

Presentation: Accurate and precise profiling of pathological proteomes by utilization of high resolution nano-LC/Orbitrap/ETD

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eRA COMMONS USER NAME JUNQU1	Chief Scientist in Bioanalysis (NYBLS)		
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Tsinghua Univ., China	Ph.D.	2002	Analytical Chemistry

Professional Experience:

4/00-10/00	Visiting Scholar	School of Chinese Medicines, Hong Kong Baptist University, Hong Kong.
08/02-9/04	Postdoctoral Fellow	Dept. of Pharmaceutical Sciences, SUNY/Buffalo
9/04-present	Asst. Professor	Dept. of Pharmaceutical Sciences, SUNY/Buffalo
01/07-present	Chief Scientist in Bioanalysis	New York Center of Excellence in Bioinformatics and Life Science
10/07-present	Member, Faculty of Graduate Committee	Dept. of Pharmaceutical Sciences, SUNY/Buffalo

Selected peer-reviewed publications:

- Luo G; Qu J; Wang S. Determination of aluminum in the extraction of mouse brain by capillary electrophoresis. *Am. Biotech. Lab.* **17**: 20-2 (1999).
- Qu J; Luo G; Wu Z. The advancement of HPLC-NMR technologies. *Chinese Journal of Analytical Chemistry* **28**: 976-81 (1999).
- Qu J; Wang Y; Luo G; Wu Z. Quantitation of denzanyisu in biological matrix by LC/MS/MS. *ACTA Pharmaceutica Sinica* **35**: 139-41 (2000).
- Qu J; Wu Z; Luo G; Liu M. Neonate screening for phenylketonuria by LC/MS/MS. *Chemical Journal of Chinese Universities* **21**: 210-2 (2000).
- Qu J; Wang Y; Luo G. Determination of scutellarin in Erigeron breviscapus extract by liquid chromatography-tandem mass spectrometry. *J Chromatogr A* **919**: 437-41 (2001).
- Qu J; Wang Y; Luo G; Wu Z. Identification and determination of glucuronides and their aglycones in Erigeron breviscapus by liquid chromatography-tandem mass spectrometry. *J Chromatogr A* **928**: 155-62 (2001).
- Qu J; Chen W; Luo G; Wang Y; Xiao S; Ling Z; Chen G. Rapid determination of underivatized pyroglutamic acid, glutamic acid, glutamine and other relevant amino acids in fermentation media by LC-MS-MS. *Analyst* **127**: 66-9 (2002).
- Qu J; Wang Y; Luo G; Wu Z; Yang C. Validated quantitation of underivatized amino acids in human blood samples by volatile ion-pair reversed-phase liquid chromatography coupled to isotope dilution tandem mass spectrometry. *Anal. Chem.* **74**: 2034-40 (2002).
- Qu J; Liang Q; Luo G; Wang Y. Screening and identification of glycosides in biological samples using energy-gradient neutral loss scan and liquid chromatography tandem mass spectrometry. *Anal. Chem.* **76**: 2239-47 (2004).
- Qu J; Straubinger RM. Improved sensitivity for quantification of proteins using triply charged cleavable isotope-coded affinity tag peptides. *Rapid Commun. Mass Spect.* **19**: 2857-64 (2005).
- Liang Q; Qu J; Luo G; Wang Y. Rapid and reliable determination of illegal adulterant in herbal medicines and dietary supplements by LC/MS/MS. *J Pharm Biomed Anal* **40**: 305-11 (2006).

12. Qu J; Jusko WJ; Straubinger RM. Utility of cleavable isotope-coded affinity-tagged reagents for quantification of low-copy proteins induced by methylprednisolone using liquid chromatography/tandem mass spectrometry. *Anal. Chem.* **78**: 4543-52 (2006).
13. Drake EJ; Cao J; Qu J; Shah MB; Straubinger RM; Gulick AM. The 1.8 Å crystal structure of PA2412, an MbtH-like protein from the pyoverdine cluster of *Pseudomonas aeruginosa*. *J. Biol. Chem.* **282**: 20425-34 (2007).
14. Qu J; Qu Y; Straubinger RM. Ultra-sensitive quantification of corticosteroids in plasma samples using selective solid-phase extraction and reversed-phase capillary high-performance liquid chromatography/tandem mass spectrometry. *Anal. Chem.* **79**: 3786-93 (2007).
15. Straubinger RM; Krzyzanski W; Francoforte CM; Qu J. Applications of quantitative pharmacodynamic effect markers in drug target identification and therapy development. *Anticancer Res.* **27**: 1237-46 (2007).
16. Gaspar JR; Qu J; Straubinger NL; Straubinger RM. Highly selective and sensitive assay for paclitaxel accumulation by tumor cells based on selective solid phase extraction and micro-flow liquid chromatography coupled to mass spectrometry. *Analyst* **133**: 1742-8 (2008).
17. Song W; Wang Y; Qu J; Lin Q. Selective functionalization of a genetically encoded alkene-containing protein via "photoclick chemistry" in bacterial cells. *J Am Chem Soc* **130**: 9654-5 (2008).
18. Song W; Wang Y; Qu J; Madden MM; Lin Q. A photoinducible 1,3-dipolar cycloaddition reaction for rapid, selective modification of tetrazole-containing proteins. *Angew Chem Int Ed Engl* **47**: 2832-5 (2008).
19. Yu H; Straubinger RM; Cao J; Wang HS; Qu J. Ultra-sensitive quantification of paclitaxel using selective solid-phase extraction in conjunction with reversed-phase capillary liquid chromatography/tandem mass spectrometry. *J. Chromatog. A* **1210**: 160-7 (2008).
20. Yu AM, Qu J, Felmler MA, Cao J, Jiang XL. Quantitation of human cytochrome P450 2D6 protein with immunoblot and mass spectrometry analysis. *Drug Metab. Dispos.* **37**: 170-7 (2009).
21. Wang H; Straubinger RM; Aletta JM; Cao J; Duan X; Yu H; Qu J. Accurate localization and relative quantification of arginine methylation using nanoflow liquid chromatography coupled to electron transfer dissociation and orbitrap mass spectrometry. *J Am Soc Mass Spectrom* **20**: 507-19 (2009).
22. Duan X; Young R; Straubinger RM; Page, BJ; Cao J; Wang H; Yu H; Canty JM; Qu J* "A Straightforward and Highly Efficient Precipitation/On-pellet Digestion Procedure Coupled to a Long Gradient Nano-LC Separation and Orbitrap Mass Spectrometry for Label-free Expression Profiling of the Swine Heart Mitochondrial Proteome". *J. Proteome Res.* **6**: 2838-2850 (2009).
23. "The 2.1 Å crystal structure of an acyl-CoA synthetase from *Methanosarcina acetivorans* reveals an alternate acyl-binding pocket for small branched acyl substrates." Shah MB, Ingram-Smith C, Cooper LL, Qu J, Meng Y, Smith KS, Gulick AM. *Proteins. In press.* (2009p).
24. "Proteomic analysis of murine Piwi proteins reveals a role for arginine methylation in specifying interaction with Tudor family members" Vagin V, Wohlschlegel J, Qu J, Jonsson X, Huang X, Chuma S, Girard A, Sachidanandam R, Hannon G. *Gene and Development. In press* (2009p).

C. Research Support:

1 S10 S10RR024521 (Straubinger)
NIH/NCRR

Role: co-PI

4/1/09 – 3/31/10

"High Performance Computational System to Support LCMS/Proteomics Analysis"

Funds the purchase of a state-of-the-art computational cluster to accelerate proteomics analysis and provide mass storage for large datasets.

5R01GM073646-02 (Blanco)
NIH/NCI

Role: co-PI

3/1/2005-2/28/2010

Pharmacogenetics Of Human Carbonyl Reductases

The proposed studies will provide essential information on the impact of CBR1 and CBR3 genetic variability on CBR mediated drug metabolism. The understanding of the molecular basis that govern the pharmacodynamics of CBR metabolized drugs will assist the design of more rational pharmacological therapies.

1 RO1 HL-61610-05 (Canty)
NIH/NCI

Role: co-I

9/1/06 - 8/31/10

Metabolic Adaptation and Functional Recovery of Hibernating Myocardium

This project evaluates the role of viable, chronically dysfunctional myocardium on the progression of chronic ischemic left ventricular remodeling. Studies are directed at identifying the role of apoptosis induced myocyte loss in ischemic and remote regions of hearts with hibernating myocardium and identify whether chronic intermittent ischemia upregulates pro and antiapoptotic proteins. Interventions to ameliorate apoptosis include studies to stimulate angiogenesis with adenoviral gene transfer of FGF- 5 as well as studies to prevent apoptosis by chronic treatment with β -blockade.

2R01AI019641-23A1 (Murphy)
NIH/NCI

Role: co-PI

9/30/1983 - 12/31/2012

Pathogenesis of Haemophilus influenzae infection in COPD

Chronic obstructive pulmonary disease (COPD) is a debilitating disease and is the fourth most common cause of death in the US. Nontypeable H. influenzae can be regarded as an opportunistic human pathogen because infections occur in two selected sites in specific host settings: 1) the lower respiratory tract of adults with COPD; and 2) the middle ear of children under 6 years of age, often preceded by viral infection. Little attention has been placed on studying strains for the possibility that different strains have different virulence potential until recently. The course of COPD is characterized by intermittent respiratory tract infections that result in hospital admissions, respiratory failure and death. This proposal includes state of the art approaches to understanding how the bacterium, Haemophilus influenzae, causes infection specifically in the setting of COPD. These results will lead directly to fresh approaches for treatment and prevention of infections by the most common cause of infection in adults with COPD.

UB Center for Protein Therapeutics (Qu)
External industry consortium funds

7/1/2008 - 6/30/2009

Ultrasensitive LC/MS Quantification of Cytokines in Biological Samples

The in vivo concentration of both therapeutic and regulatory proteins affects not only diverse biological and pathophysiological processes, but also underlies the pharmacological responses induced by many therapeutic agents. However, quantification of proteins in biological systems is challenging owing to the extreme diversity of protein chemical and physical properties, and the fact that the effector proteins of high interest are often present at relatively low abundance against an obscuring background of high-abundance "housekeeping" proteins. The purpose of this proposal is to develop a nano-LC/triple-quad MS/MS based method for the ultra-sensitive and accurate quantification of cytokines as regulated targets of therapeutic agents, using Orthogonal Array Optimization and stable isotope coded internal standards.

NIH SBIR R42/R01. (Qu)

02/01/2009-5/31/2014

KX2-391-protein interactions: Phase I

The project explores the possibility of identifying the ID and the exact binding domain of KX2-391 to cellular proteins, using a novel high-res nano_LC coupled to ETD sequencing.

Completed (last 3 years):

1 S10 RR023650 (Straubinger)
NIH/NCRR

Role: co-PI

4/1/07-3/31/09

High sensitivity liquid chromatography/tandem mass spectrometry system

Provides funds for a third high-end state-of-the-art triple quad mass spectrometer (ThermoFinnigan Quantum Ultra) for drug and peptide quantification.

1 S10 RR021221 (Straubinger)
NIH/NCRR

Role: co-PI

4/1/05 – 3/31/07

“LC/quadrupole ion trap mass spectroscopy system”

Funded the purchase of a state-of-the-art multi-dimensional capillary liquid chromatography system (GE Healthcare MDLC) and a Linear Ion Trap Quadrupole mass spectrometer (ThermoFinnigan LTQ) for peptide sequencing and drug metabolite characterization.