Current Research in Pathology

The Department of Pathology has a very strong cadre of researchers in both basic science and translational research. Major efforts are centered in the fields of cell biology, virology, cancer biology, molecular diagnosis, biotechnology, and computational biology. Researchers frequently meet and exchange ideas and novel concepts from their respective fields, creating a fertile multidisciplinary environment for graduate students and young postdoctoral trainees, including residents in Pathology. Several laboratories combine their efforts to make progress in the understanding of the causes and mechanisms of cancer.

More than ever before, biological and biomedical science is in need of theoretical modeling studies. The Department's strong computational biology group plays an increasingly enabling role in support of studies of evolutionary dynamics and selective sweeps involved in the shaping of the immune system and the progression in the biological properties of tumors. The computational team also assists laboratory scientists in displaying and analyzing large data sets as well as in producing mathematical and/or agent-based models that allow the generation of new hypotheses to be experimentally tested.

Immersed in this forever-changing and multidisciplinary landscape of scientific knowledge, the physicians in Yale Pathology Labs are ideally positioned to apply the latest insights to diagnostics and patient care.

Jeffrey Sklar

Research in the Sklar Lab concerns the molecular biology of human disease, particularly in the areas of the molecular genetics of cancer, lymphocyte biology, endometrial function, and the development of molecular methods for disease diagnosis. The research is of both a basic and translational nature.

Most recently, two previously unknown genes—*JAZF1* and *JJAZ1* (now also referred to as SUZ12)—were discovered by us to be fused head to tail in most cases of endometrial stromal tumors. These two genes are currently the focus of intense investigation within the laboratory. *JJAZ1* is a Polycomb group gene, the product of which is an essential member of the protein complex (Polycomb repressive complex 2, or PRC2) that in most or perhaps all cells catalyzes specific methylations of histone 3, leading to chromatin compaction and transcriptional silencing of DNA. The function of *JAZF1* is less well understood; however, separate single nucleotide polymorphisms (SNPs) within two introns of this gene have recently been shown to be associated with a strongly increased risk of type 2 diabetes and a decreased risk of prostate cancer. Both associations are now being investigated in the laboratory.

Alexander Vortmeyer

Dr. Vortmeyer's research interests are hereditary tumorigenesis, tissue microdissection, and tissue proteomics. His research has studied in detail tumor precursor structures arising in the context of different tumor suppressor gene syndromes. At NINDS, he developed and promoted human tissue-based research in collaboration with numerous basic and clinical laboratories within NINDS departments, NCI, and the National Human Genome Research Institute (NHGRI).

Jon Morrow

Our research focuses generally on understanding the mechanisms by which the cytoskeleton of the cell contributes to the organization of cell polarity, receptor sorting, and signal transduction, and on the diseases that result from hereditary or acquired disorders of the cytoskeleton. Current research focuses on the spectrin-ankyrin membrane skeleton, which participates in a variety of cellular processes. This work has identified the molecular basis of several blood diseases involving fragile erythrocytes; disorders of renal function that follow ischemic injury; a role in certain forms of cancer; and hereditary neurological diseases including cerebellar ataxia and certain seizure disorders. In progress studies suggest that cytoskeletal dysfunction may even play a role in the genesis of behavioral diseases such as anxiety-spectrum disorders and autism.