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## Proteomic Technologies for the Study of Rare Cells

<b>Status</b>	Current
<b>Competition</b>	Development of New Technologies Competition
<b>Sector</b>	Development of New Technologies
<b>Genome Centre</b>	Ontario Genomics Institute
<b>Project Leader</b>	Daniel Figeys

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### Project Description

We have developed a novel technology based on the efficient handling of very small volumes of samples (microfluidics) with implications across the field of protein analysis, in particular studies of proteins in cells that appear in only trace levels in the body such as stem cells. Recently, our laboratory demonstrated proof of principle for a prototype 'proteomic reactor' for efficient processing of minute levels of protein. This reactor simplifies handling of proteins, greatly reduces the volumes required for analysis and shortens processing times. It has provoked strong interest from both Canadian and international scientific equipment companies.

Improvements in the protein analytical field are concerned primarily with increasing sensitivity. Where there have been vast performance improvements in recent years in techniques like mass spectrometry and laser-induced fluorescence, these are not fully reflected in increased sensitivity because the samples are not efficiently processed prior to the analysis. This is one of the major challenges in the proteomics field.

Our prototype reactor ranks as the most efficient proteomic processing device in terms of sensitivity, speed, and simplification of process. We have demonstrated that as few as 300 living cells can be processed and analyzed by mass spectrometry and that even with higher cell numbers the reactor provides better performance than conventional protein processing approaches. We believe that we can improve on this performance, developing reactors which will provide better proteomic results for routine proteomics samples and for studies of proteins right down to the level of single cells. This would provide new applications such as single cell proteomics, with enormous implications for stem cell research and regenerative medicine.

Here we propose to further develop and expand the proteomic reactor technology in two phases. In the first, we will rapidly expand upon the current format of the proteomic reactor, building four reactor column formats covering sample needs that range from large complex proteomes such as plasma all the way down to single cells. These systems will be made faster and more efficient with automated fluidic stations. By year two we will develop automated proteomic reactor kits and demonstrate their novel applications in the field of single cell analysis. In the second phase, we will transpose and transform the proteomic reactor using microfabrication technology available at the National Research Council.

These microfluidic chips will provide further enhancement in sample processing by reducing the reaction volumes, more efficient sample handling, automation and different surface biochemistry. We expect to put in place chip proteomic reactor kits by the end of year two. Training sessions for academics and Genome Canada platforms are planned for year two and within the year following the end of this proposal.

The development of proteomic reactor column-format kits and the chip proteomic reactor will enable more efficient proteomics research in analyses ranging from plasma down to single cells. We foresee that the single-cell processing on the reactor coupled to fluorescence detection will provide a sensitivity that allows us to measure proteomic profile changes in single cells. Already, industrial partners for the fabrication and commercialization of the reactor columns and the chip proteomic reactor have provided letters of interest.