Preface

This Special Topic: Mass Spectrometry Analysis, covers recent experimental results and advances in the analytical field of Mass Spectrometry (MS) for organic and metabolic molecules, and bio-molecules. Recently, the instrumentation of mass spectrometers has been improved greatly in terms of its sensitivity, resolution, accuracy and precision. For example, the high resolution for daily running-horse instruments can now reach to 20×10^3 – 40×10^3 for time-of-flight (TOF) based MSs, and 50×10^3 – 50×10^4 for Orbitrap based ones. The data acquisition rate also becomes faster and faster, so that the speed advantage promotes metabolome and proteome to be real omic tools now. The improvements of MS instruments have provided scientist more space to explore the exciting research areas including organic chemistry, environmental chemistry, and biochemistry and life science.

We are pleased to invite ten of Chinese and Over-sea-Chinese scientists specialized in these MS topics to contribute here their research articles including one in organic reaction monitoring, two in small molecule determination, six in protein/peptide analysis, and one in protein modification profiling. Pan YuanJiang's group reports the effect of cation size on McLafferty-type rearrangement of even-electron ions in MS. Guo YinLong's group describes a reliable screening of pesticide residues in maternal and umbilical cord sera by GC-MS. Li Liang's group investigates the effect of drinking Goji-tea on urine metabolome profiling by high performance isotope-labeling LC-MS. Yang Peng-Yuan's group depicts the response of peptide intensity to

concentration in ESI-MS. Qian XiaoHong's group covers an strategy of ultra-fast and highly efficient multiple proteases digestion using graphene-oxide-based immobilization. Zhang XiangMin's group reports an efficient separation and analysis of cysteine-containing peptides by combination of extraction tip and MALDI-TOF-MS. Zhang YangJun's group provides a novel method for relative quantification of N-terminal peptides using metal-element-chelated tags coupled with MS. Zhang YunKui's and Zhang LiHua's group characterize a label-free quantification of differentially expressed proteins in mouse liver cancer cells with high and low metastasis rates by a SWATH acquisition. Xie Peng's group describes a MRM-MS method for simultaneous quantitative analysis of five plasma apolipoproteins. And Zao YingMin's and Tan WeiJia's group innovate a comprehensive profiling of lysine acetylome in *Staphylococcus aureus*.

At this moment, we would like to express our sincere thanks to all authors for their incredible contributions to this special topic, and deliver our unfeigned appreciation to editors of the journal for their well-connected organization and enthusiasm to make this special topic possible.

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Dr. YANG PengYuan is a Fudan-honorship professor in the department of chemistry, Fudan University, graduated from the Inner-Mongolian University with a major in Chemistry (1975), and received M.S. degree from the University of Science and Technology of China (1981), Ph.D from the University of Massachusetts at Amherst (USA, 1987), both in Analytical Chemistry. He was Postdoc Fellow in Indiana University at Bloomington (USA) (1987–1989) and in Xiamen University (1989–1991). He currently is the Deputy Director of Institutes of BioMedical Sciences, Fudan University, Shanghai, China.

Dr. YANG is active in bio-mass spectrometry, micro-fluidics for protein analysis, proteomics and disease proteome areas. He is specialized in mass-spectrometry-based technology and methodology. He was the Principal Scientist for the project of “Proteomics for disease study” supported by the National Basic Research Program of China (2002–2006), and for “Micro-fluidics and its application in chemistry and bio-medicine” (2007–2011), and now is the Principal Scientist for the project of “Protein sequencing instruments and related reagents” supported by the National High Technology Research and Development Program of China.