

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

Instrumentation

- QSTAR XL LC-MS/MS system (ABI/SCIEX)
- Q-ToF 2 LC-MS/MS (Waters/Micromass)
- ABI 4000 QTRAP (ABI/SCIEX)
- Autoflex MALDI-TOF (Bruker Daltonics)
- Ettan Daltsix 2D gel electrophoresis (Amersham)
- ProXPRESS imaging system (PE)
- Progenesis workstation (Nonlinear Dynamics)
- Akta FPLC and Agilent HPLC system

Research & Development

Protein Biomarker Discovery Using iTRAQ™ Reagents Proteomics in Alzheimer's Disease

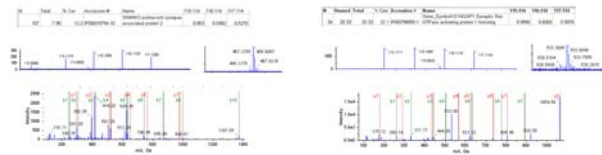
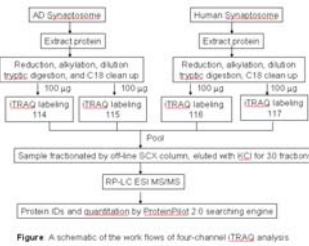


Fig 1. Example of MS/MS spectrum of peptide VQVPLQDQTK from Shank3 digest mixture by labeling 4 separate digests with tag 114-117 and combining the reaction mixture in a 1:1:1:1 ratio. A) Shank3 identification. B) Raw mass region showing the signature ions used for quantitation. C) isotopic distribution of a double charged precursor (M+2H)²⁺, (552.647.8472)

Fig 2. Example of MS/MS spectrum of peptide DAIEGFR from Shank3 digest mixture by labeling 4 separate digests with tag 114-117 and combining the reaction mixture in a 1:1:1:1 ratio. A) Shank3 identification. B) Raw mass region showing the signature ions used for quantitation. C) isotopic distribution of a double charged precursor (M+2H)²⁺, (552.533.3)

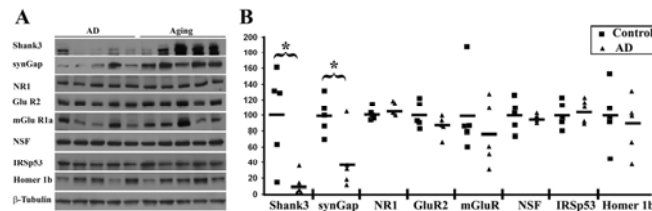


Figure 3 : Potential Biomarker candidates like Shank3, synGap... confirmed by western analysis

Identifying Subproteome of Kinetically Stable via 2D SDS/PAGE in E. Coli

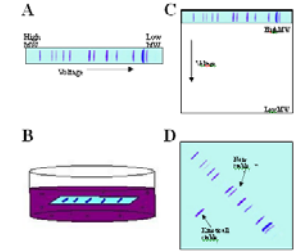


Table: Kinetically stable protein identified

Accession#	Protein name	MW	unique peptide No.	seq coverage
g02781252	Class A, Structure Of Serine Phosphatase Mutant D45a	19673	11	80%
g02781250	Class A, Structure Of Serine Phosphatase Mutant D45a	19673	7	80%
g15904817	serenase: serine phosphatase [Enterobacter coli O157:3F EDL533]	19805	12	80%
g15902070	serenase: serine phosphatase, c-10k [E coli O157:3F EDL533]	21310	12	91%
g0597572	serenase: serine phosphatase [Strain E100]	25591	12	90%
g0443293	Class A, Triphosphatase Serenase Tim (E.C.5.3.1.1)	21225	11	76%
g15904508	serenase: serine phosphatase [E coli O157:3F EDL533]	21226	10	76%
g021730071	Class A, Structure Of Cdk Uridine Phosphorylase At 2.6a	27153	12	68%
g16131660	uridine phosphorylase [Enterobacter coli K12]	27313	10	68%
g191943074	Class A, Cmp Form Deletion (Mutant Delta 109-114)	36381	28	94%
g114488510	Class A, Cmp Form Mutant T310E	37066	28	94%
g0599982	Class, The Structure of Cmp Form In a Tetragonal Crystal Form	37062	28	94%
g0599982	Class, Mutant Form (Cmp Form Mutant with Gly 119 Replaced by Asp (G119A))	37062	28	94%

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

Phosphorylation of a Cdc42 GAP by CDKs promotes polarized morphogenesis in yeast

Method: peptide shims in MudPip



Figure S5 (Zheng et al.)

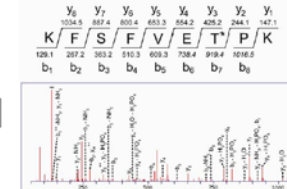


Figure S5: MS/MS of phosphopeptide

Mass-spectrometry identification of phosphorylation sites on Rga2: Purified Myc-Rga2 from hyphae

- ¹⁰⁵NLQYMNQNGSQS*GG*LLYQQNR¹²⁰ (total 1 or 2 sites)
- ²³²SLPLPFTIS*PARPTYSANSYQSK²⁵⁶
- ³⁴³VS*PPVNGVST*PPLSSDHLNDEISADTGER³⁷² (total 1 or 2 sites)
- ³⁷³IVLDVIDT*PPEQADPLAGNLKPLDVS*PGR⁴⁰⁰ (total 1, 2 or 3 sites)
- ⁴¹¹SELLS*PNQFDHNEHNR⁴¹¹
- ⁴³²PMIDS*PGT*HIS*NSNQNTK⁴⁹¹ (total 1, 2 or 3 sites)
- ⁴⁶³S*ACPS*PEAK⁴⁷¹ (total 1 or 2 sites)
- ⁴⁷⁸IVINDSITDGVDELDAIGT*PR⁵⁰⁰ (total 1 site)
- ⁵⁸⁶AGT*LKSSV*S*PPPK⁵¹⁴
- ⁵¹¹SVS*PPKVP*PST*PSR⁵²⁷
- ⁵¹⁹VPLPST*PSR⁵²⁷ (total 1 site)
- ⁵³⁵K*FVET*PK⁵⁴² (total 1 or 2 sites)
- ⁵⁴¹CLGLEGVDDYDNDHQR*S*YK⁵⁴²
- ⁵⁶⁰QHDS*EKIS*PSSMTPK⁵⁸⁶ (total 1, 3 or 4 sites)
- ⁵⁷⁶PSMSSMTPK⁵⁸⁶ (total 1 site)
- ⁵⁸⁷RVVNGS*PAVTLNPK⁶⁰²
- ⁶⁶⁰QT*S*DGS*LFSS*ANAYIS*PPITNGALGGR⁶⁹⁹ (total 1, 2 or 3 sites)
- ⁸⁰¹LS*SS*S*NSD*DPDAS*LGK⁸¹⁴ (total 1, 2 or 3 sites)
- ⁸⁴⁰ENVYSYDHL*S*PDR⁸⁵²
- ⁹²⁰PPS*FSTQALR⁹³⁰

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

Technologies being implemented

- Two dimensional gel electrophoresis
- Multi dimensional liquid chromatography
- High resolution mass spectrometry (HRMS)
- Isotope tagged quantitative LC-MS/MS protein profiling: 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 disease 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)