



September 21, 2018

Dear Colleague,

The Department of Molecular Genetics at the Ohio State University (<https://molgen.osu.edu/>) is piloting a "Connections" program to support, develop, and sustain networks between OSU and surrounding campuses and to recognize and celebrate our shared appreciation of science and scientific discovery.

Faculty participating in the Connections program are available to visit your campus at no cost to you to present a research lecture in your seminar series, a guest lecture in your classroom, and/or a topical seminar of interest to your students and faculty. We would also be happy to discuss graduate research opportunities, the graduate admissions process, and biology-related OSU graduate programs, if that is of interest to your students. Although our faculty are most familiar with the admissions process and graduate programs at OSU, much of what they share will be broadly applicable to graduate programs across the country.

The 13 Connections program faculty belong to the Ohio State Molecular Genetics graduate program, and many also participate in other topic-oriented Centers and graduate programs at OSU. Each faculty member's research expertise is highlighted in the attached Connections program materials. We are happy to work with you to tailor the visit to meet the needs of your students and faculty. Possible visit activities might include a research lecture followed by a Q&A session, a guest lecture in a specific class, involvement in a career panel, or a presentation at a Biology Club meeting. We also hope to learn more about your science and research programs.

If you are interested in participating in the Connections program, we hope to hear from you! If you are interested in a particular Connections faculty member and are flexible about the visit date, you are welcome to contact the faculty member directly to arrange a visit (contact information is available through the URL linked to each faculty name). If you have a specific date and time in mind, or a specific program type or topic, and are interested in a number of participating faculty, please contact me and I will arrange the visit for you. Please share this opportunity with your colleagues and with your departmental undergraduate affairs office. We hope to visit your campus soon.

Sincerely,

Sharon Amacher
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	Amacher	Bird	Chamberlin	Cole	Dobritsa	Fisk	Hamel	Hollick	Hopper	Mackey	Miles	Petracca	Singh
Broad Research Areas													
Cancer Biology			x		x					x	x		
Cell Biology	x			x	x	x		x		x			
Developmental Biology	x		x	x			x						
DNA replication, repair, recombination											x		
Epigenetics							x						
Evolutionary Biology		x		x			x						
Gene Expression and Regulation	x		x			x	x	x	x	x	x	x	
Genetics	x	x	x	x	x	x	x	x	x	x	x	x	
Genomics							x			x		x	
Plant Biology				x		x	x		x				
Signaling	x		x						x				
RNA Biology	x		x				x	x		x		x	
Virology/Immunology									x				
Campus Centers													
Center for Applied Plant Sciences				x		x	x		x				
Center for Muscle Health and Neuromuscular Disorders	x												
Center for RNA Biology	x		x				x	x		x		x	
Comprehensive Cancer Center			x							x			
Infectious Disease Institute									x				
Graduate Programs													
Molecular Genetics (Mol Gen)	x	x	x	x	x	x	x	x	x	x	x	x	
Molecular, Cellular and Developmental Biology (MCDB)	x		x	x	x	x	x	x	x			x	
Biophysics						x						x	
Horticulture and Crop Science (HCS)									x				
Microbiology						x							
Ohio State Biochemistry (OSBP)					x								
Ohio State Nutrition (OSUN)		x											
Translational Plant Sciences						x	x						x

The Ohio State University Department of Molecular Genetics
Connections Program Faculty



Sharon Amacher, PhD

The Amacher lab studies how cells become sequentially determined to more precisely defined fates during embryonic development, and how this process depends upon cell position and upon interactions among neighboring cells. To address these questions, we use genetics, molecular biology, and time-lapse imaging to investigate muscle development and differentiation in the zebrafish, a vertebrate model system. We collaborate with others to understand how pathway mis-regulation leads to human muscle defects and disease.



Amanda Bird, PhD

The long-term research goals of the Bird lab are to determine the basic mechanisms by which eukaryotic cells maintain optimal levels of metal ions in the cytoplasm and organelles. Metal ions including copper, zinc, iron, and manganese are required for the function of approximately half of all characterized enzymes and are therefore required for many cellular and metabolic processes including DNA replication, transcription, translation, respiration, and electron transport. Our research primarily uses the fission yeast *Schizosaccharomyces pombe* as a model system to identify new genes and proteins that are required for metal ion homeostasis, sensing, transport, and trafficking.



Helen Chamberlin, PhD

The Chamberlin research group uses the microscopic worm *C. elegans* and related nematode species to study cell-cell communication, and the evolution of developmental processes. Recent findings include the identification of genes that function in mesodermal cells to influence the excessive proliferation of epithelial cells expressing the activated form of the oncogene, RAS. Some of these new genes encode conserved proteins that may serve as novel therapeutic targets for cancer treatment.



Susan Cole, PhD

The Cole lab research program focuses on the transcriptional and post-transcriptional regulation of cell:cell signaling during embryonic development. Our major area of interest is the Notch signaling pathway, and we have used mouse models to explore how pathway signaling is regulated during vertebrate segmentation, in cardiac development, and in intestinal development. We are also interested in how dysregulation of the Notch pathway contributes to human congenital defects, disease, and cancer.



Anna Dobritsa, PhD

The Dobritsa lab is interested in learning how cells create their morphology, develop distinct cellular domains, and achieve deposition of complex extracellular structures at precise positions. As our model, we use pollen grains. Pollen surface is covered with the cell wall exine that assembles into intricate, species-specific patterns. In our studies, we ask how the patterns on the pollen surface are generated, what molecular mechanisms control exine deposition, and how these mechanisms differ between plant species that have different pollen-surface patterns.

The Ohio State University Department of Molecular Genetics
Connections Program Faculty



Harold Fisk, PhD

Centrosomes help ensure genomic integrity by forming the two poles of a bipolar mitotic spindle. Many human tumors have excess centrosomes that disrupt spindle function and generate aneuploidy, but the role of excess centrosomes in cancer is not clear. The Mps1 protein kinase regulates the assembly of centrosomes, and its misregulation leads to the production of excess centrosomes like those seen in tumors. We use biochemistry, cell biology, and animal modeling to characterize the role of Mps1 in centrosome assembly, and understand the role of excess centrosomes in tumorigenesis.



Patrice Hamel, PhD

My lab is interested in energy-transducing membranes in mitochondria and chloroplasts and uses the freshwater unicellular alga *Chlamydomonas* as an experimental system. Specifically, we are exploring the importance of forming and breaking disulfides in proteins for photosynthesis. Our goal is to discover the enzymes catalyzing these reactions and their relevant targets of action inside the chloroplast. In mitochondria, our focus is on Complex I, a multimeric enzyme whose dysfunction is the cause of severe diseases. The objective is to uncover novel factors involved in the manufacture of Complex I in order to understand the molecular basis of Complex I-linked pathologies in humans.



Jay Hollick, PhD

The Hollick lab seeks to understand the molecular mechanisms responsible for turning genes on and off. The genes they study are responsible for conditioning colorful pigments in the corn plant. This model genetic system has identified novel genomic features responsible for conferring non-Mendelian modes of inheritance and the involvement of small RNA molecules in controlling where and when specific genes are expressed.



Anita Hopper, PhD

Appropriate biogenesis and subcellular trafficking of tRNA are essential for decoding the genome and for regulating the proteome in response to nutrient availability and stress; mutations of genes involved in tRNA biology cause human disorders ranging from metabolic diseases, to neuromuscular diseases, and to cancer. We employ the powerful budding yeast model system and genetic, genomic, cell biological, and biochemical methodologies to address key issues in tRNA biology: bi-directional nuclear/cytoplasmic trafficking and its role in tRNA quality control and the appropriate localization of tRNA splicing machinery to the mitochondrial surface. These are important issues because in order to correctly decode the genome it is essential that only proper tRNAs associate with the cytoplasmic protein synthesis machinery and because other RNA processing steps in metazoans occur on mitochondria, but little is known why this organelle serves as a platform for RNA processing or how RNA processing machineries assemble there.

The Ohio State University Department of Molecular Genetics
Connections Program Faculty



David Mackey, PhD

The Mackey lab investigates the antagonistic interaction between plants and potentially pathogenic bacteria. Plants control their physiology to limit pathogen access to nutrients and water and also utilize a sophisticated innate immune system to combat infections. Conversely, bacteria promote their virulence by deploying proteins and small molecules, collectively referred to as effectors, that perturb host physiology and immune function. Through study of effectors, their host targets and the consequences of their action, we seek to gain molecular understanding that can be applied to mitigate the negative consequences of biotic stress on plant productivity.



Wayne Miles, PhD

The Miles lab is interested in understanding how loss of the Retinoblastoma 1 tumor-suppressor genes changes cells and enables their tumorigenic growth. In particular our research focuses on the role of post-transcriptional regulation in preventing the translation of proteins that either kill cells or slow their growth. To investigate these questions, my team use many “omics” approaches including RNA-seq, proteomics, Ribosome profiling and bioinformatics.



Ruben Petreaca, PhD

Our research aims to understand DNA damage repair with an emphasis on chromosomal double strand breaks. Inappropriate repair of chromosomal breaks can cause loss of genetic information as well as many forms of chromosomal re-arrangements, events that have been demonstrated to lead to cellular immortalization and cancer. Using yeast, a simple model system in which many human cellular processes can be replicated, we focus on outlining molecular mechanisms that promote accurate chromosomal break repair.



Guramrit Singh, PhD

The major goal of the Singh lab is to understand how the nuclear RNA processing history controls mRNA fate in human cells. Current projects revolve around the exon junction complex (EJC), a stable set of proteins deposited on mRNA exon-exon junctions during pre-mRNA splicing. We use an interdisciplinary approach that combines biochemical and molecular methodologies with high-throughput sequencing and proteomic technologies to investigate how nucleus-deposited EJC connects with cytoplasmic translation and mRNA degradation machineries. In collaboration with the Amacher lab, we are using the zebrafish model to study EJC functions during development.