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## **Integrated Proteomics Platforms for High-throughput Biomarker Discovery and Validation**

<b>Status</b>	Current
<b>Competition</b>	Development of New Technologies Competition
<b>Sector</b>	Development of New Technologies
<b>Genome Centre</b>	Genome Quebec
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### **Project Description**

The enormous advances in genomics in recent years have enabled the mapping of the human genome (DNA), the “*blueprint*” for the human body. Genes, the “information units” in the genome, are instructions for generating proteins, the molecular workhorses in biological systems. Recent progresses in proteomics (the study of proteins) have allowed the discovery and analysis of large numbers of individual proteins. In many respects, however, proteomics offers more difficult technological and analytical challenges than genomics, both because of greater numbers (20,000 to 25,000 genes vs. about 1,000,000 proteins in humans) and because protein molecules are much more fragile than DNA. To screen a large number of proteins in parallel for medical applications has proven to be very difficult because of combinatorial possibilities resulting from cross-affinities across a large number of candidate molecules and their propensity for non-specific binding. As a result, technological advances in proteomics have progressed at a relatively slow pace (compared to genomics) and significant progress in health care has been slow in coming.

Despite many attempts by groups worldwide to do so, success to date in this area has been modest at best, due to the difficult nature of the challenge. The present project brings together a very strong interdisciplinary team proposing a highly novel technological solution to this challenge, which builds on recent proven work by individual members of this group.

The proposal described here is a technology development project for efficiently and reliably screening large number of candidates for the identification of protein biomarkers of disease and scaling the technology to a miniaturized form that will allow its widespread use. Indeed, the proposal describes a two-pronged approach to this difficult challenge. Initially, based on recently demonstrated technology developed at McGill and at the Université de Sherbrooke for screening large numbers of protein candidates based on colocalization arrays and multimodal sensing, the team will develop a platform capable of analysing large numbers of candidate molecules in parallel – with high specificity and sensitivity. This platform is intended for use as a service facility by Genome Québec/Canada researchers. Finally, based on recently demonstrated technology developed at McGill and IMI, a miniaturized and highly portable version of the technology based on digital microfluidics and integrated optical instrumentation

will be made available to individual partner research groups for on-site analysis of protein candidates in targeted applications.

The short term impact of the platform will be on biomarker discovery as the proteomics platform will bridge the gap between MS based biomarker discovery and clinical diagnostics. The targeted platform which allows for the analysis of 100 spots in parallel could revolutionize biomarker and biomarker validation because it could be run easily by individuals in laboratories.

This integrated proteomics platforms has a strong focus on technology, more specifically on the development and integration of enabling platforms. During the course of this project, we expect the GE3LS (Ethical, Environmental, Economic, Legal and Social Issues stemming from the Research) issues requiring attention to be minor and not any different from those raised by normal research practices in biomedical sciences.

Our system which will allow screening of multiple protein based biomarkers with high throughput and sensitivity would be a tremendous breakthrough in medicine because proteins are the molecular machines of life, and powerful surrogate indicators of disease.