TARGETED LC-MS/MS WORKFLOW FOR MEASURING QUANTITATIVE CHANGES IN THE TEAR PROTEOME. **Lekha Sleno**[1*,] Maggy Lépine[1], Marie-Claude Robert[2], [1] University of Quebec in Montreal (UQAM), Chemistry department, Montreal, QC, Canada. [2] Hospital Research Center of the University of Montreal, Ophthalmology department, Montréal, QC, Canada. (sleno.lekha@uqam.ca)

Proteins in tears play a central role in eye health and changes in some of these proteins has been shown to correlate with certain diseases. Quantitative analysis of tear proteins is a promising approach to identify biomarkers to help diagnose pathologies and help to better characterize the biological pathways involved. We have developed a non-invasive method to monitor changes in the tear proteome of healthy patients and those with eye diseases.

Using targeted LC-sMRM analysis, a method was developed for 226 consistently detected proteins. This list of proteins was first used to investigate inter-day and inter-individual variations in a healthy population. This work was useful in providing information to prioritize disease-related biomarkers, relative to their normal variations. This method was also used to investigate changes in tear proteome from patients with two ocular surface diseases: a rare multisystemic autoimmune disease, mucous membrane pemphigoid (MMP), and Sjogren's syndrome (SS), an autoimmune rheumatic disorder causing severe aqueous dry eyes. From both MMP and SS, several pathways were perturbed, including neutrophil degranulation and oxidative stress. Proteins secreted by the lacrimal gland were more enriched in SS, whereas extracellular matrix proteins were more implicated in MMP. Ongoing work includes further development of targeted assays of specific families of proteins in ocular fluids, including S100 and annexin proteins.