

The Dr. Don Rix Protein Identification Facility

With the mapping of the human genome complete, the focus in the world of bioinformatics has turned to proteomics, a discipline that involves unravelling the structure and function of proteins. In 2001, in an effort to be at the forefront of this research movement, The University of Western Ontario opened the Dr. Don Rix Protein Identification Facility and recruited professor Gilles Lajoie to head a world-class proteomics centre dedicated to mapping the human proteome with the ultimate goal of understanding human biology and disease.

What is the Dr. Don Rix Protein Identification Facility?

Named after Western medical school graduate Don Rix, who donated \$1 million to assist in the construction of the laboratory, the Dr. Don Rix Protein Identification Facility has established Western as a leading proteomics research hub in Ontario. With exceptional resources for investigating the sequence, abundance and post-translational modifications of proteins, researchers at the facility are discovering the precise role that proteins play in the development of numerous diseases with the hopes of finding better ways to diagnose and, eventually, cure them.

Instrumentation

The facility houses a host of state-of-the-art mass spectrometers that complement other comprehensive devices at Western for identifying and characterizing proteins, including nuclear magnetic resonance imaging and x-ray crystallography machinery. The Don Rix facility was the first facility in the world to acquire a Fourier transform ion cyclotron resonance mass spectrometer with a 12 Tesla magnet—a cutting-edge tool that allows protein mass to be measured with extreme accuracy. It is part of the Biological Mass Spectrometry Laboratory, which is equipped to analyze other biomolecules such as lipids and carbohydrates.

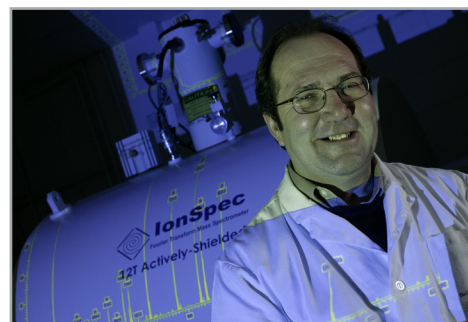
Research

Proteomics research at the facility relies heavily on extensive collaborations that cross many research disciplines. This work involves computer scientists who are developing better software, chemists who are improving technology for separating proteins and clinicians interested in finding the underlying causes of diseases. The facility's researchers are engaged in a wide range of projects, including studies of pre-eclampsia, stem cells, Alzheimer's disease, mechanisms of transmembrane transport and the relationship of protein structure to function. The Centre is part of the Ontario-Wide Protein Identification Facility, an initiative that was spearheaded by Western. In conjunction with collaborators at the University of Toronto, York University, McMaster University and the Hospital for Sick Children, the facility's researchers are focusing on advancing proteomics research and understanding the molecular basis of neonatal diseases, cancer, multiple sclerosis and diabetes.

One of the group's major research areas is designing new drugs and understanding how they interact with their target proteins. A high priority project led by professors David Litchfield and Shawn Li is the study of kinases—cellular signalling enzymes that have been implicated in the development of a number of diseases such as cancer. By identifying the proteins targeted by these kinases, scientists hope to design better anticancer drugs. Another high-priority research project involves the antifungal human salivary proteins known as histatins. Because organisms such as *Candida albicans* proliferate unabated in immune-compromised patients, researchers are using proteomic approaches to reveal how histatins kill such fungi.

Notable Achievements

The facility's researchers and collaborators recently published work in the prestigious journal *Nature* showing that human embryonic stem cells produce their own supporting cells or 'niche' cells, which are critical to stem cell production. Because stem cells have this support system and are sustained by one key secreted protein, they are promising to be particularly useful agents for therapies such as tissue regeneration. Protein researcher Lars Konermann has developed a unique method of stopped-flow electrospray mass spectrometry, a powerful tool for analyzing the kinetics of protein folding. Professor Ken Yeung is developing advanced capillary electrophoresis techniques for performing fast, automated and highly efficient protein separations, while professors Bin Ma and Kaizhong Zhang have developed new software and sophisticated computational algorithms for de-novo peptide sequencing from tandem mass spectrometry data.



Proteomics researcher Gilles Lajoie at the Dr. Don Rix Protein Identification Facility

For more information, please visit: www.biochem.uwo.ca/wits/bmsl/