

Supporting information for:
Selective Enrichment and Sensitive Detection of Peptide and Protein Biomarkers in
Human Serum Using Polymeric Reverse Micelles and MALDI-MS

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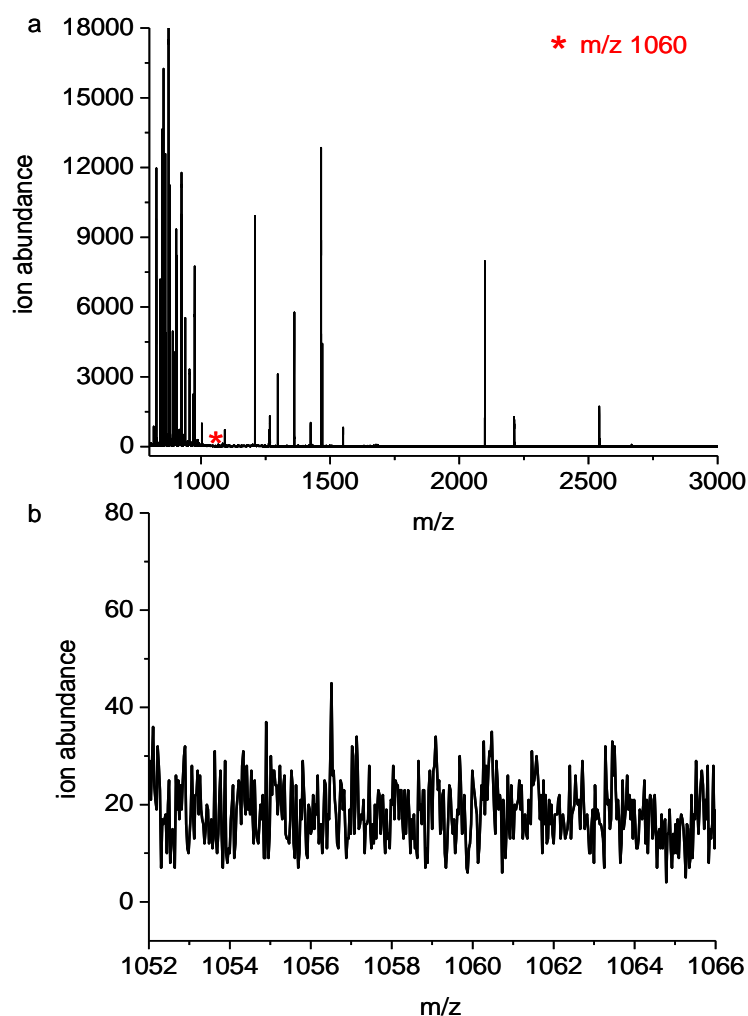


Figure S1. MALDI mass spectrum of a control experiment of human serum after HSA/IgG depletion extracted by the negatively charged polymers at pH 7.7 (a) an enlarge MALDI mass spectrum of figure S1a with m/z range of 1052-1066 (b).

Table S1. m/z ratio of all peptides that are observed in Figure 2a, 2d and Figure 3 within a mass range of 1000-3000 and S/N \geq 3.0. The m/z ratios in bold are found in more than one spectrum.

Figure 2a (organic phase with 5.0 x 10 ⁻¹⁰ M bradykinin extracted by negative polymer at pH 6.8)	Figure 2d (organic phase with 5.0 x 10 ⁻¹¹ M C4a extracted by negative polymer at pH 6.8)	Figure 3 (organic phase with 1.0 x 10 ⁻¹⁰ M ITIH ₄ extracted by positive polymer at pH 7.4)
1034.5, 1080.1, 1158.2, 1175.1, 1207.8, 1248.9 , 1289.1, 1335.5, 1465.9, 1604.9, 1647.9, 1719.0 , 2000.2 , 2099.2, 2338.7, 2495.0, 2752.9	1034.5, 1148.0, 1158.2, 1175.1, 1187.2, 1192.5, 1248.9 , 1271.6, 1289.1, 1335.5, 1465.9, 1574.6, 1647.9, 1719.0 , 2000.2 , 2099.2, 2338.7, 2495.0	1015.1, 1037.6, 1094.4, 1107.2, 1212.5, 1248.9 , 1425.5, 1668.5, 1719.0 , 1775.1, 1924.5, 2000.2 , 2104.1, 2358.6, 2432.5, 2613.7

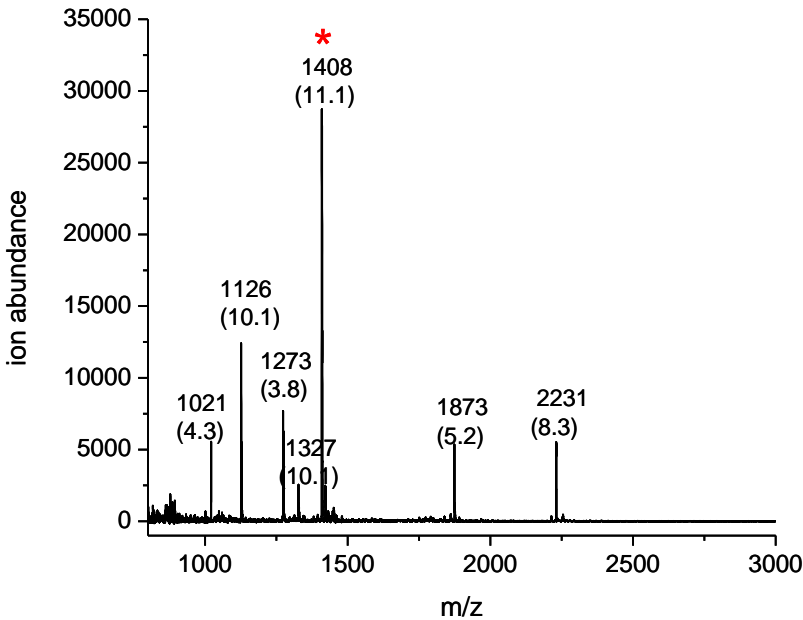


Figure S2. MALDI mass spectrum of peptide fragments of PSA digested by immobilized trypsin. The numbers above the peak indicate m/z and pI value of each PSA peptide fragment.