How Genes and Proteins Make Us Fat:
New Technologies for Research on Obesity-Related Health Complications

Genome-wide association studies and resequencing efforts have identified large numbers of sequence variants in the human genome that contribute to common disorders such as obesity, diabetes, or heart disease. However, it has become clear that these approaches are unlikely to unravel the entire complement of genetic variants that contribute to the risk for these disorders. Furthermore, the functional characterization and mechanistic interpretation of the effect of the identified variants has been slow and challenging. As an alternative, we have used integrated genomic and proteomic approaches to dissect the genetic basis of obesity-associated lipid abnormalities in humans. These combined approaches have revealed novel genes and pathways, and we are currently developing additional tools that will allow the functional characterization of these variants in vivo.

Michael Olivier, Ph.D.
Scientist & Director, Wisconsin Center of Excellence in Genomics Science
Texas Biomedical Research Institute