

Identification of *Pseudomonas aeruginosa* Using Functional Magnetic Nanoparticle-Based Affinity Capture Combined with MALDI MS Analysis

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Supporting Information

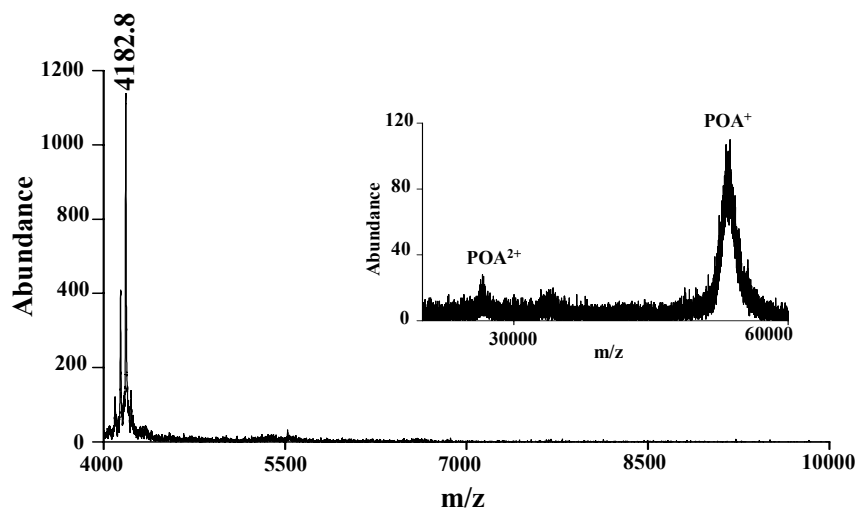


Figure S1. MALDI mass spectrum of the POA-Fe₃O₄@Al₂O₃. CHCA (25 mg/mL, 1 μ L) containing 1% TFA was used as the MALDI matrix. The peak at m/z 4182.8 dominates the mass spectrum. Presumably, it was derived from the acid-hydrolysis product of POA since the matrix contained 1% TFA. Additionally, the singly-charged (POA⁺) and doubly charged ions of POA (POA²⁺) at m/z ~53 kDa and ~26.5 kDa, respectively, appear in the mass spectrum indicated as inset.

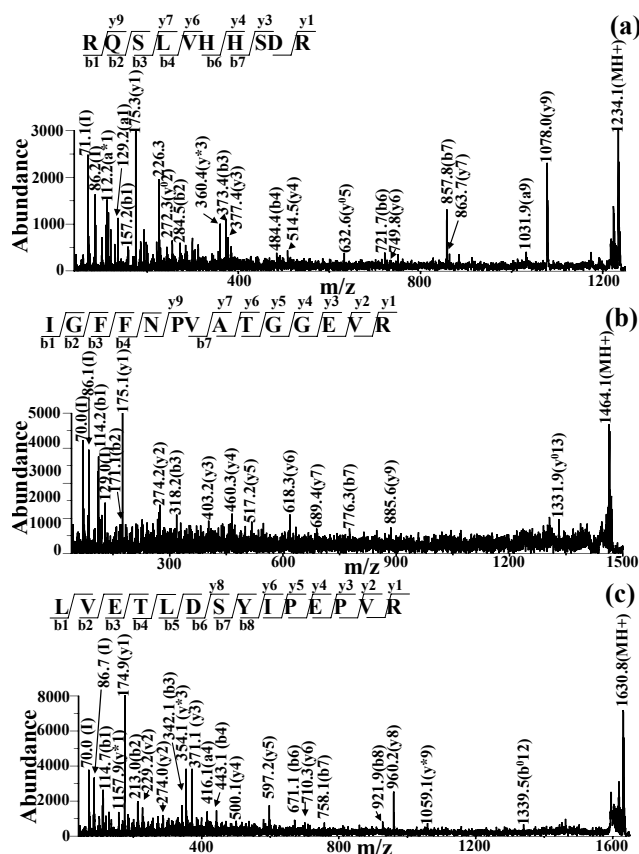


Figure S2. The tryptic digest of the bacteria targeted by the POA-Fe₃O₄@Al₂O₃ NPs from the same sample (1.5 mL) as that used to obtain Figure 8b. Gb3 (6 mg/mL, 10 μ L) was used to elute the bacteria from the NPs prior to tryptic digestion. Bacterial tryptic digestion was performed in the presence of the Fe₃O₄@Al₂O₃ NPs under microwave heating (power: 900 W) for 1 min. The peaks at *m/z* (a) 1234.1 (b) 1464.1 and (c) 1630.8 were selected as the precursor ions. CHCA (25 mg/mL, 1 μ L) containing 1% TFA was used as the MALDI matrix.

Table S1. Proteins Identified in panels a-c of Figure S2.

species	AC	protein	peptide sequence	MH _{obs} ⁺	size(a.a)	score
<i>P. aeruginosa</i>	gi 152989588	hypothetical protein	RQSLVHHSR	1234.2	263	56
	gi 152987689	hypothetical protein			116	
	gi 14195196	30S ribosomal protein S16	IGFFNPVATGGEVR	1464.1	83	90
	gi 15599461	Elongation factor Tu	LVETLDSYIPEPVR	1630.8	397	98

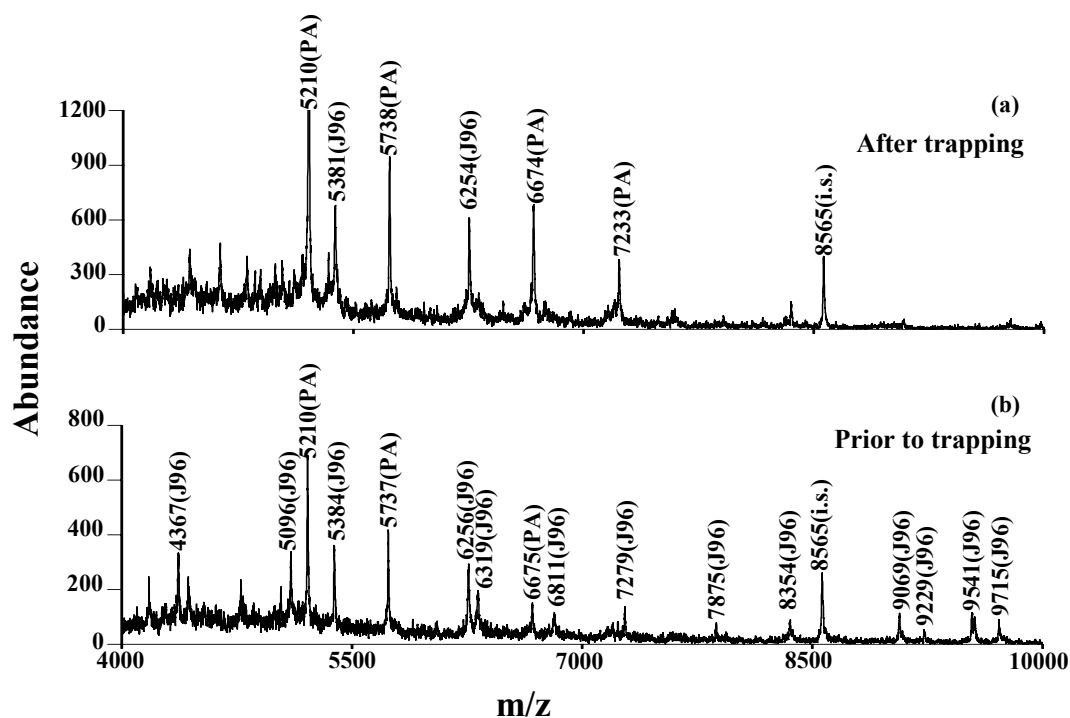


Figure S3. (a) MALDI mass spectrum obtained after using the POA-Fe₃O₄@Al₂O₃ NPs (40 µg) as affinity probes to selectively enrich target bacterial cells from a sample (0.8 mL) containing *E. coli* J96 (J96) (6.43×10^7 cells/mL) and *P. aeruginosa* (PA)(8.25×10^7 cells/mL). (b) MALDI mass spectrum of the same sample as used for obtaining Panel a prior to enrichment. CHCA (25 mg/mL, 1 µL) containing 1% TFA was used as the MALDI matrix.