

Program in Cellular, Molecular and Computational Proteomics

Objectives

Add modern proteomics capabilities to UK

Strengthen protein production and characterization facilities

Proteomics is an emerging post-genomic field of study that provides the tools with which to examine the sequences, three-dimensional structures and cellular levels of protein molecules and their regulatory modifications, qualitatively and quantitatively, in living cells and tissues and from studies of purified proteins.

Approach

Recruit two new faculty members:

- Cellular Proteomics
- Molecular/Computational Proteomics

Add instrumentation:

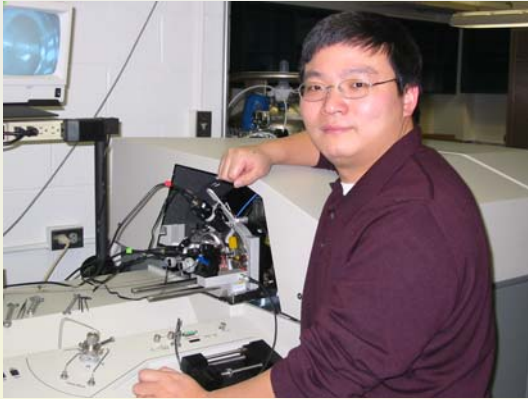
- Mass spectrometry and related techniques for cellular proteomics
- Protein production and characterization
- Computational resources

Organization/integration:

- Proteomics and protein production/characterization service facilities both established under the existing Center for Structural Biology

Faculty Recruitment in Cellular Proteomics

Dr. Haining Zhu
Appointed Sept., 2002



Projects:

Mitochondrial proteomics of familial
Lou Gehrig's disease

SOD1 conformation and aggregation in
cells and relevance to Lou Gehrig's disease

Cell surface proteomics and significance
in cancer metastasis

Proteomics studies of lipid rafts and
relevance to diabetes

Active funding:

NIH R01, \$925,000 total direct

NIH R21, \$301,291 total direct

NIH COBRE project, \$902,974 total direct

Pending requests:

Six total to NIH and DOD (PI on two)

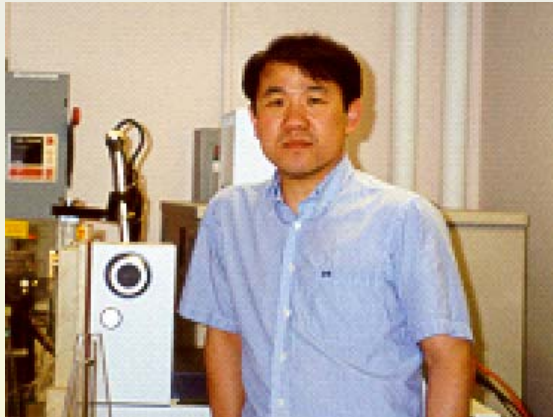
Recent publications/submissions:

Fukada, K., Zhang, F., Vien, A., Cashman, N.
R. and **Zhu, H.** "Mitochondrial proteomic
analysis of motor neuron-like cells expressing
superoxide dismutase 1 mutants linked with
familial amyotrophic lateral sclerosis", (2004)
Molecular and Cellular Proteomics, 3, 1211-
1223.

Lu, X. and **Zhu, H.** "A novel protocol for
efficient LC-MS/MS characterization of
membrane proteins", submitted to *Molecular
and Cellular Proteomics*.

Faculty Recruitment in Molecular/Computational Proteomics -

**Dr. Young-in Chi Appointed
September 2003**



Projects:

Multi-protein complex formation by HNF1 α
and HNF4 α : beta cell master regulators

Enhanceosome complex formation by c-AMP
responsive element binding proteins.

Structural and functional studies of the tumor
suppressor Menin

Active funding:

Juvenile Diabetes Fdn., \$479,026 total direct
NIH COBRE project, \$964,508 total direct

Recent publications:

Duda, K., Chi, Y.-I., and Shoelson, S. E.
(2004) Structural basis for HNF-4 α
activation by ligand and coactivator binding.
J. Biol. Chem. 279: 23311-6.

Dhe-Paganon S., Werner E.D., Nishi M.,
Hansen L., Chi Y.I., Shoelson S.E. (2004)
A phenylalanine zipper mediates APS
dimerization. Nat. Struct. Mol. Biol.
11(10):968-74.

Chi, Y.-I. (2005) Homeodomain revisited: a
lesson from disease-causing mutations.
Human Genetics, 116: 433-44.

Major equipment acquired

Proteomics

- ABI QStar XL Mass Spectrometer – \$475,000 (\$125,000 provided by institution)
- Two 2D gel systems – \$22,500 (\$7,000 provided by institution)
- Bio-Rad ProteomeWorks Spot Cutter system – \$84,917
- Ciphergen Protein profiling Seldi-TOF Mass spectrometry system - \$400,000 (entirely funded by institution)
- Molecular Dynamics Typhoon phosphorimager – \$105,000 (\$75,000 provided by institution)



Protein production/characterization

- New Brunswick Bioreactor/fermenter - \$39,290
- Jasco J810 Spectrapolarimeter – \$83,313
- P/E LS 55 Fluorescence Spectrometer – \$40,000
- Waters Breeze Preparative HPLC System – 30,442
- TIRF microscopy system - \$70,000 (\$35,000 provided by institution) →



Computation

- Microway, Inc 16 node Beowulf Linux Cluster – \$78,000
- 10 Linux workstations -- \$14,000

Facilities

Proteomics facility

- Staffed by one Ph.D. research analyst and one technician
- 2D gel electrophoresis, mass spectrometry based proteomics, Ciphergen based protein profiling
- Users from 22 groups

Protein production/characterization

- Staffed by one Ph.D. research analyst
- Large scale fermentation and cell culture, protein purification, light scattering, circular dichroism, fluorescence spectroscopy, kinetics, crystallization, structure determination, single molecular fluorescence, protein interactions in cells
- Users from 16 groups

Future: Both facilities funded for five years via NIH COBRE grant (Louis Hersh, PI)!