Electronic Supplementary Material (ESI) for RSC Advances.

Electronic Supporting Information

Exposure to microwave irradiation at constant culture temperature slows the growth of *Escherichia coli* DE3 cells, leading to modified metabolic profiles

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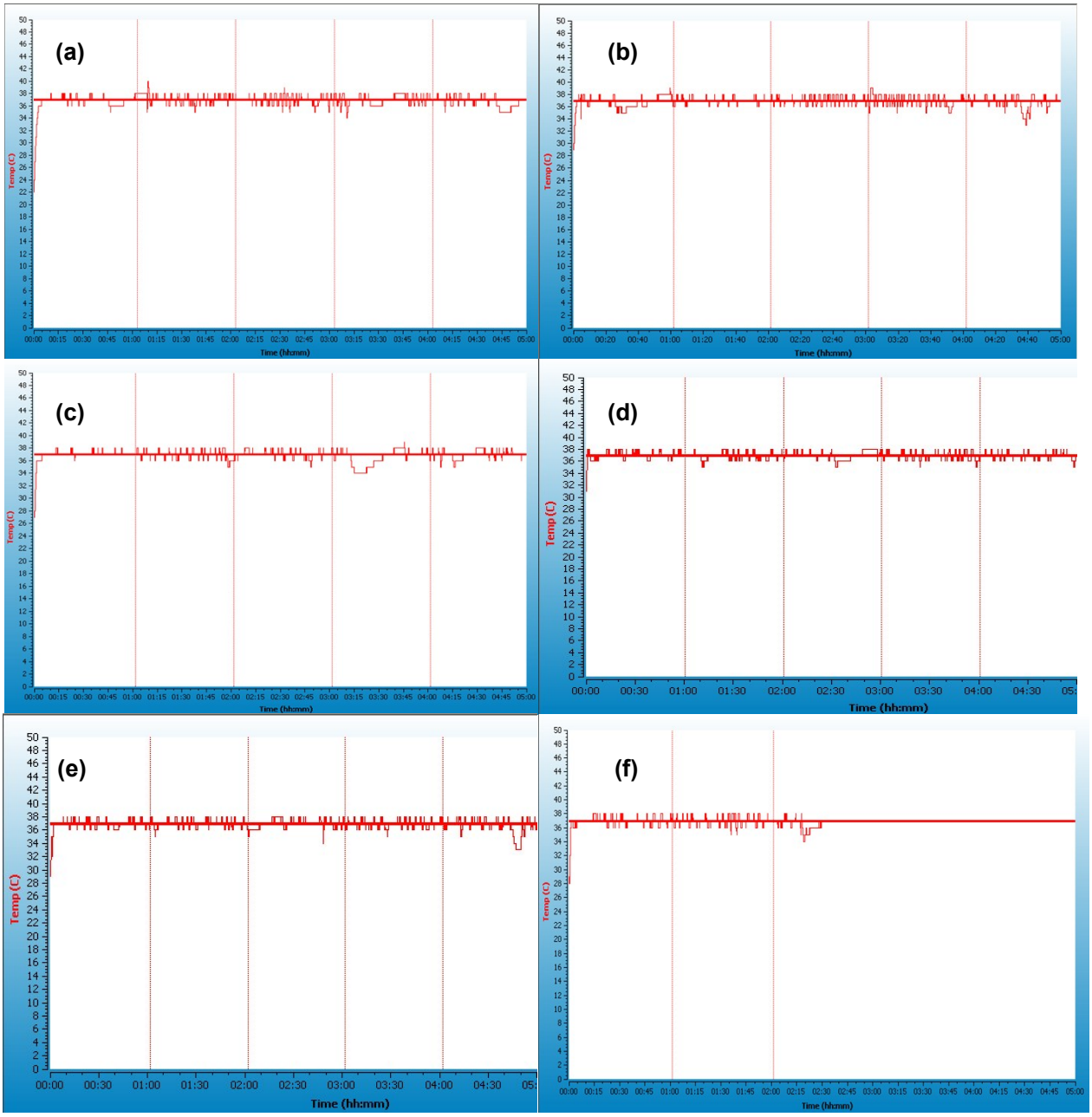


Figure S1. Temperature profiles of cultures throughout the growth period (total 27.5 hours). Note: as the Synergy software keeps track of temperature profiles on five-hour frames, multiple frames (a-f) were provided to cover the entire growth period.

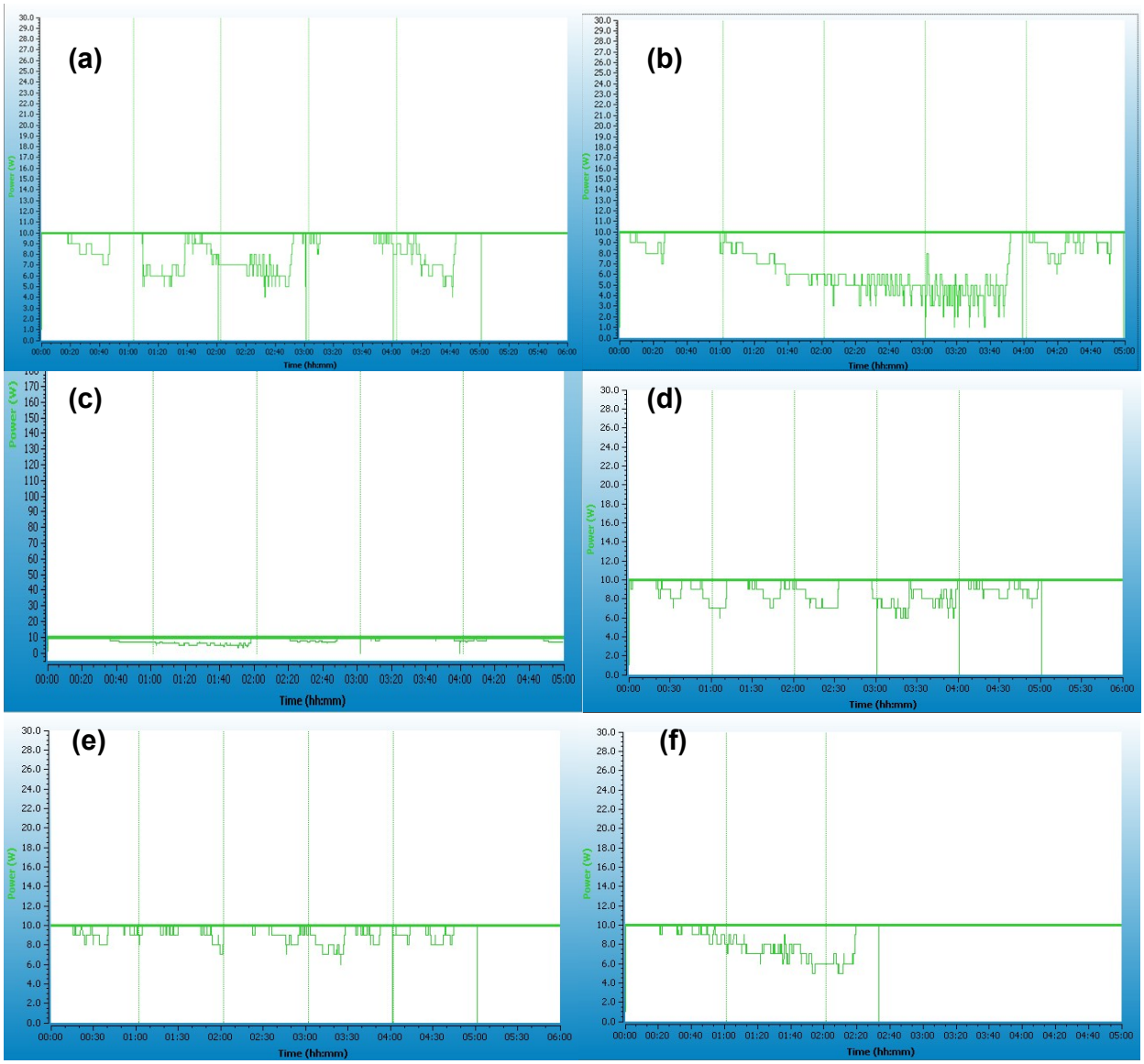


Figure S2. Profiles of microwave power output throughout the growth period (total 27.5 hours). Note: as the Synergy software only keeps track of power output profiles on five-hour frames, multiple frames (a-f) were provided to cover the entire growth period.

Table 1S. DO levels in LB media.

	DO concentration (mg/L) average of two replicate experiments	
	1 hour	2 hour
Control	7.19 (7.23/7.15)	6.98 (6.94/7.01)
Microwave exposed	6.50 (6.46/6.55)	6.40 (6.37/6.44)

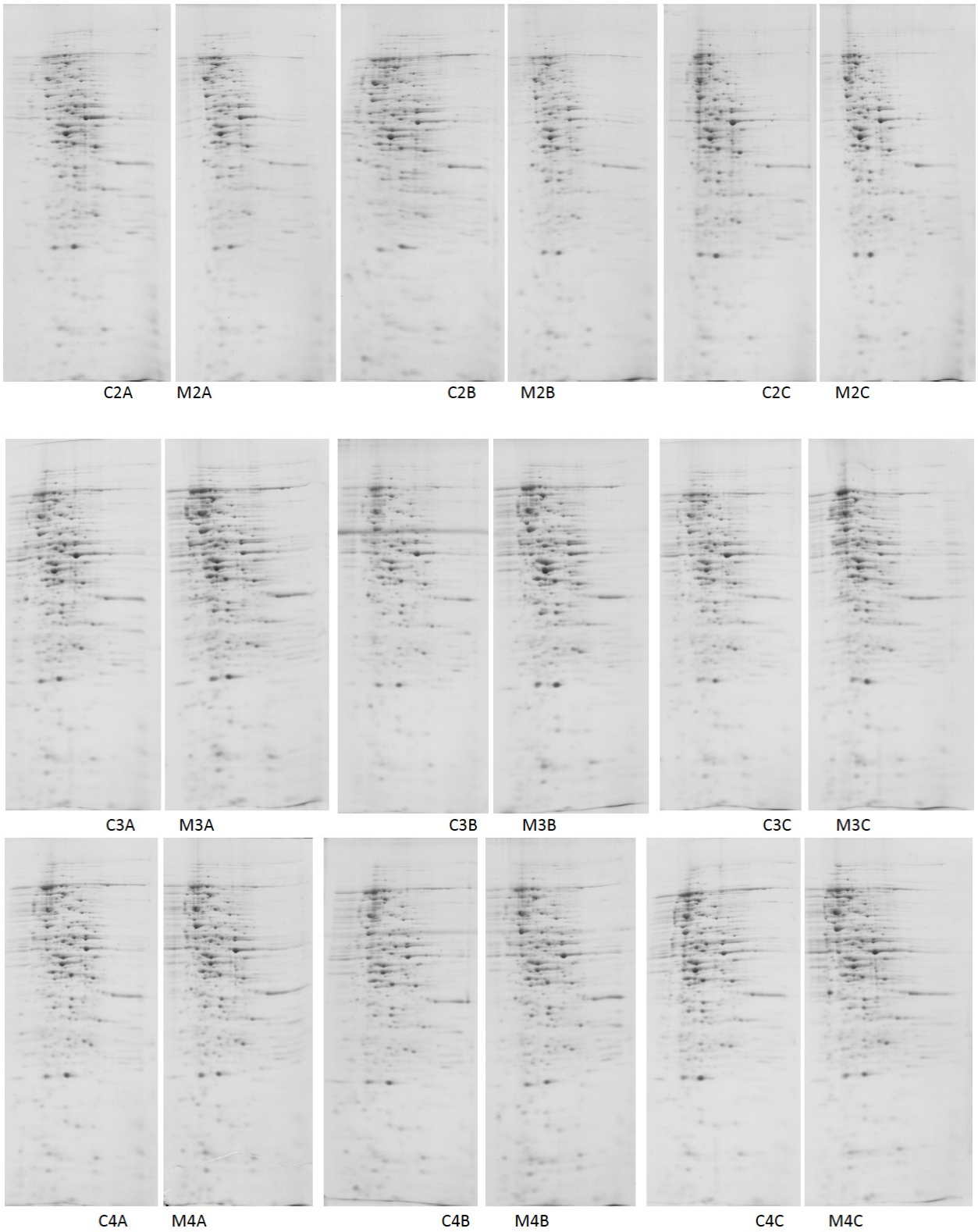
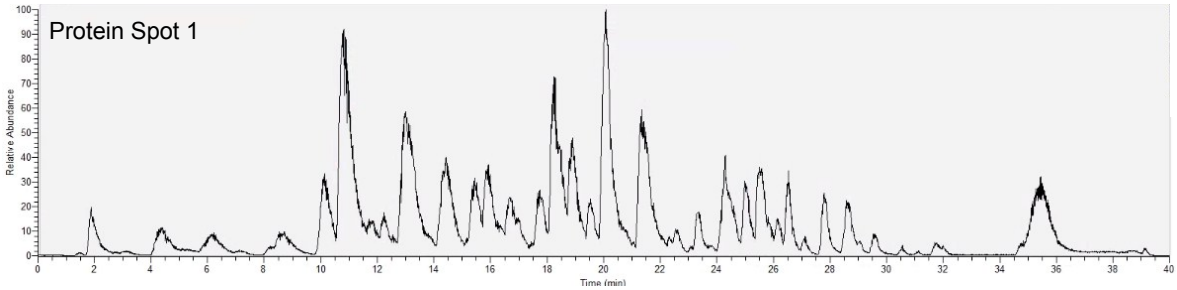


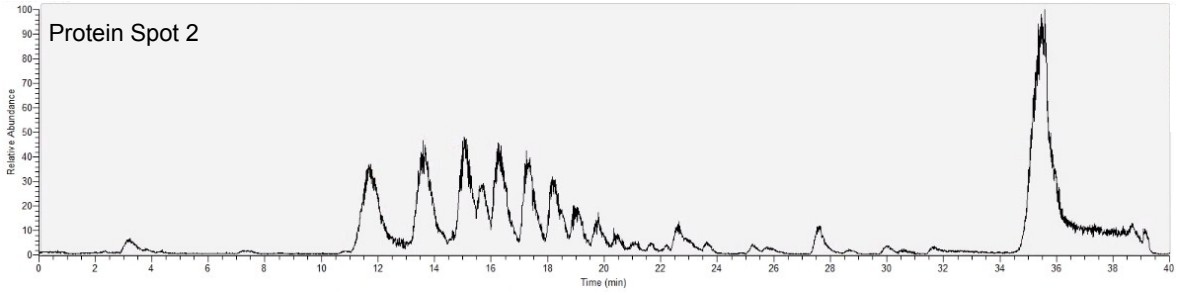
Figure S3. 2-D gel images of protein samples isolated from *E. coli* culture treated with microwave (M) and incubated in oil bath (Control).

C = control, M = microwave, 100 µg total protein, 12.5% T mini-tall SDS-PAGE
Loading and IEF order: Run 1 (C2-ABC; M2-ABC); Run 2 (C3-ABC; C4-ABC; M3-ABC; M4-ABC). 2, 3 and 4 represent biological replicates; A, B and C are technical replicates. For SDS-PAGE, a single gel was shared between corresponding strips, i.e. C2A M2A were resolved together. C2 and M2 were resolved on gels cast in parallel; C3, C4, M3 and M4 were resolved on gels cast in parallel.

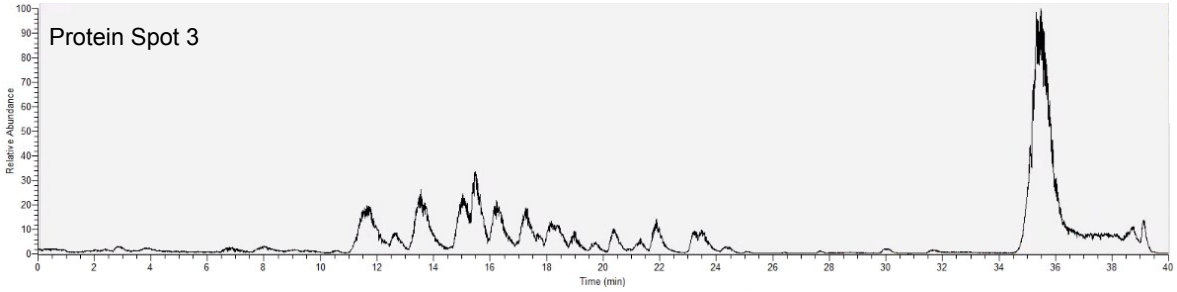
A



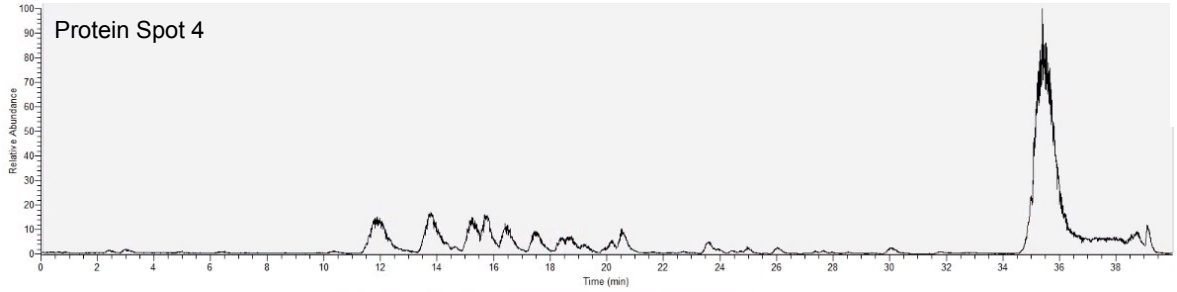
B



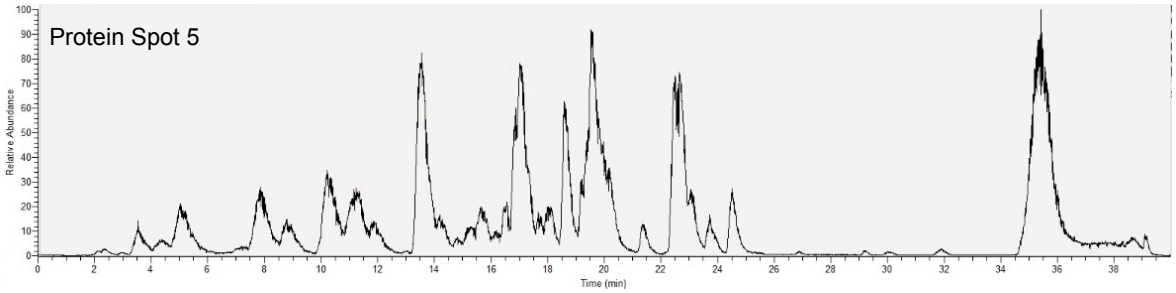
C



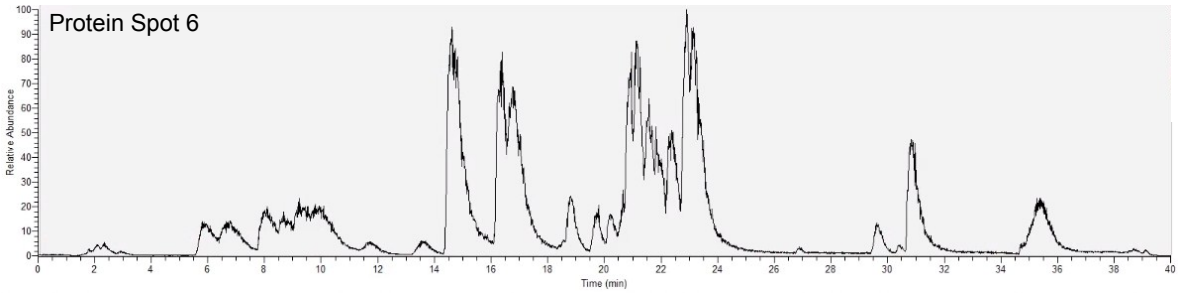
D



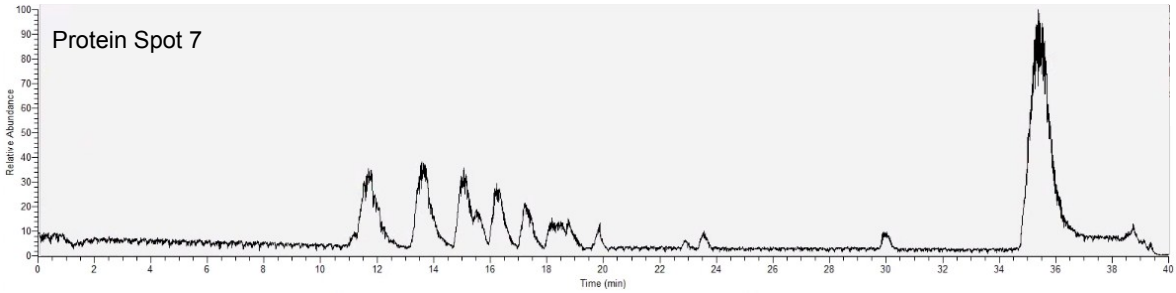
E


Protein Spot 5
Relative Abundance
Time (min)

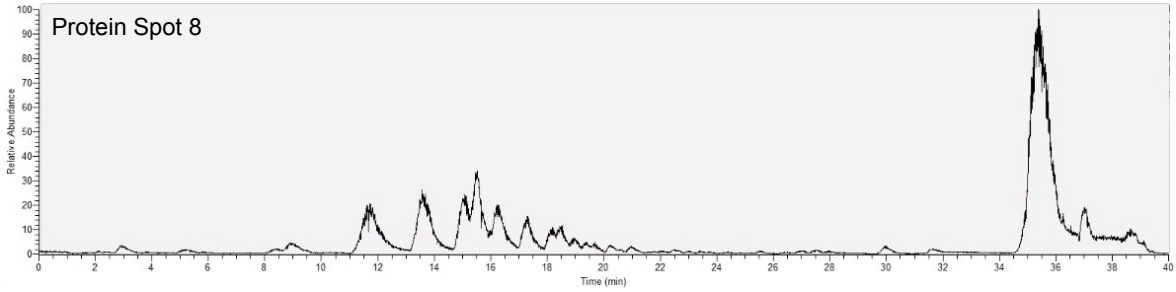
F


Protein Spot 6
Relative Abundance
Time (min)

G


Protein Spot 7
Relative Abundance
Time (min)

H


Protein Spot 8
Relative Abundance
Time (min)

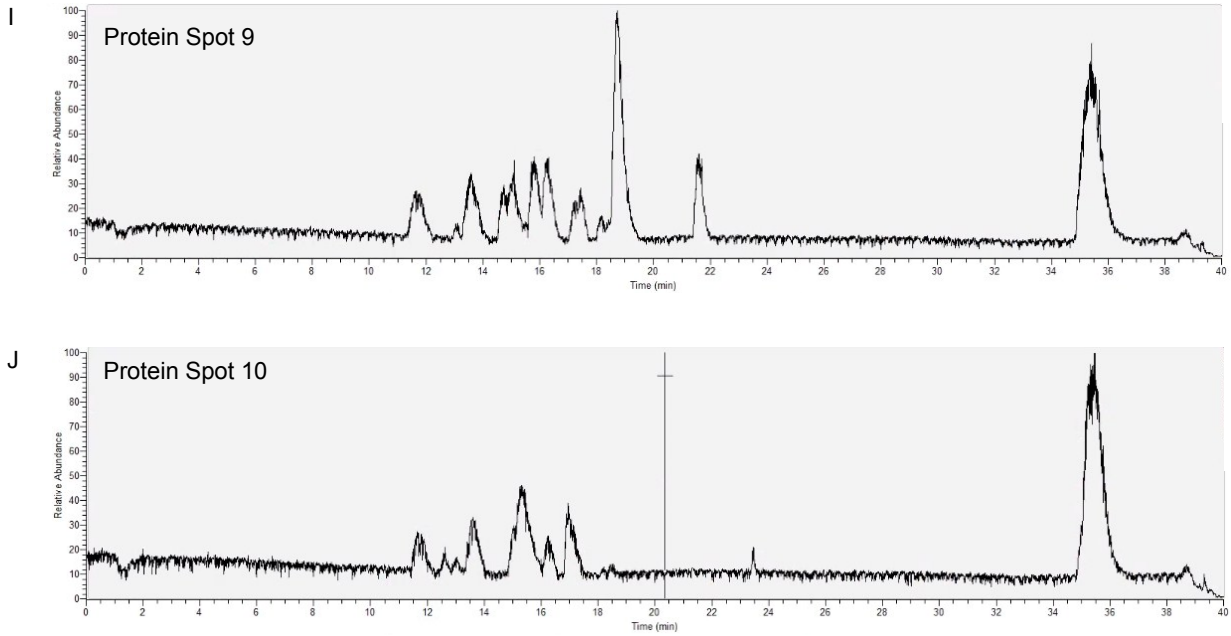


Figure S4. LC-MS chromatograms of the 10 resolved protein spots. Chromatographic separation of peptides was carried out using a Zorbax 300SB-C18 column (3.5 µm i.d. × 150 mm, particle size 5 µm, pore size 100 Å, Agilent Technologies, Wilminton, DE). Peptides were loaded onto a Zorbax 300SB-C18 trap cartridge at a flow rate of 2 µl per minute for 10 min. After washing with 0.1% formic acid the peptides were eluted using a 5–40% B gradient for 30 min at a flow rate of 250 nl/min acid (mobile phase A = 0.1% formic acid; mobile phase B = 0.1% formic acid in acetonitrile) on an Agilent 1260 capillary/nano system.