Electronic Supplementary Information (ESI)

Table S1. Peptide mapping results of the tryptic digests of BSA and MYO obtained by using a core-changeable GO-based microchip bioreactor and in-solution digestion coupled with MALDI-TOF MS.

Digestion methods	Protein	Concentration (ng/μL)	Digestion time	Sequence coverage, (%)	Peptides matched	Amino acids identified
Microreactor	BSA	200	<10 s	49	33	296
Microreactor	BSA	20	<10 s	28	16	173
In-solution	BSA	200	12 h	38	18	236
Microreactor	MYO	200	<10 s	78	16	120
Microreactor	MYO	20	<10 s	64	12	99
In-solution	MYO	200	12 h	69	10	107

Fig. S1 Schematic showing the layer-by-layer self-assembly process of CTS and GO on a piece of glass fiber. (A) Dipping the glass fiber (a) in 10 mg/mL CTS aqueous solution containing 20 mg/mL acetic acid (b) for 5 min; (B) rinsing the modified fiber in doubly distilled water (c) for 30 s; (C) dipping the modified fiber in 2 mg/mL GO aqueous solution (d) for 5 min; (D) rinsing the modified fiber in (c) for 30 s; (E) immobilizing trypsin in the LBL-assembled coating on (a) by dipping the modified fiber in a 5 mg/mL trypsin in 50 mM Tris-HCl buffer (pH 8.0) containing 20 mM $CaCl_2$ (e) in a 4 °C refrigerator for 2 h.

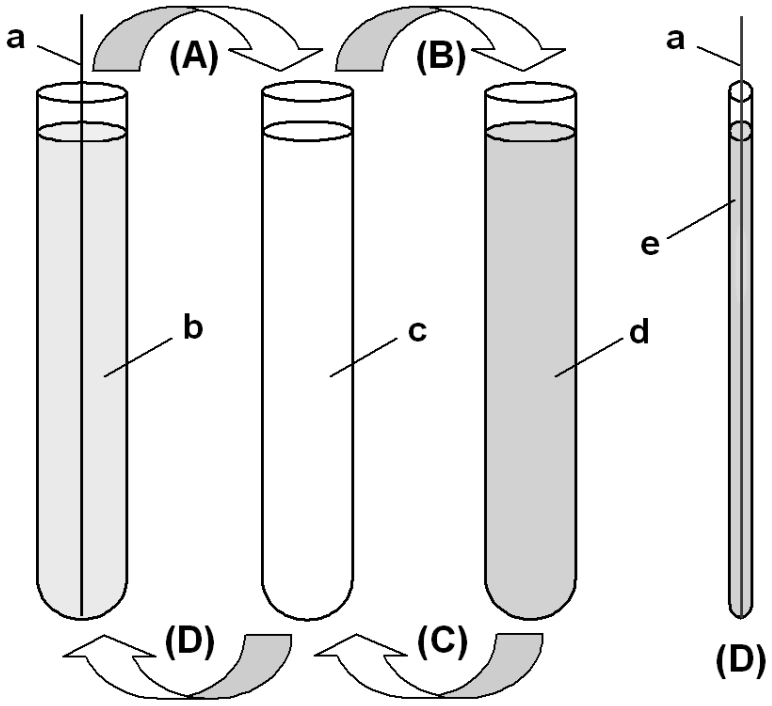

Fig. S2 SEM images of GO sheets. Conditions: accelerating voltage, 20 kV; magnification, ×5000.

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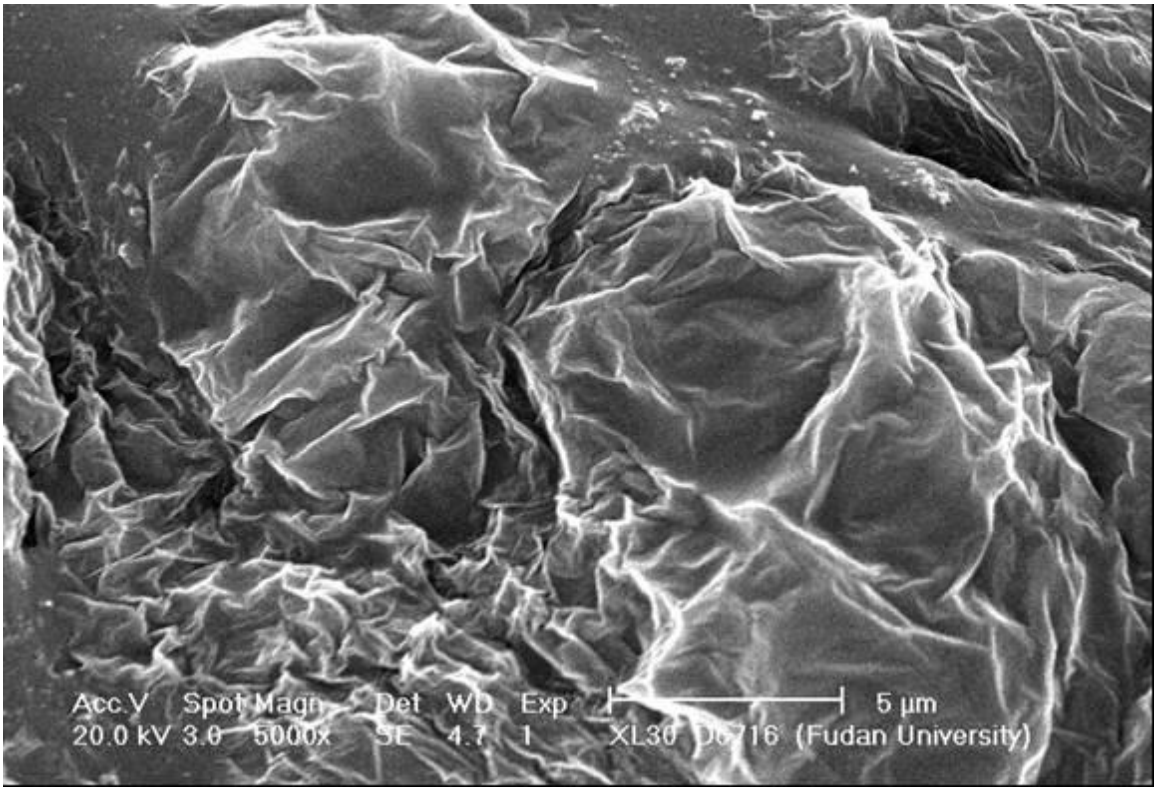

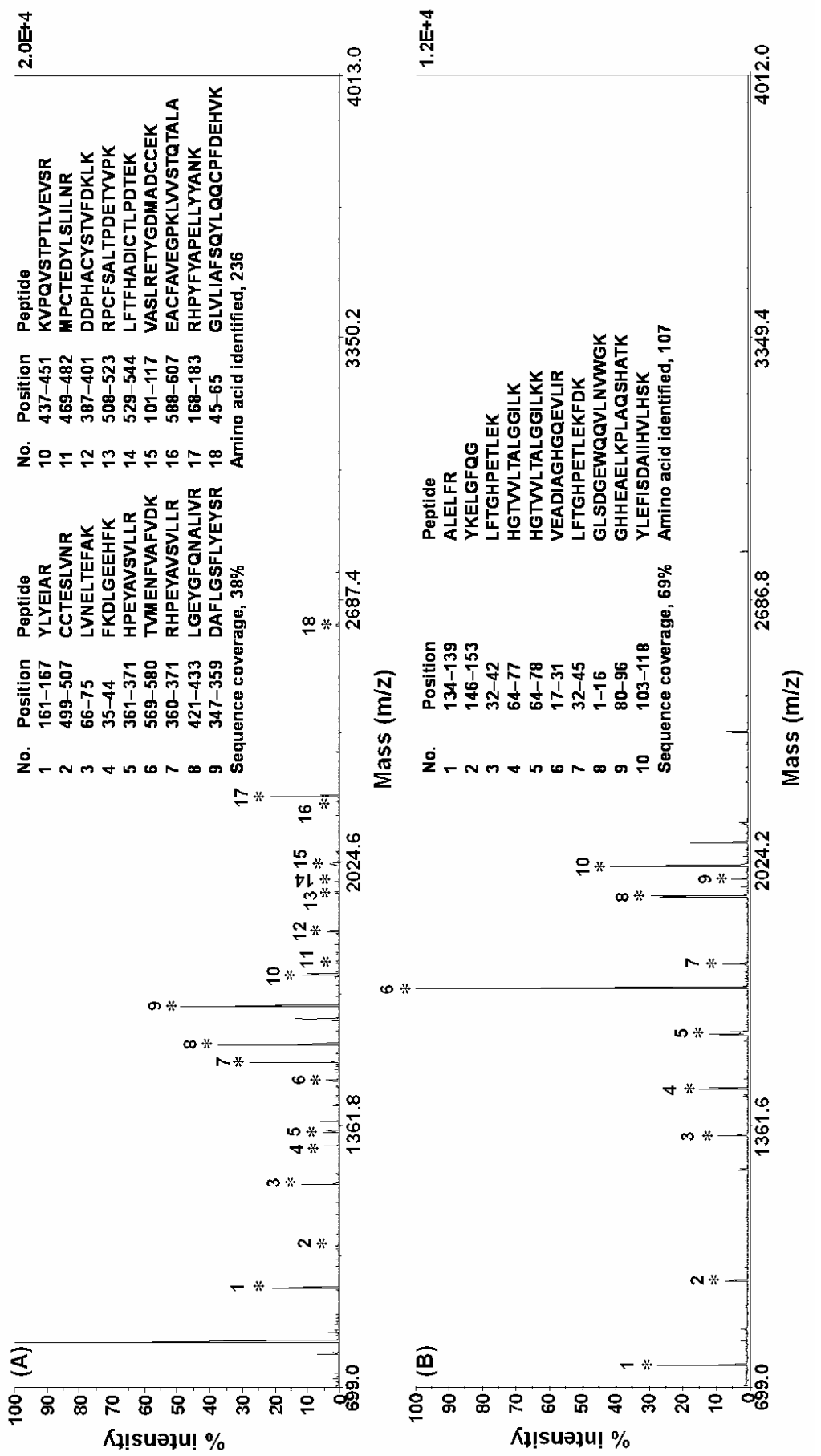

Fig. S3 MALDI TOF mass spectra of the digest of (A) BSA and (B) MYO (200 ng/μL) obtained by using conventional in-solution proteolysis in 10 mM NH_4HCO_3 buffer (pH 8.1). Digestion time, 12 h; trypsin/substrate ratio, 1:40; all matched peptides were marked with "*".

Fig. S4 MALDI-TOF mass spectra of the digests of (A) Cyt-*c* and (B) HEM obtained by using a core-changeable GO-based microchip bioreactor at a flow rate of 2.0 μL/min (digestion time, <10 s; all peptides matched were marked with "*"). The concentrations of proteins were 200 ng/μL in 10 mmol/L NH_4HCO_3 (pH 8.1).