

# innovations

from The University of Vermont

**TITLE:** PROTEIN FRACTIONATION FOR HIGH-THROUGHPUT PROTEOMICS

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**DESCRIPTION:** The invention provides a novel method for fractionating a sample of biological cellular material into a subset of proteins and other components according to their association with subcellular compartments. The method is part of a new proteomics platform employing single polymer matrix unit chromatography. Fractionation of protein mixtures and separation of individual proteins are generally rate-limiting steps in proteomic data collection. The invention platform is designed to overcome shortcomings in the present state of the art by facilitate the rate of proteomic analysis. Increased rates of 2-3 orders of magnitude can be expected, depending upon down-stream methods of protein separation, mass spectrometry, and data processing.

The invention (protein fractionation) involves 1) injecting a fractionating solution into a perfusion chamber at a rate that permits fractionation and equilibration of the subset of cellular components released by the fractionating solution, and 2) collecting the protein-loaded solution as it flows out of the chamber for downstream processing and analysis. One important aspect of the invention is that the sample material to be fractionated may be provided in amounts as small as 1 mg (or less). Another important aspect is that liquid aliquots from the protein fractions may be provided on an even smaller scale, in amounts as small as 1 pl (or less).

**ADVANTAGES:** The separation of proteins in a complex mixture is one of the most important challenges of modern proteomics. Sub-cellular fractionation, protein enrichment, and protein separation in liquid aliquots are key features of the proposed proteome platform that enable separation of complex mixtures of proteins from animal tissue biopsies. The proteomics platform combining subcellular fractionation (Invention 1) and single polymer matrix unit chromatography (Invention 2) has applications across the broad field of proteomics. The system can be automated to provide high throughput proteomic analysis of biological samples, including assessment of protein synthesis patterns or post-translational modifications. High throughput analysis will facilitate identification and evaluation of drug targets, mechanisms of drug action, and pharmacological and/or toxicological effects.

**PATENT STATUS:** US Patent applied for May, 2001.

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