Intramural Continuing Umbrella of Research Experiences (iCURE) – 2021 Possible Projects

Possible Projects in the Center for Cancer Research (CCR)

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
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 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	Bethesda
Joseph Barchi Jr. PhD	All	Carbohydrates are displayed in various forms on all cells but they are modified when a cell becomes cancerous. Many of these are considered Tumor-Associated carbohydrate antigens (TACA's) because they initiate an immunes response to the tumor. We are interested in what the function of these modified structures are relating to tumor development and antigenicity. We do this through synthesis of TACA's, probes and novel TACA-based antigens. We study the structures and conformation of these probes by techniques like NMR spectroscopy. We then use these for vaccinations or in vitro assays to develop new therapeutics for hard to treat cancers. https://ccr2.cancer.gov/resources/cbl/OurScience/Barchi.aspx	Frederick
Pedro J. Batista, PhD	Post-Baccaualreate 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

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Deborah Citrin, MD	All	Major projects in the laboratory focus on the identification of molecules involved in determining cell/tissue radioresponse and the development of target-based therapies. Opportunities are available for using a variety of genetic and molecular biology approaches to delineate the molecules/processes that regulate cellular radiosensitivity. Studies will also involve translating fundamental information relating to molecular radioresponse to strategies aimed at increasing the sensitivity of tumor cells. https://ccr.cancer.gov/Radiation-Oncology-Branch/deborah-e-citrin	Bethesda
Erin L Davies, PhD	Postdoctoral Fellow	My team seeks an iCURE postdoctoral fellow to determine how life-long pluripotency is established during planarian embryogenesis. Planarians rely on pluripotent adult stem cells for homeostasis, reproduction, and regeneration. The fellow will determine the developmental antecedents of adult pluripotent stem cells and will investigate the mechanisms that regulate the transition from embryonic to adult pluripotency. To achieve these objectives, the fellow will employ single cell RNA-sequencing, lineage tracing, cell transplantation, and RNAi knock-down assays. This study will generate resources and testable hypotheses for comparative studies of potency regulation in planarians and mammalian stem cell and cancer models. https://ccr.cancer.gov/cancer-and-developmental-biology-laboratory/erin-l-davies	Frederick
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	Bethesda

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		cholangiocarcinoma. https://ccr.cancer.gov/thoracic-and-gi-malignancies-branch/tim-f-greten	
Sridhar Hannenhalli, PhD	Postdoctoral Fellow	Hannenhalli lab harnesses a variety of high-throughput omics data (primarily transcriptomic and epigenomic) to address fundamental biological questions as they pertain to both normal organismal functions, as well as diseases, with a special emphasis on cancer. The work involves both methodological development as well as collaborative basic science and clinical applications. Examples of current projects include: (1) non-genetic origins of cancer, (2) functional assessment of non-coding cancer mutations, (3) molecular links between oncogenesis and embryonic development, (4) Inferring miRNA activities in single cell RNA-seq data, (5) tissue-specific effects of genetic mutations, and (6) genetic interactions in cancer. https://ccr.cancer.gov/cancer-data-science-laboratory/sridhar-hannenhalli	Bethesda
Christine M. Heske, MD	Post-baccalaureate and Post-master	The focus of our lab is to elucidate and target the mechanisms behind therapeutic resistance in pediatric-type sarcomas, especially as related to metabolism and DNA damage repair. Our group conducts translational studies in sarcoma biology, which range from basic to clinical research. Our goal is to identify vulnerabilities specific to sarcoma cells, effectively target them in our disease models, and bring the most promising novel agents into early phase clinical trials for our patients. https://ccr.cancer.gov/Pediatric-Oncology-Branch/christine-m-heske	Bethesda
Ramiro Iglesias-Bartolome, PhD	All	Our lab research focuses on elucidating the signaling mechanisms that control and drive tissue specific stem cell self-renewal and differentiation and their connections to tumor initiation and growth. In particular, our goal is to identify particular G-protein-coupled receptors (GPCRs) and their linked signaling partners that function as master regulators of epithelial stem cells during skin development, tissue homeostasis and cancer. https://ccr.cancer.gov/Laboratory-of-Cellular-and-Molecular-Biology/ramiro-iglesias-bartolome	Bethesda
Sadhana Jackson, MD	Post-masters Postdoctoral Fellow	One of the major obstacles to effectively treating central nervous system (CNS) tumors is the integrity of the blood-brain barrier (BBB). The BBB prevents systemic drug delivery from reaching the brain and brain tumor tissue. While previous studies have mainly focused on circumventing the BBB, very few agents or mechanisms have been explored that modulate	Bethesda

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		the tumor microenvironment to enhance effective therapies for malignant brain tumors. Our collaborative laboratory and clinical investigations center around BBB biology, cancer biology, pharmacokinetics and pharmacodynamics related to optimal CNS drug delivery. As a lab member, your studies will aim to better understand heterogeneity of BBB permeability amongst malignant glioma cells to improve therapeutic options. https://ccr.cancer.gov/pediatric-oncology-branch/sadhana-jackson	
Peng Jiang, PhD	All	Dr. Jiang's research is focused on developing integrative frameworks that leverage the big-data resource in public domains to identify regulators of cancer therapy resistance. A general challenge in cancer research is the lack of data to understand the clinical efficacy of each treatment, while new drugs with distinct mechanisms of action get approved every year. To fill in the gap, we are developing statistical and machine learning infrastructures that transfer knowledge from a vast amount of previous data cohorts to the study of new cancer biology problems. Potential iCURE project: 1. Inference of cytokine activity through large-scale data integration. This project aims to create a computational framework to infer cytokine activities from the single-cell and spatial transcriptomics data through integrating data in the NCBI GEO and ArrayExpress databases. 2. Develop machine-learning frameworks to identify image features of cancer clinical outcomes. This project aims to develop feature selection algorithms for the deep neural networks to achieve knowledge discovery from cancer imaging data, especially high-content tissue imaging. https://ccr.cancer.gov/cancer-data-science-laboratory/peng-jiang	Bethesda
Peter F. Johnson, PhD	All	Our research focuses on mechanisms that regulate signal transmission from RAS oncoproteins to downstream targets in tumor cells and in cells undergoing oncogene-induced senescence (OIS, an intrinsic tumor suppression mechanism). We have found that subcellular localization of RAS effector kinases and mRNAs encoding their target proteins play a key role in determining cellular responses to oncogenic RAS. Our studies involve understanding how these spatial patterns are established and how they lead to oncogenic RAS-induced transformation in cancer cells or, alternatively, elicit OIS in normal cells expressing the same oncogene. The lab uses molecular and RNA biology techniques,	Frederick

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		biochemistry of signaling proteins, microscopic imaging of proteins and mRNAs, and mouse genetics to address these questions. Projects are available in each of these areas. https://ccr.cancer.gov/Mouse-Cancer-Genetics-Program/peter-f-johnson	
Anupama Khare, PhD	All	Our lab is interested in dissecting the mechanistic basis of complex microbial behaviors, with the ultimate goal of defining novel targets for designing antimicrobial treatments. We are specifically interested in identifying the molecules and genetic pathways that underlie interactions between different bacterial species in a polymicrobial community, and how these affect fitness and community dynamics. Our lab also studies the evolution of antibiotic resistance. https://ccr.cancer.gov/Laboratory-of-Molecular-Biology/anupama-khare	Bethesda
Shioko Kimura, PhD	Graduate Student Postdoctoral Fellow	One of the projects in our laboratory is to understand the molecular mechanism of thyroid carcinogenesis. We plan to carry out RNAseq and single cell sequencing analysis of human thyroid cancer specimens that we will receive from our collaborator, the George Washington University, Head and Neck surgery department. The changes in gene expression patterns from normal to adenoma to carcinoma will be analyzed to understand the underlying mechanism(s) of normal cells becoming cancerous and cancer cells acquiring aggressiveness. Once particular pathways and/or genes are found, whether they are indeed responsible for thyroid carcinogenesis, will be confirmed by studies using cell lines and/or mouse. https://ccr.cancer.gov/Laboratory-of-Metabolism/shioko-kimura	Bethesda
Laurie T. Krug, PhD	All	The Krug laboratory is seeking highly motivated individuals to join our team to investigate how the oncogenic viruses Epstein-Barr virus and Kaposi sarcoma herpesvirus alter host defenses and the microenvironment to promote life-long infection and cancer. Our projects integrate molecular virology in cell culture, animal pathogenesis studies, and monitoring of the host immune response to infection in mice and in clinical samples. A deeper understanding of the virus interplay with the host is key to the identification of novel, effective interventions to treat and prevent cancers driven by these oncogenic viruses, an urgent need especially for patients infected with HIV. https://ccr.cancer.gov/HIV-and-AIDS-Malignancy-Branch/laurie-t-krug	Bethesda
Daniel Larson, PhD	All	The primary goal of my laboratory is to understand gene expression in eukaryotic cells, starting from the mechanistic behavior of individual macromolecules and proceeding to their regulation in cells and tissue.	Bethesda

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		Recently, we have begun to apply these experimental and theoretical approaches to the study of hematopoiesis. The differentiation of hematopoietic stem cells into committed lineages in the blood is the result of concerted regulation between transcription, splicing and translation, and a goal of the laboratory is to understand the dynamic interplay between these processes in space and time in single cells. https://ccr.cancer.gov/Laboratory-of-Receptor-Biology-and-Gene-Expression/daniel-r-larson	
Andres Lebensohn, PhD	All	We study how cell signaling pathways produce different physiological outcomes in diverse biological contexts, such as during embryonic development and in adult tissue homeostasis. We focus on WNT signaling, a fundamental pathway that orchestrates patterning and morphogenesis during development and promotes tissue renewal and regeneration in adults. We use powerful genetic screens in human cells to discover new regulatory mechanisms and probe their molecular underpinning through biochemistry and cell biology to understand how they enable the pathway to generate distinct physiological outcomes. Based on this understanding we hope to devise more selective therapeutic strategies to target tumors driven by dysregulation of WNT signaling. https://ccr.cancer.gov/Laboratory-of-Cellular-and-Molecular-Biology/andres-m-lebensohn	Bethesda
W. Marston Linehan, MD	All	The Urologic Oncology Branch conducts clinical and basic research designed to develop better methods for detecting, preventing, and treating patients with kidney cancer. We aim to develop novel forms of targeted precision therapy for patients affected with renal cell carcinoma. We study the genetic and metabolic basis of renal cell carcinoma (RCC), including VHL, MET, FLCN, TFE3, fumarate hydratase and succinate dehydrogenase B pathways and have shown that renal cell carcinoma is fundamentally a metabolic disease. We identified the VHL clear cell renal cell carcinoma gene, helped characterized the VHL/HIF oxygen sensing pathway and are studying novel approaches to targeting the VHL/HIF2 pathway in in-vitro as well as in-vivo models. We have shown that fumarate hydratase-deficient type 2 papillary renal cell carcinoma is characterized by a Warburg metabolic shift to aerobic glycolysis with impaired oxidative phosphorylation and a dependence of glucose for its rapid proliferation and aggressive growth and that in FH-deficient RCC there is an	Bethesda

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		accumulation of fumarate. We use quantitative, isotope-resolved metabolomics on tumor samples removed surgically and tumor derived renal cell carcinoma cell lines to characterize the metabolic basis of FH-deficient RCC which allows for identification and quantification of intermediary metabolites of intermediary metabolism in renal cell carcinoma. We conduct synthetic lethal CRISPR-Cas9 studies MIPE library screening of therapeutic agents to target RCC gene pathways to identify novel therapeutic agents and to evaluate for combinations of agents in in-vitro as well as in-vivo screens. Based on these findings we have developed therapeutic approaches which are currently being evaluated in a clinical trial in patients with localized as well as advanced RCC. https://ccr.cancer.gov/urologic-oncology-branch/w-marston-linehan	
Stan Lipkowitz, MD, PhD	All	My laboratory investigates signal transduction pathways that regulate growth and programmed cell death in epithelial cancer cells. The ongoing projects in my laboratory are: 1) Regulation of signaling by Cbl proteins; 2) Activation of TRAIL death receptor pathways to kill breast cancer cells; and 3) CLPP agonists as treatment for breast cancer. Each project has basic and translational components. https://ccr.cancer.gov/womens-malignancies-branch/stanley-lipkowitz	Bethesda
Zheng-Gang 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	Bethesda

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		tumor cells leads to tumor necrosis and promotes tumor metastasis. Currently, we are trying to understand how necroptosis promotes metastasis. https://irp.nih.gov/pi/zheng-gang-liu	
Beverly A. Mock, PhD	All	Project 1: Precision Medicine in Multiple Myeloma This project utilizes drug-response data we collected at NCATS on 43 multiple myeloma cell lines tested for 1900 compounds. We have developed a predictive pipeline for biomarker detection by combining single agent screen data with large-scale disease-specific data integration. The goal of this project is to develop a flexible precision medicine pipeline, capable of incorporating a wide range of data types and biological knowledge in the form of pathway and gene set annotations, related experimental datasets (including clinical trial data), and known drug-gene interactions to bear on the prediction outcome. We have been able to parse the 1900 compounds into roughly 27 drug clusters, (as defined by their similarity in dose response profiles across all cell lines). In the current iteration of the pipeline, we have observed strong enrichment for drugs with similar classes/mechanism in the detected drug clusters. We will examine the top performing drug/biomarker combination in each of the drug clusters for which the pipeline is able to accurately predict cell line sensitivity. The iCURE scholar would be involved in assessing viability and target/biomarker responses in a set of myeloma cell lines treated with the candidate compounds: myeloma cell lines ranked for their overall sensitivity/resistance to the 1900 compounds, and MM cell line pairs (4 parental and 4 drug resistant lines) which were selected in vitro for their resistance to proteasome inhibitor or dexamethasone treatment, two agents used in myeloma standard of care. Project 2: Proteasome Inhibitor Resistance in Myeloma Two cell line pairs selected for proteasome inhibitor resistance will be utilized to determine which genes/pathways are involved in promoting drug resistance to a third generation proteasome inhibitor, oprozomib. The iCURE scholar would be involved in validating a series of potential target genes/pathways already identified by a combination of gene expression profiling, siRNA screens and analysis of extracellular vesicle cargo	Bethesda

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		https://ccr.cancer.gov/Laboratory-of-Cancer-Biology-and-Genetics/beverly-mock	
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
Hyun Park, PhD	All	The Park lab seeks to understand the role of cytokine receptor expression and signaling in T cell development, differentiation and homeostasis. Specifically, we aim to decipher the transcriptional and post-transcriptional mechanisms of cytokine receptor expression and downstream signaling in T cells that controls their survival and effector function. The lab has generated a series of mouse models using CRISPR/Cas9 technology and conventional gene targeting that replicate human diseases and immune deficiencies. In this context, we generated new mouse strains that links aberrant cytokine receptor signaling to inflammation and autoimmune diseases. The lab utilizes cutting-edge techniques such as RNA-seq, multi-color flow cytometry but also high-dimension analytic tools, such as CyTOF and single cell RNA sequencing (scRNA-seq), to understand the molecular mechanisms in these processes. https://irp.nih.gov/pi/jung-hyun-park	Bethesda
Christina Schroeder, PhD	All	In my group we discover and develop bioactive peptides from venomous creatures and marine extracts that target ion channels upregulated in cancer. We use these peptides to gain understanding into how overexpression of ion channels leads to more aggressive cancers, increased metastasis and poor prognosis with the aim of developing novel diagnostic tools, probes and therapeutics. Our multidisciplinary lab offers projects in areas including natural product peptide discovery, peptide chemistry and structural biology as well as ion channel pharmacology, electrophysiology and cell biology. https://ccr.cancer.gov/chemical-biology-laboratory/christina-i-schroeder	Frederick
Dinah Singer, PhD	Post-baccalaureate	Our research program is focused on characterizing the molecular mechanisms regulating gene expression, especially transcription factors associated with cancer. Recent studies in the lab have identified novel enzymatic properties of the factor BRD4 and a novel cytoplasmic role for the transcription factor TAF7. Post-baccalaureates would under projects	Bethesda

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		focused on further structure/function characterization. https://ccr.cancer.gov/Experimental-Immunology-Branch/dinah-s-singer	
Ramaprasad Srinivasan, MD, PhD	All	Our research group studies the role of key biological pathways driving distinct forms of kidney cancer, including metabolic alterations and DNA damage repair, in order to develop novel therapeutic strategies. iCURE scholars will work with experienced lab members on a translational research project. The goals of the project are to evaluate the importance of various biological pathways in kidney cancer cell growth and survival, and to determine the effects and potential clinical value of inhibiting specific enzymes necessary for energy metabolism and DNA damage repair. https://ccr.cancer.gov/urologic-oncology-branch/ramaprasad-srinivasan	Bethesda
Anish Thomas, MBBS, MD	Graduate Student Postdoctoral Fellow	Our primary goal is to identify novel therapeutics targeting DNA damage response and chromatin and to characterize biomarkers of response for patients with small cell lung cancer, one of the most aggressive and recalcitrant cancers. For our highly translational work, we employ a variety of model systems including patient derived cell lines and PDXs, and extensively study patient tumors and blood harnessing the power of high throughput genomic, epigenomic and proteomic techniques. We are looking for highly motivated scholars interested in bench work or computational research or a combination of both, with immediate clinical impact. https://ccr.cancer.gov/Developmental-Therapeutics-Branch/anish-thomas	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 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	Bethesda

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Brigitte Widemann, MD	All	My team has the primary goal to develop effective therapies for children and adults with rare solid tumors and for patients with genetic tumor predisposition syndromes such as neurofibromatosis type 1 and 2, hereditary medullary thyroid carcinoma and SDH-deficient Gastrointestinal stromal tumors. Our research spans from laboratory research such as preclinical trials to the development and conduct of cutting edge clinical trials with investigational agents and innovative trial designs and endpoints. Students can learn about many aspects of drug development and gain clinical experience as well. https://ccr.cancer.gov/pediatric-oncology-branch/brigitte-c-widemann	Bethesda
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 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 and identifying new RNA surveillance pathways in mammalian cells. https://ccr.cancer.gov/RNA-Biology-Laboratory/sandra-l-wolin	Frederick
Chuan Wu, MD, PhD	All	The neuroimmune interactions within the gut involve the actions of neurotransmitters, neuromodulators and cytokines that carry signals, often bidirectionally, between enteric neurons and immune cells. Our lab focuses on understanding how the interactions between immune system, nervous system and microbiome regulate intestinal and systemic homeostasis. https://ccr.cancer.gov/Experimental-Immunology-Branch/chuan-wu	Bethesda
Ryan Young, PhD	All	Multiple myeloma (MM) is an incurable malignancy of plasma cells marked by extreme genetic and phenotypic heterogeneity. While the genetics of MM have been well-annotated, much less is known about pathogenic signaling in MM and how common mutations contribute to oncogenic signaling. My research program utilizes cutting-edge proteogenomic techniques, high-resolution microscopy imaging and biochemical approaches to elucidate molecular mechanisms underlying oncogenic signaling in MM. The goal of my lab is to find new opportunities for the targeted treatment of MM by exploiting druggable pathways, even in tumors with undruggable driver oncogenes. https://ccr.cancer.gov/Lymphoid-Malignancies-Branch/ryan-m-young	Bethesda

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

Name	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Amy Berrington de González, D Phil.	Postdoctoral Fellow	As cancer treatment and screening has improved markedly the number of cancer survivors is continuing to grow. There are currently 17 million cancer survivors in the USA and this is expected to reach 22 million by 2030. In REB we are studying the long-term impact of cancer treatment on health including the late-effects of radiotherapy, chemotherapy and hormonal therapy. We have several studies underway to investigate the late effects of treatment including the U.S. Pediatric Proton Therapy Cohort, which is a collaboration with the Pediatric Proton Consortium Registry and Massachusetts General Hospital. The Kaiser Breast Cancer Survivors Study. is an electronic medical record linkage study of the late effects of breast cancer treatments in more than 15,000 women from Kaiser Colorado, Washington and Northwest. We have opportunities for post-doctoral fellows to work with these study populations as well as other studies we collaborate on including the Childhood Cancer Survivor Study and the National Wilms Tumor Study. https://dceg.cancer.gov/about/organization/tdrp/reb	Shady Grove
David Borrego, PhD	All	Dr. Borrego's research focuses on improving our understanding of ionizing radiation, associated health risks, and the development of models to clarify how ionizing radiation, like medical x rays from radiography and fluoroscopy, deposits energy in the tissues of the human body. Selected scholar will have an opportunity to apply their knowledge and skills to tackle important questions on occupational dose to medical workers in a large cohort of occupational exposed workers, such as the U.S. Radiologic Technologists Study. This project will provide valuable research and a hands-on experience with large datasets of occupational work history questionnaire data, annual dose of records, and monthly measurement data of occupational doses. In addition, scholars will receive one-on-one mentoring, be able to make valuable contributions to an active cohort study, and have the opportunity to engage with a multi-disciplinary group of researchers eager to welcome a new generation of scientists. https://dceg.cancer.gov/about/staff-directory/borrego-david	Shady Grove

Jiyeon Choi, PhD	All	Our research aim is to understand molecular mechanisms of how heritable genetic variants confer increased cancer risk. We focus on lung cancer risk in smokers and non-smokers from diverse ethnic populations. We use techniques and analytical tools involving functional genomics, bioinformatics, molecular biology, cell biology, and human genetics. To identify functional variants and affected genes from genomic loci associated with lung cancer risk through GWAS, we use approaches including massively parallel reporter assays, CRISPR-based screening, and chromatin interaction studies. We are also building single-cell lung expression quantitative loci (eQTL) dataset to understand genetic regulation of cell-type specific gene expression. We further investigate susceptibility gene function in cell-based systems to elucidate their roles in tumor evolutionary trajectory in the context of somatic driver events. https://dceg.cancer.gov/about/staff-directory/choi-jiyeon	Shady Grove
Neal Freedman, PhD, MPH	All	My research group conducts classical and molecular epidemiologic studies that aim to understand the contributions of common, potentially modifiable, exposures to cancer and disease: including tobacco, coffee, alcohol, and opioids. Our work characterizes the disease risks of these exposures, tracks their prevalence and impact over time, and investigates underlying mechanisms. We are also interested in characterizing, understanding, and tracking premature mortality and health disparities in the US population. https://dceg.cancer.gov/about/staff-directory/freedman-neal	Shady Grove
Hormuzd Katki, PhD	All	Developing individualized lung cancer risk calculators that accurately estimate risks for minorities and subgroups, for use in selecting people for screening: Individualized lung cancer risk calculators are being used to recommend ever-smokers for lung cancer screening. However, current individualized lung cancer risk calculators do a poor job of estimating risk for minorities, women, and other subgroups (Katki et al, Ann Intern Med 2018). We propose to combine big data from nationally-representative surveys, cancer registries, trials, and epidemiologic cohorts, to develop calculators that accurately estimate risk for minorities, women, and other subgroups. The project will be heavily statistical and data-science oriented, and epidemiology training would also be valuable. (Postdoctoral Fellow Specific Project Idea) Quantifying disparities in lung cancer screening:Current lung cancer screening guidelines account for smoking history, but not race/ethnicity/gender, and thus under-select African-Americans and women for screening. However, some of the under-selection is due to African-Americans and women smoking less than other groups. I propose	Shady Grove

		using the Peters-Belson method for quantifying the contributions of known factors towards explaining an observed disparity. This project will identify the reasons for the observed disparities in screening eligibility, to help suggest guidelines that mitigate the disparities. The ideal candidate would have knowledge of R computer programming, statistics, and epidemiology, but a willingness to independently learn these on-the-job would suffice. https://dceg.cancer.gov/about/staff-directory/katki-hormuzd	
Stella Koutros, PhD	Postdoctoral Fellow	Genomic characterization of urologic cancers (prostate/bladder) in large epidemiologic studies: Opportunities to study the genomics of urologic cancer in human study populations available. DNA (somatic mutations/copy number alterations) and RNA (gene expression)-based molecular characterization of tumors are underway to understand the etiology of bladder and prostate cancer. Many opportunities exist to incorporate these data with detailed risk factors, special exposures and germline genetic susceptibility to conducted integrative studies on etiology, disease heterogeneity and mechanisms for cancer. Access to large existing datasets (questionnaires from epidemiologic studies, biological samples, and genomics) for novel hypotheses and studies are also available. https://dceg.cancer.gov/about/staff-directory/koutros-stella	Shady Grove
Mitchell Machiela, ScD MPH	Graduate Student Postdoctoral Fellow	Dr. Machiela's research program is focused on understanding the role of germline variation and somatic mosaicism in relation to cancer risk. He is leading studies of mosaic chromosomal alterations to investigate the risk factors associated with acquired chromosomal alterations and the impact acquired chromosomal alterations have on cancer risk. He also conducts and analyzes genetic association studies to investigate the underlying genetic architecture of both pediatric and common adult cancers. https://dceg.cancer.gov/about/staff-directory/machiela-mitchell	Shady Grove
Meredith Shiels, PhD	Graduate Student	My research largely uses surveillance and descriptive epidemiology to quantify trends in cancer incidence and mortality and premature mortality, and to understand the drivers behind these trends. Potential projects could focus on the following areas: 1) quantifying the role of major risk factors on changing national cancer rates over time; 2) estimating changing cancer risk and burden among HIV-infected people; and 3) conducting detailed analyses of rising premature death rates in the United States. https://dceg.cancer.gov/about/staff-directory/shiels-meredith	Shady Grove
Mary H. Ward, PhD	All	Dr. Ward's research focuses on environmental causes of cancer, with emphasis on drinking water contaminants, pesticides, and other chemicals in relation to childhood cancers and adult gastrointestinal and thyroid cancers. Dr. Ward uses geographic information systems (GIS) to develop	Shady Grove

		new methods for exposure assessment. In cohort and case-control studies, drinking water nitrate increased the risk of thyroid, bladder, kidney, and ovarian cancers. Following up upon these findings, Dr. Ward is using GIS-based models to estimate nitrate levels in drinking water supplies for the Agricultural Health Study, a cohort of pesticide applicators and their spouses with high exposure to nitrate through their private wells. Dr. Ward and her colleagues are also evaluating residential exposures to agricultural pesticides and animal operations in studies of childhood cancers in California and Denmark. https://irp.nih.gov/pi/mary-ward	
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 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	Shady Grove