ZnO-Poly (methyl methacrylate) Nanobeads for Fast Enriching and Desalting Low Abundant Proteins Followed by Directly MALDI-TOF MS Analysis

Wenwen Shen,[1,2] Huanming Xiong,[1] Ye Xu,[3] Sanjun Cai,[3] Haojie Lu,[1,2] Pengyuan Yang [1,2]*

[1]Department of Chemistry, Fudan University, Shanghai 200433, China

[2]Institutes of Biomedical Sciences, [3]Affiliated Tumor Hospital, Fudan University, Shanghai 200032, China

* Corresponding author. Tel: 86-21-54237416. Fax: 86-21-54237416. Email: luhaojie@fudan.edu.cn

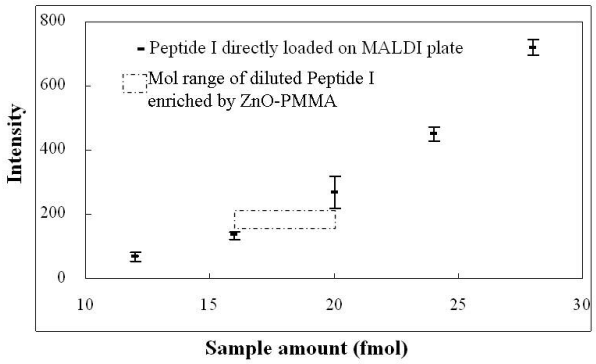

Figure S-1. MS intensity-concentration curve of Peptide I (digested from BSA) in the range of 12-28 fmol directly loaded on MALDI plate. From the curve, the mol range of the diluted Peptide I enriched by ZnO-PMMA can be calculated by average intensity (RSD%=15, n=6) obtained by MALDI-TOF MS. MALDI-TOF MS experiments were performed on a 4700 Proteomics Analyzer (Applied Biosystems, USA), with the Nd-YAG laser at 355 nm, a repetition rate of 200 Hz, and an acceleration voltage of 20 kV. Analysis of peptides was performed in the reflector TOF detection mode. All spectra were taken from a signal averaging of 2000 laser shots. Peptide I: amino acid sequence: HPEYAVSVLLR; m/z: 1283.4; PI: 6.75.

Figure S-2. 2-DE map of Human Colorectal Cancer. 200 μg proteins extracted from CRC were firstly separated by 18-cm nonlinear pH 3-10 IPG strips (GE Healthcare). After reduced and alkylated, the proteins were secondly separated by a 12% SDS-PAGE gel. After the electrophoresis separation, the gel was visualized by silver staining method. The stained gel was scanned using the ImageScanner and analyzed with ImageMaster 2D software (GE Healthcare). Arabic numerals make spots assigned to the newly reported proteins in CRC proteome research, also shown in Table 1.