Functional Nanoparticle-Based Proteomic Strategies for Rapid Characterization of Pathogenic Bacteria

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Supporting Information

Figure S1 presents the MS/MS spectrum by selecting the peak at m/z 1603, which is derived from *Shigella sonnei*. The inset displays the peptide sequence that was obtained by combing the MS/MS result with protein database searching. The searching result confirmed that the peak at m/z 1603 is derived from elongation factor Tu of *S. sonnei*. Fragment peaks ($S/N > 3$) resulting from precursor ions ($S/N > 3$) were submitted via Biotoools (v. 3.0) to MASCOT (www.matrixscience.com) using the following search parameters: the database searched was NCBI nr 20080616; taxonomy was limited to eubacteria; the enzyme was trypsin; MS and MS/MS tolerances were set at ± 0.5 and ± 0.8 Da, respectively; the number of missed cleavages was set to 1; the significance threshold was set at $p < 0.05$ because the score was over 50.

Figure S1. MS/MS spectrum of the ion at m/z 1603 and its corresponding peptide sequence obtained via protein database searching.