

09/15/2016

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OFFICE:

Center for Biologics Evaluation and Research (CBER)
U.S. Food and Drug Administration (FDA)
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EDUCATION:

Ph.D. (1985), Pharmaceutical Sciences
University of Kentucky, Lexington, KY 40536
Dissertation: Thromboxane Synthase: purification, characterization and immunological studies.

M.S. (1979), Agricultural Chemistry
National Taiwan University, Taipei, Taiwan
Thesis: Enzymatic oxidation of glucose using crab chitin-immobilized glucose oxidase and catalase in a fluidized-bed reactor.

B.S. (1975), Agricultural Chemistry
National Taiwan University, Taipei, Taiwan
Thesis: Production of single-cell protein using methanol as the sole source of carbon.

POSTDOCTORAL TRAINING (85-89)

Howard Hughes Medical Institute, Dept. of Cell Biology
Baylor College of Medicine, Houston, TX 77030
Mentor: Savio LC Woo, Ph.D.
Research Project: Transcriptional regulation of human α 1-antitrypsin gene expression *in vitro* and *in vivo*.

EMPLOYMENT:

03/2011-present

Director, Facility for Biotechnology Resources, CBER, FDA

Major roles: Developing and managing a Center wide, multi-functional "Facility for Biotechnology Resources (FBR)" at FDA. Lead a team of 8 scientists providing technical consultation as well as experimental execution on macromolecule synthesis and characterization. At present, the following analytical/synthetic services are offered:

Next Generation Sequencing: Based on Illumina platform using HiSeq 2500, NextSeq & MiSeq sequencers. Sample preparation is assisted by Corvaris S220 focused ultrasonicator (DNA fragmentation), Promega AS4500 (RNA/DNA extraction), Illumina

NeoPre (library construction), Agilent Bioanalyzer (DNA/RNA QC), and Sage Pipin Pre (DNA fragment isolation). Data analysis is performed using programs on NIH Helix (Biowulf) supercomputer, IlluminaCompute, Illumina BaseSpace, Genomatix GGA, or CLC Genomics Workbench.

Proteomics: Protein identification, quantification, and posttranslational modifications are analyzed by LC-MS, using Thermo Q Exactive and Orbitrap Fusion mass spectrometers equipped with a micro- or nano-flow HPLC. Database search and analysis are performed with Proteome Discoverer, PepFinder, Protein Deconvolution, ProSight PC, Byonic, and Byologic software programs.

Capillary DNA Sequencing: Sanger's dideoxy DNA sequencing analysis is conducted on 2 ABI Genetic Analyzers (3500xL, 24 capillaries) for plasmids or PCR products.

Peptide Synthesis, Modifications, and Conjugation: Two ABI 433A and 2 Tribute peptide synthesizers are used to provide synthetic, modified, or conjugated peptides.

Oligonucleotide Synthesis: Four ABI 394 and one 12-channel MerMade oligo synthesizers are used to provide synthetic, modified (e.g., biotinylated or thiolated oligos and Taqman probes), or degenerate oligonucleotides.

N-terminal Protein/Peptide Sequencing: An ABI 494A Procise sequencer is used for protein/peptide N-terminal Edman sequencing.

Macromolecule Purification and Quality Control: Two Walters' preparative HPLC systems with PDA detectors are used for peptide/oligonucleotide purification; ABI Voyager and SumulTOF mass spectrometers are used for the QC.

Large-scale protein expression, purification, and conformational characterization: Using Eppendorf Bioflo 320 fermentor, Specpturm KR2i TFF (tangential flow filtration) system, FPLC, Mass spectrometers, and Leap HDx (hydrogen-deuterium exchange).

02/2003-03/2011

Director, Proteomics and Analytical Biochemistry Unit (at NIA) and Proteomics Core Facility (at NHLBI)

Major Roles: Established and managed Proteomic Cores for NHLBI (2003-2008) and NIA (2008-2011) of NIH, respectively. Both had 2D gel-based and LC-based mass spectrometric capabilities. Provided project consultation, sample preparation, and mass spectrometry to intramural investigators (~55 each), and directed staff scientists on methods development and biomedical applications. Contributed ~50 peer-reviewed publications on protein ID, PTMs, quantitative proteomics, and software programs.

01/2001-02/2003

Senior Scientist, Division of Proteomics, Thermo Finnigan Inc., 355 River Oak Pkw, San Jose, CA

Major Roles: Established the 1st "sample preparation lab" for Thermo Finnigan's San Jose Factory. Participated in the specification, applications, and marketing of the 1st fully automated commercial 2D-LC/MS system, the ProteomeX. Conducted phosphoprotein and

phosphopeptide capture and LC-MS analysis using magnetic bead-coated anti-p-Tyr or the IMAC strategy. Presented seminars on behalf of Thermo Finnigan at biotechnology workshops and research Institutes around US and Canada cities.

10/1989-12/2000

Assistant (89-97)/Associate (97-2000) Professor, Programs in Human Genetics & Molecular and Cell Biology, University of Maryland School of Medicine, Baltimore, MD 21201

Major roles: Mentored/Supervised Ph.D. graduate students and Postdocs in Program in Human Genetics; Lectured on Human Genetics (I and II) and Transcriptional Regulation to medical and graduate students. Conducted research on gene characterization of thromboxane synthase (TS), mapping TS genes to human chromosomes 7q and mouse chromosome 6, respectively; Identifying CA repeat polymorphism and its association with pre-eclampsia; elucidating NF-E2 and AP-1 as the major transcription regulators, while methylation at gene promoter as a determinant factor in cell-specific expression; producing chimeric mice from TS +/- ES cells via homologous recombination.

OTHER PROFESSIONAL ACTIVITIES AT NIH and FDA:

Member, FDA Shared Resources Committee (2011-present).
 Member, CBER Computational Science Review Committee (2011-present)
 Member, CBER White Oak Laboratory Planning Committee (2011-present)
 Member, NIH Proteomics Interest Group Steering Committee (2003-2011)
 Member, Review Committee on NINDS Protein and Peptide Sequencing Facility (2007)

HONORS/AWARDS:

- Member. Special Emphasis Panel (RO3 grants), NIDCD, NIH (1996-97).
- AHA Established Investigator Grantee (1/1997-12/2000), entitled "AHA-Genetech Special Awardee in Thrombosis".
- Senior Advisor in genomics and proteomics, Industrial and Technology Research Institute (ITRI) USA (2001-05).
- NIH Cash Award recipient, 2005.
- Member, study section of the National Research Program in Genomic Medicine, National Science Council, Taiwan, 2006.
- Consultant, Biomedical Engineering Center, ITRI, Taiwan (01/07-02/08).
- CBER/FDA Group Award (2015)

PROFESSIONAL MEMBERSHIP: American Society for Mass Spectrometry (ASMS); ASBMB

TEACHING EXPERIENCE (University of Maryland School OF Medicine, Baltimore, MD):

1990-2000 HGEN 601 and 602, "Introduction to Human Genetics", lectured on "Genome Complexity and Eukaryotic Gene Expression and Regulation" (Course Master 1994-1996, co-course master 1999).

1992-1996 HGEN 740 "Molecular Aspects of Human Disease", an advanced course for graduate students in Human Genetics Graduate Program (co-course master 1992, course master 1994, 1996).

1997-1998 Member, the faculty of "Cell & Molecular Biology" conferences on "α1-antitrypsin

deficiency" and "fatty acid oxidation" for medical students.

SUPERVISORY EXPERIENCES:

At CBER, FDA (2011-present)

Supervisor for:

Wells Wu, Ph.D., Research Chemist (2011-)
 Chun-Ting Lee, Ph.D., Staff Fellow (2016-)
 Galina Abduolaeva, Ph.D., Research Chemist (2011-)
 Joey Lin, Ph.D. ORISE Research Fellow (2016-)
 Je Nie Phue, Ph. D., Staff Fellow (2012-)
 Irina Zhul, MS, Chemist (2011-)
 Sang Eun Lee, BS, Chemist (2011-)
 Rong Wang, Ph.D., Visiting Associate (2012-2015)
 Tung-Chin Chiang, Ph.D., ORISE Research Fellow (2013-2016)
 Danielle Goecke, ORISE post-bac trainee (2015-2016)
 Hailey Dahae Bae, ORISE post-bac trainee (2015-2016)
 Cheryl Hart, Administrative Assistant (2011-2015)

At NIH (2003-2011)

Supervisor for:

Charlie Hsiao, M.S. (Special Volunteer, 3/09-10/2010)
 Wells W. Wu, Ph.D., Research Chemist (11/2003-3/2011)
 Sajni Patel, M.S., Res. Associate (12/07-10/2010)
 Hem Shukla, Ph.D., Research Scientist (9/08-9/09)
 Guanghui Wang, Ph.D., Research Fellow (2003-2008)
 Angel Aponte, Biologist (2003- 2008)
 Panthip Rattanasinganchan, Ph.D. (4/07-10//07), Mahidol Univ., Bangkok, Thailand)
 Meghan Morgan, M.S., Res Associate (2005-2007)

At University of Maryland School of Medicine, Baltimore, MD (1989-2000):

Mentor/Dissertation Advisor for:

Yoshiyasu Ogata, M.D./Ph.D., postdoc (4/99-3/01)
 Shigeyasu Inada, M.D./Ph.D., postdoc (5/97-4/99)
 Seung Joon Baek, Ph.D. (1998); Liqun Zhang, Ph.D. (1997)
 Kuan-Der Lee, M.D./Ph.D.(1996); Dionyssia Avrith, MS (2001)

Thesis Committee Member for:

Peter Kuehl, MD./PhD. 2000; Susan Janicki, Ph.D., 1999;
 Kara Smolinsky, MD/PhD, 1999; Erin Thompson, Ph.D., 1999;
 Robyn Starr, Ph.D., 1995; Jinsong Xia, Ph.D., 1995;
 Hao Jiang, Ph.D., 1994; Jackie Andrews, M.S., 1994

RESEARCH AND OPERATION SUPPORTS AT FEDERAL INSTITUTES (2003-Present):

At FDA, Office of the CBER Center Director (2011-Present)

At NIA, Intramural Support from the Research Resources Branch (2008-2011)

At NHLBI, Intramural Support from Office of the Scientific Director (2003-2008)

PAST GRANT SUPPORT (1989-2000 at Univ. of Maryland School of Medicine):

NIH: 9/01/97-6/30/00 "Collaborative study on the genetics of asthma" (Co-PI);

American Heart Association, National Center and Maryland Affiliate:

01/01/97-12/31/00 Established Investigator Grant
"Molecular Genetics of thromboxane synthase" (PI)
07/01/96-06/30/99 "Transcriptional control of thromboxane synthase gene expression" (PI)
07/01/93-06/30/96 "Structure/function relationship and gene organization of thromboxane synthase" (PI)
07/01/91-06/30/93 "Molecular cloning and regulation of the thromboxane synthase gene". (PI)

University of Maryland School of Medicine:

09/01/90-08/31/92 Frank C. Bressler Research Fund
"Cloning and expression of the thromboxane synthase cDNA" (PI)
07/01/92-06/30/93 UMAB Graduate School
"Activation of gene expression in differentiating HL-60 Cells" (PI)
07/01/93-06/30/94 Special Research Initiative Support, UMB
"Prostacyclin synthase: cDNA cloning using sequence information of conserved functional domains" (PI)
07/01/94-06/30/95 UMB Graduate School
"Up-regulation of thromboxane synthase gene expression" (PI)
07/01/96-06/30/97 Intramural grant, UMB School of Medicine
"Identification of a trans-acting factor modulating the activity of human thromboxane synthase gene promoter" (PI)

Ad Hoc REVIEW FOR SCIENTIFIC JOURNALS:

Journal of Proteome Research;	Proteomics
Journal of Biological Chemistry;	Molecular and Cell Biology;
Biochemistry;	Kidney International
J Chromatography B;	American Journal of Physiology
Analytical Chemistry;	J Protein Science

PEER-REVIEWED PUBLICATIONS:

1. Liu WH, Shen R-F, Lee FF, and Su YC: Enzymatic oxidation of glucose via crab chitin-immobilized glucose oxidase and catalase. Proc Natl Sci Council (ROC) 4:338-344 (1980).
2. Liu Y, Yoden K, Shen R-F, and Tai HH: 12-L-Hydroxy-5,8,10-heptadecatrienoic acid (HHT) is an excellent substrate for NAD⁺-dependent 15-hydroxy-prostaglandin dehydrogenase.

- Biochem Biophys Res Commun 129:268-274 (1985).
3. Shen R-F, and Tai HH: Monoclonal antibodies to thromboxane synthase: production and application to development of a tandem immunoradiometric assay. *J Biol Chem* 261:11585-11591 (1986).
 4. Shen R-F, and Tai HH: Immunoaffinity purification and characterization of thromboxane synthase from porcine lung. *J Biol Chem* 261:11592-11599 (1986).
 5. Shen R-F, Li Y, Sifers RN, Wang H, Hardick C, Tsai SY, and Woo SLC: Tissue-specific expression of the human alpha-1-antitrypsin gene is controlled by multiple cis-regulatory elements. *Nucleic Acid Res* 15:8399-8415 (1987).
 6. Li Y, Shen R-F, Tsai SY, and Woo SLC: Multiple hepatic trans-acting factors are required for *in vitro* transcription of the human α_1 -antitrypsin gene. *Mol Cell Biol* 8:4362-4369 (1988).
 7. Peng H, Armentano D, MacKenzie-Graham L, Shen R-F, Darlington G, Ledley F, Woo SLC: Retroviral-mediated gene transfer and expression of human phenylalanine hydroxylase in primary mouse hepatocytes. *Proc Natl Acad Sci (USA)* 85:8146-8150 (1988).
 8. Shen R-F, Clift SM, DeMayo JL, Sifers RN, Finegold MJ, and Woo SLC: Tissue-specific regulation of human α_1 -antitrypsin gene expression in transgenic mice. *DNA* 8:111-118 (1989).
 9. Sepulveda AR, Finegold MJ, Smith B, Slagle BL, DeMayo JL, Shen R-F, Woo SLC, and Butel JS: SV40 Large T-antigen expression controlled by regulatory elements of the human α_1 -antitrypsin gene: A transgenic mouse system for the analysis of stages in liver carcinogenesis. *Cancer Res* 49:6108-6117 (1989).
 10. Sifers RN, Shen R-F, and Woo SLC: Genetic control of the human α_1 -antitrypsin. *Mol Biol and Med.* 6:127-135 (1989) (invited review).
 11. Lee T-H, Finegold MJ, Shen R-F, DeMayo JL, Woo SLC, and Butel JS: Hepatitis B virus transactivator X protein is not tumorigenic in transgenic mouse. *J Virol* 64:5939-5947 (1990).
 12. Chase MB, Baek, SJ, Purtell D, Schwartz S, and Shen R-F: Mapping of the human thromboxane synthase (TXBAS1) gene to chromosome 7q34-35 by two color fluorescence *in situ* hybridization. *Genomics* 16: 771-773 (1993).
 13. Zhang L, Chase MB, and Shen R-F: Molecular cloning and expression of murine thromboxane synthase. *Biochem Biophys Res Commun* 194: 741-748 (1993).
 14. Xia, Z, Shen R-F, Baek SJ, and Tai H-H: Expression of two different forms of cDNA for thromboxane synthase in insect cells and site-directed mutagenesis of a critical cysteine residue. *Biochem J* 295: 457-461 (1993).
 15. Lee KD, Baek S-J, and Shen R-F: Cloning and characterization of human thromboxane synthase gene promoter. *Biochem Biophys Res Comm* 201:379-387 (1994).
 16. Shen R-F, Zhang L, Baek SJ, Tai H-H, and Lee K-D: The porcine thromboxane synthase-encoding cDNA: sequence, mRNA expression, and enzyme production in Sf9 insect cells. *Gene* 140:261-265 (1994).
 17. Baek SJ, Lee K-D, and Shen R-F: Genomic structure and polymorphism of the human thromboxane synthase gene. *Gene*, 173:251-256 (1996).
 18. Lee K-D, Baek SJ, and Shen R-F: Multiple factors regulating the expression of human thromboxane synthase gene. *Biochemical J* 319:783-791 (1996).
 19. Zhang L, H Xiao, RA Schultz, and Shen R-F: Genomic organization, chromosomal localization and expression of the murine thromboxane synthase gene (*Tbxas1*). *Genomics* 45:519-528 (1997).
 20. Shen R-F and Tai H-H: Thromboxanes: Synthase and Receptors, *J Biomed. Sci.* 5:153-172 (1998) (invited review).
 21. Chelius D, Zhang T, Wang G, and Shen R-F: Global protein identification and quantitation technology using two-dimensional liquid chromatography nanospray mass spectrometry. *Anal Chem* 75: 6658-65 (2003).

22. Carlson KA, Ciborowski P, Schellpeper CN, Biskup TM, Shen R-F, Luo X, Destache CJ, Gendelman HE: Proteomic fingerprinting of HIV-1-infected human monocyte-derived macrophages: a preliminary report. *J Neuroimmunol* 147:35-42 (2004).
23. Li T, Edokimov E, Shen R-F, Chao C-C, Tekle E, Statman ER, Wang T, Young D, and Chock PB: Sumoylation of heterogeneous nuclear ribonucleoproteins, zinc finger proteins, and nuclear pore complex proteins: A proteomic analysis. *Proc Natl Acad Sci (USA)* 101:8551-8556 (2004).
24. Pisitkun T, Shen R-F, and Knepper MA: Identification and proteomic profiling of exosomes in human urine. *Proc Natl Acad Sci (USA)*, 101:13368-13373 (2004).
25. Ryu OH, Choi SJ, Erhan F, Choi SW, Hart P, Shen R-F, Wang G, Wu WW and Hart TC: Proteolysis of LD78 β or LD78 α by neutrophil granule serine proteinases. *J Biol Chem* 280:17415-21 (2005).
26. Barile M, Pisitkun T, Chou C-L, Verbalis MJ, Shen R-F, and Knepper MA: Large-scale protein identification in intracellular aquaporin-2 vesicles immunisolated from renal inner medullary collecting duct. *Mol. Cell. Proteomics*, 4(8):1095-106 (2005).
27. Zhou XW, Kafsack BF, Cole RN, Beckett P, Shen R-F, and Carruthers VB: The opportunistic pathogen *Toxoplasma gondii* deploys a diverse legion of invasion and survival proteins. *J Biol Chem*, 280(40):34233-34244 (2005).
28. Hortin GL, Shen R-F, Martin B, Thomas F, and Remaley A: Diverse range of small peptides associated with high-density lipoprotein. *Biochem Biophys Res Commun*, 340:909-915 (2006).
29. Hopper RK, Carroll S, Aponte AM, Johnson DT, French S, Shen R-F, Witzmann FA, Harris RA, and Balaban RS: Mitochondria matrix phosphoproteome: Effect of extra mitochondrial calcium. *Biochemistry* 45(8):2524-2536 (2006).
30. Wu WW, Wang G, Baek SJ, and Shen R-F: A comparative study of three quantitative methods, DIGE, cICAT, and iTRAQ, using 2D gel- or LC-MALDI TOF/TOF. *J Proteome Res* 5:651- 658 (2006). (Most cited and accessed article of *J Proteome Res* in 2006).
31. Pisitkun T, Bieniek J, Tchapyjnikow D, Wang G, Wu W, Shen R-F, and Knepper MA: High-Throughput Identification of IMCD Proteins Using LC-MS/MS. *Physiol Genomics*, 25(2): 263-76 (2006).
32. Wang G, Wu WW, Zheng W, Chou CL, and Shen R-F: Label-free protein quantification using LC-coupled ion trap or FT mass spectrometry. *J Proteome Res*, 5(5):1214-23 (2006).
33. Hoffert, JD, Pisitkun T, Wang G, Shen R-F, and Knepper MA: Phosphoproteomic analysis of rat inner medullary collecting duct during short-term vasopressin treatment: Identification of novel aquaporin-2 phosphorylation sites. *Proc Natl Acad Sci*, 103:7159-7164 (2006).
34. Simons BL, Wang G, Shen R-F, and Knepper MA: *In vacuo* isotope coded alkylation technique (IVICAT); a selective N-terminal stable isotopic label for quantitative LC-MS proteomics. *Rapid Commun Mass Spectrom* 20:2463-2477 (2006).
35. Li T, Santockyte R, Shen R-F, Tekle E, Wang G, Yang DCH, and Chock PB: A general approach to identify enzymatic pathways and substrates for ubiquitin-like modifiers. *Arch Biochem. Biophys*, 453:68-72 (2006).
36. Wang G, Wu WW, Pisitkun T, Hoffert JD, Knepper MA, and Shen R-F: An automated quantification tool for high-throughput proteomics using stable isotope labeling and LC-MSⁿ. *Anal Chem*, 78:5752-61 (2006).
37. Schieke SM, Phillips D, McCoy JP, Jr. Aponte AM, Shen R-F, Malide D, Combs CA, Balaban RS, and Finkel T: The mTOR pathway regulates mitochondrial oxygen consumption and oxidative capacity. *J Biol Chem*, 281:27643-52 (2006).
38. Yu MJ, Pisitkun T, Wang G, Shen R-F, and Knepper MA: LC/MS analysis of apical and basolateral membranes of rat renal collecting duct cells. *Mol. Cell. Proteomics*, 5(11):2131-2145 (2006).
39. Zhou H, Pisitkun T, Aponte A, Yuen P, Yasuda H, Hu X, Chawla L, Shen R-F, Knepper MA,

- and Star R: Exosomal Fetuin-A identified by proteomics: a novel urinary biomarker for detecting acute kidney injury. *Kidney Intl.*, 70(10):1847-57 (2006).
40. Li T, Santockyte R, Shen R-F, Tekle E, Wang G, Yang D, and Chock PB: Expression of SUMO-2/3 induced senescence through p53- and pRB-mediated pathway. *J Biol Chem*, 281(47):36221-7 (2006).
 41. Chen Y, Schenetz M, Irarrazabal C, Shen R-F, Williams CK, Burg MB, and Ferraris JD: Proteomic identification of proteins associated with the osmoregulatory transcription factor TonEBP/OREBP. Functional effects of Hsp90 and PARP-1. *Amer. J Physiol-Renal physiol*, 292:F981-992 (2007).
 42. Ngo T, Peng T, Liang XJ, Akeju O, Pastorino S, Zhang W, Fine HA, Maric D, Wen PY, Girolami UD, Black PM, Wu WW, Shen R-F, Kang D-W, and Park JK. The 1p encoded protein stathmin modulates the response of malignant gliomas to nitrosourea. *J. Natl Cancer Inst.* 99(8):639-52 (2007).
 43. Wu WW, Wang G, and Shen R-F: Identification and quantification of basic and acidic proteins using solution-based 2D protein fractionation and label-free and ¹⁸O-label mass spectrometry. *J Proteome Res*, 6:2447-2459 (2007).
 44. Zhou XW, Mudannayake M, Green M, Gigena MS, Wang G, Shen R-F, and Rogers TB: Proteomic studies of PP2A-B56 γ 1 phosphatase complexes reveal phosphorylation-regulated partners in cardiac local signaling. *J Proteome Res*, 6:3433-3442 (2007).
 45. Hoffert J, Wang G, Pisitkun T, Shen R-F, and Knepper: An automated platform for analysis of phosphoproteomic datasets: application to kidney collecting duct phosphoproteins, *J Proteome Res*, 6:3501-3508 (2007).
 46. Sun J, Morgan M, Shen R-F, Steenbergen C, and Murphy E: Preconditioning results in S-nitrosylation involved in regulation of mitochondrial energetics and calcium transport. *Circulation Res*, 101:1155-1163 (2007).
 47. Noda Y, Berlett B, Stadtman ER, Aponte A, Morgan M, and Shen R-F: Identification of enzymes and regulatory proteins in *E. coli* that are preferentially oxidized under nitrogen, carbon or phosphate starvation. *Proc. Natl. Acad. Sci.*, 104(27):18456-60 (2007).
 48. Alves G, Ogurtsov A, Wu WW, Wang G, Shen R-F, and Yu YK: Calibrating E-values for MS² library search methods. *Biology Direct*, 2:26 (2007).
 49. Choi S, Song I, Ryu O, Choi S, Hart P, Wu WW, Shen R-F, and Hart T: A 4 bp deletion mutation in DLX3 enhances osteoblastic differentiation and bone formation in vitro. *Bone*, 42(1):162-171 (2008).
 50. Wu WW, Wang G, Liang X-J, Park J, and Shen R-F: Covalent modification of stathmin by CCNU determined by FTMS analysis of modified proteins and tryptic peptides. *Biochem Biophys Res Commun*, 367: 7–13 (2008).
 51. Hao JJ, Wang G, Pisitkun T, Patino-Lopez G, Knepper MA, Shen R-F, Shaw S: Enrichment of distinct microfilament-associated and GTP-binding-proteins in membrane/microvilli fractions from lymphoid cells. *J Proteome Res*, 7:2911-2927 (2008).
 52. Alves G, Wu WW, Wang G, Shen R-F, and Yu YK: Enhancing Peptide Identification Confidence by Combining Search Methods. *J Proteome Res*, 7:3102-2113 (2008).
 53. Yu MJ, Pisitkun T, Wang G, Aranda JF, Gonzales PA, Tchapyjnikov D, Shen R-F, Alonso MA, and Knepper MA: Large-scale quantitative LC-MS/MS analysis of detergent-resistant membrane proteins from rat renal collecting duct. *Amer J Physiol-Cell Physiol*, 5(3):C661-78 (2008).
 54. Alves G, Ogurtsov AY, Kowk S, Wu WW, Wang G, Shen R-F, and Yu YK: Detection of co-eluted peptides using database search methods. *Biology Direct*, 3(1):27 (2008).
 55. Wang G, Wu WW, Zhang Z, Masilamani S, and Shen R-F: Decoy methods for assessing false positives and false discovery rates in shotgun proteomics. *Anal Chem*, 81(1):146-59 (2009).
 56. Looze C, Yui D, Leung L, Ingham M, Kaler M, Yao X, Wu WW, Shen R-F, Daniels MP,

- Levine SJ: Proteomic Profiling of Human Plasma Exosomes Identifies PPAR γ as an Exosome-associated Protein, *Biochem Biophys Res Commun*, 378(3):433-8 (2009).
57. Yuditskaya S, Tumblin A, Hoehn GT, Wang G, Drake S, Xu X, Ying S, Chi A, Remaley AT, Shen R-F, Munson PJ, Suffredini AF, and Kato GJ: Proteomics identification of dysregulated apolipoprotein expression in pulmonary hypertension and vasculopathy of sickle cell disease. *Blood*, 113(5):1122-8 (2009).
 58. Eyster CA, Hgginson J, Huebner R, Porat-Shlioni N, Weigert R, Wu WW, Shen R-F, and Donaldson, JG: Discovery of new cargo proteins that enter cells through clathrin-independent endocytosis, *Traffic*, 10:590-599 (2009).
 59. Tsai S-Y, Hayashi T, Harvey B, Wang Y, Wu WW, Shen R-F, Zhang Y, Becker K, Hoffer B, and Su T-P: Sigma-1 receptors regulate hippocampal dendritic spine formation via a free radical-sensitive mechanism involving Rac1•GTP pathway. *Proc Natl Acad Sci*, 106:22468-73 (2009).
 60. Kunin M, Dmitrieva NI, Gallazzini M, Shen R-F, Wang G, Burg MB, and Ferraris JD: Mediator of DNA Damage Checkpoint 1 (MDC1) Contributes to High NaCl-Induced Activation of the Osmoprotective Transcription Factor TonEBP/OREBP. *PLoS ONE*, 5(8): e12108 (2010).
 61. Giannone R, McDonald H, Hurst G, Shen R-F, Wang Y, and Liu Y: "The protein network surrounding the human telomere repeat binding factors TRF1, TRF2, and POT1". *PLoS ONE*, 5(8): e12407 (2010).
 62. Vangala K, Yanney M, Hsiao CT, Wu WW, Shen R-F, Zou S, Sygula A, and Zhang D: Sensitive carbohydrate detection using surface enhanced Raman tagging. *Anal Chem*, 82:10164-71 (2010).
 63. Zhou Y, Yi T, Park SS, Chadwick W, Shen R-F, Wu WW, Martin B, and Maudsley S: Rapid and enhanced proteolytic digestion using electric field-oriented enzyme reactor. *J Proteomics*, 74:1030-35 (2011).
 64. Li T, Santockyte R, Yu S, Shen R-F, Tekle E, Lee CG, Yang DC, and Chock PB: FAT10 modifies 53 and upregulates its transcriptional activity. *Arch Biochem Biophys*, 509:164-9 (2011).
 65. Wu WW, Wang G, Insel PA, Hsiao CT, Zou S, Maudsley S, Martin B, and Shen R-F: Identification of proteins and phosphoproteins using pulsed Q collision induced dissociation (PQD). *JASMS*, 22:1753-62 (2011).
 66. Obolensky OI, Wu WW, Shen R-F, Yu YK: Using dissociation energies to predict observability of b- and y-peaks in mass spectra of short peptides. *Rapid Commun Mass Spectrom*, 26:915-20 (2012).
 67. Wu WW, Wang G, Insel PA, Hsiao CT, Zou S, Martin B, Maudsley S, Shen R-F: Discovery- and target-based protein quantification using iTRAQ and pulsed Q collision induced dissociation (PQD). *J Proteomics*, 75:2480-7 (2012).
 68. Park SS, Wu WW, Zhou Y, Shen R-F, Martin B, Maudsley S: Effective correction of experimental errors in quantitative proteomics using stable isotope labeling by amino acids in cell culture (SILAC). *J Proteomics*, 75:3720-32 (2012).
 69. Wu WW, Shen R-F, Park SS, Martin B, Maudsley S: Precursor ion exclusion for enhanced identification of plasma biomarkers. *Proteomics Clin Appl*, 6:304-8 (2012).
 70. Shen X, Li CC, Aponte AM, Shen R-F, Billings EM, Moss J, Vaughan M: Brefeldin A-inhibited ADP-ribosylation factor activator BIG2 regulates cell migration via integrin β 1 cycling and actin remodeling. *Proc Natl Acad Sci*, 109:14464-9 (2012).
 71. Obolensky OI, Wu WW, Shen R-F, Yu YK: Using dissociation energies to predict observability of b- and y-peaks in mass spectra of short peptides. II. Results for hexapeptides with non-polar side chains. *Rapid Comm Mass Spectrom*, 27:152-6 (2013).
 72. Laslo M, Sun X, Hsiao CT, Wu WW, Shen R-F, Zou S: A botanical containing freeze dried açai pulp promotes healthy aging and reduces oxidative damage in sod1

- knockdown flies. *Age (Dordor)*, 35(4):1117-32 (2013).
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