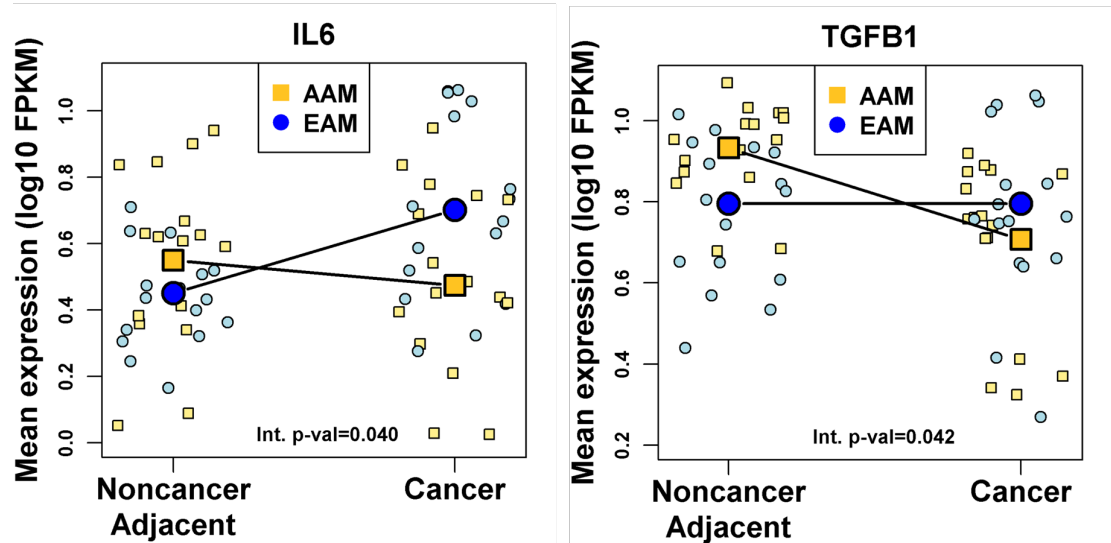
Guidelines for Lead Time

Researchers are encouraged to contact the Core early in the formulation of a research project to allow sufficient time for collaboration. Meaningful collaboration requires time for familiarization with research problems, communication, review of the literature in the particular research field, tailoring the appropriate statistical methods. Requests for statistical collaboration are addressed based on Core priorities and within a priority in the order in which they are received. Because requests for collaboration on grant proposals have the highest priority, the Core may be unable to respond immediately to other types of requests. It is recommended that researchers provide sufficient lead-time to Core members:

- **External grants:** two months before the grant is due at funding source
- **Abstracts:** one month before the abstract deadline

Research:

Teslow E et al. (2018) Exogenous IL-6 induces mRNA splice variant MBD2_v2 to promote stemness in TP53 wild-type, African American PCa cells. Mol Oncol.

**Acknowledgement Text:**

Publications that result from Core involvement should include following statement:

“The Biostatistics and Bioinformatics Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

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<https://www.karmanos.org/karmanos/cyclotron-pet-radiochemistry-core>



Mission of the Core:

The Cyclotron & Radiochemistry (C&R) Core is an FDA regulated facility responsible for research & development of novel PET radiotracers to advance early diagnosis and treatment of diseases.

Core Services Available:

- (A)NDA PET radiotracer routine manufacturing.
- Research PET radiotracer development, including novel radiotracers for preclinical animal imaging, Radioactive Drug Research Committee (RDRC) and Investigational New Drug (IND) study.
- PET radiotracers productions to meet preclinical and clinical needs.

Resources (Clinical):

- GE PETtrace 800 cyclotron for PET radioisotopes production, such as F-18, C-11, N-13 and O-15.
- cGMP compatible clean room for PET drug production and dose preparation.
- Four Comcer mini hot cells for PET drug synthesis and two vertical ISO 5 hot cells with manipulators and dose calibrators for dose preparation.
- Two GE Fastlab modules for FDG production.
- Capintec CRC-25 PET radioisotope dose calibrator.
- Rotem radiation monitoring system with multiple detectors.
- Comcer fume hood for QC test.
- Canberra multi-channel analyzer.
- EZ Radio-TLC scanner.
- Agilent 7890A gas chromatography.
- Hydrogen generator.
- Endosafe PTS pyrogen testing module.
- Thermo Heratherm incubation oven for sterility test.
- Ludlum model 375 hand and foot radiation monitor.
- Ludlum model 14C radiation monitor with pancake detector
- Millipore deionized water unit.
- Mettler Analytical Balance AE260.
- LabrepcO Futura refrigerator.
- Epson WF-6090 printer.



Resources (Research):

- Four Von Galen vertical hot cells for radiation shielding.
- Synthra MelPlus research module for C-11 radiotracer R&D.

- Synthra RNplus research module for F-18 radiotracer R&D.
- In-house built F-18/C-11 modules for research PET radiotracers production.
- Hydrogen generator for C-11 radiochemistry.
- Waters UPLC system with UV and NaI Rad detector.
- Bioscan AR-2000 Radio-TLC scanner with control computer and software.
- Endosafe PTS pyrogen testing module.
- Laminar flow hood for quality control test.
- Isotemp incubator for sterility test.
- VMware radiation monitoring system with multiple detectors.
- Three Capintec 712M control modules with ionization chambers.
- Capintec CAPRAC-R radiation counter.
- Ludlum model 14C radiation monitor with pancake detector
- Ludlum model 177 ratemeter with detector
- Millipore deionized water unit.
- Mettler AT261 analytical balance.
- Lexmark X656DTE printer.
- Epson WF-6090 printer.

Research:

Over 20 PET radiotracers have been developed and/or investigated in the C&R Core. Currently, the Core is focused on RDRC/IND research projects using [¹⁸F]FDG, [¹⁸F]FLT and its analogs, [¹¹C]AMT, [¹¹C]PK11195, [¹¹C]acetate, [¹⁸F]FMPEP-d2 and [¹⁸F]FETrp. Meanwhile, work is also in progress on novel radiotracers, such as [¹⁸F]TFAHA and [¹⁸F]Diabody, for animal microPET imaging. Table 1, below, lists the current radiotracers in production in the C&R Core.

Table 1. List of PET radiotracers in the C&R Core.

PET drugs	Target	Application
[¹⁵ O]H ₂ O	Blood flow, oxygen	Brain activation, heart
[¹⁵ O]O ₂	Brain oxygen utilization	Stroke, fMRI validation
[¹⁵ O]CO	Oxidative metabolism	Brown fat
[¹³ N]ammonia	Myocardial perfusion	Coronary artery disease
[¹⁸ F]FDG (2-[¹⁸ F]fluoro-2-deoxy-glucose)	Glucose metabolism	Epilepsy, heart, tumor
[¹⁸ F]FLT, [¹⁸ F]FAU, [¹⁸ F]FMAU, [¹⁸ F]FBAU, [¹⁸ F]FIAU, [¹⁸ F]FAG	DNA synthesis, thymidine analog	Tumor, epilepsy
[¹⁸ F]FMPEP-d2	Cannabinoid CB1 receptors	Depression, schizophrenia, and obesity
[¹⁸ F]TFAHA	Histone deacetylases IIa	Brain
[¹⁸ F]Diabody	Interferon-γ	Tumor
[¹⁸ F]FETrp (1-(2- ¹⁸ F-fluoroethyl)-L-tryptophan)	F-18 version AMT	F-18 version AMT
[¹¹ C]AMT (a-11C-methyl-L-tryptophan)	Serotonin synthesis, kynurenine pathway metabolism	Autism, epilepsy, migraine, Tourette syndrome, tumor
[¹¹ C]PK11195	Peripheral benzodiazepine receptors	Inflammation
[¹¹ C]acetate	Oxidative metabolism	Cardiomyopathy
[¹¹ C]HED, [¹¹ C]FMZ, [¹¹ C]DWAY, [¹¹ C]methionine, [¹¹ C]leucine, [¹¹ C]Doxepine	Sympathetic innervation, GABAA, protein synthesis 5HT1A, Histamine H1 receptors	Epilepsy, seizures, autism, brain development

Acknowledgement Text:

Publications that result from Core involvement should include following statement:

The Cyclotron & Radiochemistry (C&R) Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

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Epidemiology Research Core (ERC)

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Web: <https://www.karmanos.org/ERC>



Mission of the Core:

The Epidemiology Research Core (ERC) mission is to support population-based research by accessing Metropolitan Detroit Cancer Surveillance System (MDCSS) cancer cases and their data for use in approved research. The ERC provides epidemiology expertise and collaborates with researchers conducting investigations in cancer prevention, etiology, treatment and outcomes. This type of population-based cancer research is made possible by ERC accessing this data on behalf of researchers, which ensures confidentiality.

Core Services Available:

- Consultation. Consultation and collaborative research expertise focused on study design, proposal development, IRB applications, and interpretation of population-based local and national SEER data. (\$0.00)
(Free initially, but salary support for MDCSS-affiliated faculty with appropriate expertise is requested for ongoing funded projects.)
- Rapid Case Ascertainment. Rapid identification and ascertainment of eligible study participants, requiring review of all pathology reports indicating a cancer diagnosis at approximately 60 metropolitan area hospitals, clinics, pathology laboratories and radiation therapy facilities and rapid collection of patient demographic information. This speeds up case identification for population-based studies, with most cases identified within two to three months of diagnosis. (\$55.00/case)
- Control Identification. Identification of population-based control groups for case-control study designs via Centers for Medicaid and Medicare Services (CMS) records, Department of Motor Vehicles (DMV) records, and other mechanisms. (\$36.37/hour)
- Research Support and Training: Regulatory oversight and research training support of study staff involved in studies in which participants are being contacted. (\$53.43/hour)
- Collection and Abstraction of Medical Records. Collection of medical records and abstraction of study-specific data that are not available in the MDCSS registry. (\$51.64/hour)
- Biospecimen Collection. Collection of biologic specimens, including blood, buccal cells, saliva, urine and spirometry, from study participants and/or diagnosing hospitals including KCI and non-KCI facilities. (\$75.00/specimen)
- Tissue Retrieval. Collection of biologic tissue specimens, including tumor blocks and H&E stained slides and unstained slides from diagnosing hospitals including KCI and non-KCI facilities. Tumor Collection from KCI facilities is coordinated with the KCI Biorepository Core. (\$49.51/specimen)
- Database Query: Response to requests for population-based data requiring query of the MDCSS and/or the national SEER de-identified research data files for descriptive analyses. (\$49.00/hour)
- Database Linkage. Linkage of outside data sources to MDCSS data for the collection of patient demographics, treatment and survival data. Use of the linked SEER-Medicare files is included in this service line. (\$49.00/hour)

Resources:

The MDCSS data system contains all cancer diagnosis and survival information for the Metropolitan Detroit area from 1973 forward, housed in the SEER Data Management System (SEER*DMS). SEER*DMS is a relational database that supports central cancer registry operations and includes features for importing, editing, consolidating, exporting and reporting on cancer-related data. This database currently houses data on in excess of 1,060,000 patients and 1,200,000 cancers. In addition, ERC analyst(s) have access to the national de-identified SEER Research data, as well as Statistical Analysis System (SAS©) and ArcGIS© softwares.

Research:

The Epidemiology Research Core (ERC) supports a broad array of research. Set forth below are selected projects currently being supported by the ERC.

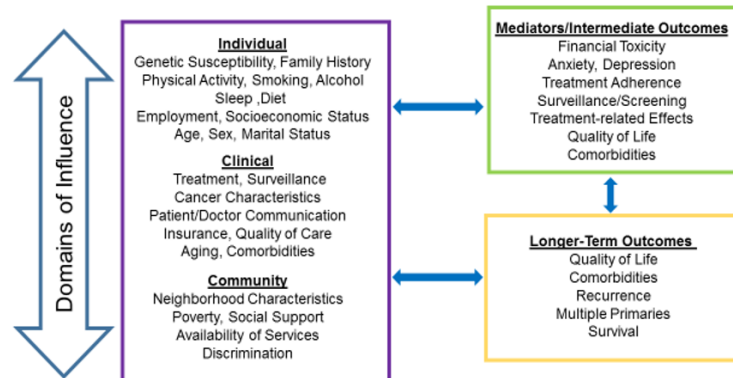
The Detroit Research on Cancer Survivorship (ROCS) study PIs: Schwartz A. and Beebe-Dimmer J., NCI 2U01 CA199240, (03/01/2022-02/28/2027)



There are an estimated 15.5 million cancer survivors in the US so that understanding the unique issues cancer survivors face is essential. African Americans (AA) with cancer experience the highest death rate and shortest survival for most cancers. The Detroit ROCS study is the largest case cohort of AA cancer survivors with over 5,000 patients diagnosed with female breast, prostate, colorectal, lung,

endometrial, and any cancer diagnosed under the age of 50 enrolled. In addition, 1,000 patient caregivers have been enrolled in a separate cohort. Case participants complete an enrollment survey and annual surveys for up to 9 years, and caregiver participants complete an enrollment survey and a follow-up survey. Blood and tumor specimens are collected and banked for projects focused on germline genetics, plasma biomarkers, and tumor molecular profiling. Addresses at each survey are geocoded and linked to several area-based measures of poverty and environmental exposures.

Research Framework



More information on the study, including an on-line form for researchers to request data, can be found at the following website: <https://www.detroitrocs.org/>

The **Epidemiology Research Core** supports this project with Rapid Case Ascertainment (RCA), Database Query, Database Linkage, Research Support and Training (RST), Biospecimen Collection, and Tissue Retrieval.

Disparities and Cancer Epidemiology (DANCE) Study

MPIs: Purrington K., Rozek L.*, Stoffel E. *, NCI R01CA259420, (06/01/21 - 05/31/26)

*University of Michigan



The overall goal of the study is to identify genomic and social factors associated with colorectal (CRC) pathogenesis in African American and non-Hispanic White CRC cases from Detroit, MI and Louisiana. We hypothesize that tumor biology, here defined by somatic and epigenetic alterations in tumors, explains a substantial proportion of the racial disparities in CRC outcomes, and area-level factors modify this relationship. Our long-term goal is to improve our ability to diagnose, treat and prevent CRC through a comprehensive understanding of the molecular events in tumors that arise in diverse populations.

The **Epidemiology Research Core** supports this project with Database Query, Research Support and Training (RST), Biospecimen Collection, and Tissue Retrieval.

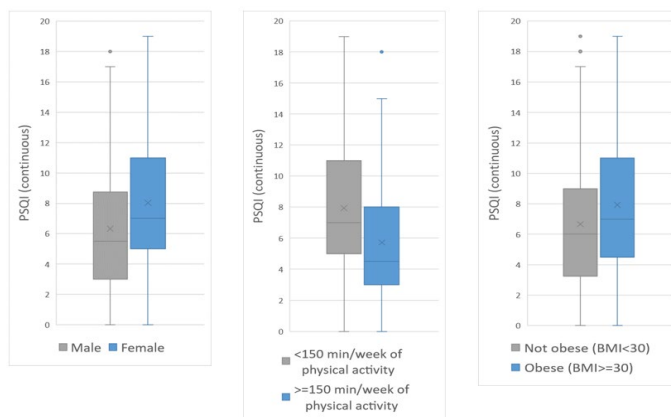
Sleep Health in African American Cancer Survivors: A Focus on Outcomes

PI: Beebe-Dimmer, J, U01CA199240-04 (2/1/20 - 1/31/22)



Sleep disturbances are relatively common in cancer survivors (and their caregivers) and can include delayed sleep onset and frequent waking during the night, reducing overall sleep time. These sleep disturbances correlate with fatigue, can exacerbate existing or cause depression, and negatively impact health related quality of life. This study added a sleep questionnaire to the ROCS survey at both enrollment and follow-up to examine association between sleep quality and reported anxiety, depression, quality of life, health behaviors, and financial hardship. In addition, among a subset of those who complete the sleep questionnaire, measures of sleep quality will be collected from a wearable actigraph monitor to address the validity of self-reported data.

Pittsburgh sleep quality index (PSQI) stratified by select variables among ROCS cancer survivors.



*Higher PSQI scores indicate poorer sleep quality

To date, we have collected sleep questionnaire data on 1,391 ROCS case participants (388 at enrollment and 1,003 at follow-up) along with actigraphy data from 53 survivors. We have also collected sleep questionnaire data on 91 caregivers. Preliminary analyses show that there are significant differences in the quality of sleep reported by demographic variables as well as health behaviors. When looking at the associations between health-related quality of life (HRQOL) and different variable groups (sleep quality, health behaviors, comorbidities, demographics, and cancer characteristics), sleep quality explained the most variability in HRQOL.

The **Epidemiology Research Core** supports this project with Database Query and Research Support and Training (RST).

Acknowledgement Text:

Publications that result from Core involvement should include following statement:

“The Epidemiology Research Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

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Starting at Top Left: Terri Essex, Julie Ruterbusch, Terry Smith, Jaclyn Kyko, Sharon Moton, Jennifer Beebe-Dimmer, Ron Shore, Tara Baird, Angie Bernat, Randell Seaton, and Arkeshia Barnes

Microscopy, Imaging, and Cytometry Resources Core (MICR)

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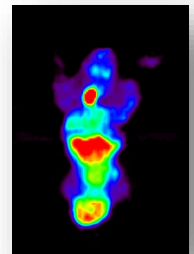


Mission of the Core:

The mission of the Microscopy, Imaging & Cytometry Resources (MICR) core is to enhance the peer reviewed funded research activities of KCI members whose research requires confocal microscopy, flow cytometry, small animal imaging and related techniques. We provide KCI members with expert scientific consultation and access to state-of-the-art instrumentation.

Core Services Available:

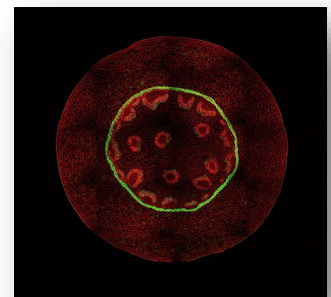
- Confocal Microscopy, including both point scanning and spinning disk technologies
- Multiphoton Microscopy, including Second Harmonic Generation imaging
- Conventional, widefield epifluorescence
- Optical sectioning using Structured Illumination (via the Zeiss ApoTome system)
- In vivo small animal SPECT/CT
- In vivo small animal and large animal PET/CT
- In vivo small animal X-Ray, fluorescence, and bioluminescence imaging
- In vitro and in vivo X-Ray Irradiation
- Multi-parameter Flow Cytometry (both traditional and spectral)
- Cell Sorting
- Imaging Cytometry
- Advanced Data Analysis, including 3D and 4D image reconstruction and quantitative measurements
- Expert consultation, including advice on application choice and experimental design
- Instrument-specific training for users as well as workshops on data analysis and advanced techniques
- Grant collaboration and assistance with application preparation



Resources:

Microscopy

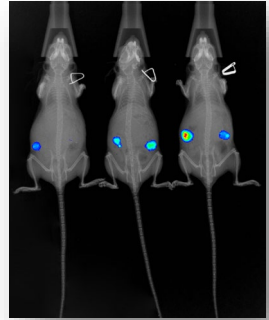
- Zeiss LSM-800 Laser Scanning Confocal microscope with Airyscan Super Resolution detector
- Zeiss LSM-780 Laser Scanning Confocal
- Zeiss LSM-510 META NLO MP Laser Scanning Confocal microscope
- Leica TCS SP5 MP Laser Scanning Confocal microscope
- Leica TCS SP8 Laser Scanning Confocal microscope
- Zeiss Cell Observer Spinning Disk Confocal microscope
- Leica DMI8 inverted epifluorescence microscope
- Incucyte Live-Cell Analysis System
- Andor Dragonfly Spinning Disk Confocal microscope
- Zeiss LSM-410 Laser Scanning Confocal microscope
- Zeiss ApoTome Structured Illumination microscopes (2)



- Zeiss Axiovert inverted epifluorescent microscope

In Vivo Imaging

- Siemens Inveon SPECT/CT
- Bruker Albira 2-ring uPET/CT
- Bruker *In Vivo* Xtreme
- Bruker MS FX Pro
- GE Discovery LS4 large animal PET/CT
- Precision X-Ray XRAD 320 Irradiator



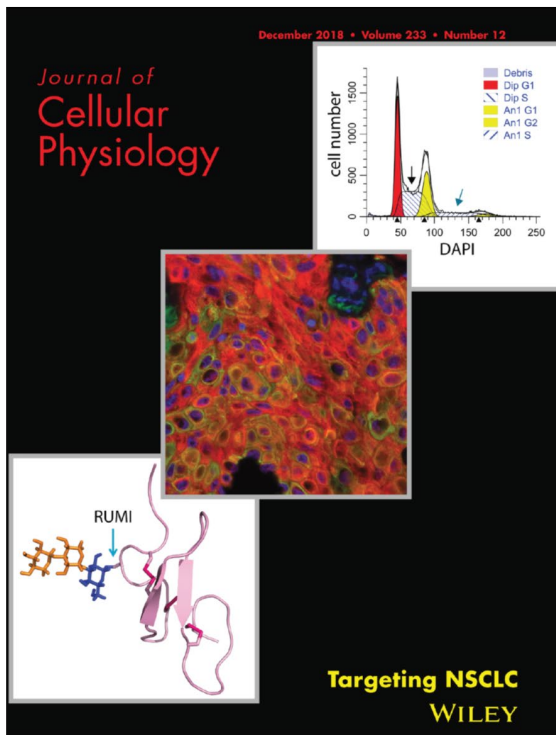
Cytometry

- Cytek Northern Lights Spectral Cytometer
- BD LSR II SORP
- BD FACSCanto II
- Sony SY3200 Cell Sorter
- Sony SH800 Cell Sorter (2)
- Amnis ImageStream^X MarkII Imaging Cytometer

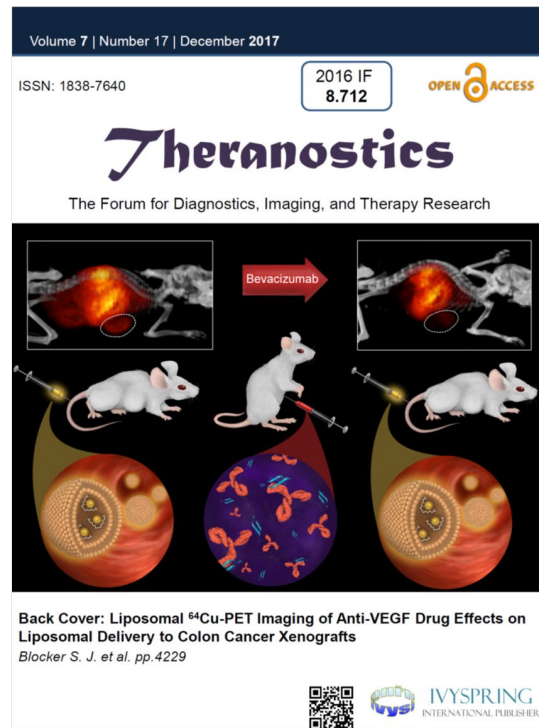
Supporting equipment

- Molecular Imaging Portal (MIP), a high capacity image server module
- Computer workstations with analytical imaging and cytometry software (Velocity and SVI)
- In-house cell culture facility

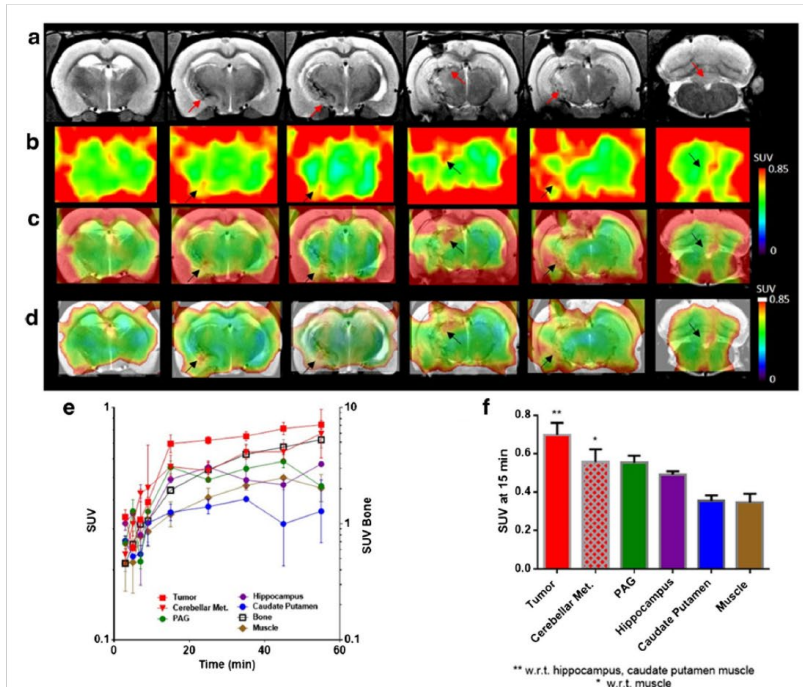
Research:



Chammaa, et al. *J Cell Physiol.* 2018;233:9548–9562
 Funding: 11-053-01-IRG
 14-238-04-IRG



Funding: T32-CA009531



a T2-weighted MR image sliced coronally through the 9L glioma lesion and hippocampus with red arrows indicating areas of tumor lesion. **b** Dynamic PET images at 15-min post administration of 12-[¹⁸F]DDAHA NIH lookup table (LUT). **c** Dynamic PET images post administration of 12-[¹⁸F]DDAHA overlaid onto T2-weighted MR images using the NIH LUT. **d** The same images as in **c**, but with the NIH + white LUT, to better visualize the internal structures due to the high degree of defluorination occurring, which is seen as F-18 accumulation in the bone causing a "halo" effect around the cortical region due to partial volume effect of bone signal into cortex. **e** Time activity curves for each region of interest within the brain over 60 min of dynamic PET images displayed as long (SUV) vs time. The error bars represent standard deviation of the voxel values within each ROI. **f** A visual representation of differential washout between tumor and other regions of the brain at 15-min post i.v. administration of 12-[¹⁸F]DDAHA, where error bars represent standard deviations and * or ** represent $P < 0.05$ as found from one-way ANOVA.

Bonomi, et al. *Mol Imaging Biol* (2018) 20:594-604

Acknowledgement Text:

Publications that result from Core involvement should include following statement:

"The Microscopy, Imaging, and Cytometry Resources Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute and NIH R50 CA251068 to Dr. Moin at Wayne State University."

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Mission of the Core:

To provide state-of-the-art bioanalytical technology and a broad range of pharmacology and metabolomics expertise to support basic, translational, and clinical research.

Core Services Available:

The Pharmacology and Metabolomics Core offers the following services based on fee-for-service:

- **Biospecimen Processing** service provides a centralized resource for the acquisition, processing, and shipment of patient specimens that are required for evaluation of pharmacokinetics or pharmacodynamics according to clinical protocol specifications. All specimens are collected from patients who provided informed consent following an Institutional Review Board approved protocol. Specimen handling, processing, and shipment are in compliance with good laboratory practice procedures, approved standard operating procedures, and regulatory requirements to ensure sample integrity and quality. A secure database that includes detailed information on the acquisition, processing, distribution of samples, along with related clinical data, is maintained.
- **Bioanalysis service** provides development, validation, and implementation of liquid chromatography coupled with tandem mass spectrometer (LC-MS/MS) based analytical methods for quantitative determination of drugs and their metabolites as well as endogenous chemicals (metabolites) in biological samples (including biofluid, tissue, cell culture samples). Method validation is provided based on the United States Food and Drug Administration Guidance for Bioanalytical Method Validation to ensure that a particular method is specific, sensitive, reliable, reproducible, and suitable for the intended analytical use. Rigorous quality assurance and quality control are provided for the analyses of clinical and preclinical samples. The list of established LC-MS/MS methods for quantitation of drugs and their metabolites is presented in **Table 1**.
- **LC-MS/MS based targeted metabolomics** enables quantitative determination of ~ 300 small molecule endogenous metabolites that are involved in major human metabolic pathways, including but not limited to, glycolysis, pentose phosphate pathway, tricarboxylic acid cycle, one-carbon metabolism, as well as amino acid and nucleotide metabolism. **Table 2** summarizes the major metabolic pathways (classes) measured by our targeted metabolomics platform. **Table 3** lists the individual metabolites measured by the targeted metabolomics platform.
- **Metabolic flux analysis** applies LC-MS/MS or high-resolution LC-MS to determine the metabolite labeling patterns from stable isotope-labeled tracers (e.g., [1,2-¹³C]glucose, [U-¹³C]glucose, [U-¹³C]glutamine, [2,3,3-²H]Serine), which can reveal metabolic pathway activities and determine the contribution of specific metabolic pathways to the prevailing levels of particular metabolites.

In addition, the Core provides a broad range of pharmacology support including:

- **PK study design** provides the design of PK studies in clinical trials and preclinical studies.
- **PK data analysis and modeling** provides traditional compartmental and non-compartmental analysis, nonlinear mixed-effect (population) PK modeling, and physiologically based pharmacokinetic modeling for characterization of PK profiles, determination of dose-exposure-response relationship, and optimization of dosing regimens.

- **In vitro pharmacology** provides assays for determination of in vitro drug metabolism (enzyme identification, inhibition and induction, metabolite identification), drug protein/tissue binding, and drug transporters.

Table 1 The list of established LC-MS/MS methods for quantitation of drugs and their metabolites

Assay #	Drugs, Metabolites	Assay #	Drugs, Metabolites
1	AG127	23	Irinotecan, SN-38, SN-38G
2	Aminoflavone, AFP464	24	Isoflavones (Daidzein, Genistein)
3	AZD1775	25	Lapatinib
4	Betulinic acid	26	Methotrexate, DAMPA
5	Carboplatin	27	Pazopanib
6	CDF (difluorinated-curcumin)	28	Phenylethylamine
7	Ceritinib	29	Ribociclib
8	Combretastatin A4	30	RO4929097
9	Compound #9 (Rad6 inhibitor)	31	Sertaline, Venlafaxine
10	CP-1	32	Sorafenib
11	Cu27	33	Temozolomide, AIC
12	CuDDSF2	34	Thiourea
13	Curcumin	35	Tunicamycin A
14	Decetaxel	36	UTL-5g, DCA, ISOX
15	Dexamethasone	37	Veliparib, M8
16	Hydroxyflavone (di, tri, and tetra-)	38	Pamiparib
17	DIM (Diindolmethane)	39	Tucatinib
18	Erlotinib	40	Neratinib
19	Everolimus	41	Abemaciclib
20	FAU, FMAU	42	Ribociclib
21	Gefitinib	43	Pabociclib
22	HBC (Hydrazinobenzoylcurcumin)	44	Olaparib

Table 2: Typical metabolic pathways and classes covered by the targeted metabolomics platform*

Classes or Pathways	Number of Metabolites Determined
Glycolytic, TCA cycle, and pentose phosphate pathway	25
Nucleosides, nucleotides and NAD-related metabolites	40
Amino acid and related metabolites	60
Acyl CoAs	10
Acyl Carnitines	20
Bile acids	15
Ceramides	10
Steroids	10
Short chain fatty acids	8
Phospholipids	15
Gut microbial related metabolites	15
Miscellaneous Metabolites	65
Total	293

*Typical metabolites measured are listed above but the capacity is not limited to these. Assays can be tailored to investigators' needs.

Table 3 The list of metabolites measured by the targeted metabolomics platform

ID	Metabolite name	Calibration curve range
M001	M001_Tryptophan	0.01 - 10
M002	M002_L-kynurenine	0.01 - 10
M003	M003_Serotonin	0.01 - 5
M004	M004_5-Hydroxyindoleacetic acid (5'-HIAA)	0.01 - 10
M005	M005_Kynurenic acid	0.01 - 1
M006	M006_Quinolinic acid	0.2 - 10
M007	M007_Cis aconitic acid	0.02 - 2
M008	M008_Succinic acid	0.5 - 5
M009	M009_Fumaric acid	0.5 - 10
M010	M010_DL-isocitric acid	0.1 - 5
M012	M012_L-malic acid	0.02 - 5
M013	M013_Succinyl coenzyme A	0.01 - 10
M015	M015_Acetyl coenzyme A	0.01 - 10
M016	M016_α- ketoglutaric acid	0.1 - 10
M019	M019_fructose 6-phosphate	0.01 - 2
M020	M020_D-fructose 1,6-bisphosphate	0.02 - 0.5
M021	M021_D(+) 2 phosphoglyceric acid	0.01 - 10
M022	M022_Phosphoenolpyruvic acid(s)	0.2 - 10
M023	M023_DL-Valine	0.01 - 2
M024	M024_DL-Leucine (s)	0.01 - 1
M025	M025_DL-Histidine	0.01 - 1
M026	M026_DL-Phenylalanine	0.01 - 10
M027	M027_DL-Glutamine	0.02 - 10
M028	M028_DL-Tyrosine	0.01 - 10
M029	M029_DL-Isoleucine (s)	0.1 - 10
M030	M030_DL-Threonine (s)	0.05 - 1
M031	M031_DL-Glutamic acid	0.02 - 2
M032	M032_DL-Arginine	0.01 - 0.5
M033	M033_DL-Lysine(s)	0.02 - 0.5
M034	M034_S-Adenosyl-L-methionine	0.02 - 2
M035	M035_Dihydroxyacetone phosphate	0.05 - 1
M036	M036_2-Picolinic acid	0.01 - 10
M038	M038_Palmitic acid	0.5 - 5
M039	M039_NADP+ (Nicotinamide adenine dinucleotide phosphate, oxidized)	0.02 - 10
M041	M041_NAD+ (Nicotinamide adenine dinucleotide, oxidized)	0.01 - 1
M043	M043_3'-Dephosphocoenzyme A	0.05 - 10
M046	M046_DL-3-hydroxy-3- methyl glutaryl -CoA	0.01 - 10
M047	M047_Nicotinamide	0.01 - 5
M048	M048_S-Aminoimidazole-4-carboxamide 1-B-D-ribofuranosyl 5-monophosphate (Aminoimidazole-4-carboxamide)	0.01 - 5
M049	M049_S-5'-adenosyl-L- homocysteine	0.01 - 10
M050	M050_2-Deoxyribose -5-phosphate	0.01 - 2
M051	M051_Alpha D-glucose 1- phosphate	0.01 - 0.5
M052	M052_dUMP (deoxyuridine monophosphate)	0.01 - 5
M054	M054_Hypoxanthine	0.01 - 2
M055	M055_D-ribose 5- phosphate	0.01 - 2
M056	M056_Glutathione	0.01 - 10
M057	M057_D-gluconate	0.01 - 2
M058	M058_Uric acid (s)	0.01 - 2
M062	M062_1-Methyl-Histidine	0.01 - 1
M063	M063_1-Methylnicotinamide	0.01 - 2
M064	M064_2,5-dihydroxybenzoic acid (2,5-DHBA)	0.2 - 10

M065	M065_2-deoxycytidine	0.01 - 2
M068	M068_2-ketohexanoic acid	0.05 - 5
M069	M069_5-methoxytryptophan	0.01 - 10
M070	M070_Acetyl-DL-carnitine	0.01 - 10
M071	M071_Acetyllysine	0.01 - 2
M072	M072_aconitate	0.02 - 2
M073	M073_adenosine	0.01 - 1
M074	M074_adenosine-5-diphosphoribose	0.01 - 2
M075	M075_ADP (adenosine 5'-diphosphate)	0.01 - 2
M076	M076_Agmatine	0.02 -0.5
M077	M077_Aminoadipic acid	0.05 - 2
M078	M078_aminolevulinic acid	0.1 - 10
M079	M079_AMP (adenosine 5'-monophosphate)	0.01 - 10
M080	M080_Biotin	0.01 - 10
M082	M082_Butrylcholine	0.01 - 1
M083	M083_carnitine	0.01 - 2
M084	M084_Chlorzoxazone	0.5 - 10
M085	M085_Citraconic acid	0.1 - 10
M086	M086_citrulline	0.01 - 10
M087	M087_CMP (cytidine 5'-monophosphate)	0.01 - 10
M089	M089_cytosine	0.01 - 0.5
M090	M090_dAMP (deoxyadenosine monophosphate)	0.01 - 10
M091	M091_Dehydro-L-(+)-ascorbic acid	0.5 - 5
M092	M092_deoxyinosine(s)	0.1 - 2
M093	M093_deoxyuridine	0.1 - 10
M096	M096_DL-2-Aminocaprylic acid (2-Aminooctanoic acid)	0.01 - 10
M097	M097_DL-Glyceraldehyde-3-phosphate (s)	0.05 - 2
M099	M099_FAD:flavin adenine dinucleotide	0.01 - 10
M100	M100_Flavone	0.01 - 10
M101	M101_Folic acid	0.01 - 2
M103	M103_Gluconic acid	0.05 - 1
M105	M105_glucosamine	0.02 - 2
M106	M106_glucose-6-phosphate	0.01 - 2
M107	M107_glucuronic acid	0.01 - 2
M108	M108_Glycerate	0.5 - 10
M109	M109_GMP (guanosine 5'-monophosphate)	0.05 - 10
M112	M112_Guanidoacetic acid	0.05 - 5
M113	M113_guanine	0.01 - 10
M114	M114_guanosine	0.01 - 10
M117	M117_homoserine(s)	0.01 - 5
M118	M118_Hydroxyisocaproic acid	0.01 - 10
M119	M119_Hydroxyphenylacetic acid	0.2 - 10
M121	M121_Imidazole	0.02 - 2
M122	M122_Imidazoleacetic acid	0.01 - 2
M123	M123_IMP (inosine 5'-monophosphate)	0.02 - 1
M124	M124_indole	0.1 - 10
M125	M125_Indole-3-carboxylic acid	0.01 - 10
M126	M126_Indoleacrylic acid	0.01 - 10
M127	M127_lipoate	0.2 - 5
M128	M128_L-Pipecolic acid(s)	0.02 - 5
M129	M129_Methionine sulfoxide	0.01 - 10
M131	M131_N-acetyl-aspartate	0.02 - 1
M132	M132_N-acetyl-glucosamine	0.01 - 1
M133	M133_N-Acetyl-L-alanine(s)	0.02 - 10

M134	M134_N-acetyl-L-ornithine	0.01 - 2
M137	M137_Niacin (Vitamin B3)	0.01 - 2
M138	M138_NMDA (N-Methyl-D-aspartic acid)	0.05 - 1
M139	M139_O-Acetyl-L-serine	0.1 - 2
M140	M140_ornithine	0.01 - 0.5
M141	M141_Orotate	0.02 - 5
M142	M142_oxaloacetate	0.02 - 10
M143	M143_pantothenic acid	0.01 - 10
M144	M144_Perfluoroheptanoic acid	0.01 - 5
M145	M145_Phenyllactic acid	0.05 - 10
M146	M146_Phenylpropionic acid	0.05 - 10
M147	M147_Phenylpyruvate	0.1 - 10
M149	M149_p-hydroxybenzoate (4-hydroxybenzoic acid)	0.05 - 10
M150	M150_proline	0.05 - 2
M151	M151_purine	0.01 - 10
M152	M152_pyridoxal 5'-phosphate	0.01 - 5
M153	M153_Pyridoxamine (s)	0.01 - 0.5
M154	M154_pyridoxine	0.01 - 1
M155	M155_Pyroglutamic acid(s)	0.1 - 2
M157	M157_riboflavin-5-monophosphate	0.2 - 10
M158	M158_shikimate	0.05 - 5
M160	M160_sorbitol	0.1 - 5
M161	M161_taurine	0.02 - 10
M162	M162_thiamine	0.01 - 10
M163	M163_thymidine	0.01 - 1
M164	M164_thymine	0.01 - 5
M166	M166_UDP-N-acetylglucosamine (uridine diphosphate-N-acetylglucosamine)	0.01 - 10
M167	M167_UMP (uridine 5'-monophosphate)	0.01 - 2
M168	M168_uracil	0.01 - 10
M169	M169_uridine	0.01 - 2
M170	M170_xanthine	0.01 - 5
M171	M171_Xanthosine	0.01 - 5
M172	M172_Xanthosine 5'-monophosphate	0.05 - 5
M173	M173_Xanthurenic acid	0.01 - 2
M174	M174_ATP (adenosine triphosphate)	0.05 - 5
M175	M175_CTP (cytidine 5'-triphosphate) (s)	0.5 - 10
M176	M176_GTP (guanosine triphosphate)	0.05 - 5
M177	M177_UTP (uridine triphosphate)	0.02 - 5
M178	M178_dATP (deoxyadenosine triphosphate)	0.01 - 10
M179	M179_dCTP (deoxycytidine triphosphate)	0.01 - 10
M180	M180_dGTP (deoxyguanosine triphosphate)	0.05 - 2
M181	M181_dTTP (deoxythymidine triphosphate)	0.01 - 5
M182	M182_L-cysteine	0.1 - 1
M183	M183_L-Alanine	0.5 - 10
M183	M183_L-Alanine(s)	0.5 - 10
M184	M184_L-Asparagine	0.1 - 10
M185	M185_Glycine	0.5 - 10
M186	M186_L-Aspartic acid	0.01 - 1
M187	M187_Argininosuccinic acid	0.01 - 2
M188	M188_Sarcosine(s)	0.2 - 10
M189	M189_Dimethylglycine+M191	0.01 - 1
M190	M190_Betaine	0.05 - 5
M191	M191_Choline	0.01 - 1

M192	M192_Cystathionine	0.01 - 1
M194	M194_Urea	0.02 - 1
M195	M195_Cytidine	0.01 - 2
M196	M196_CDP (cytidine diphosphate)	0.01 - 5
M197	M197_GDP (guanosine diphosphate)	0.02 - 10
M198	M198_UDP (uridine diphosphate)	0.01 - 10
M199	M199_5'-Deoxyadenosine+M268+M092	0.02 - 2
M200	M200_dCMP (deoxycytidine monophosphate)	0.01 - 2
M201	M201_dCDP (deoxycytidine diphosphate)	0.01 - 10
M202	M202_dGMP (deoxyguanosine monophosphate)	0.05 - 10
M203	M203_dGDP (deoxyguanosine diphosphate)	0.05 - 10
M204	M204_dTMP (deoxythymidine monophosphate)	0.01 - 5
M205	M205_dTDP (doxythymidine diphosphate)	0.01 - 10
M206	M206_UDP-glucose (uridine diphosphate-glucose)	0.01 - 2
M207	M207_ADP-glucose (adenosine 5'-diphosphate-glucose)	0.01 - 1
M211	M211_Maleic acid	0.1 - 10
M214	M214_Methylmalonic acid	0.1 - 2
M216	M216_Anthranilic acid	0.01 - 10
M217	M217_4-Aminobenzoic acid	0.01 - 5
M219	M219_a-keto-4-methylthio-2-oxobutanoate	0.02 - 10
M220	M220_2,3-Dihydroxybenzoic acid	0.01 - 10
M221	M221_DL-Dihydroorotic acid	0.01 - 2
M224	M224_4-Pyridoxic acid	0.01 - 1
M225	M225_2-keto-D-gluconic acid	0.01 - 2
M226	M226_D-Erythrose 4-phosphate	0.01 - 2
M227	M227_D-Glucarate	0.05 - 2
M228	M228_Inosine	0.01 - 2
M229	M229_D-Sedoheptulose-1-7-phosphate	0.01 - 1
M230	M230_N-Acetyl-glucosamine-1-phosphate	0.01 - 2
M231	M231_Cyclic AMP (cyclic adenosine monophosphate)	0.01 - 2
M232	M232_Sucrose	0.01 - 5
M238	M238_Thiamine diphosphate	0.05 - 10
M239	M239_Adenosine 5'-phosphosulfate	0.01 - 10
M241	M241_Cholesteryl sulfate	0.01 - 10
M242	M242_Cytidine-5'-diphosphocholine	0.01 - 10
M243	M243_Taurodexoycholate	0.01 - 2
M245	M245_Coenzyme A	0.1 - 10
M246	M246_n-Propionyl Coenzyme A	0.01 - 10
M247	M247_DL-3-hydroxybutyryl CoA	0.01 - 5
M248	M248_L-alpha-hydroxyglutaric acid	0.01 - 2
M249	M249_Ethanlamine	0.01 - 1
M251	M251_4-Aminobutyric acid	0.01 - 2
M254	M254_Creatinine	0.01 - 1
M255	M255_Creatine(s)	0.01 - 1
M256	M256_N-Acetylputrescine	0.01 - 1
M257	M257_Trans-4-hydroxy-L-proline(s)	0.02 - 5
M258	M258_Adenine	0.02 - 10
M259	M259_L-homocysteine	0.05 - 2
M260	M260_L-histidinol	0.01 - 1
M262	M262_Phosphocholine	0.02 - 1
M263	M263_3-Phospho-L-serine	0.5 - 10
M264	M264_N-Acetyl L-glutamine	0.01 - 2
M265	M265_N-Acetyl L-glutamic acid	0.01 - 5
M266	M266_N ^G , N ^G -Dimethyl arginine	0.01 - 2

M267	M267_L-Cystine	0.02 - 1
M268	M268_2'-Deoxyadenosine(s)	0.01 - 1
M269	M269_Acadesine	0.01 - 10
M271	M271_7-Methylguanosine	0.01 - 1
M272	M272_Beta-nicotinamide mononucleotide	0.01 - 5
M273	M273_Riboflavin	0.01 - 10
M276	M276_3,5-Diiodo-L-thyronine	0.01 - 2
M277	M277_Putrescine	0.01 - 0.5
M278	M278_Spermidine	0.01 - 0.5
M279	M279_Spermine	0.01 - 1
M280	M280_Acetone	0.2 - 10
M281	M281_Alpha-Hydroxyisobutyric acid	0.01 - 10
M282	M282_4-Hydroxyphenyl acetic acid	0.01 - 10
M283	M283_APCI_7-Dehydrocholesterol	0.01 - 10
M284	M284_Chenodeoxycholic acid as M294 Hyodeoxycholic acid M303	0.02 - 1
M285	M285_APCI_Cholesterol	
M286	M286_APCI_Cholesterol	0.01 - 10
M287	M287_APCI_Coprostan-3-ol	
M288	M288_APCI_Desmosterol	0.01 - 10
M289	M289_Dimethylamine	0.05 - 2
M290	M290_Glycocholic acid	0.01 - 10
M291	M291_Glycoursodeoxycholic acid +M297 Glycodeoxycolic acid+M313	
M291	Glycochendeoxychlate	0.01 - 10
M293	M293_Hippurate	0.01 - 10
M294	M294_Hyodeoxycholic acid same as M284_Chenodeoxycholic acid M303	0.02 - 1
M295	M295_APCI_Lanosterol	0.01 - 10
M296	M296_APCI_Lathosterol	
M297	M297 Glycodeoxycolic acid+M313 Glycochendeoxychlate	0.01 - 10
M298	M298_Stigmasterol	0.01 - 10
M299	M299_Taurochenodesoxycholic acid	0.01 - 10
M300	M300_Taurocholic acid	0.01 - 10
M302	M302_Taurolithocholic acid	0.01 - 10
M303	M303_Ursodeoxycholic acid_ss	0.01 - 10
M304	M304_Campesterol	0.01 - 5
M305	M305_3-Phosphoglyceric acid	0.01 - 10
M306	M306_Thiamine monophosphate	0.01 - 10
M307	M307_2'-Deoxyguanosine	0.01 - 10
M308	M308_Malonyl CoA	0.05 - 1
M309	M309_R-2-Hydroxy-2-phenylpropionic acid	0.2 - 10
M310	M310_D-Citramalic acid	0.01 - 2
M311	M311_L-Homocysteic acid	0.01 - 2
M312	M312_Serine	0.02 - 10
M313	M313 Glycochendeoxychlate + M297 Glycodeoxycolic acid	0.01 - 10
M314	M314_CDP-ethanolamine	0.01 - 10
M315	M315_p-cresyl sulfate	0.01 - 10
M316	M316_Glycolithocholic acid	0.01 - 10
M317	M317_Dihydro thymine	0.01 - 0.2
M318	M318_Alpha-N-Phenylacetyl- L-glutamine	0.01 - 10
M319	M319_N-Phenylacetyl glycine	0.01 - 10
M322	M322_06:0 Lyso PC	0.01 - 10
M323	M323_14:0 Lyso PC	0.01 - 10
M324	M324_16:0 Lyso PC	0.01 - 10
M325	M325_18:0 Lyso PC	0.01 - 10
M327	M327_Lithocholic acid	0.01 - 10

M328	M328_Linoleyl Carnitine	0.01 -10
M329	M329_C5:0 Carnitine (Valeryl-L carnitine)	0.01 -10
M330	M330_C12:0 Carnitine (Lauroyl-L carnitine)	0.01 -10
M331	M331_C16:0 Carnitine (Palmitoyl-L carnitine)	0.01 -10
M332	M332_18:1 Lyso PC	0.01 -10
M333	M333_17:0 Lyso PC	0.01 -10
M335	M335_26:0 Lyso PC	0.01 -10
M336	M336_18:1 SM	0.01 -10
M337	M337_24:1 SM	0.01 - 5
M338	M338_16:0 SM	0.01 - 5
M339	M339_18:0 SM	0.01 - 2
M340	M340_24:0 SM	0.01 - 10
M341	M341_C14 Carnitine (Myristoyl-L-carnitine)	0.01 - 5
M342	M342_C3 Carnitine (Propionyl-L-carnitine)	0.01 - 10
M343	M343_C8 Carnitine (Octanoyl-L-carnitine)	0.01 - 10
M344	M344_C10 Carnitine (Decanoyl-L-carnitine)	0.01 - 5
M345	M345_C4-OH Carnitine (Malonyl-L-carnitine)	0.01 - 5
M346	M346_C18 Carnitine (Stearoyl-L-carnitine)	0.01 - 5

Resources:

Major analytical instrumentation includes:

- AB SCIEX QTRAP 6500 LC-MS/MS system: Consisting of an enhanced high performance hybrid triple quadrupole/linear ion trap mass spectrometer, interfaced with a SHIMADZU Nexera UPLC system, and associated software for operation and data analysis (Analyst™ for system control and data acquisition/processing; LightSight™ for metabolite identification).
- Waters Xevo TQ-XS LC-MS/MS system: Consisting of a Waters AQUITY UPLC system coupled with a Waters Xevo TQ-XS triple quadrupole mass spectrometer, and associated software for operation and data analysis (MassLynx™ for system control and data acquisition and processing).

Major instrumentation for sample processing and storage includes:

- Revco -300C and -800C freezers with liquid nitrogen have alarms and temperature chart recorders for the proper documentation of storage conditions
- SpeedVac vacuum concentrator (Thermo Fisher Scientific)
- Centrifuges include 1 Beckman Coulter GS-15R, 1 Beckman Allegra 21, and 2 Beckman Allegra X-22R
- Other instrumentation includes homogenizers, sonicators, incubators, shakers, water bath

Software for pharmacokinetic data analysis and metabolomics data analysis:

- WinNonlin (Pharsight Corp., Mountain View, CA)
- NONMEM (ICON Development Solutions, Ellicott City, MD)
- Simcyp® Physiologically based pharmacokinetic modeling software (Simcyp Limited, United Kingdom)
- On-line free software for metabolomics data analysis: MetaboAnalyst (<http://www.metaboanalyst.ca/>)

Research:

Robust and cutting-edge analytical methods developed by the Core are essential to the evaluation of pharmacokinetics and biomarkers in clinical trials and preclinical studies. The Core has developed more than 60 LC-MS/MS methods for quantitative determination of small molecule drugs and drugs metabolites in biological matrix (1-10). These methods have used to evaluate pharmacokinetics in either clinical trials or preclinical study (11-16). A cutting-edge method developed for quantitation of oncometabolites in both frozen and formalin-fixed paraffin-embedded (FFPE) specimens (17) has enabled inter-institutional collaborations with Yale University and University of California at Los Angeles, leading to the successful funding of NIH R01 (PI, Bindra; Co-I, Li), SWOG/Hope Foundation Impact Award (MPI, Shuch/Li/Bindra), and CureSearch Catapult Impact Fund (MPI, Bindra/Li). In addition, this method has supported research published in Nature Genetics and Nature (18,19), and is currently being applied in 5 active NIH-supported clinical trials to explore oncometabolite tumor levels as a potential biomarker for prediction of tumor sensitivity to DNA-damaging agents.

Advanced PK models developed by the Core provide valuable tools for better understanding of the pharmacokinetics and response of anticancer drugs in patients. Two examples are highlighted. FAU, which was evaluated in UM1-supported phase I study (NCI #7916; PI, Shields), acts as a prodrug requiring sequential bioactivation by intracellular thymidine kinase and thymidylate synthase to form FMAU that is incorporated into DNA thereby causing cell death. In collaboration with the Biostatistics (Dr. Kim), Dr. Li developed a parent-metabolite population PK model that could be used for the prediction of the bioactivation of FAU and retention of FMAU in tumor and normal tissues (20). Mechanistic understanding and early, quantitative prediction of drug penetration into human brain and brain tumors is critical to rational drug development and treatment for brain cancer. In conjunction with the Ivy Brain Cancer Clinical Trial Programs (PI, Nader Sanai, Barrow Neurological Institute), Dr. Li has developed a physiologically based pharmacokinetic model platform that offers a mechanistic tool for the prediction of the human central nervous system pharmacokinetics and target engagement of anticancer drugs, informing selection of right drug and design of optimal dosing regimen for the treatment of brain cancer patients (21,22). This line of research is supported by the NIH R01 CA255124 (PI, Li).

Targeted metabolomics and metabolic flux analysis provide a powerful tool for mapping biochemical pathways implicated in diseases and in response to drug treatment. The Core has become one of the premier institutional-based metabolomics laboratories in the nation, providing a critical infrastructure and laying a foundation for a cancer metabolomics research program, one of KCI's priority research areas for 2019 - 2024. The targeted metabolomics service has supported a number of national funded grants and publications (23-29).

Selected Recent Publications:

1. Bao X, Wu J, Sanai N, Li J. A liquid chromatography with tandem mass spectrometry method for quantitating total and unbound ceritinib in patient plasma and brain tumor. *J Pharm Anal* **2018**;8(1):20-6 doi 10.1016/j.jpba.2017.07.007.
2. Bao X, Wu J, Sanai N, Li J. Determination of total and unbound ribociclib in human plasma and brain tumor tissues using liquid chromatography coupled with tandem mass spectrometry. *J Pharm Biomed Anal* **2019**;166:197-204 doi 10.1016/j.jpba.2019.01.017.
3. Shaw J, Wiegand R, Wu J, Bao X, Valeriote F, Li J. A liquid chromatography with tandem mass spectrometry method for simultaneous determination of UTL-5g and its metabolites in human plasma. *J Chromatogr B Analyt Technol Biomed Life Sci* **2015**;991:92-8 doi 10.1016/j.jchromb.2015.04.015.
4. Wiegand R, Wu J, Sha X, LoRusso P, Heath E, Li J. Validation and implementation of a liquid chromatography/tandem mass spectrometry assay to quantitate aminoflavone (NSC 686288) in human plasma. *J Chromatogr B Analyt Technol Biomed Life Sci* **2009**;877(14-15):1460-4 doi 10.1016/j.jchromb.2009.03.015.
5. Wiegand R, Wu J, Sha X, LoRusso P, Li J. Simultaneous determination of ABT-888, a poly (ADP-ribose) polymerase inhibitor, and its metabolite in human plasma by liquid chromatography/tandem mass

- spectrometry. *J Chromatogr B Analyt Technol Biomed Life Sci* **2010**;878(3-4):333-9 doi 10.1016/j.jchromb.2009.11.037.
6. Wiegand R, Wu J, Shields AF, Lorusso P, Li J. Simultaneous determination of 1-(2'-deoxy-2'-fluoro-beta-D-arabinofuranosyl) uracil (FAU) and 1-(2'-deoxy-2'-fluoro-beta-D-arabinofuranosyl) 5-methyluracil (FMAU) in human plasma by liquid chromatography/tandem mass spectrometry. *J Chromatogr B Analyt Technol Biomed Life Sci* **2012**;891-892:64-70 doi 10.1016/j.jchromb.2012.02.030.
 7. Wu J, Sanai N, Bao X, LoRusso P, Li J. An aqueous normal-phase chromatography coupled with tandem mass spectrometry method for determining unbound brain-to-plasma concentration ratio of AZD1775, a Wee1 kinase inhibitor, in patients with glioblastoma. *J Chromatogr B Analyt Technol Biomed Life Sci* **2016**;1028:25-32 doi 10.1016/j.jchromb.2016.05.050.
 8. Wu J, Wiegand R, LoRusso P, Li J. Validation and implementation of a liquid chromatography/tandem mass spectrometry assay for quantitation of the total and unbound RO4929097, a gamma-secretase inhibitor targeting Notch signaling, in human plasma. *J Chromatogr B Analyt Technol Biomed Life Sci* **2011**;879(19):1537-43 doi 10.1016/j.jchromb.2011.03.045.
 9. Wu J, Wiegand R, LoRusso P, Li J. A stable isotope-labeled internal standard is essential for correcting for the interindividual variability in the recovery of lapatinib from cancer patient plasma in quantitative LC-MS/MS analysis. *J Chromatogr B Analyt Technol Biomed Life Sci* **2013**;941:100-8 doi 10.1016/j.jchromb.2013.10.011.
 10. Wu J, Zhang Y, Wiegand R, Wang J, Bepler G, Li J. Quantitative analysis of intracellular nucleoside triphosphates and other polar metabolites using ion pair reversed-phase liquid chromatography coupled with tandem mass spectrometry. *J Chromatogr B Analyt Technol Biomed Life Sci* **2015**;1006:167-78 doi 10.1016/j.jchromb.2015.10.030.
 11. Bellail AC, Jin HR, Lo HY, Jung SH, Hamdouchi C, Kim D, *et al.* Ubiquitination and degradation of SUMO1 by small-molecule degraders extends survival of mice with patient-derived tumors. *Sci Transl Med* **2021**;13(615):eabh1486 doi 10.1126/scitranslmed.abh1486.
 12. Mehta S, Fiorelli R, Bao X, Pennington-Krygier C, Derogatis A, Kim S, *et al.* A Phase 0 Trial of Ceritinib in Patients with Brain Metastases and Recurrent Glioblastoma. *Clin Cancer Res* **2022**;28(2):289-97 doi 10.1158/1078-0432.CCR-21-1096.
 13. Sanai N, Li J, Boerner J, Stark K, Wu J, Kim S, *et al.* Phase 0 Trial of AZD1775 in First-Recurrence Glioblastoma Patients. *Clin Cancer Res* **2018**;24(16):3820-8 doi 10.1158/1078-0432.CCR-17-3348.
 14. Tien AC, Li J, Bao X, Derogatis A, Kim S, Mehta S, *et al.* A Phase 0 Trial of Ribociclib in Recurrent Glioblastoma Patients Incorporating a Tumor Pharmacodynamic- and Pharmacokinetic-Guided Expansion Cohort. *Clin Cancer Res* **2019**;25(19):5777-86 doi 10.1158/1078-0432.CCR-19-0133.
 15. Rosati R, Polin L, Ducker C, Li J, Bao X, Selvakumar D, *et al.* Strategy for Tumor-Selective Disruption of Androgen Receptor Function in the Spectrum of Prostate Cancer. *Clin Cancer Res* **2018**;24(24):6509-22 doi 10.1158/1078-0432.CCR-18-0982.
 16. Saadat N, Liu F, Haynes B, Nangia-Makker P, Bao X, Li J, *et al.* Nano-delivery of RAD6/Translesion Synthesis Inhibitor SMI#9 for Triple-negative Breast Cancer Therapy. *Mol Cancer Ther* **2018**;17(12):2586-97 doi 10.1158/1535-7163.MCT-18-0364.
 17. Bao X, Wu J, Shuch B, LoRusso P, Bindra RS, Li J. Quantitative Profiling of Oncometabolites in Frozen and Formalin-Fixed Paraffin-Embedded Tissue Specimens by Liquid Chromatography Coupled with Tandem Mass Spectrometry *Scientific Report* **2019**; 9: 11238
 18. Sulkowski PL, Sundaram RK, Oeck S, Corso CD, Liu Y, Noorbakhsh S, *et al.* Krebs-cycle-deficient hereditary cancer syndromes are defined by defects in homologous-recombination DNA repair. *Nat Genet* **2018**;50(8):1086-92 doi 10.1038/s41588-018-0170-4.
 19. Sulkowski PL, Oeck S, Dow J, Economos NG, Mirfakhraie L, Liu Y, *et al.* Oncometabolites suppress DNA repair by disrupting local chromatin signalling. *Nature* **2020**;582(7813):586-91 doi 10.1038/s41586-020-2363-0.
 20. Li J, Kim S, Shields AF, Douglas KA, McHugh CI, Lawhorn-Crews JM, *et al.* Integrating Dynamic Positron Emission Tomography and Conventional Pharmacokinetic Studies to Delineate Plasma and Tumor

- Pharmacokinetics of FAU, a Prodrug Bioactivated by Thymidylate Synthase. *J Clin Pharmacol* **2016**;56(11):1433-47 doi 10.1002/jcph.751.
21. Li J, Wu J, Bao X, Honea N, Xie Y, Kim S, *et al.* Quantitative and Mechanistic Understanding of AZD1775 Penetration across Human Blood-Brain Barrier in Glioblastoma Patients Using an IVIVE-PBPK Modeling Approach. *Clin Cancer Res* **2017**;23(24):7454-66 doi 10.1158/1078-0432.CCR-17-0983.
 22. Li J, Jiang J, Wu J, Bao X, Sanai N. Physiologically Based Pharmacokinetic Modeling of Central Nervous System Pharmacokinetics of CDK4/6 Inhibitors to Guide Selection of Drug and Dosing Regimen for Brain Cancer Treatment. *Clin Pharmacol Ther* **2021**;109(2):494-506 doi 10.1002/cpt.2021.
 23. Udumula MP, Sakr S, Dar S, Alvero AB, Ali-Fehmi R, Abdulfatah E, *et al.* Ovarian cancer modulates the immunosuppressive function of CD11b(+)Gr1(+) myeloid cells via glutamine metabolism. *Mol Metab* **2021**;53:101272 doi 10.1016/j.molmet.2021.101272.
 24. Qiao X, Ma J, Knight T, Su Y, Edwards H, Polin L, *et al.* The combination of CUDC-907 and gilteritinib shows promising in vitro and in vivo antileukemic activity against FLT3-ITD AML. *Blood Cancer J* **2021**;11(6):111 doi 10.1038/s41408-021-00502-7.
 25. Wallace-Povirk A, Tong N, Wong-Roushar J, O'Connor C, Zhou X, Hou Z, *et al.* Discovery of 6-substituted thieno[2,3-d]pyrimidine analogs as dual inhibitors of glycinamide ribonucleotide formyltransferase and 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase in de novo purine nucleotide biosynthesis in folate receptor expressing human tumors. *Bioorg Med Chem* **2021**;37:116093 doi 10.1016/j.bmc.2021.116093.
 26. Mpilla G, Aboukameel A, Muqbil I, Kim S, Beydoun R, Philip PA, *et al.* PAK4-NAMPT Dual Inhibition as a Novel Strategy for Therapy Resistant Pancreatic Neuroendocrine Tumors. *Cancers (Basel)* **2019**;11(12) doi 10.3390/cancers11121902.
 27. Moriyama T, Liu S, Li J, Meyer J, Zhao X, Yang W, *et al.* Mechanisms of NT5C2-Mediated Thiopurine Resistance in Acute Lymphoblastic Leukemia. *Mol Cancer Ther* **2019**;18(10):1887-95 doi 10.1158/1535-7163.MCT-18-1112.
 28. Dekhne AS, Shah K, Ducker GS, Katinas JM, Wong-Roushar J, Nayeem MJ, *et al.* Novel Pyrrolo[3,2-d]pyrimidine Compounds Target Mitochondrial and Cytosolic One-carbon Metabolism with Broad-spectrum Antitumor Efficacy. *Mol Cancer Ther* **2019**;18(10):1787-99 doi 10.1158/1535-7163.MCT-19-0037.
 29. Zhang K, Kim H, Fu Z, Qiu Y, Yang Z, Wang J, *et al.* Deficiency of the Mitochondrial NAD Kinase Causes Stress-Induced Hepatic Steatosis in Mice. *Gastroenterology* **2018**;154(1):224-37 doi 10.1053/j.gastro.2017.09.010.

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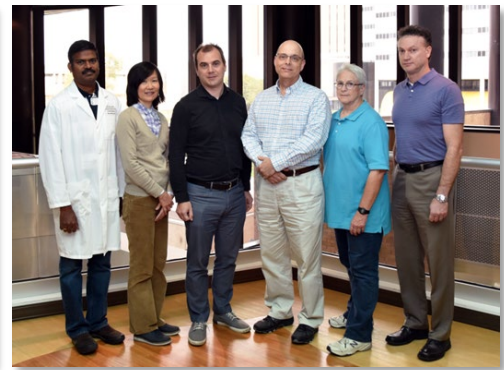
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<https://www.karmanos.org/Proteomics>



Mission of the Core:

The mission of the Proteomics Core is to enhance research productivity of WSU/KCI researchers by providing the equipment and expertise necessary for analysis of cellular protein composition and protein-protein interactions. These two objectives require different instrumentation, but they both rely on expertise in protein chemistry, separation and analysis.

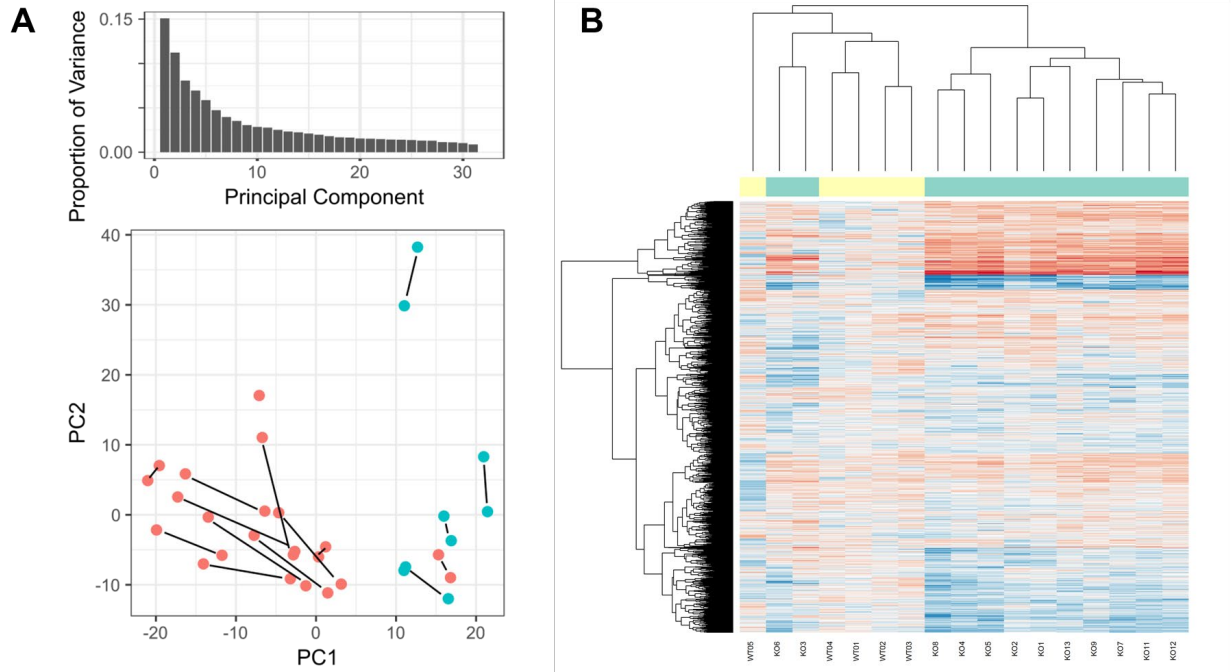
Core Services Available:

- Protein identification using nano-LC/MS/MS instruments
- Protein quantitation using spectral counting or isobaric tags with data acquired on the Orbitrap Fusion and Orbitrap QExactive systems and the Multiple Reaction Monitoring strategy using the TSQ Vantage system.
- Proteomic profiling using two-dimensional chromatographic separations or MuDPIT technologies
- Analysis of post translational modifications using nano-LC/MS/MS with fragmentation by CID, HCD and ETD
- Robotic sample preparation using the AssayMap Bravo robot.
- Sample fractionation Alkaline Reversed Phase spin columns.
- Peptide labeling and purification using an HPLC with UV and Fluorescence Detectors
- Surface Plasmon Resonance (SPR) using a Biacore 3000. Investigators performing SPR analysis must have appropriately trained personnel
- Biolayer Interferometry (BLI) for molecular interaction analysis using an Octet Red96.
- Data Analysis using MaxQuant, Mascot, Sequest, X!tandem and Peaks algorithms with data compilation and secondary analysis using Scaffold.

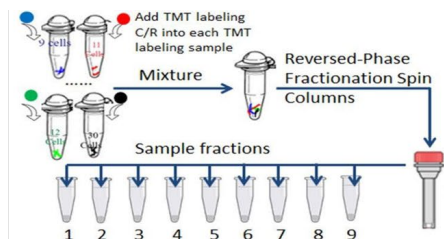
Resources:

- Thermo Orbitrap Fusion nano-LC/MS/MS with ETD
- Thermo Orbitrap QExactive nano-LC/MS/MS
- Thermo Finnigan TSQ Vantage triple quadrupol nano-LC/MS/MS
- AssayMap Bravo sample preparation robot
- HPLC system for peptide purification, which includes UV and Fluorescence Detectors
- Biacore 3000 for molecular interaction analysis by Surface Plasmon Resonance
- Octet Red96 for molecular interaction analysis by Biolayer Interferometry

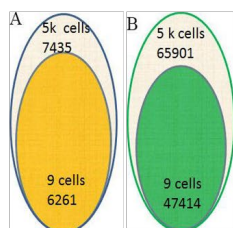
Research:



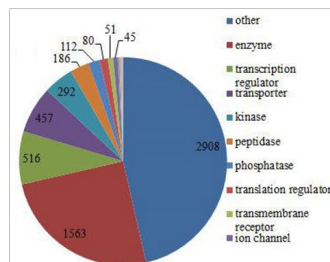
Project 1. Evaluation of mDig CRISPR-Cas9 KO clones. Proteome profiling of 12 KO and 5 control clones in duplicate to a depth of greater than 5,000 proteins demonstrates that mDig KO has consistent as well as variable effects on the proteome. Panel A shows the PCA analysis and panel B the heat map grouping the clones by protein abundance. PI: Fei Chen. R01 ES028263 & R01 ES028335.



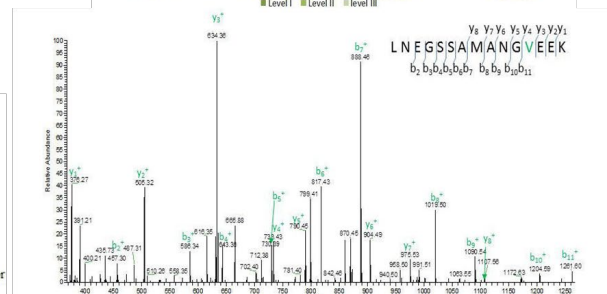
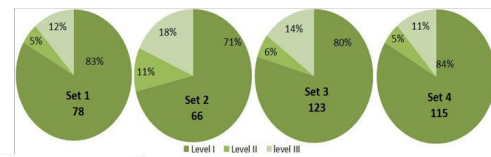
1. The Carrier/Reference Strategy for micro sample proteomics.



2. Protein (A) and peptide (B) coverage for Panc1 cells.



3. GO analysis demonstrates coverage of regulatory proteins.



4. Single Amino Acid Variant (SAAV) identification in samples of 9 cells, (upper panel). Spectrum of SAAV peptide from Septin 9, (lower panel).

Project 2. The carrier/reference (C/R) proteome allowed us to detect 47,414 unique peptides derived from 6,261 proteins in as few as 9 cells providing sufficient coverage to search for single amino acid variants (SAAVs) related to cancer. Tan Z, Yi X, Carruthers NJ, Stemmer PM, Lubman DM. J Proteome Res. 2018 Nov 7. doi: 10.1021/acs.jproteome.8b00694. [Epub ahead of print] PubMed PMID: 30404448.

Acknowledgement Text:

Publications that result from Core involvement should include following statement:

“The Proteomics Core is supported, in part, by NIH Center grant P30 CA022453 to the Karmanos Cancer Institute at Wayne State University.”

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Mission of the Clinical Trials Office:

The mission of the Clinical Trials Office (CTO) is to provide outstanding support to clinical trials at the Karmanos Cancer Institute (KCI) with the goal of improving cancer therapy and patient quality of life through research.

Goals and Services Available:

- Ensure that all clinical trials conducted at KCI are managed in strict compliance with the Food and Drug Administration's (FDA) Code of Federal Regulations (CFR) and in accordance with International Conference on Harmonisation (ICH) Good Clinical Practice (GCP) guidelines.
 - Coordinating and managing all clinical trials conducted at KCI in strict compliance with the FDA CFR, ICH GCP standards and institutional policies and regulations
 - Ensuring the safety of patients participating in clinical trials
 - Coordinating and tracking National Cancer Institute (NCI) registrations and annual updates for KCI investigators
 - Coordinating registration and maintenance of all interventional and observational research with ClinicalTrials.gov and the NCI's Clinical Trials Reporting Program (CTRP)
- CTO is an integral component of the NCI Cancer Center Support Grant (CCSG)
 - Provides ongoing support for the required Cancer Center committees, including the Protocol Review and Monitoring Committee (PRMC), Quality Assurance Committee (QAC), and Data and Safety Monitoring Committee (DSMC), in accordance with our NCI approved Data and Safety Monitoring Plan
- Facilitate and optimize accrual to clinical trials by providing well-qualified, specifically trained regulatory and study coordinators and research nurse support to KCI physicians and clinical support staff.
 - Facilitating increasing accrual to clinical trials
 - Maintaining protocol registry and accrual data utilizing OnCore®, KCI's Clinical Trials Management System
 - Liaise between Principal Investigators, IRBs, and study sponsors
- Ensure research coordination by facilitating and optimizing physician-patient-CTO staff interaction, communication, and collaboration.
 - Increasing awareness and education of all KCI and affiliate institution staff in the clinical trials arena
 - Facilitate a robust research investigator and staff onboarding for participation in clinical trials
- Facilitate regulatory approval and oversight to rapidly review and activate appropriate trials.
 - Serving as an interface with the various Institutional Review Boards (IRB), including Wayne State University IRB and the NCI Central IRB, to facilitate preparation of the required consent and privacy forms and other regulatory documents necessary to expedite effective and timely approval of KCI protocols

Research Administration

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Mission of Research Administration

The mission of Research Administration is to reliably and consistently provide cost-effective administrative services that further the conduct of efficient and effective research efforts.

Services Available:

Research Administration strives to provide the best support to the researchers of the Karmanos Cancer Institute by providing expert assistance in the following areas:

- **Pre-Award Services** - Research Administration has staff members with decades of experience in meeting the requirements of funding agencies and navigating the intricacies of the submission process through Wayne State University. Research Administration staff members review and provide the final polish to grant applications for Cancer Center members, provide regular reports to senior leadership on the health of our funding portfolio, and play a vital role in the administration of the Cancer Center Support Grant (CCSG).
- **Post-Award/Billing**
 - Research Administration plays an ongoing role in assisting researchers to maximize the use of their grant funding, long after the original award date. Post award staff provide monthly reports on spending, ensure correct distribution of effort for researcher salaries, meet regularly with faculty and staff to answer questions, and play an active role in the final closeout of grant funding.
 - Billing specialists review the charges of all patients enrolled on clinical trials at KCI and bill the appropriate healthcare payer, whether insurance, government program, or the clinical trial itself. These staff are more than typical medical billers. They possess the knowledge of current CPT coding practices along with a deep understanding of clinical trial budgeting and reimbursement. No other team could perform this task for the Cancer Center.
- **CCSG Administration** - Research Administration plays a pivotal role in coordinating the various components of the CCSG application itself along with the day-to-day activities that support the Cancer Center structure: program meetings and retreats, Core business operations, institutional support for new initiatives, space allocation, and working closely with the Development and Marketing departments to increase awareness of and enthusiasm for cancer research.
- **Research Finance** - Research Administration employs dedicated accountants and budget specialists to keep a careful eye on the precious financial resources for research. Developing and managing budgets within both KCI and WSU, these financial managers develop a strategy for making the best use of available funding and provide a valuable service in purchasing and financial reporting for Cancer Center members. The finance team of Research Administration plays a critical role in the overall strategy of the Institute and provides direct support to senior leaders in their decision-making.