After four years of serving numerous investigators inside and outside of Vermont, the Vermont Genetics Network (VGN) Proteomics Core has a new home in a newly renovated laboratory in Marsh Life Science Building Room 335 as of August 2010. Routine operations and services resumed after only a short one-week hiatus.

The VGN Proteomics Facility has improved its ability to provide its users with cutting edge technologies for analyzing proteins and peptides through the combination of current equipment (three mass spectrometers—two Thermo-Finnigan LTQ Linear Quadrupole Ion Traps and one Thermo-Finnigan LTQ-Orbitrap) as well as the addition of new equipment. The facility has added a new SpeedVac, which is used for sample preparation and a Laser Puller P-2000 for use in making packed separation columns.

Since last year over 2000 samples have been analyzed, eight peer-reviewed papers have been published and three new grants have been funded due to expertise from the VGN Proteomics Facility. The user base is growing and includes over 59 active faculty, post docs and staff; 35 graduate students; and 40 undergraduates. At least 25 seminars and poster presentations have been presented by users/staff that included data from the VGN Proteomics Facility. Since its beginnings in 2006 the VGN Proteomics Facility has experienced a rapid growth in its user base and in total samples analyzed. However, we are expecting even more users and collaborative projects in the facility given the critical nature of proteomic data to various lines of biological inquiry.

Please visit the following link to sign up for a consultation or to fill out an online sample submission form: http://vgn.uvm.edu/proteomics/
The purine-rich element binding proteins are a small, evolutionarily-conserved family of nucleic acid-binding proteins whose signature biochemical feature is specific and high affinity interaction with guanosine-rich single-stranded DNA (ssDNA) or RNA sequences. The founding member of this family, Pura, has been linked to aspects of nucleic acid homeostasis required for regulated cell growth and genome stability. On the other hand, we hypothesized that the protein might fold development of a simplified method for site-specific profiling of the glycans on proteins. These analyses revealed the presence and composition of the N-linked glycans at asparagines 11, 124, and 137 in TF, and indicated that there are substantial differences in the composition of carbohydrates at each site between the recombinant and natural forms. Combining the data from these detailed glycan characterizations with enzymatic deglycosylation and functional studies of the different TF forms demonstrated that glycosylation had significant impact on the biological activity of TF. A second UVM study in Dr. Paula Tracy’s laboratory has been applying the same technique to characterize the glycans of factor Va (FVa), an essential cofactor for clot formation. Two different forms of the FVa protein exist, with differences in PTMs that are thought to be responsible for their dramatic functional differences. To address this hypothesis, Drs. Jeremy Wood and Jay Silveira in collaboration with the VGN, are characterizing glycosylation differences in the proteins. Analyses of plasma-derived FVas have identified and characterized the N-linked glycans at asparagines 269, 432, 439, 1675, and 218. Detailed compositional analyses have identified high mannose and complex glycan chains with relatively little compositional heterogeneity, as well as potential N-linked glycosylation sites that appear to lack glycan addition. Similar analyses are currently being

---

**Characterization of carbohydrates found on coagulation proteins**

Hemostasis is the process in which bleeding is stopped by the formation of a clot, and numerous plasma and integral membrane proteins are essential components. Studies of these proteins at the molecular level are defining how their structure dictates their function, and how those relationships may be altered by post-translational modifications (PTMs) such as glycosylation. In collaboration with the VGN, two hemostasis research groups at UVM are employing some exciting new methodologies to define how differences in glycosylation alter protein function.

---

**References**


---

**Picture:** Pictured are the first author Ph.D. student, Amy Rumora, and her advisor, Dr. Robert Kelm Jr. who was the senior author of the study. Both are members of the UVM Biochemistry Department.