**Comprehensive “Omics”**

**Milk Glycomics**

Oligosaccharides in human milk (HMOs) represent an abundant and diverse group of bioactive molecules. Although they do not provide direct nutritional value to the infant, they are beneficial to the growth and development of the infant gut flora. The protective and probiotic effects of HMOs are being studied more today. Recently, we have been investigating their binding activity to certain strains of bacteria.

**Milk Peptidomics**

Milk is a self-digesting biological-rich in proteomics. A comprehensive study of the peptide content in human milk has revealed a wide diversity of naturally occurring peptides (NHPs). A human NHP library has been generated with more than 800 unique sequences from 54 proteins.

**Clinical Glycomics/Biomarkers**

 Glycosylation is an important determinant of protein function and has been shown to mediate many post-translational processes and has recently been acknowledged as potential markers for several diseases. Many groups have reviewed the relationships with associated with the structural features of the glycoconjugates in certain cancerous conditions. We aim to apply a well-developing structural serum-based library-based approach to develop patient-specific classifiers using algorithms for relative abundances, retention times, accurate masses, and tandem MS spectra to perform clinical research.

We have recently optimized a rapid-throughput method for comprehensive, tumor-specific chromatographic profiling of native human glycans and applied it to glycan biomarker discovery. In the near future, we will apply a well-developing structural serum-based library-based approach to develop patient-specific classifiers using algorithms for relative abundances, retention times, accurate masses, and tandem MS spectra to perform clinical research.

**Effect of Cell Surface Glycosylation**

Glycosylation on the cell surface membrane plays an important role in cell-cell interactions. We have optimized a method to enrich for cell membrane glycans and use analytical tools to study them. In recent studies, we isolated cell membrane glycans from a variety of cell lines, and found that the same glycans displayed similar trends. Glycosylation is a key to the color-coded representation of the Pearson correlation coefficient (R^2) between each pair of cell lines. Red: highly correlating blue: low correlating. Relative abundances are shown for each glycan. E.R. is clearly distinct from the green lymphoid cell lines. Recent Publications: Peao et al. Proteinome Res. 2018; An et al. Mol. Cell. Proteomics 2011.

**Markers for Autointolerance**

Over the last decades, several successful studies have emerged on the detection of candidate glycan biomarkers for several diseases including auto-immune diseases. Most studies have focused on disease-specific differences and changes in glycobiological profiles of disease may result in more important biomarkers, with improved sensitivity and specificity, hence we present here different methods to detect and apply unique glycan profiles of the immunoglobulins A, G, and M in a quantitative manner.

**Software**

High-throughput software platforms are now in constant development, providing easy access to the discovery and annotation of glycans, including a variety of post-translational processes. Custom bioinformatics tools in our group allow us to run high-throughput extracts on glycans in order to annotate their differences.

**Cancer Biomarkers**

Cancer biomarkers can be divided into several categories: cell surface markers, tumor suppressor genes, and protease inhibitors. Cell surface markers are the most well-known, and they are often used as targets for therapeutic interventions. Tumor suppressor genes are important for controlling cell growth and proliferation, and they are frequently mutated in cancer. Protease inhibitors are important for regulating the activity of proteases, which are involved in many cellular processes, including cancer progression.