NIH NATIONAL CANCER INSTITUTE

iCURE

Intramural Continuing Umbrella of Research Experiences (iCURE) – 2025 Possible Projects

This document includes tables listing NCI PIs who have expressed interest in hosting an iCURE scholar. Possible projects or information on their research groups are described in the table but do not represent an inclusive description of all research activities.

If you are interested in working with PIs from the

- **Center for Cancer Research (CCR)**
- **Center for Global Health (CGH)**
- **Division for Cancer Control and Population Sciences (DCCPS)**
- **Division for Cancer Epidemiology and Genetics (DCEG)**

Possible Projects in the Center for Cancer Research (CCR)

Investigator	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Jairaj Acharya, MBBS, PhD	Post-Baccalaureate	Our laboratory studies Sphingolipid/Phospholipid Metabolic Signaling using in vivo model organisms Drosophila and mice. Projects in the laboratory include evaluating effects of mutations in de novo sphingolipid biosynthetic pathway during hematopoiesis, lymphocyte differentiation and function, in natural killer cells, and in tumor susceptibility. At the cellular levels we examine gene regulation, metabolic and lipidomic changes and establish if the observed changes contribute to phenotypic changes observed in the mutants. The fellow will have an opportunity to work with a senior staff scientist in the laboratory in the design and execution of a screen to evaluate lipid modulators of insulin secretion using an in vivo model. The fellow will be trained and encouraged to employ standard laboratory techniques such as tissue culture, cloning, Western analysis , confocal and high resolution microscopy in their studies. https://ccr.cancer.gov/staff-directory/jairaj-k-acharya	CCR Frederick
Mirit 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	CCR Bethesda
Leslie Aldrich, PhD	Post-Baccalaureate, Postdoctoral Candidate	Our primary research focus is the discovery and development of small-molecule modulators of challenging biological targets and pathways. A major area of interest is the autophagy pathway, which is important for metabolism and cellular homeostasis. Recent efforts to target autophagy in cancer have focused on late-stage inhibition with compounds that disrupt lysosome function, which is not specific for autophagy, or early-stage kinase inhibition, which has led to molecules that lack specificity due to the multiple roles of the kinases involved in the autophagy pathway. For example, the lipid kinase VPS34 is present in two multi-protein complexes, and inhibition of VPS34 enzymatic activity inhibits both autophagy and	CCR Frederick

		vesicle trafficking due to inhibition of both complexes. An alternative approach to potentially provide selective autophagy inhibitors is to target key protein-protein interactions that are required for the initiation of autophagy. We recently identified a small-molecule inhibitor of the Beclin1-ATG14L protein-protein interaction, which is required for the formation, proper localization, and function of VPS34 Complex I, that does not affect the Beclin1-UVRAG protein-protein interaction found in VPS34 Complex II, and thus does not cause vesicle trafficking defects like treatment with VPS34 inhibitors. Additionally, our group has developed a high-throughput screen to identify small-molecule inhibitors of the ATG5-ATG16L1 protein-protein interaction, which is involved in LC3 lipidation and autophagosome formation. Current work in our lab combines several interdisciplinary approaches, including medicinal chemistry to improve the properties/potency of initial hits, chemical biology to study binding modes of the small molecules with target proteins and the impact of protein-protein interaction inhibition on the autophagy pathway and other cellular pathways, and cell biology to evaluate the efficacy of autophagy inhibition as a therapeutic strategy in cancer. https://ccr.cancer.gov/staff-directory/leslie-n-aldrich	
Gregoire Altan-Bonnet, PhD	Graduate Student, Postdoctoral Candidate	Discovering the hidden rules of tissue-specific responses to inflammation How organs mount distinct site-specific inflammatory responses despite sharing common components like immune cells, fibroblasts, and extracellular matrix (ECM) is a completely unresolved question in immunology. This project (in collaboration with teams in the UK, Netherlands & Canada) aims to discover the molecular, cellular, and tissue-level rules for organ-specific responses to inflammation. We reimagine how cells perceive signals and interact by proposing: (1) tissue context and cellular experience shape the perception of inflammatory signals, and (2) tissue-specific hierarchies govern the integration of responses by all cell types into coordinated tissue-level outcomes. Our multidisciplinary team has designed a data-driven cycle between in vitro and in silico tissue models. We will use high-throughput robotics to systematically implement and test different in vitro tissue models of mouse organs with different sensitivities for infection or immunopathology. We will interrogate these systems to generate multimodal datasets and ultimately understand how tissue-specific responses emerge. Machine learning analysis of our multimodal datasets yields generative computational models, revealing how cellular responses integrate into tissue-level outcomes. These predictions will guide mechanistic studies in our tissue models, creating an iterative cycle of discovery. Together, this project will transform tissue biology by providing a unified conceptual and methodological framework to solve the riddle of tissue-specific inflammatory	CCR Bethesda

		responses, unlocking future opportunities to treat inflammation across tissues. We seek budding scientists with expertise in bioengineering and/or computer science and/or immunology to join this highly interdisciplinary project. https://ccr.cancer.gov/staff-directory/gregoire-altan-bonnet	
Suresh Ambudkar, PhD	All	Our group studies the role of ABC transporters in the development of multidrug resistance in cancer cells. Emphasis is upon elucidating the mechanism of action of ABC transporters. Biochemical, molecular biological, biophysical, molecular pharmacological, and molecular modeling approaches are used (see review: https://www.nature.com/articles/s41568-023-00612-3). https://ccr.cancer.gov/staff-directory/suresh-v-ambudkar	CCR Bethesda
Andrea Apolo, MD	All	Studying the effectiveness and resistance mechanisms of antibody drug conjugates in urothelial carcinoma and rare genitourinary tumors. Work on developing and characterizing new models of therapy resistance in both in vitro and in vivo settings. https://ccr.cancer.gov/staff-directory/andrea-b-apolo	CCR Bethesda
A Rouf Banday, PhD	All	The overarching goal of my laboratory is to explore molecular mechanisms and delineate therapeutically actionable pathways in bladder cancer. We specifically focus on two key research areas: I. APOBEC3-mediated mutagenesis: This is one of the predominant mutational processes in cancers, driven by APOBEC3 deaminases, and accounts for over 70% of mutations (both coding and non-coding) in bladder cancer. II. Alterations in RNA regulators: These include changes in RNA regulators, such as splicing factors, which occur in more than 20% of bladder tumors. We employ advanced genetic and functional genomics approaches. Trainees will have the opportunity to develop their own research projects that align with the overarching goals of the lab or work on a project proposed by the principal investigator (PI). One such project involves investigating how RNA alterations modulate the tumor immune microenvironment and influence immune therapies. This exciting project will provide trainees with the opportunity to learn a multitude of interdisciplinary approaches, including: a) computational tools for analyzing single-cell and long-read RNA sequencing data, and b) developing and applying CRISPR libraries to evaluate the role of RNA alterations in tumor immunity. In addition to these high-throughput methods, trainees will gain experience in fundamental cell and molecular biology techniques to address specific research questions. Our mentoring approach is tailored to the individual needs of students, combining rigorous training with fostering critical thinking and building a strong scientific foundation. https://ccr.cancer.gov/staff-directory/a-rouf-banday	CCR Bethesda

Pedro Batista, PhD	All	The primary objective of our lab is to investigate how RNA post-transcriptional modifications, known as the epitranscriptome, enable tumor cells to evade treatment. To achieve this, we use genome engineering techniques and patient-derived tumor cell lines as model systems. Currently, we are focusing on the role of RNA-binding proteins in mediating tumor cells' resistance to natural killer (NK) cell cytotoxicity. Ultimately, our research aims to identify novel therapeutic targets for cancer treatment. https://ccr.cancer.gov/staff-directory/pedro-j-batista	CCR Bethesda
Avinash Bhandoola, MB, BS, PhD	Graduate Student, Postdoctoral Candidate	The project follows up on our studies indicating that bone marrow but not splenic plasma cells depend on extracellular ATP, released by Panx3 that binds P2rx4 on plasma cells (Ishikawa et al., Nature, 2024). It is a collaboration with my colleague David Allman at the University of Pennsylvania. One set of proposed studies would extend our observations of plasma cells to niches other than bone marrow and spleen, beginning with intestinal plasma cells. Other select subsets of plasma cells are present in meninges, thymus, and inflammed joints, all of which we wish to assess. Another set of proposed studies addresses transformed plasma cells, termed multiple myeloma. We wish to determine whether at least some human myelomas remain sensitive to inhibition of P2rx4, suggesting drugs that target P2rx4 might be a potential treatment for this disease. Thus, we wish to determine if human myeloma cells remain sensitive to P2rx4 inhibition, and whether P2rx5 might also be implicated in the survival of multiple myeloma, as suggested by early collaborative studies with Ryan Young at the NCI. https://ccr.cancer.gov/staff-directory/avinash-bhandoola#research	CCR Bethesda
Lisa Boxer, PhD	All	The Boxer lab studies chromatin and epigenetics in brain development and how mutations in chromatin regulators lead to neurodevelopmental disorders and cancer. Current projects in the lab focus on the specific types of DNA methylation found in neurons and the proteins associated with these modifications. In most differentiated cell types, DNA methylation is found primarily in the CG sequence, but during postnatal brain development, neurons accumulate high levels of CA methylation and CG hydroxymethylation. Mutations in the known writers, readers, and erasers of these modifications cause neurodevelopmental disorders and cancer, but the function of these modifications in neurons is not understood. One project in our lab uses molecular and genomic approaches to understand the function of these specific types of DNA methylation in neurons. We are investigating why these modifications accumulate specifically in neurons, what proteins associate with these modifications, how these modifications regulate transcription and genome integrity, and how disruption of these modifications leads to neurodevelopmental disorders and cancer. Another project focuses on a specific methyl-DNA-binding protein, MeCP2. Loss-of-	CCR Bethesda

		function mutations in MeCP2 cause the neurodevelopmental disorder Rett syndrome, and MeCP2 is overexpressed in multiple cancers. To investigate the function of MeCP2, we developed an approach to rapidly degrade the MeCP2 protein in the mouse brain. We are using this system to distinguish the primary and secondary consequences of acute loss of MeCP2. These experiments will lend insight into the primary function of MeCP2, and this approach can be broadly applied to other chromatin regulators implicated in neurodevelopmental disorders and cancer. https://ccr.cancer.gov/staff-directory/lisa-d-boxer	
Chongyi Chen, PhD	Post-Baccalaureate, Postdoctoral Candidate	Our lab investigates the topological tension of DNA, known as DNA supercoiling, in the context of chromatin organization and gene expression in human cells. By leveraging our expertise in developing novel genomic technologies and single-cell assays, we aim to understand how DNA supercoiling interacts with other chromatin features, shaping the chromatin environment and regulating gene expression. We also study the regulatory mechanisms and functions of DNA supercoiling across various biological and biomedical settings, with a focus on DNA topoisomerase, the primary modulator of DNA supercoiling and a key target in cancer chemotherapy. Our long-term goal is to translate these discoveries in DNA topology and chromatin biology, together with our advanced genomic and single-cell methodologies, into breakthroughs in cancer biology and medicine. https://ccr.cancer.gov/staff-directory/chongyi-chen	CCR Bethesda
Peter Choyke, MD, FACR	All	Recently, a new type of cancer therapy, radioligand therapy (RLT) was introduced for prostate cancer. In patients with metastatic disease, Lu-177 is conjugated to a molecule that targets an antigen on prostate cancer cells called PSMA. This conjugate targets prostate cancer cells and results in selective cancer killing which greatly improves symptoms and prolongs time to recurrence and overall survival. Based on the success of Lu-177-PSMA my lab is developing other RLTs to target other cancers. For instance, we are developing a nanobody-based conjugate that targets multiple myeloma cells with I-131 nanobody(nb)BCMA. In animals this has shown amazing efficacy with minimal toxicity and we hope to translate this into the clinic. Similarly, we are working on agents that have multiple targets on neuroendocrine tumors to improve the efficacy of treatment of those cancers. This is a very exciting field. We have a team of radiochemists (headed by Orit Jacobson PhD) and biologists (headed by Behnaz Ghaemi PhD) who work together in animal models of cancers to develop new RLT agents against cancer. We are working on a variety of targets and should you choose to join our lab you would work on one or more of these. There is a high likelihood of one or more publications resulting from your work. You must be willing to work with animals and work with small amounts of radioactivity. We operate under the safest conditions in our laboratory and always design experiments	CCR Bethesda

		to minimize exposure to the researcher. If you are interested in research that could translate into clinical application, you should consider our laboratory! https://ccr.cancer.gov/molecular-imaging-branch	
Alex Compton, PhD	All	Projects in the Compton lab (Antiviral Immunity and Resistance Section) focus on the innate immune response to virus infections. We study the processes by which individual cells defend themselves against virus infection, and in doing so, we learn new things about how viruses enter our cells. Our work examines host-virus interactions on multiple scales, from atoms to whole animals. Specifically, we are known characterizing the antiviral functions performed by interferon-induced transmembrane proteins that inhibit the cellular entry of a broad number of pathogenic viruses, including HIV-1, Influenza A virus, Zika virus, and SARS-CoV-2. iCURE scholars would be able to participate in multiple ongoing projects in the lab as well as lead their own independent project. https://ccr.cancer.gov/staff-directory/alex-compton	CCR Frederick
Leah Cook, PhD	Post-baccalaureate, Postdoctoral Candidate	Prostate cancer (PCa) metastasizes to the bone more frequently than any other tissue site. There are limited options for patients with metastatic disease, which is the major contributor of PCa-associated deaths. Our lab previously identified that neutrophils, myeloid immune cells that are generated and stored within bone marrow, are initially protective against BM-PCa that has disseminated into the bone compartment. However, we found that the tumor inevitably becomes resistant to neutrophil anti-tumor responses and suppresses neutrophil function, a finding that can be leveraged for the development of novel immunotherapeutic treatment options. Additionally, a major focus of the Cook Lab is to interrogate mechanisms of the prostate tumor-bone microenvironment that contribute to the progression of bone metastatic prostate cancer (BM-PCa). Further, African American men, compared to European American, are at the highest risk of developing prostate cancer and dying from it. Although some genetic signatures have been identified that may contribute to more aggressive disease in AA men, including increase inflammation and fatty acid synthesis, there is very little know about the key mechanisms of the bone microenvironment that contributes to the propensity of prostate cancer in AA men to spread to and thrive in bone. This project will examine 3 primary mechanisms as a method for specific targeting of BM-PCa in AA men: 1) understanding the role of fatty acid metabolism in prostate cancer racial disparities and 2) defining the importance of citrate and niche-specific metabolism in BM-PCa and 3) delineating the importance of neutrophils in the immune microenvironment of PCa in AA men. We will do this utilizing a combination of preclinical mouse metastasis models, in vitro cell line assays, and indepth, unbiased of BM-PCa patient samples for translating our preclinical studies. https://ccr.cancer.gov/staff-directory/leah-m-cook	CCR Frederick

Dan Crooks, PhD	All	The CCR Clinical Cancer Metabolism Facility (CCM) is housed within NIH Building 10 for the conduct of metabolomics studies and metabolic imaging with a focus on isotope-resolved analysis of clinical samples and patient-based studies. The Mass Spectrometry and Sample Preparation Core Facility is geared toward targeted, ultra-high resolution stable isotope-resolved metabolomics as well as careful sample extraction and preparation methodologies. The Clinical NMR Metabolomics Facility is equipped with a powerful 700MHz magnet with probes available for both targeted, isotope-resolved studies of polar and non-polar metabolite and lipid extracts, as well as high-throughput untargeted discovery by virtue of a high-capacity chilled autosampler. Pre-clinical metabolic imaging resources are available for dynamic small animal metabolic imaging via Dynamic Nuclear Polarization (hyperpolarization) as well as non-hyperpolarized deuterium and 13C metabolic imaging using image deconvolution algorithms developed at CCR. Finally, clinical 13C-hyperpolarized metabolic imaging is made possible via a specialized 13C MRI scanner with custom-made 13C coils and clinical polarizer located in the Molecular Imaging Branch. Trainees will take on isotope-resolved metabolomics and multinuclear MRI-based projects directed toward identifying altered central metabolic pathways in human cancers with the goal of selecting rational therapeutic strategies and novel diagnostic imaging contrasts based on the unique metabolism of human tumors. There are also opportunities for assay and method development on both the high resolution Orbitrap-based mass spectrometry platforms, NMR-based method development and pulse sequence optimization, development and adaptation of multinuclear MRI imaging strategies, and utilization of EPR oximetry imaging for measurement of tissue oxygen concentrations in vivo. https://ccr.cancer.gov/staff-directory/daniel-r-crooks; https://ccr.cancer.gov/staff-directory/w-marston-linehan	CCR Bethesda
Ira Daar, PhD	Post-Baccalaureate	The student will be taught to use the Xenopus (Frog) system and the project will involve completing the functional and molecular characterization of the cellular and developmental effects mediated by the EphrinB transmembrane Eph ligand and Wnt pathway proteins. EphrinB and Wnt receptor mutants will be expressed in developing embryos to determine structural motifs that are important for EphrinB and Wnt receptor-induced developmental effects. EphrinB and Wnt pathway molecules will be co-expressed with proteins found to be associated with EphrinB. The ability of these proteins to physically interact and modulate EphrinB-induced developmental effects will also be assessed. https://ccr.cancer.gov/staff-directory/ira-o-daar	CCR Frederick

Yamini Dalal, PhD	All	Micronuclei are strongly associated with degeneration of the nucleus in human aging, cancer and other diseases. We are interested in studying micronuclei purified from human cells, in order to understand mechanistic and mechanical forces driving chromosome instability in senescence-associated cancers. Our research team is composed of a diversity of award-winning and friendly colleagues engaged in intellectually and technologically cutting-edge interdisciplinary research, with a singular expertise in atomic force microscopy to visualize chromosome and nuclear dynamics. A highly motivated graduate student, postdoc or postbac fellow is welcome to join our eclectic group to take ownership of an exciting and impactful project in chromosome cancer biology. https://ccr.cancer.gov/staff-directory/yamini-dalal	CCR Bethesda
Erin Davies, PhD	Post-Baccalaureate, Postdoctoral Candidate	The Davies lab investigates the developmental and evolutionary origins of stem cell-dependent regenerative abilities in marine and freshwater flatworms. We are determining when and how regenerative abilities are established during embryogenesis in the planarian flatworm, Schmidtea polychroa. Our results suggest that the ability to dynamically regulate positional information after amputation is critical for the establishment of head regeneration abilities and that this may be rate-limiting for the acquisition of regeneration competence. My team seeks to recruit an NCI iCURE Fellow to determine how evolutionarily conserved signaling pathways influence body axis establishment and cell fate specification during S. polychroa embryogenesis. We will determine how positional information is codified during embryogenesis, and how processes used to establish positional identities during embryogenesis compare with those used during regeneration. The Fellow will receive training in visualization of gene expression, transcriptomics, brightfield and confocal microscopy, and functional assay development (RNAi knock-downs, small molecule agonist and inhibitor studies to perturb signaling pathway function). https://ccr.cancer.gov/staff-directory/erin-l-davies	CCR Frederick
William Figg, Pharm.D., MBA	All	Our laboratory research is focused on (1) understanding the (epi)genetics and molecular mechanisms that drive prostate cancer (PCa) progression; (2) elucidating mechanisms responsible for cancer drug resistance; and (3) developing novel treatment strategies for patients with advanced prostate cancer who have progressed on standard regimens. The focus is on translating basic discoveries into novel therapeutics. We are currently investigating novel rationally targeted drug combinations for metastatic castration-resistant prostate cancer (CRPC). The iCURE scholar will be involved with characterizing these compounds in preclinical models (e.g., in vitro spheroid models, ex vivo patient-derived organoid cultures, in vivo PDX/CDX xenografts) to help move the potential drug candidates into the clinic. The project will provide opportunities to acquire expertise in drug development, from drug/target discovery, validation, and advance mechanism of action studies to preclinical and clinical development. Advanced technologies include 3D/organoid	CCR Bethesda

		cell culture systems, next-generation sequencing (RNAseq, single cell), proteomics, CRISPR-based drug screens, bioinformatics analysis, and in vitro/ex vivo assays.https://ccr.cancer.gov/staff-directory/william-douglas-figg	
Eric Freed, PhD	All	The overall goal of our lab is to elucidate basic mechanisms of retroviral replication at the molecular level, with an emphasis on the late stages of the HIV-1 replication cycle. Specifically, much of our current effort is aimed at understanding HIV-1 assembly, envelope glycoprotein (Env) incorporation and function, virus budding, and maturation. We have a special interest in the complex relationship between viral proteins and cellular factors and pathways. We believe that characterizing fundamental aspects of the HIV-1 replication cycle will suggest novel targets for the development of antiretroviral therapies; with the exception of the protease (PR) inhibitors (PIs), there are no approved drugs that target the late stages of the replication cycle. In this regard, we continue to play an important role in the development of HIV-1 maturation inhibitors (MIs). https://ccr.cancer.gov/staff-directory/eric-o-freed	CCR Frederick
Takeo Fujii, MD, MPH	Post-Baccalaureate, Postdoctoral Candidate	Our lab is studying how the immune cells in the context of thromboembolic events (e.g. stroke and deep venous thrombosis [DVT]) affect breast cancer metastasis. My vision is improving survival outcomes of patients with aggressive types of breast cancer such as triple negative breast cancer (TNBC), inflammatory breast cancer (IBC), and brain metastasis by bringing new clinical trials through mechanistic understanding of the role of immune cells in distant organ metastasis. Patients with cancer have a high risk of developing thromboembolic events and the prognosis of the cancer patients with thromboembolic events is significant poor. We have previously reported that DVT is associated with high incidence of brain metastasis among patients with metastatic breast cancer. However, it is not fully understood whether and how thromboembolic events facilitate breast cancer metastasis. More importantly, there is no difference in the cancer treatment after diagnosis of stroke or DVT. Therefore, developing novel therapeutic strategies for patients with breast cancer who develop stroke or DVT by elucidating the role of thromboembolic events in breast cancer metastasis is an unmet clinical need. We have developed novel animal models demonstrating that small ischemic strokes or DVT promote breast cancer brain metastasis. By using these animal models, we are conducting experiments to comprehensively understand how the immune cell profile in the brain and blood circulation make distant organ suitable for breast cancer brain metastasis. Particularly, our research focuses on myeloid cells such as neutrophils, neutrophil extra cellular traps (NETs), and microglia/macrophages/monocytes. Our lab analyzes samples collected from experimental animals and patients by utilizing techniques such as flow cytometry, tissue clearing, immunofluorescence staining, and bulk- and single-cell RNA sequencing. https://ccr.cancer.gov/staff-directory/takeo-fujii	CCR Bethesda

Jeffrey Gildersleeve, PhD	All	Carbohydrates play critical roles in numerous biological processes and disease states. Antibodies that target carbohydrates are useful for a wide range of basic research and clinical applications. For example, two monoclonal antibodies that bind the carbohydrate GD2 are FDA approved for treating children with neuroblastoma. While there are many important and useful carbohydrate targets, there are very few good antibodies that recognize carbohydrates. Our laboratory is addressing this major gap in the field via two new technologies. First, we are developing strategies for directed evolution of carbohydrate-binding antibodies by building libraries of antibodies displayed on cell surfaces and then selecting good binders via FACS. Second, we are developing multiplexed strategies for discovering new antibodies from human B cells, the immune cells that make antibodies. These projects are enabling the development of new diagnostics, therapeutics, and research tools, and they encompass a wide range of techniques and approaches, including antibody expression and evaluation, protein engineering, next-generation sequencing, mammalian cell culture, glycan microarray technology, flow cytometry, and molecular biology. https://ccr.cancer.gov/staff-directory/jeffrey-c-gildersleeve	CCR Frederick
John Glod, MD, PhD	Post-Baccalaureate	P1: Studying Mechanisms of Drug Response and/or Resistance in New Models of Rare Pediatric Cancer Based on current results of ongoing experiments at the time the fellow starts, the fellow will use a cell- or mouse-based model of a pediatric rare tumor in the Rare Tumor Initiative section to examine tumor growth/death response to select FDA-approved or late-phase investigational drugs. The fellow will use molecular biology techniques to probe the mechanism of drug response or resistance. Previous lab experience in molecular biology, cell biology, and/or mouse models is strongly preferred for this project. The project may also involve characterization of new models of rare tumors for how well they represent patient tumors. P2: Correlation of clinical characteristics and course with genomic findings and/or immunoprofile in rare solid tumors. The Natural History Study of Rare Solid Tumors in Pediatrics and Adults has enrolled more than 660 participants particularly with tumors where data and knowledge are lacking. This protocol includes robust clinical data collection, tumor profiling (mutation analysis), and research blood draws to analyze immune subsets which are collected longitudinally. This project would involve the analysis of these data either across multiple tumors or for a specific tumor type to elucidate a better understanding of these rare tumors. P3:Identifying new human genes related to retroviral envelopes as potential	CCR Bethesda

		metabolic regulators We have identified 187 new human genes that derive from ancient retroviral infections related to retroviral envelope glycoproteins (Envs) that bind nutrient transporters. At least 50 of these new genes match structures of receptor-binding domains (RBDs) of retroviral Envs that are highly conserved during primate evolution. Those for which a receptor has been identified bind a metabolic transporter. We will assess the role of of these new endoRBDs as a new network of metabolic regulators and potential drug target. https://ccr.cancer.gov/pediatric-oncology-branch	
Thomas Gonatopoulos-Pournatzis, PhD	All	Alternative pre-mRNA splicing is a dynamic process that enables a single gene to produce multiple mRNA and protein variants, driving transcriptomic and proteomic diversity. Remarkably, over 10% of pathogenic mutations affect alternative splice site activation, and dysregulation of splicing has been implicated in complex diseases, including cancer. Despite its significance, many human alternative exons remain poorly understood, both in terms of their functional roles and the regulatory mechanisms controlling them. Our research group develops and applies cutting-edge functional genomics approaches to study the regulation and biological impact of pre-mRNA processing. We focus on addressing two critical questions: 1. Identifying Functionally Relevant Alternative Exons We aim to uncover which alternative exons in the human genome are functionally significant and contribute to phenotypes associated with cancer, particularly renal cell carcinoma. 2. Decoding the Regulatory Mechanisms of RNA Processing We investigate the factors that control—or misregulate—RNA processing decisions in cancer cells, with the goal of identifying novel regulatory pathways and potential therapeutic targets. If you are interested in these fundamental questions and would like to learn more about our work, please contact Thomas Gonatopoulos-Pournatzis at thomas.gonatopoulos@nih.gov. https://ccr.cancer.gov/staff-directory/thomas-gonatopoulos-pournatzis	CCR Frederick

Michael Gottesman, MD	Post-Baccalaureate	Small cell lung cancer (SCLC) is a recalcitrant disease with poor survival outcomes due to the rapid onset of disease progression and the development of resistance to chemotherapy (cisplatin and etoposide). While SCLC cases have a nearly universal inactivation of the TP53 and RB1 tumor suppressor genes, there is a limited frequency of known oncogenic mutations, suggesting that the disease is largely driven by epigenetic mechanisms. Therefore, we are focused on identifying the epigenetic regulators driving SCLC drug resistance. We recently conducted an open-reading frame (ORF) screen in two SCLC cell lines to identify transcription factors (TFs) that increase resistance to cisplatin. The goals of the project going forward are to confirm our findings and determine the downstream mechanisms by which these TFs confer resistance by regulating the transcription of downstream target genes. We are interested in a student who is enthusiastic about learning about drug resistance and how to quantify drug efficacy in vitro through cell-based assays. Additionally, the student should be interested in understanding how cells regulate gene expression and learning how to assess altered expression through basic molecular techniques. https://ccr.cancer.gov/staff-directory/michael-m-gottesman	CCR Bethesda
Susan Gottesman, PhD	All	Our laboratory uses a range of molecular and genetic approaches to uncover novel regulatory mechanisms in bacteria and to understand how signal transduction works to optimize the organism's growth and response to stress. Trainees develop specific project plans in collaboration with me and other members of the group and will meet with me at least weekly to discuss findings, plans, and the deeper background for the science that we are investigating. Postbaccalaureate fellows, in particular, will work closely with senior members of the lab to learn techniques, as needed. Because the non-pathogenic bacteria we study, E. coli K12, has a large array of genetic tools and decades of previous work, it serves as an excellent easily manipulable model system to probe deeply into regulatory mechanisms, which can then be extrapolated to pathogenic bacteria. While not directly applicable to cancer research, mechanisms of cell response are frequently shared and understanding how the microbiome respond to changing conditions is critical to fully understanding how we are affected and affect our bacterial symbionts and pathogens. Among the possible projects for an iCure scholar: 1) Understanding the roles of a protease adaptor and the proteins it interacts with. 2) Investigating novel small regulatory RNAs and their targets and effects on bacterial physiology. 3) Identifying and investigating the roles of novel regulatory proteins involved in small RNA function.	CCR Bethesda

		https://ccr.cancer.gov/staff-directory/susan-gottesman	
Tim Greten, MD	Post-Baccalaureate, Postdoctoral Candidate	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-baccs, 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/staff-directory/tim-f-greten	CCR Bethesda
Shuo Gu, PhD	All	Our lab is dedicated to uncovering the molecular mechanisms of RNA interference (RNAi) and microRNA (miRNA) pathways, with a particular emphasis on their roles in cancer biology. miRNAs, small noncoding RNAs that act as master regulators of gene expression, influence critical processes in mammalian development and disease. The 2024 Nobel Prize, awarded to pioneers of miRNA research, underscores the transformative impact of miRNAs on our understanding of gene regulation and human health, making this an exciting and dynamic field to explore. Our research focuses on the regulatory mechanisms governing miRNA biogenesis and function, with the ultimate goal of developing new cancer treatments. We take a multidisciplinary approach that integrates genetic studies in cells and animal models, biochemical and structural analyses, next-generation sequencing (NGS), and bioinformatics. A key area of investigation is the role of recurrent mutations in miRNA biogenesis factors, particularly DICER1, which are frequently observed in pediatric cancers and are hallmark features of DICER1 syndrome-related tumors. We have shown that hotspot mutations in the RNase IIIb domain of DICER1 not only disrupt the production of 5p-miRNAs but also lead to a gain of function for specific 3p-miRNAs, which may drive tumorigenesis and represents a promising therapeutic target. We are committed to translating our findings into RNA-based therapies. By identifying cancer-specific miRNA alterations and deciphering their roles in tumor initiation and progression, we aim to develop targeted interventions that could improve outcomes for patients with cancers driven by miRNA dysregulation. Our	CCR Frederick

		research bridges basic science and translational applications, providing a unique opportunity to contribute to cutting-edge cancer biology while working toward real-world therapeutic solutions. We are seeking passionate and driven trainees at all levels to join our team. https://ccr.cancer.gov/staff-directory/shuo-gu	
Sridhar Hannenhalli, PhD	All	We are a purely dry lab with expertise in computational and statistical methods, machine learning, and analysis of a variety of high-throughput omics data. We strongly believe in team science and welcome collaborations. We are broadly interested in Cancer Gene Regulation. Our projects are organized into four broad areas: (1) Transcriptional heterogeneity, cellular plasticity, and regulatory mechanisms underlying oncogenesis, metastasis, and therapy response, (2) Developmental and homeostatic origins of cancer, (3) Development of deep learning models to identify functional non-coding polymorphisms and mutations underlying cancer, and (4) Intrinsic and extrinsic context-specific functionality of genes and cells. https://ccr.cancer.gov/staff-directory/sridhar-hannenhalli	CCR Bethesda
Christine Heske, MD	Post-Baccalaureate, Postdoctoral Candidate	The Translational Sarcoma Biology Section of the Pediatric Oncology Branch is seeking collaborative, inquisitive, and committed applicants to join our team and be part of bench-to-bedside efforts to improve outcomes for patients. The focus of our lab is to elucidate and target the mechanisms behind therapeutic resistance in pediatric-type sarcomas, especially as related to tumor 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 exploitable vulnerabilities specific to sarcoma cells, characterize and evaluate them in relevent disease models, and bring the most promising novel agents and combinations into early phase clinical trials for our patients. As a mentor, I am dedicated to fostering a collaborative research environment that values respect, communication, and diversity of ideas. For more information on our lab and work, see: https://ccr.cancer.gov/staff-directory/christine-m-heske/lab#about For more in-depth project specifics, please feel free to reach out to me by email: christine.heske@nih.gov https://ccr.cancer.gov/staff-directory/christine-m-heske	CCR Bethesda
Mitchell Ho, PhD	All	Our lab studies cell surface glypicans as new cancer therapeutic targets, with a focus on the generation of antibody engineering-based immunotherapies. Our area of research ranges from the investigation of molecular and cellular mechanisms by which glypicans such as GPC1, GPC2, and GPC3 regulate Wnt and Yap signaling to the design of antibody and T cell-based therapeutics. We established mammalian cell display technology and built shark and camel single-domain antibody phage libraries as new high-throughput protein engineering tools to advance drug	CCR Bethesda

		discovery. The immune therapeutics, including CAR-T cells, created in our laboratory, are being tested at clinical stages for treating liver cancers, pediatric cancers, mesothelioma, and other cancers. We are committed to inclusivity and diversity in laboratory research. https://ccr.cancer.gov/staff-directory/mitchell-ho	
James Hodge, PhD, MBA	All	The main objective of the Immunotherapeutics Section of the Center for Immuno-oncology is the development of rationally designed novel immunotherapy combinations for the treatment of cancer. Our lab is specifically focused on two areas: A. Utilizing experimental therapies to modulate immune cells to enable productive immune interactions in the tumor microenvironment Our lab is interested in developing strategic therapeutic combinations that induce immune subset conditioning that results in a) the establishment of effector cells, b) functional enabling/preservation of effector cells, and c) the reduction of negative regulatory elements. We have previously demonstrated that using multiple agents targeting diverse immune-tumor interactions that engage, expand, enable, and evolve the adaptive immune response is effective in controlling established tumors in mouse models. We are currently investigating combination therapies that reprogram the TME to license effector cell populations to treat checkpoint refractory tumors and rare tumors. B. Exploiting immunogenic modulation with standard-of-care and experimental therapies to render cancer cells more sensitive to immune-mediated killing Our group has previously shown that malignant cells that survive or are exposed to nonlethal/sublethal doses of standard-of-care therapies (ex. chemotherapy, radiation, PARP inhibitors, tyrosine kinase inhibitors) may undergo immunogenic modulation, which sensitizes the tumor cells to immune cell targeting. Furthermore, we have demonstrated these FDA-approved agents improve tumor targeting and augment antitumor effects when combined with novel immunotherapy. We are currently investigating several experimental small molecules for their capability to induce immunogenic modulation, the pathways that are central to the treatment-mediated immunogenic modulation, and the antitumor effects of these molecules when combined with other immunotherapeutic agents.https://ccr.cancer.gov/staff-directory/james-w-hodge	CCR Bethesda
Jing Huang, PhD	All	The primary objective of our laboratory is to elucidate the molecular mechanisms underlying gene expression dysregulation in cancer. Our current research centers on the role of the RUNX family proteins, specifically in osteosarcoma (OS) and breast cancer (BC). The RUNX family, consisting of RUNX1, RUNX2, and RUNX3, shares a common cofactor, CBFB, forming transcriptional complexes crucial to physiological processes. Disruption of these complexes is a hallmark of cancer	CCR Bethesda

		progression, exemplified by RUNX2 amplification in OS and CBFB/RUNX1 mutations in BC. Research Projects Our ongoing research is divided into two major projects: Project 1: The RUNX2 Transcriptional Network in Osteosarcoma Project 1 addresses OS, a particularly devastating cancer affecting the younger population, for which no FDA-approved targeted therapies exist. We have identified pro-survival factors in OS cells linked to RUNX2. Utilizing an integrative approach, we aim to unravel the functions of these epigenetic regulators in OS cells. Our ultimate goal is to identify critical factors for OS cell survival and, through mechanistic insights, design innovative strategies for targeted therapy and immunotherapy. Project 2: Roles of CBFB and RUNX1 in Breast Cancer Project 2 focuses on BC. Whole-genome sequencing studies have identified frequent mutations in BC, with CBFB and RUNX1 collectively representing 10-15% of these mutations. Recently, our lab uncovered a surprising dual role of CBFB in BC, regulating not only transcription but also cytosolic and mitochondrial translation. These findings form the basis for a highly effective combination strategy, combining a PIK3CA inhibitor (BYL719) and an autophagy inhibitor (Hydroxychloroquine). Ongoing research aims to unveil additional functions of CBFB in BC cells, with the overarching objective of designing novel therapeutic strategies. https://ccr.cancer.gov/staff-directory/jing-huang	
Kazusa Ishii, MD, MPH	Post-Baccalaureate, Postdoctoral Candidate	Our group discover, develop, and clinically translate T cell receptor-transduced T (TCR-T) cell therapies for the treatment of leukemia, lymphoma, and other incurable cancers. The projects open for the prospective trainees include: 1. Dissect the mechanism of how co-receptors modulate the effector functions of TCR-T cells and apply the findings for the purpose of improving the therapeutic potency of TCR-T cells 2. Elucidate leukemia intrinsic mechanism of resistance to CAR-T cells vs. TCR-T cells 3. Study synergistic effects of CAR-T cells plus TCR-T cells 4. TCR discovery and pre-clinical development of TCRs for the treatment of a). chordoma, b). myeloid malignancies, c). metastatic cancers https://ccr.cancer.gov/staff-directory/kazusa-ishii	CCR Bethesda

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/staff-directory/anupama-khare	CCR Bethesda
Mardo Koivomagi, PhD	Post-Baccalaureate	The overarching goal of our research is to determine the biochemical mechanisms cyclin-dependent kinase use to control cell division. Specifically, much of our current effort is aimed at understanding how the first steps in cell division are controlled and to use the gained knowledge for finding novel therapeutics against cancer. New projects in the laboratory build upon our previous work. Basis for the first project is the discovery of a novel mechanism by which cyclin-dependent kinases drive G1-S transition. This highly unexpected finding linked cell cycle for the first time directly to transcriptional activation of G1/S genes and contrasts with the prevailing model that RNA Polymerase II phosphorylation is merely a basal step in transcriptional activation. In our future research we want to understand more thoroughly how cell cycle cyclin-Cdk complexes are recruited to specific promoters, how they regulate gene expression and study if there are other promoter-specific kinases capable of regulating RNA Polymerase II. The second project builds upon our previous work identifying a novel helix-based docking mechanism for cyclin D, a key driver of cell cycle entry whose major target is the retinoblastoma protein Rb. This finding allows us to search for other substrates potentially using the same docking mechanism to understand the fundamental molecular mechanisms controlled by these kinase complexes. In addition, we are trying to find novel therapeutics that target this novel type of interaction between cyclin D and Rb. To get more insight about the ongoing and starting research in our lab, please visit: https://ccr.cancer.gov/staff-directory/mardo-koivomagi	CCR Bethesda
Mikhail Kolmogorov, PhD	All	Cancer is a disease of the genome. Most cancers are driven by somatic mutations, such as single nucleotide variations (SNVs) that can alter protein sequence and function. Another hallmark of cancer is structural variation (SV), a process that can insert, delete or rearrange large chromosomal fragments. SVs vary greatly in size and complexity: from local oncogene amplifications to catastrophic events that shuffle megabase-scale fragments from one or multiple chromosomes. Recent analysis of 2,658 tumors by the Pan-Cancer Analysis of Whole Genomes	CCR Bethesda

		project showed that ~50% of cancer driver mutations are explained by SVs. Despite that, somatic SVs in cancer remain understudied because of technological and methodological challenges. Most current cancer genomics projects rely on short-read sequencing data, which systematically miss certain classes of somatic SVs and often produce many false-positive calls. Our lab is developing new computational approaches that utilize novel sequencing technologies (such as long-read sequencing or chromatin conformation capture) to better understand the prevalence and role of SV in cancer. In collaboration with other NIH and extramural investigators, we apply these new methods to various cancer types and patient cohorts. We also aim to improve scalability and democratize the cost of long-read sequencing projects, paving the road towards the complete variational landscape of the human genome and microbiome. The potential project for the iCURE scholar include the development of new algorithm and methods for cancer genomics, or applying existing methods to analyze large-scale datasets. The projects will be in collaboration with other members of our lab, and together with many other groups at NCI and NIH. https://ccr.cancer.gov/staff-directory/mikhail-kolmogorov	
Sri Krishna, PhD	All	Metastatic solid tumors remain the leading cause of cancer deaths worldwide. Cancer immunotherapies have provided the promise of long durable regressions for some types of solid tumors. However, many metastatic solid epithelial tumors, including colon, rectal, breast, ovarian and pancreatic cancers, do not respond well to immunotherapies. Central to the success of cancer immunotherapies including T cell-based therapies lie in the 1) accurate identification of antitumor T cells, 2) overcoming profound T cell exhaustion within tumors, and 3) overcoming resistance mechanisms employed by tumors. At the NCI Surgery Branch, we have a unique research environment where basic scientists and clinicians interact to develop unique personalized immunotherapies targeting each patient's tumors. My lab is focused in utilizing this unique human patient samples to discover basic immune principles to understand tumor immunology and develop next-generation immunotherapies. Below are potential projects: 1. We are interested in studying the phenotypic states of antitumor T cells targeting tumor mutations (neoantigens) in humans. These investigations include basic research studies to identify the various states that antitumor T cells can attain across space and time within a human along with primary tumor resistance mechanisms to escape our cell therapies. 2. We are interested in studying and reversing exhausted antitumor T cells from human patient-derived samples through genetic, epigenetic, and immune	CCR Bethesda

		manipulation. 3. We are interested in identifying antitumor T cell receptors (for TCR therapy) against tumor drivers that are shared across patients (including against viral antigenss to develop "off-the-shelf" gene engineered cell therapies for patients with cancer. Keywords: Cancer Immunology and Immunotherapy, T cell dysfunction, Adoptive Cell therapy, Cancer Vaccines, Neoantigens, TCR therapy, Gene therapy https://ccr.cancer.gov/staff-directory/sri-krishna	
Mioara Larion, PhD	Postdoctoral Candidate	One postdoctoral position is available in the Larion laboratory at the Neuro-Oncology Branch, National Cancer Institute. The laboratory is focused on understanding the metabolic changes in brain tumors. In particular, we are interested in revealing the lipid alterations of isocitrate dehydrogenase (IDH1)-mutated gliomas and in exploiting these deregulations for therapeutic applications. We employ a combination of methods such as molecular biology, animal models, as well as in vitro and in vivo metabolomics using Raman Imaging Microscopy, and Mass Spectrometry (MS). The postdoctoral fellow will explore the link between lipid gene alterations in brain tumors and their biology. This position requires expertise in Western Blotting, mammalian cell culture and other common biomedical techniques used in cancer biology labs such as handling tissue samples, preparing tissue slides, staining, and extracting of proteins from brain tissue. https://ccr.cancer.gov/staff-directory/mioara-larion	CCR Bethesda
Vanja Lazarevic, PhD	All	Our laboratory investigates the dynamic immune cell interactions in the meninges and the central nervous system (CNS). Utilizing a multidisciplinary approach, our research aims to mechanistically understand how transcription factors influence the behavior and adaptation of innate lymphoid cells (ILCs) and CD4+ T helper cells within the CNS environment. Our objective is to pinpoint molecular pathways in ILCs and T cells that are key drivers of neuroinflammation and neurodegeneration. Current projects: Transcriptional regulation of CD4+ T cell responses in autoimmunity: This project examines the molecular underpinnings governing the developmental plasticity and tissue adaptation of CD4+ T helper cells. Utilizing the experimental autoimmune encephalomyelitis (EAE) model of multiple sclerosis, we focus on identifying key transcription factors and their gene targets that orchestrate inflammatory responses in the CNS. Immunoregulatory role of ILCs in the CNS:	CCR Bethesda

		The CNS is an immune-privileged site that carefully regulates interactions with immune cells to protect neurons from inflammation. However, the meninges and CNS bone marrow niches are populated by diverse immune cells engaged in immunosurveillance. Despite this presence, CNS borders act as selective gateways, controlling immune cell entry into the parenchyma. Our research aims to understand how these interactions at CNS borders impact immune responses in CNS autoimmunity. Our previous studies revealed that T-BET-dependent NKp46+ ILCs regulate adaptive immune responses in the meninges, influencing the reactivation and stability of myelin-reactive CD4+ Th17 cells. This project focuses on understanding the functions and regulatory mechanisms of ILCs, particularly in the meninges, exploring their tissue origin, and their role in maintaining CNS integrity and contributing to neuroinflammatory diseases. https://ccr.cancer.gov/staff-directory/vanja-lazarevic	
Susan Lea, D.Phil, F.Med.Sci, FRS	Post-Baccalaureate, Postdoctoral Candidate	We use advanced structural biology methods to determine the structures of membrane-embedded protein complexes relevant to human health and disease. In this project we will seek to express, purify and solve the structures of protein complexes related to bacterial infection in key pathogens. The project will give the candidate experience in cutting edge biochemistry of membrane proteins and structure determination by cryo electron microscopy using the advanced facilities in the CSB, Frederick. The work relates to the following recent papers from the laboratory: The project will be the new Center for Structural Biology https://ccr.cancer.gov/staff-directory/susan-m-lea	CCR Frederick
Andres Lebensohn, PhD	All	We are interested in how a small number of cell signaling pathways can orchestrate the thousands of cellular events that give rise to complex organisms during development and maintain tissues in adults. We focus on the WNT pathway, which controls embryonic patterning and morphogenesis, promotes tissue regeneration, and can be a potent cancer driver. We use functional genomics to discover new regulatory mechanisms and probe their molecular underpinnings through biochemistry and cell biology. We use organoids and mouse models to understand how this new regulation enables the WNT pathway to generate distinct physiological outcomes. One possible project focuses on the regulation of WNT signaling by distinct R-spondin receptors. R-spondins are secreted stem cell growth factors that modulate sensitivity to WNT ligands by regulating the abundance of WNT receptors at the cell surface. R-spondins regulate two transmembrane ubiquitin ligases, ZNRF3 and RNF43 (Z/R), which in turn target WNT receptors for internalization and degradation. We found that R-spondins can use two different cell-surface co-receptors, LGRs or heparan sulfate proteoglycans (HSPGs), to regulate Z/R. This project aims to dissect the mechanisms by which R-spondins regulate Z/R, and to determine which	CCR Bethesda

		physiological and pathological processes are regulated by LGR- or HSPG-dependent R-spondin signaling during embryonic development, tissue homeostasis and in cancer. https://ccr.cancer.gov/staff-directory/andres-m-lebensohn	
Kyung Lee, PhD	All	The architecture of a cell is established through varying degrees of hierarchical organizations from single molecules to macromolecular assemblies. Investigating how these molecules interact with one another to form a higher-order structural entity with a new biological function is a key step to unlocking the mystery of life. We are mainly interested in understanding the molecular bases of how the physicochemical properties of pericentriolar scaffold proteins drive the formation of micron-scale self-assemblies with distinct cellular functions. Recently, we found that human polo-like kinase 4, a key regulator of centriole duplication, forms a high M.W. complex with centrosomal scaffold proteins, which cooperatively self-assemble into a higher-order architecture around a centriole in a concentration-dependent manner. Notably, a failure in these events can result in abnormal centrosome numbers, improper spindle formation, and chromosome missegregation that ultimately lead to the development of various human diseases, including cancer, ciliopathy, and microcephaly. Thus, we aim to elucidate the molecular mechanism underlying the assembly of pericentriolar architectures to ultimately understand the etiology of centrosome-associated human diseases. Our work covers various expertise, including biochemistry, biophysics, cell biology, single molecule nanoscopy, structural biology, and computational biology. https://ccr.cancer.gov/Laboratory-of-Metabolism/kyung-s-lee	CCR Bethesda
W. Marston Linehan, MD	All	The CCR Clinical Cancer Metabolism Facility (CCM) is housed within NIH Building 10 for the conduct of metabolomics studies and metabolic imaging with a focus on isotope-resolved analysis of clinical samples and patient-based studies. The Mass Spectrometry and Sample Preparation Core Facility is geared toward targeted, ultra-high resolution stable isotope-resolved metabolomics as well as careful sample extraction and preparation methodologies. The Clinical NMR Metabolomics Facility is equipped with a powerful 700MHz magnet with probes available for both targeted, isotope-resolved studies of polar and non-polar metabolite and lipid extracts, as well as high-throughput untargeted discovery by virtue of a high-capacity chilled autosampler. Pre-clinical metabolic imaging resources are available for dynamic small animal metabolic imaging via Dynamic Nuclear Polarization (hyperpolarization) as well as non-hyperpolarized deuterium and 13C metabolic imaging using image deconvolution algorithms developed at CCR. Finally, clinical 13C-hyperpolarized metabolic imaging is made possible via a specialized 13C MRI scanner with custom-made 13C coils and clinical polarizer located in the Molecular Imaging Branch. Project 1: Trainees will take on isotope-resolved metabolomics and multinuclear MRI-based projects directed toward identifying altered central metabolic pathways in	CCR Bethesda

		human cancers with the goal of selecting rational therapeutic strategies and novel diagnostic imaging contrasts based on the unique metabolism of human tumors. There are also opportunities for assay and method development on both the high resolution Orbitrap-based mass spectrometry platforms, NMR-based method development and pulse sequence optimization, development and adaptation of multinuclear MRI imaging strategies, and utilization of EPR oximetry imaging for measurement of tissue oxygen concentrations in vivo. Project 2: The Linehan Lab is investigating the efficacy of therapeutic agents in our RCC cell models, with a particular focus on fumarate hydratase-deficient RCC in patients affected by Hereditary Leiomyomatosis and Renal Cell Cancer, and FLCN-deficient RCC in patients affected by Birt-Hogg Dube syndrome. We utilize small-scale screens to investigate novel targeted agents in the lab, and in collaboration with the National Center for Advancing Translational Science (NCATS), we perform high throughput drug screening utilizing a library of FDA approved drugs and compounds. The most effective agents are further investigated in 3-D spheroid assays, anchorage-independent growth assays, invasion assays, and finally *in vivo* in xenograft models. These methodologies have already proved successful, with publications in *Cancer Cell*, *Oncotarget*, *J Exp Clin Cancer Res,* and others, and we have numerous models that require further investigation. https://ccr.cancer.gov/staff-directory/daniel-r-crooks; https://ccr.cancer.gov/staff-directory/w-marston-linehan	
Stan Lipkowitz, MD, PhD	All	My laboratory investigates signal transduction pathways that regulate growth and programmed cell death in breast cancer cells. Our goal is to integrate laboratory and clinical research findings into mechanism-based, hypothesis-driven clinical trials for patients with breast cancer. There are three ongoing projects in my laboratory each with basic and translational components. 1) Regulation of signaling by Cbl proteins. In this project we are focused on inhibitors of Cblb, which increase immune mediated killing of tumors due to activation of the T Cell costimulatory pathway. 2) Tumor Necrosis Factor Related Apoptosis Inducting Factor (TRAIL) as an apoptosis induced in triple negative breast cancer (TNBC). We have shown that a subgroup of TNBC cell lines are most sensitive to TRAIL- induced apoptosis and are exploring the mechanisms underlying sensititity or resistance to TRAIL. 3) CLPP agonists as treatment for breast cancer. We demonstrated that a family of drugs inhibits breast cancer cells by imparing their mitochondrial function. We are conducting preclinical studies to bring these to the clinic. https://ccr.cancer.gov/Womens-Malignancies-Branch/stanley-lipkowitz	CCR Bethesda
Jadranka Loncarek, PhD	All	Our lab studies the molecular mechanisms that govern centrosome and centriole assembly in human cells. We explore how centrosome-assembly steps are coordinated with other cell cycle events and how that coordination is perturbed in	CCR Frederick

		pathologies. We are keenly interested in elucidating the role of cell cycle regulators such as mitotic Polo-like kinase 1 in centriole formation and maturation, centrosome copy control, and in understanding how centrosomes and centrosome-associated processes go awry in cancer. Our experimental approaches range from cutting-edge microscopy (light and electron) to high-content transcriptomics and various biochemical and cell biology methods. The successful candidate in this position will be part of a vibrant, collaborative, multi-disciplinary environment and outstanding research infrastructure. They will participate in ongoing, novel projects and collaborative efforts with our colleagues inside and outside NIH. https://ccr.cancer.gov/staff-directory/jadranka-loncarek#research	
Lichun Ma, PhD	Postdoctoral Candidate	Tumor heterogeneity is a major hurdle to effective interventions. While single-cell approaches reveal the diverse molecular landscapes within tumors, they fall short of capturing tumor spatial organization and the interactions between tumor cells and their surrounding microenvironments, which are crucial for understanding how tumor heterogeneity arises and is maintained. This project aims to dissect the spatial dynamics that drive intratumor heterogeneity (ITH) and influence therapeutic outcomes by leveraging cutting-edge spatial omics approaches. We will integrate spatial transcriptomics, spatial proteomics, and single-cell RNA sequencing to map the molecular and spatial landscapes of tumor ecosystems in liver cancer. By analyzing both the spatial context and molecular profiles of millions of individual cells, we aim to uncover how distinct tumor cell populations interact with their surrounding microenvironments, including immune, stromal, and vascular compartments. Key objectives of this project include: 1. Mapping Spatial Heterogeneity: Using spatial omics approaches, we will create high-resolution maps of cells in liver cancer to understand the spatial dynamics of tumor cells. 2. Linking Spatial and Molecular Data: By integrating spatial data and single-cell transcriptome data, we seek to understand the signaling pathways and gene expression programs unique to specific spatial niches. 3. Identifying Therapeutic Targets: Through spatial analysis, we will identify molecular targets linked to patient outcome. The insights gained from this project will advance our understanding of how spatial	CCR Bethesda

		dynamics influence tumor heterogeneity and may lead to the identification of novel therapeutic strategies to overcome the challenges of intratumor heterogeneity. https://ccr.cancer.gov/staff-directory/lichun-ma	
Yuichi Machida, PhD	All	The research in the Machida lab explores the molecular mechanisms responsible for the repair of damaged DNA within cells, with a specific focus on their implications for genomic stability and tumorigenesis. We are particularly interested in proteolytic enzymes that play a crucial role in repairing DNA-protein crosslinks (DPCs), a form of bulky DNA damage blocking DNA replication and transcription. DPCs are prevalent DNA damage that require constant repair. Using a mouse model, our laboratory has successfully demonstrated that the insufficiency of SPRTN, a critical metalloprotease involved in DPC repair, leads to genomic instability premature aging, and the early onset of liver cancer. This mirrors the phenotypes observed in Ruijs-Aalfs Syndrome, which is caused by mutations in the SPRTN gene. Furthermore, the Machida lab investigates the impact of inhibiting DPC repair mechanisms on chemotherapies. We aim to sensitize tumors to DPC-inducing drugs by developing inhibitors for DPC repair enzymes. In summary, our research not only contribute to a deeper understanding of fundamental DNA repair processes but also provide new insights into innovative therapeutic approaches for combating cancer. https://ccr.cancer.gov/staff-directory/yuichi-machida	CCR Bethesda
Christian Mayer, PhD	Postdoctoral Candidate	The laboratory is interested how programmed cell death regulates the development, differentiation and function of the immune system. We are particularly interested in B lymphocyte development and B cell receptor repertoire selection. Moreover, the group explores how these regulatory pathways contribute to self-tolerance, autoimmunity, inflammatory diseases, protective immunity and/or malignancies. The long-term goals are to identify new therapeutic strategies to (1) inhibit unwanted immune responses against self-antigens and harmless environmental antigens, (2) enhance immune responses against tumors and pathogens. https://ccr.cancer.gov/staff-directory/christian-t-mayer	CCR Bethesda
Beverly Mock, PhD	All	Our lab is interested in pharmacologically modulating targets for intervention in multiple myeloma by studying the responses of preclinical cell line and animal models to various single agent and combination drug treatments. Our studies utilize data from a high throughput drug screen that we performed at NCATS to identify new drug combinations that target oncogenes for suppression (eg., MYC, mTOR) and tumor suppressors (eg., p16, MNDA) for re-expression. We have more than 30 myeloma cell lines for use and several animal models, some of which develop bone lesions. The iCURE Scholar would be involved in assessing viability and target biomarker responses of drug treatments in cell lines selected for drug resistance to standard of care options. We are also involved in drug discovery projects to identify and validate small molecules binding to ADRM1 ((hRpn13), a component of the proteasome or mEAK-7, a protein that forms a complex with mTOR. In both projects,	CCR Bethesda

		target engagement and eventually PK/PD studies will be performed to confirm that small molecules are directly affecting their targets –ADRM1 and MEAK7, and also inhibiting cell proliferation or inducing apoptosis. Both molecules have been implicated in various cancers including lung and myeloma. We would evaluate promising candidates in longer term efficacy studies in mouse models. Project 1 is a collaboration with Kylie Walters (CSB) and Deb Citrin (ROB), and project 2 is in collaboration with John (Jay) Schneekloth (CBL). Project 2 will also involve screening for compounds at NCATs with Craig Thomas (LYMB adjunct PI). We have cell lines available to us that have deleted these targets to allow for assessment of off-target defects, and to identify compounds which may be synthetically lethal in combination. Other projects in the lab include an analysis of several mutations occuring in the HEAT domains of mTOR to determine if they are activating or inactivating with respect to mTOR signaling.https://ccr.cancer.gov/laboratory-of-cancer-biology-and-genetics; https://ccr.cancer.gov/staff-directory/beverly-mock	
Diana Monteiro, PhD	Graduate Student, Postdoctoral Candidate	The Monteiro Lab is looking for an iCURE scholar to join our team and pursue a project in protein crystallography/organic chemistry for drug discovery. We're looking for applicants with either a background in biochemistry/biophysics/molecular biology or organic chemistry with an interest in drug discovery from structure-activity relationships. The project will consist of expressing, purifying and crystallizing an oncogenic drug target, characterization using biophysical techniques (e.g. DSF, ITC, MS), collecting diffraction data and solving the structure and determining structure-activity relationships either by high-throughput compound screening or from specific protein-ligand complexes. The project will then progress into a lead compound design stage with activity/binding studies for characterization. Our group has state-of-the-art robotics to aid and streamline protein crystallography, strong connections to accelerator facilities for access to high-brilliant X-rays for data collection on large numbers of samples and collaborations across NCI and CCR for translational purposes. https://ccr.cancer.gov/staff-directory/diana-cf-monteiro	CCR Frederick
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. Diffuse large B-cell lymphoma (DLBCL) is an aggressive malignancy that has a high degree of clinical and genetic heterogeneity. Recent classification systems have identified several novel subgroups of DLBCL with distinct gene expression and outcomes to therapy. Two of these subgroups, BN2 and N1 are enriched for gain-of-function mutations in NOTCH2 and NOTCH1, respectively. However, little is known about the molecular and cellular underpinnings of these subsets due to the lack of model systems. This project aims to define the	CCR Bethesda

		pathogenesis for the BN2 and N1 classes of DLBCL and generate pre-clinical models that could shed light on therapeutically actionable vulnerabilities for these DLBCL subclasses using novel genetically engineered mouse models that have recently been generated within the lab. https://ccr.cancer.gov/staff-directory/jagan-r-muppidi	
Senthil Muthuswamy, PhD	All	The research program at the Muthuswamy laboratory combines mechanistic basic science with translational research opportunities at the NCI intramural program to identify new regulators of resistance to therapies and challenge the notion that cell polarity proteins are tumor suppressors by defining their role as promoters of resistance to cancer therapy. *The Problem and Impact:* Cancer patients receive many treatments, including but not limited to radiotherapy, chemotherapy, molecularly targeted treatments, and immunotherapies. Irrespective of the stage and location of the disease within a patient, the development of resistance to these treatment modalities is arguably the single most important factor contributing to the fatality of cancer patients. Thus, preventing or overcoming treatment resistance is a critical unmet need for controlling cancer and decreasing mortality. *Knowledge gap*: Despite the advances in our understanding of resistance, how cell biological properties such as cell polarity, intracellular protein trafficking, and cellular metabolism regulate therapy resistance are poorly understood; hence, it is an underexplored research area that offers new opportunities for understanding mechanisms and developing therapeutics. *Approach*: We will use a combination of patient-tumor-derived organoids, established cancer cell lines, and T-cell co-culture models of breast and pancreatic cancer to investigate how changes in cell membrane composition and cell polarity proteins affect the development of resistance to therapeutic drugs or immune evasion. The goals are: 1) To identify cell surfaceome changes associated with resistance to therapeutic drugs and T cell killing and understand their mechanisms of action. 2) To identify cell polarity proteins that promote resistance to therapeutic drugs and T-cell-mediated killing and define their mechanisms of action. https://ccr.cancer.gov/staff-directory/senthil-k-muthuswamy/lab	CCR Bethesda
Samuel Ng, MD, PhD	Post-Baccalaureate	Part of the NCI Center for Cancer Research Lymphoid Malignancies Branch, the Ng lab seeks to understand the mechanistic underpinnings of T-cell Non-Hodgkin Lymphoma through basic and translational research using preclinical models and clinical samples. The primary focus of the laboratory is to identify and exploit genetic and chemical vulnerabilities specific to malignant cells. Two major genetic	CCR Bethesda

		vulnerabilities previously identified in the lab include the BATF3/IRF4 transcription factor complex and the SLC7A1 cationic amino acid transporter. We have initiatives in the lab testing means of directly exploiting these vulnerabilities. BATF3 is an AP-1 transcription factor that is physiologically expressed in CD8 memory T cell and CD8 dendritic cell subsets, but which is also upregulated in the majority of T-cell lymphoma cell lines we have profiled. One project involves identifying upstream regulators of BATF3 expression that might provide a means of exploiting the T-cell lymphoma cell line addiction to the transcription factor. SLC7A1 has a critical role in transporting arginine in activated naive T cells and we have shown that our T-cell lymphoma lines are exquisitely sensitive to low arginine concentrations. We have performed whole genome CRISPR screens in cell lines grown with limiting arginine concentrations to identify partners that might be combined with SLC7A1 inhibition to treat T-cell Lymphoma, and a second project includes validation of these targets and assessment of whether these provide a synergistic means of killing lymphoma cells. The Ng lab utilizes a broad range of wet and dry lab techniques to achieve its aims and would welcome an enthusiastic addition willing to learn and to troubleshoot a broad range of these methods in the projects outlined above. https://irp.nih.gov/pi/samuel-ng	
Joe Nguyen, DDS, PhD	All	Head and neck cancer (HNC) is the seventh most common cancer in the world, with an estimated 890,000 new cases and 450,000 deaths annually. While early stage HNC has a high survival rate, more advanced HNC has roughly a 50% survival rate after 5 years. Our project aims to leverage Single-Cell Resolved Spatial Transcriptomics via Visium HD analyses of patient tumor resections to better understand the genes found within the "malignant transformation zone" of epithelial cells. This would allow for us to identify oncogenes or modulators of the immune system for which we can genetically deplete with specially derived cell lines from our lab, murine Cas9+ oral squamous cell carcinoma, mCas9-OSCC-1, -2. These cells were derived by processing oral cancers that formed after 4NQO treatment, a tobacco mimetic, of mice for 4-6 months. Aim 1: To determine the genes of the Malignant Transformation Zone (MTZ) in HNC patients. We will perform Visium HD spatial transcriptomics on HNC patient samples to analyze up to 10 tissue sections. Our focus is on identifying genes differentially expressed between normal epithelium and malignant cells, pinpointing drivers of transformation. Aim 2: To utilize CRISPR/Cas9 to genetically ablate key genes within the MTZ in	CCR Bethesda

		vivo. Leveraging our mCas9-OSCC-1 and mCas9-OSCC-2 cell lines, we will conduct a focused CRISPR screen targeting 1,000-2,000 genes identified from Aim 1. These cells, derived from 4NQO-induced oral carcinomas, will serve as a powerful in vivo model to validate the roles of MTZ-specific genes. This project will advance our understanding of the molecular events driving malignant transformation in HNC, with a particular focus on the MTZ. By combining state-of-the-art spatial transcriptomics with functional genetic screening, we aim to discover actionable targets for intervention. These findings will contribute to the development of precision therapies, potentially improving outcomes for patients with advanced HNC. https://ccr.cancer.gov/staff-directory/joe-t-nguyen	
Rosa Nguyen, MD, PhD	Graduate Student, Postdoctoral Candidate	CAR T-cell therapy is an exciting new treatment modality for diffuse midline gliomas, such as diffuse pontine glioma (DIPG). DIPG is a devastating brain cancer of early childhood with less than 10% survival rate beyond 5 years. Anti-GD2 CAR T-cells have shown in trials to decrease tumor burden and improve clinical symptoms in patients with DIPG. However, further improvement of this treatment is needed to increase objective responses. DIPG is an immunologically "cold" tumor. We will use focused ultrasound to bridge the blood-brain barrier and enhance GD2-CAR T-cell delivery to the tumor. We will also leverage hyperthermia by ultrasound to remodel the tumor microenvironment and enhance the anti-DIPG immune response. Selected skills and knowledge learned through this project: stereotactic brain tumor implantation, Omaya catheter implantation in the brain, CAR T-cell manufacturing and design, CAR T-cell correlative studies, tumor immunology, blood-brain barrier biology, focused ultrasound application, imaging acquisition and analysis skills. https://ccr.cancer.gov/staff-directory/rosa-nguyen	CCR Bethesda
Terren Niethamer, PhD	All	Respiratory disease is a leading cause of death worldwide. This includes chronic lung diseases; infections such as influenza and COVID-19; pediatric lung disease associated with premature birth; and lung cancer, which accounts for over 20% of all cancer deaths. After injury, the normally quiescent lung activates progenitor cells to regenerate the tissue and reestablish its major function, gas exchange with the external environment. However, regeneration is a lengthy process that does not always restore full function. To combat lung disease and improve human health, we must improve existing regenerative strategies and pursue new therapeutic avenues in the lung. My laboratory studies the complex interactions between the pulmonary epithelium and the endothelial cells (ECs) lining capillaries in the lung. Interactions between these cells form and maintain the gas exchange interface of the lung alveolus. We and others have recently discovered that after lung injury, a subpopulation of injury-associated capillary ECs arises. These ECs express inflammatory marker genes,	CCR Frederick

		genes associated with the fetal or immature lung, and genes associated with hypoxia and a switch to glycolytic metabolism. Many of these changes are also associated with cancer cells. This project will use mouse genetics, mouse lung injury models, and primary human cells to determine the role of inflammation and hypoxia in changes to lung EC fate and function. We will determine the role of interferon signaling in inducing aberrant EC fates, the function of hypoxia and hypoxia-induced genes, and the effects of changing EC metabolism on the overall response to tissue damage in the lung. We will use this knowledge to define factors that can shift the balance from dysplastic towards functional regeneration and improve repair of diseased lung tissue. Ultimately, this work will lead to the identification of novel strategies for targeting the lung endothelium to improve respiratory health. https://ccr.cancer.gov/staff-directory/terren-k-niethamer	
Barry O'Keefe, PhD	Postdoctoral Candidate	The Protein Chemistry and Molecular Biology Section (PCMBS) of the Molecular Targets Program (MTP) offers and inclusive, successful, and invigorating research experience on the interface of biochemistry/molecular biology and natural products discovery. The project offered is centered on the discovery and characterization of new potential biotherapeutics from a unique library of partially-purified marine aqueous natural product samples. The library (~100,000 samples) will be tested in MTP bioassays in our high throughput screening laboratory to identify potential anti-cancer activities. The successful iCURE researcher will work with dedicated, experienced PCMBS personnel to isolate, characterize, sequence and potentially recombinantly express in E. coli, novel proteins and peptides with potential anticancer activity. We have already begun screening the library for activity against mesothelioma and will be screening it in additional assays (both cell-based and biochemical) starting next year. The MTP and PCMBS are well equipped and staffed in protein chemistry, natural products chemistry, bioassay development, high throughput screening, functional genomics, and chemical biology. We are a very interdisciplinary laboratory that offers a broad research experience to iCURE candidates. https://ccr.cancer.gov/staff-directory/barry-r-okeefe	CCR Frederick
Francis O'Reilly, PhD	All	Project Title: Comprehensive Mapping of the Protein-Interactome of the Nucleus with Structural Proteomics Currently, structural data is sorely lacking across much of the nuclear protein interactome. The nucleus is a dynamic environment where proteins interact in complex networks to control gene expression, replication, and repair. Understanding these interactions is crucial for unraveling the molecular underpinnings of various diseases. Our lab combines structural biology approaches with proteomics to map	CCR Frederick

		the structure of protein complexes in the nucleus of the cell and identify how these change during the development of cancer. We then seek to develop drugs to that target these protein-protein interactions to act as cancer therapeutics. Our lab also does significant technical development in the field of crosslinking mass spectrometry. This and other approaches that you will learn and develop as a member of our group in structural biology and proteomics are highly sought-after in academia and industry. Our lab is young and collaborative, with projects spanning molecular biology, proteomics, and informatics. You will be instrumental in developing and applying advanced proteomic technologies to systematically identify and quantify protein-protein interactions. We invite applications from motivated students or postdocs who are ready to contribute to this cutting-edge exploration in a multidisciplinary environment. There is excellent support for professional development in the vibrant research community of the NCI. https://ccr.cancer.gov/staff-directory/francis-j-oreilly	
Claudia Palena, PhD	Postdoctoral Candidate	The main goal of our research is to design novel immunotherapies that address two central features of metastatic disease: tumor dissemination and resistance to therapy. Towards this goal, our laboratory has been focused on understanding the process of cancer cell plasticity, i.e., the ability of epithelial cancer cells to undergo phenotypic changes, and how these changes affect anti-tumor immune responses. We have shown that this phenomenon can promote the acquisition of resistance to immunotherapy and have been working on the characterization of drives of cancer plasticity for potential targeting and improvement of anti-tumor responses. In this context, our laboratory has been exploring the targeting of IL-8, TGF-beta, and collagens in the extracellular matrix, which are associated with tumor resistance to immune cytotoxicity, the presence of an unfavorable tumor microenvironment, and immune cell exclusion. Various therapeutics directed against these targets are currently being evaluated in preclinical studies in murine models of cancer, in combination with checkpoint inhibition, vaccines, and other immune-based therapies. The research conducted in our laboratory has a component of basic discovery and a strong component of translational research. https://ccr.cancer.gov/claudia-m-palena	CCR Bethesda
Hyun Park, PhD	All	The laboratory's research interest focuses on understanding the role of cytokine receptor expression and signaling in T cell development and differentiation. Specifically, we seek to understand the transcriptional and post-transcriptional mechanisms of cytokine receptor expression and downstream signaling in T cells. To this end, we employ a variety of genetically engineered mouse models that we have generated in the lab using cutting-edge CRISPR technology and conditional genetic deletion or tissue-specific overexpression. Recently, we generated a new mouse model that links aberrant cytokine signaling to autoimmune inflammation, and	CCR Bethesda

		we plan to use high-dimension analytic tools, such as CyTOF, CITE-seq and scRNA sequencing, to understand the mechanisms. https://ccr.cancer.gov/staff-directory/jung-hyun-park	
Christopher Ricketts, PhD	All	Genetic and genomic alterations in renal cell carcinoma (RCC), at both the germline and somatic level, are known to have direct and profound effects on tumor biology and metabolism. This includes activating the HIF pathway from loss of the VHL and ELOC genes, influencing major cellular growth pathways such as the PI3K/AKT/MTOR pathways through alterations of the PTEN, FLCN, MET, and TFE3/TFEB genes, and disruption of the Krebs cycle via inactivation of key enzymes such as FH and SDH. The Urologic Oncology Branch surgically manages a large cohort of patients that present with a range of different types of renal cell carcinoma that require comprehensive genetic and genomic characterization to better understand their specific tumor biology and highlight potential therapeutic targets. Currently, a major aspect of our work is the characterization of different histologically or genetically defined RCC subtypes utilizing several next-generation sequencing technologies, including whole genome sequencing, whole exome sequencing, transcriptomic sequencing, and DNA methylation analysis. Bioinformatic analysis of these multi-omic approaches allows us to highlight key gene losses or chromosomal alterations and correlate these observations to differences in RNA expression and alterations in pivotal pathways. Additionally, we have NCI patient derived tumor cell line models that represent the majority of the RCC subtypes that can be genetically manipulated to demonstrate the biological relevance of observations gained by tumor characterization. This can demonstrate the potential therapeutic value of targeting specific pathways by direct alteration of these cell lines using techniques such as CRISPR. The analysis of a specific RCC subtype provides an excellent project for an iCURE fellow and they would also benefit from the exposure to a large, multidisciplinary team of scientists, physician-scientists, surgeons, nurses and patient care professionals. https://ccr.cancer.gov/urologic-oncology-branch	CCR Bethesda
Nitin Roper, MD, MSc	All	The Roper laboratory is focused on studying neuroendocrine tumors. The laboratory uses multipronged experimental approaches, including in vivo approaches, to address clinically relevant research questions. In particular, the laboratory seeks to develop new immuno-oncology focused therapeutic strategies for these cancers. The Developmental Therapeutics Branch offers a highly collaborative and interactive research environment with opportunities available to interact with members of a multidisciplinary research community. We are committed to creating an inclusive	CCR Bethesda

		research environment and to supporting the successful research careers of all trainees. https://ccr.cancer.gov/staff-directory/nitin-roper	
Sergio Ruiz Macias, PhD	All	Our program within the Laboratory of Genome Integrity is interested in understanding the molecular mechanisms driving cell fate decisions. For this, we use human and mouse embryonic stem cells (ESCs) as well as mouse embryos to study cell plasticity, pluripotency and differentiation. We leverage the use of these in vitro and in vivo models to get a better comprehension of embryonic development, cell transformation and cancer. In the last few years we focused our efforts to study the molecular determinants of totipotency, the cell state of maximum developmental plasticity on which a single cell can originate a whole organism and is associated to early blastomeres in the embryo, mainly those found in the 2-cell embryo in mice. Our current projects examine the role of new regulators involved in the acquisition and the exit from totipotency and the relevance of the genome architecture in these transitions. https://irp.nih.gov/pi/sergio-ruiz-macias	CCR Bethesda
John Schiller, PhD	Post-Baccalaureate	We are engaged in the development of cancer therapies that are applicable across a broad range of cancer types without molecular profiling and that could be implemented at modest cost, to address the large disparities in access to cancer control in low resource settings. To this end, the project will optimize and characterize a treatment strategy based on recruitment of preexisting T cell immunity generated in response to persistent viral infection or antiviral vaccines via intratumoral injection of their cognate minimal peptide epitopes together with an immuno-stimulant. It will involve tumor challenge studies in mice and in-depth in vitro analyses of the changes in the tumor microenvironment in response to treatment. https://ccr.cancer.gov/staff-directory/john-t-schiller	CCR Bethesda
Martin Schnermann, PhD	All	This project will apply in vivo optical imaging to the design of new ADC chemistry. While the potential of ADCs has been validated, existing agents have proven much more toxic than anticipated. Critically, much of this toxicity is mAb target-independent and due to deleterious effects of the payload and linker. Our approach applies new imaging probes to the development of strategies addressing questions in the field of ADC design. These include: 1) What role do payload properties and labeling chemistries have on tumor and off-target distribution? 2) Are linkers activated by the tumor microenvironment preferred to those cleaved after internalization? We are translating efforts from these imaging studies into the design, synthesis and testing of novel linker-payload combinations. These studies will combine insights and techniques ranging from natural products and fluorophore synthesis to cellular and in vivo characterization. We are creating novel hydrophilic ADC payloads designed to maintain mAb tumor-targeting properties, but then be converted to cell-	CCR Frederick

		permeable active species following tumor localization. These will be applied with the novel linkers and optimized conjugation chemistry that will be defined through our imaging studies. Overall, our goal in these studies is to establish an “imaging-first” workflow for the design and testing of novel targeted drug delivery agents. https://ccr.cancer.gov/staff-directory/martin-j-schnermann	
Jack Shern, MD	All	The Tumor Evolution and Genomics Section located within the Pediatric Oncology Branch, develops and integrates chemical and functional genomic approaches to define mechanisms of molecular evolution that cancer cell populations use in their response to treatment pressures. The work focuses on high-risk sarcomas including rhabdomyosarcoma and malignant peripheral nerve sheath tumors that occur in the pediatric and young adult populations and are notable for aberrant epigenetic modification and/or oncogenic activation of transcription factors. Several potential projects are available in the laboratory including: 1. Use of high-throughput proteomic, functional genomic, and small molecule screening to identify drugs that induce the cancer cell to upregulate cell surface targets which are targetable with antibody-drug conjugates (ADCs) or CAR T cells. 2. Use of single-cell multiomic solution and spatial sequencing to identify and profile tumor cell subpopulations that are resistant to therapy in clinical samples and patient derived xenograft models of sarcomas. A highly motivated graduate student, postdoc or postbac fellow is welcome to join our group to take ownership of an exciting and impactful project that would have the potential to change how we treat patients with pediatric cancer.https://ccr.cancer.gov/staff-directory/jack-f-shern	CCR Bethesda
Ramaprasad Srinivasan, MD, PhD	Post-Baccalaureate, Postdoctoral Candidate	Over the past three decades, it has become increasingly clear that kidney cancer encompasses a diverse group of malignancies that arise in the kidney but are characterized by different genetic, molecular, and clinical features. Therefore, the primary goal of our research is to provide a better understanding of the biological underpinnings of distinct subtypes of kidney cancer, and to develop novel therapeutic strategies for these cancers. Specific projects in the lab focus on: (1) Examining the role of metabolic alterations and DNA damage in distinct forms of kidney cancer by targeting enzymes necessary for energy metabolism and DNA repair. (2) Evaluating novel cellular immunotherapeutic strategies including CAR T cells, as well as other targeted approaches including antibody-drug conjugates (ADCs) in TFE3 translocation renal cell carcinoma.	CCR Bethesda

		(3) Targeting the antioxidant response pathways in fumarate hydratase(FH)-deficient Hereditary Leiomyomatosis and Renal Cell Cancer (HLRCC). Our lab is also interested in leveraging our findings to identify novel synergistic drug combinations. iCURE scholars will have access to state-of-the-art equipment and core facilities, and will work in a dynamic, translational research environment with the opportunity to impact clinical trials and patient care. Our work has led to improvement in the standard of care for patients with Von Hippel-Lindau (VHL)-associated tumors, notably the FDA- approval of the HIF2 alpha inhibitor, belzutifan, the first systemic therapy agent approved for the treatment of patients with organ confined, VHL-associated tumors (NEJM 2021), as well as tumors associated with fumarate hydratase alterations. https://ccr.cancer.gov/staff-directory/ramaprasad-srinivasan	
Gabriel Starrett, PhD	All	Polyomaviruses are ubiquitous non-enveloped double stranded DNA viruses that can cause cancer in humans, especially those that are immune suppressed. Merkel cell polyomavirus is the best studied as the etiologic agent of most cases of Merkel cell carcinoma, a rare, aggressive, neuroendocrine skin cancer. However, a growing body of evidence supports the idea that BK polyomavirus plays (BKPyV) a causal role in bladder cancer carcinogenesis. These viruses are wholly dependent on host DNA damage response machinery and usurp these processes for their own replication. Our lab is interested in understanding how polyomavirus infection can result in host genome mutagenesis, genome instability, and ultimately virus integration that frequently precedes tumorigenesis. To do so we develop and implement a variety of sequencing approached to measure mutation rates, chromatin alterations, and gene expression changes in clinical specimens. We then use this information to build cellular model systems to further dissect polyomavirus-mediated mechanisms of tumorigenesis with the goals of preventing disease and improving therapies in immunosuppressed patients and the general population. https://ccr.cancer.gov/staff-directory/gabriel-j-starrett	CCR Bethesda
Louis Staudt, MD, PhD	All	We are very interested in studying the molecular basis for constitutive signaling by the B cell receptor (BCR) in lymphomas, which is essential for their malignant survival and is an ideal therapeutic target. This phenomenon is particularly important in diffuse large B cell lymphoma (DLBCL), the most common and aggressive lymphoma subtype. In certain molecular subtypes of DLBCL, we have visualized the BCR in the plasma membrane of lymphoma cells using super-resolution microscopy and observed an dense clusters of 50-200 BCR molecules that are the site of constitutive BCR signaling. We have recently generated an array of "nanobodies" that bind to the BCR and other cell surface molecules in lymphomas. Nanobodies are antibodies made by alpacas and other camelids that are compact, single chain binding domains, making them easy to engineer as molecular probes by attaching	CCR Bethesda

		fluorescent proteins or functionally useful enzymes. The project will focus on understanding the protein neighborhood of the clustered BCRs in lymphoma by engineering an anti-BCR nanobody with a highly efficient enzyme that attaches biotin to neighboring proteins. The neighboring proteins can then be easily identified by enrichment of biotinylated proteins using streptavidin beads, following by mass spectroscopy. This is an exciting project because it may reveal protein-protein interactions that are necessary for BCR signaling in lymphomas that could served as new therapeutic targets. https://ccr.cancer.gov/staff-directory/louis-m-staudt	
Esta Sterneck, PhD	Post-Baccalaureate, Postdoctoral Candidate	Mechanisms and targeting of Breast Cancer Cell Plasticity in Metastasis. Our laboratory conducts basic research using breast cancer cell lines, xenograft mouse models, genetic models, and PDX models to characterize the molecular signaling pathways that regulate breast cancer cell biology. In studies involving inflammatory breast cancer and a novel 3D culture systems, we have discovered a signaling pathway that is implicated in cluster dissemination, circulating tumor cell survival, and metastasis (Balamurugan et al., 2023; PMID: 36757813). Ongoing studies are investigating prostaglandin signaling pathways as potential molecular targets to disrupt cell-cell adhesion and tumor cell survival through its effects on mitochondrial metabolism. The trainee shall develop/participate in projects within that framework, which may include one or more of the following: (1) identify the molecular pathways that lead to hybrid epithelial-mesenchymal cell states, cell-cell adhesion, and mitochondrial metabolism, (2) determine pharmacological means to disrupt cell-cell adhesion, (3) employ genetic mouse models and xenograft PDX to study and target breast cancer metastasis, (4) perform genetic screens to identify important pathways in cancer cell survival and metastasis. Through the support of state-of-the art core facilities, the project will provide opportunities to acquire expertise in advanced technologies such as single cell RNA-Seq, proteomics and high-resolution microscopy and/or multiplex image analysis. The laboratory has an adjunct affiliation with the Women's Malignancies Brach at NCI Bethesda, and the Mouse Cancer Genetics Program at NCI-Frederick. https://ccr.cancer.gov/staff-directory/esta-sterneck	CCR Frederick
David Takeda, MD, PhD	All	About the Takeda laboratory: The overall goal of the lab is to understand how cancers rewire their epigenome to evade treatment. The lab uses observations generated from clinical biospecimens such as surgical biopsies or circulating cell free DNA, to guide functional studies in model systems including organoids or patient derived xenografts. We combine genome-scale profiling methods such as ChIP-seq, ATAC-seq, RNA-seq with functional genomic approaches leveraging recent advances in genome editing and CRISPR screening. About the role: The candidate will become proficient with genome editing, genome-scale profiling methods, and CRISPR-based genetic screening. By having access to	CCR Bethesda

		the nation's largest hospital dedicated entirely to clinical research, there are opportunities to study different stages of cancer including disease progression and treatment resistance. This is a great opportunity for candidates to work at the interface of basic science and clinical medicine by using patient samples to design and perform functional mechanistic studies. https://ccr.cancer.gov/staff-directory/david-takeda	
Masaki Terabe, PhD	Postdoctoral Candidate	The Basic Immunology Lab in the Neuro-Oncology Branch is focused on uncovering the immunobiology of glioblastoma, a type of primary brain cancer. Although immunotherapy has transformed cancer treatment over the past five years—gaining approval for over 13 different cancers—its benefits have not yet extended to primary brain cancer. This gap highlights the urgent need for a deeper understanding of the immune responses associated with this disease. Our research centers on unconventional T cells, specifically NKT and MAIT cells, capable of regulating tumor immunity but remain underexplored in brain cancer immunology. NKT cells recognize lipids rather than peptides via CD1d-restricted T cell receptors (TCRs). We found that the products of altered lipid metabolism in glioblastoma are recognized by NKT cells and manipulate the functions of NKT cells. MAIT cells, on the other hand, are MR1-restricted cells that recognize riboflavin (vitamin B2) intermediates as antigens. Our studies show that MAIT cells infiltrate glioblastoma tissue, with their gene signature correlating with patient outcomes. By understanding and potentially modulating the functions of NKT and MAIT cells, we hope to develop novel therapeutic strategies. Our ultimate goal is to combine these approaches with other immunotherapies, such as vaccines and immune checkpoint inhibitors, to improve the outcomes of glioblastoma patients. https://ccr.cancer.gov/staff-directory/masaki-terabe	CCR Bethesda
Carole Thiele, PhD	All	The Cell & Molecular Biology Section (CMBS) of the Pediatric Oncology Branch is a translational research group that aims to develop new therapies for high-risk solid tumors by systematic analysis of the underlying genomics and epigenomics that contribute to tumor growth and resistance to therapy. 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. The CMBS has developed pre-clinical models using patient derived tumors to study mechanisms of neuroblastoma tumorigenesis and assess novel therapeutic interventions. Ongoing studies are aimed at understanding epigenetic/chromatin-	CCR Bethesda

		based mechanisms to re-program and differentiate neuroblastoma tumor cells. These studies include genome-wide assessments of transcriptomic and epitranscriptomic changes that regulate tumor growth, differentiation and response to therapy. Areas of interest include, tumor cell heterogeneity, tumor cell plasticity and tumor microenvironmental pressures that contribute to tumor phenotypic switching. https://ccr.cancer.gov/staff-directory/carol-j-thiele	
Anish Thomas, MBBS, MD	All	Small cell lung cancer is one of the most recalcitrant and chemo-resistant cancers affecting >30,000 individuals in US alone. Most patients with SCLC die within a year of their diagnosis. We have a number of spanning basic, translational, and clinical focusing on SCLC. On the basic side we investigate novel drugs aiming to understand their mechanisms and determinants of response with the goal of clinical translation. On the translational side, we seek to understand and define subtypes of tumors that are most likely to respond to specific therapies, using tools such as WGS, RNA-seq, methylation, scRNA etc on tumor and ctDNA datasets. On the clinical side, we conduct clinical trials of cutting edge therapeutics with a focus on agents targeting DNA replication, repair, and chromatin remodeling. Overall, our findings have contributed to the understanding that SCLC is not just one disease but many subtypes, each with its own vulnerabilities. More recently, we have started to learn about the drivers of SCLC heterogeneity and plasticity between subtypes. Cancer Cell 2021, J Clin Oncol 2018, JAMA Oncol 2023, Clin Cancer Res 2023, Nat Commun 2021, Sci Transl Med 2021, bioRxiv 2023, Cancer Discovery 2023, Cell Rep Med 2024. Our trainees have been recognized by ASCO Young Investigator Awards, International Association for the Study of Lung Cancer (IASLC) Early Career Award, NIH Physician-Scientist Early Investigator Award, Lasker Clinical Research Scholar Award, NCI Pathway to Independence Award for Outstanding Early Stage Postdoctoral Researchers (K99/R00), and have presented their findings at oral presentations at the World Conference on Lung Cancer (WCLC) and the American Association for Cancer Research (AACR) annual meetings. I received the 2022 NCI Director's Outstanding Mentor Award, and the 2024 NIH Postbac Mentor of the Year Award. https://ccr.cancer.gov/staff-directory/anish-thomas#research	CCR Bethesda
Giovanna Tosato, MD	Graduate Student, Postdoctoral Candidate	The laboratory has a longstanding interest in the biology, pathology, molecular biology and biochemistry of endothelial cells and blood vessels, with a focus on their role in cancer. It is well established that endothelial cells and blood vessels play a critical role in the development and growth of many cancer types, since angiogenesis (the process by which new vessels are formed) is necessary to support the progressive expansion of tumors, responding to the increased demand	CCR Bethesda

		of nutrients and oxygen. Current anti-angiogenic therapy of cancer targets only Vascular Endothelial Growth factor (VEGF). This therapy has not substantially improved the survival of cancer patients. Since the principle of reducing the tumor vasculature to reduce cancer growth is well supported by many studies, there is an increased need to understanding how tumor angiogenesis is regulated and how to improve current anti-angiogenic treatment of cancer. Recently, our laboratory has identified a set of ~20 vascular regulators that, together, control tumor angiogenesis. When we reduce levels of these factors, tumor vascularization and tumor growth are substantially reduced. This approach also induces “normalization” of the tumor vasculature (changing the disorderly tumor vasculature into one resembling the normal vasculature), subverts the tumor architecture by clustering the tumor cells into “tumor islands” and alters the metabolic requirements of tumor cells. This transformation is associated with the emergence of new vulnerabilities in the tumor cells, now amenable to treatment. Single-cell spatial transcriptome analyses combined with other biochemical, histochemical and functional studies in vitro and in the mouse provide an opportunity to investigate the biochemical underpinning of the changes in the tumor vasculature induced by the successful approach we have identified. Such studies will be of fundamental to the design of new anti-angiogenic drugs for the treatment of cancer. https://ccr.cancer.gov/staff-directory/giovanna-tosato	
Eugene Valkov, D.Phil	Post-Baccalaureate, Postdoctoral Candidate	Our laboratory focuses on unraveling the molecular mechanisms governing messenger RNA (mRNA) stability, with a particular emphasis on mRNA-based therapeutics. As a junior researcher, you will contribute to an exciting project at the forefront of this rapidly evolving field. Key aspects of the project are as follows: Objective: Develop an optimal set of parameters to control the stability and expression of synthetic mRNA for therapeutic applications. Methodology: - Utilize cutting-edge, high-throughput sequencing techniques - Combine sequencing with in vitro biochemical assays - Analyze large datasets to identify key factors influencing mRNA stability Industry Collaboration: Work alongside pharmaceutical partners, gaining invaluable experience in translational research and drug development processes.	CCR Frederick

		Impact: Contribute to the advancement of mRNA-based therapeutics, a revolutionary approach in treating cancer and other diseases. Skill Development: - Hands-on experience with state-of-the-art sequencing technologies - Data analysis and bioinformatics - Experimental design and execution of biochemical assays - Collaboration with industry professionals This project offers a unique opportunity to participate in groundbreaking research that bridges fundamental molecular biology and real-world therapeutic applications. You will gain comprehensive experience in a field that represents the future of personalized medicine and targeted therapeutics. https://ccr.cancer.gov/staff-directory/eugene-valkov	
Lalage Wakefield, D.Phil	Post-Baccalaureate	Cancer stem cells (CSCs) are a very small “bad actor” subpopulation of tumor cells. The CSCs are the main drivers of tumorigenesis and metastasis and they are very resistant to most cancer therapies. Thus we need a good understanding of these cells to generate more effective cancer treatments. Our lab developed a novel fluorescent reporter that colors the CSCs and allows us to follow their fates and behavior by live-cell imaging both in culture and in the whole animal. We combine fluorescent imaging, single cell fate-mapping, cell and molecular biology techniques and animal modeling to gain mechanistic insights into CSC regulation in breast cancer models. We find that CSCs are hyper-responsive to microenvironmental signals and serve as sensors of microenvironmental quality for the tumor as a whole. We are now dissecting underlying molecular mechanisms and leveraging mechanistic insights to come up with more effective combination therapies. The iCURE Fellow will work closely with our Section’s Staff Scientist (a previous winner of the Staff Scientist Mentoring Award) and will be able to take advantage of all the many additional didactic and skill-training programs offered by the Lab of Cancer Genetics and Biology. https://ccr.cancer.gov/staff-directory/lalage-m-wakefield	CCR Bethesda
Kylie Walters, PhD	Graduate Student, Postdoctoral Candidate	Our group studies naturally existing pathways for protein quality control and degradation and engineer chemical tools to induce the degradation of cancer-associated proteins through these pathways. We pursue our research goals by integrating structural, chemical, and cellular biology approaches, allowing trainees to learn multiple techniques and disciplines. We have focused on the ubiquitin-proteasome pathway, which performs regulated protein degradation. Inhibition of the	CCR Frederick

		proteasome is standard of care for treating hematological cancers and PROTACs, which induce the degradation of proteins of interest by usurping ubiquitination machinery, are in clinical trials for breast and prostate cancer. In our previous studies, we have discovered two of the proteasome ubiquitin receptors and a binding site in the proteasome for an E3 ligase. These discoveries have inspired new therapeutic approaches and provide fundamental insights into how protein lifespans are regulated. We have open projects to apply structural techniques to newly discovered proteasome-associating proteins and to other cancer targets. https://ccr.cancer.gov/staff-directory/kylie-j-walters	
Xin Wei Wang, PhD	All	Primary liver cancer (PLC) is among the top five deadliest cancers in the world. Chronic liver diseases, resulting from complex etiologies such as viral hepatitis, alcohol consumption, parasites, chemical carcinogens, unhealthy diets, or sedentary lifestyle, are significant global health burdens that increase the risk of PLC. We seek to investigate the causes of PLC and to uncover the underlying mechanisms for the development of PLC and to identify functional biomarkers for improving early detection, diagnosis, and therapy. We are currently focusing on three main projects. 1) Exploring molecular heterogeneity and mechanistic insights of PLC across diverse populations with complex etiologies. We have established several national and international collaborative projects. We employ molecular-based technologies such as genomics, transcriptomics, metabolomics, and microbiomics, including single-cell omics to characterize liver specimens across diverse populations. This approach aims to better define liver tumor molecular subtypes with unique tumor biology and develop predictive tools for early onset and treatment response. 2) Investigating synthetic circulating biomarkers for cancer risk assessment and early detection. We utilize the phage display immunoprecipitation sequencing approach to determine serological responses to the human virome as potential functional biomarkers for risk stratification and early onset of liver cancer. We also examine intratumor microbiota linked to tumor biology and liver cancer prognosis. 3) Studying the potential of beneficial viral antigens as a cancer vaccine against PLC. We recently identified a set of viral antigens that exhibited stronger immunoreactivity in healthy individuals than in PLC patients. This discovery us to hypothesize that viral antigens showing robust serological reactivity in healthy individuals may provide protective effects against PLC. https://ccr.cancer.gov/staff-directory/xin-wei-wang	CCR Bethesda
Roberto Weigert, PhD	Graduate Student, Postdoctoral Candidate	Our lab is interested in the mechanisms that trigger the transition from pre-cancerous to cancerous lesions. Specifically, we focus the role played by immune evasion that is based on a variety of processes, including the reprogramming of select immune cell populations. Early responders such as neutrophils, macrophages	CCR Bethesda

		and other myeloid cells have been shown to undergo changes in gene expression and behavior, therefore becoming de facto new cell types that facilitate tumor progression and malignant transformation. This project is aimed at defining the sequence of events leading to this switch in the myeloid linages at early stages of cancer. To this end, we will use a combination of cutting-edge technologies including the combination of intravital microscopy and correlative spatial multi-omics in a oral cancer carcinogen mouse model. https://ccr.cancer.gov/staff-directory/roberto-weigert	
Christopher Westlake, PhD	All	Defects in the formation and function of primary cilia are linked to various cancers and genetic disorders, including polycystic kidney disease. My laboratory has demonstrated that cilium assembly begins within the cell through a vesicular transport-dependent mechanism regulated by the PI3K-Akt signaling pathway, which is often dysregulated in many cancers. This project aims to investigate the dysfunction of ciliogenesis in cancer cells related to PI3K-Akt signaling and its impact on tumorigenesis pathways, such as Hedgehog signaling. We have also recently identified a rare genetic disorder associated with this pathway involving the protein WDR44. In a related project, we are investigating WDR44 patient variants links to ciliogenesis dysfunction and its role in disease development. The Westlake laboratory employs advanced cellular imaging techniques, including super-resolution microscopy and volume electron microscopy, alongside genetic tools like CRISPR-Cas9. We utilize a variety of model systems, including mice and zebrafish, to explore these processes comprehensively. https://ccr.cancer.gov/staff-directory/christopher-j-westlake	CCR Frederick
Brigitte Widemann, MD Co PI's John Glod, PhD	Post-Baccalaureate, Graduate Student	Project 1: Identifying Germline Findings and Additional Risks in Chordoma Patients: Strategies for Prevention and Risk Management In chordoma patients, cancer susceptibility and hereditary cancer syndromes (HCS) are frequently overlooked. In a recent study of 24 chordoma patients, we discovered germline mutations in established cancer-predisposing genes in 38% of the cohort, even though none had a contributory family history or met current criteria for clinical genetic testing. These findings were clinically significant and influenced patient management, underscoring the potential benefits of implementing universal germline testing for patients with solid tumors. By expanding genetic testing in future studies, we aim to deepen our understanding of the genetic basis of chordoma and other solid tumors, while developing tailored counseling, management, and preventive strategies. This will be particularly valuable in addressing the current uncertainties around genetic testing and patient care in this population.	CCR Bethesda

		Project 2: Analysis of Patient Reported Outcomes (PROs) and Neurocognitive Functioning in Patients with Clival Chordoma. There is a dearth of literature characterizing the patient reported outcomes (PRO) and neurocognitive functioning in patients with clival chordoma. The current Rare Tumor Natural History study has collected longitudinal PRO data and cross-sectional neurocognitive data for pediatric and adolescent and young adult (AYA) patients with clival chordoma. The iCURE selectee will assist in literature searches, PRO scoring, and data cleaning and manuscript preparation for the obtained data. This project will allow us to characterize the physical, social-emotional, and cognitive functioning of our sample of Chordoma patients Project 3: Studying Mechanisms of Drug Response and/or Resistance in New Models of Rare Pediatric Cancer Based on current results of ongoing experiments at the time the fellow starts, the fellow will use a cell- or mouse-based model of a pediatric rare tumor in the Rare Tumor Initiative section to examine tumor growth/death response to select FDA-approved or late-phase investigational drugs. The fellow will use molecular biology techniques to probe the mechanism of drug response or resistance. Previous lab experience in molecular biology, cell biology, and/or mouse models is strongly preferred for this project. The project may also involve characterization of new models of rare tumors for how well they represent patient tumors. Project 4: Correlation of clinical characteristics and course with genomic findings and/or immunoprofile in rare solid tumors. The Natural History Study of Rare Solid Tumors in Pediatrics and Adults has enrolled more than 660 participants particularly with tumors where data and knowledge are lacking. This protocol includes robust clinical data collection, tumor profiling (mutation analysis), and research blood draws to analyze immune subsets which are collected longitudinally. This project would involve the analysis of these data either across multiple tumors or for a specific tumor type to elucidate a better understanding of these rare tumors. Project 5: Identifying new human genes related to retroviral envelopes as potential metabolic regulators We have identified 187 new human genes that derive from ancient retroviral infections related to retroviral envelope glycoproteins (Envs) that bind nutrient	

		transporters. At least 50 of these new genes match structures of receptor-binding domains (RBDs) of retroviral Envs that are highly conserved during primate evolution. Those for which a receptor has been identified bind a metabolic transporter. We will assess the role of of these new endoRBDs as a new network of metabolic regulators and potential drug target. https://ccr.cancer.gov/pediatric-oncology-branch	
Matthew Wolf, PhD	Post-Baccalaureate, Postdoctoral Candidate	This project is in the Cancer Biomaterials Engineering Section at NCI Frederick. My lab investigates immunomodulatory biomaterials for use in next-generation cancer immunotherapies. We aim to integrate immunomodulatory biomaterials with immune oncology – the study of the immune system's role in recognizing and fighting cancer. This project aims to study how biomaterial scaffold properties such as architecture and composition affect immune cell recruitment and activation. These findings are applied in a cancer immunotherapy delivery and tissue repair, in vivo. This project has a strong emphasis on cancer immunology, using techniques such as FACS, confocal imaging, and gene expression analysis. Our goals are translational, ultimately to develop strategies that merge tissue repair and cancer therapy after tumor surgery. https://ccr.cancer.gov/staff-directory/matthew-t-wolf	CCR Frederick
Sandra Wolin, MD, PhD	All	We study how noncoding RNAs function, the RNA surveillance pathways that remove defective and harmful RNAs and the mechanisms by which defects in these pathways contribute to diseases such as cancer and autoimmunity. Our approach is multidisciplinary, as we combine molecular biology, genetics, biochemistry and structural biology to discover novel functions for noncoding RNAs and to identify novel RNA surveillance pathways. Projects include deciphering the functions of novel noncoding RNAs and studying how RNA surveillance pathways contribute to disease. https://ccr.cancer.gov/staff-directory/sandra-l-wolin	CCR Frederick
Colin Wu, PhD	All	Numerous human diseases are associated with ribosome dysfunction. These include inherited diseases such as ribosomopathies, a group of mostly congenital diseases caused by mutations in ribosomal proteins or ribosome biogenesis factors, as well as diseases such as cancer and numerous neurodegenerative disorders, which appear later in life. Notably, damage to rRNA can be readily observed in numerous neurodegenerative diseases, including Alzheimer's disease. The involvement of ribosomes in cancer and neurodegeneration may be due to the fact that the ribosome is one of the most long-lived macromolecules in cells, and its ribosomal RNA and protein components are sensitive to environmental insults, such as oxidative stress that can occur during aging or upon exposure to sunlight or some toxins. This susceptibility can lead to accumulation of damaged ribosomes, eventually resulting in aberrant translation and dysregulated gene expression. The pathological consequences of ribosome damage may also be impacted by the complex cellular responses to ribosome-mediated stress. Therefore, a detailed understanding of the stress responses triggered by damaged ribosomes is needed	CCR Frederick

		to distinguish between beneficial and adverse outcomes. Defining the stress responses induced by aberrant translation and deciphering the mechanisms of ribosome quality control pathways that safeguard cells against production of defective proteins from aberrant ribosomes may allow these pathways to be manipulated for therapeutic use. My lab focuses on translational control of gene expression by the ribosome, with particular emphasis on two research projects aiming at deciphering the molecular mechanisms by which mammalian cells degrade nonfunctional rRNAs. To address this, we established a human orthogonal rRNA expression system for molecular and functional dissection of NRD and its interconnected biological processes. https://ccr.cancer.gov/staff-directory/colin-wu	
Chunzhang Yang, PhD	All	Glioma, particularly glioblastoma (GBM), is an aggressive brain cancer with a poor prognosis and limited treatment options. Current therapies—surgery, radiation, and chemotherapy—primarily provide palliative care, leading to minimal disease control and limited improvements in patient survival. Factors contributing to these poor outcomes include genomic heterogeneity, the infiltrative nature of the tumor, and a complex tumor microenvironment. Additionally, gliomas exhibit robust resistance mechanisms, mainly through enhanced DNA repair pathways and dysregulated cell cycle checkpoints, allowing cancer cells to evade treatment. To tackle these challenges, our research team is conducting genome-wide CRISPR guide RNA screens to identify novel biomarkers linked to therapy resistance in glioma. This approach aims to uncover vulnerabilities within glioma cells that can be targeted for more effective therapies. Preliminary results suggest that cell cycle-related kinases play a crucial role in establishing therapy resistance. Our current project goal is to validate these therapeutic vulnerabilities in cell culture and preclinical animal models. The prospective scholar will be actively involved in ongoing genetic screens, managing glioma cell lines, and validating potential therapeutic compounds. This hands-on research will deepen our understanding of glioma biology and facilitate the development of next-generation therapeutics, ultimately aiming to improve outcomes for patients facing this challenging disease. https://ccr.cancer.gov/staff-directory/chunzhang-yang	CCR Bethesda
Li Yang, PhD	All	Tumor dormancy is a critical mechanism in treatment resistance and relaspe. The ability of residual tumor cells to persist in a dormant state can occur during metastatic progression and/or following extended periods of clinical remission that may last decades. The mechanisms for tumor dormancy induction or tumor cell reactivation remain unclear. We are currently using in vitro and in vivo molecular imaging, single-cell RNA sequencing, and mouse models of breast cancer to investigate the molecular and cellular mechanisms mediated by the immune	CCR Bethesda

		microenvironment in tumor dormancy. The candidate will join a team of staff scientist, postdoc, postbac as well as collaborators across institutes. https://ccr.cancer.gov/staff-directory/li-yang	
Robert Yarchoan, MD	Post-Baccalaureate, Postdoctoral Candidate	Research in the Yarchoan laboratory is focused on HIV-associated malignancies and especially those caused by Kaposi sarcoma-associated herpesvirus (KSHV) and other oncogenic viruses. KSHV causes Kaposi sarcoma (KS), multicentric Castleman disease (MCD), primary effusion lymphoma (PEL), and KSHV inflammatory cytokine syndrome (KICS), a disease first identified by our group. I have a translational research program that includes clinical studies and also basic research. iCure scholars would be able to work on one or more of several ongoing projects, including: (1) development of new therapeutic agents for KSHV-associated diseases; (2) dissecting the pathogenesis of KICS, MCD, and other KSHV-associated diseases; (3) analyzing the potential role of somatic mutations in the development of KS. Also, we are currently studying several patients with a very rare form of KS in which the disease has evolved to an anaplastic form associated with somatic mutations and deletions of part of the KSHV genome. The Yarchoan lab collaborates with a number of other laboratories, including other PIs in the HIV and AIDS Malignancy Branch and the laboratory of Denise Whitby in Frederick. https://ccr.cancer.gov/staff-directory/robert-yarchoan	CCR Bethesda
Ryang Young, PhD	All	Multiple myeloma is an incurable malignancy of plasma cells characterized by extensive genetic and phenotypic diversity. My research program leverages advanced proteogenomic techniques, high-resolution microscopy, and biochemical approaches to uncover the molecular mechanisms underlying pathogenic signaling in multiple myeloma. Our ultimate goal is to identify novel therapeutic targets for the precision treatment of multiple myeloma. https://ccr.cancer.gov/staff-directory/ryan-m-young	CCR Bethesda
Ying Zhang, PhD	All	Investigating the Molecular Mechanisms of TGF-β Signaling in Tumor Progression through Smad3-Mediated Transcription and Alternative Splicing. Background: The Transforming Growth Factor-beta (TGF-β) signaling pathway is pivotal in regulating a variety of cellular functions such as proliferation, differentiation, apoptosis, migration, and adhesion, and has critical roles in cancer and other diseases. TGF-β initiates signaling by activating a complex of two types of transmembrane serine/threonine kinase receptors, which in turn activate Smad proteins. Smad3, a key downstream protein in this pathway, regulates transcription by interacting with transcription factors on chromatin. Our recent studies have shown that Smad3 not only impacts transcription but also influences alternative splicing events, which can contribute to processes such as epithelial-mesenchymal transition (EMT) and cancer cell invasion. Project Objectives:	CCR Bethesda

		1. To characterize the mechanisms by which Smad3 regulates long-range chromatin interactions during TGF-β-mediated transcription. 2. To investigate Smad3's role in alternative splicing and its impact on cancer progression, particularly in the context of EMT and invasion. Methods: 1. Chromatin Immunoprecipitation (ChIP) and Chromatin Conformation Capture (3C/Hi-C) to examine Smad3's interactions with chromatin and identify its regulatory regions during TGF-β signaling. 2. RNA-seq Analysis to determine alternative splicing events regulated by Smad3, particularly those that may be altered in cancer progression. 3. Gene Knockdown/Knockout Studies using CRISPR/Cas9 or siRNA targeting tumor suppressors to assess changes in Smad3 function in transcription and splicing regulation. 4. Functional Assays: Conduct EMT and invasion assays in cancer cell models to examine how Smad3-regulated transcriptional and splicing changes impact tumor progression. https://ccr.cancer.gov/staff-directory/ying-e-zhang	

Possible Projects in the Center for Global Health (CGH)

Investigator	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
		More details coming soon	

Possible Projects in the Division of Cancer Control and Population Sciences (DCCPS)

Investigator	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Nicole Everson, PhD	All	The National Cancer Institute's (NCI's) Health Communication and Informatics Research Branch advances research on the processes and effects of communication and health information technology across the cancer control continuum. Research priorities include digital health, health literacy, communication inequalities, social media use and health, health-related misinformation, communication surveillance, patient- provider communication, global cancer stigma, public policy support and multilevel communication interventions. Priority content areas that intersect with health communication include cancer health disparities; health behaviors (e.g. tobacco use, diet, physical activity, alcohol use, cannabis); lung cancer screening; environmental justice/climate change and cancer; early onset cancers. We are looking for a fellow to support the branch's research activities in one or more of these areas. Responsibilities may include data management and analysis to support HCIRB's partnership with the NCI's Cancer Information Service (CIS), which provides smoking cessation counseling and evidence-based information to patients, caregivers, healthcare providers, and researchers about all aspects of cancer, including cancer clinical trials, cancer risks, and survivorship. The CIS' rich database includes documentation of each interaction which can be used to understand cancer information needs and inform NCI's research priorities. Fellows may also collaborate with program directors in new and ongoing analyses of the Health Information National Trends Survey (HINTS), a nationally representative survey of the American public's access to and use of cancer- and health- related information, or other federal datasets, as well as collaborate in systematic literature reviews and portfolio analyses. https://cancercontrol.cancer.gov/brp/hcirb	Shady Grove
Paul Han, MD, MA, MPH	All	Two projects are available for interested candidates, involving primary data collection and secondary data analysis. Project 1 is a qualitative sub-study of the HPV-automated visual evaluation (PAVE) study, a large multi-site global health study evaluating a novel cervical screen-triage-treat strategy in low and middle-income countries (LMICs). This qualitative study aims to understand how patients and health professionals participating in the PAVE study perceive the value of risk communication and shared decision making in cervical cancer prevention and screening. The study involves conducting and analyzing data from individual interviews with patients and physicians in 4 countries (Brazil, El Salvador, Nigeria, and Tanzania). Project 2 is a set of online experimental studies aimed at understanding the effects of	Shady Grove

		different strategies for communicating about the cancer risk associated with alcohol consumption. This study uses online surveys of the general public to experimentally test the effectiveness of different messaging strategies; participants are randomly assigned to different messages (e.g., “alcohol causes cancer” vs. “alcohol increases the risk of cancer”) and then complete surveys measuring their responses to these messages. Quantitative data analyses are conducted to compare the effects of different messages. Project 3 is a qualitative sub-study of the Connect for Cancer Prevention Study (CONNECT), a large prospective cohort of 200,000 adults in the United States designed to further investigate the etiology of cancer and its outcomes. This qualitative study aims to understand the extent to which participants perceive environmental risk information generated by the study as valuable, and their preferences for receiving such information. A diverse sample of participants from different geographic regions of the US will be recruited to explore how sociodemographic factors might influence participants’ views. https://staffprofiles.cancer.gov/brp/prgmStaffProfile.do?contactId=1532&name=Paul-Han&bioType=stf	
William Klein, PhD	All	My colleagues and I in the Behavioral Research Program are engaged in several projects that test and apply risk communication science to behavioral risk factors for cancer. In one set of studies, we are applying principles from the literature on risk communication to design effective methods of communicating lung cancer risk to smokers engaged in lung cancer screening. In another, we are exploring how best to communicate the carcinogenic nature of alcohol in public health messages and in warning labels. In a third set of studies, we are assessing how risk perceptions for genetic disease are related to interest in genetic testing, with the ultimate goal of designing better ways to communicate genetic risk. We also have a team focusing on risk communication regarding climate change and cancer risk. Our program also collects national data using the Health Information National Trends Survey (HINTS) to assess knowledge, attitudes, and risk perceptions regarding behavioral risk factors such as tobacco, alcohol, diet, and physical activity, allowing us to assess determinants of health risk behaviors. Fellows have full access to these and other data sets (e.g., the Tobacco Use Supplement to the Current Population Survey) and can also contribute content for future administrations of these surveys. We have a strong mentorship culture, and our fellows (including iCURE fellows) have gone on to many excellent positions in academia, government, and industry. Fellows have many opportunities for publication, conference attendance/presentation, and collaboration. Fellows also have the chance to participate in our collaborations with other NCI research programs such as the Clinical Genetics Branch in DCEG, which conducts research on individuals at high genetic risk (e.g., Li-Fraumeni Syndrome). Moreover, fellows can get involved in workshop and program planning as desired. https://staffprofiles.cancer.gov/brp/prgmStaffHome.do	Shady Grove

Stephanie Land, PhD	All	The Smoking Cessation at Lung Examination (SCALE) Collaboration is an initiative sponsored by the National Cancer Institute (NCI) to conduct research on lung cancer screening and smoking cessation treatment with a specific group: long-term smokers who are screened for lung cancer using low-dose computed tomography (LDCT). The purpose of the SCALE Collaboration is to share data and methods from funded randomized controlled trials to enable cross-project research on smoking cessation interventions in the setting of lung cancer screening. Numerous research ideas are being generated in this group, such as which types of cessation interventions were most effective. To pursue these ideas, NCI scientists are collaborating with the investigators of the SCALE trials, at 8 academic medical institutions in the United States. Our group is a nice environment for fellows, with interesting work and collegial interactions. We have an active mentorship program with many opportunities for networking, training, and other types of career development. We seek to ensure that projects and types of tasks are matched to the interests of the fellow. https://cancercontrol.cancer.gov/brp/tcrb	Shady Grove
Richard P. Moser, PhD	Post-Baccalaureate, Postdoctoral Candidate	This is an opportunity for someone with interests in behavioral research including health communication, survey and research methods, statistical analysis, and data harmonization. One set of projects would involve joining a team that administers the Health Information National Trends Survey (HINTS), a population-based survey of US adults. This would involve doing data management, running statistical analyses, creating reports based on these analyses, helping to prepare documents to support researchers to use the data, and contributing to publications created by the team, and leading your own analyses, related presentations, and publications. Also, you would be part of a working group with Healthy People 2030 as HINTS supports 5 objectives and you could be part of this trans-HHS initiative. In addition, you would be involved with developing the GEM portal, to promote and disseminate the use of common measures for prospective research to increase data harmonization for merging and comparability. https://hints.cancer.gov/	Shady Grove
Jill Reedy, PhD, MPH, RDN	All	The Risk Factor Assessment Branch (RFAB), in the Epidemiology and Genomics Research Program of the Division of Cancer Control and Population Science (DCCPS), develops, supports, and stimulates assessment of modifiable risk factors among individuals and diverse populations across the cancer continuum to inform and advance health promotion. Below is an example of project that a fellow could lead or contribute to, depending on their skills and experience. There are other examples, but we did not have enough space to include them all here. Project 1: User testing of the Diet History Questionnaire's Personalized Healthy Eating Index Report: Participant and Researcher/Clinician Perspective Background: The Healthy Eating Index (HEI) is a measure of diet quality, independent of quality, that assesses alignment with the Dietary Guidelines for Americans. To extend the application of the HEI, an HEI Report was developed to provide personalized feedback to	Shady Grove

		research participants. The report has been through two rounds of mixed-methods usability testing. The current study will pilot test the HEI report and gather feedback from participants (Aim 1) and researchers (Aim 2) with the goal of revising the report and supporting information to enhance its comprehension and usability. This usability study is nested within the DC Community Organizing for Optimal culinary Knowledge Study (DC Cooks) with Heart. The objective of DC Cooks is to learn about the cooking behaviors of African American adults at risk for heart disease and determine if a community-based cooking intervention will affect home-cooking behaviors. Participants will complete the Diet History Questionnaire III, a food frequency questionnaire, at baseline and then again after receiving an intervention. The study is currently enrolling participants and data collection will conclude in early 2025. An iCure fellow would have the opportunity to conduct qualitative and quantitative analyses addressing Aims 1 and 2. https://epi.grants.cancer.gov/risk/	
Emily Tonorezos, MD, MPH	All	The Office of Cancer Survivorship supports research that both examines and addresses the long and short-term physical, psychological, social, and economic effects of cancer and its treatment among pediatric and adult survivors of cancer and their families. We have a range of research projects in development or in process at any given time, representing a number of opportunities for students or trainees. Our values include scientific integrity, collaboration, creativity, and autonomy. http://survivorship.cancer.gov	Shady Grove
Robin Vanderpool, DrPH	All	The National Cancer Institute's (NCI's) contact center, known as NCI's Cancer Information Service (CIS), was established in 1975 as an essential part of NCI's communication infrastructure and information dissemination efforts. For over 40 years, NCI's CIS has been providing compassionate and scientifically based information to patients, their families and friends, health providers, researchers, and the general public about all aspects of cancer including: cancer clinical trials, cancer prevention, risk factors, symptoms, early detection, diagnosis, treatment, and survivorship. CIS also provides tobacco and cessation counseling and information. The CIS documents each interaction across its contact points (i.e., telephone, LiveHelp, email, social media) using an OMB-approved coding schema, resulting in a rich database profiling active information-seekers that can be used to inform NCI's research priorities. As collaborative partners, DCCPS – specifically the Health Communication and Informatics Research Branch (HCRIB) – and the CIS have established an agenda focused on secondary data analyses of CIS contact data for research and programmatic planning purposes; increasing CIS connections throughout NCI Divisions, Offices, and Centers; and disseminating findings through reports, manuscripts, and presentations. We are looking for a fellow to assist with execution of data management protocols, including quarterly data updates from the CIS Contact Center, and ongoing data cleaning and preparation for analytic activities as well as provision of quantitative analytic support to understand cancer information-seeking on topics that address NCI initiatives and research priorities. This project would result in numerous publication and presentation	Shady Grove

		opportunities, therefore, high quality writing and presentation skills are required. The fellowship would be based in DCCPS/HCIRB and the fellow would also work with the CIS program and Westat, a research services contractor. https://cancercontrol.cancer.gov/brp/hcirb; https://www.cancer.gov/contact	

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

Investigator	Scholar Level	Currently Available Research Areas and Projects	Location (In Maryland)
Mustapha Abubakar, MD, PhD	Post-Baccalaureate, Postdoctoral Candidate	The position is seeking an individual with experience in epidemiology, biostatistics, or bioinformatics interested in understanding the role of disruptive changes in native tissue architecture and cell composition in the etiology, pathogenesis, and natural history of screening-detectable cancers, with a focus on prostate and colorectal cancers. Carcinogenesis is a multistep process, involving progressive morphological and molecular changes that begin in normal tissues and culminate in the emergence of invasive disease. Most epithelial cancers, including colorectal and prostate cancers, are thought to arise via the multistep model of carcinogenesis. With advances in genomic, transcriptomic, and proteomic profiling, it is now evident that colorectal and prostate tumors are not homogenous entities, but aggregations of subtypes with distinct morphological, molecular, and clinical characteristics. Within-tumor-site differences in survival are, therefore, partly attributable to subtype differences (indolent versus aggressive), varying modes of detection (i.e., screening-detected versus symptomatic), clinical presentation (localized versus advanced), and response to treatment (good versus poor), all of which are driven by unique tumor biology that is rooted in the etiopathogenesis of these cancers. Accordingly, improved understanding of the etiopathogenesis and natural history of these cancers is critical towards informing targeted prevention and treatment strategies. Participants in this study are from the Prostate, Lung, Colorectal, and Ovarian cancer (PLCO) screening trial, a large randomized controlled study that recruited men and women 55-74 years across 10 centers in the US between 1993-2001. The candidate would assist with statistical analyses and manuscript preparation and learn about the use of state-of-the-art computational pathology approaches for the in-situ phenotyping the tissue ecosystem. The candidate would be mentored by Mustapha Abubakar, M.D., Ph.D. https://dceg.cancer.gov/about/staff-directory/abubakar-mustapha	Shady Grove
Jonas Almeida, PhD	All	Epidemiological AI trackers - the Data Science and Engineering group at DCEG is focused on real-time, consumer-facing analytical solutions to the analytics of real world data. These are composed of modular software development projects that, collectively, articulate the development of cancer precision prevention solutions. Unsurprisingly, these modular research projects rely heavily on web and cloud computing. AI-based analytics and modeling have risen to the level of a core component for modular software development. The data types tracked vary widely,	

		for example, from mortality data (https://episphere.github.io/mortalitytracker) to consumer genomics (https://episphere.github.io/prs) and digital pathology (https://mathbiol.github.io/tcgatil). Recently, the previously untrackable human-machine configuration of applications like these, has been amply addressed by advancements in generative AI (https://episphere.github/gemini). In particular, multimodal classification such as what takes place in tumor boards has become an key area of integrative data-systems research. If you like coding, algorithms, and data, and want to change the world in real-time, there is probably a DSERG (Data Science and Ebginering Research) project for you. https://dceg.cancer.gov/about/organization/tdrp/dserg	
Laura Beane Freeman, PhD	Post-Baccalaureate, Postdoctoral Candidate	Studies around the world have observed that farmers and other agricultural workers are at elevated risk of several specific cancers, despite lower incidence of cancer overall. In this occupational group, excess risks are observed for Hodgkin lymphoma, non-Hodgkin lymphoma, leukemia, multiple myeloma, and cancers of the brain, skin, lip, stomach, and prostate. Exposures suspected of contributing to the excesses include pesticides, viruses, water contaminants, and a variety of other agents encountered in the agricultural environment. There are a variety of projects related to these and other exposures conducted primarily within the context of the Agricultural Health Study cohort, www.aghealth.nih.gov Current projects involve epidemiologic evaluations of occupational and non-occupational pesticide exposure, and early life agricultural exposures and their influence on risk of cancer and other diseases later in life. https://dceg.cancer.gov/about/staff-directory/beane-freeman-laura	Shady Grove
Li Cheung, PhD	All	I would like to develop methods to accurately estimate the years of life lost due to cancer and the years of life gainable by secondary prevention. Current estimation of the years of life lost are biased as they compare ages of cancer death against either a specific attained age or to actuarial tables estimates of life expectancy, but this approach does not account for differences between those who acquire cancer and the general population. Similarly the years of life-gainable is often estimated as the difference in death age between those diagnosed with localized, distant, and regional stage cancers, but the two populations may not be directly comparable. https://dceg.cancer.gov/about/staff-directory/cheung-li	Shady Grove
Diptavo Dutta, PhD	Postdoctoral Candidate	Advances in high throughput technologies has presented unprecedented opportunities of investigating the complex interplay between genetic and external risk factors in cancer susceptibility. In particular, bulk tissue profiling like gene expressions, proteomics, metabolomics, as well as granular single-cell multi-omics has provided important insights into cancer etiology. Below I list a few projects in the immediate future in the domain which will evolve over time and definitely will not be restricted to these:	Shady Grove

		(1) Identify shared and specific proteomic biomarkers for related cancers: Proteomics have emerged as an exciting candidate in biomarker research due to its stability and druggability. Integrating data across GWAS studies and proteomic studies, we will develop new methods to identify proteins that have similar effects across related cancers as well as proteins which are more cancer-specific. (2) Genetic regulation of longitudinal variation in omics levels: Analysis of omics data have been restricted to cross-sectional/snapshot studies. In earlier smaller-scale candidate studies, temporal fluctuations in omics levels have been shown to be associated to cancers as well as to be hotspots for gene-environment interactions. We will devise novel methods to identify genetic variants associated with longitudinal variation in gene expressions/protein levels and characterize them for different cancers. (3) Partitioned polygenic risk scores (PRS): PRS has, almost exclusively, been used as a predictive tool for cancer risk. However complex diseases like cancers, arise due to the converge of multiple heterogeneous distinct processes/mechanisms. Using multiple omics data modalities, we will partition the PRS into "components" pertaining to such relevant biological mechanisms, which will add critical interpretability and improve personalized risk stratification. https://diptavo.github.io/, https://dceg.cancer.gov/about/staff-directory/dutta-diptavo	
Gretchen Gierach, PhD, MPH	Post-Baccalaureate, Postdoctoral Candidate	The position is seeking an individual with experience in epidemiology or biostatistics interested in hormonally-related exposures and health outcomes, including breast cancer, to work on studies from The NCI DES Follow-up Study, which is a nationwide research study following more than 21,000 women and men to learn as much as possible about the long-term health effects of exposure to diethylstilbestrol (DES): https://dceg.cancer.gov/research/what-we-study/des-study Diethylstilbestrol (DES) is a known human carcinogen. DES was the first estrogen pill, produced in 1938 and widely used from the mid-1940s until the early 1970s as a treatment for women who were at risk of miscarriages. It is estimated that millions of Americans (mothers, daughters, and sons) may have been exposed to DES. The NCI DES Follow-up Study is the largest ongoing study on long-term health and DES exposure. The candidate would assist with statistical analyses and manuscript preparation, and will learn about DES as a model for studying endocrine-disrupting agents and cancer risk as well as the potential clinical impact of study findings. The candidate would be mentored by Gretchen Gierach, Ph.D., M.P.H. https://dceg.cancer.gov/about/staff-directory/gierach-gretchen	Shady Grove
Jonathan Hoffman, PhD, MPH	All	The objective of my research is to understand the role of pesticides and other agricultural exposures, per- and polyfluoroalkyl substances (PFAS), and other risk factors in the development of various malignancies, focusing in particular on multiple	Shady Groce

		myeloma and kidney cancer. Specifically, I am conducting classical and molecular epidemiology studies in the following three areas: 1) agricultural exposures and cancer; 2) PFAS and cancer risk; and 3) the biological mechanisms of multiple myeloma development and progression. In particular, there are opportunities for projects within the Biomarkers of Exposure and Effect in Agriculture (BEEA) study, a molecular epidemiologic subcohort within the Agricultural Health Study. The BEEA study is designed to facilitate investigations of the potential biological mechanisms through which pesticides and other agricultural exposures influence cancer risk. I am also exploring opportunities to follow up on findings from BEEA in other agricultural populations. In addition, there would be opportunities for classical, molecular, and genetic epidemiologic studies of multiple myeloma and kidney cancer, including investigations of racial and ethnic disparities in these malignancies. Ultimately, the goal of this work is to better characterize the carcinogenic potential of these high priority and widespread environmental and occupational exposures, and to generate new insights into the etiology of multiple myeloma, kidney cancer, and other cancers. https://dceg.cancer.gov/about/staff-directory/hofmann-jonathan	
Sadie Hutson, PhD, RN, FAAN, Co-PIs: Camella Rising, PhD, MS, RDN	Project 1- Graduate Student, Postdoctoral Candidate Project 2- Post-Baccalaureate	**Project 1:** The Clinical Genetics Branch of the National Cancer Institute (NCI) is seeking a post-doctoral fellow to work with the psychosocial and behavioral science research program. This program conducts translational research to improve the psychosocial well-being and biobehavioral outcomes of individuals, families, and communities at elevated risk of cancer. The post-doctoral fellow will work with an interprofessional team of scientists focused on examining the psychosocial consequences of living at high genetic risk of cancer among patients, family members, and care partners. Specifically, an opportunity exists to conduct psychosocial and behavioral research in Inherited Bone Marrow Failure Syndromes (IBMFS). IBMFS are a group of rare disorders of the bone marrow that can result in a number of medical conditions, including a high risk of cancer. A new initiative to explore the needs of patients with Fanconi Anemia (FA) as well as the needs of their care partners is underway. This study will implement qualitative and quantitative methods in a multi-site and global team effort to ensure rigorous attention to the psychosocial needs of this unique aggregate. This mixed methods study includes a combination of survey and interviewing approaches, complemented by thematic and content analysis of participant stories. **Project 2:**	Shady Grove

		Our interprofessional team of clinicians and researchers examine psychosocial and behavioral aspects of living with rare cancer syndromes using quantitative, qualitative, and mixed methods research approaches. Project 1 offers the opportunity to investigate health behaviors (e.g., diet, physical activity, sleep) and associated psychosocial factors among Li-Fraumeni syndrome (LFS) populations (e.g., adolescents and young adults with LFS, adults with LFS). Project 2 involves working on a team that will conduct community-engaged research to identify intervention targets, components, and outcome measures to include in a future digital psychological intervention for adolescents and young adults with LFS. Project 3 provides an opportunity to study clinically relevant psychosocial and behavioral needs surrounding topics such as end of life care and advanced care planning for adolescents and young adults with LFS. Your role as an iCure scholar will depend on your level of training, education, and goals. Ideally, though not mandatory, you have some knowledge of psychological, social, and behavioral aspects of living with cancer. You will be mentored by a staff research fellow and/or a post-doctoral fellow, with the support of senior staff. Through this project, you will develop analytic skills, learn about the psychosocial and behavioral implications of LFS and cancer on individuals and families, and learn how to summarize and disseminate research findings. You will have opportunities to co-author publications and/or scientific abstracts.https://dceg.cancer.gov/research/what-we-study/psychosocial-effects	
Sarah Jackson, PhD, MPH	All	This fellowship will involve work on sex differences in cancer incidence and survival and/or cancer among sexual and gender minority (SGM) adults. The selected fellow could work on one or both of these topics depending on their interests and qualifications. Research projects related to sex differences would entail conducting research on the role of sex differences in the immune response to viruses and cancer, as well as examining the role of sex hormones in the development of cancer. Research projects related to SGM populations would include a range of topics related to screening, risk factors, incidence, and outcomes of cancer among transgender and gender diverse adults. All these projects will involve analyses of data from surveys, registries, cohort studies, and electronic health records. The fellow will develop and enhance their analytic skills in SAS or R, and their scientific writing and presentation skills. Postbac fellows will be given increasing independence as the fellowship progresses. Postdoc fellows will be encouraged to develop their own collaborations and resources. For projects related to SGM populations, a demonstrated experience working with the LGBTQ+ community is preferred. https://dceg.cancer.gov/about/staff-directory/jackson-sarah	Shady Grove
Rena Jones, PhD, MS	All	I work on studies to investigate the association of environmental contaminants with cancer risk in both adults and children. Main research areas include air pollution and drinking water contaminants. I also study industrial exposures (e.g., fracking sites, oil refineries), wildfires, and agricultural exposures, including pesticides and	Shady Grove

		concentrated animal feeding operations. The application of geospatial methods and data is a major component of this work. Studying exposure disparities and how they may translate to cancer disparities is also of interest. There are opportunities for the iCURE scholar to learn how to incorporate survey, regulatory, environmental and biological monitoring and other data to construct environmental exposure assessments for epidemiologic studies, and evaluate their associations with cancer risks in both case-control and cohort study designs. They can also expect to develop analytic skills in SAS, R, and/or Excel, work with GIS-based exposure data and linkages, and also develop their scientific writing, reviewing, and presentation skills. I have a broad research program that focuses on exposures that are widespread and have important public health impacts. Our team is diverse, close-knit, and fun to work with. Come join us! https://dceg.cancer.gov/about/organization/tdrp/oeeb	
Alexander Keil, PhD	All	I conduct research into the epidemiologic and causal inferential methods underlying studies of health effects of exposure mixtures. I have several possible projects at multiple levels: Environmental epidemiology has increasingly taken a mixtures-based approach to estimating health effects of the environment in which many exposures are measured simultaneously. Routinely, analyses are performed on these data using default statistical approaches. Alternatively, methods are available to tailor mixtures' analyses directly to urgent categories of public health questions, such as identifying joint effects of receiving many harmful exposures at once and quantifying whether environmental exposure disparities could be contributing to health disparities. I could greatly use your help in these projects, where you could learn a) how to organize data for epidemiologic analyses using open source statistical software like R or Julia and perform basic data summarization; b) the use of publicly available data to characterize how effectively the exposures we face can be used to estimate effects of independent or joint exposure to multiple chemicals; or c) how to assist with and carry out simulation studies on new methods for estimating health effects of exposure mixtures. Applicants at the post-doctoral level are also welcome to help me brainstorm new ideas on integrating causal inference approaches with exposure mixtures using the wealth of epidemiologic data here in DCEG. Applicants at all levels will be encouraged to help or lead the writing-up of study results with the goal of scientific publication. Existing skills in programming, environmental epidemiology, and causal inference are most welcome, but I am also seeking candidates who are enthusiastic about learning in these areas and have not yet had the chance to do so. https://dceg.cancer.gov/about/staff-directory/keil-alexander	Shady Grove
Jill Koshiol, PhD	Postdoctoral Candidate	Biliary tract cancers (BTCs), including gallbladder (GBC), intrahepatic bile duct (IHBDC), extrahepatic bile duct, and ampulla of Vater cancer, are rare in much of the world but constitute a major public health burden in some areas. In the US, the burden is disproportionately high among underrepresented racial and ethnic groups.	Shady Grove

		For example, GBC incidence has decreased in the US until recently when it stabilized in most racial and ethnic groups; it is predicted to increase among Black males and females. IHBDC incidence rates are increasing in all racial and ethnic groups in the US, as well as globally. Unfortunately, given their rarity, little work has been done to understand the etiology of these cancers. BTCs are often combined for research studies, masking true associations for individual sites. Thus, a critical question is how do risk factors vary by anatomic site? To address this gap, we created the Biliary Tract Cancer Pooling Project (BiTCaPP), a consortium of 30 cohorts in 17 countries with nearly 3 million participants and over 5000 biliary tract cancer cases. One project for an iCURE candidate could be to complete a study of non-steroidal anti-inflammatory drugs (NSAIDs) and acetaminophen (Tylenol) in BiTCaPP. This project could provide valuable information about whether NSAIDs might help reduce risk of BTCs, especially in high-risk populations, and whether acetaminophen increases the risk and should be avoided in high-risk populations. An iCURE fellow could also participate in research in Chile Biliary Longitudinal Study (Chile BiLS), a cohort of women with gallstones in Chile, which has among the highest rates of GBC in the world. GBC is one of the top 10 causes of cancer death in Chilean women, and the rates are especially high among people of Mapuche (the predominant ethnic group in the high-risk region) ancestry. Research in Chile BiLS will help elucidate the reasons for the high risk of GBC and explore differences by Mapuche status. https://dceg.cancer.gov/about/staff-directory/koshiol-jill	
Maria Teresa Landi, MD, PhD	Post-Baccalaureate, Postdoctoral Candidate	Project 1 - Sherlock-Lung study aims to characterize the genomic and evolutionary landscape of lung cancers in never smokers (LCINS) and to develop an integrated molecular, histological, and radiological classification of these tumors. The target sample size is 2,000 multi-ethnic and geographically diverse LCINS. Currently, we are analyzing deep whole-genome sequencing data from >1,200 tumor/normal samples and RNA-seq and methylation tumor/normal data from >1,800 samples in collaboration with genomics leaders worldwide. To further characterize LCINS tumor evolution and cell-of-origin, we are also conducting long-read Nanopore DNA sequencing, single-cell sequencing, and spatial transcriptomics. We are also developing genomic analysis algorithms, pipelines and web-based interactive tools for genomics analyses and data visualization. Project 2 - Melanoma studies: 1. Acral lentiginous melanoma (ALM) is a rare subtype of melanoma occurring in typically non sun-exposed anatomical sites. We are collecting >1000 biospecimens from diverse populations, particularly from various Latin American countries to	Shady Grove

		perform the largest investigation of ALM to date to define molecular and immune landscape, and the association of host factors with molecular and clinical features of ALM. 2. We are collaborating with others, especially those from Latin America, to join the effort for the Phase III melanoma GWAS meta-analysis, with large sample size (>75,000) and controls. These data will increase power for subtype specific analysis of genetic loci predisposing to melanoma. 3. We are leading MelaNostrum, a consortium that conducts familial cutaneous melanoma studies using homogeneous procedures for data and sample collection, and the largest WES analysis of >3,000 melanoma-prone families. We have identified new genes responsible for melanoma https://dceg.cancer.gov/about/staff-directory/landi-maria	
Choonsik Lee, PhD	Post-Baccalaureate, Graduate Student	The project includes three independent but closely-related radiation dosimetry projects as follows: 1. Internal Dosimetry for Nuclear Medicine Participants will explore techniques for assessing radiation doses in nuclear medicine patients. This includes calculating S values and organ dose coefficients using anatomical models and Monte Carlo radiation transport methods. Emphasis will be placed on radionuclide-specific dose distributions for commonly used radiopharmaceuticals, such as Tc-99m, Ga-68, I-123, and I-131. Mentors will guide participants through the process of estimating patient-specific doses and understanding the impact of factors such as age, organ mass, and radionuclide energy. 2. Radiation Dose Assessment for Environmental Exposure Participants will also focus on environmental dosimetry related to radiation accidents, such as the Chernobyl nuclear power plant disaster. Through this, they will learn to assess radiation exposure in affected populations by analyzing environmental data, contamination levels, and dose reconstruction techniques. The mentoring will cover methodologies for evaluating long-term radiation exposure effects on health and strategies for effective risk communication in such incidents. 3. Radiation Accidents and Emergency Dosimetry This segment will prepare participants for radiation accident scenarios, providing them with the knowledge and skills to perform emergency radiation dose	Shady Grove

		assessments. Case studies of accidents, like Chernobyl, will be used to demonstrate real-world applications of internal and external dosimetry techniques. Participants will gain experience in using dosimetry tools and models to support emergency response efforts, including assessing exposure risks and determining appropriate protective actions. https://dceg.cancer.gov/about/staff-directory/lee-choonsik	
Mitchell Machiela, ScD, MPH	Graduate Student, Postdoctoral Candidate	Germline variation and somatic mutations are important contributors to cancer risk. My research program focuses on integrative analysis of germline and somatic variation to better understand the etiology of cancer, with a focus on germline-somatic interactions that could elevate risk. My group utilizes population-based data from large, international biobank studies (>100K participants) and applies integrative methods to help disentangle the genetic etiology of cancer. Most projects focus on hematologic cancer risk, but opportunities are available to investigate solid tumors and pediatric malignancies (e.g., Ewing sarcoma). Trainees will gain experience with a variety of genomic approaches including genome-wide association studies, whole-genome sequencing, whole-exome sequencing, targeted sequencing, long-read sequencing, RNA sequencing, DNA methylation, telomere length assays, and single-cell technologies. https://dceg.cancer.gov/about/staff-directory/machiela-mitchell	Shady Grove
Jessica Madrigal, PhD, MS	Post-Baccalaureate, Graduate Student	In collaboration with Dr. Rena Jones, I work on studies using geographic information systems for environmental exposure assessment and to identify determinants of environmental exposures and their association with cancer risk in adults and children. A large part of my work focuses on describing underlying patterns of exposure to environmental pollutants, the non-chemical environment, and social-structural factors among diverse population groups within the US and using those data to conduct multifactorial studies of cancer etiology among these participants from various US-based cohorts. This could included describing population-level patterns of proximity to emissions of perfluorinated substances from industrial sources across the US. Alternatively, I have a project to describe population-level patterns of agricultural pesticide exposures in California and evaluate if Hispanic and Latino population groups experience an unequal burden of exposure. This project is a precursor to a study I am developing to evaluate associations of agricultural pesticide exposure and childhood leukemia risk. Another project that is more cancer-outcome oriented is to evaluate the associations of air emissions of known and probable carcinogens from industrial sources with risk of cancer in adults in the AARP diet and health study. There are also opportunities to use national surveys like the NHANES to conduct exposure validation studies of linked exposure data. The iCURE scholar can expect to develop analytic skills in SAS, R, and Excel, work with geographic exposure datasets that are linked to cohort data, and develop their scientific writing. Ultimately, the goal of this work is to characterize environmental	Shady Grove

		causes of cancer disparities among different population groups in the US and to generate new insights into the etiology of multiple cancer types. https://dceg.cancer.gov/fellowship-training/fellowship-experience/meet-fellows/oeeb/madrigal-jessica	
Katherine McGlynn, PhD, MPH	Postdoctoral Candidate	My research interests are focused on two areas: the epidemiology of liver cancers (with special emphasis on hepatocellular carcinoma and intrahepatic cholangiocarcinoma) and the epidemiology of testicular cancer (with special emphasis on testicular germ cell tumors). My group conducts cross-sectional, case-control and cohort studies to study the etiology of these tumors and associated conditions, such as non-alcoholic fatty liver disease, and the testicular dysgenesis syndrome. We employ biosamples from these studies to examine a variety of serologic, metabolomic, and genetic hypotheses. We also use existing data sources (e.g., data from SEER, SEER-Medicare, CRPD, Cancer in 5 Continents, NHANES) to examine trends in these cancers and to address etiologic hypotheses. https://dceg.cancer.gov/about/staff-directory/mcglynn-katherine	Shady Grove
Mark Purdue, PhD	All	I am seeking an iCURE fellow interested in gaining experience conducting classical and molecular epidemiologic research involving investigations of (1) cancer associations with occupational and environmental exposures in active-duty military personnel, and/or (2) differences by race and ethnicity in kidney cancer etiology. A major part of my research involves investigating cancer risks associated with exposures to per- and polyfluoroalkyl substances (PFAS), highly persistent chemicals that have become widespread water contaminants due to environmental releases from military bases and civilian airports using PFAS-containing firefighting foams, among other sources. In particular, I have been conducting studies investigating testicular cancer risk among active-duty military personnel in relation to serum PFAS concentrations as well as military occupational histories. There are opportunities to analyze data from these studies as well as a planned cohort study of military firefighters. I also conduct epidemiologic studies to better understand factors underlying the disparity in kidney cancer incidence and survival between Black and White Americans. This work includes analyses of questionnaire data on known and suspected risk factors, investigations of genetic susceptibility through genome-wide association studies, and racial comparisons of tumors molecularly characterized using sequencing, gene expression profiling and genome-wide methylation analysis. There will also be opportunities to help develop new research ideas to pursue. https://dceg.cancer.gov/about/staff-directory/purdue-mark	Shady Grove

Rachael Stolzenberg-Solomon, PhD, MPH, RD	All	Fellows will work with a multidisciplinary team that includes epidemiologists, statisticians, and/or bioinformaticians. There are several potential project(s) that fellows can work on. Opportunities include but are not limited to 1) evaluating nutrition and dietary disparities across race and ethic groups within the National Health and Nutrition Examination Survey (NHANES), 2) dietary pattern and/or other risk factor exposures analyses within prospective cohorts with pancreatic cancer as an outcome, and 3) molecular epidemiologic studies that utilize omics (metabolomic, lipidomic, and genomic) data for cancer risk factors and/or pancreatic cancer outcomes employing novel statistical approaches. The applicants ideally should have training in epidemiologic methods and statistics, strong quantitative skills, and an understanding of biological and molecular processes. Training in nutrition or population genetics is beneficial. Good writing skills are also desirable. https://dceg.cancer.gov/about/staff-directory/stolzenberg-solomon-rachael	Shady Grove
Jacqueline Vo, PhD, RN, MPH	All	1) Project 1 examines health disparities in cancer incidence, mortality, or outcomes by race and ethnicity or socioeconomic status. There is a special emphasis on examining health disparities for Asian American vs Native Hawaiian and other Pacific Islander populations, who represent distinct and different racial groups in the U.S. Research will focus on conducting analyses using SEER data, creating graphs, and drafting manuscript. There will be opportunities for first author or co-authorship. 2) Project 2 includes joining a dynamic research team for the NCI-Kaiser Permanente Breast Cancer Survivors Cohort. Research focuses on treatment-related second cancers, cardiovascular disease, and mortality, among a racially diverse breast cancer survivor cohort. Research opportunities include conducting a scoping literature review on health disparities in cardiovascular diseaese among breast cancer survivors, conducting descriptive analyses examining treatment patterns by race and ethnicity, and conducting survival analyses examining the risk of treatment-related cardiovascular disease by race and ethnicity. Future expansions include geospatial linkages to county- and census-tract level outcomes, and opportunities include leading analyses, drafting conference abstracts, and leading or co-authoring manuscripts. https://dceg.cancer.gov/research/what-we-study/contralateral-breast-cancer; https://dceg.cancer.gov/about/staff-directory/vo-jacqueline	Shady Grove
Emily Vogtmann, PhD	All	Microbes, including bacteria and fungi, are essential for numerous physiological processes and likely play multiple roles in health and disease. However, the relationship between the microbiome and cancer remains understudied and previous studies have often not included diverse participants. My ongoing research focuses on 1) understanding the relationship between the oral and fecal microbiome with	Shady Grove

		cancer risk; and 2) methodologic studies of the microbiome to evaluate optimal methods to collect, store, and process oral and fecal samples for microbiome analyses. Data include newly generated 16S rRNA gene data and shotgun metagenomic sequencing data from samples analyzed in DCEG and large, existing datasets of the microbiome and microbiome-related exposures with various outcomes. In addition, I am planning qualitative studies, including focus groups, to evaluate how to recruit more diverse individuals to microbiome studies. https://dceg.cancer.gov/about/staff-directory/vogtmann-emily	
Rose Yang, PhD, MPH	All	Dr. Yang (https://dceg.cancer.gov/about/staff-directory/yang-rose) at the Integrative Tumor Epidemiology Branch is seeking applicant with training in epidemiology, computational biology, genetics/genomics, or a related field in cancer epidemiology studies. Dr. Yang's research focuses on investigating the etiologic and molecular heterogeneity of breast cancer, finding novel susceptibility genes for familial melanoma and chordoma, and characterizing the somatic genomic landscape of chordoma, by integrating molecular and genomic technologies as well as digital pathology to well-characterized tissues in epidemiologic studies. Projects may include analysis of histologic/radiologic images and omics data for molecular and spatial characterization of tumor and TME, next-generation sequencing analysis to identify germline susceptibility genes, and statistical analysis of risk factor and clinical data. Various approaches may be used to test hypotheses, including epidemiologic/statistical, computational pathology, and integrative genomic analyses. The successful candidate will be mentored to achieve their goals, progressing to greater independence during the fellowship. https://dceg.cancer.gov/about/staff-directory/yang-rose	Shady Grove
Tongwu Zhang, PhD	All	Our research group specializes in investigating cancer genetics and genomics using advanced computational methods and diverse sequencing technologies. Our primary focus is on understanding tumor heterogeneity and evolution in the context of specific genetic backgrounds and causative factors. We delve deep into the intricacies of tumor heterogeneity and evolution, exploring how they vary across diverse populations, exposures, and genetic interactions. Our projects also delve into cutting-edge cancer genomic features, including mutational signatures, retrotransposable elements, and extrachromosomal DNA (ecDNA). To achieve our goals, we employ intensive computational resources and diverse cancer genomic approaches. We utilize pan-cancer genomic datasets from prominent international studies such as TCGA, PCAWG, ICGC, Genomics England, Hartwig Medical Foundation, ALCHEMIST, and AACR GENIE, as well as internal cancer genomic datasets from underrepresented populations within DCEG.	Shady Grove

		In addition to our research endeavors, we are committed to developing innovative computational methods, interactive visualization tools, and data portals. These resources facilitate a deeper understanding of complex cancer genomic features, enabling researchers to explore and analyze data comprehensively. As a member of our team, you will have the opportunity to lead or co-lead international collaborative projects focused on cancer genomics analyses and studies. You will receive mentorship to acquire new methods and approaches for analyzing large-scale and high-dimensional genomic data. Moreover, you will have the chance to develop new projects and collaborate closely with experts in diverse fields, including bioinformatics, data science, biostatistics, epidemiology, cancer genomics, and genetics. This collaborative environment extends beyond NIH, allowing you to work with experts outside the organization. https://dceg.cancer.gov/about/staff-directory/zhang-tongwu	