

Electronic Supplementary Information

Characterization of Efficient Proteolysis by Trypsin Loaded Macroporous Silica

Weichao Guo¹, Hongyan Bi², Liang Qiao², Jingjing Wan¹, Kun Qian¹,

Hubert H. Girault,² Baohong Liu^{1}*

1. Department of Chemistry and Institute of Biomedical Sciences, Fudan University, Shanghai, 200433,

P. R. China,

2. Laboratoire d'Electrochimie Physique et Analytique, Station 6, Ecole Polytechnique Fédérale de

Lausanne, CH-1015 Lausanne, Switzerland.

*: To whom correspondence should be addressed. Prof. Baohong Liu, Department of Chemistry, Fudan University, Shanghai, 200433, P. R. China, Tel: +86-21-65642405, Fax: +86-21-65641740, Email:

bhliu@fudan.edu.cn

SI-1: Characterization of employed porous material

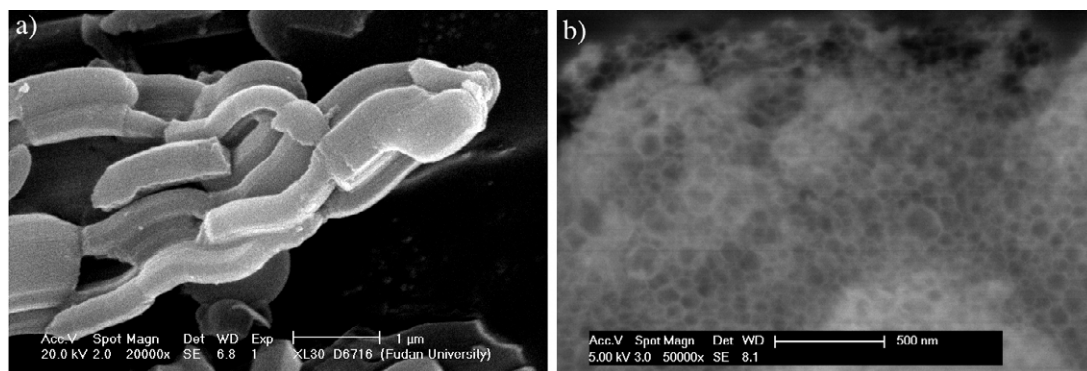


Figure SI-1. Scanning electron micrographs of SBA-15 a) and MOSF b), respectively

Table SI-1. Physical parameters of the chosen porous materials, calculated from nitrogen sorption data.

	SBA-15	MOSF
Cell/window size	~10nm pore size	~100nm in pore diameter
Pore volume	1.14cm ³ /g	1.3cm ³ /g
Surface area	503m ² /g	430m ² /g

SI-2: Electric double layer formation in the nanoporous silica

Assuming that the surface property of porous silica is similar as glass, the surface of silica inner pore should be negatively charged with a coulomb intensity around $1\text{mC}\cdot\text{m}^{-2}$, when the silica is separated in a buffer with pH 8. (Analytical and Physical Electrochemistry, Hubert H. Girault, Presses Polytechniques Universitaires Romandes, 2004) To compensate these negative charges, positive ions could be confined in the nanopores with a concentration calculated as $qA/(FV)$, where q is the surface charge intensity ($\text{C}\cdot\text{m}^{-2}$), A is the specific surface area of porous silica, V is the total pore volume of porous silica and F is the Faraday constant. For MOSF and SBA-15, the specific surface areas are both around $500\text{m}^2/\text{g}$, and the total pore volumes are both around $1\text{cm}^3/\text{g}$. The positive ion concentration in the nanopores of both MSOF and SBA-15 can be roughly calculated as $\sim 5\text{mM}$, indicating an electric double layer thickness of $\sim 10\text{nm}$ generated on the surface of the inner pores of the porous silica (Analytical and Physical Electrochemistry, Hubert H. Girault, Presses Polytechniques Universitaires Romandes, 2004).

SI-3: Interference of SDS and urea on the reactor catalyzed digestion.

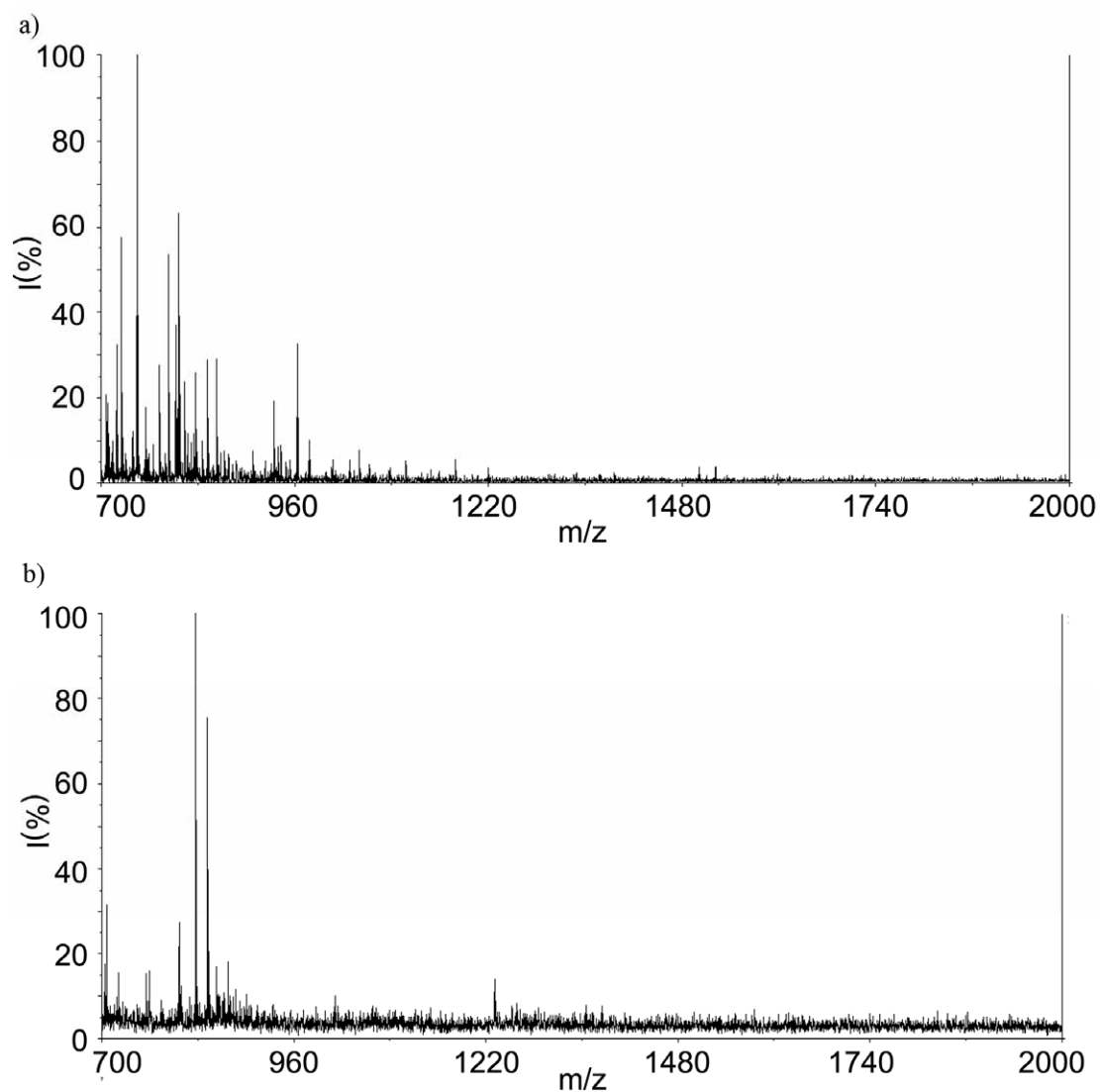


Figure SI-2. Mass spectra of proteolysis products from 20min trypsin-MOSF catalyzed digestion of myoglobin (20ng/ μ L) that is dissolved with a) 0.1% SDS and b) 500mM urea. The SDS and urea were removed by using SCX Zip Tips before MS identification.

SI-4: RPLC spectrum of the rat liver cytoplasm sample

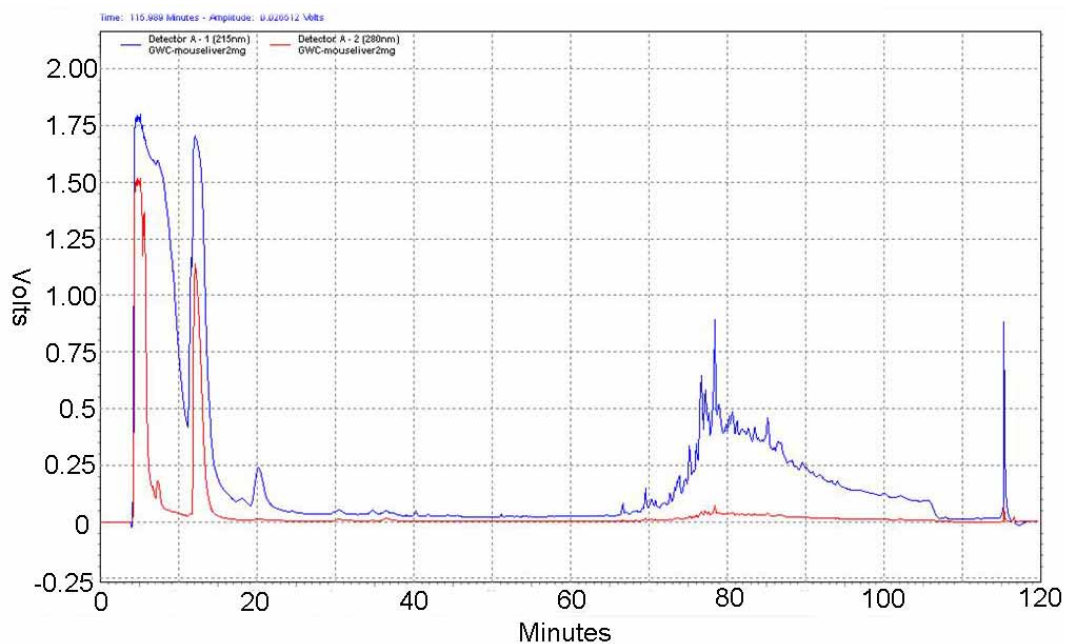


Figure SI-3. RPLC spectrum of the rat liver cytoplasm sample carried out on Agilent ZORBAX SB-C18 column (4.6 ×250 mm, 5 μm, 300Å, C18, Hypersil, EliteHPLC, China) for 120 min by using 0.05%(v/v) TFA in water as mobile phase A and 0.05%(v/v) TFA in acetonitrile as mobile phase B on a Shimadzu LC-20AD capillary pumping system. The fraction separated from 77min to 78min was chosen to be digested. The blue curve was recorded by detecting the UV light absorption of separated fractions under 215nm wavelength; while the red curve was recorded by detecting the UV light absorption of separated fractions under 280nm wavelength.

SI-5: Identified proteins from rat liver tissue RPLC fraction 77-78min

Table SI-2. The proteins identified from the tryptic peptides generated after 3h of digestion with free trypsin.

No.	protein	pI	Mw	No.	protein	pI	Mw
1	sp O08709 PRDX6_MOUSE	5.71	24870.64648	34	sp P19639 GSTM4_MOUSE	7.62008	25701.607
2	sp O35490 BHMT1_MOUSE	8.01	45020.53125	35	sp O70591 PFD2_MOUSE	6.190047	16533.701
3	sp P00329 ADH1_MOUSE	8.43	39771.45703	36	sp P08228 SODC_MOUSE	6.020043	15942.667
4	sp P01942 HBA_MOUSE	7.96	15085.1709	37	sp P09671 SODM_MOUSE	8.790106	24602.928
5	sp P02088 HBB1_MOUSE	7.12	15840.17383	38	sp P10648 GSTA2_MOUSE	8.880108	25532.957
6	sp P02089 HBB2_MOUSE	7.84	15878.25	39	sp P11352 GPX1_MOUSE	6.730059	22179.254
7	sp P07309 TTHY_MOUSE	5.76	15775.92481	40	sp P15532 NDKA_MOUSE	6.840062	17207.795
8	sp P07724 ALBU_MOUSE	5.74	68692.60156	41	sp P18760 COF1_MOUSE	8.210093	18559.545
9	sp P10649 GSTM1_MOUSE	7.71	25969.98047	42	sp P20029 GRP78_MOUSE	5.060021	72422.164
10	sp P10853 H2B1F_MOUSE	10.3	13936.16309	43	sp P20152 VIME_MOUSE	5.060021	53687.738
11	sp P12710 FABPL_MOUSE	8.58	14245.55078	44	sp P25688 URIC_MOUSE	8.480099	35039.191
12	sp P16015 CAH3_MOUSE	6.89	29366.27539	45	sp P35979 RL12_MOUSE	9.480122	17804.557
13	sp P17742 PPIA_MOUSE	7.73	17971.33789	46	sp P56480 ATPB_MOUSE	5.190024	56300.539
14	sp P19221 THRB_MOUSE	6.03	70268.86719	47	sp P99027 RLA2_MOUSE	4.420006	11650.907
15	sp P24270 CATA_MOUSE	7.72	59765.35547	48	sp P99029 PRDX5_MOUSE	9.090113	21897.473
16	sp P25444 RS2_MOUSE	10.3	31231.32031	49	sp Q60668 HNRPD_MOUSE	7.610079	38354.117
17	sp P26443 DHE3_MOUSE	8.05	61336.86719	50	sp Q64433 CH10_MOUSE	7.900086	10962.703
18	sp P27773 PDIA3_MOUSE	5.88	56678.46484	51	sp Q8BIQ5 CSTF2_MOUSE	6.35005	61341.168
19	sp P32020 NLTP_MOUSE	7.15	59125.73047	52	sp Q99J08 S14L2_MOUSE	6.680058	46300.316
20	sp P62908 RS3_MOUSE	9.68	26674.30469	53	sp Q9CQ48 NUDC2_MOUSE	4.980019	17659.871
21	sp Q5EBG8 CA050_MOUSE	5.29	21862.71094	54	sp Q9CXI5 ARMET_MOUSE	8.340096	20373.684
22	sp Q64523 H2A2C_MOUSE	10.9	13988.36719	55	sp Q9CY58 PAIRB_MOUSE	8.600101	44714.145
23	sp Q8QZT1 THIL_MOUSE	8.7	44816.14063	56	sp Q9DCX2 ATP5H_MOUSE	5.510031	18749.449
24	sp Q8VBW8 TTC36_MOUSE	5.12	20132.50195	57	sp Q9JII6 AK1A1_MOUSE	6.890063	36586.938
25	sp Q91X83 METF1_MOUSE	5.51	43508.66406	58	sp P10126 EF1A1_MOUSE	9.100113	50113.898
26	sp Q91Y97 ALDOB_MOUSE	8.52	39506.98047	59	sp Q99020 ROAA_MOUSE	7.680081	30831.271
27	sp Q99PL5 RRBP1_MOUSE	9.35	172878.1875	60	sp P49429 HPPD_MOUSE	6.580056	45054.254
28	sp Q9CPU0 LGUL_MOUSE	5.24	20809.59961	61	sp P56391 CX6B1_MOUSE	8.96011	10071.45
29	sp Q9CZX8 RS19_MOUSE	10.4	16085.49121	62	sp P0C0S6 H2AZ_MOUSE	10.580147	13552.732
30	sp Q9D6J6 NDUV2_MOUSE	6.99	27285.36328	63	sp P10639 THIO_MOUSE	4.790015	11675.441
31	sp Q9DCW4 ETFB_MOUSE	8.24	27623.30273	64	sp Q99KB8 GLO2_MOUSE	6.490054	28901.016
32	sp Q9R257 HEBP1_MOUSE	5.18	21052.82422	65	sp P46656 ADX_MOUSE	5.370028	20122.869
33	sp Q9WVA2 TIM8A_MOUSE	5.1	11042.44336	66	sp P62991 UBIQ_MOUSE	6.560055	8564.8428

Table SI-3. The isoelectric point and molecular weight of proteins identified from the tryptic peptides generated after 3h digestion with MOSF-trypsin nanoreactor (right, black characters) and from standard overnight in-solution digestion method (left, red characters). The proteins existing in both lists are characterized as bold and italic type.

No.	pI	Mw	No.	pI	Mw	No.	pI	Mw	No.	pI	Mw
1	<i>4.330004</i>	47994.6	57	<i>7.340073</i>	68091.02	1	3.979997	28537.53	83	7.070067	102088.2
2	<i>4.420006</i>	11650.91	58	<i>7.62008</i>	25701.61	2	4.330004	47994.6	84	7.090067	32675.22
3	<i>4.910017</i>	34384.79	59	<i>7.65008</i>	34108.37	3	4.420006	11650.91	85	7.120068	15840.17
4	<i>5.060021</i>	72422.16	60	<i>7.700081</i>	33465.91	4	4.610011	32560.05	86	7.150069	59125.73
5	5.060021	53687.74	61	7.710082	25969.98	5	4.680012	32862.82	87	7.340073	68091.02
6	5.100022	11042.44	62	7.720082	59765.36	6	4.740014	92475.85	88	7.62008	25701.61
7	5.120022	20132.5	63	7.730082	17971.34	7	4.790015	32838.08	89	7.63008	44729.57
8	5.130023	71973.5	64	7.840085	15878.25	8	4.890017	48699.59	90	7.65008	34108.37
9	5.150023	33406.85	65	7.960087	15085.17	9	4.900017	31293.03	91	7.670081	21984.06
10	5.180024	21052.82	66	8.010088	45020.53	10	4.980019	17659.87	92	7.700081	33465.91
11	5.190024	56300.54	67	8.030088	35490.41	11	5.00002	50006.88	93	7.700081	13559.46
12	5.190024	20830.44	68	8.030088	59335.16	12	5.01002	26791.2	94	7.710082	25969.98
13	5.240025	20809.6	69	8.050089	61336.87	13	5.02002	52572.75	95	7.720082	59765.36
14	5.350028	48968.5	70	8.210093	18559.54	14	5.060021	72422.16	96	7.730082	17971.34
15	5.380028	53600.41	71	8.240093	27623.3	15	5.060021	53687.74	97	7.750082	18235.85
16	5.510031	43508.66	72	8.250093	70922.81	16	5.060021	61422.24	98	7.840085	15878.25
17	5.510031	18749.45	73	8.320095	41857.93	17	5.100022	11042.44	99	7.900086	10962.7
18	5.630034	31380.98	74	8.350096	16665.11	18	5.100022	61172.12	100	7.910086	51340.84
19	5.680035	22165.33	75	8.360096	30048.64	19	5.120022	20132.5	101	7.960087	15085.17
20	5.690035	54565.35	76	8.430098	39771.46	20	5.150023	33406.85	102	8.000088	48297.27
21	5.710036	24870.65	77	8.430098	35810.03	21	5.180024	21052.82	103	8.010088	45020.53
22	5.740036	68692.6	78	8.460098	14957.21	22	5.190024	20830.44	104	8.030088	35490.41
23	5.760037	15775.92	79	8.480099	35039.19	23	5.190024	56300.54	105	8.030088	59335.16
24	5.840039	68600.97	80	8.490099	37047.68	24	5.230025	11777.88	106	8.050089	61336.87
25	5.870039	52514.07	81	8.5201	39506.98	25	5.240025	20809.6	107	8.070089	85463.54
26	5.88004	56678.46	82	8.580101	14245.55	26	5.290026	21862.71	108	8.210093	18559.54
27	5.91004	34216.42	83	8.700104	44816.14	27	5.290026	41736.76	109	8.240093	27623.3
28	5.950041	17270.54	84	8.790106	24602.93	28	5.350028	48968.5	110	8.320095	41857.93
29	5.990042	30448.64	85	8.850107	35000.2	29	5.370028	32667.05	111	8.340096	32314.11
30	5.990042	29546.54	86	8.870108	50906.22	30	5.380028	53600.41	112	8.350096	16665.11
31	6.020043	15942.67	87	8.880108	25532.96	31	5.47003	16131.43	113	8.360096	30048.64
32	6.090044	32804.31	88	8.97011	37402.68	32	5.500031	46415.53	114	8.430098	35810.03
33	6.100045	33023.19	89	9.000111	54540.88	33	5.510031	43508.66	115	8.480099	35039.19
34	6.100045	41525.52	90	9.090113	39652	34	5.510031	18749.45	116	8.490099	37047.68
35	6.130045	15137.4	91	9.100113	50113.9	35	5.510031	88847.04	117	8.5201	39506.98

36	6.170046	24324.58	92	9.140114	38284.98	36	5.530032	21066.6	118	8.5301	30641.21
37	6.35005	13776.89	93	9.170115	12096.96	37	5.620034	31875.64	119	8.580101	14245.55
38	6.420052	141742.5	94	9.220116	59752.64	38	5.680035	22165.33	120	8.640102	33880.5
39	6.430052	44698.85	95	9.230116	66765.57	39	5.690035	54565.35	121	8.640102	56822.82
40	6.480053	164617.2	96	9.230116	82669.94	40	5.710036	24870.65	122	8.640102	74634.73
41	6.490054	28901.02	97	9.330118	52443.5	41	5.740036	68692.6	123	8.700104	44816.14
42	6.500054	13770.28	98	9.350119	172878.2	42	5.760037	15775.92	124	8.770105	10000.43
43	6.580056	45054.25	99	9.350119	9117.577	43	5.840039	68600.97	125	8.770105	66414.57
44	6.690058	31319.58	100	9.39012	220599	44	5.88004	56678.46	126	8.790106	24602.93
45	6.730059	22179.25	101	9.42012	51386.37	45	5.88004	38752.32	127	8.850107	35000.2
46	6.840062	17207.79	102	9.460121	48136.83	46	5.950041	17270.54	128	8.870108	50906.22
47	6.890063	29366.28	103	9.480122	17804.56	47	5.990042	29546.54	129	8.880108	25532.96
48	6.890063	36586.94	104	9.650126	12784.05	48	5.990042	30448.64	130	8.890108	46589.65
49	6.910063	27497.62	105	9.680126	26674.3	49	6.020043	15942.67	131	8.96011	10071.45
50	6.940064	76723.88	106	9.960133	21881.43	50	6.020043	38988.21	132	8.97011	37402.68
51	6.990065	27285.36	107	10.13014	8469	51	6.070044	16101.47	133	9.000111	54540.88
52	7.060067	72585.46	108	10.25014	31231.32	52	6.090044	32804.31	134	9.090113	39652
53	7.090067	32675.22	109	10.31014	13936.16	53	6.090044	52003.64	135	9.100113	50113.9
54	7.120068	15840.17	110	10.40014	16085.49	54	6.100045	33023.19	136	9.140114	38284.98
55	7.150069	59125.73	111	10.58015	13552.73	55	6.130045	15137.4	137	9.140114	31994.32
56	7.170069	85004.53	112	11.04016	14135.49	56	6.160046	36511.18	138	9.220116	59752.64
						57	6.250048	129684.5	139	9.230116	66765.57
						58	6.260048	37798.63	140	9.340118	8235.602
						59	6.35005	61341.17	141	9.350119	172878.2
						60	6.360051	47140.86	142	9.350119	9117.577
						61	6.420052	141742.5	143	9.41012	40035.92
						62	6.430052	44698.85	144	9.42012	51386.37
						63	6.480053	164617.2	145	9.450121	75441.9
						64	6.490054	28901.02	146	9.480122	33363.22
						65	6.580056	45054.25	147	9.480122	17804.56
						66	6.610056	35334.47	148	9.480122	23274.81
						67	6.630057	42119.68	149	9.510122	22030.8
						68	6.640057	13048.85	150	9.550123	23713.48
						69	6.660058	37057.8	151	9.650126	12784.05
						70	6.660058	32951.46	152	9.680126	26674.3
						71	6.700058	27901.84	153	9.780128	34400.63
						72	6.710059	52227.2	154	9.84013	15524.08
						73	6.730059	22179.25	155	9.870131	35729.97
						74	6.840062	34357.07	156	9.890131	15081.29

					75	6.860062	34460.75	157	9.950132	10344.23
					76	6.890063	29366.28	158	10.13014	8469
					77	6.890063	36586.94	159	10.14014	14839.5
					78	6.910063	46103.74	160	10.25014	31231.32
					79	6.940064	76723.88	161	10.31014	13936.16
					80	6.970065	17363.06	162	10.58015	13552.73
					81	6.990065	27285.36	163	10.90015	13988.37
					82	7.060067	72585.46			
