Intramural Continuing Umbrella of Research Experiences (iCURE) – 2019 Possible Projects

Possible Projects in the Center for Cancer Research (CCR)

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Jairaj Acharya, MBBS, PhD	All	Our long-term objective is to understand the complex interrelationship between phospholipid and sphingolipid metabolism and metabolic signaling *in vivo*. Intermediates of phospholipid (PL) and sphingolipid (SL) metabolism serve as second messengers for a number of signaling cascades. Sphingolipid composition in membranes influence a wide range of processes from protein secretion to activation of apoptosis. We have initiated studies to understand several aspects of lipid signaling *in vivo* using Drosophila and mouse models. https://ccr.cancer.gov/Cancer-and-Developmental-Biology-Laboratory/jairaj-k-acharya	Frederick
Mirit I. Aladjem, PhD	All	The DNA Replication Group at the NCI's Developmental Therapeutics Branch investigates cellular signaling pathways that monitor and direct DNA synthesis. Since many regulatory networks affecting chromosome duplication are deregulated in cancer, such studies can help portray critical aspects of cancer biology and elucidate the cellular responses to chemotherapeutic drugs. Specifically, our studies use a combination of biochemistry, cell biology and bioinformatics to reveal regulatory pathways that coordinate chromosome duplication with gene expression, chromatin condensation and cellular stress responses to preserve genomic stability. https://ccr.cancer.gov/Developmental-Therapeutics-Branch/mirit-i-aladjem	Bethesda
Suresh V. Ambudkar, PhD	All	P-glycoprotein (P-gp) and ABCG2 transporters also play an important role in drug-drug interactions, and in the bioavailability and pharmacokinetics of several drugs. Our long-term aim is to elucidate the role of ABC drug transporters in the development of multidrug resistance (MDR) in cancers and to aid the discovery of new therapeutic strategies to increase the efficiency of chemotherapy for cancer patients. We are elucidating molecular mechanisms of the ATP hydrolysis cycle and drug transport and the molecular basis of the polyspecificity of these transporters. For these studies we are employing innovative approaches	Bethesda

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		including biochemical and biophysical techniques, cell-based transport assays, genetic manipulation and molecular modeling. https://ccr.cancer.gov/Laboratory-of-Cell-Biology/suresh-v-ambudkar	
Efsun Arda, PhD	Post-baccalaureate Postdoctoral Fellow	My group's research focus is to delineate genomic elements that govern human pancreas cell identity and function. We are developing methods to understand how these molecular pathways are disrupted in diabetes or pancreas cancer. The lab is highly interdisciplinary and uses state-of-the-art technologies to address outstanding questions in human pancreas biology. Possible projects include the following areas of interest: single-cell analysis, chromatin structure and regulation, gene networks, stem cell differentiation, CRISPR gene editing and organoid systems. https://ccr.cancer.gov/Laboratory-of-Receptor-Biology-and-Gene-Expression/h-efsun-arda	Bethesda
Yawen Bai, PhD	All	The Bai group investigates chromatin structure, dynamics and function using a broad range of biophysical methods (nuclear magnetic resonance, X-ray crystallography, cryo-electron microscopy, isothermal titration calorimetry, analytical ultracentrifugation…). Current projects include structural studies on interactions between histone chaperones and histones and between nucleosomes and various proteins such as centromere proteins, transcription factors, heterochromatin protein 1, chromatin remodelers, etc. The proteins we study play important functional roles in biological function and are closely related to cancer biology. https://ccr.cancer.gov/Laboratory-of-Biochemistry-and-Molecular-Biology/yawen-bai	Bethesda
Joseph J. Barchi Jr., PhD	All	The Barchi lab studies the function of tumor-associated carbohydrate antigens (TACAs), aberrant glycan structures present on tumor cells that contribute to both the immune response to tumors and their aggressiveness. Organic synthesis is used to design probes and vaccine constructs of TACA-peptide conjugates as antitumor therapeutic agents. The vaccine constructs are comprised of TACA-based glycopeptides and molecular adjuvant molecules bound to gold nanoparticles. A current project is to design and find optimum conditions for the synthesis of novel nanoparticles that can activate antigen-presenting cells (APCs). https://ccr.cancer.gov/Chemical-Biology-Laboratory/joseph-j-barchi	Frederick

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Munira A. Basrai, PhD		https://ccr.cancer.gov/Genetics-Branch/munira-a-basrai	Bethesda
Pedro J. Batista, PhD	Post-baccalaureate Postdoctoral Fellow	The goal of the lab is to understand how the epitranscriptome responds to changes in the cellular metabolic environment. We use genome engineering and cell lines derived from patient tumors as model systems to determine how RNA biogenesis and function is disrupted to facilitate the establishment and proliferation of cancer. Ultimately, understanding this process will uncover new targets for cancer therapy, as both metabolic pathways and RNA methylation dependent gene regulation can be targeted to sensitize cancer cells. https://ccr.cancer.gov/Laboratory-of-Cell-Biology/pedro-j-batista	Bethesda
Yamini Dalal, PhD	Graduate Student Postdoctoral Fellow / MD/PhD Fellow	The Dalal lab is interested in chromatin structure and epigenetic mechanisms that underpin normal and diseased states. Using high speed video nanomicroscopy (AFM) we would like to extend our interdisciplinary tools to visualize and quantify nanoscale looping and real-time changes in chromatin structure deriving from alterations in histone variants, chaperones, histone modifications, remodelers, and breaks. We are particularly interested in dissecting mutant forms of chromatin states found in cancer cells. https://ccr.cancer.gov/Laboratory-of-Receptor-Biology-and-Gene-Expression/yamini-dalal	Bethesda
Jeffrey Gildersleeve, PhD	All	Cancer cells undergo major changes in glycosylation during the onset and progression of the disease. Antibodies to carbohydrates are critical for studying these changes and for targeting tumor associated carbohydrate antigens for diagnostic and therapeutic applications. Unfortunately, there are very few good antibodies to carbohydrates available. The goal of my lab is to understand how antibodies to carbohydrates are generated, what they do, and how we can use them to improve cancer care. To help us with these projects we have developed a carbohydrate antigen microarray. The array provides a unique tool for high-throughput analysis of antibody selectivity and affinity. In addition, it can be used to rapidly profile the repertoire of antibodies in human serum. There are several projects that a candidate could work on, including engineering antibodies to carbohydrates, developing platforms for directed evolution of antibodies, or developing screening strategies for obtaining antibodies to carbohydrates. https://ccr.cancer.gov/Chemical-Biology-Laboratory/jeffrey-c-gildersleeve	Frederick

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Tim Greten, MD	All	The Greten lab is studying the immune system and how it can be used to treat patients with gastrointestinal cancer. We conduct basic research in cancer immunology of the liver, perform pre-clinical studies to evaluate novel treatment approaches and conduct clinical trials in patients with different types of GI cancer. The lab conducts complex animal studies and uses techniques such as flow cytometry, immunohistochemistry, cell culture, gene expression studies including single-cell RNA sequencing as well as whole exome sequencing, microbiome studies and metabolism studies. We use samples derived from patients treated on clinical trials to better understand how and why treatments work or are not as effective as we want them to be. Currently there are a number of open projects for post-bacs, graduate students and post-docs. Topics include microbiome studies in mice and patient derived samples, metabolism studies in mice with cancer undergoing immunotherapy and novel immune based approaches to treat cholangiocarcinoma. https://ccr.cancer.gov/thoracic-and-gi-malignancies-branch/tim-f-greten	Bethesda
Steven Hou, PhD	All	The Hou's lab studies Central Mechanisms of Metabolic Stress and Stem Cell Regulation in Development and Cancer. In our paper published on *Nature* not too long ago, we found that stem cells and cancer stem cells (CSCs), like hibernating animals, rely primarily on lipid reserves for energy, so that ablation of the Arf1-mediated lipid metabolism results in lipid droplet accumulation and metabolic stress, which promotes CSCs necrosis. In our papers in submission, we identified the detail molecular mechanisms in both mice and *Drosophila*. We found that ablation of the Arf1 pathway triggers a chain reaction of multiple cells that coordinately promotes death of stem cells or CSCs. The stressed cells first release danger signals that activate neighboring cells or immune cells, which then feedback to kill the affected cells. In cancer mice, ablation of the Arf1 pathway can kill two birds with one stone: not only does it kill CSCs, but it also releases danger signals to activate a tumor-specific immune response in which dying CSCs are converted into a therapeutic vaccine to attract and activate immune cells for destroying the bulk tumors and resulting in durable efficacy of the treatment. This is a unique and innovative system. We are using the both mouse and *Drosophila* genetic models to explore specific molecular	Frederick

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		mechanisms as well as identify new drug targets for the treatment of cancer and other human diseases. https://ccr.cancer.gov/Basic-Research-Laboratory/steven-x-hou	
Sadhana Jackson, MD		https://ccr.cancer.gov/Neuro-Oncology-Branch/sadhana-jackson	Bethesda
Javad Khan, MD	Graduate Student Postdoctoral Fellow	Pediatric cancers are known to have a low mutational burden, and fusion-positive sarcomas have the very lowest. Our hypothesis is that fusion gene driven pediatric sarcomas, expresses a set of unique fusion gene-derived epitopes (neoepitopes) as well as other epitopes induced by the effect of the fusion gene and these can act as targets for recombinant T cell receptors (TCRs). The postdoc or graduate student will identify potent TCRs specific for sarcoma-associated antigens through in vitro antigen-driven T cell expansion and use single-cell sequencing and functional screening in order to employ optimal TCRs for developing novel immunotherapeutics. https://ccr.cancer.gov/Genetics-Branch/javed-khan	Bethesda
Shioko Kimura, PhD	Graduate Student Postdoctoral Fellow	We have identified a novel cytokine called Secretoglobin (SCGB) 3A2, predominantly expressed in lung airways. We have demonstrated that SCGB3A2 has anti-inflammatory, growth factor, anti-fibrotic, and recently anti-cancer activities in lung. Mice intravenously injected with mouse Lewis lung carcinoma (LLC) cells develop lung cancer within several weeks. When progression of lung cancer was monitored using *ex vivo* culture of mouse lungs that were taken out right after injection of LLC cells to mice, the addition of SCGB3A2 in culture media slowed the cancer development. We plan to examine the effect of SCGB3A2 at cell levels using electron microscope. https://ccr.cancer.gov/Laboratory-of-Metabolism/shioko-kimura	Bethesda
Kyung S. Lee, PhD	Graduate Student Postdoctoral Fellow	We have been studying the architecture and function of the centrosome, a membraneless organelle composed of two microtubule-derived structures called centrioles and an amorphous mass of pericentriolar material (PCM). We discovered that two human PCM scaffolds, Cep63 and Cep152, cooperatively generate a heterotetrameric alpha-helical bundle, which in turn self-assembles into a nanoscale cylindrical architecture critical for cell division and proliferation. Abnormal regulation of this process leads to the development of diverse human diseases, such as cancer and microcephaly. Potential projects may involve	Bethesda

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		investigating the cellular, structural, or biophysical aspect of forming a higher-order self-assembly by the PCM scaffolds and the biological significance of this event. Another potential project is to carry out structure-based drug discovery aimed at developing small molecule anticancer therapeutics against the polo-box domain of a Ser/Thr protein kinase, Plk1, an attractive anti-cancer drug target. Fellows with an expertise in cell biology, biochemistry, X-ray crystallography/NMR, single-molecule tracking, or cryo-EM are desired. https://ccr.cancer.gov/Laboratory-of-Metabolism/kyung-s-lee	
Stan Lipkowitz, MD, PhD	Post-baccalaureate Postdoctoral Fellows	The Lipkowitz lab investigates signal transduction pathways that regulate growth and programmed cell death in epithelial cancer cells. Ongoing projects include: 1) Regulation of signaling by Cbl proteins RTKs, such as EGFR, HER2, MET and RET, that are often inappropriately active (due to mutation or overexpression) in a wide array of epithelial malignancies, 2) Activation of death receptor pathways to kill breast cancer cells, 3) Inhibition of breast cancer cells by the novel drug ONC201. https://ccr.cancer.gov/Womens-Malignancies-Branch/stanley-lipkowitz	Bethesda
Zhenggang Liu, PhD	All	TNF regulates many cellular processes including cell proliferation, differentiation and cell death and is involved in many types of diseases such as cancer. Inappropriate production of TNF plays a critical role in the pathogenesis of both acute and chronic inflammatory diseases. The deregulation of programed cell death such as apoptosis and necroptosis has been suggested to be pivotal for tumor development. Therefore, revealing the molecular mechanism of TNF signaling and the regulation of apoptosis and necroptosis will not only help to understand the biology of TNF function and programmed cell death but also provide insights for developing novel treatments of inflammatory diseases and cancer. Of particular significance is our work that helped to elucidate the molecular mechanism of TNF-induced necroptosis. Necroptosis, as apoptosis, is an important cell death mode that is both physiologically and pathologically relevant. However, the regulation of necrotic cell death is poorly understood. My lab has identified the most critical executor of necroptosis, MLKL, and demonstrated the mechanism of its function in necroptosis. Most recently, my lab demonstrated that necroptosis of tumor cells leads to tumor necrosis and promotes tumor metastasis.	Bethesda

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		Currently, we are trying to understand how necroptosis promotes metastasis. https://irp.nih.gov/pi/zheng-gang-liu	
Daniel W. McVicar, PhD	All	The McVicar group studies the regulation of innate immune cells in the context of cancer with a current emphasis on regulation of metabolism. The studies use in vitro biochemical approaches, metabolomics, metabolic flux analysis, heavy isotope tracing, and animal models to dissect metabolic pathways. The laboratory currently has projects running investigating metabolic control of NK cells, monocytes/macrophages, and neutrophils. In addition, as part of the NCI Cancer and Inflammation Program (CIP), the group translates these projects into in vivo models of inflammation and carcinogenesis. https://ccr.cancer.gov/Cancer-and-Inflammation-Program/daniel-w-mcvicar	Frederick
Tom Misteli, PhD	Postdoctoral Fellows	The Misteli lab studies the 3D organization of the genome in the context of health and disease. Methods include a combination of high-end imaging techniques, molecular tools and biochemistry approaches, and specific projects suitable for a post-doc fellow include the mapping of 3D genome organization using high-throughput imaging or the generation of novel sensors of nuclear function. https://ccr.cancer.gov/Laboratory-of-Receptor-Biology-and-Gene-Expression/tom-misteli	Bethesda
Jagan Muppidi, MD, PhD	All	The Muppidi lab studies the intersection of the immune response and generation of malignancies derived from B cells. The lab uses genetically engineered animal models to define how genetic changes found in B cell lymphomas contribute to altered B cell behavior within the microenvironment and the subsequent development of malignancy. https://ccr.cancer.gov/Lymphoid-Malignancies-Branch/jagan-r-muppidi	Bethesda
Shalini Oberdoerffer, PhD	All	https://ccr.cancer.gov/Laboratory-of-Receptor-Biology-and-Gene-Expression/shalini-oberdoerffer	Bethesda
Hyun Park, PhD	All	The laboratory's research interest focuses on understanding the role of cytokine receptor expression and signaling in T cells. Specifically, we seek to understand the transcriptional and post-transcriptional mechanisms of cytokine receptor expression and downstream signaling in T cells. Recently, we generated a new mouse model that links	All

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		aberrant cytokine signaling to autoimmune inflammation, and we plan to use high-dimension analytic tools, such as CyTOF and single cell RNA sequencing, to understand the mechanisms. https://irp.nih.gov/pi/jung-hyun-park	
Eytan Ruppin, MD, PhD	All	The Ruppin lab is focused on developing and harnessing data science approaches for the integration of multi-omics data to better understand the pathogenesis of cancer, its evolution and treatment. We collaborate with many experimental cancer labs, aiming to develop and utilize computational approaches to jointly gain a network-level integrative view of the systems we study. From a translational perspective, together with our collaborators, we aim to predict and test novel drug targets and biomarkers to treat cancer more effectively. https://ccr.cancer.gov/cancer-data-science-laboratory/eytan-ruppin	Bethesda
DeeDee Smart, MD, PhD	Post-baccalaureate Postdoctoral Fellow	Metabolic regulators of the radiation response and brain radiosensitivity. This is a collaborative project with Dr. Ravinder Reddy of the University of Pennsylvania Department of Radiology and Dr. Alan Koretsky of the National Institute of Neurologic Diseases and Stroke and is focused on defining changes in metabolism in the normal brain from radiation treatment using chemical exchange saturation transfer (CEST) MRI imaging techniques, and correlating observed metabolic changes with clinical outcomes as well as investigational therapeutic interventions. https://ccr.cancer.gov/Radiation-Oncology-Branch/deedee-k-smart	Bethesda
Gilbert H. Smith, PhD	Post-baccalaureate	An important issue that overarches all of our research is the notion that cellular behavior is the result of signals emanating from the microenvironment and not necessarily from characteristics that are inherent to individual cells. While mutations play an important part in the reaction of a given cell to these signals, the evidence as a whole argues that malignant transformation and its progression to frank malignancy and metastasis is strongly dictated by the signals engendered by the “normal” stroma and non-transformed cells in their immediate neighborhood. https://ccr.cancer.gov/Basic-Research-Laboratory/gilbert-howlett-smith	Bethesda
Esta Sterneck, PhD	Graduate Student	Immune-oncology: Analysis of the myeloid lineage response to tumor development in mice. The importance of the immune system in modulating tumor initiation, development, progression, as well as	Frederick

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
	Postdoctoral Fellow	response to therapeutics, is well established. In addition, exploitation of the host defense system for novel therapeutic strategies is one of the most promising frontiers in cancer management. My laboratory conducts basic research on the molecular mechanisms underlying tumor biology. Specifically, we study the functions of the transcription factor *CEBPD.* To dissect the cell-type specific roles of C/EBPδ, we generated mice with a floxed allele of *Cebpd*. Because C/EBPδ is expressed in mature myeloid cells and myeloid-derived suppressor cells (MDSCs), we chose the LysM-Cre mouse to delete *Cebpd* in these cell types. The goal of this Project is to characterize myeloid-lineage specific functions of C/EBPδ that modulate tumor biology and thereby advance our mechanistic understanding of the tumor-host interactions that control tumor progression. This project will involve extensive molecular and functional analysis of the myeloid cell lineage in the context of mouse tumor models. State of the art core support including imaging and singe-cell sequencing will be part of the analysis. The project will be in collaboration with Dr. J. Keller (MCGP, CCR, NCI) and other investigators at NIH. https://ccr.cancer.gov/Laboratory-of-Cell-and-Developmental-Signaling/esta-sterneck	
Yousuke Takahama, PhD	All	Our laboratory is interested in understanding molecular mechanisms that: 1) build functionally competent thymus microenvironments, which are capable of supporting the production and selection of T cells, 2) govern thymic selection to establish a functionally competent and self-tolerant repertoire of T cells, 3) position developing T cells to localize within the thymus microenvironments for production and selection of T cells. https://ccr.cancer.gov/Experimental-Immunology-Branch/yousuke-takahama	Bethesda
Masaki Terabe, PhD	Postdoctoral Fellow	The Neuro-Oncology Branch Immunology program primarily focuses on regulatory mechanisms of immune responses against brain tumors. Candidates will be part of a basic, translational, and collaborative research program mainly focusing on the roles of CD1d-restricted NKT cells and other T cells in the regulation of tumor immunity in the brain. This is an exciting opportunity to join a growing trans-institutional research team that promotes and supports collaborations across the	Bethesda

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		basic, translational, and clinical research spectrum to develop novel therapeutics for individuals with primary central nervous system malignancies that will globally influence the field. Interested in applicants with a strong background in brain biology/science (cancer biology, cell biology or molecular biology). Immunology background is NOT required if the applicant has a strong interest in immunology. https://ccr.cancer.gov/Neuro-Oncology-Branch/masaki-terabe	
Lino Tessarollo, PhD	All	My laboratory is using the mouse as a genetically amenable *in vivo* tool to address the physiological roles of neurotrophins and their receptors. Drugs to target neurotrophin signaling are already in clinical trials for cancer treatments but their long-term effects in mammalian physiology is unknown. We are interested in dissecting the cell specific neurotrophin signaling pathways and their role in the nervous and cardiovascular system. Our effort is aimed at understanding the specific roles of neurotrophins during development and in the mature organism and the impact that disruption of these signaling pathways may have in mammals. https://ccr.cancer.gov/Mouse-Cancer-Genetics-Program/lino-tessarollo	Frederick
Carol J. Thiele, PhD	All	Dr. Thiele leads a research program which develops novel therapies for children with solid tumors using state-of-the-art biologic and genomic analyses of tumors and normal counterparts. She pioneered studies using retinoids to “target” the MYCN oncogene and control tumor growth. These led to clinical studies which showed that retinoids improved outcomes for children with high-risk neuroblastoma. Her section has developed pre-clinical models and genetically engineered mice (GEMs) to study mechanisms of neuroblastoma tumorigenesis and assess novel therapeutic interventions. Ongoing studies are aimed at understanding epigenetic/chromatin based mechanisms to re-program and differentiate tumor cells. https://ccr.cancer.gov/Pediatric-Oncology-Branch/carol-j-thiele	Bethesda
Xin Wei Wang, PhD	All	Dr. Wang’s research centers on functional genomics of liver cancer using genome-scale technologies paired with several national/international collaborative initiatives and clinical studies. His lab focuses on basic/translational research by building a comprehensive global liver cancer data ecosystem and employing integrated genomics to address liver cancer heterogeneity. His lab emphasizes new	Bethesda

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		molecular approaches such as genomics, transcriptomics, metabolomics, microbiomics, viromics and single cell analysis to define tumor subtypes and identify biomarkers for early detection, diagnosis, prognosis and prediction, and to delineate the molecular mechanisms of liver cancer initiation and metastasis with applications towards precision oncology. https://ccr.cancer.gov/laboratory-of-human-carcinogenesis/xin-wei-wang	
Roberto Weigert, PhD	All	Our lab has developed an imaging approach called Intravital Subcellular Microscopy (ISMic) that enables the visualization of cellular and subcellular processes in live animals with an unprecedented resolution. We have developed a model system that permits to image the initiation, progression and metastasis of tumors generated by carcinogen exposure, and at the same time, to investigate the contribution of the tumor micro-environment. This model will be exploited to investigate, at a molecular level, the role of membrane remodeling, cellular metabolism and the immune system during tumor progression, with the potential of unraveling novel cellular mechanisms that will lead to more effective therapies for cancer treatment. https://ccr.cancer.gov/Laboratory-of-Cellular-and-Molecular-Biology/roberto-weigert	Bethesda
Allan M. Weissman, MD	All	Our laboratory is focused on the ubiquitin-proteasome system in cancer and other diseases. We have determined that gp78, which is a ubiquitin ligase of the endoplasmic reticulum, plays a causal role in cancer aggressiveness and is expressed at higher levels in breast cancers from African-Americans than European-Americans. Studies utilize human tissue samples, our mouse models, genetically manipulated cell lines, and biochemical approaches. Using these, a recruit will have the opportunity to undertake a project to assess molecular mechanisms of gp78-mediated cancer aggressiveness and participate in development of therapeutic interventions to manipulate the function of gp78 and related molecules in cancer. https://ccr.cancer.gov/Laboratory-of-Protein-Dynamics-and-Signaling/allan-m-weissman	Frederick
Sandra Wolin, MD, PhD	All	The Wolin lab studies how noncoding RNAs function, how cells recognize and degrade defective RNAs, and how failure to degrade these RNAs contributes to human disease. One pathway that we study	Frederick

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		involves noncoding RNA-protein complexes known as Ro60 ribonucleoproteins (RNPs). In all studied organisms, Ro60 binds noncoding RNAs called Y RNAs. Current projects include uncovering new roles for Ro60 and Y RNAs in mammalian cells and bacteria, obtaining a high-resolution structure of the new RNA degradation machine and identifying new RNA surveillance pathways in mammalian cells. https://ccr.cancer.gov/RNA-Biology-Laboratory/sandra-l-wolin	
Jing Wu, MD, PhD	Postdoctoral Fellow	We are seeking a highly motivated and postdoctoral fellow, preferably a recent graduate (PhD and/or MD), with a background in Cancer Biology/Molecular and Cellular Biology to join the Translational Research Program at the NOB laboratory of NCI/NIH. The mission for the Translational Research Program at NOB laboratory is to develop hypothesis-driven laboratory projects, leading to testing in preclinical models, and ultimately developing clinical trials based on these preclinical studies to determine predictors and mechanisms of treatment responses or resistance in diffuse gliomas, particularly in IDH mutant gliomas and glioblastoma. https://ccr.cancer.gov/Neuro-Oncology-Branch/jing-wu	Bethesda

Possible Projects in the Division of Cancer Epidemiology and Genetics (DCEG)

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Ludmila Prokunina, PhD	All	Genetics and translational genomics of cancer and immune response. We start from germline variations identified by GWAS and perform computational and laboratory investigations to identify molecular phenotypes and translational applications of these findings. https://dceg.cancer.gov/about/staff-directory/biographies/K-N/prokunina-olsson-ludmila	Rockville
Rose Yang, PhD, MPH	All	My research has focused on the molecular epidemiology of breast cancer and gene identification in cancer-prone families. *Breast cancer:* I am currently leading breast cancer studies in several Asian populations with the main goals of identifying distinct genomic alterations in tumors and adjacent normal tissues among Asian women and examining the	Rockville

		associations of these changes with risk factors, breast tissue composition and density, and breast cancer subtypes. *Melanoma and chordoma:* The goals of these studies are to identify novel high-penetrance genes or genetic/ epigenetic factors that modify susceptibility in familial melanoma and chordoma. In addition, in collaboration with a neurosurgery hospital in Beijing, China, we are characterizing the genomic landscape of chordoma tumors using whole genome sequencing and RNA sequencing. https://dceg.cancer.gov/about/staff-directory/biographies/O-Z/yang-rose	