Supporting Information

Facile Synthesis of Magnetic Mesoporous Hollow Carbon Microspheres for Rapid Capture of Low-concentration Peptides

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Figures:

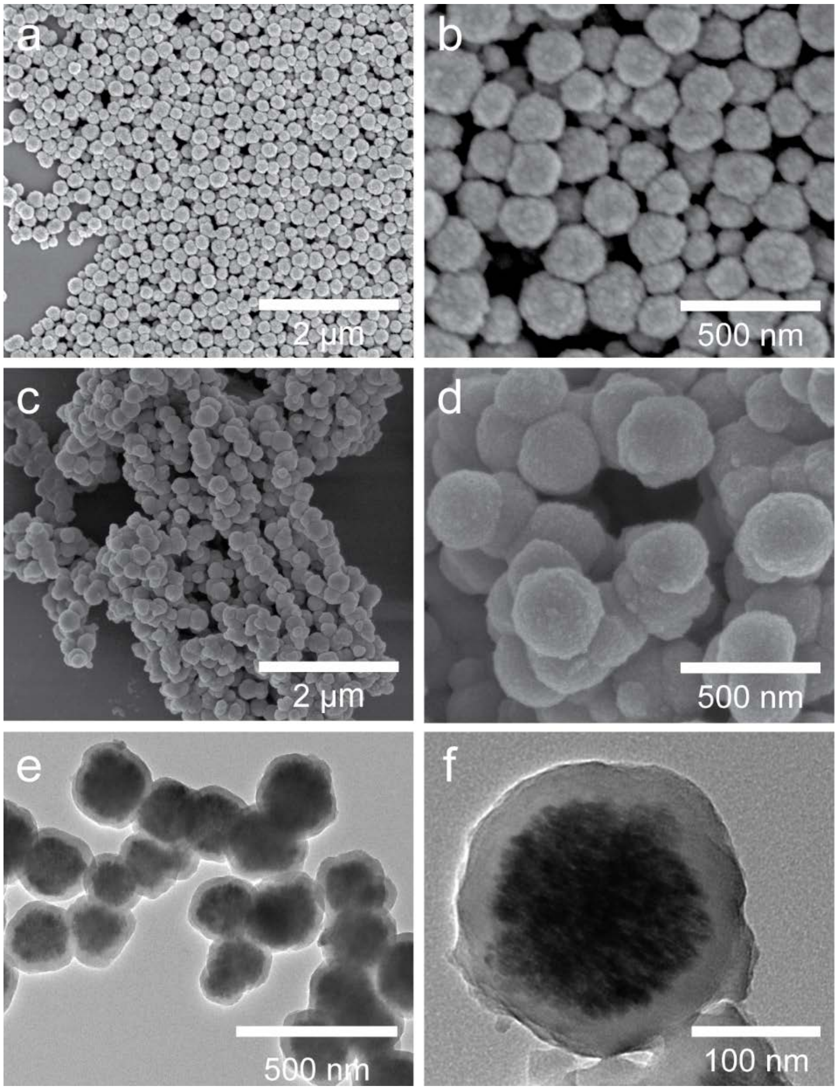

Fig. S1 SEM (a-d) and TEM (e and f) images of prepared Fe_3O_4 (a and b) and Fe_3O_4@PDA microspheres (c-f)

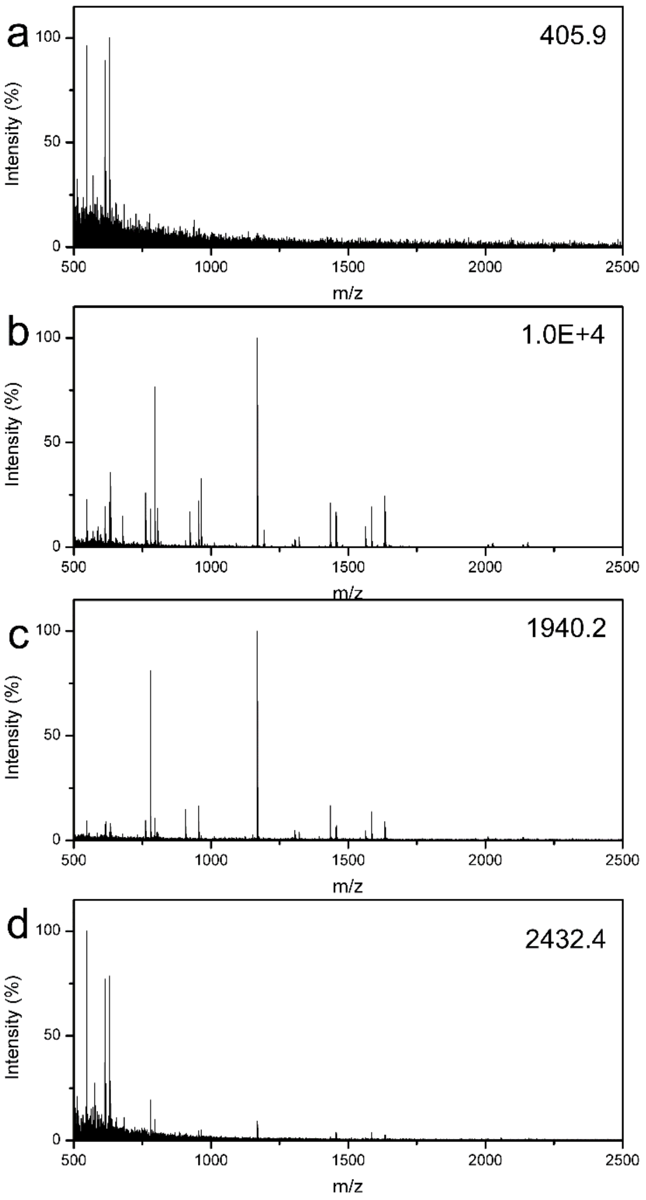

Fig. S2 MALDI-TOF mass spectra of the diluted Cyt-C digest (2.5 nM): direct detection (a) and after enrichment with the MPC affinity microspheres (b), the ZipTipC18 pipette tip (c), and the magnetic mesoporous silica microspheres (d), respectively. The number in the top right corner is the highest peak intensity.

Tables:

Table S1 The peptides captured from BSA digest by different affinity materials and identified by MALDI-TOF MS. M@mSiO$_2$ stands for magnetic mesoporous silica microspheres.

Start–End	MW	Sequence	MHM	Zip-tip C18	M@mSiO$_2$
20-24	633.3711	R.GVFRR.D			√
24-28	655.3402	R.RDTHK.S			√
29–34	711.3664	K.SEIAHR.F	√		
35–44	1248.614	R.FKDLGEEHFK.G	√	√	√
37–44	973.4505	K.DLGEEHFK.G	√		
66–75	1162.623	K.LVNELTEFAK.T	√	√	√
101-105	544.3333	K.VASLR.E	√	√	
118-122	657.3082	K.QEPER.N		√	
156-160	664.3697	K.KFWGK.Y	√	√	√
157-160	536.2747	K.FWGK.Y	√	√	
161–167	926.4861	K.YLYEIAR.R	√	√	√
198–204	700.3942	K.GACLLPK.I	√		
219-222	572.3221	R.QRLR.C	√	√	
223-228	648.3265	R.CASIQK.F	√		√
229-232	507.2441	K.FGER.A	√	√	
236-241	688.3656	K.AWSVAR.L	√	√	
242–248	846.4963	R.LSQKFPK.A	√		√
249-256	921.4807	K.AEFVEVTK.L	√		
257-263	788.4644	K.LVTDLTK.V	√		
281-285	516.2907	R.ADLAK.Y	√	√	
341–346	751.35	K.NYQEAK.D	√		

347–359	1566.735	K.DAFLGSFLYEYSR.R	√		√
360–371	1438.805	R.RHPEYAVSVLLR.L	√	√	√
361–371	1282.703	R.HPEYAVSVLLR.L	√		√
402–412	1304.709	K.HLVDEPQNLIK.Q	√	√	√
421–433	1478.788	K.LGEYGFQNALIVR.Y	√	√	√
434-437	566.3176	R.YTRK.V	√		
437–451	1638.931	R.KVPQVSTPTLVEVSR.S	√		√
438–451	1510.836	K.VPQVSTPTLVEVSR.S	√		√
490-495	659.349	K.TPVSEK.V	√	√	
499–507	1023.448	K.CCTESLVNR.R	√		
524-528	608.2806	K.AFDEK.L	√		√
548–557	1141.707	K.KQTALVELLK.H	√		√
549–557	1013.612	K.QTALVELLK.H	√		√
558-561	508.3121	K.HKPK.A	√		
562–568	817.4181	K.ATEEQLK.T	√		
598–607	1001.576	K.LVVSTQTALA.-	√		
Matched peptides			34	16	19
Sequence coverage (%)			37	20	22

Table S2 The peptides captured from Cyt-c digest by different affinity materials and identified by MALDI-TOF MS

Start-End	MW	Peptide Sequence	MHM	Zip-tip	M@mSiO$_2$
1-6	677.3054	-.MGDVEK.G	√		
2-6	546.264	M.GDVEK.G	√	√	√
9-14	761.4800	K.KIFVQK.C	√		√
10-14	633.3850	K.IFVQK.C	√	√	√

10-23	1632.8116	K.IFVQKCAQCHTVEK.G	√	√	√
24-28	525.3023	K.GGKHK.T		√	
27-39	1432.768	K.HKTGPNLHGLFGR.K	√		√
29-39	1167.6149	K.TGPNLHGLFGR.K	√	√	√
40-54	1583.7580	R.KTGQAPGFSYTDANK.N	√	√	√
41-54	1455.6630	K.TGQAPGFSYTDANK.N	√	√	√
57-73	2008.9452	K.GITWGEETLMEYLENPK.K	√		√
57-74	2137.0401	K.GITWGEETLMEYLENPKK.Y	√		√
74-80	805.4698	K.KYIPGTK.M	√		√
81-87	778.4411	K.MIFAGIK.K	√	√	√
81-88	906.5361	K.MIFAGIKK.K	√		
90-100	1305.6928	K.GEREDLIAYLK.K	√		√
93-100	963.5277	R.EDLIAYLK.K	√		
93-101	1091.622	R.EDLIAYLKK.A	√		
101-105	561.2758	K.KATNE.-	√	√	
Matched peptides			19	9	14
Sequence coverage (%)			92	59	86

Table S3 The peptides captured from human urine

m/z	S/N	m/z	S/N
757.4	33.2	2212.7	65.6
982.6	39.4	2216.7	19.9

1148.5	10.7	2228.7	16.2
1188.7	51.7	2436.8	102.2
1204.7	104.8	2674.9	12.3
1218.6	11.9	2787.9	513.9
1251.6	11.6	2790.9	270.43
1406.5	11.4	2805.9	17.9
1912.1	125.1	2809.9	56.21
2079.7	10.2	2814.9	19.68
2192.8	278.5	2825.9	21.0