Supporting Information

Post synthetic modification of amino-functionalized metal-organic framework for the efficient enrichment of N-linked glycopeptides

Wen Ma,[a] Linnan Xu,[a] Ze Li,[a] Yunlong Sun,[b] Yu Bai*[a] and Huwei Liu [a]
[a]*Beijing National Laboratory for Molecular Sciences, Key Laboratory of Bioorganic Chemistry and Molecular Engineering of Ministry of Education, College of Chemistry and Molecular Engineering, Institute of Analytical Chemistry, Peking University, Beijing 100871, China.*
[b]*Center for Soft Matter Science and Engineering, Peking University, Beijing, 100871*
**Tel: +86 10 6275 8198; E-mail: yu.bai@pku.edu.cn*

Experimental Section

Chemicals and Materials

Trypsin, horseradish peroxidase (HRP), human serum immunoglobulin G (human IgG), azidotrimethylsilane ($TMSN_3$), acetonitrile (ACN) were purchased from Sigma-Aldrich. Amberlite IR-120 resin (H^+ form), tert-butyl nitrate (tBuONO), 2,5-dihydroxybenzoic acid (DHB), dithiothreitol (DTT) and iodoacetamide (IAA) were purchased from J&K Scientific Ltd. Tetrahydrofuran (THF), anhydrous potassium carbonate, copper(II) sulfate ($CuSO_4 \cdot 5H_2O$) and ureawere from Xilong Chemical Co., Ltd. Ammonium bicarbonate (NH_4HCO_3) was from Fluka. Ethanol and phosphoric acid (H_3PO_4) were from Beijing Chemical Works. Chromic nitrate hydrate, sodium methoxide and boron trifluoride/ether were from Sinopharm Chemical Reagent Co., Ltd. 2-aminoterephthalic acid was from AlfaAesar China Chemical Co., Ltd. Anhydrous methanol and dichloromethane (CH_2Cl_2) were from Beijing Tong Guang Fine Chemicals Company. β-D-maltose octaacetate was purchased from Energy Chemical. Ascorbic acid was purchased from Aladdin Industrial Inc. Trifluoroacetic acid (TFA) was obtained from Acros Organics. Peptide-N-glycosidase (PNGase F) was from New England Biolabs (Ipswich, MA, USA). Water used for digestion and enrichment analysis was from Wahaha Group Co., Ltd. All chemicals were of analytical grade except ACN, which were of HPLC grade. Human serum of a healthy person was

obtained from Peking University Hospital.

Preparation of MIL-101(Cr)-maltose

Preparation of parent MIL-101(Cr)-NH_2

MIL-101(Cr)-$NH_2$was synthesized according to a previous report[S1]. Briefly, 1500mg chromic nitrate hydrate and 690mg 2-aminoterephthalic acid were dispersed in 21mL deionized water in a 30mL Teflon-lined stainless steel autoclave, the reaction was conducted at 130℃ for 24h. The product was then washed by ethanol for several times and dried in vacuum.

Preparation of MIL-101(Cr)-N_3

The post synthetic modification of MIL-101(Cr)-NH_2 was conducted according to a generic post functionalization method[S2] starting from amino-derived metal-organic frameworks. The freshly preparedMIL-101(Cr)-NH_2(80mg) was treated with tBuONO(0.3mL) and $TMSN_3$(0.27mL) in THF for 20min at room temperature. The resulting compound was washed three times by THF and three times by CH_2Cl_2.

Preparation of 1-propargyl-O-maltose

1-propargyl-O-maltose was synthesized according to a reported method[S3]. In detail, under nitrogen atmosphere, 25.0g β-D-maltose octaacetate was dissolved in 350mL CH_2Cl_2 in a dried flask, then 2.5mL propargylalcohol was added. The suspention was stirred at 0℃ for1h after the addition of 7.5mL boron trifluoride/ether and at room temperature for another 4h. After 12.5g anhydrous potassium carbonate was added, the solution continuously stirred for 30min. The unreacted solid was filtered out and the filtrate was concentrated. 1-propargyl-acetyl-maltose was obtained with m/z=697.0 ($[M+Na]^+$) by MALDI-TOF MS. The obtained solid was further dissolved in 750mL anhydrous methanol solution. Then, 250mL sodium methoxide in methanol (1 M) was added dropwise. The reaction was conducted at room temperature for 6h, and the resulting solution was neutralized by Amberlite IR-120 resin (H^+ form). The solution was then filtered out and the filtrate was concentrated. 1-propargyl-O-maltose was obtained with m/z=402.6 ($[M+Na]^+$) by MALDI-TOF MS.

Preparation of MIL-101(Cr)-maltose

The obtained MIL-101(Cr)-N_3(170mg) and an excess of 1-propargyl-O-maltose was

dispersed in 40mL methanol/water(v/v=1:1) solution in a 100mL flask and sonicated for 20min. Then 2mL solution containing 138mg $CuSO_4 \cdot 5H_2O$ and 323 mg ascorbic acid was added. The mixture continuously stirred for 72 h at 40 ℃. The obtained solid was washed by water, methanol, ethanol nine times anddried in the vacuum oven.

Characterization

Fourier-transformed infrared spectroscope (FT-IR) characterization was measured with KBr pellet by Bruker Tensor 27 FT-IR. Transmittance spectrum was acquired with resolution of 4 cm^{-1} and average spectrum of 32-time measurements was recorded. ^{1}H-NMR spectra were recorded on a Bruker ARX400 FT-NMR spectrometer(at 400 MHz). All samples were digested in $NaOD/D_2O$. Power X-ray diffraction pattern was carried out on a Bruker D2 diffractometer with Cu Kα radiation (λ=1.5406Å) at an accelerating potential of 40kV and a scanning speed of 2° min^{-1}. For transmission electron microscopy (TEM) characterization, the NPs were collected on carbon-coated copper grids. TEM images were recorded on a JEOL JEM-2100 at 200kV. N_2 adsorption-desorption experiment was conducted in ASAP 2020M apparatus. MIL-101(Cr)-NH_2 was degassed at 120℃ and MIL-101(Cr)-N_3, MIL-101(Cr)-maltose were degassed at 100℃ in case of decomposition. The BET surface area was calculated over the range of relative pressures between 0.05 and 0.20. It revealed that the surface area were 2357.4 m^2 g^{-1}, 1518.6 m^2 $g^{-1}$and 250.2 m^2 g^{-1} for MIL-101(Cr)-NH_2, MIL-101(Cr)-N_3, and MIL-101(Cr)-maltose, respectively.

Tryptic digest of glycoproteins

2mg HRP or IgG was dissolved in 1mL solution containing 50mM NH_4HCO_3 and 8M urea. After that, proteins were reduced with 20μL DTT (1M) at 60℃ for 1 h and alkylated by 7.4 mg IAA at 37℃ in the dark for 45 min. Then, the solution was diluted ten-fold with 50mM NH_4HCO_3, followed by the addition of trypsin at enzyme-protein ratio of 1: 20 (w/w). The solution was incubated at 37℃ for 18h, and the tryptic digests were stored at -20℃ for further use. For human serum sample, the preparation was almost the same. In detail, 5μL human serum was diluted by 40μL denaturing solution containing 50mM NH_4HCO_3 and 8M urea. Then, the sample was reduced with 5 μL DTT (200 mM) at 60℃ for 1 h and alkylated by 7.2

mg IAAat 37℃ in the dark for 45 min. The resulting solution was diluted by 350μL 50mM NH_4HCO_3 and digested with trypsin (protein: enzyme = 20:1, w/w) for 20 h.The peptides mixture were lyophilized and kept at -20℃for further use.

Enrichment of glycopeptides in standard glycoprotein and human serum sample

20μg MIL-101(Cr)-maltose was suspended in 150μL loading buffer containingACN/H_2O/TFA (88:7:5, v/v/v). Then10μL tryptic digest HRP (2μg) or 15μL human IgG (3μg) was added and the solution was incubated for 30min. After washed by loading buffer three times to remove non-glycopeptides, the adsorbed glycopeptides were eluted with elution buffer containing ACN/H_2O/TFA (30:69.9:0.1, v/v/v). The collected peptides were analyzed by MALDI-TOF MS. For human serum sample, peptides were redissolved in 200μLACN/H_2O/TFA (88:7:5, v/v/v), then 200μg MIL-101(Cr)-maltose was added. The enrichment was gently carried out for 30min, then washed by loading buffer for three times. The glycopeptides were eluted with 2×30μL elution buffer and lyophilized. The collected peptides weredeglycosylation for LC-MS/MS analysis.

Deglycosylation of glycopeptides by PNGase F

The lyophilized glycopeptides were redissolved in 50mM NH_4HCO_3, followed by addition of 1μL PNGaseF. The reaction was carried out at 37℃ for 16h.The resulting solution was further analyzed by MALDI-TOF MS or LC-MS/MS.

Mass spectrometry analysis

MALDI-TOF MS analysis

MALDI-TOF MS spectra were obtained by a Bruker Daltonics ultraflex TOF mass spectrometer in reflection mode. A mixture of 25mg/mL DHB in ACN/H_2O/H_3PO_4 (70:29:1, v/v/v) was prepared as the matrix. For eluted glycopeptides, 0.5μL elute was mixed with 0.5μL matrix on the steel plate for MS analysis.

LC-MS/MS Analysis

All LC-MS/MS were performed on a Velos Pro Orbitrap Elite mass spectrometer (Thermo Scientific, USA) equipped with a nano-ESI source. The samples were vacuum-centrifuged to

dryness, reconstituted in 0.2% formic acid, loaded onto a pre-column and separated on a C18 column. For a gradient separation, 5-30% B in 121min, 30%-75% B in 4min, then held at 75% B for 20 min (A = 0.1% formic acid in water, B = 0.1% formic acid in acetonitrile). Full MS scan was obtained from m/z=375-1600 at a resolution of 120000 followed by CID (Collision Induced Dissociation) MS/MS scans.

Database search and data analysis

All the raw data files were converted to mascot generic format before submitted for Mascot (version 2.3.02) database search. The search parameters were set as follows: fixed modification of cysteine residues (+57.0215 Da), variable modification of methionine oxidation (+15.9949 Da) and deamidation (+0.9840 Da). The mass tolerances were 5 ppm for initialprecursor ions and 0.5 Da for fragment ions. Two missed cleavages were allowed for trypsin restriction. Only glycopeptides with N-!P-S/T were considered as highly reliable results.

Reference:

S1.D. M. Jiang, L. L. Keenan, A. D. Burrows and K. J. Edler, *Chem. Commun.*, 2012, **48**, 12053-12055.

S2.M. Savonnet, D. Bazer-Bachi, N. Bats, J. Perez-Pellitero, E. Jeanneau, V. Lecocq, C. Pinel and D. Farrusseng, *J. Am. Chem. Soc.*, 2010, **132**, 4518-4519.

S3.Z. C. Xiong, L. Zhao, F. J. Wang, J. Zhu, H. Q. Qin, R. A. Wu, W. B. Zhang and H. F. Zou, *Chem. Commun.*, 2012, **48**, 8138-8140.

Figures and Table

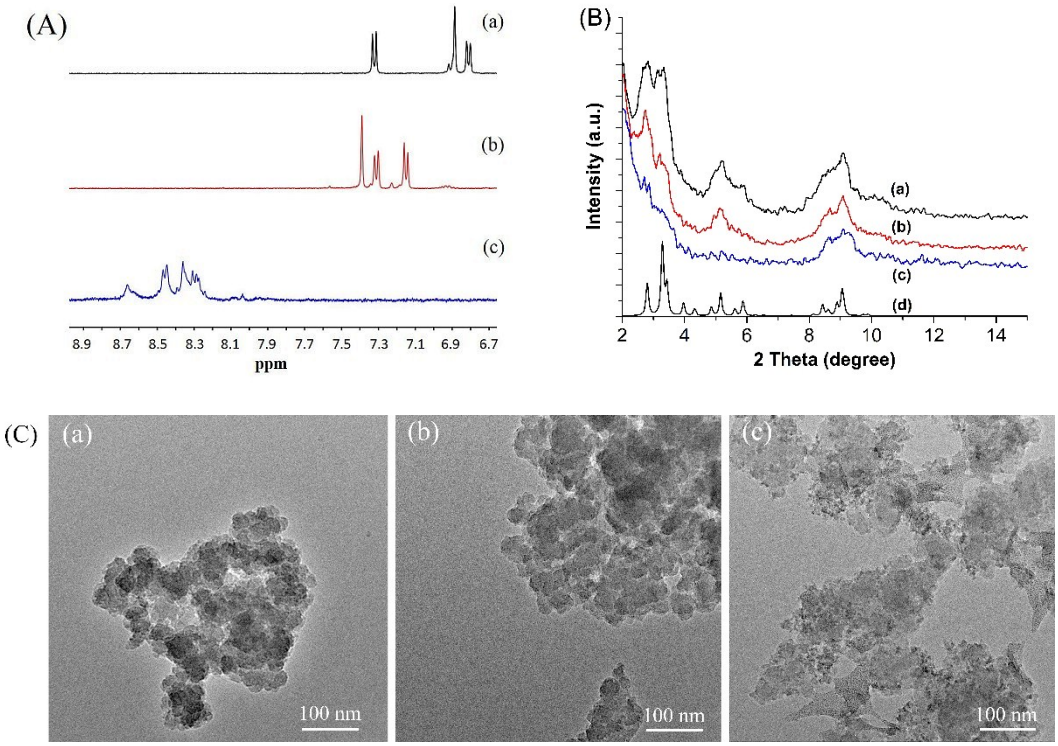

Fig. S1 (A)^{1}H-NMR spectra, (B) PXRD pattern and (C) TEM image of (a) MIL-101(Cr)-NH_2, (b) MIL-101(Cr)-N_3, (c) MIL-101(Cr)-maltose and (d) the simulated PXRD pattern calculated from MIL-101(Cr) structure.

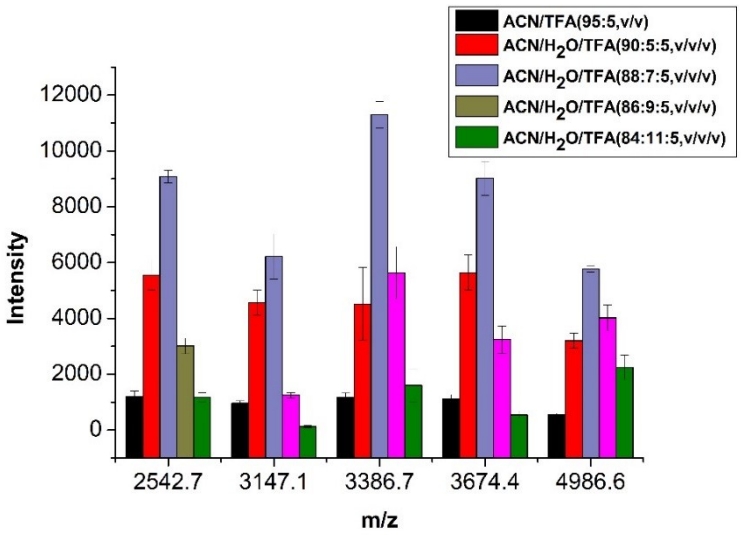

Fig. S2 The effect of different acetonitrile concentration in loading buffer on intensity of five seleced glycopeptides captured by MIL-101(Cr)-maltose from HRP digest.

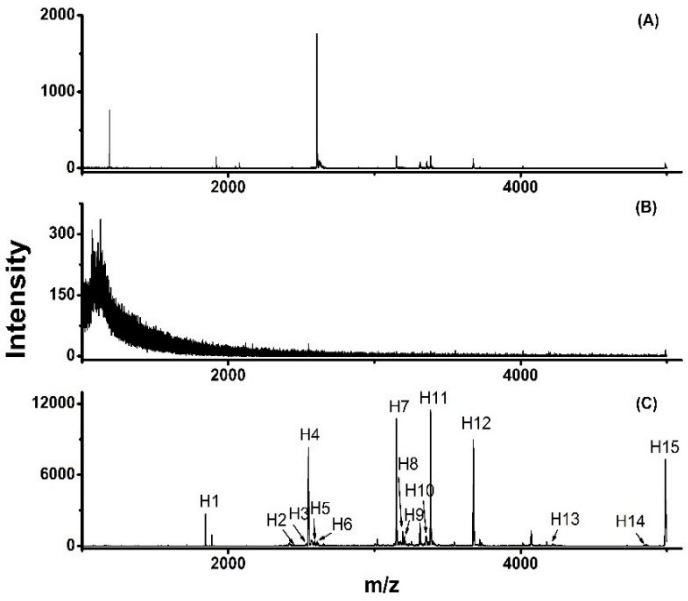

Fig. S3 MALDI-TOF MS spectra of HRP tryptic digest (1.0 pmol/μL)(A) by direct analysis, (B) after MIL-101(Cr)-N_3 enrichment and (C) afterMIL-101(Cr)-maltose enrichment.

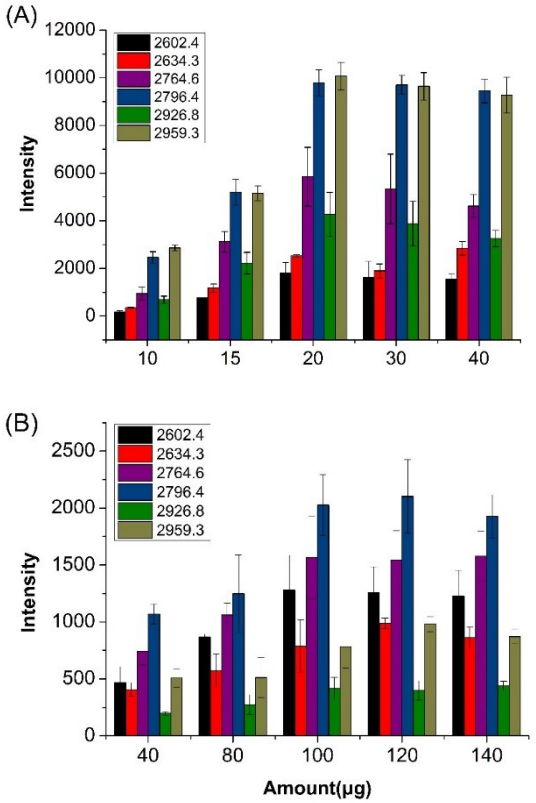

Fig. S4 The intensity of six selected glycopeptides from 3 μg human IgG trypticdigest after enrichment by different amount of (A) MIL-101(Cr)-maltose and (B) MIL-101(Cr)-NH_2.

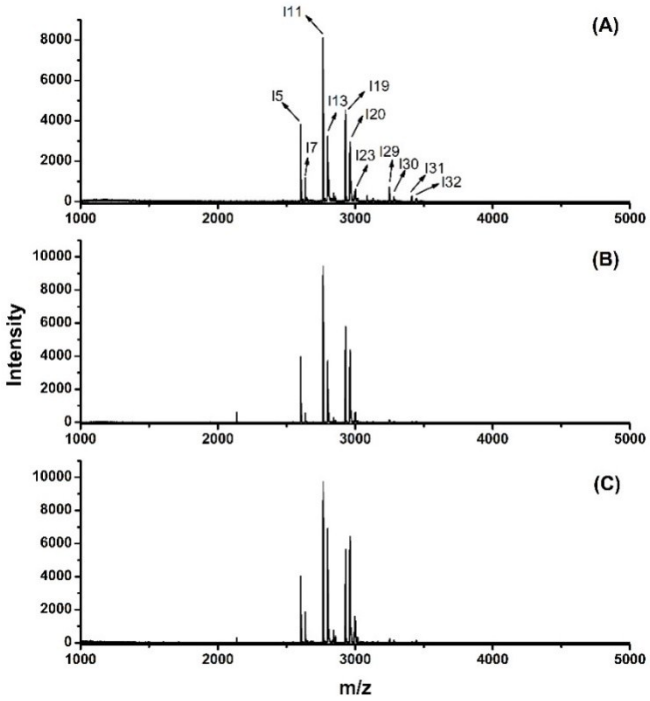

Fig. S5 MALDI-TOF MS of glycopeptides enriched from human IgGdigest (3μg) using MIL-101(Cr)-maltose nanoparticles, (A) for the first time, (B) for the third time and (C) for the fifth time.

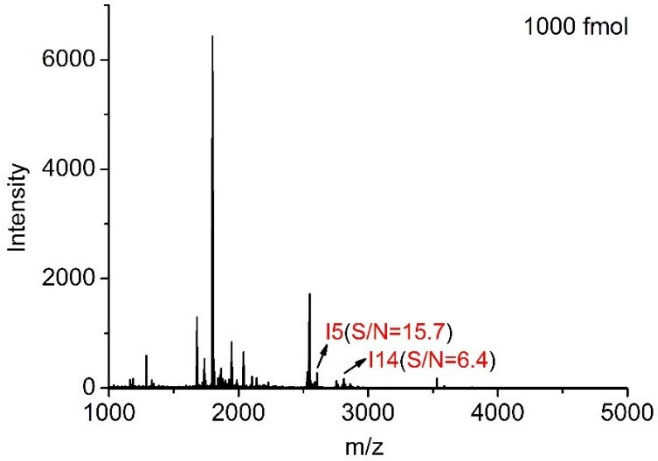

Fig. S6 MALDI-TOF-MS spectra of IgG tryptic digest without enrichment 1000 fmol (0.5μL).

Table S1 Observed glycopeptides and glycan composition of HRP tryptic digests enriched by MIL-101(Cr)-maltose. N* denotes the N-linked glycosylation sites.

Peak number	Observed *m/z*	Glycan composition	Peptide sequence
H1	1843.9	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	NVGLN*R
H2	2445.1	[Hex]3[HexNAc]2 [Xyl]1	PTLN*TTYLQTLR
H3	2531.1	[HexNAc]1[Fuc]1	SFAN*STQTFFNAFVEAMDR
H4	2542.7	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	SSPN*ATDTIPLVR
H5	2590.2	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	PTLN*TTYLQTLR
H6	2613.9	[Hex]3[HexNAc]2 [Xyl]1	MGN*ITPLTGTQGQIR
H7	3147.1	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	GLCPLNGN*LSALVDFDLR
H8	3190.3	[HexNAc]1[Fuc]1	LHFHDCFVNGCDASILLDN*TTSFR
H9	3206.4	[Hex]3[HexNAc]2 [Xyl]1	SFAN*STQTFFNAFVEAMDR
H10	3353.5	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	SFAN*STQTFFNAFVEAMDR
H11	3386.7	[Hex]6[HexNAc]4[Fuc]2[Xyl]1	DSFRNVGLN*R
H12	3674.4	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	GLIQSDQELFSSPN*ATDTIPLVR
H13	4221.0	[Hex]3[HexNAc]2[Fuc]1[Xyl]1	QLTPTFYDNSC(AAVESACPR)PN*V SNIVR
H14	4840.7	[Hex]3[HexNAc]2[Fuc]1[Xyl]1 [Hex]3[HexNAc]2 [Xyl]1	LYN*FSNTGLPDPTLN*TTYLQTLR
H15	4986.6	[Hex]3[HexNAc]2[Fuc]1[Xyl]1 [Hex]3[HexNAc]2[Fuc]1[Xyl]1	LYN*FSNTGLPDPTLN*TTYLQTLR

Table S2 Observed glycopeptides and glycan composition of human IgG tryptic digests enriched by MIL-101(Cr)-maltose. N* denotes the N-linked glycosylation sites.

Peak number	Observed *m/z*	Glycan composition	Peptide sequence
I1	2400.1	[Hex]3[HexNAc]3[Fuc]1	EEQFN*STFR
I2	2433.0	[Hex]3[HexNAc]3[Fuc]1	EEQYN*STYR
I3	2490.1	[Hex]3[HexNAc]4	EEQYN*STYR
I4	2562.3	[Hex]4[HexNAc]3[Fuc]1	EEQFN*STFR
I5	2602.4	[Hex]3[HexNAc]4[Fuc]1	EEQFN*STFR
I6	2618.2	[Hex]4[HexNAc]4	EEQFN*STFR
I7	2634.3	[Hex]3[HexNAc]4[Fuc]1	EEQYN*STYR
I8	2650.3	[HexNAc]4[HexNAc]4	EEQYN*STYR
I9	2660.2	[Hex]3[HexNAc]5	EEQFN*STFR
I10	2691.7	[Hex]3[HexNAc]5	EEQYN*STYR
I11	2764.6	[Hex]4[HexNAc]4[Fuc]1	EEQFN*STFR
I12	2780.6	[Hex]5[HexNAc]4	EEQFN*STFR
I13	2796.4	[Hex]4[HexNAc]4[Fuc]1	EEQYN*STYR
I14	2805.9	[Hex]3[HexNAc]5[Fuc]1	EEQFN*STFR
I15	2812.7	[Hex]5[HexNAc]4	EEQYN*STYR

I16	2822.6	[Hex]4[HexNAc]5	EEQFN*STFR
I17	2838.3	[Hex]3[HexNAc]5[Fuc]1	EEQYN*STYR
I18	2853.9	[Hex]4[HexNAc]5	EEQYN*STYR
I19	2926.8	[Hex]5[HexNAc]4[Fuc]1	EEQFN*STFR
I20	2959.3	[Hex]5[HexNAc]4[Fuc]1	EEQYN*STYR
I21	2967.7	[Hex]4[HexNAc]5 [Fuc]1	EEQFN*STFR
I22	2984.5	[Hex]5[HexNAc]5	EEQFN*STFR
I23	2999.8	[Hex]4[HexNAc]5 [Fuc]1	EEQYN*STYR
I24	3016.1	[Hex]5[HexNAc]5	EEQYN*STYR
I25	3057.3	[Hex]4[HexNAc]4[Fuc]1[NeuAc]1	EEQFN*STFR
I26	3085.3	[Hex]4[HexNAc]4[Fuc]1[NeuAc]1	EEQYN*STYR
I27	3130.9	[Hex]5[HexNAc]5[Fuc]1	EEQFN*STFR
I28	3162.6	[Hex]5[HexNAc]5[Fuc]1	EEQYN*STYR
I29	3247.5	[Hex]4[HexNAc]4[Fuc]1	TKPREEQFN*STFR
I30	3279.6	[Hex]4[HexNAc]4[Fuc]1	TKPYEEQYN*STYR
I31	3409.6	[Hex]5[HexNAc]4[Fuc]1	TKPREEQFN*STFR
I32	3441.8	[Hex]5[HexNAc]4[Fuc]1	TKPYEEQYN*STYR
I33	3452.0	[Hex]5[HexNAc]5[Fuc]1[NeuAc]1	EEQYN*STYR

Table S3 Observed glycopeptides of human serum tryptic digests without enrichment. OS=Organism Name, GN=Gene Name, PE=Protein Existence, SV=SequenceVersion. N* denotes the N-linked glycosylation sites.

Protein	Description	Peptide Sequence
CERU_HUMAN	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	DVDKEFYLFPTVFDEN*ESLLLEDNIR
WDR33_HUMAN	WD repeat-containing protein 33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	KTIDYN*PSVIK

Table S4 Observed glycopeptides of human serum tryptic digests enriched by MIL-101(Cr)-maltose. OS=Organism Name, GN=Gene Name, PE=Protein Existence, SV=Sequence Version. N* denotes the N-linked glycosylation sites.

Protein	Description	Peptide Sequence
A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	YLGN*ATAIFFLPDEGK ADTHDEILEGLNFN*LTEIPEAQIHEGFQEL LR
AACT_HUMAN	Alpha-1-antichymotrypsin OS=Homo sapiens	YTGN*ASALFILPDQDK FN*LTETSEAEIHQSFQHLLR

	GN=SERPINA3 PE=1 SV=2	
A2MG_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2	SLGNVN*FTVSAEALESQELCGTEVPSVPEHGR GCVLLSYLN*ETVTVSASLESVR VSN*QTLSLFFTVLQDVPVR
A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	EN*GTISR QDQCIYN*TTYLNVQR NEEYN*K
ANT3_HUMAN	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	SLTFN*ETYQDISELVYGAK WVSN*KTEGR LGACN*DTLQQLMEVFK LGACN*DTLQQLMEVFKFDTISEK
APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	ADGTVNQIEGEATPVN*LTEPAK ADGTVNQIEGEATPVN*LTEPAKLEVK
APOB_HUMAN	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=1	FN*SSYLQGTNQITGR YDFN*SSMLYSTAK FVEGSHN*STVSLTTK VNQNLVYESGSLN*FSK
APOC4_HUMAN	Apolipoprotein C-IV OS=Homo sapiens GN=APOC4 PE=1 SV=1	ELLETVVN*R
A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	QNQCFYN*SSYLNVQR
ATRN_HUMAN	Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2	GICN*SSDVR IDSTGN*VTNELR
APOH_HUMAN	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	VYKPSAGN*NSLYR LGN*WSAMPSCK
AFAM_HUMAN	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	YAEDKFN*ETTEK DIENFN*STQK
CERU_HUMAN	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	EHEGAIYPDN*TTDFQR EN*LTAPGSDSAVFFEQGTTR ELHHLQEQN*VSNAFLDK ELHHLQEQN*VSNAFLDKGEFYIGSK
CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	HN*STGCLR EDALN*ETR KEDALN*ETR KKEDALN*ETR LAN*LTQGEDQYYLR MLN*TSSLLEQLNEQFNWVSR
CO4A_HUMAN	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	GLN*VTLSSTGR FSDGLESN*SSTQFEVK
CBG_HU	Corticosteroid-binding globulin	AQLLQGLGFN*LTER

MAN	OS=Homo sapiens GN=SERPINA6 PE=1 SV=1	
CO8A_HUMAN	Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	GGSSGWSGGLAQN*R
CO4B_HUMAN	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=1	FSDGLESN*SSTQFEVK GLN*VTLSSTGR
CO6_HUMAN	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	VLN*FTTK
CO7_HUMAN	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	N*YTLTGR
CO9_HUMAN	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	AVN*ITSENLIDDVVSLIR
CO3_HUMAN	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	TVLTPATNHMGN*VTFTIPANR
C1S_HUMAN	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	NCGVN*CSGDVFTALIGEIASPNYPKPYPE NSR
CFAI_HUMAN	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=1	FLNN*GTCTAEGK
C4BPA_HUMAN	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	LSVDKDQYVEPEN*VTIQCDSGYGVVGPQ SITCSGN*R
C4BPB_HUMAN	C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1	LGHCPDPVLVNGEFSSSGPVN*VSDK
CPN2_HUMAN	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=2	AFGSNPN*LTK
CHP1_HUMAN	Calcium-binding protein p22 OS=Homo sapiens GN=CHP PE=1 SV=3	GEN*GTLSR
CFAH_HUMAN	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	IPCSQPPQIEHGTIN*SSR
FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	VCQDCPLLAPLN*DTR AALAAFNAQNN*GSNFQLEEISR KVCQDCPLLAPLN*DTR
FHR1_HUMAN	Complement factor H-related protein 1 OS=Homo sapiens	LQNNENN*ISCVER

	GN=CFHR1 PE=1 SV=2	
FA10_HUMAN	Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2	GDNN*LTR
FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=3	LDAPTNLQFVN*ETDSTVLVR DQCIVDDITYNVN*DTFHK
HRG_HUMAN	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	VIDFN*CTTSSVSSALANTK
HPT_HUMAN	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	NLFLN*HSEN*ATAK VVLHPN*YSQVDIGLIK MVSHHN*LTTGATLINEQWLLTTAK
HEMO_HUMAN	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	SWPAVGN*CSSALR ALPQPQN*VTSLLGCTH
HEP2_HUMAN	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	DFVN*ASSK
IGHG1_HUMAN	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	EEQYN*STYR
IGHG2_HUMAN	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	EEQFN*STFR TKPREEQFN*STFR
IGHG3_HUMAN	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	EEQYN*STFR
IGHG4_HUMAN	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	EEQFN*STYR
IGHA1_HUMAN	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	LSLHRPALEDLLLGSEAN*LTCTLTGLR
IGHA2_HUMAN	Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3	TPLTAN*ITK LSLHRPALEDLLLGSEAN*LTCTLTGLR
IGHM_HUMAN	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	N*NSDISSTR YKN*NSDISSTR GLTFQQN*ASSMCVPDQDTAIR THTN*ISESHPN*ATFSAVGEASICEDDWNSGER
IGJ_HUMAN	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	EN*ISDPTSPLR
IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens	DTFVN*ASR VLSN*NSDANLELINTWVAK

	GN=SERPING1 PE=1 SV=2	
ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	NAHGEEKEN*LTAR
ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	DQFNLIVFSTEATQWRPSLVPASAENVN*K
KV203_HUMAN	Ig kappa chain V-II region MIL OS=Homo sapiens PE=1 SV=1	FSGSGSGTN*FTLK
KLKB1_HUMAN	Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1	IYSGILN*LSDITK GVNFN*VSK IYPGVDFGGEELN*VTFVK
KNG1_HUMAN	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	YNSQN*QSNNQFVLYR LNAENN*ATFYFK
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	ALGFEN*ATQALGR
LUM_HUMAN	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	LHINHNN*LTESVGPLPK AFEN*VTDLQWLILDHNLLENSK
LV202_HUMAN	Ig lambda chain V-II region NEI OS=Homo sapiens PE=1 SV=1	RPSGVSN*R
PEDF_HUMAN	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=3	VTQN*LTLIEESLTSEFIHDIDR
PON1_HUMAN	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=2	HAN*WTLTPLK VTQVYAEN*GTVLQGSTVASVYK
PLTP_HUMAN	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	VSN*VSCQASVSR
TRFE_HUMAN	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=2	CGLVPVLAENYN*K QQQHLFGSN*VTDCSGNFCLFR
THRB_HUMAN	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	N*FTENDLLVR GHVN*ITR
TNPO3_HUMAN	Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3	DAN*CSVMR
TTHY_HUMAN	Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	ALGISPFHEHAEVVFTAN*DSGPR
WDR33_HUMAN	WD repeat-containing protein 33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	KTIDYN*PSVIK
VTNC_HUMAN	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	NN*ATVHEQVGGPSLTSDLQAQSK

ZA2G_HUMAN	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=1	FGCEIENN*R DIVEYYN*DSN*GSHVLQGR
ZN750_HUMAN	Protein ZNF750 OS=Homo sapiens GN=ZNF750 PE=2 SV=1	LN*PSDPNR