BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Rong Zeng	Professor
CURRENT AFFILIATION Shanghai Institutes for Biological Sciences	

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
Shanghai Institute of Biochemistry	Ph. D	1995-2000	Biochemistry
Hunan Normal University	Bachelor	1991-1995	Biology

List of five recent publications by the candidate:

1. Tang LY, Deng N, Wang LS, Dai J, Wang ZL, Jiang XS, Li SJ, Li L, Sheng QH, Wu DQ, Li L, **Zeng R***. Quantitative Phosphoproteome Profiling of Wnt3a-mediated Signaling Network: Indicating the Involvement of Ribonucleoside-diphosphate Reductase M2 Subunit Phosphorylation at Residue Serine 20 in Canonical Wnt Signal Transduction.Mol Cell Proteomics. 2007, 6:1952-67.

2. Dai J, Jin WH, Sheng QH, Shieh CH, Wu JR, **Zeng R***. Protein Phosphorylation and Expression Profiling by Yin-Yang Multidimensional Liquid Chromatography (Yin-yang MDLC) Mass Spectrometry. J Proteome Research. 2007, 6:250-62

3. Sheng QH, Wang LS, Dai J, Jiang XS, Li RX, Ma DJ, Li YX, **Zeng R***, Wu JR. Comparison of a proteomic approach with a microarray-based approach to detect exons in the mouse genome. Nat Genet. 2006, 38:1223-4.

4. Dai J, Shieh CH, Sheng QH, Zhou H, **Zeng R***. Proteomic analysis with integrated multiple dimensional liquid chromatography/mass spectrometry based on elution of ion exchange column using pH steps. Anal Chem. 2005, 77:5793-9.

5. Jiang XS, Dai J, Sheng QH, Zhang L, Xia QC, Wu JR, **Zeng R*.** A comparative proteomic strategy for subcellular proteome research: ICAT approach coupled with bioinformatics prediction to ascertain rat liver mitochondrial proteins and indication of mitochondrial localization for catalase. Mol Cell Proteomics. 2005, 4:12-34.

* Corresponding author

Please indicate in 200 words or less the reason(s) why you would be a suitable candidate for the HUPO Council elections.

Dr. Rong Zeng is one of the founders of Research Center for Proteome Analysis (RCPA) in Shanghai Institute of Biological Sciences，Chinese Academy of Sciences. The mission of the center is to develop methodologies to probe protein dynamic behaviors associated with cell signaling and human diseases. In the past five years, Dr. Zeng developed a pH-elution strategy in multiple-dimensional liquid chromatography mass spectrometry, which facilitated the high-coverage identification of protein expression and modification. In addition, Dr Zeng is trying to integrate proteomics with transcriptome, MiRNA, etc., aiming to elucidate protein behaviors at a

level of systems biology. Dr. Zeng also involved in HPPP and HLPP projects of HUPO.