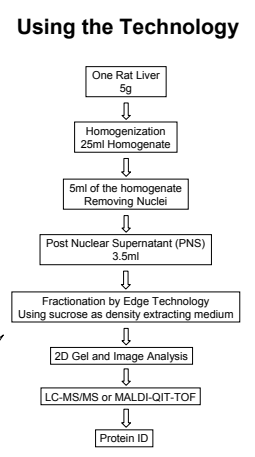
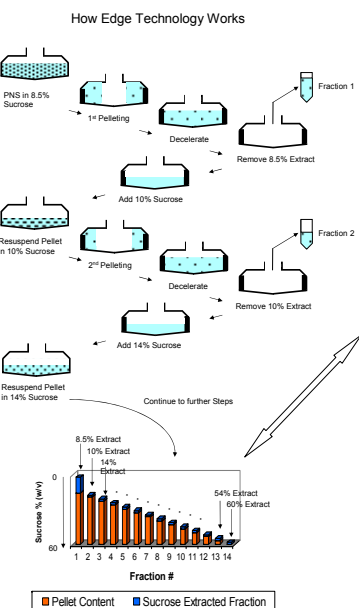
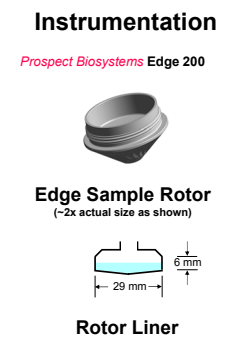
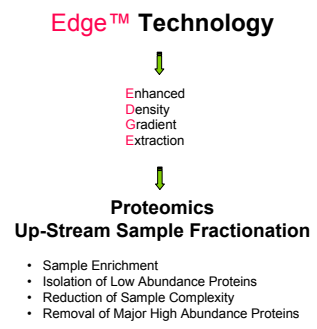


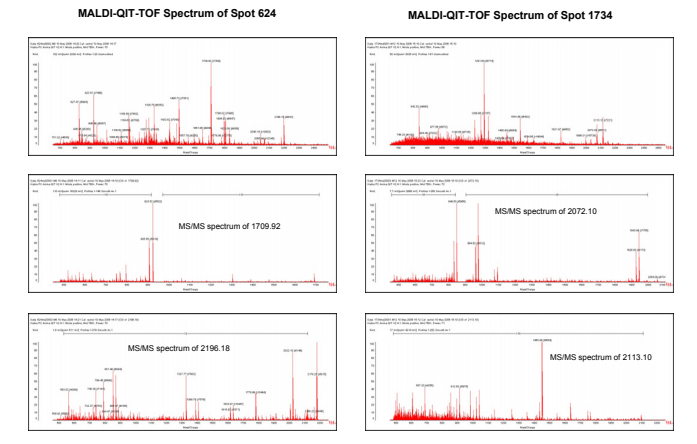
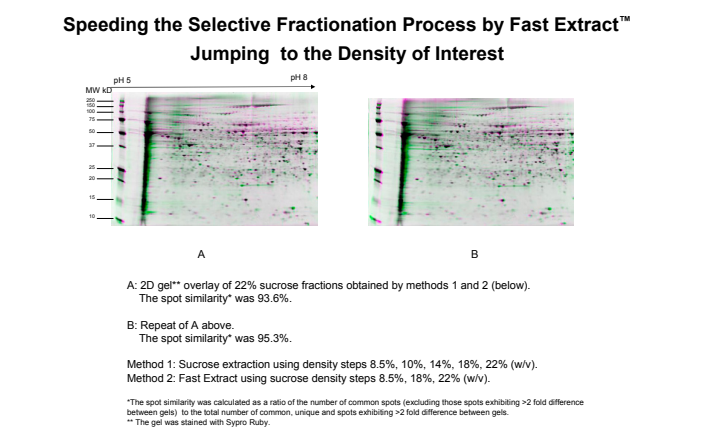
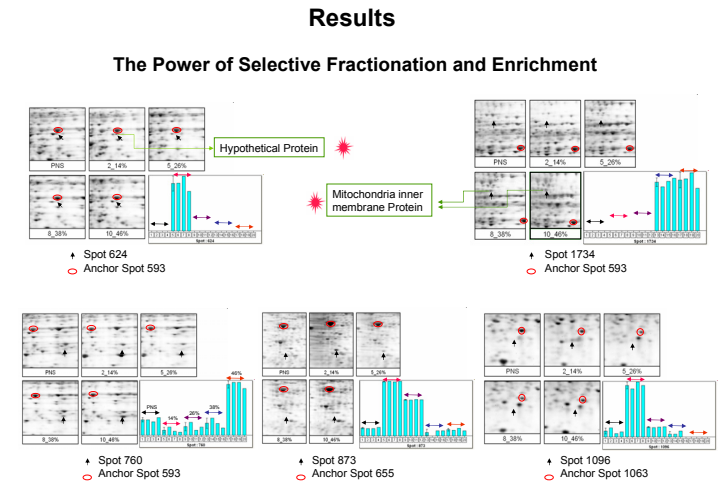
# Edge™: A Powerful Technology for Selective Proteomics Sample Fractionation Using Step-wise Gradient Density Extraction

Wenkui Lan & Marc J. Horn, Prospect Biosystems, LLC, Newark, NJ  
 Douglas Hinerfeld & Sun W. Tam, UMass Medical School Proteomics Consortium, Shrewsbury, MA



**For more information, Visit Booth #8**

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 www.prospectbiosys.com



#### Anchor Spot Point Protein ID Using LC-MS/MS

Spot #	Protein
505	Calreticulin precursor (gi 117505)
655	Actin, Cytoplasmic 2 (Gamma-actin) (gi 54036665)
1063	Peroxisredoxin 1 (gi 16923958)
593	Argininosuccinate synthetase (gi 25453414)
233	Formyltetrahydrofolate dehydrogenase (gi 57921067)

#### Selected Spot Point Protein ID Using MALDI-QIT-TOF

Spot #	Protein
624	Predicted: Similar to Psmc6 protein (gi 34869622)
1096	Ferritin light chain (gi 204123)
760	Urate Oxidase (gi 56971244)
873	40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (gi 730681)
1734	Electron transfer flavoprotein-ubiquinone oxidoreductase precursor (gi 34419911)

## Edge Technology Benefits

- Edge Technology provides a powerful, selective sample fractionation tool for proteomics analysis, including low abundance protein isolation and enrichment, as well as information on subcellular location.
- Sample complexity is reduced significantly.
- Starting sample volume is less than 4 ml.
- Extraction volume is flexible and can be as low as 100 µl.
- Each extraction step takes about 5 minutes.
- Extraction may start at any density step of interest without the need for going through the whole gradient.
- The recovery yield is > 90%.
- The method DOES NOT need any density gradient medium and does not need any gradient mixer.
- The density of the extraction medium at each step is defined and no other instrument is needed for density determination.
- Fractionation conditions are non-denaturing.

## Potential Applications

- Subcellular biology, cell biology and subcellular proteomics
- Drug target discovery and characterization
- Binding studies and protein-protein interactions
- Biomarker discovery