

1 **Hydrophilic glutathione-modified flower-like hollow covalent**
2 **organic frameworks for highly efficient capture of N-linked**
3 **glycopeptides**

4
5 Yin Ji^a, Yanting He^b, Ruibing chen^c, Chao Zhong^a, Heming Li^a, Yijing Wu^a, Zian Lin^{a*}

6
7 ^a Ministry of Education Key Laboratory of Analytical Science for Food Safety and
8 Biology, Fujian Provincial Key Laboratory of Analysis and Detection Technology for
9 Food Safety, College of Chemistry, Fuzhou University, Fuzhou, Fujian, 350108, China

10 ^b School of Pharmacy, Bengbu Medical University, 2600 Donghai Avenue, Bengbu,
11 Anhui, 233000, China

12 ^c School of Pharmaceutical Science and Technology, Tianjin University, Tianjin
13 300072, China

14

15

16 ● **Corresponding author:** Zian Lin;

17 ● **Postal address:** College of Chemistry, Fuzhou University,

18 Fuzhou, Fujian, 350108, China

19 ● **Fax:** 86-591-22866135

20 **E-mail:** zianlin@fzu.edu.cn (Z. Lin)

21

22

23

24

25

26 **Experimental Section**

27 **Chemicals and reagents**

28 All chemicals and reagents were analytical grade or better and used without further
29 purification. 1,3,5-Tris(4-aminophenyl)benzene (TPB), 2,5- divinylnitroterephthalaldehyde
30 (DVA) were obtained from Jilin Chinese Academy of Sciences-Yanshen Technology
31 Co., Ltd. Ethanol, acetonitrile (ACN, HPLC grade) were purchased from Sinopharm
32 Chemical Reagent, Co., Ltd (Shanghai, China). Hydrogen tetrachloroaurate (III)
33 trihydrate ($\text{H}_7\text{AuCl}_4\text{O}_3$), sodium citrate (SC), tannic acid (TA), and potassium
34 carbonate (K_2CO_3), glutathione (GSH), acetic acid and trifluoroacetic acid (TFA) were
35 purchased from Aladin (Shanghai, China). Iodacetamide (IAA), 1,4-dithiothreitol
36 (DTT), 2,5-dihydroxybenzoic acid (2,5-DHB), horseradish peroxidase (HRP), bovine
37 serum albumin (BSA), PNGase F (Glycerol-free) and TPCK-treated trypsin were
38 purchased from Sigma-Aldrich (St. Louis, MO). Healthy human serum was supplied
39 by Fujian Provincial Official Hospital (Fuzhou, China). Deionized water ($18.2 \text{ M}\Omega$
40 cm^{-1}) was purified with Milli-Q water system (Millipore, USA).

41 **Characterization**

42 Transmission electron microscopies (TEM) images were obtained by the Hitachi
43 HT7700 with an accelerating voltage of 100 kV. Scanning electron microscopies
44 (SEM) measurement was performed on a Verios G4 scanning electron microscope. The
45 high-angle annular dark-field scanning TEM (HAADF-STEM) was carried out by a
46 FEI Tecnai G2 F20 S-Twin HRTEM operating at 200 kV. A Micromeritics 3020M was
47 used to analysis the N_2 adsorption/desorption isotherms at 77K. The samples were

48 degassed by vacuum at 120 °C for 10 h before analysis. Powder X-ray diffraction
49 (XRD) patterns were conducted at a scan rate of 5° min⁻¹ over a range of 2.5-80° (2θ)
50 on a X'Pert-Pro MPD (Philips, Holland) power diffractometer with Cu-Kα source
51 (λ=1.5418 Å). Fourier-transform infrared spectra (FT-IR) were collected by attenuated
52 total reflectance (ATR) on a Nicolet iS50 spectrometer (Thermo Fisher, USA) with the
53 wave number range of 4000-400 cm⁻¹. The contact angles were measured by a contact
54 angle analyzer (HAKER-SPCAX1). Thermogravimetric analysis (TGA) was carried
55 out on a STA449C/6/G analyzer from 30 to 1000 °C under Ar₂ atmosphere with a ramp
56 rate of 10 °C min⁻¹. The zeta potential was measured by dynamic light scattering
57 (Zetasizer NanoZS90, Malvern). The X-ray photoelectron spectra (XPS) was analyzed
58 by a Thermo Scientific ESCALAB 250. All matrix-assisted laser desorption ionization
59 time-of-flight mass spectrometry (MALDI-TOF MS) analysis were performed in
60 reflector positive-ion mode on a Bruker autoflex speed MALDI-TOF/TOF MS
61 equipped with the Nd: YAG laser at 355 nm.

62 **Synthesis of the HFH-COFs@Au@GSH**

63 **Synthesis of the HFH-COFs**

64 The HFH-COFs were prepared at room temperature according to the previous
65 literature with slight modification. In brief, 1,3,5-tris(4-aminophenyl)benzene (TPB,
66 0.04 mmol) and 2,5-divinylterephthalaldehyde (DVA, 0.06 mmol) were dispersed in 5
67 mL of ACN with 8% H₂O and sonicated for 20 s to dissolve the building blocks
68 completely. After that, 1.0 mL of HAc (17.4 M) was added and sonicated for 10 s. Then
69 the mixture was incubated at room temperature for 72 h. The obtained yellow

70 precipitates were collected by centrifugation at 12000 rpm for 3 min and washed with
71 acetonitrile and ethanol for three times, respectively. Eventually, the yellow powders
72 were dried overnight at 60 °C under vacuum for use.

73 **Synthesis of the HFH-COFs@Au**

74 The yellow product (20 mg) was dispersed in 4 mL of deionized water and the
75 mixture was sonicated for 10 min to completely disperse the HFH-COFs. 7.5 mg of
76 $H_7AuCl_4O_3$ was added to the above mixture solution and shaken for 30 min vigorously.
77 Sodium citrate (SC, 75.0 mg), tannic acid (TA, 0.30 mg) and potassium carbonate
78 (K_2CO_3 , 15.80 mg) were added in a round-bottom flask (100 mL) along with 50 mL of
79 water. After heating the flask to 70°C, the prepared above solution was injected and
80 was kept at 70 °C under strenuous stirring for 20 min to get brown product HFH-
81 COFs@Au. The obtained brown precipitates were collected by centrifugation at 12000
82 rpm for 3 min and washed with deionized water for three times and dried for 16 h at 60
83 °C in vacuum to give brown powders.

84 **Synthesis of the HFH-COFs@Au@GSH**

85 The HFH-COFs@Au@GSH were obtained through the reaction between the
86 HFH-COFs@Au (20 mg) and glutathione (100 mg) at room temperature for 24 h. The
87 obtained precipitates were washed with deionized water for three times and dried in
88 vacuum at 60 °C for 16 h.

89 **Digestion of standard proteins and biosample**

90 1 mg of HRP was added to 1 mL of NH_4HCO_3 solution (50 mM, pH 8.3). The protein
91 solution was kept at 100 °C for 10 min to denature the proteins. After cooled to room

92 temperature, 20 μg of trypsin was added to digest the proteins at 37 $^{\circ}\text{C}$ for 16 h. The
93 procedure of digest of BSA was different from that of HRP. 10 mg of BSA was added
94 to 500 μL of NH_4HCO_3 solution (50 mM, pH 8.3) containing urea (8 M) and denatured
95 at 56 $^{\circ}\text{C}$ for 15 min. The protein solution was then reduced by 110 μL 100 mM DTT at
96 56 $^{\circ}\text{C}$ for 1 h and further alkylated by 270 μL 100 mM IAA at 37 $^{\circ}\text{C}$ for 30 min in the
97 dark. Finally, the protein solution was diluted to 2 mL and digested by 200 μg of trypsin
98 at 37 $^{\circ}\text{C}$ for 16 h. These resulted tryptic digests were stored at -20 $^{\circ}\text{C}$ for further use. 5
99 μL of human serum was firstly diluted with 50 μL NH_4HCO_3 solution (50 mM, pH 8.3)
100 and denatured at 100 $^{\circ}\text{C}$ for 10 min. The mixture was reduced by using 100 μL DTT
101 (1M) at 60 $^{\circ}\text{C}$ for 1h and alkylated by 7.5mg IAA at 37 $^{\circ}\text{C}$ for 1 h in the dark. After
102 that, the obtained solution was digested with trypsin (trypsin:protein, 1:40, w/w) at 37
103 $^{\circ}\text{C}$ for 16 h. Finally, the tryptic digest was lyophilized and stored at -20 $^{\circ}\text{C}$ until use.

104 **Enrichment protocol for standard proteins and complex biological samples.**

105 For standard proteins, the HFH-COFs@Au@GSH (200 μg) were suspended into
106 100 μL of loading buffer (95% ACN/0.1% TFA including 10 μL of the HRP tryptic
107 digest). The above mixture was sonicated for a few seconds and incubated for 30 min
108 at room temperature. After centrifugation and removal of supernatant, the HFH-
109 COFs@Au@GSH were washed with 100 μL of washing buffer (95% ACN involving
110 0.1% TFA) for three times to remove nonspecific binding. Eventually, the target N-
111 glycopeptides were eluted with elution buffer (30% ACN containing 0.1% TFA) by
112 sonication for 20 min and then analyzed by MALDI-TOF MS.

113 For the enrichment of N-linked glycopeptides in human serum, first of all, 200 μg

114 of the HFH-COFs@Au@GSH were suspended into 100 μL of loading buffer (95%
115 ACN/0.1% TFA including 10 μL of tryptic digest of serum supernatant). After
116 incubated for 30 min, the above mixture was washed with washing buffer (95% ACN
117 involving 0.1% TFA), and eluted with elution buffer (30% ACN containing 0.1% TFA).
118 The eluent was lyophilized and redissolved into a lysis solution containing 17 μL of
119 H_2O , 2 μL of glycobuffer and 1 μL of PNGase F. After 16 h of the deglycosylation
120 process at 37 $^\circ\text{C}$, the obtained peptides were lyophilized for timsTOF Pro analysis.

121 **MALDI-TOF MS analysis**

122 In brief, 1 μL of eluate was dropped on the sample plate and air-dried. Subsequently,
123 1 μL of matrix solution (25 mg mL^{-1} DHB in 50% ACN/49% H_2O /1% H_3PO_4) was
124 covered on the eluate. The captured phosphopeptides were identified by Bruker
125 autoflex speed MALDI-TOF/TOF MS in reflector positive-ion mode equipped with the
126 Nd: YAG laser (355 nm), the repetition rate (2000 Hz), and the acceleration voltage (20
127 kV).

128 **TimsTOF Pro MS analysis**

129 Human serum samples were analyzed on a nanoElute (Bruker) coupled to a timsTOF
130 Pro (Bruker) equipped with a Captive Spray source. Peptides were dissolved in 10 μL
131 of 0.1% formic acid and were auto-sampled directly onto a homemade C18 column (35
132 $\text{cm} \times 75 \mu\text{m}$ i.d., 1.9 μm 100 \AA). Samples were then eluted for 60 min with linear
133 gradients of 3–35% acetonitrile in 0.1% formic acid at a flow rate of 300 nL/min . Mass
134 spectra data were acquired with a timsTOF Pro mass spectrometer (Bruker) operated in
135 PASEF mode. The raw files were analyzed by Peaks Studio X software against uniprot

136 database.

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

157

158

159

160 **Supplementary figures**

161

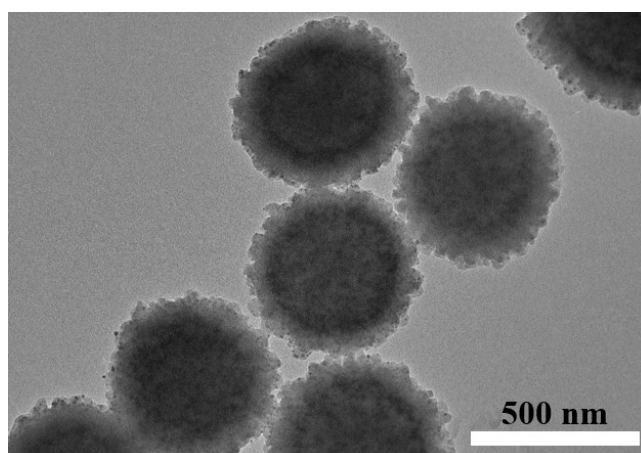
162

163

164

165

166



167

168

Fig. S1 TEM images of the HFH-COFs@Au.

169

170

171

172

173

174

175

176

177

178

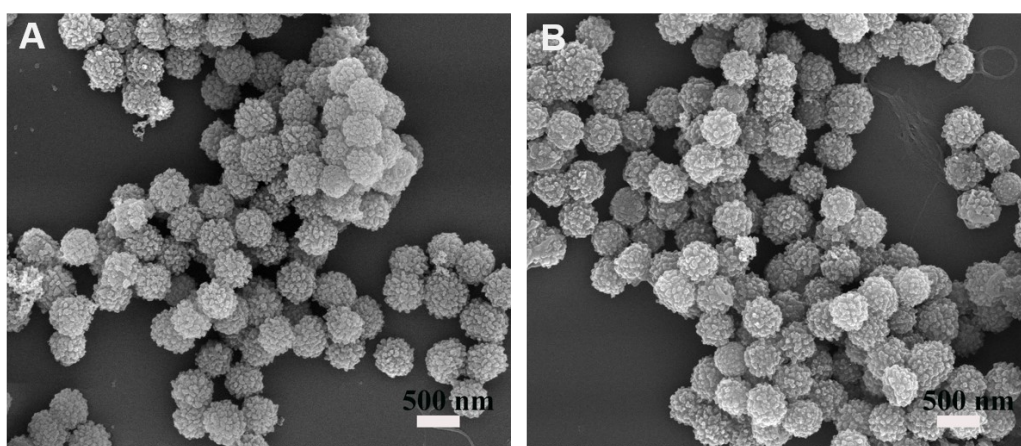
179

180

181

182

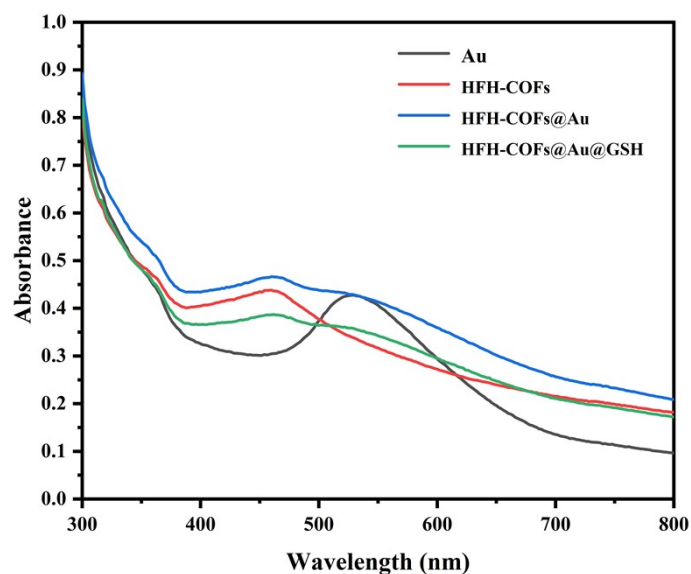
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199



200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215

Fig. S2 SEM images of (A) HFH-COFs@Au, and (B) HFH-COFs@Au@GSH.

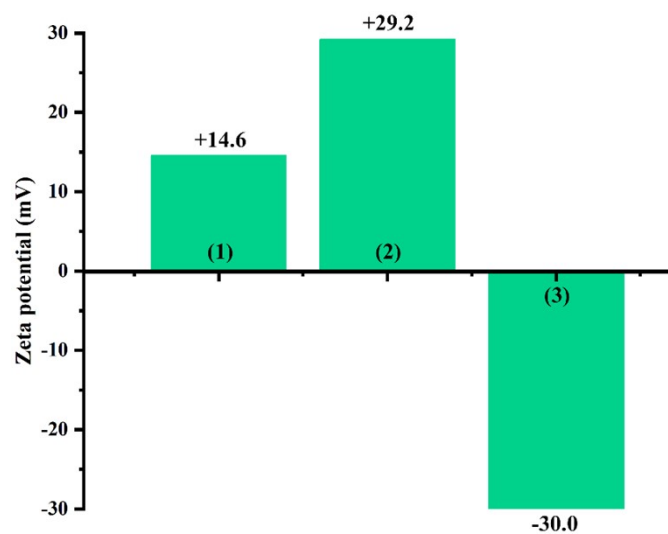
216
217
218
219
220
221
222
223
224
225
226
227



228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246

Fig. S3 UV-visible spectra of Au NPs, HFH-COFs, HFH-COFs@Au, and HFH-COFs@Au@GSH

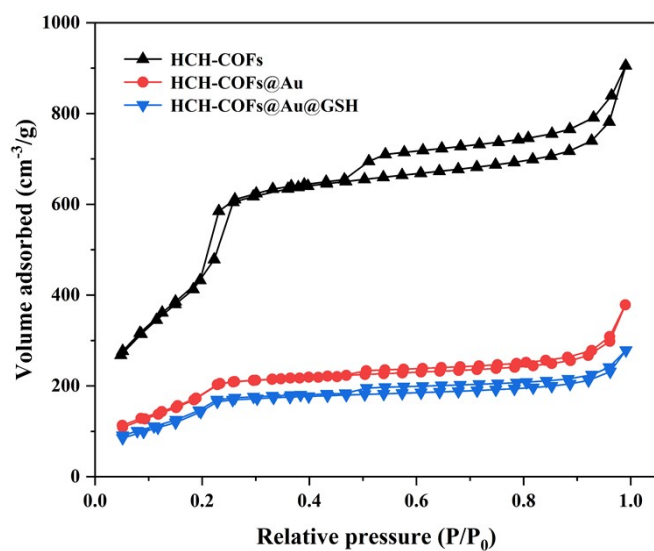
247
248
249
250
251
252
253
254
255
256



257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278

Fig. S4 Zeta potential of (1) HFH-COFs, (2) HFH-COFs@Au and (3) HFH-COFs@Au@GSH.

279
280
281
282
283
284
285
286
287
288



289

290 **Fig. S5** Nitrogen adsorption and desorption isotherms of the HFH-COFs, HFH-

291

COFs@Au, and HFH-COFs@Au@GSH.

292

293

294

295

296

297

298

299

300

301

302

303

304

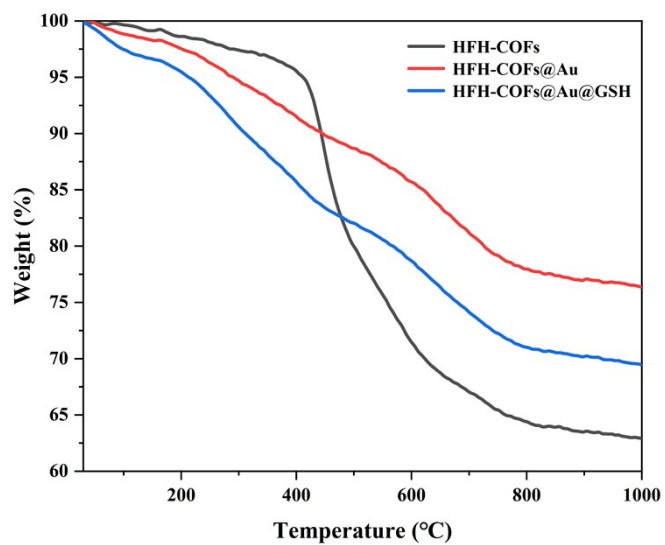
305

306

307

308

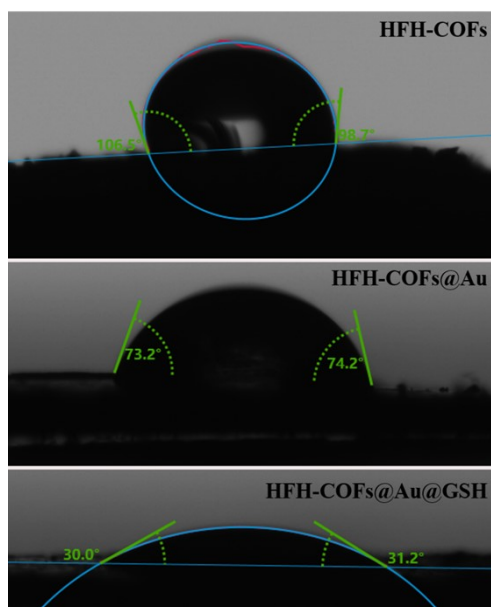
309
310
311
312
313
314
315
316
317
318



319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339

Fig. S6 TGA analysis of the HFH-COFs, HFH-COFs@Au and HFH-COFs@Au@GSH.

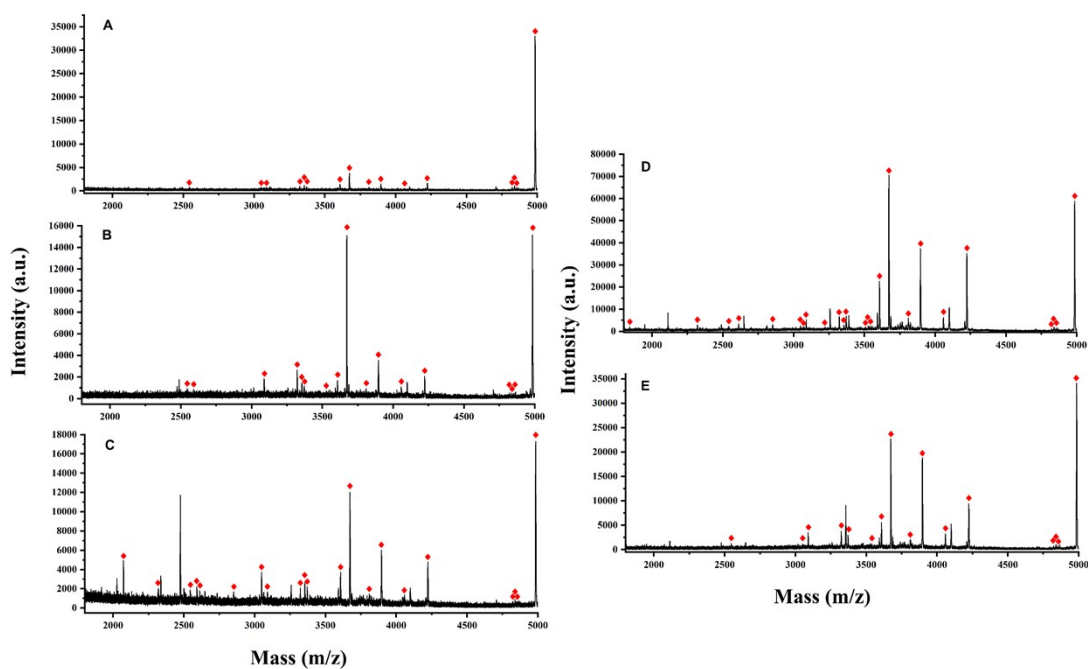
340
341
342
343
344
345
346



347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368

Fig. S7 Contact angles of the HFH-COFs, HFH-COFs@Au and HFH-COFs@Au@GSH.

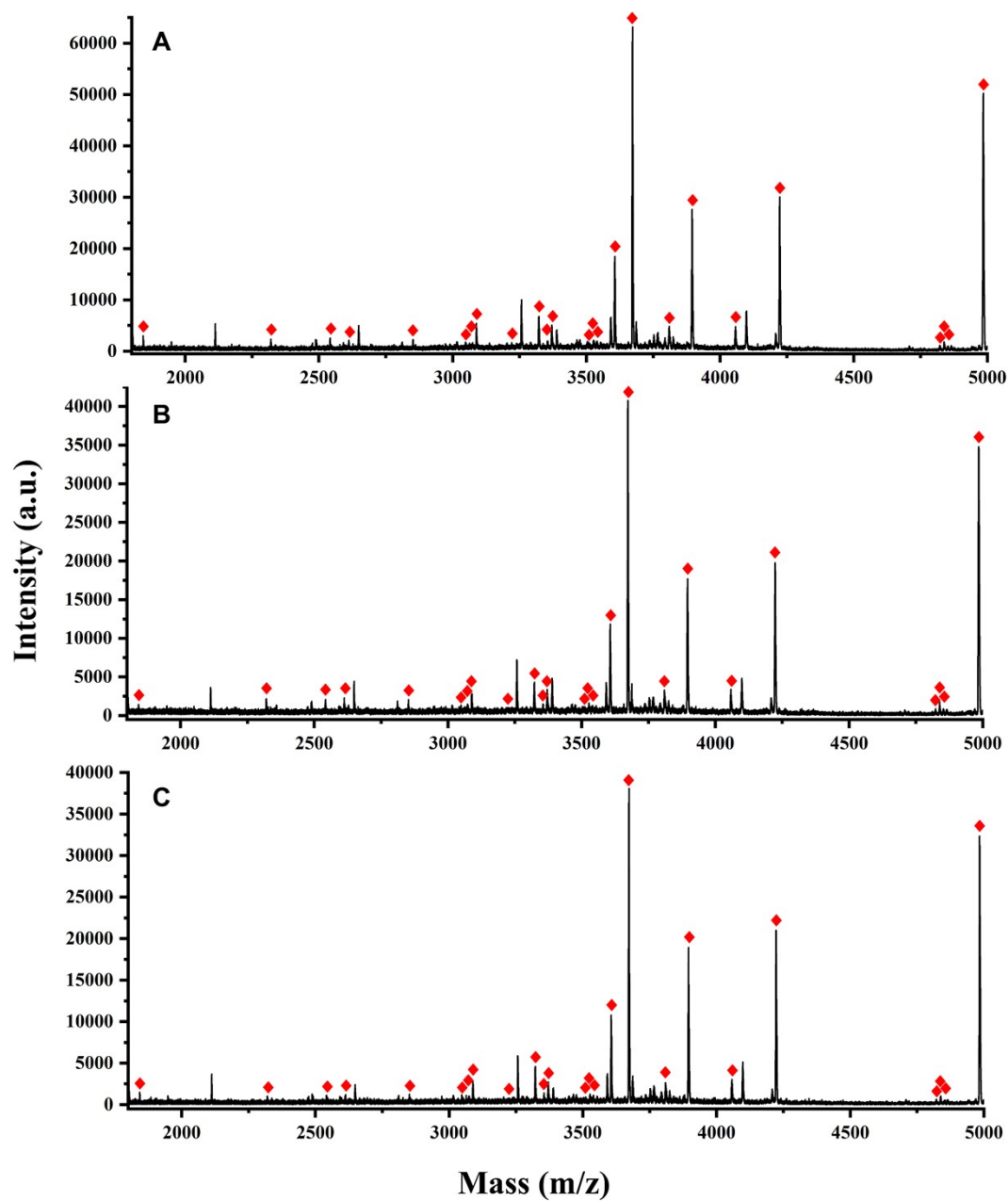
369
370
371
372
373
374
375



376

377 **Fig. S8** MALDI-TOF mass spectrometry of HRP trypsin digest by the HFH-
378 COFs@Au@GSH with different gold content (A) 1.0 mg, (B) 2.5 mg (C) 5.0 mg (D)
379 7.5 mg, and (E) 10.0 mg. Glycopeptide peaks are marked with “*”

380
381
382
383
384
385
386
387
388



390

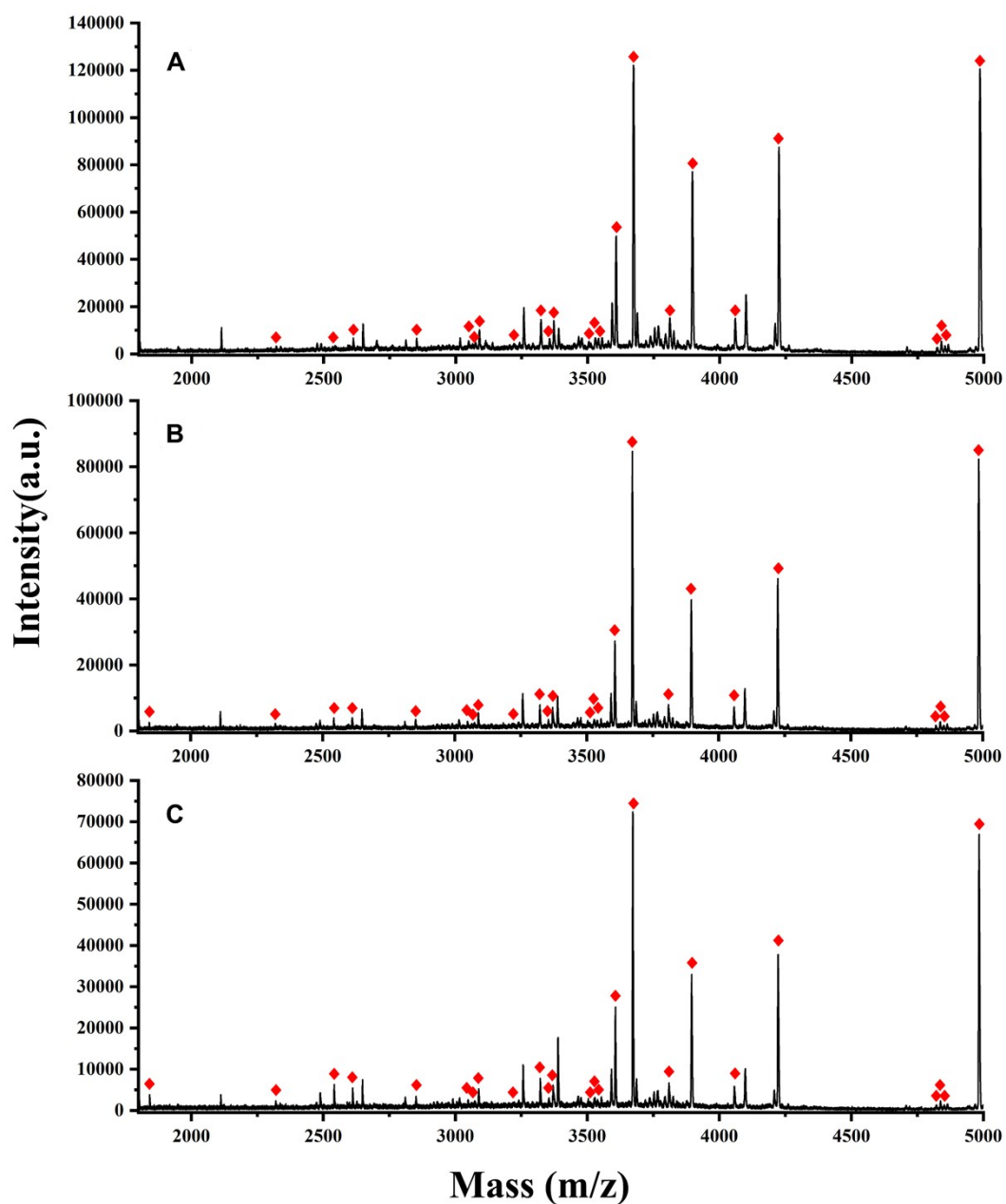
391 **Fig. S9** MALDI-TOF mass spectra of the tryptic digests of HRP after enrichment by
392 the same batch of the HFH-COFs@Au@GSH for the (A) first time, (B) third time, and

393 (C) fifth time. Glycopeptide peaks are marked with “*”

394

395

396



398

399 **Fig. S10** MALDI-TOF mass spectra of HRP tryptic digest after enrichment by the
400 HFH-COFs@Au@GSH stored in water for (A) one months, (B) three months, and (C)

401 five months, respectively. Glycopeptide peaks are marked with “*”

402

403

404

405

406

407

408 Table S1 XPS element analysis of the HFH-COFs@Au@GSH.

Element	Weight%	Atomic%
C	44.18	70.12
N	5.76	7.84
O	13.92	16.57
S	3.98	2.37
Au	32.16	3.11
Total	100	100

409

410

411

412

413

414

415

416

417

418

419

420

421

422 Table S2 Detailed information about the identified N-glycopeptides captured by the
423 HFH-COFs@Au@GSH from the tryptic digest of HRP. The lower case letter n represent
424 N-glycosylation site.

NO.	Glycan composition	Peptide sequence	Observed m/z
1	XylMan3FucGlcNAc2	NVGLnR	1842
2	Man2GlcNAc2	MGnITPLTGTQGQIR	2320
3	XylMan3FucGlcNAc2	SSPnATDTIPLVR	2541
4	XylMan3GlcNAc2	MGnITPLTGTQGQIR	2611
5	FucGlcNAc	GLIQSDQELFSSPnATDTIPLVR	2851
6	XylMan2GlcNAc2	SFAnSTQTFNFAFVEAMDR	3048
7	FucGlcNAc	LHFHDCFVNGCDASILLDnTTSFR	3074
8	XylMan3FucGlcNAc2	GLCPLNGnLSALVDFDLR	3089
9	Man3FucGlcNAc2	SFAnSTQTFNFAFVEAMDR	3222
10	XylMan3FucGlcNAc2	QLTPTFYDNSCPnVSNIVR	3322
11	XylMan3FucGlcNAc2	SFAnSTQTFNFAFVEAMDR	3354
12	XylMan3FucGlcNAc2	SFAnSTQTFNFAFVEAM*DR	3370
13	XylMan2FucGlcNAc2	GLIQSDQELFSSPnATDTIPLVR	3511
14	XylMan3GlcNAc2	GLIQSDQELFSSPnATDTIPLVR	3527
15	Man3FucGlcNAc2	GLIQSDQELFSSPNATDTIPLVR	3539
16	XylMan3FucGlcNAc2	NQCRGLCPLNGnLSALVDFDLR	3607
17	XylMan3FucGlcNAc2	GLIQSDQELFSSPnATDTIPLVR	3672
18	Man2GlcNAc2	LHFHDCFVNGCDASILLDnTTSFRTEK	3812
19	XylMan3FucGlcNAc2	LHFHDCFVNGCDASILLDnTTSFR	3894
20	XylMan3GlcNAc2	QLTPTFYDNSC(AAVESACPR)PnVSNIVR-H2O	4057
21	XylMan3FucGlcNAc2	QLTPTFYDNSC(AAVESACPR)PnVSNIVR	4221
22	XylMan2FucGlcNAc2, XylMan2GlcNAc2	LYnFSNTGLPDPTLnTTYLQTLR	4821
23	XylMan3FucGlcNAc2, XylMan3GlcNAc2	LYnFSNTGLPDPTLnTTYLQTLR	4838
24	Man3FucGlcNAc2, XylMan3FucGlcNAc2	LYnFSNTGLPDPTLnTTYLQTLR	4852
25	XylMan3FucGlcNAc2, XylMan3GlcNAc2	LYnFSNTGLPDPTLnTTYLQTLR	4984

425

426

427

428

429

430

432 Table S3 Detailed information about the identified N-glycopeptides captured by the
 433 HFH-COFs@Au@GSH from human serum. The lower case letter n represent N-
 434 glycosylation site.

NO.	Protein ID	Protein Accession	Peptide	Mass
1	1	P02768 (ALBU_HUMAN)	R.nECFLQHKDD.N	1304.5455
2	1	P02768 (ALBU_HUMAN)	R.nECFLQHK.D	1074.4917
3	1	P02768 (ALBU_HUMAN)	R.nECFLQHKD.D	1189.5186
4	1	P02768 (ALBU_HUMAN)	R.nECFLQHKDDNP.L	1996.9061
5	1	P02768 (ALBU_HUMAN)	Q.EPERnECFLQHKDDNP.L	2507.1611
6	1	P02768 (ALBU_HUMAN)	R.nECFLQHKDDNP.L	1629.6842
7	1	P02768 (ALBU_HUMAN)	A.DCCAKQEPERnECFLQHKDDNP.L	3269.4399
8	1	P02768 (ALBU_HUMAN)	R.nECFLQHKDDN.P	1418.5885
9	1	P02768 (ALBU_HUMAN)	n.ECFLQHKDDNP.L	1881.8792
10	1	P02768 (ALBU_HUMAN)	R.nECFLQH.K	946.3967
11	1	P02768 (ALBU_HUMAN)	C.AKQEPERnECFLQHKDDNP.L	2834.3518
12	1	P02768 (ALBU_HUMAN)	K.QEPERnECFLQHKDDNP.L	2636.2036
13	1	P02768 (ALBU_HUMAN)	R.ETYGEMADCCAKQEPERnECFLQHKDDNP.L	4050.7354
14	4	P00738 (HPT_HUMAN)	K.VVLHPnYSQVDIGLIK.L	2036.167
15	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnATAK.D	1574.7212
16	4	P00738 (HPT_HUMAN)	E.nATAKDIAPTLTLYVGKK.Q	1904.0618
17	4	P00738 (HPT_HUMAN)	K.VVLHPnYSQVDIGLIK.L	1794.9879
18	4	P00738 (HPT_HUMAN)	N.LFLnHSEnATAK.D	1345.6514
19	4	P00738 (HPT_HUMAN)	K.MVSHHnLTTGATLINEQWLLTTAK.N	2695.364
20	4	P00738 (HPT_HUMAN)	L.TTAKNLFLnHSEnATAK.D	1860.9218
21	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnATAK.D	1460.6783
22	4	P00738 (HPT_HUMAN)	K.MVSHHnLTTG.A	1096.4972
23	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnATAKDIAPTLTLYVGKK.Q	2859.5017
24	4	P00738 (HPT_HUMAN)	K.MVSHHnLTT.G	1039.4757
25	4	P00738 (HPT_HUMAN)	F.LnHSEnATAK.D	1085.4989
26	4	P00738 (HPT_HUMAN)	L.FLnHSEnATAK.D	1232.5673
27	4	P00738 (HPT_HUMAN)	K.MVSHHnLT.T	938.428
28	4	P00738 (HPT_HUMAN)	K.MVSHHnLTTGA.T	1167.5343
29	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnA.T	1159.5145
30	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnATA.K	1331.5994
31	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnATAKDIAPTLTLY.V	2447.2219
32	4	P00738 (HPT_HUMAN)	K.NLFLnHSE.N	973.4505
33	4	P00738 (HPT_HUMAN)	K.NLFLnHSEnAT.A	1260.5623
34	9	P0C0L4 (CO4A_HUMAN)	R.FSDGLESnSSTQFEVK.K	1774.7897
35	9	P0C0L4 (CO4A_HUMAN)	R.GLnVTLSSTGR.N	1104.5775

36	9	P0C0L4 (CO4A_HUMAN)	G.LnVTLSSSTGR.N	1047.556
37	9	P0C0L4 (CO4A_HUMAN)	R.FSDGLESnSSTQFEVKK.Y	1902.8846
38	10	P0C0L5 (CO4B_HUMAN)	R.FSDGLESnSSTQFEVKK.K	1774.7897
39	10	P0C0L5 (CO4B_HUMAN)	R.GLnVTLSSSTGR.N	1104.5775
40	10	P0C0L5 (CO4B_HUMAN)	G.LnVTLSSSTGR.N	1047.556
41	10	P0C0L5 (CO4B_HUMAN)	R.FSDGLESnSSTQFEVKK.Y	1902.8846
42	3	P63261 (ACTG_HUMAN)	M.EEEIAALVIDnGSGMCK.A	1877.8386
43	3	P63261 (ACTG_HUMAN)	M.EEEIAALVIDnGSGM.C	1604.7239
44	14	P02671 (FIBA_HUMAN)	N.NPDWGTFFEEVSGnVSPGTR.R	2047.9235
45	11	P01857 (IGHG1_HUMAN)	K.TKPREEQYnSTYR.V	1671.7853
46	11	P01857 (IGHG1_HUMAN)	R.EEQYnSTYR.V	1189.4888
47	11	P01857 (IGHG1_HUMAN)	R.EEQYnSTYRVVSVL.T	1686.8101
48	11	P01857 (IGHG1_HUMAN)	K.TKPREEQYnSTYRVV.S	1869.922
49	11	P01857 (IGHG1_HUMAN)	K.TKPREEQYnSTYRVVSVL.T	2169.1064
50	11	P01857 (IGHG1_HUMAN)	N.AKTKPREEQYnSTYR.V	1870.9172
51	54	P02765 (FETUA_HUMAN)	N.AQNnGSNFQLEEISR.A	1706.786
52	54	P02765 (FETUA_HUMAN)	K.VCQDCPLLAPLnDTR.V	1771.8232
53	54	P02765 (FETUA_HUMAN)	L.APLnDTRVVHAAK.A	1391.7521
54	54	P02765 (FETUA_HUMAN)	A.AFNAQNnGSNFQLEEISR.A	2038.9344
55	54	P02765 (FETUA_HUMAN)	R.KVCQDCPLLAPLnDTR.V	1899.9182
56	54	P02765 (FETUA_HUMAN)	Q.NnGSNFQLEEISR.A	1507.6903
57	54	P02765 (FETUA_HUMAN)	N.nGSNFQLEEISR.A	1393.6473
58	54	P02765 (FETUA_HUMAN)	n.DTRVVHAAK.A	995.5512
59	54	P02765 (FETUA_HUMAN)	K.AALAAFNAQNnGSNFQLEEISR.A	2366.1138
60	54	P02765 (FETUA_HUMAN)	Q.DCPLLAPLnDTR.V	1384.6656
61	54	P02765 (FETUA_HUMAN)	A.LAAFNAQNnGSNFQLEEISR.A	2223.0557
62	54	P02765 (FETUA_HUMAN)	K.AALAAFNAQNnGSNFQLE.E	1879.87
63	54	P02765 (FETUA_HUMAN)	L.APLnDTR.V	786.3871
64	54	P02765 (FETUA_HUMAN)	L.AAFNAQNnGSNFQLEEISR.A	2109.9714
65	2	P60709 (ACTB_HUMAN)	M.DDDIAALVVDnGSGMCK.A	1821.776
66	26	P02787 (TRFE_HUMAN)	R.QQHLFGSnVTDCSGNFCLFR.S	2515.1008
67	26	P02787 (TRFE_HUMAN)	S.nVTDCSGNFCLFR.S	1589.6603
68	26	P02787 (TRFE_HUMAN)	F.GSnVTDCSGNFCLFR.S	1733.7137
69	26	P02787 (TRFE_HUMAN)	R.QQHLFGSnVTDCSGNF.C	1938.8167
70	26	P02787 (TRFE_HUMAN)	K.ILRQQHLFGSnVTDCSGNFCLFR.S	2897.3701
71	26	P02787 (TRFE_HUMAN)	K.ILRQQHLFGSnVTD.C	1755.8904
72	26	P02787 (TRFE_HUMAN)	H.LFGSnVTDCSGNFCLFR.S	1993.8662
73	26	P02787 (TRFE_HUMAN)	K.ILRQQHLFGSnVTDCSGNF.C	2321.0859
74	26	P02787 (TRFE_HUMAN)	R.QQHLFGSnVTD.C	1373.6211
75	21	P04264 (K2C1_HUMAN)	M.DNnRSLDLSIIAEVK.A	1800.9218
76	21	P04264 (K2C1_HUMAN)	M.QTQISETNVILSMDNnR.S	1977.9426
77	21	P04264 (K2C1_HUMAN)	Q.TQISETNVILSMDNnR.S	1833.889
78	21	P04264 (K2C1_HUMAN)	Q.ISETNVILSMDNnR.S	1620.7777
79	21	P04264 (K2C1_HUMAN)	S.ETNVILSMDNnR.S	1420.6616

80	21	P04264 (K2C1_HUMAN)	L.SMDNnRSLDLDSIIAEVK.A	2018.9943
81	24	P01859 (IGHG2_HUMAN)	K.TKPREEQFnSTFR.V	1639.7954
82	24	P01859 (IGHG2_HUMAN)	R.EEQFnSTFR.V	1157.4989
83	24	P01859 (IGHG2_HUMAN)	K.TKPREEQFnSTFRVVSVL.T	2137.1167
84	24	P01859 (IGHG2_HUMAN)	K.TKPREEQFnSTFRVV.S	1837.9323
85	24	P01859 (IGHG2_HUMAN)	N.AKTKPREEQFnSTFR.V	1838.9275
86	13	P08670 (VIME_HUMAN)	R.DGQVInETSQHDDLE	1835.7922
87	13	P08670 (VIME_HUMAN)	R.QDVDnASLAR.L	1087.5258
88	18	P01860 (IGHG3_HUMAN)	R.EEQYnSTFR.V	1173.4938
89	48	P01591 (IGJ_HUMAN)	R.NIRIIVPLNNREnISDPTSPLR.T	2531.3818
90	48	P01591 (IGJ_HUMAN)	R.IVLVDnKCKCAR.I	1474.7748
91	48	P01591 (IGJ_HUMAN)	N.NREnISDPTSPLRTR.F	1755.8864
92	48	P01591 (IGJ_HUMAN)	R.IIVPLNNREnISDPTSPLR.T	2149.1379
93	48	P01591 (IGJ_HUMAN)	R.NIRIIVPLNNREnIS.D	1764.9846
94	48	P01591 (IGJ_HUMAN)	R.NIRIIVPLNNREnISD.P	1880.9956
95	48	P01591 (IGJ_HUMAN)	R.EnISDPTSPLR.T	1228.5935
96	48	P01591 (IGJ_HUMAN)	R.IVLVDnKCK.C	1088.59
97	48	P01591 (IGJ_HUMAN)	R.NIRIIVPLNNREnISDPTSPLRTR.F	2788.5308
98	48	P01591 (IGJ_HUMAN)	R.IIVPLNNREnISD.P	1497.7675
99	48	P01591 (IGJ_HUMAN)	R.IVLVDnK.C	799.4803
100	48	P01591 (IGJ_HUMAN)	R.IIVPLNNREnIS.D	1382.7405
101	48	P01591 (IGJ_HUMAN)	L.NNREnISDPTSPLRTR.F	1869.9293
102	48	P01591 (IGJ_HUMAN)	L.NNREnISDPTSPLR.T	1612.7805
103	48	P01591 (IGJ_HUMAN)	R.IIVPLNNREnISDPTSPLR.R	1992.0527
104	48	P01591 (IGJ_HUMAN)	R.IIVPLNNREnISDPTSPLRTR.F	2406.2866
105	48	P01591 (IGJ_HUMAN)	N.NREnISDPTSPLR.T	1497.7535
106	27	P01024 (CO3_HUMAN)	K.SLKVVPEGIRMnKTVAVR.T	1997.1455
107	27	P01024 (CO3_HUMAN)	R.MnKTVAVR.T	918.4957
108	27	P01024 (CO3_HUMAN)	K.SLKVVPEGIRMnK.T	1470.8228
109	27	P01024 (CO3_HUMAN)	K.TVLPATNHMGnVFTFIPANR.E	2255.137
110	27	P01024 (CO3_HUMAN)	E.GIRMnKTVAVR.T	1244.7023
111	27	P01024 (CO3_HUMAN)	K.VVPEGIRMnKTVAVR.T	1667.9504
112	27	P01024 (CO3_HUMAN)	K.VVPEGIRMnK.T	1142.6117
113	27	P01024 (CO3_HUMAN)	G.IRMnKTVAVR.T	1187.6808
114	74	P25311 (ZA2G_HUMAN)	R.FGCEIEnR.S	1138.4713
115	49	P02790 (HEMO_HUMAN)	R.NGTGHGnSTHHGPEYMR.C	1852.7548
116	49	P02790 (HEMO_HUMAN)	K.ALPQPQnVTSLLGCTH	1735.8563
117	49	P02790 (HEMO_HUMAN)	N.AAKALPQPQnVTSLLGCTH	2006.0255
118	49	P02790 (HEMO_HUMAN)	R.SWPAVGnCSSALR.W	1404.6456
119	49	P02790 (HEMO_HUMAN)	A.LPQPQnVTSLLGCTH	1664.8192
120	49	P02790 (HEMO_HUMAN)	L.PQPQnVTSLLGCTH	1551.7351
121	49	P02790 (HEMO_HUMAN)	A.AKALPQPQnVTSLLGCTH	1934.9884
122	49	P02790 (HEMO_HUMAN)	Q.nVTSLLGCTH	1101.5125
123	49	P02790 (HEMO_HUMAN)	Q.PQnVTSLLGCTH	1326.6238

124	49	P02790 (HEMO_HUMAN)	n.VTSLLGCTH	986.4855
125	49	P02790 (HEMO_HUMAN)	G.nSTHHGPEYMR.C	1328.5568
126	49	P02790 (HEMO_HUMAN)	Y.SDVEKLNAAKALPQPQnVTSLLGCTH	2791.4175
127	49	P02790 (HEMO_HUMAN)	S.DVEKLNAAKALPQPQnVTSLLGCTH	2704.3853
128	49	P02790 (HEMO_HUMAN)	P.QnVTSLLGCTH	1229.571
129	49	P02790 (HEMO_HUMAN)	A.KALPQPQnVTSLLGCTH	1863.9513
130	49	P02790 (HEMO_HUMAN)	K.SLGPhSCSANGPGLYL.I	1605.7457
131	49	P02790 (HEMO_HUMAN)	K.SLGPhSCSANGPGLYLIH.G	1855.8887
132	49	P02790 (HEMO_HUMAN)	K.ALQPQnVTSLG.C	1337.719
133	49	P02790 (HEMO_HUMAN)	K.ALQPQnVTSLG.G	1280.6976
134	49	P02790 (HEMO_HUMAN)	P.QPQnVTSLGCTH	1454.6824
135	49	P02790 (HEMO_HUMAN)	G.nCSSALR.W	807.3545
136	19	P05787 (K2C8_HUMAN)	K.AQYEDIA n.R.S	1078.5043
137	19	P05787 (K2C8_HUMAN)	R.GGLGGGYGGASGMGGITAVTV n.QSLLSPLVLEVDPNIA VR.T	3941.0203
138	19	P05787 (K2C8_HUMAN)	R.LESGM n.MSIHTK.T	1506.6807
139	28	P10909 (CLUS_HUMAN)	R.EIRH n.STGCLR.M	1342.6411
140	28	P10909 (CLUS_HUMAN)	R.H n.STGCLR.M	944.4134
141	28	P10909 (CLUS_HUMAN)	K.KKKEDAL n.ETR.E	1331.7045
142	28	P10909 (CLUS_HUMAN)	K.KKEDAL n.ETR.E	1203.6095
143	28	P10909 (CLUS_HUMAN)	K.KKEDAL n.ETRESETK.L	1777.8694
144	28	P10909 (CLUS_HUMAN)	K.KEDAL n.ETRESETK.L	1649.7744
145	28	P10909 (CLUS_HUMAN)	K.KEDAL n.ETR.E	1075.5145
146	38	P02749 (APOH_HUMAN)	K.LG n.WSAMPSCK.A	1250.5424
147	38	P02749 (APOH_HUMAN)	D.TITCTTHG n.WTKLPECR.E	2074.9565
148	38	P02749 (APOH_HUMAN)	n.DTITCTTHG n.WTKLPECR.E	2189.9834
149	38	P02749 (APOH_HUMAN)	F.G n.DTITCTTHG n.WTKLPECR.E	2362.0317
150	38	P02749 (APOH_HUMAN)	G.nWTKLPECR.E	1203.5707
151	38	P02749 (APOH_HUMAN)	F.ECLPQHAMFG n.DTITCTTHG n.WTKLPECR.E	3475.5054
152	38	P02749 (APOH_HUMAN)	R.VYKPSAG n.NSLYR.D	1469.715
153	38	P02749 (APOH_HUMAN)	H.G n.WTKLPECR.E	1260.592
154	38	P02749 (APOH_HUMAN)	C.TTHG n.WTKLPECR.E	1599.7463
155	38	P02749 (APOH_HUMAN)	R.VYKPSAG n.NSLYRDTAVF.E	2001.9795
156	38	P02749 (APOH_HUMAN)	R.VYKPSAG n.NSLY.R	1312.6299
157	38	P02749 (APOH_HUMAN)	R.VYKPSAG n.NSLYRDTAVFECLPQH.A	2765.323
158	38	P02749 (APOH_HUMAN)	H.AMFG n.DTITCTTHG n.WTKLPECR.E	2726.1887
159	38	P02749 (APOH_HUMAN)	G.nDTITCTTHG n.WTKLPECR.E	2304.0264
160	38	P02749 (APOH_HUMAN)	R.DTAVFECLPQHAMFG n.DTITCTTHG n.WTKLPECR.E	4024.7488
161	31	P13645 (K1C10_HUMAN)	R.nVSTGDVNVEMNAAPGVDLTQLLN.N	2486.1958
162	31	P13645 (K1C10_HUMAN)	R.nVSTGDVNVEMNAAPGVDLTQLLNNMR.S	2903.3752
163	31	P13645 (K1C10_HUMAN)	n.LTTDNANILLQIDNAR.L	1783.9427
164	31	P13645 (K1C10_HUMAN)	R.nVSTGDVNVEMNAAPGVDLTQLLN.N	2372.1528
165	30	P01876 (IGHA1_HUMAN)	G.SEA n.LTCTLTGLR.D	1435.6976
166	30	P01876 (IGHA1_HUMAN)	E.DLLGSEA n.LTCTLTGLR.D	1946.9983

167	30	P01876 (IGHA1_HUMAN)	K.TIDRLAGKPTHVnVSVVM.A	1937.0404
168	30	P01876 (IGHA1_HUMAN)	R.LAGKPTHVnVSVVMAEVDGTC.Y	2184.0554
169	30	P01876 (IGHA1_HUMAN)	L.GSEAnLTCTLTGLR.D	1492.7191
170	30	P01876 (IGHA1_HUMAN)	R.LAGKPTHVnVS.V	1122.6033
171	30	P01876 (IGHA1_HUMAN)	K.TIDRLAGKPTHVnVS.V	1607.863
172	30	P01876 (IGHA1_HUMAN)	R.LAGKPTHVnVSVVM.A	1451.7806
173	41	P01861 (IGHG4_HUMAN)	R.EEQFnSTYR.V	1173.4938
174	41	P01861 (IGHG4_HUMAN)	K.TKPREEQFnSTYR.V	1655.7903
175	44	P01877 (IGHA2_HUMAN)	T.AAHPELKTPLTAnITK.S	1704.941
176	44	P01877 (IGHA2_HUMAN)	K.TPLTAnITK.S	958.5335
177	44	P01877 (IGHA2_HUMAN)	K.SVTCHVKHYTnSSQDVTVPCR.V	2475.1272
178	44	P01877 (IGHA2_HUMAN)	K.HYTnSSQDVTVPCR.V	1663.7261
179	44	P01877 (IGHA2_HUMAN)	G.SEAnLTCTLTGLR.D	1435.6976
180	44	P01877 (IGHA2_HUMAN)	W.SESGQnVTAR.N	1048.4785
181	44	P01877 (IGHA2_HUMAN)	E.DLLLGSEAnLTCTLTGLR.D	1946.9983
182	44	P01877 (IGHA2_HUMAN)	L.GSEAnLTCTLTGLR.D	1492.7191
183	44	P01877 (IGHA2_HUMAN)	S.VTWSESGQnVTAR.N	1434.674
184	96	P01009 (A1AT_HUMAN)	R.QLAHQSnSTNIFFSPVS.I	1876.8955
185	96	P01009 (A1AT_HUMAN)	R.QLAHQSnSTNIFF.S	1506.7103
186	67	Q562R1 (ACTBL_HUMAN)	R.GYnFTTTAER.E	1159.5145
187	105	P01008 (ANT3_HUMAN)	R.AAINKWVSnKTEGR.I	1574.8052
188	105	P01008 (ANT3_HUMAN)	K.WVSnKTEGR.I	1076.525
189	97	P12259 (FA5_HUMAN)	R.HLIGKNSVlnSSTAETHSSPYSE.D	2357.1135
190	97	P12259 (FA5_HUMAN)	K.NSVLlnSSTAETHSSPYSED.P	1923.797
191	97	P12259 (FA5_HUMAN)	K.NSVLlnSSTAETHSSPYSE.D	1808.77
192	97	P12259 (FA5_HUMAN)	R.SFRnSSLNQEEEEEF.N	1715.7274
193	97	P12259 (FA5_HUMAN)	R.SFRnSSLNQEEEEFNLT.A.L	2115.9233
194	97	P12259 (FA5_HUMAN)	R.SFRnSSLNQEEEEFNLTALALE.N	2542.1711
195	60	Q15149 (PLEC_HUMAN)	R.NLVDnITGQR.L	1128.5887
196	116	P04004 (VTNC_HUMAN)	N.nATVHEQVGGPSLTSDLQAQSK.G	2267.103
197	116	P04004 (VTNC_HUMAN)	D.DGEEKNnATVHEQVGGPSLTSDLQAQSK.G	2939.3745
198	116	P04004 (VTNC_HUMAN)	Y.DGEEKNnATVHEQVGGPSLTSDLQAQSK.G	3053.4172
199	78	P01871 (IGHM_HUMAN)	R.TVDKSTGKPTLYnVSLVMSDTAGTC	2808.3198
200	78	P01871 (IGHM_HUMAN)	K.YKnNSDISSTR.G	1284.5946
201	78	P01871 (IGHM_HUMAN)	F.SWKYKnNSDISSTR.G	1685.8009
202	78	P01871 (IGHM_HUMAN)	R.TVDKSTGKPTLYnVSLVMSDTA.G	2327.1567
203	78	P01871 (IGHM_HUMAN)	R.GLTFQQnASSMCVDPQDTAIR.V	2339.0522
204	111	P04196 (HRG_HUMAN)	R.VIDFnCTTSSVSSALANTK.D	2014.9518
205	59	P02545 (LMNA_HUMAN)	R.TALInSTGEEVAMR.K	1506.7347
206	153	P05155 (IC1_HUMAN)	R.VLSnNSDANLELINTWVAK.N	2101.0691
207	153	P05155 (IC1_HUMAN)	R.VLSnNSDANLELINTWVAK.N	2101.0691
208	153	P05155 (IC1_HUMAN)	S.NPhATSSSSQDPESLQDR.G	1932.8297
209	153	P05155 (IC1_HUMAN)	R.DTFVnASR.T	909.4192
210	153	P05155 (IC1_HUMAN)	P.nATSSSSQDPESLQDRGEGK.V	2092.9146

211	153	P05155 (IC1_HUMAN)	S.NPnATSSSSQDPESLQDRGEGK.V	2303.0261
212	77	P11142 (HSP7C_HUMAN)	K.VEIIANDQGnR.T	1227.6207
213	77	P11142 (HSP7C_HUMAN)	K.TVTNAVVTVPAYFnDSQR.Q	1980.9905
214	95	P00747 (PLMN_HUMAN)	R.FSPATHPSEGLEEnYCR.N	1992.8635
215	95	P00747 (PLMN_HUMAN)	K.NLDEnYCR.N	1082.4451
216	95	P00747 (PLMN_HUMAN)	R.FSPATHPSEGLEEnYCRNPdND.P	2548.0562
217	95	P00747 (PLMN_HUMAN)	K.TPENYPNAGLTmYCR.N	1899.8243
218	104	O95678 (K2C75_HUMAN)	K.AQYEDIAnR.S	1078.5043
219	80	P00734 (THRB_HUMAN)	R.GHVnITR.S	796.4191
220	80	P00734 (THRB_HUMAN)	R.SRYPHKPEINSTTHPGADLQEnFCR.N	2954.3728
221	80	P00734 (THRB_HUMAN)	E.GNCAEGLGTNYRGHVnITR.S	2088.9758
222	80	P00734 (THRB_HUMAN)	A.ACLEGNCAEGLGTNYRGHVnITR.S	2562.1704
223	80	P00734 (THRB_HUMAN)	G.NCAEGLGTNYRGHVnITR.S	2031.9545
224	80	P00734 (THRB_HUMAN)	N.CAEGLGTNYRGHVnITR.S	1918.8955
225	98	P01042 (KNG1_HUMAN)	R.HGIQYFNnTQH.S	1472.6433
226	98	P01042 (KNG1_HUMAN)	K.LNAENnATFYFK.I	1431.667
227	98	P01042 (KNG1_HUMAN)	R.HGIQYFNnTQHSSLF.M	1906.8599
228	151	P0DMV9 (HS71B_HUMAN)	K.VEIIANDQGnR.T	1227.6207
229	158	P17066 (HSP76_HUMAN)	R.VEILANDQGnR.T	1227.6207
230	81	P00751 (CFAB_HUMAN)	R.SPYnVSDEISFHCY.D	1880.7563
231	81	P00751 (CFAB_HUMAN)	R.GSAnRTCQVNGR.W	1320.5841
232	102	P08238 (HS90B_HUMAN)	R.GVVDESLPLnISR.E	1512.7783
233	102	P08238 (HS90B_HUMAN)	R.ELISnASDALDK.I	1274.6354
234	102	P08238 (HS90B_HUMAN)	R.IMKAQALRDnSTMGYMAK.K	2208.0046
235	99	P35221 (CTNA1_HUMAN)	K.nTSDVISAAsK.K	1004.5138
236	113	P13639 (EF2_HUMAN)	K.AYLPVnESFGFTADLR.S	1798.8889
237	131	P19338 (NUCL_HUMAN)	K.TLVLSnLSYSATEETLQEVFEK.A	2500.2583
238	123	P05156 (CFAI_HUMAN)	K.FLNnGTCTAEGK.F	1311.5765
239	123	P05156 (CFAI_HUMAN)	K.nGTAVCATNRR.S	1219.5728
240	106	Q13813 (SPTN1_HUMAN)	K.EELYQnLTR.E	1164.5775
241	125	P08603 (CFAH_HUMAN)	R.ISEEnETTCYMGK.W	1561.6276
242	125	P08603 (CFAH_HUMAN)	K.MDGASnVTCINSR.W	1424.6024
243	125	P08603 (CFAH_HUMAN)	K.IPCSQPPQIEHGTLnSSR.S	2020.9636
244	125	P08603 (CFAH_HUMAN)	N.GnWTEPPQCK.D	1216.5183
245	188	P35542 (SAA4_HUMAN)	G.nSSTVLEDSKSNEKAEEWGR.S	2266.0349
246	178	P04003 (C4BPA_HUMAN)	C.DSGYGVVGPQSITCSGnR.T	1853.8214
247	178	P04003 (C4BPA_HUMAN)	R.LSVDKDQYVEPEnVTIQCDSGYGVVGPQS.I	3183.4553
248	178	P04003 (C4BPA_HUMAN)	R.LSVDKDQYVEPEnVTIQC.D	2136.9885
249	256	P01019 (ANGT_HUMAN)	H.LVIHnESTCEQLAK.A	1641.8032
250	256	P01019 (ANGT_HUMAN)	H.nESTCEQLAK.A	1179.5078
251	138	Q9BVA1 (TBB2B_HUMAN)	K.MSATFIGnSTAIQELFK.R	1872.9291
252	138	Q9BVA1 (TBB2B_HUMAN)	K.nSSYFVEWIPNNVK.T	1695.8257
253	139	Q13885 (TBB2A_HUMAN)	K.MSATFIGnSTAIQELFK.R	1872.9291
254	139	Q13885 (TBB2A_HUMAN)	K.nSSYFVEWIPNNVK.T	1695.8257

255	126	P07437 (TBB5_HUMAN)	K.nSSYFVEWIPNNVK.T	1695.8257
256	126	P07437 (TBB5_HUMAN)	K.MAVTFI _{Gn} STAIQELFK.R	1884.9655
257	191	P05090 (APOD_HUMAN)	R.ADGTVNQIEGEATPV _{nL} TEPAK.L	2254.0964
258	191	P05090 (APOD_HUMAN)	R.ADGTVNQIEGEATPV _{nL} TEPAKLEVK.F	2723.3865
259	191	P05090 (APOD_HUMAN)	A.nYSLMENGKIK.V	1297.6224
260	230	P07195 (LDHB_HUMAN)	V.SLQELNPEMGTD _n DSENWK.E	2222.9272
261	128	P17936 (IBP3_HUMAN)	Y.KVDYESQSTDTQ _n FSSSESKR.E	2335.0564
262	128	P17936 (IBP3_HUMAN)	R.GLCV _n ASAVSR.L	1133.5499
263	177	P07900 (HS90A_HUMAN)	R.GVVDEDLPL _n ISR.E	1512.7783
264	221	P02748 (CO9_HUMAN)	R.CNGD _n DCGDFSEDDCESEPRPCR.D	3004.0125
265	194	P02763 (A1AG1_HUMAN)	R.QDQCIY _n TTYLNVQR.E	1915.8734
266	194	P02763 (A1AG1_HUMAN)	Y. _n TTYLNVQR.E	1108.5513
267	194	P02763 (A1AG1_HUMAN)	F.FYFTPhKTEDTIFLR.E	1891.9355
268	194	P02763 (A1AG1_HUMAN)	F.YFTPhKTEDTIFLR.E	1744.8672
269	194	P02763 (A1AG1_HUMAN)	R.QDQCIY _n TTYLNVQRE _n GTISR.Y	2674.2292
270	180	Q16643 (DREB_HUMAN)	K.VAEFFQGV _{DVIVn} ASSVEDIDAGAIGQR.L	2905.4458
271	196	P19652 (A1AG2_HUMAN)	N.LVPVPI _{Tn} ATLDR.I	1408.7926
272	196	P19652 (A1AG2_HUMAN)	A.NLVPVPI _{Tn} ATLDR.I	1522.8354
273	196	P19652 (A1AG2_HUMAN)	R.QNQCFY _n SSYLVNQR.E	1920.8424
274	196	P19652 (A1AG2_HUMAN)	C.ANLVPVPI _{Tn} ATLDR.I	1593.8726
275	196	P19652 (A1AG2_HUMAN)	A.QIPLCANLVPVPI _{Tn} ATLDR.I	2205.1826
276	196	P19652 (A1AG2_HUMAN)	F.FYFTPhKTEDTIFLR.E	1891.9355
277	196	P19652 (A1AG2_HUMAN)	F.YFTPhKTEDTIFLR.E	1744.8672
278	196	P19652 (A1AG2_HUMAN)	L.VPVPI _{Tn} ATLDR.I	1295.7085
279	196	P19652 (A1AG2_HUMAN)	Y. _n SSYLVNQR.E	1080.52
280	187	P35579 (MYH9_HUMAN)	K.IAQLEEQLD _n ETK.E	1529.7573
281	362	P68104 (EF1A1_HUMAN)	R.VETGVLPKPGMVVTFAPV _n VTTEVK.S	2530.3716
282	363	Q5VTE0 (EF1A3_HUMAN)	R.VETGVLPKPGMVVTFAPV _n VTTEVK.S	2530.3716
283	280	P01011 (AACT_HUMAN)	K.LINDYVK _n GTR.G	1292.6725
284	280	P01011 (AACT_HUMAN)	K.KLINDYVK _n GTR.G	1420.7673
285	176	O43790 (KRT86_HUMAN)	R.VSSVPSNSNVVGT _{Tn} AC.A	1791.8309
286	265	P60842 (IF4A1_HUMAN)	R.DIETFY _n TSIEEMPLNVADLI	2442.1511
287	213	Q08380 (LG3BP_HUMAN)	R.TVIRPFYL _{Tn} SSGVD	1668.8358
288	213	Q08380 (LG3BP_HUMAN)	R.ALGFEnATQALGR.A	1347.6782
289	213	Q08380 (LG3BP_HUMAN)	R.DAGVVCT _n ETR.S	1221.5295
290	296	Q03591 (FHR1_HUMAN)	R.LQNNEN _n ISCVER.G	1589.7103
291	296	Q03591 (FHR1_HUMAN)	N.G _n WTEPPQCK.D	1216.5183
292	432	P36980 (FHR2_HUMAN)	R.LQNNEN _n ISCVER.G	1589.7103
293	328	Q6UXB8 (PI16_HUMAN)	K.SLPNFP _h TSAT _{An} ATGGR.A	1776.8279
294	328	Q6UXB8 (PI16_HUMAN)	K.SLPNFPNTSAT _{An} ATGGRALA.L	2031.9861
295	456	P07357 (CO8A_HUMAN)	R.VRGSSGWSGGLAQ _n R.S	1588.7706
296	456	P07357 (CO8A_HUMAN)	R.GGSSGWSGGLAQ _n R.S	1333.6011
297	192	P19823 (ITIH2_HUMAN)	K.GAFIS _n FSMTVDGK.T	1473.6809
298	254	P43652 (AFAM_HUMAN)	R.YAEDKFnETTEK.S	1474.6464

299	254	P43652 (AFAM_HUMAN)	R.DIENFnSTQK.F	1195.5356
300	298	Q68DL7 (CR063_HUMAN)	R.LAPAWnRTGH.L	1121.573
301	215	O95445 (APOM_HUMAN)	M.LnETGQGYQR.F	1165.5364
302	339	O75882 (ATRN_HUMAN)	K.AATCINPLnGSVCERPA _n HSAK.Q	2368.0898
303	509	P37802 (TAGL2_HUMAN)	R.YGlnTTDIFQTVDLWEGK.N	2099.021
304	548	Q9H9S0 (NANOG_HUMAN)	L.SNILnLSYKQVK.T	1405.7928
305	548	Q9H9S0 (NANOG_HUMAN)	I.LnLSYKQVK.T	1091.6339
306	551	Q8N7R0 (NANG2_HUMAN)	L.SNILnLSYKQVK.T	1405.7928
307	551	Q8N7R0 (NANG2_HUMAN)	I.LnLSYKQVK.T	1091.6339
308	574	Q6NSW7 (NANP8_HUMAN)	I.LnLSYKQVK.T	1091.6339
309	574	Q6NSW7 (NANP8_HUMAN)	L.SNILnLSYKQVK.T	1406.7769

435

436

437

438

439

440

441

442

443

444

445

446

447

448