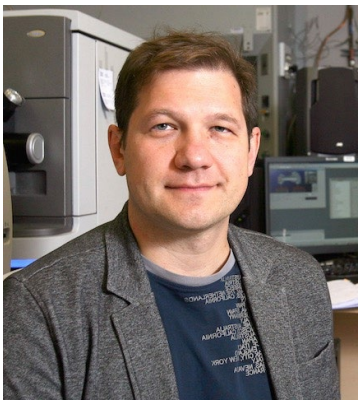

Maxim V. Berezovski is a Full Professor of Bioanalytical Chemistry at the University of Ottawa in Canada. He received a Ph.D. from York University (Canada) in 2005 and did an NSERC postdoc at the University of Toronto (Canada). His research focuses on bioanalytical chemistry, biological mass spectrometry, and molecular diagnostics. He develops analytical methods for studying biomolecular interactions with capillary electrophoresis and mass spectrometry, discovers protein biomarkers of extracellular vesicles, and makes aptamer-based sensors for tumour cells, viruses, and exosomes. Prof. Berezovski published 104 articles, 5 book chapters, and 3 patents. He has an h-index of 42 with >6000 citations. He is an Editor for Molecular Therapy-Nucleic Acids (a journal of the American Society of Gene & Cell Therapy) and Editor for Cancers (MDPI). Maxim was awarded a Visiting Professorship from the Royal Netherlands Academy of Arts and Sciences, and a Friedrich Wilhelm Bessel Research Award from the Alexander von Humboldt Foundation of Germany. Before academia, he served as CEO of a pharmaceutical company for six years. Now, Maxim leads the Laboratory of Molecular Diagnostics and Proteomic Mass Spectrometry Core Facility at the University of Ottawa.

"**Discovery of DNA Aptamers Targeting SARS-COV-2 Proteins and Identification of Protein Binding Epitopes For Label-Free COVID-19 Diagnostics**"

The spread of COVID-19 has affected billions of people across the globe with the challenges of less accurate and time-consuming detection approaches. Especially, new variants with various mutations in the spike protein can escape immune responses as well as a low viral load in clinical samples can trigger a false-negative test result. Due to high immunogenicity and abundant expression during viral infection, SARS-CoV-2 nucleocapsid (N) protein could be an alternative diagnostic marker, together with targeting the S1 subunit of SARS-CoV-2 spike protein. This study aimed to develop a label-free optical aptasensor fabricated with novel ssDNA aptamers to detect the N and S1 proteins. The aptamers selected using asymmetric emulsion PCR-SELEX and their binding affinity and cross-reactivity were characterized by using bio-layer interferometry. The tNSP3 aptamer (44 nt) was identified to bind the N protein of wild type and Delta and Omicron variants with high affinity (KD in the range of 0.6 – 3.5 nM). Furthermore, the aptamers targeting the S1 subunit were also discovered in order to expand an additional tool for aptamer-based biosensors used in COVID-19 detection. The S1-tSP10 aptamer with 40 nt performed better affinity than other S1-targeting aptamers, and this aptamer possessed the KD about 15 nM binding to the S1 protein of wild type and Omicron variant. Utilizing tNSP3 and S1-tSP10 aptamers to separately detect the N and S1 proteins spiked in human saliva evinced the potential of these

aptamers in the function of aptamer-based BLI with LODs of 4.5 nM and 19 nM corresponding to tNSP3 and S1-tSP10 aptamers, respectively. To get insight into where the aptamers bind to their target proteins, mass spectrometry analysis was performed along with the molecular dynamic simulation. The identified epitope peptides are localized within the RNA-binding domain and CTD of the N protein as well as RBD of the S1 protein. Hence, we confirmed the performance of the aptamers as a label-free analytical tool for COVID-19 diagnosis, and also knowing the binding epitopes can be essential for improving biomedical applications in therapeutics.

"**The proteomic analyses of extracellular vesicles reveal enzymes as potential biomarkers of breast cancer.**"

We performed a phosphoproteomic analysis of breast cancer-derived exosomes to provide insight into the molecular and cellular regulatory mechanisms important for breast cancer tumor progression and metastasis. We examined three cell line models for breast cancer: MCF10A (non-malignant), MCF7 (estrogen and progesterone receptor-positive, metastatic), and MDA-MB-231 (triple-negative, highly metastatic). To obtain a comprehensive overview of the exosome phosphoproteome derived from each cell line, effective phosphopeptide enrichment techniques IMAC and TiO2, followed by LC-MS/MS, were performed. Among 855 distinct phosphoproteins, we validated four enzymes associated with cancer and present only in exosomes isolated from MCF7 and MDA-MB-231 cell lines: ATP citrate lyase (ACLY), phosphofructokinase-M (PFKM), sirtuin-1 (SIRT1), and sirtuin-6 (SIRT6). With the exception of PFKM, the specific activity of these enzymes was significantly higher in MDA-MB-231 when compared with MCF10A-derived exosomes. This study demonstrates that exosomes contain functional metabolic enzymes that could be further explored for their potential use in early breast cancer diagnostic and therapeutic applications.