

Instrumentation



Research & Development

Protein Biomarker Discovery Using Quantitative Proteomics

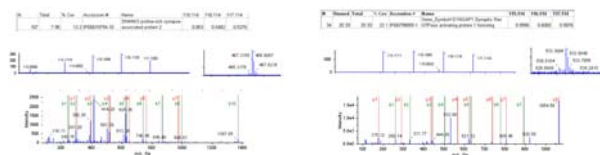
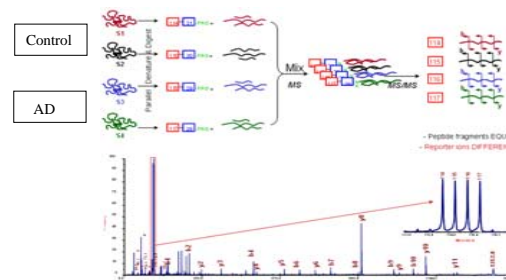


Fig 1. Example of MS/MS spectrum of peptide VQIPQLCQTK from Shank3 digest mixture by labeling 4 separate digests with tag 118-117 and combining the reaction mixture in a 1:1:1:1 ratio. A) Shank3 identification; B) low mass region showing the signature ion used for quantification; C) isotopic distribution of a double-charged precursor (M+2H)²⁺, m/z 547.5472

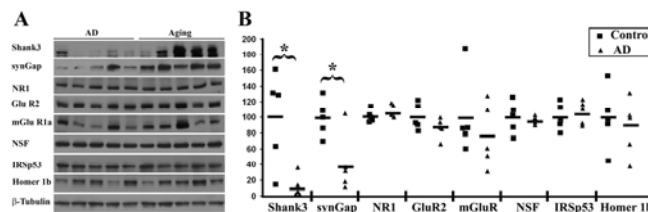


Figure 3 : Potential Biomarker candidates like Shank3, synGap... confirmed by blotting analysis

Objective

- To develop new technologies in proteomics for use in the prevention, diagnosis and treatment of disease
- To Improve and develop new protein profiling technologies to identify proteins that play key roles and/or serve as biomarkers for cancer
- To Provide state of the art technologies in protein identification and characterization
- To develop novel methods for high throughput protein identification
- To provide consultancy on protein separation methodologies for effective proteomic analysis
- To provide consultancy for mass spectrometry data interpretation
- To promote economic development with pharmaceutical and biotechnology industries

Technologies Being Implemented

- Two dimensional gel electrophoresis
- Multidimensional liquid chromatography (MudPIT)
- High resolution mass spectrometry (HRMS)
- Isotope tagged quantitative LC-MS/MS protein profiling: ICAT, iTRAQ and SILAC
- Differential (fluorescence) 2D gel electrophoresis protein profiling (DIGE)
- Phosphoproteome analysis based on MS analysis of phosphopeptide-enriched fractions from digests of cell extracts
- Protein biomarker analysis of serum and other biological fluids
- Gel imaging and analysis
- MALDI-TOF peptide mass fingerprint (PMF)
- Metabolite ID and quantitation
- Amino acid analysis (AccQ tag)

Identifying Subproteome of Kinetically Stable via 2D SDS/PAGE-Mass Spectrometry

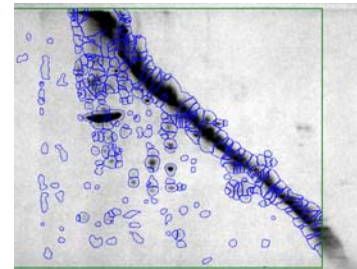
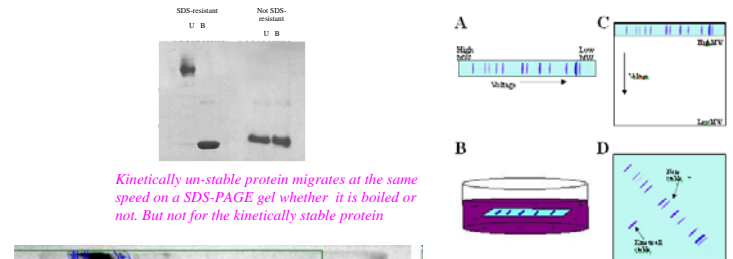


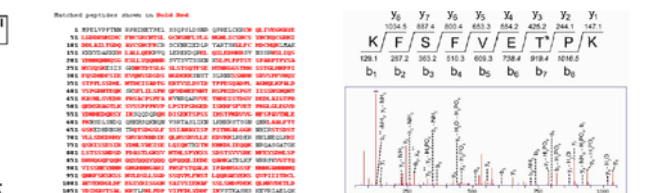
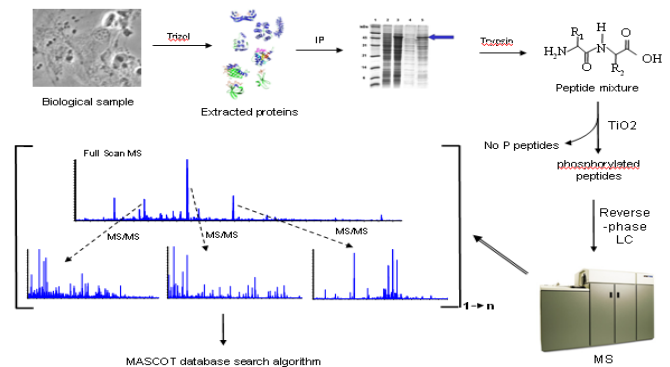
Table: Kinetically stable protein identified

Accession#	Protein name	MW	unique peptide No.	req coverage
gi2781252	Chain A, Structure Of Inorganic Pyrophosphatase Mutant D45a	19473	11	80%
gi2781250	Chain A, Structure Of Inorganic Pyrophosphatase Mutant D42a	19473	7	80%
gi15804817	inorganic pyrophosphatase [Escherichia coli O157:H7 EDL933]	19805	12	80%
gi15802070	inorganic pyrophosphatase [Escherichia coli O157:H7 EDL933]	21310	12	91%
gi9597572	Adenosine triphosphatase [Paramecium B100]	23991	12	90%
gi15804309	inorganic pyrophosphatase [Escherichia coli O157:H7 EDL933]	21125	11	76%
gi21730871	Chain A, Structure Of E. Coli Uridine Phosphorylase At 2.0a	27153	12	69%
gi16131680	uridine phosphorylase [Escherichia coli K12]	27313	10	68%
gi1943074	Chain, OmpF Pore Domain (Mutant Delta 109-114)	36381	20	94%
gi14488510	Chain A, OmpF Pore Mutant T306F	37066	20	94%
gi999992	Chain, The Structure Of OmpF Pore In A Tetragonal Crystal Form	37062	20	94%
gi999973	Chain, Matrix Pore (OmpG Mutant with Gly 119 Replaced by Asp (D119A))	37120	20	94%

K. Xia, ..., Q. Lin et al. PNAS, 2007, 104(44), 17329-44

Phosphorylation Site Mapping of a Kinase - Cdc42 GAP

Phosphoproteomics: General Experimental Design



X. Zheng, ..., Q. Lin et al. EMBO J, 2007, 26, 3760-9

Figure 5: MS/MS of phosphopeptide