

## Microfluidic microarrays for multiplex protein analysis

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### Information Summary

Reference Code:	ROI 07084
Technology overview:	Microfluidic system
Applications:	Research tool to identify drug candidates. The invention could be used also for diagnostic/prognostic applications
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### Technology Description

Moore's law describes the exponential growth of computers with a doubling of performance roughly every year that lead to a billion fold performance enhancement over 30 years and trillion dollar markets. The key ingredient to this technological and economic success has been the scalability of computers because the number of elements in an integrated circuits could be reduced and doubled in number without need to change the basic operating principles. The same concepts were translated to genomic analysis where we have experienced an exponential growth much faster than in computer sciences over the last 10 years, and which has transformed life sciences research and already resulted in novel diagnostic applications. Proteins, which are the machines of life, have not benefited from such technological advances. We have invented a scalable technology for protein analysis which will allow doubling the number of proteins being analyzed for years to come and rapidly lead to a platform where whole organism proteomics can be performed.

### Performance

The invention describes a device that can complete multiplex analysis of biomolecules with limited sample

volume. The multiplex assay is achieved by delivering multiple sample solutions in parallel to a plurality of microcompartment arrays partitioned into a number of macrocompartments. The microfluidic liquid delivery and the microcompartment arrays can easily be scaled.

### Benefits

Proteins have historically been used as biomarkers for a vast array of diseases and health conditions such as pregnancy tests and cancer, and heart diseases. With a few notable exceptions such as pregnancy, the conventional single biomarker tests are inaccurate and are only used as adjuvant markers with other diagnostics tools. It has become clear that the use of multiple biomarkers in parallel strongly improves the diagnostic and prognostic accuracy of different tests. DNA based Gene expression arrays provide the strongest support for this argument and the recent FDA approval of tests such as Oncotype underline it further. The drawback of DNA analysis is that it is done with tissue which requires a surgical intervention, whereas proteins can be measured in blood. Multiplexed protein diagnostics have been slow to emerge because of lack of technologies that can be used for multiplexed validation of thousands of identified biomarker candidates, and lack of technology for diagnostics. Beyond diagnostics, a high throughput proteomics analysis techniques would find widespread application in research because proteins are the ultimate effectors of activity in the cell, and because the network activity of proteins cannot be detected using gene chips.

### Market Need and Opportunity

The market for proteomic technologies in the year 2005 was about \$6 billion and is expected to increase to \$10 billion by the year 2010 and \$18 billion by the year 2015. The largest expansion will be in bioinformatics and protein biochip technologies. Important areas of application are cancer and neurological disorders.



**Dr. David Juncker**

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Micro and Nanotechnologies supported the integration, miniaturization, and large scale parallelization of microelectronics along with an exponential growth that has already lasted over 40 years and has come to be known as Moore's law. This exponential growth has fueled the "digital revolution". The power of miniaturization and parallelization, enabled by microtechnologies, has started to bear on the life sciences, and already revolutionized them, by means of DNA microarrays and high throughput DNA sequencers running millions of biochemical reactions in parallel, as opposed to a single reaction at a time just a few years ago.

We are designing and developing micro and nanobioengineering technologies – with a strong focus on microfluidic systems – and are using these technologies for miniaturizing and parallelizing the protein analysis (proteomics) and cell biology. We aspire to emulate the parallelization of DNA microarrays and sequencers,, and enable systematic, quantitative, and comprehensive approach for protein analysis and ultimately for cell biological experimentation. Systematic and quantitative biological experimentation will in turn help achieve full modeling of cells such as neurons and of diseases such as cancer as complex (biological) systems. These new approaches will transform biology into a predictive science and will help increase exponentially our understanding of the human brain and of cancerous diseases.