Supporting information

In situ Synthesis of Magnetic Mesoporous Phenolic Resin for the Selective Enrichment of Glycopeptides

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Experimental Section

Sample preparation

IgG (1 mg) or HRP (1 mg) were dissolved in an NH_4HCO_3 solution (50 mM, 1 mL) and treated with trypsin (2 %, w/w) for 16 h at 37°C for direct digestion. The obtained IgG or HRP digests were stored at -20°C until further use.

Human serum (20 μL) was diluted in an NH4HCO3 solution (50 mM, pH = 8.3, 220 μL) and denatured by adding urea (8 M), DTT (10 mM) for 45 min at 60°C. Then, IAA (1.1 mg) was added to the reaction mixture and mixtures are kept in dark for 45 min at room temperature. The solution was diluted to 1.2 mL and then treated with trypsin (2 %, w/w, 24 μg) for 16 h at 37°C. The tryptic digests were desalted by C18-SPE and stored at -20°C until further use.

Mass spectrometry analysis

MALDI–TOF MS experiments were operated in positive ion mode on a 5800 Proteomics Analyzer (Applied Biosystems, Framingham, MA, USA) with the Nd-YAG laser at 355 nm, a repetition rate of 400 Hz and an acceleration voltage of 20 kV.

For experiment of nano-LC-MS/MS anaylsis, the sample was loaded on the trap column (Thermo Scientific Acclaim PepMap C18, 100 μm × 2 cm) in 3 min at a flow rate of 10 μL/min. The sample was subsequently separated with an analytical column (Thermo Scientific Acclaim PepMap C18, 75 μm × 25 cm). For gradient separation, H2O/FA (99.9: 0.1) was used as the mobile phase A, and ACN/FA (99.9:0.1) was the mobile phase B. The gradient elution was performed as follows: 4 % B was held for 10 min. Then, from 4 % to 50 %, B was held for 150 min, and from 50 % to 80 %, B was held for 5 min. Next, the mobile phase B was held at 80 % for 10 min, and then from 80 % to 4 % for 0.1 min. Finally, at 4 %, B was held for 10 min. The column flow rate was maintained at 300 nL/min and column temperature was maintained at 40°C. The electrospray voltage of 2.0 kV versus the inlet of the mass spectrometer was used. The Nano Aquity UPLC system (Waters Corp.) was coupled to a Orbitrap Fusion mass spectrometer equipped with a nanospray source. Survey full-scan MS spectra (m/z 350−1600) were acquired in Orbitrap with a mass resolution of 120000 at m/z. The AGC target was set to 1000000, and the maximum injection time was 50ms. MS/MS acquisition was performed in Orbitrap in 3s cycle time. The intensity threshold was 50000, and the isolation window was 2m/z. Ions with charge states 2+, 3+, and 4+ were orderly fragmented by HCD with NCE of 35% and fixed first mass was set at 110.

Database Search

Thermo Scientific Proteome Discoverer software version 1.4 with the MASCOT v2.3.2 search engine was used for all searches of the database. The database was the Human UniProtKB/Swiss-Prot database (Release 2014-04-10, with 20264 sequences). The mass tolerance of the precursor ion was set to 10 ppm and that of the fragment ions was set to 50 mmu. The peptide false discovery rate (FDR) was set to 1%. Trypsin was chosen as the proteolytic enzyme and up to two miss cleavages were allowed. Carbamidomethyl on cysteine was set as a fixed modification. Oxidation on methionine and Deamidation on asparagine were set as variable modifications.

The Asn modification that did not occur in the N-X-S/T/C (X≠P) sequon was eliminated to ensure the false

positive rate below 1% for the identified glycosylation sites.

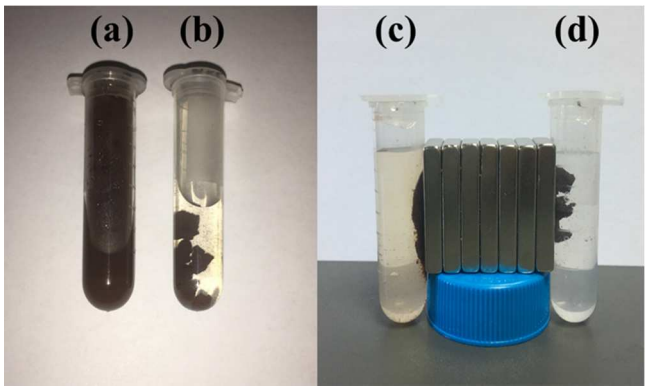


Figure S1. Photographs of the MMP dispersion solution before (a), (b) and after (c), (d) the placement of a magnet, and the MMP was ground (a), (c) or not (b), (d).

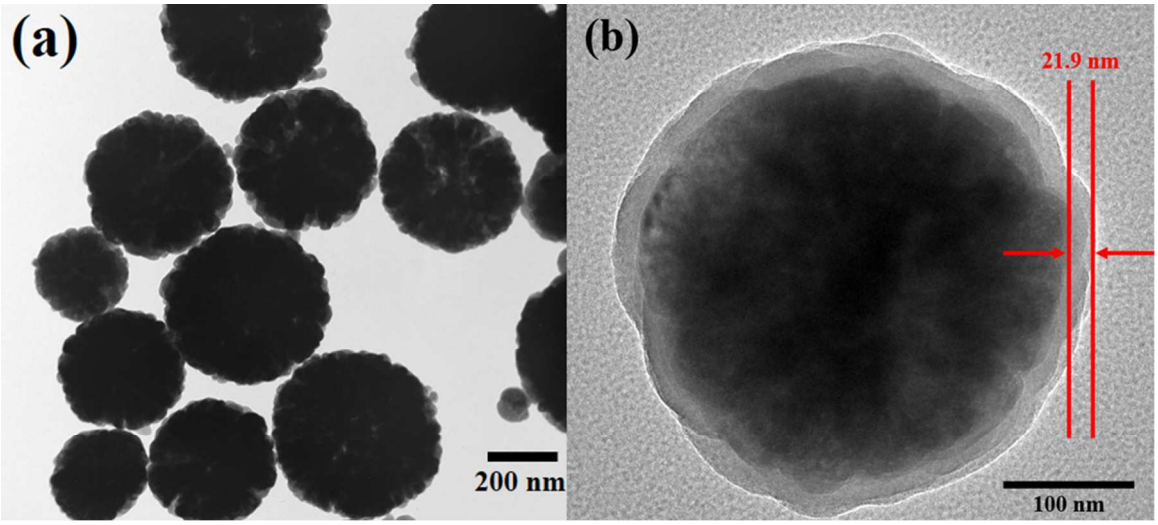


Figure S2. TEM images of (a) magnetic Fe_3O_4 core and (b) Fe_3O_4@SiO_2.

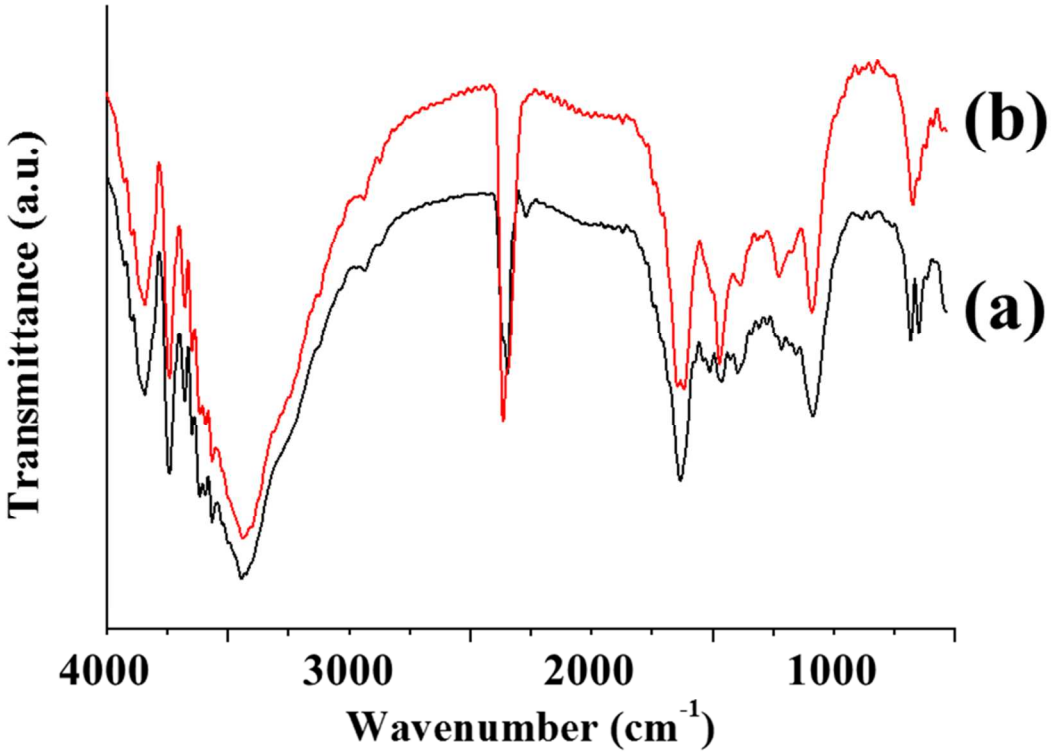


Figure S3. FT-IR spectra of (a) MMP and (b) MP.

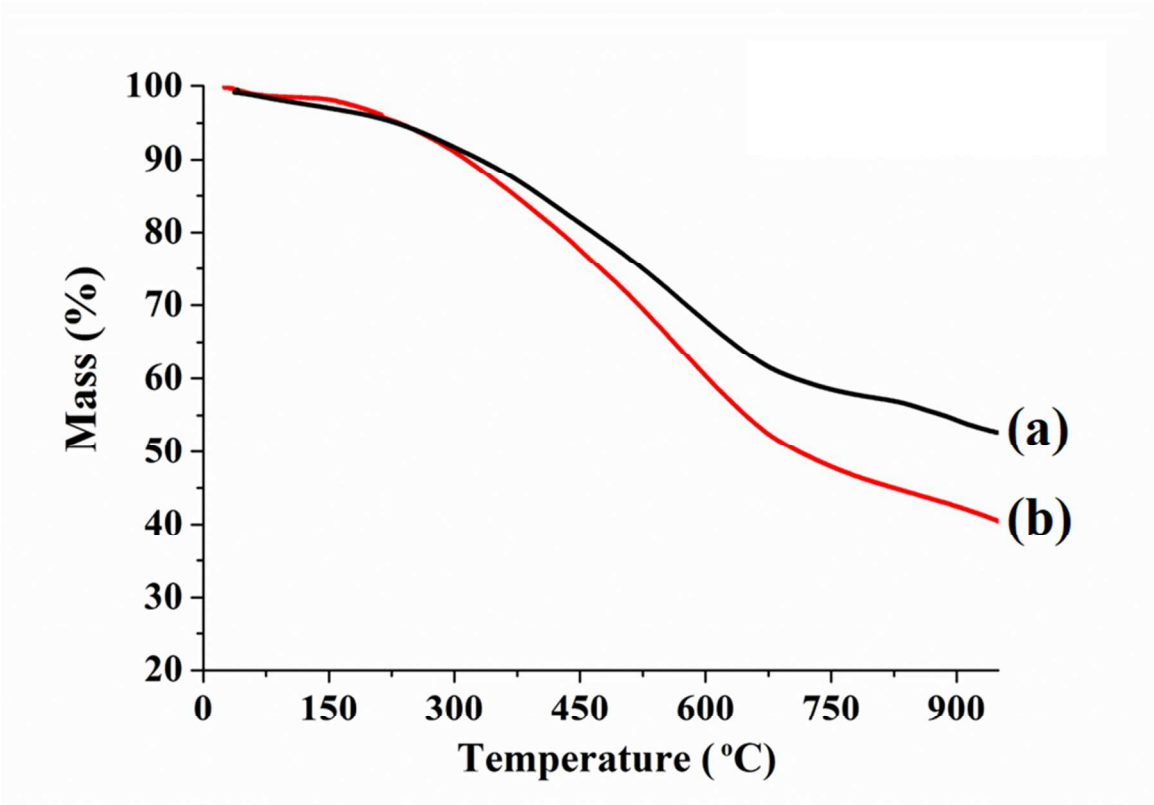
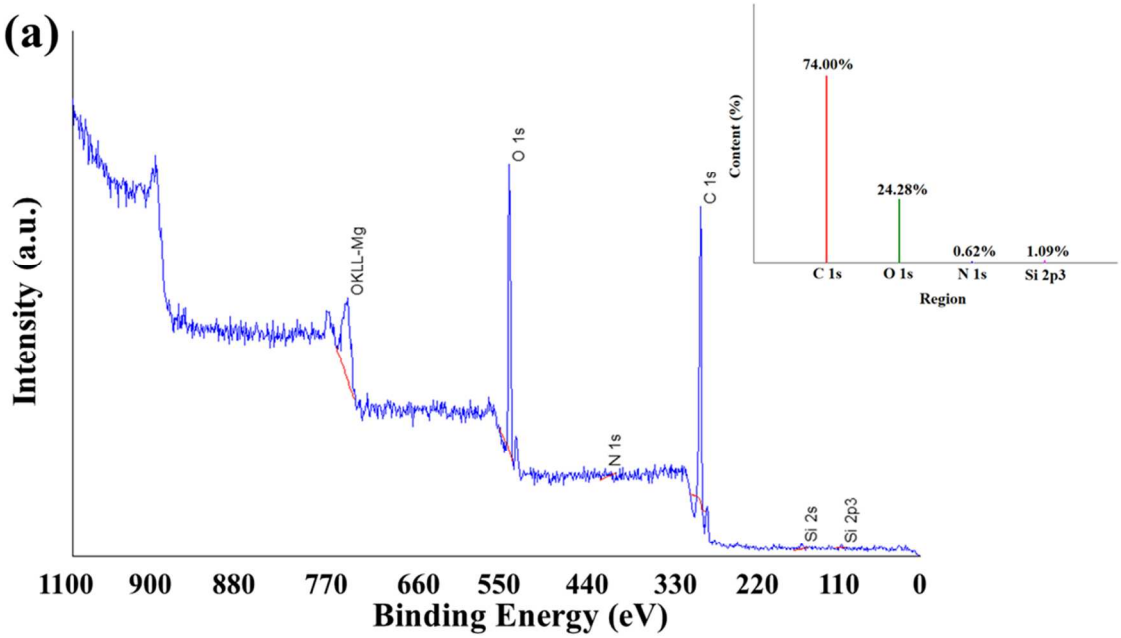


Figure S4. TGA curves of (a) MMP and (b) MP.



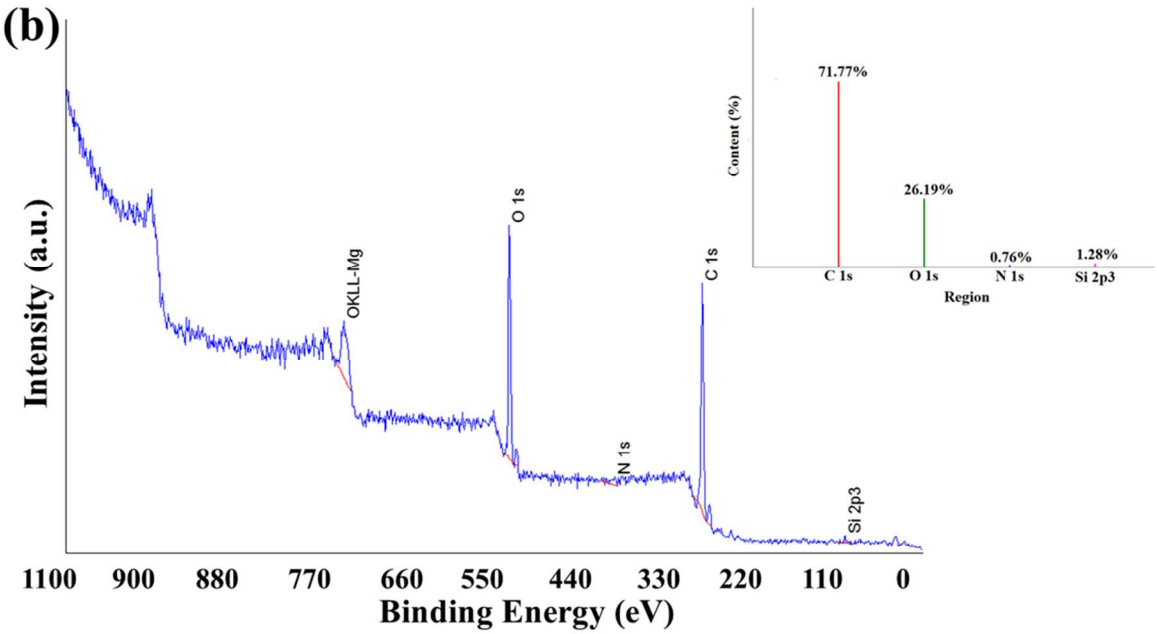


Figure S5. XPS patterns of the (a) MMP (Inset: the elemental analysis of the MMP) and (b) MP (Inset: the elemental analysis of the MP).

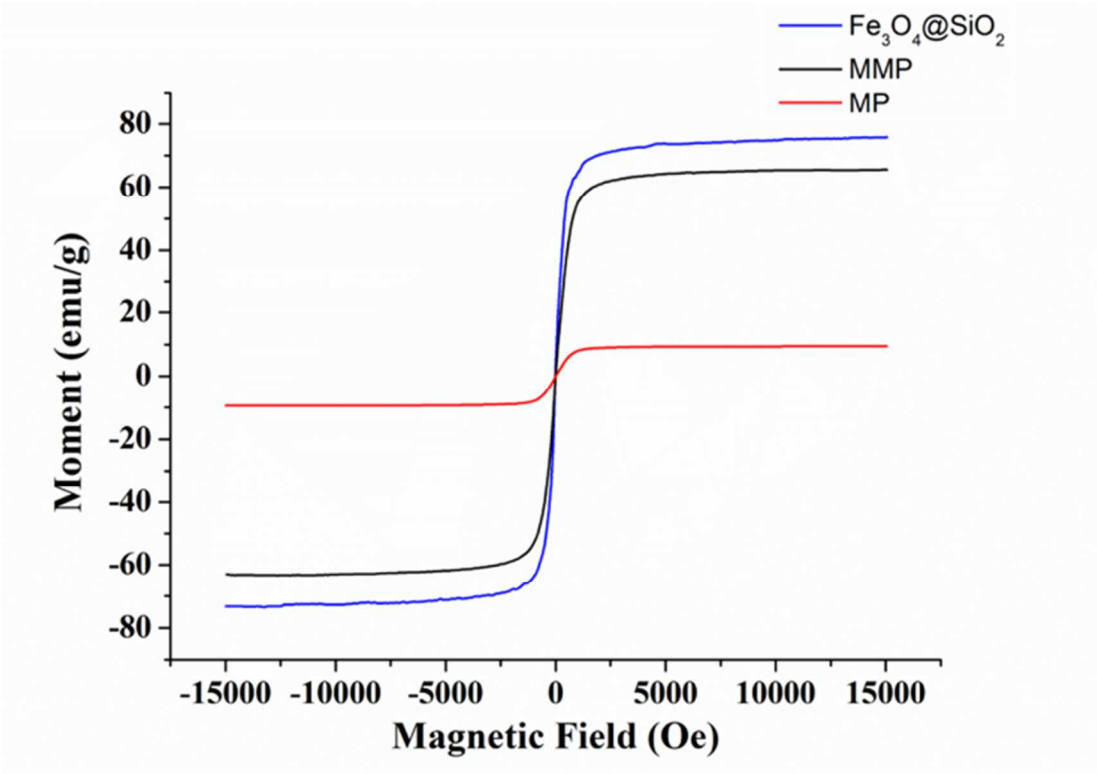


Figure S6. Magnetic hysteresis curves of Fe_3O_4@SiO_2, MMP and MP.

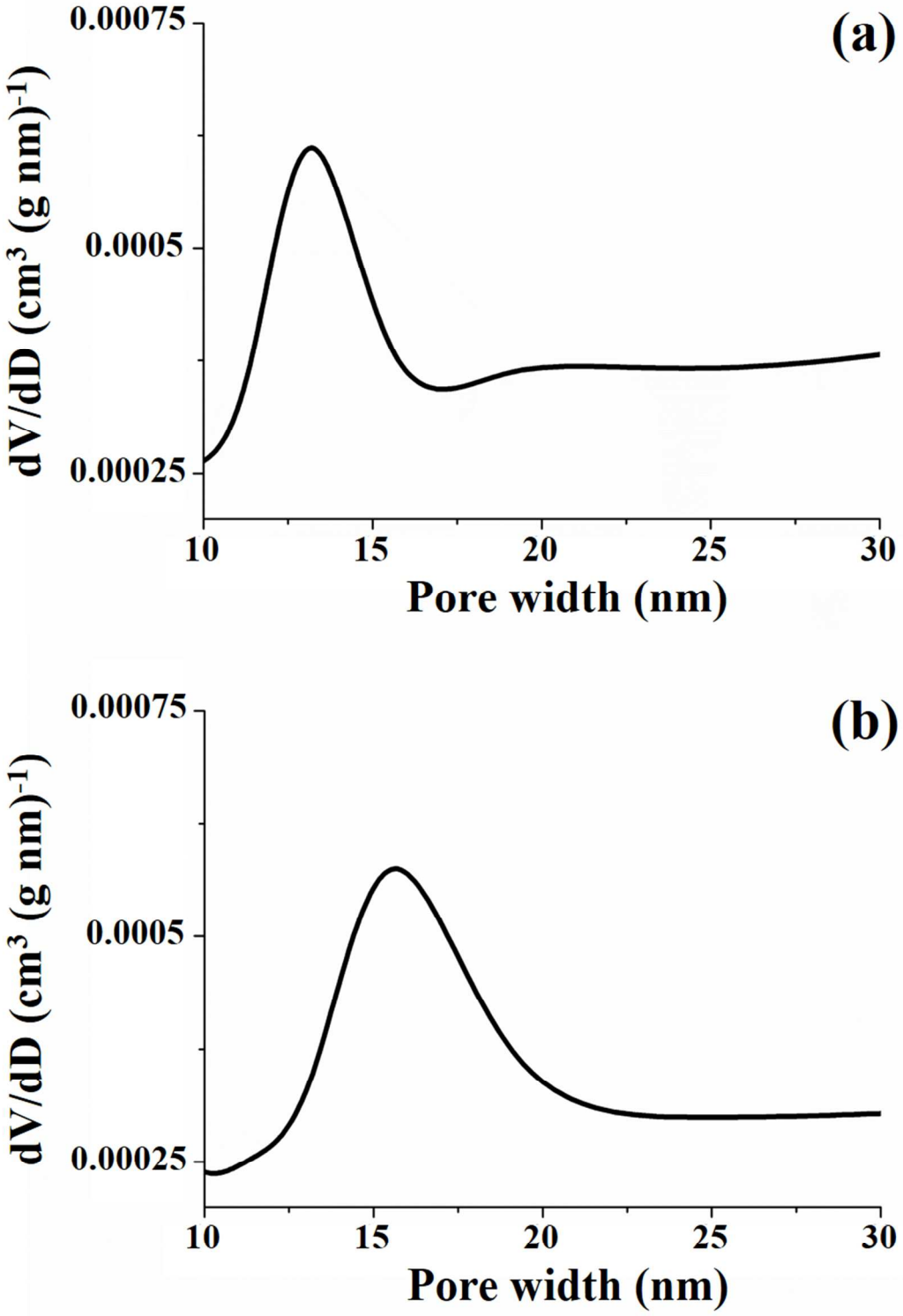


Figure S7. The pore size distribution (PSD) of MMP (a) concentrated at 13.2 nm and MP (b) concentrated at 15.6 nm.

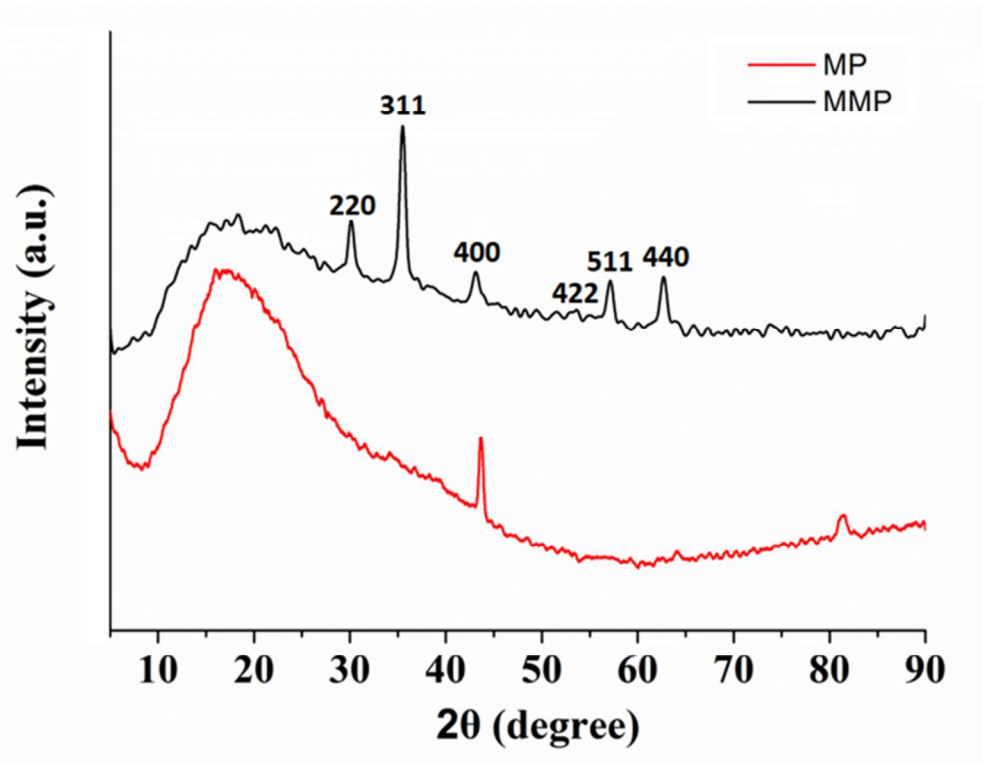


Figure S8. PXRD patterns of the MMP and MP.

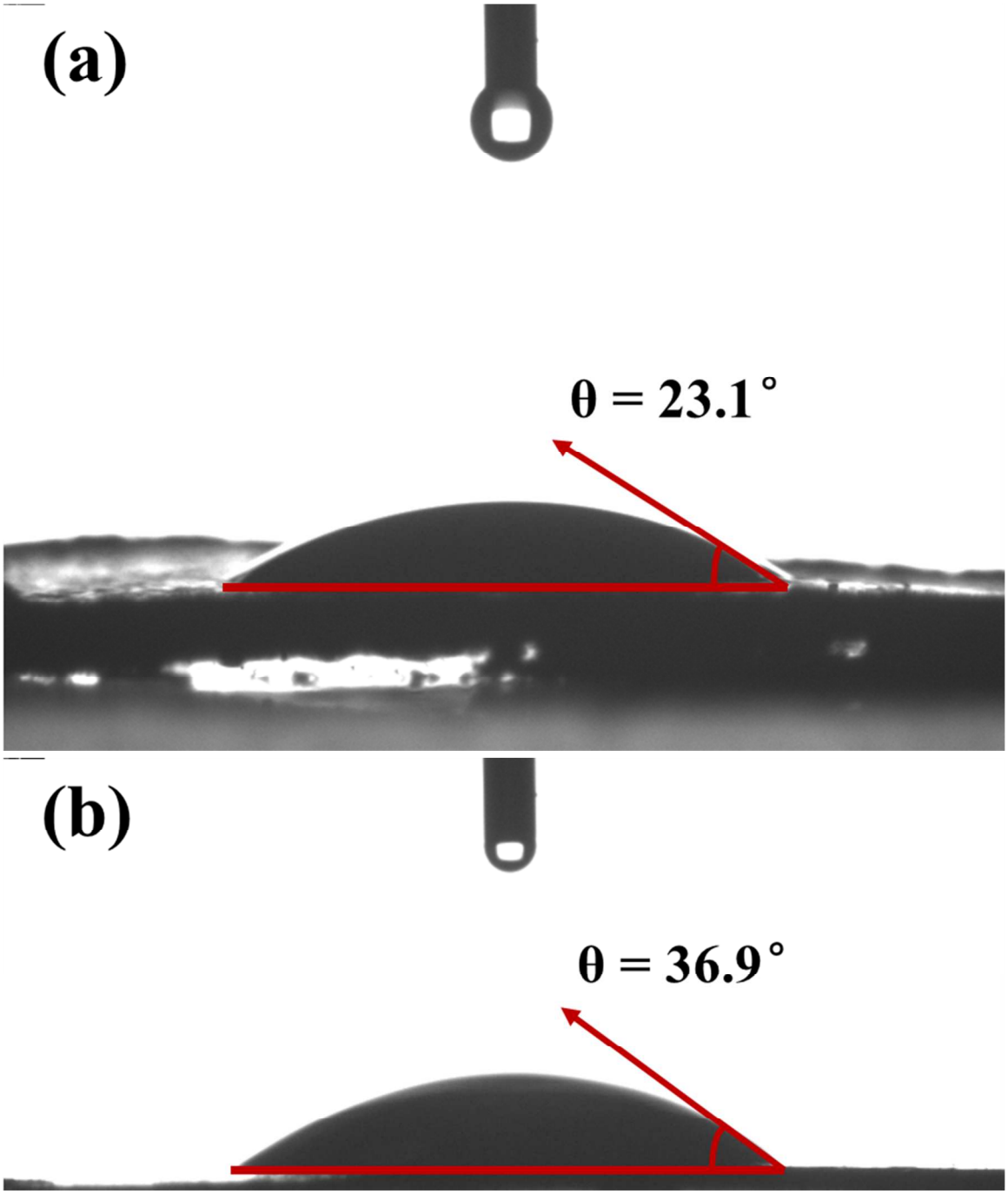


Figure S9. Water contact angles of (a) MP and (b) MMP.

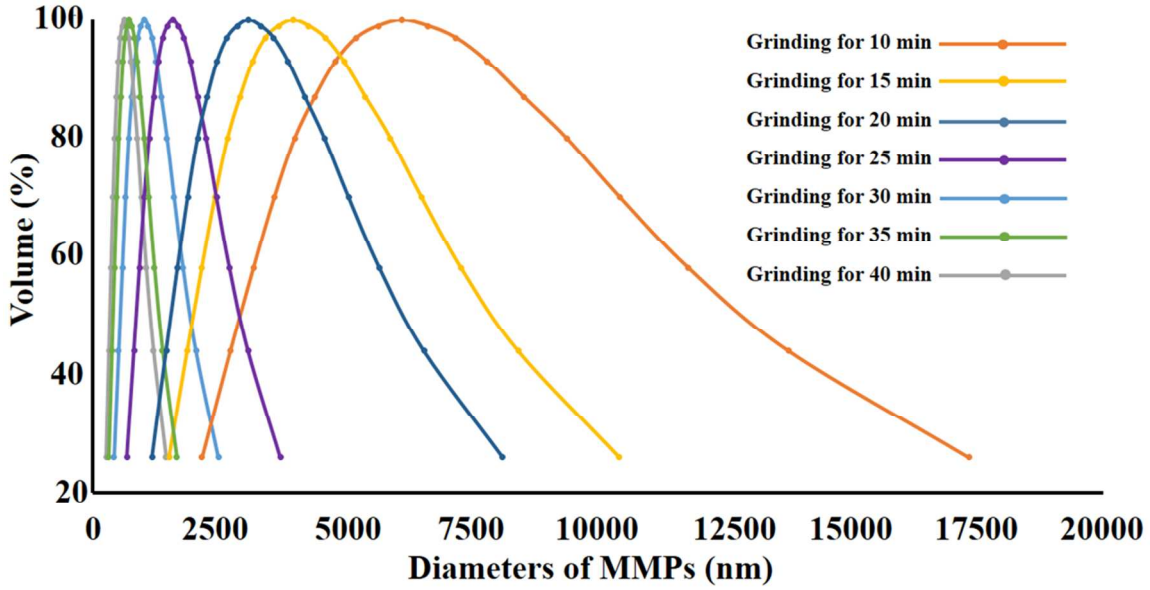


Figure S10. Dynamic light scattering (DLS) detections of MMPs with different grinding time.

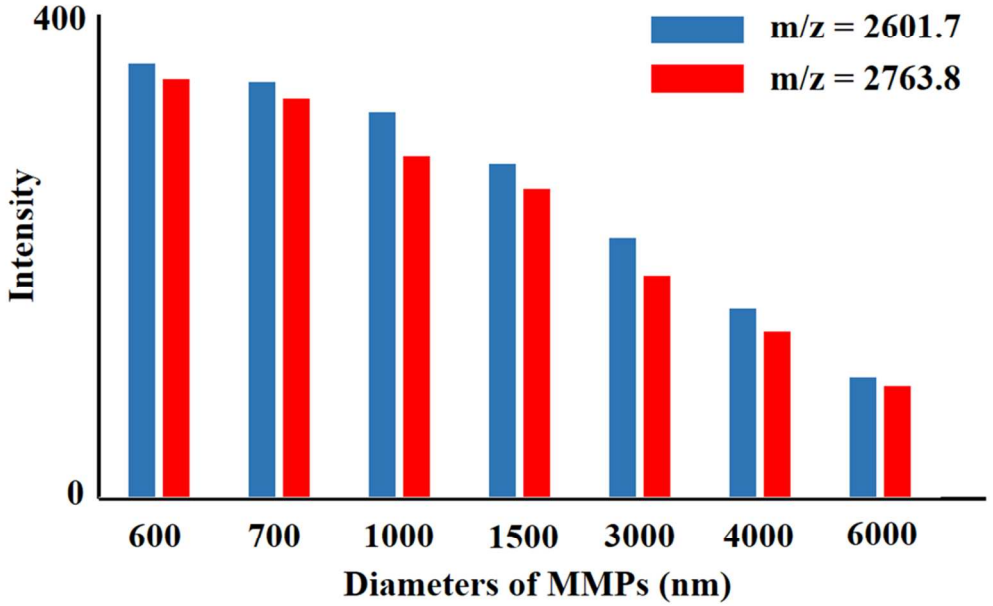


Figure S11. The MS intensities of two selected glycopeptides from tryptic digests of human IgG (3 μg) after enrichment with different size distributions of MMPs.

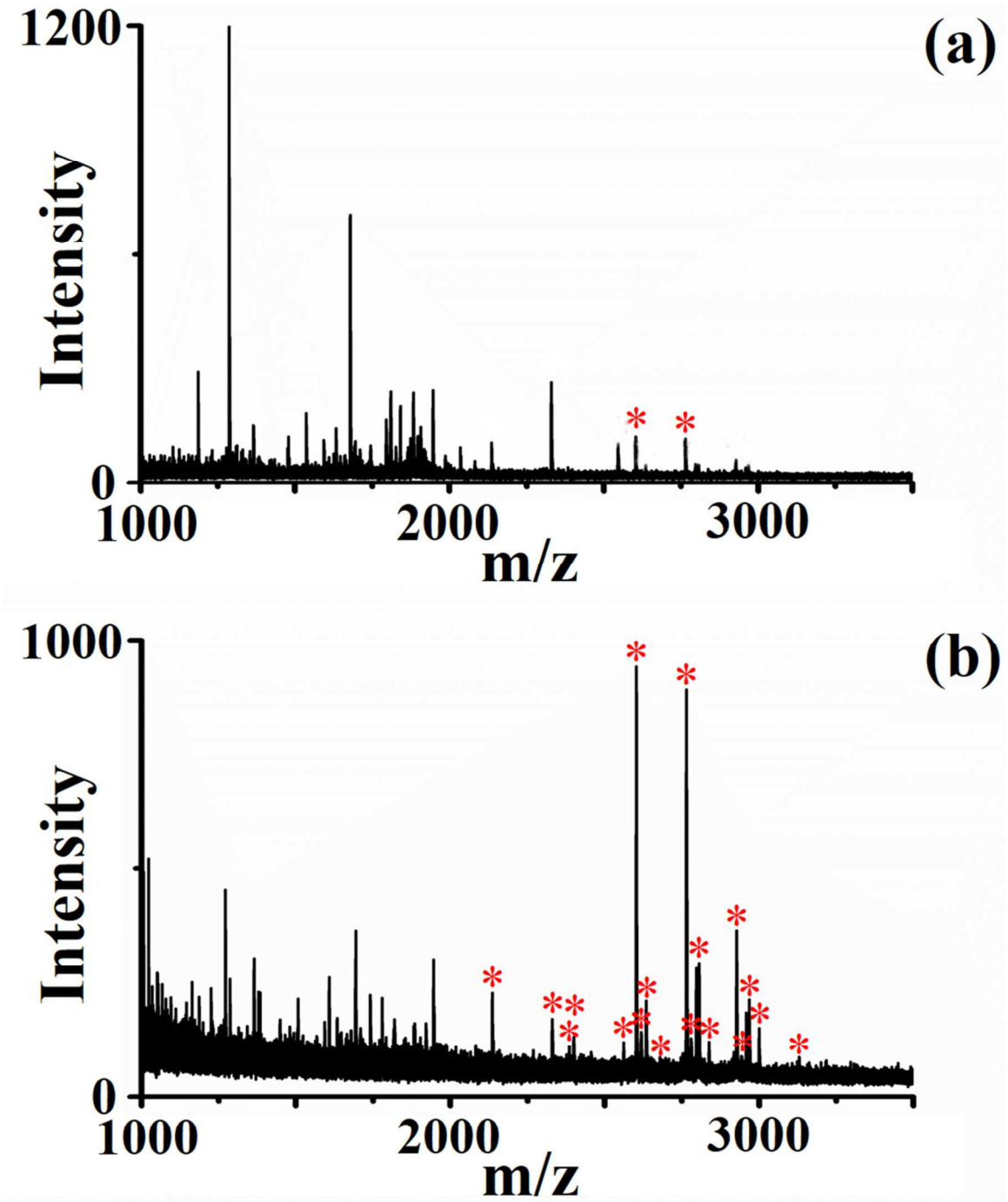


Figure S12. MALDI mass spectra of the tryptic digest human IgG without (a) or with MMP (b) enrichment. The m/z ranges from 1000 to 3500.The glycopeptides are marked with "*".

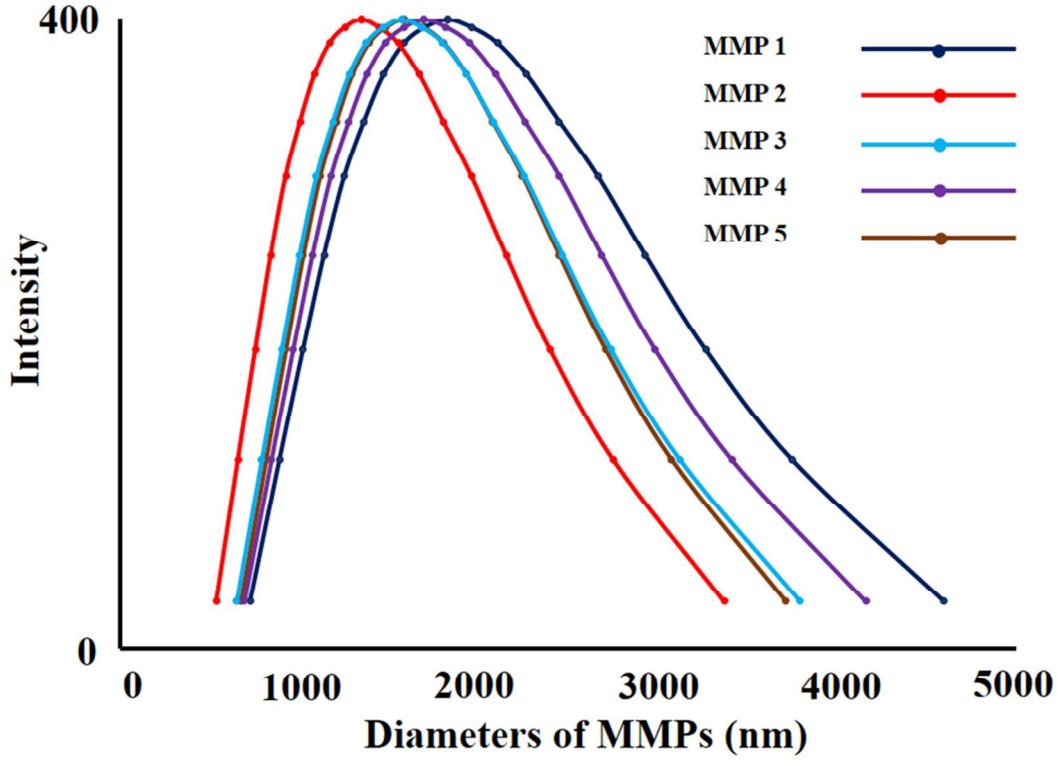


Figure S13. Size distributions reproducibility of 5 batches of MMPs grinded for 25 min.

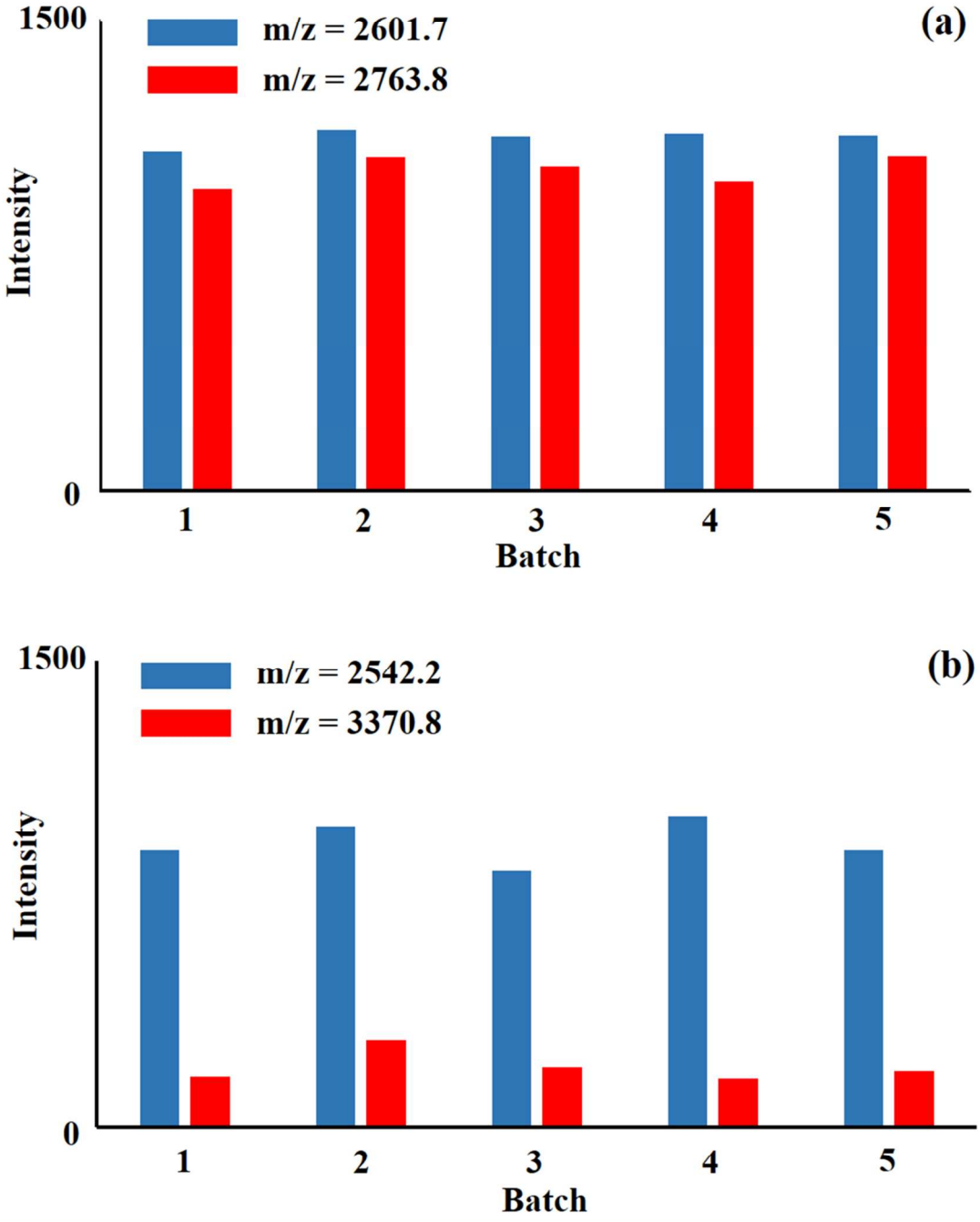


Figure S14. The enrichment reproducibility of 5 batches MMPs: MS intensity of four selected glycopeptides from tryptic digests of (a) human IgG (5 μg) and (b) HRP (5 μg).

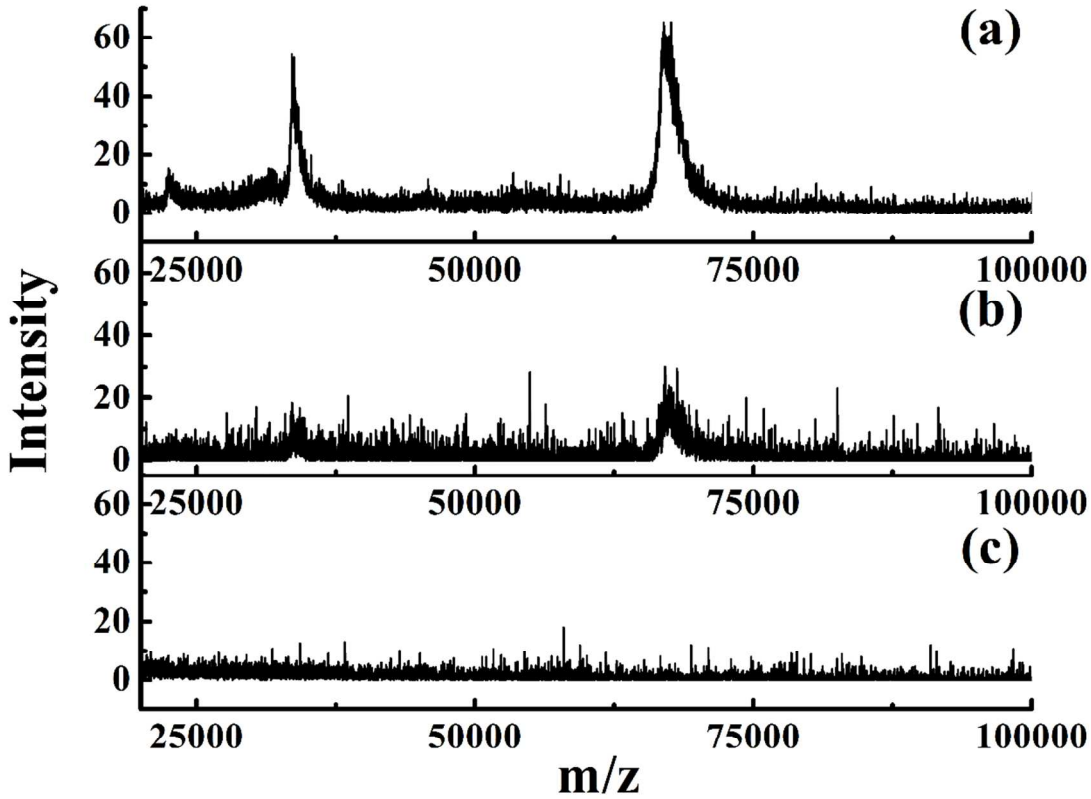


Figure S15. MALDI-MS of (a) the mixture of BSA proteins and tryptic digest of human IgG (BSA: IgG = 50:1), (b) the supernatant of the mixture after enrichment, (c) the elution of the mixture after enrichment.

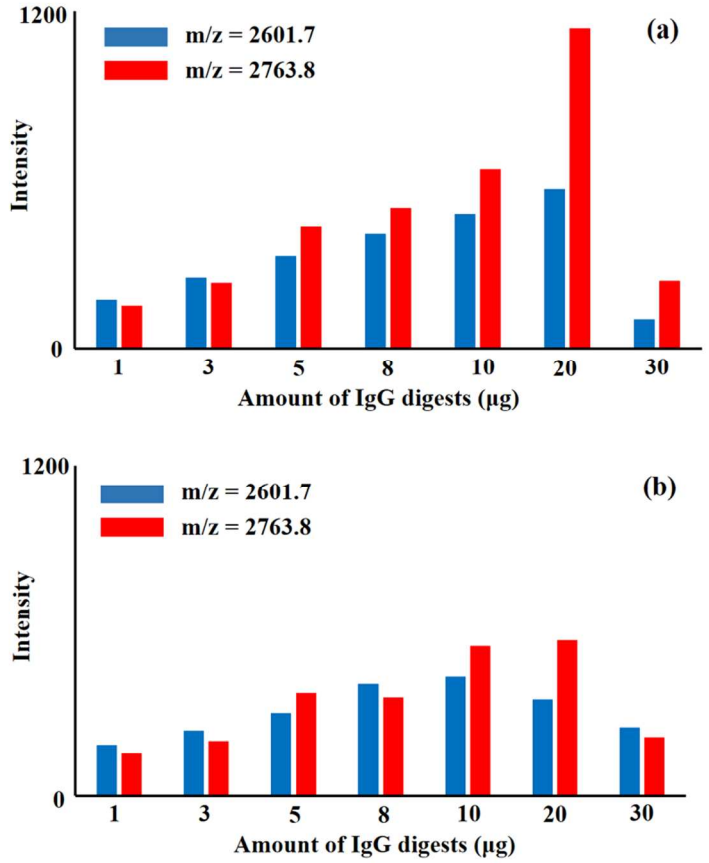


Figure S16. The MS intensities of two selected glycopeptides from different amounts of tryptic digests of human IgG after enrichment with MMP (50 μg).

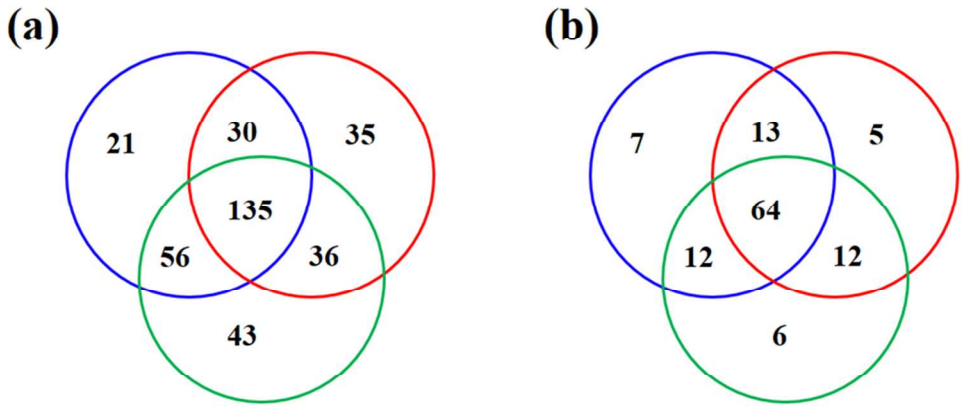


Figure S17. The analysis of 0.35 μL tryptic digests from human serum enriched by 100 μg MMP in three replicate analyses. Venn diagrams of identified (a) glycopeptide and (b) glycoprotein number.

Table S1. Detailed information of the glycopeptides enriched by MMP from human IgG tryptic digest. N* denotes the N-linked glycosylation site.

No	Observed m/z	Glycan composition	Amino acid sequence
1	2236.7	[Hex]3[HexNAc]2[Fuc]1	EEQFN*STFR
2	2398.7	[Hex]3[HexNAc]3[Fuc]1	EEQFN*STFR
3	2413.8	[Hex]3[HexNAc]3[Fuc]1	EEQFN*STFR
4	2431.7	[Hex]3[HexNAc]3[Fuc]1	EEQYN*STYR
5	2472.8	[Hex]3[HexNAc]4	EEQFN*STYR
6	2487.7	[Hex]3[HexNAc]4	EEQYN*STYR
7	2560.8	[Hex]4[HexNAc]3[Fuc]1	EEQFN*STFR
8	2593.7	[Hex]4[HexNAc]3[Fuc]1	EEQYN*STYR

9	2601.7	[Hex]4[HexNAc]4[Fuc]1	EEQFN*STFR
10	2618.7	[Hex]4[HexNAc]4[Fuc]1, or [Hex]4[HexNAc]4	EEQFN*STYR, or EEQFN*STFR
11	2633.7	[Hex]4[HexNAc]4[Fuc]1, or [Hex]4[HexNAc]4	EEQYN*STYR, or EEQFN*STYR
12	2649.7	[Hex]4[HexNAc]4	EEQYN*STYR
13	2763.8	[Hex]4[HexNAc]4[Fuc]1	EEQFN*STFR
14	2783.8	[Hex]4[HexNAc]4[Fuc]1, or [Hex]5[HexNAc]4	EEQFN*STYR, or EEQFN*STFR
15	2795.7	[Hex]4[HexNAc]4[Fuc]1, or [Hex]5[HexNAc]4	EEQYN*STYR, or EEQFN*STYR

16	2804.8	[Hex]3[HexNAc]5[Fuc]1	EEQFN*STFR
17	2811.7	[Hex]4[HexNAc]4[Fuc]1	EEQYN*STYR
18	2836.8	[Hex]3[HexNAc]5[Fuc]1, or [Hex]4[HexNAc]5	EEQYN*STYR or EEQFN*STYR
19	2852.8	[Hex]4[HexNAc]5	EEQYN*STYR
20	2925.8	[Hex]5[HexNAc]4[Fuc]1	EEQFN*STFR
21	2944.8	[Hex]5[HexNAc]4[Fuc]1	EEQFN*STYR
22	2957.8	[Hex]5[HexNAc]4[Fuc]1	EEQYN*STYR
23	2966.8	[Hex]4[HexNAc]5[Fuc]1	EEQFN*STFR
24	2982.0	[Hex]4[HexNAc]5[Fuc]1, or [Hex]5[HexNAc]5	EEQFN*STYR, or

			EEQFN*STFR
25	2998.8	[Hex]4[HexNAc]5[Fuc]1, or [Hex]5[HexNAc]5	EEQYN*STYR, or EEQFN*STYR
26	3014.9	[Hex]5[HexNAc]5	EEQYN*STYR
27	3129.9	[Hex]5[HexNAc]5[Fuc]1	EEQFN*STFR
28	3160.8	[Hex]5[HexNAc]5[Fuc]1	EEQYN*STYR

Table S2 Detailed information of the glycopeptides enriched by MMP from HRP tryptic digest. N* denotes the N-linked glycosylation site.

No	Observed m/z	Glycan composition	Amino acid sequence
1	2288.0	XylMan2GlcNAc2	SILLDN*TTSFR
2	2319.0	Man2GlcNAc2	MGN*ITPLTGTQGQIR
3	2531.2	FucGlcNAc	SFAN*STQTFFNAFVEAMDR
4	2542.2	XylMan3FucGlcNAc2	SSPN*ATDTIPLVR
5	2592.2	XylMan3FucGlcNAc2	PTLN*TTYLQTLR
6	3073.6	FucGlcNAc	LHFHDCFVNGCDASILLDN*TTSFR
7	3089.6	XylMan3FucGlcNAc2	GLCPLNGN*LSALVDFDLR
8	3370.8	XylMan3FucGlcNAc2	SFAN*STQTFFNAFVEAM*DR

9	3525.1	XylMan3GlcNAc2	GLIQSDQELFSSPN*ATDTIPLVR
10	3541.2	Man3FucGlcNAc2	GLIQSDQELFSSPN*ATDTIPLVR
11	3608.2	XylMan3FucGlcNAc2	NQCRGLCPLNGN*LSALVDFDLR
12	3673.3	XylMan3FucGlcNAc2	GLIQSDQELFSSPN*ATDTIPLVR
13	3895.4	XylMan3FucGlcNAc2	LHFHDCFVNGCDASILLDN*TTSFR
14	4058.5	XylMan3GlcNAc2	QLTPTFYDNSC(AAVESACPR)PN*VSNIVRH_2O
15	4221.7	XylMan3FucGlcNAc2	QLTPTFYDNSC(AAVESACPR)PN*VSNIVR
16	4721.3	Man3FucGlcNAc2, Man3FucGlcNAc2	LYN*FSNTGLPDPTLN*TTYLQTLR

17	4822.3	XylMan2FucGlcNAc2, XylMan2GlcNAc2	LYN*FSNTGLPDPTLN*TTYLQTLR
18	4839.5	XylMan3FucGlcNAc2, XylMan3GlcNAc2	LYN*FSNTGLPDPTLN*TTYLQTLR
19	4854.4	Man3FucGlcNAc2, XylMan3FucGlcNAc2	LYN*FSNTGLPDPTLN*TTYLQTLR
20	4985.6	XylMan3FucGlcNAc2, XylMan3FucGlcNAc2	LYN*FSNTGLPDPTLN*TTYLQTLR

Table S3. The recovery yields of six synthesized standard glycopeptides using MMP and MP. N* denotes the N-linked glycosylation site.

Numbers	Observed m/z	Oligosaccharides sequences	Peptides sequences	Recovery of MMP %	Recovery of MP %
1	2183.25	$GalGlcNAcMan_3GlcNAc$	LLNINPN*K	95.71±5.68	98.46±14.77
2	2578.61	$GalGlcNAc_2Man_3GlcNAc$	VQPFN*VTQGK	70.18±16.03	75.62±13.94
3	2782.80	$Gal_2GlcNAc_2Man_3GlcNAc$	GHTLTLN*FTR	89.29±9.84	90.06±1.54
4	2780.69	$Gal_2GlcNAc_2Man_3GlcNAc$	EEQFN*STFR	83.20±6.42	82.55±5.69
5	3715.83	$Sia_2Gal_2GlcNAc_2Man_3GlcNAc$	NVN*ISYTVNDSFFPQRPQK	96.66±12.52	95.05±13.74
6	3715.83	$Sia_2Gal_2GlcNAc_2Man_3GlcNAc$	NVNISYTVN*DSFFPQRPQK	97.23±2.93	102.64±0.33

Table S4. Detailed information of the observed N-glycopeptides obtained from tryptic digests of human serum of 25 nL.

Number	Accessions	Sequences	Scores
1	SP|P01023| A2MG_HUMAN	GcVLLSYLNETVTVSASLESVR	85.79
2	SP|P01023| A2MG_HUMAN	VSNQTLSLFFTVLQDVPVR	75.96
3	SP|P01009| A1AT _HUMAN	YLGNATAIFFLPDEGK	69.85
4	SP|P01009| A1AT _HUMAN	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	68.53
5	SP|P01009| A1AT _HUMAN	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	68.53
6	SP|P01009| A1AT _HUMAN	LYHSEAFTVNFGDTEEAKK	47.06
7	SP|P01009| A1AT _HUMAN	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	44.81
8	SP|P01834| IGKC _HUMAN	VDNALQSGNSQESVTEQDSK	32.86
9	SP|Q86W47| KCMB4_HUMAN	GTSQYPcVQVYVNNSESNSR	24.29
10	SP|P01859| IGHG2_HUMAN	EEQFNSTFR	45.29
11	SP|P0C0L4| CO4A _HUMAN	FSDGLE NSSTQFEVK	67.11
12	SP|P00738| HPT _HUMAN	NLFLNHSENATAK	47.27
13	SP|P00738| HPT _HUMAN	NLFLNHSENATAK	47.27
14	SP|P00738| HPT _HUMAN	VVLHPNYSQVDIGLIK	25.57
15	SP|P01857| IGHG1 _HUMAN	EEQYNSTYR	16.64
16	SP|P02765| FETUA _HUMAN	AALAAFNAQNNGSNFQLEEISR	31.03

Table S5. Detailed information of the observed N-glycopeptides identified in three replicate analyses of tryptic digests of human serum of 0.35 μL.

Numbers	Accessions	Sequences	Scores
1	SP|P02768|ALBU_HUMAN	YICENQDSISSK	18.13
2	SP|P02768|ALBU_HUMAN	YICENQDSISSKLK	53.52
3	SP|P02787|TRFE_HUMAN	CDEWSVNSVGK	37.28
4	SP|P02787|TRFE_HUMAN	LKCDEWSVNSVGK	44.11
5	SP|P02787|TRFE_HUMAN	LCMGSGLNLCEPNNK	99.35
6	SP|P02787|TRFE_HUMAN	INHCRFDEFFSEGCAPGSK	45.91
7	SP|P02787|TRFE_HUMAN	QQQHLFGSNVTDCSGNFCLFR	41.08
8	SP|P02787|TRFE_HUMAN	ILRQQQHLFGSNVTDCSGNFCLFR	56
9	SP|P02787|TRFE_HUMAN	LCMGSGLNLCEPNNKEGYYGYTGAFR	14.66
10	SP|P02787|TRFE_HUMAN	CDEWSVNSVGKIECVSAETTEDCIAK	80.04
11	SP|P02787|TRFE_HUMAN	AVANFFSGSCAPCADGTDFPQLCQLCPGCGCSTLNQYFGYSGAFK	26
12	SP|P01023|A2MG_HUMAN	TEVSSNHVLIYLDK	61.28
13	SP|P01023|A2MG_HUMAN	SSSNEEVMFLTVQVK	39.61
14	SP|P01023|A2MG_HUMAN	VSNQTLSLFFTVLQDVPVR	16.75
15	SP|P01023|A2MG_HUMAN	GCVLLSYLNETVTVSASLESVR	81.01
16	SP|P01023|A2MG_HUMAN	SSSNEEVMFLTVQVKGPTQEFK	20.63
17	SP|P01023|A2MG_HUMAN	SLGNVNFTVSAEALESQELCGTEVPSVPEHGR	88
18	SP|P01023|A2MG	SLGNVNFTVSAEALESQELCGTEVPSVPEH	26.74

	_HUMAN	GRK	
19	SP|P01023|A2MG_HUMAN	HNVYINGITYTPVSSTNEKDMYSFLEDMGLK	26.41
20	SP|P01023|A2MG_HUMAN	TEVSSNHVLIYLDKVSNQTLSLFFTVLQDVPVR	79.12
21	SP|P02765|FETUA_HUMAN	AALAAFNAQNNGSNFQLEEISR	109.39
22	SP|P02765|FETUA_HUMAN	HTLNQIDEVKVWPQQPSGELFEIEIDTLETTCHVLDPTPVAR	120.57
23	SP|P01876|IGHA1_HUMAN	LAGKPTHVNVSVVMAEVDGTCY	27.8
24	SP|P01876|IGHA1_HUMAN	TIDRLAGKPTHVNVSVVMAEVDGTCY	14.21
25	SP|P01876|IGHA1_HUMAN	LSLHRPALEDLLLGSEANLTCTLTGLR	40.89
26	SP|P02774|VTDB_HUMAN	LCDNLSTK	15.25
27	SP|P02774|VTDB_HUMAN	GQELCADYSENTFTEYK	66.35
28	SP|P02774|VTDB_HUMAN	SLGECCDVEDSTTCFNAK	62.23
29	SP|P02774|VTDB_HUMAN	ELSSFIDKGQELCADYSENTFTEYK	37.55
30	SP|P02774|VTDB_HUMAN	SDFASNCCSINSPPLYCDSEIDAELK	64.43
31	SP|P02774|VTDB_HUMAN	RSDFASNCCSINSPPLYCDSEIDAELK	102.61
32	SP|P02774|VTDB_HUMAN	EYANQFMWEYSTNYGQAPLSLLVSYTK	85.39
33	SP|P02774|VTDB_HUMAN	SDFASNCCSINSPPLYCDSEIDAELKNIL	53.25
34	SP|P01834|IGKC_HUMAN	SFNRGEC	22.21
35	SP|P01834|IGKC_HUMAN	VDNALQSGNSQESVTEQDSK	77.51
36	SP|P01834|IGKC_HUMAN	VQWKVDNALQSGNSQESVTEQDSK	108.03
37	SP|P01834|IGKC_HUMAN	VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK	25.79
38	SP|P01871|IGHM_	GLTFQQNASSMCVPDQDTAIR	45.22

	HUMAN		
39	SP|P01871|IGHM_HUMAN	STGKPTLYNVSLVMSDTAGTCY	23.76
40	SP|P01871|IGHM_HUMAN	TVDKSTGKPTLYNVSLVMSDTAGTCY	77.13
41	SP|P08603|CFAH_HUMAN	SSNLIILEEHLK	42.4
42	SP|P08603|CFAH_HUMAN	MDGASNVTCINSR	17.53
43	SP|P08603|CFAH_HUMAN	ISEENETTCYMGK	20.14
44	SP|P08603|CFAH_HUMAN	SCDNPYIPNGDYSPLR	15.37
45	SP|P08603|CFAH_HUMAN	DTSCVNPPTVQNAYIVSR	59.01
46	SP|P08603|CFAH_HUMAN	IPCSQPPQIEHGTINSSR	14.58
47	SP|P08603|CFAH_HUMAN	SPYEMFGDEEVMCLNGNWTEPPQCK	46.36
48	SP|P08603|CFAH_HUMAN	CGPPPPIDNGDITSFPLSVYAPASSVEYQCQNLYQLEGNKR	13.44
49	SP|P00450|CERU_HUMAN	ENLTAPGSDSAVFFEQGTTR	65.48
50	SP|P00450|CERU_HUMAN	ELHHLQEQNVSNAFLDKGEFYIGSK	20.02
51	SP|P00450|CERU_HUMAN	DVDKEFYLFPTVFDENESLLLEDNIR	98.87
52	SP|P00450|CERU_HUMAN	GDSVVWYLFSAGNEADVHGIYFSGNTYLWR	21.04
53	SP|P00450|CERU_HUMAN	NLASRPYTFHSHGITYYKEHEGAIYPDNTTDFQR	35.42
54	SP|P00450|CERU_HUMAN	DTANLFPQTSLTLHMWPDTEGTFNVECLTTDHYTGGMK	42.25
55	SP|P00450|CERU_HUMAN	HYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTR	26.18
56	SP|P0C0L5|CO4B_HUMAN	GLNVTLSSTGR	39.28
57	SP|P0C0L5|CO4B_HUMAN	TTNIQGINLLFSSR	99.57
58	SP|P0C0L5|CO4B	FSDGLESNSSTQFEVK	13.7

	_HUMAN		
59	SP|P0C0L5|CO4B _HUMAN	FSDGLESNSSTQFEVKK	25.98
60	SP|P0C0L5|CO4B _HUMAN	LQETSNWLLSQQQADGSFQDLSPVIHR	92.29
61	SP|P0C0L5|CO4B _HUMAN	VLSLAQEQVGGSPEKLQETSNWLLSQQQA DGSFQDLSPVIHR	35.72
62	SP|P0C0L4|CO4A _HUMAN	LQETSNWLLSQQQADGSFQDPCPVLDR	82.87
63	SP|P00738|HPT_H UMAN	VVLHPNYSQVDIGLIK	17.7
64	SP|P00738|HPT_H UMAN	MVSHHNLTTGATLINEQWLLTTAK	36
65	SP|P02790|HEMO _HUMAN	SWPAVGNCSSALR	13.93
66	SP|P02790|HEMO _HUMAN	ERSWPAVGNCSSALR	23.14
67	SP|P02790|HEMO _HUMAN	ALPQPQNVTSLLGCTH	25.25
68	SP|P02790|HEMO _HUMAN	CSDGWSFDATTLDDNGTMLFFK	49.23
69	SP|P02790|HEMO _HUMAN	SLGPNSCSANGPGLYLIHGPNLYCYSDVEK	40.22
70	SP|P02790|HEMO _HUMAN	SLGPNSCSANGPGLYLIHGPNLYCYSDVEKL NAAK	64.43
71	SP|P19823|ITIH2_ HUMAN	GAFISNFSMTVDGK	18.21
72	SP|P19823|ITIH2_ HUMAN	VVNNSPQPQNVVFDVQIPK	77.27
73	SP|P19823|ITIH2_ HUMAN	ENIQDNISLFSLGMGFDVDYDFLKR	46.09
74	SP|P19823|ITIH2_ HUMAN	SILQMSLDHHIVTPLTSLVIENEAGDER	26.29
75	SP|P19823|ITIH2_ HUMAN	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVV AGK	26.18
76	SP|P05155|IC1_H UMAN	VLSNNSDANLELINTWVAK	17.16
77	SP|P05155|IC1_H UMAN	VGQLQLSHNLSLVILVPQNLK	22.63
78	SP|P00747|PLMN	FSPATHPSEGLEENYCR	95.73

	_HUMAN		
79	SP|P02751|FINC_ HUMAN	QDGHLWCSTTSNYEQDQK	111.9
80	SP|P02751|FINC_ HUMAN	RPGGEPSPEGTTGQSYNQYSQR	138.76
81	SP|P02751|FINC_ HUMAN	SYTITGLQPGTDYKIYLYTLNDNAR	39.85
82	SP|P02751|FINC_ HUMAN	GFNCESKPEAEETCFDKYTGNTYR	26.03
83	SP|P01008|ANT3_ HUMAN	LVSANRLFGDK	26.48
84	SP|P01008|ANT3_ HUMAN	SLTFNETYQDISELVYGAK	57.08
85	SP|P01008|ANT3_ HUMAN	LGACNDTLQQLMEVFKFDTISEK	76.93
86	SP|P01008|ANT3_ HUMAN	LFGDKSLTFNETYQDISELVYGAK	44.98
87	SP|P01042|KNG1_ HUMAN	YNSQNQSNNQFVLYR	24.96
88	SP|P01042|KNG1_ HUMAN	KYNSQNQSNNQFVLYR	35.5
89	SP|P01042|KNG1_ HUMAN	SLWNGDTGECTDNAYIDIQLR	28.54
90	SP|P01042|KNG1_ HUMAN	IASFSQNCDIYPGKDFVQPPTK	40.43
91	SP|P01042|KNG1_ HUMAN	HGIQYFNNNTQHSSLFMLNEVK	26.66
92	SP|P01042|KNG1_ HUMAN	ITYSIVQTNCSKENFLFLTPDCK	24.2
93	SP|P04004|VTNC _HUMAN	NNATVHEQVGGPSLTSDLQAQSK	89.71
94	SP|P04004|VTNC _HUMAN	NISDGFDGIPDNVDAALALPAHSYSGR	49.11
95	SP|P04004|VTNC _HUMAN	FEDGVLDPDYPRNISDGFDGIPDNVDAALA LPAHSYSGR	32.2
96	SP|P04003|C4BPA _HUMAN	SHSTQTLTCNSDGEWVYNTFCIYK	123.11
97	SP|P04003|C4BPA _HUMAN	SRPANHCVYFYGDEISFSCHETSR	33.65
98	SP|P04003|C4BPA	KSRPANHCVYFYGDEISFSCHETSR	44.25

	_HUMAN		
99	SP|P04003|C4BPA _HUMAN	SHSTQTLTCNSDGEWVYNTFCIYKR	92.45
100	SP|P04003|C4BPA _HUMAN	FSLLGHASISCTVENETIGVWRPSPPTCEK	21.71
101	SP|P04003|C4BPA _HUMAN	LSVDKDQYVEPENVTIQCDSGYGVVGPQSI TCSGNR	39.77
102	SP|P00751|CFAB_ HUMAN	VSEADSSNADWVTK	61.48
103	SP|P00751|CFAB_ HUMAN	FLCTGGVSPYADPNTCR	94.64
104	SP|P00751|CFAB_ HUMAN	SPYYNVSDEISFHCYDGYTLR	44.35
105	SP|P00751|CFAB_ HUMAN	WSGQTAICDNGAGYCSNPGIPIGTR	83.04
106	SP|P00751|CFAB_ HUMAN	WSGQTAICDNGAGYCSNPGIPIGTRK	69.99
107	SP|O43866|CD5L_ HUMAN	LVGGDNLCSGR	30.59
108	SP|O43866|CD5L_ HUMAN	EATLQDCPSGPWGKNTCNHDEDTWVECED PFDLR	27.07
109	SP|P19827|ITIH1_ HUMAN	FAHYVVTSQVVNTANEAR	122.96
110	SP|P19827|ITIH1_ HUMAN	ANLSSQALQMSLDYGFVTPLTSMSIR	27.54
111	SP|P02649|APOE_ HUMAN	VQAAVGTSAAPVPSDNH	90.51
112	SP|P10909|CLUS_ HUMAN	EILSVDCSTNNPSQAK	77.15
113	SP|P10909|CLUS_ HUMAN	MLNTSSLLEQLNEQFNWVSR	70.09
114	SP|P04196|HRG_ HUMAN	VIDFNCTTSSVSSALANTK	89.41
115	SP|P04196|HRG_ HUMAN	VENTTVYYLVLDVQESDCSVLSR	45.32
116	SP|P04196|HRG_ HUMAN	IADAHLDRVENTTVYYLVLDVQESDCSVLS R	16.39
117	SP|P00734|THRB_ HUMAN	HQDFNSAVQLVENFCR	66.8
118	SP|P00734|THRB_	SEGSSVNLSPPLEQCVPDRGQQYQGR	54.08

	HUMAN		
119	SP|P02748|CO9_HUMAN	TSNFNAAISLK	36.97
120	SP|P02748|CO9_HUMAN	AVNITSENLIDDVVSLIR	77.73
121	SP|P02748|CO9_HUMAN	GTVIDVTDFVNWASSINDAPVLISQK	86.87
122	SP|P02748|CO9_HUMAN	QCVPTEPCEDAEDDCGNDFQCSTGR	92.2
123	SP|P02749|APOH_HUMAN	LGNWSAMPSCK	21.56
124	SP|P02749|APOH_HUMAN	YTTFEYPNTISFSCNTGFYLNGADSAK	37.13
125	SP|P01031|CO5_HUMAN	ANISHKDMQLGR	75.42
126	SP|P01031|CO5_HUMAN	MVETTAYALLTSLNLK	41.15
127	SP|P01031|CO5_HUMAN	YGGGFYSTQDTINAIEGLTEYSLLVK	149.8
128	SP|P06396|GELS_HUMAN	ATEVPVSWESFNNGDCFILDLGNNIHQWCGSNSNRYER	28.36
129	SP|P0DOY2|IGLC2_HUMAN	AGVETTTPSKQSNNK	72.19
130	SP|P0DOY2|IGLC2_HUMAN	QSNNKYAASSYLSLTPEQWK	50.08
131	SP|P10643|CO7_HUMAN	AASGTQNNVLR	22.6
132	SP|P10643|CO7_HUMAN	NVVYTCNEGYSLIGNPVAR	82.89
133	SP|P10643|CO7_HUMAN	INNDFNYEFYNSTWSYVK	40.17
134	SP|P27169|PON1_HUMAN	IFFYDSENPPASEVLR	68.73
135	SP|P27169|PON1_HUMAN	VVAEGFDFANGINISPDGK	17.19
136	SP|P27169|PON1_HUMAN	VTQVYAENGTVLQGSTVASVYK	58.5
137	SP|P27169|PON1_HUMAN	VTQVYAENGTVLQGSTVASVYKGK	52.92
138	SP|P27169|PON1_	IQNILTEEPKVTQVYAENGTVLQGSTVASVY	120.71

	HUMAN	K	
139	SP|P27169|PON1_HUMAN	FDVSSFNPHGISTFTDEDNAMYLLVVNHPDAK	90.27
140	SP|P01011|AACT_HUMAN	YTGNASALFILPDQDK	25.77
141	SP|P01011|AACT_HUMAN	FNLTETSEAEIHQSFQHLLR	25.72
142	SP|P01011|AACT_HUMAN	YTGNASALFILPDQDKMEEVEAMLLPETLK	43.29
143	SP|P05156|CFAI_HUMAN	LSDLSINSTECLHVHCR	22.53
144	SP|P05156|CFAI_HUMAN	ACDGINDCGDQSDELCCK	54.21
145	SP|P05156|CFAI_HUMAN	SIPACVPWSPYLFQPNDTCIVSGWGR	17.3
146	SP|Q96PD5|PGRP2_HUMAN	LEPVHLQLQCMSQEQLAQVAANATK	48.13
147	SP|Q96PD5|PGRP2_HUMAN	LYHFLLGAWSLNATELDPCPLSPELLGLTK	69.71
148	SP|Q96PD5|PGRP2_HUMAN	LEPVHLQLQCMSQEQLAQVAANATKEFTEAFLGCPAIHPR	61.78
149	SP|P04114|APOB_HUMAN	FNSSYLQGTNQITGR	54.25
150	SP|P04114|APOB_HUMAN	FEVDSPVYNATWSASLK	17.51
151	SP|P04114|APOB_HUMAN	KYTYNYEAESSSGVPGTADSR	130.54
152	SP|P04114|APOB_HUMAN	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	61.19
153	SP|P03952|KLKB1_HUMAN	IYSGILNLSDITK	14.95
154	SP|P03952|KLKB1_HUMAN	LQAPLNYTEFQKPICLPSK	29.82
155	SP|P03952|KLKB1_HUMAN	IYSGILNLSDITKDTPFSQIK	43.46
156	SP|P03952|KLKB1_HUMAN	IVGGTNSSWGEWPWQVSLQVK	20.01
157	SP|P02745|C1QA_HUMAN	SLGFCDTTNK	21.66
158	SP|P02745|C1QA_	NPPMGGNVVIFDTVITNQEEPYQNHSGR	20.86

	HUMAN		
159	SP|P02745|C1QA_HUMAN	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	21.51
160	SP|P07358|CO8B_HUMAN	QCNNPPPQNGGSPCSGPASETLDCS	28.35
161	SP|P43652|AFAM_HUMAN	DIENFNSTQK	13.32
162	SP|P43652|AFAM_HUMAN	FTDSENVCQER	67.43
163	SP|P43652|AFAM_HUMAN	EGKFTDSENVCQER	15.25
164	SP|P43652|AFAM_HUMAN	ELISLVEDVSSNYDGCCEGDVVQCIR	13.24
165	SP|P43652|AFAM_HUMAN	TYVPPPFSQDLFTFHADMCQSQNEELQR	66.38
166	SP|P43652|AFAM_HUMAN	IEFKELISLVEDVSSNYDGCCEGDVVQCIR	25.71
167	SP|Q14624|ITIH4_HUMAN	LAILPASAPPATSNPDPAVSR	14.12
168	SP|Q14624|ITIH4_HUMAN	LPTQNITFQTESSVAEQEAEFQSPK	29.22
169	SP|P00736|C1R_HUMAN	QRPPDLDTSSNAVDLLFFTDESGDSR	114.06
170	SP|P13671|CO6_HUMAN	QIVVDKYYQENFCEQICSK	64
171	SP|P01591|IGJ_HUMAN	ENISDPTSPLR	13.08
172	SP|P01591|IGJ_HUMAN	IIVPLNNRENISDPTSPLR	21.21
173	SP|P01591|IGJ_HUMAN	KCDPTEVELDNQIVTATQSNICDEDSATETCYTYDR	14.11
174	SP|P22792|CPN2_HUMAN	LGSLQELFLDSNNISELPPQVFSQLFCLER	65.35
175	SP|P05090|APOD_HUMAN	NILTSNNIDVK	39.44
176	SP|P05160|F13B_HUMAN	SGYLLHGSNEITCNR	37.89
177	SP|P05160|F13B_HUMAN	HGVIISSTVDTYENGSSVEYR	43.67
178	SP|P51884|LUM_	LHINHNNLTESVGPLPK	19.46

	HUMAN		
179	SP|P51884|LUM_HUMAN	AFENVTDLQWLILDHNLLENSK	45.03
180	SP|P51884|LUM_HUMAN	LSHNELADSGIPGNSFNVSSLVELDLSYNK	55.91
181	SP|P51884|LUM_HUMAN	NNQIDHIDEKAFENVTDLQWLILDHNLLENSK	14.54
182	SP|P09871|C1S_HUMAN	SSNNPHSPIVEEFQVPYNK	50.79
183	SP|P02763|A1AG1_HUMAN	SVQEIQATFFYFTPNKTEDTIFLR	49.82
184	SP|O95445|APOM_HUMAN	TELFSSSCPGGIMLNETGQGYQR	54.82
185	SP|P00748|FA12_HUMAN	TTLSGAPCQPWASEATYRNVTAEQAR	32.46
186	SP|P01624|KV315_HUMAN	ASQSVSSNLAWYQQKPGQAPR	61.3
187	SP|P07996|TSP1_HUMAN	VVNSTTGPGEHLR	57.3
188	SP|P07996|TSP1_HUMAN	FTGSQPFGQGVEHATANK	99.12
189	SP|P07996|TSP1_HUMAN	KVSCPIMPCSNATVPDGECCPR	22.04
190	SP|P08697|A2AP_HUMAN	MSLSSFSVNRPFLFFIFEDTTGLPLFVGSVRNPNPSAPR	35.86
191	SP|Q03591|FHR1_HUMAN	LQNNENNISCVER	21.32
192	SP|Q03591|FHR1_HUMAN	STDTSCVNPPTVQNAHILSR	19.4
193	SP|P02671|FIBA_HUMAN	QFTSSTSYNRGDSTFESK	20.49
194	SP|P35858|ALS_HUMAN	AGAFLGLTNVAVMNLSGNCLR	38.68
195	SP|P43251|BTD_HUMAN	NPVGLIGAENATGETDPSHSK	56.16
196	SP|Q9UGM5|FETUB_HUMAN	VLYLAAYNCTLRPVSK	19.9
197	SP|P49908|SEPP1_HUMAN	EGYSNISYIVVNHQGISSR	52.07
198	SP|P49908|SEPP1	VSEHIPVYQQEENQTDVWTLLNGSKDDFLI	34.33

	_HUMAN	YDR	
199	SP|Q96IY4|CBPB2_HUMAN	QVHFFVNASDVDNVK	16.8
200	SP|P00742|FA10_HUMAN	LSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTR	71.84
201	SP|A0A075B6I0|LV861_HUMAN	TLIYSTNTR	13.18
202	SP|P55058|PLTP_HUMAN	VSNVSCQASVSR	15.46
203	SP|P55058|PLTP_HUMAN	IYSNHSALESLALIPLQAPLK	15.46
204	SP|O75882|ATRN_HUMAN	VFHIHNESWVLLTPK	34.03
205	SP|O75882|ATRN_HUMAN	ISNSSDTVECECSENWKGEACDIPHCTDNCGFPHR	23.51
206	SP|P06276|CHLE_HUMAN	DNNSIITR	14.81
207	SP|P06276|CHLE_HUMAN	DNYTKAEEILSR	42.41
208	SP|P12259|FA5_HUMAN	NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR	22.85
209	SP|Q9NZP8|C1RL_HUMAN	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	50.46
210	SP|P09172|DOPO_HUMAN	SLEAINGSGLQMGLQR	36.69
211	SP|Q02985|FHR3_HUMAN	FVQGNSTEVACHPGYGLPK	23.17
212	SP|Q9Y6R7|FCGBP_HUMAN	YLPVNSSLLTSDCSER	29.91
213	SP|P27918|PROP_HUMAN	GLLGGGVSVEDCCLNTAFAYQK	22.04
214	SP|Q15166|PON3_HUMAN	VSTVYANNGSVLQGTSVASVYHGK	24.52
215	SP|P08185|CBG_HUMAN	AVLQLNEEGVDTAGSTGVTLNLTSKPIILR	22.42
216	SP|P33981|TTK_HUMAN	SECINQNPAASSNHWQIPELAR	21.2
217	SP|P05546|HEP2_HUMAN	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	20.74
218	SP|P40197|GPV_	NLSSLESVQLDHNQLETLPGDVFGALPR	21.76

	HUMAN		
219	SP|Q8TD07|N2DL4_HUMAN	EFLGHWEAMPEPTVSPVNASDIHWSSSSLPDR	16.83
220	SP|Q9UHG3|PCYOX_HUMAN	GELNTSIFSSRPIDK	14.13
221	SP|P02768|ALBU_HUMAN	DVCKNYAEAK	24.65
222	SP|P02768|ALBU_HUMAN	QEPERNECFLQHK	21.34
223	SP|P02765|FETUA_HUMAN	VCQDCPLLAPLNDTR	27.81
224	SP|P02765|FETUA_HUMAN	KVCQDCPLLAPLNDTR	30.25
225	SP|P01024|CO3_HUMAN	VFLDCCNYITELR	131.15
226	SP|P01024|CO3_HUMAN	KVFLDCCNYITELR	93.91
227	SP|P01024|CO3_HUMAN	VFLDCCNYITELRR	15.81
228	SP|P08603|CFAH_HUMAN	AVYTCNEGYQLLGEINYR	23.57
229	SP|P08603|CFAH_HUMAN	AVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVK	23.7
230	SP|P00747|PLMN_HUMAN	NLDENYCRNPDGK	20.96
231	SP|P00747|PLMN_HUMAN	TPENYPNAGLTMNYCR	13.51
232	SP|P00747|PLMN_HUMAN	NPDGDVGGPWCYTTNPR	79.88
233	SP|P00747|PLMN_HUMAN	NYCRNPDGDVGGPWCYTTNPR	61.5
234	SP|P02751|FINC_HUMAN	WCGTTQNYDADQK	95.85
235	SP|P02751|FINC_HUMAN	DQCIVDDITYNVNDTFHK	15.79
236	SP|P02751|FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	70.42
237	SP|P01008|ANT3_HUMAN	LGACNDTLQQLMEVFK	70.32
238	SP|O43866|CD5L_	NTCNHDEDTWVECEDPFDLR	24.47

	HUMAN		
239	SP|P10909|CLUS_HUMAN	ELPGVCNETMMALWEECKPCLK	28.78
240	SP|P00734|THRB_HUMAN	ITDNMFCAGYKPDEGK	30.65
241	SP|P01031|CO5_HUMAN	KCCYDGACVNNDETCEQR	35.55
242	SP|P10643|CO7_HUMAN	MHVLHCQGRNYTLTGR	26.38
243	SP|P05156|CFAI_HUMAN	FLNNGTCTAEGK	31.64
244	SP|P03952|KLKB1_HUMAN	GVNVCQETCTK	51.71
245	SP|P43652|AFAM_HUMAN	TINPAVDHCCK	26.73
246	SP|P13671|CO6_HUMAN	TLNICEVGTIR	49.81
247	SP|P02763|A1AG1_HUMAN	QDQCIYNTTYLNVQR	42.95
248	SP|P26927|HGFL_HUMAN	GTANTTTAGVPCQR	28.11
249	SP|P20851|C4BPB_HUMAN	EWDNTTTECR	24.63
250	SP|P02768|ALBU_HUMAN	YICENQDSISSK	77.1
251	SP|P01023|A2MG_HUMAN	AVDQSVLLMKPDAELSASSVYNLLPEKDLTGFPGPLNDQDNEDCINR	20.2
252	SP|P00450|CERU_HUMAN	MFTTAPDQVDKEDEDFQESNK	99.3
253	SP|P00738|HPT_HUMAN	VSVNER	14.18
254	SP|P05155|IC1_HUMAN	GVTSVSQIFHSPDLAIRDTFVNASR	18.49
255	SP|P02790|HEMO_HUMAN	CSPHLVLSALTSDNHGATYAFSGTHYWR	77.26
256	SP|P02751|FINC_HUMAN	QKTGLDSPTGIDFSDITANSFTVHWIAPR	87.11
257	SP|P19827|ITIH1_HUMAN	IYEDHDATQQLQGFYSQVAKPLLVDVDLQYPQDAVLALTQNHHK	70.13
258	SP|P01042|KNG1_	HGIQYFNNNTQHSSLFMLNEVKR	77.59

	HUMAN		
259	SP|P27169|PON1_HUMAN	SFNPNSPGK	39.72
260	SP|P04004|VTNC_HUMAN	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLKNGSLFAFR	19.37
261	SP|P00734|THRB_HUMAN	SEGSSVNLSPPLEQCVPDR	43.12
262	SP|P00734|THRB_HUMAN	SRYPHKPEINSTTHPGADLQENFCR	30.98
263	SP|P00734|THRB_HUMAN	YPHKPEINSTTHPGADLQENFCRNPDSSTTGPWCYTTDPTVR	21.16
264	SP|P04196|HRG_HUMAN	VIDFNCTTSSVSSALANTKDSPVLIDFFEDTER	56.01
265	SP|P00739|HPTR_HUMAN	VGYVSGWGQSDNFK	22.85
266	SP|P01011|AACT_HUMAN	TLNQSSDELQLSMGNAMFVK	60.75
267	SP|P00751|CFAB_HUMAN	KIVLDPSGSMNIYLVLDGSDSIGASNFTGAK	17.08
268	SP|P03952|KLKB1_HUMAN	LQAPLNYTEFQKPICLPSKGDTSTIYTNCWVTGWGFSK	49.06
269	SP|P05090|APOD_HUMAN	NILTSNNIDVKK	43.6
270	SP|P05090|APOD_HUMAN	CIQANYSLMENGK	13.16
271	SP|P05156|CFAI_HUMAN	FKLSDLSINSTECLHVHCR	38.61
272	SP|P22792|CPN2_HUMAN	LSNNALSGLPQGVFGK	21.44
273	SP|P04217|A1BG_HUMAN	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	18.41
274	SP|P04217|A1BG_HUMAN	REGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	13.67
275	SP|P51884|LUM_HUMAN	SLEYLDLSFNQIAR	15.64
276	SP|P51884|LUM_HUMAN	KLHINHNNLTESVGPLPK	37.88
277	SP|P36955|PEDF_HUMAN	VTQNLTLIEESLTSEFIHDIDRELK	37.32

278	SP|P35858|ALS_HUMAN	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	27.35
279	SP|P49908|SEPP1_HUMAN	CGNCSLTTLKDEDFCK	15.82
280	SP|P23142|FBLN1_HUMAN	CATPHGDNASLEATFVKR	24.39
281	SP|P01701|LV151_HUMAN	VTISCSGSSSNIGNNYVSWYQQLPGTAPK	97.66
282	SP|P04264|K2C1_HUMAN	MSGECAPNVSVSVSTSHTTISGGGSR	48.5
283	SP|Q08380|LG3BP_HUMAN	TVIRPFYLTNSSGVD	21.37
284	SP|P08571|CD14_HUMAN	AFPALTSLDLSDNPGLGER	13.17
285	SP|P08571|CD14_HUMAN	CMWSSALNSLNLSFAGLEQVPK	47.55
286	SP|P19652|A1AG2_HUMAN	QNQCFYNSSYLNVQR	32.63
287	SP|P04278|SHBG_HUMAN	SHEIWTHSCPQSPGNGTDASH	44.38
288	SP|P07996|TSP1_HUMAN	NKGCSSSTSVLLTLDNNVVNGSSPAIR	31.27
289	SP|P02750|A2GL_HUMAN	QLDMLDLSNNSLASVPEGLWASLGQPNWDMR	40.07
290	SP|O75144|ICOSL_HUMAN	TVVTYHIPQNSSLENVDSR	29
291	SP|Q13201|MMRN1_HUMAN	TQAALSNLTCCIDR	17.16
292	SP|Q13201|MMRN1_HUMAN	FNPGAESVVLSNSTLK	20.62
293	SP|P05452|TETN_HUMAN	NWETEITAQPDGGKTENCAVLSGAANGK	23.35
294	SP|Q04756|HGFA_HUMAN	CQIAGWGHLDENVSGYSSSLR	22.91
295	SP|Q13873|BMPR2_HUMAN	IPSPETSVTSLSTNTTTTNTTGLTPSTGMTTISEMPYPDETNLHTTNVAQSIGPTPVCLQLTEEDLETNK	19.48
296	SP|P11279|LAMP1_HUMAN	SSCGKENTSDPSLVIAFGR	16.88
297	SP|P16070|CD44_	AFNSTLPTMAQMEK	14.88

	HUMAN		
298	SP|P04180|LCAT_HUMAN	AELSNHTRPVILVPGCLGNQLEAK	13.71
299	SP|Q16581|C3AR_HUMAN	NVGMACSICGCIWVVAFVMCIPVFVYREIFTTDNHNR	13.4
300	SP|P02768|ALBU_HUMAN	NECFLQHKDDNPNLPR	26.44
301	SP|P01023|A2MG_HUMAN	IITILEEEMNVSVCGLYTYGKPVPGHVTVSICR	72.83
302	SP|P02765|FETUA_HUMAN	HTLNQIDEVK	53.77
303	SP|P01024|CO3_HUMAN	DQLTCNKFDLK	25.23
304	SP|P01024|CO3_HUMAN	TVLTPATNHMGNVTFTIPANR	15.9
305	SP|P01024|CO3_HUMAN	TMQALPYSTVGNSNNYLHLSVLR	15.38
306	SP|P01876|IGHA1_HUMAN	SGNTFRPEVHLLPPPSEELALNELVTLTCLAR	31.94
307	SP|P00450|CERU_HUMAN	EHEGAIYPDNTTDFQR	39.54
308	SP|P0C0L4|CO4A_HUMAN	TYNVLDMK	28.3
309	SP|P0C0L4|CO4A_HUMAN	VGDTLNLNLR	41.86
310	SP|P0C0L4|CO4A_HUMAN	TYNVLDMKNTTCQDLQIEVTVK	24.68
311	SP|P0C0L4|CO4A_HUMAN	VLSLAQEQVGGSPEKLQETSNWLLSQQQADGSFQDPCPVLDR	37.21
312	SP|P00738|HPT_HUMAN	TEGDGVYTLNDK	48.17
313	SP|P00738|HPT_HUMAN	TEGDGVYTLNDKK	50.88
314	SP|P00738|HPT_HUMAN	LRTEGDGVYTLNNEK	30.38
315	SP|P02751|FINC_HUMAN	HEEGHMLNCTCFGQGR	26.75
316	SP|P01042|KNG1_HUMAN	LNAENNATFYFK	16.83
317	SP|P01042|KNG1_	LNAENNATFYFKIDNVK	25.79

	HUMAN		
318	SP|P01042|KNG1_HUMAN	DIPTNSPELEETLTHTITKLNAENNATFYFK	15.57
319	SP|P27169|PON1_HUMAN	HANWTLTPLK	16.88
320	SP|P02647|APOA1_HUMAN	QLNLKLLDNWDSVTSTFSK	26.87
321	SP|P01011|AACT_HUMAN	GLKFNLTETSEAEIHQSFQHLLR	38.72
322	SP|P10909|CLUS_HUMAN	LANLTQGEDQYYLR	35.19
323	SP|P10909|CLUS_HUMAN	CREILSVDCSTNNPSQAK	65.34
324	SP|P10909|CLUS_HUMAN	LKELPGVCNETMMALWEECKPCLK	25.3
325	SP|P02749|APOH_HUMAN	ATFGCHDGYSLDGPEEIECTKLGNWSAMPSCK	32.47
326	SP|P00734|THRB_HUMAN	ETWTANVGK	25.18
327	SP|P00734|THRB_HUMAN	VTGWGNLKETWTANVGK	18.08
328	SP|P00734|THRB_HUMAN	WVLTAAHCLLYPPWDKNFTENDLLVR	48.03
329	SP|P43652|AFAM_HUMAN	FTDSENVCQERDADPDTFFAK	19.21
330	SP|Q96PD5|PGRP2_HUMAN	GFGVAIVGNYTAALPTEAALR	36.49
331	SP|P02748|CO9_HUMAN	FSYSKNETYQLFLSYSSK	27.27
332	SP|P00736|C1R_HUMAN	EHEAQSNASLDVFLGHTNVEELMK	61.76
333	SP|P03952|KLKB1_HUMAN	IYPGVDFGGEELNVTFVK	16.69
334	SP|P01009|A1AT_HUMAN	YLGNATAIFFLPDEGK	32.49
335	SP|P01009|A1AT_HUMAN	YLGNATAIFFLPDEGKLQHLENELTHDIITK	34.64
336	SP|P05090|APOD_HUMAN	ADGTVNQIEGEATPVNLTEPAK	23.97
337	SP|P05090|APOD	ADGTVNQIEGEATPVNLTEPAKLEVK	35.53

	_HUMAN		
338	SP|P05160|F13B_HUMAN	KEHETCLAPELYNGNYSTTQK	17.69
339	SP|P02766|TTHY_HUMAN	ALGISPFHEHAEVVFTANDSGPR	27.05
340	SP|P51884|LUM_HUMAN	NIPTVNENLENYYLEVNQLEKFDIK	61.93
341	SP|P43251|BTD_HUMAN	DVQIIVFPEDGIHGFNFTR	15.35
342	SP|P07477|TRY1_HUMAN	TLNNDIMLIK	35.06
343	SP|P17936|IBP3_HUMAN	AYLLPAPPAPGNASESEEDRSAGSVESPSVSSTHR	42.43
344	SP|P48740|MASP1_HUMAN	NNLTTYKSEIK	31.08
345	SP|P48740|MASP1_HUMAN	MLNNNTGIYTCSAQGVWMNK	30.56
346	SP|P00748|FA12_HUMAN	RNHSCEPCQTLAVR	25.96
347	SP|Q9HDC9|APMAP_HUMAN	AGPNGTLFVADAYK	28.93
348	SP|P29622|KAIN_HUMAN	FLNDTMAVYEAK	28.54
349	SP|P13473|LAMP2_HUMAN	VASVININPNTTHSTGSCR	26.8
350	SP|P02675|FIBB_HUMAN	AHYGGFTVQNEANKYQISVNK	20.78
351	SP|P11597|CETP_HUMAN	GHFIYKNVSEDLPLPTFSPTLLGDSR	20.25
352	SP|Q08380|LG3BP_HUMAN	ALGFENATQALGR	13.08
353	SP|P01023|A2MG_HUMAN	VSVQLEASPAFLAVPVEKEQAPHCICANGR	16.1
354	SP|P43652|AFAM_HUMAN	AESPEVCFNEESPK	23.08
355	SP|P07357|CO8A_HUMAN	ALDQYLMEFNACR	32.71
356	SP|O95445|APOM_HUMAN	NQEACELSNN	52.97

Table S6. Properties and enrichment performances of different materials.

Materials	Glycopeptides enriched from complex biosamlpes	Binding capacity ($mg \cdot g^{-1}$)	Rapid separation properties	Pore structures	Recovery yields
Magnetic Mesoporous Phenolic Resin (MMP)	15 N-glycosylation sites from 25 nL of human serum and 356 N-linked glycopeptides from 0.35 μL of human serum	400	Magnetic component	Mesoporous structure (13.2 nm)	70.18-97.23%
Fe_3O_4@CS MCNCs	283 N-glycosylation sites of 45 mg protein from HeLa cells	17.5	Magnetic component	ND[a]	ND[a]
Fe_3O_4-DA-Maltose NPs	115 N-linked glycopeptides in HRMC	43	Magnetic component	ND[a]	85−110%
Boronic acid-functionalized mesoporous silica	15 endogenous glycopeptides in rat serum	40	ND[a]	Small pore entrance size (2–3 nm)	88.10%
Histidine-Bonded Silica (HBS)	487 glycosites from 2 μL of human serum	ND[a]	Switchable surface charge structures	ND[a]	ND[a]
cross-linked chitosan microspheres (CSMs)	194 and 947 N-glycosylation sites from 2 μL of human serum and 0.1 mg of rat brain	100	ND[a]	Nanosize pore microstructure (10 nm)	74.9−106.4%
Graphitic Carbon Nitride	17 Sialoglycopeptides tryptic digests of haptoglobin separated from human serum	148	ND[a]	ND[a]	89.2%

[a]ND: not determined.

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