James S. McDonnell Department of Genetics

Website: http://genetics.wustl.edu

Research Electives

Genetics Research Electives

During the fourth year, opportunities exist for many varieties of advanced clinical or research experiences.

Barak Cohen, PhD
Couch Biomedical Research Building, Room 4308
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Functional genomics in yeast; gene regulatory networks, complex trait genetics, and synthetic biology studies of cis-regulation.

Joseph Dougherty, PhD
Couch Biomedical Research Building, Room 6316
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Our laboratory utilizes a variety of techniques spanning from human molecular genetics and informatics to mouse behavioral neuroscience and neuroanatomy. We develop and employ mouse models of psychiatric disorders, particularly those that mimic genetic variations that we have identified in human patient populations, with the goal of trying to understand the cellular and molecular underpinnings of these disorders.

Susan K. Dutcher, PhD
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dutcher@wustl.edu

Studies of the role of centrioles and basal bodies in ciliary signaling, assembly, and motility using molecular genetics and computational and biochemical approaches.

Gabor Egervari, MD, PhD
Couch Biomedical Research Building, Room 6313
Phone: 314-362-6741
gabor@wustl.edu

Our lab combines genomic, proteomic and metabolomic approaches with animal behavioral models to understand how metabolic fluctuations influence gene expression in the brain, particularly in the context of substance use disorders and neurodegeneration.

Sheng Chih (Peter) Jin, PhD
Couch Biomedical Research Building, Room 5206
jin810@wustl.edu
Phone: 314-273-2710

We use human genetic, genomic, and bioinformatic approaches to identify mutations underlying human diseases and their molecular mechanisms.

Tristan (Qingyun) Li, PhD
McDonnell Medical Sciences Building, 8th Floor
Phone: 314-273-1422
qingyunli@wustl.edu

Our lab is broadly interested in neuroimmunology, with a focus on microglial biology. We combine cutting-edge, single-cell genomic technologies with in vitro and in vivo genetic, molecular, and cellular tools to investigate microglial functions in the establishment of the nervous system as well as how changes in these functions contribute to neurological diseases.
**Michael Meers, PhD**  
Couch Biomedical Research Building, Room 5308  
Phone: 314-747-4061  
meers@wustl.edu

The Meers Lab studies how transcription factors interact with and overcome barriers presented by chromatin landscapes to specify developmental and disease outcomes. To do so, we develop cutting-edge epigenomics techniques to map transcription factor binding and chromatin structure in the same context at high resolution.

**Jeffrey Milbrandt, MD, PhD**  
Couch Biomedical Research Building, Room 6306  
Phone: 314-362-4651  
jmilbrandt@wustl.edu

We are performing Cas9/CRISPR activation and repression screens in iPSC-derived neurons together with single-cell transcriptomics analysis to evaluate the causal effects of genetic variants associated with neuropsychiatric diseases. We are also studying how metabolism influences the axonal/glial interactions important for proper nerve function. We use genetic and metabolomic analysis to identify molecular mechanisms of axonal degeneration, a self-destructive process that plays an important role in many neurodegenerative conditions, particularly motor neuron diseases like ALS and peripheral neuropathy.

**Rob Mitra, PhD**  
Couch Biomedical Research Building, Room 4301  
Phone: 314-362-2751  
rmitra@wustl.edu

Our focus is on systems biology, gene regulation and technology development. Projects in the lab fall into three general categories: (1) understanding the molecular logic of transcription factor cooperativity; (2) mapping the gene regulatory networks that control developmental processes and using this knowledge to reprogram fibroblasts into useful cell types; and (3) developing novel technologies to more efficiently achieve the first two aims.

**Samantha Morris, PhD**  
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s.morris@wustl.edu

This lab strives to engineer cell fate to generate clinically valuable cell populations via stem cell and developmental biology. Our research focuses on dissecting the gene regulatory networks that define cell identity, using the developing embryo and tissue regeneration as a guide to engineer fate in vitro. We apply insight from these analyses to generate clinically relevant populations by differentiating cells from a pluripotent state or by directly converting cells between mature fates. We employ a combination of computational, single-cell transcriptomics with cell and developmental biology approaches.