Electronic Supplementary Material (ESI) for Analyst.

Supporting Information(SI)
A novel microscale preparative gel electrophoresis system

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Table S1 Protein relative mobility and the RSD values

Protein	Relative mobility			RSD(%)
	Group 1	Group 2	Group 3	
β-galactosidase	0.08	0.08	0.08	0.18
BSA	0.16	0.18	0.15	1.4
ovalbumin	0.27	0.29	0.27	1.0
CA	0.47	0.48	0.46	0.84
soybean trypsin inhibitor	0.68	0.70	0.69	0.78
α-lactalbumin	0.88	0.89	0.89	0.54

As shown in Table S1, the maximum RSD value was 1.4% and the average RSD value was 0.79%, which indicated a good reproducibility of the protein separation.

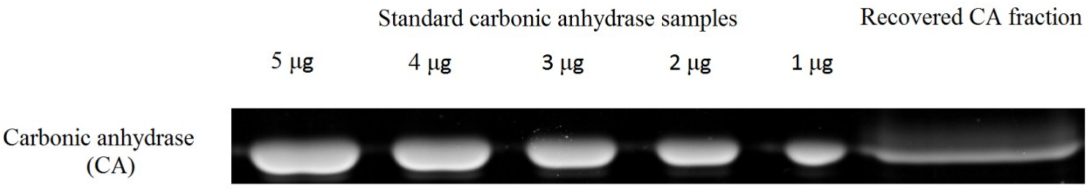

Fig. S1 Densitometric analysis of recovered CA fraction using the ImageJ software.

Table S2 Densitometric analysis data

Lane number	OD($\times 10^6$)	Protein amount (μg)
1	1.45	5
2	1.23	4
3	1.01	3
4	0.817	2
5	0.488	1
6	1.37	4.59

As shown in Table S2, the OD value (y) and the protein amount (x) was fitted through linear regression. The regression equation was

$$y \times 10^{-5} = 2.33x + 3.01$$

$$R^2 = 0.990$$

Therefore, protein amount in recovered CA fraction was 4.59 μg.

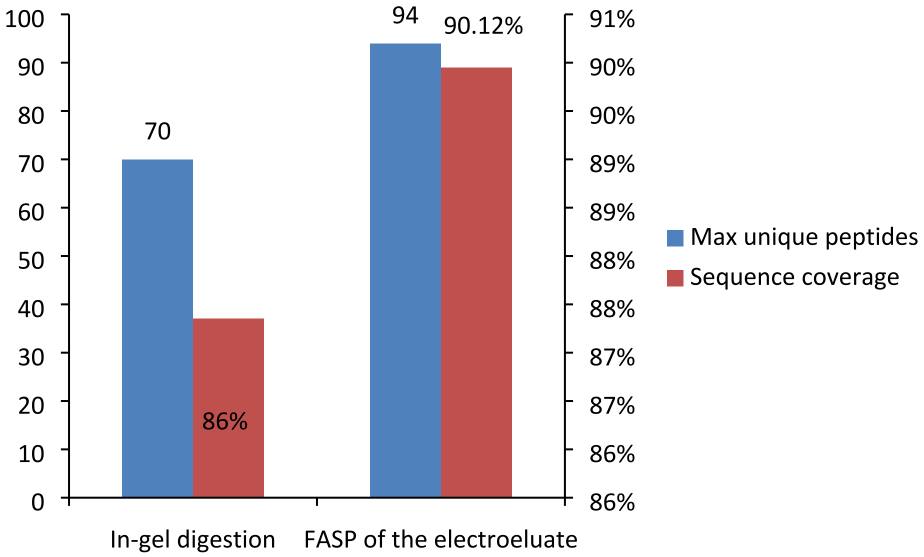

Fig. S2 Comparison of maximum unique peptides and the average sequence coverage of the in-gel digestion and FASP of the electroeluate.

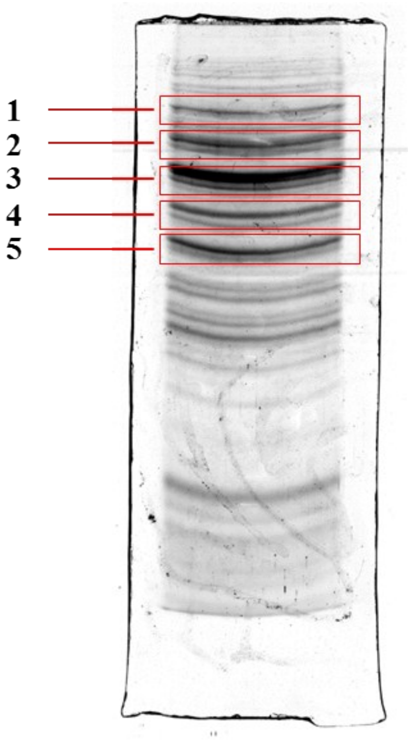

Fig. S3 Separation of 20 μg of yeast extract using the separation apparatus. The red wireframes represent the eluted/sliced areas.