



## **ProteoSolve<sub>LRS</sub>** Innovation at its finest

*Cutting edge method for detergent-free protein extraction  
from lipid-rich samples using PCT*

**Important New Biomarker Discovery Tool  
and Winner of the 2007 Frost & Sullivan  
North American Technology Innovation Award**

PBI recently announced the development of a novel, potentially revolutionary, PCT-dependent method for the safe, rapid, efficient, and reproducible extraction of proteins from lipid-rich samples such as adipose and brain tissues, organelles, and membrane preparations. Proteomic analysis of such samples is widely used in the study of diabetes, cancer, ALS, heart disease, and a number of other serious human disorders related to obesity. We believe that our PCT-dependent method of protein extraction from lipid-rich samples offers significant advantages over current extraction techniques, especially the ability to process samples without the addition of harsh detergents in the extraction process.

ProteoSolve<sub>LRS</sub> combines specific buffers, solvents, PULSE Tubes, and instructions in a single kit. All the researcher needs to do is to purchase or lease the Barocycler instrument and purchase the kit from PBI and they will have everything they need to enhance their protein extraction from lipid-rich samples. Our novel, patent-pending, PCT-dependent method for the detergent-free extraction of proteins from lipid-rich samples will benefit the thousands of researchers around the world who are working on new approaches for the prevention, detection, and treatment of diseases related to obesity - including diabetes, heart disease, and stroke.

## CALENDAR OF EVENTS

**BIOWEST 2007**  
DENVER, COLORADO  
DECEMBER 6 & 7, 2007

**PLANT & ANIMAL GENOMICS XV**  
SAN DIEGO, CA  
JANUARY 12-16, 2008

## **ProteoSolve<sub>LRS</sub> Wins** the Prestigious 2007 Frost & Sullivan North American Technology Innovation Award

### PCT Used to Study Colon Cancer

**Colon Cancer: Protein Biomarkers in Tissue and Body  
Dr. Paul Pevsner, Department of Pharmacology,  
New York University School of Medicine, New York, NY, USA**

The aim of the study was to achieve proof of principal that potential biomarkers of colon cancer can be identified from body fluids, and that tumor margins could be confidently identified with MALDI imaging. Proteins were extracted from tissue and stool using the PCT System with pressures between ambient and 35K PSI. Proteins recovered from tumor, urine, saliva, and stool were separated by either two-dimensional gel electrophoresis or HPLC. Control and tumor samples were reduced (DTT), alkylated (iodoacetamide), and trypsin digested. The protein digests were applied to MALDI target plates for MALDI mass spectrometry and MALDI MS tandem mass spectrometry. Tumor tissue sections were applied to target plates for direct MALDI protein identification from tissue and MALDI imaging.

### Application Focus

**Analysis of the Daphnia Proteome  
Using Pressure Cycling Technology (PCT)**

Daphnia are parthenogenic microcrustacea belonging to the family Daphniidae. Under normal environmental conditions, Daphnia populations are exclusively female and reproduction is clonal. However, in response to adverse environmental stimuli, sexual reproduction is induced, enabling genetic recombination and allowing rapid adaptive response. Sexual daphnids produce resting eggs, termed ephippia, which can remain viable for centuries. Thus, the analyses of Daphnids grown from ephippia isolated from layers of lake or stream sediment could potentially provide a chronology of environmental changes over several decades. It would be advantageous to derive sufficient protein from minimal number of Daphnia organisms to enable phenotypic analyses. Standard sample preparation methods are inadequate to provide sufficient protein from a single Daphnia. However, Pressure Cycling Technology proved to be an excellent method for the extraction of proteins from extremely small samples. Proteins isolated by the PCT System and analyzed on two-dimensional gel electrophoresis were capable of resolving differences between asexual and sexual phenotypes from single *Daphnia magna*. For the smaller *Daphnia pulex*, 2DGE resolved  $904 \pm 7$  protein spots from a single organism, and  $1,267 \pm 3$  protein spots from a pool of five organisms and demonstrated high reproducibility of the combined methods. These data suggest the feasibility of using 2DGE for following phenotypic response to environmental stimuli such as hepatotoxin contamination during cyanobacterial blooms.