

## **Proteomic analysis of endoplasmic reticulum in C57BL/6J mouse liver**

Yanping Song<sup>1</sup>, Ying Jiang<sup>1</sup>, Fuchu He<sup>1,2</sup>

1. Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, 33 Life Science Road, Beijing 102206, China.
2. Institutes of Biomedical Sciences, Fudan University, Shanghai 200032, China

Endoplasmic reticulum (ER) takes part in the protein synthesis, glycogenolysis and biosynthesis of lipid and cholesterol. It also has a close relationship with membrane-bound and secretory proteins. For liver tissue, ER plays a great role in the biotransformation of hydrophobic endogenous metabolites and xenobiotics. The disorder of ER function can cause cell dysfunction and diseases. To gain a better understanding of the critical role of ER function in liver, we present the ER proteome study on C57BL/6J mouse liver. In contrast to other proteome studies we focused on the multiple fractionation strategy to make full use of sample and to compare different subcellular fractions from single homogenate as well. The purity evaluation method was also applied to obtain highly purified organelle. Subsequently, ER proteins were separated by SDS-PAGE prior to nano-LC-ESI-MS/MS analysis with gas phase fractionation by mass range selection. 2018 and 1735 proteins were identified separately in rough and smooth endoplasmic (rER, sER), in which 1232 and 1177 proteins matched by over two peptides.