Supplementary information

Synthesis of magnetic Fe_3O_4 nanoparticles

$FeCl_3 \cdot 6H_2O$ (1.08 g, 4.0 mmol) and CH_3COONa (2.88 g, 35 mmol) were dissolved in ethylene glycol (60 mL), the homogeneous solution was sealed in stainless-steel autoclave and reacted at 200 °C for 16 h. The resulted product was collected, washed three times with deionized water and ethanol successively, and dried under vacuum at 60 °C overnight.

Synthesis of mCOF

Fe_3O_4 (300 mg), Tb (100 mg, 0.6 mmol) and DHBD (200 mg, 0.9 mmol) were dispersed in DMSO (100 mL). Being sonicated for 5 min, acetic acid (4 mL) was slowly added dropwise to the above mixture. After standing at room temperature for 24 h, the resulted precipitate was collected by magnet, washed three times with tetrahydrofuran and ethanol successively, and dried under vacuum at 60 °C overnight.

Synthesis of mCOF-GLYMO

mCOF (300 mg) and GLYMO (2400 μL) were mixed in 240 mL of toluene, which was reacted at 80 °C for 12 h. Next, the precipitate was collected by magnet, washed three times with ethanol and dried under vacuum at 60 °C overnight.

The pretreatment of standard proteins digests and actual biological samples

β-casein (1 mg) was dispersed in NH_4HCO_3 (50 mM, 100 μL) and denatured at 100℃ for 10 minutes. After natural cooling, it was digested with trypsin at a mass ratio of 1:40 (trypsin/protein, w/w) for 16 h at 37 ℃, and the final digests were saved at -20 °C. The digestion of serum was similar to that of β-casein, but protein quantification

was required prior to the procedure.

BSA was pretreated with DTT and IAA. BSA (1 mg) dispersed in NH_4HCO_3 (50mM, 185 μL) was denatured at 100℃ for 10 minutes. After the addition of DTT (40mM, 5 μL), the mixture was reduced at 37℃ for 1 h. Subsequently, IAA (40mM, 10 μL) was added for alkylation at 37℃ in the dark for 1 h. Finally, it was digested with trypsin (25 μg) at 37℃ under the dark condition for 16 hours, the digests were saved at -20 °C.

Fresh saliva of healthy human (2 mL) was added into 0.2% TFA aqueous solution (2 mL) under low temperature environment, and the supernatant was collected by centrifugation at 8000 rpm for 10 min. The samples were saved at -20 °C.

Characterization

Scanning electron microscopy (SEM) and energy-dispersive X-ray spectroscopy (EDX) were recorded on ZEISS Sigma 300 (German). Transmission electron microscope (TEM) image was conducted on a JEOL 2100F microscope (Japan). X-ray diffraction (XRD) was carried out by Bruker D8 Advance (Germany). Fourier transform infrared spectra (FT-IR) were performed on a Nicolet 6700 infrared spectrometer analysis (USA).

MALDI-TOF MS analysis

MALDI-TOF mass spectra were recorded on autoflex max MALDI-TOF(Bruker, German) with an upgraded Nd:YAG laser at 355 nm, an acceleration voltage of TOF at 20 kV and a detection frequency of 1000 Hz. The detection range of the mass-to-charge ratio was 1000–3500Da. 2,5-dihydroxybenzoic acid (DHB, 2mg) dissolved in

100 μL of buffer (ACN/H_2O/H_3PO_4, 50/49/1, v/v/v) was prepared as matrix solution for use.

Nano LC-MS/MS analysis

Phosphopeptides of human serum tryptic digests were analyzed on a Vanquish Neo UHPLC system coupled with Thermo Scientific Orbitrap Eclipse mass spectrometer with nanoelectrospray ion source. Lyophilized sample was redissolved in 0.1% FA aqueous solution (10 μL), loaded on a Thermo Scientific trap column (300μm×0.5 cm, 5μm, 100Å, C18) and then separated through an analytical chromatography column (75μm×15 cm, 2 μm, 100 Å, C18) with mobile phase A (0.1% FA aqueous solution) and mobile phase B (80% ACN with 0.1% FA) for 70 min. The elution gradient was set as follows: 0–1 min, 5-6% B; 1–43 min, 6–20% B; 43–63 min, 20–35% B; 63–67 min, 35-100% B; 67–70 min, 100% B. The flow rate was 300 nL min^{-1}.

The mass spectrometer was set as follows: Analysis time: 70min; Detection mode: positive mode; Parent ion scanning range: 350-1800 m z^{-1}; MS resolution: 60000 at 200 m z^{-1}; Scanning mode: Top-Speed; AGC target:$4e^5$; Maximum IT: 50 ms; Number of scan ranges: 1; Dynamic exclusion: 40.0 s; Data Dependent Mode: Cycle Time; Time between Master Scan: 1.5 s. The mass-charge ratio of peptides and peptide fragments were collected and set as follows: MS/MS scan was performed at the same time of each MS scan (Master scan); Activation Type: HCD; resolution: 30000 at 200 m z^{-1}; Microscan: 1; Maximum IT: 22 ms; AGC target: $1e^5$.

Data analysis

The original data of mass spectrometry analysis was RAW file, and the built-in software Proteome Discoverer 2.5 (Thermo Scientific) was used for library identification and quantitative analysis. The uniprot database is used this time: uniprot_human_reviewed(Swiss-Prot)_2023.02.14.fasta with 26554 entries. When searching the library, submitting the RAW file to SequestHT through Proteome Discoverer, selecting the established database, and then searching the database. The search parameters were as follows: monoisotopic mass, trypsin digestion, maximum 2 missing cut sites, peptides Charged number: 2^+, 3^+ and 4^+, fixed modification to carbamidomethylation (C), dynamic modification to oxidation (M), Acethyl (protein N-term) and Deamidated [N]. The maximum error of the precursor ion was 10 ppm, and the maximum error of the fragment ion was 0.02 Da. Proteome Discoverer 2.5 performs Peptide high Confidence screening based on the peptide identification results and outputed the results.

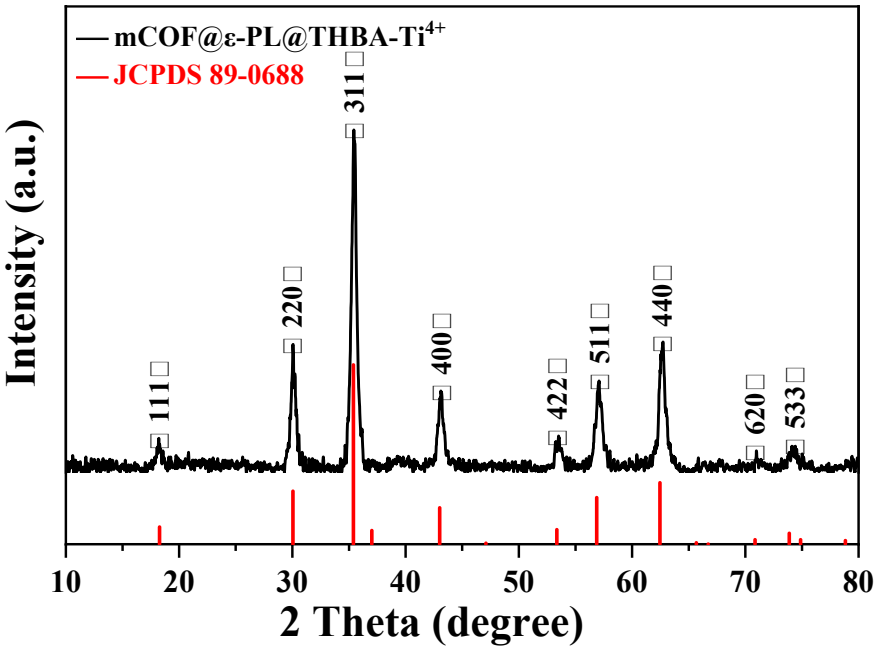

Fig. S1 Powder XRD pattern of mCOF@ε-PL@THBA-Ti^{4+}.

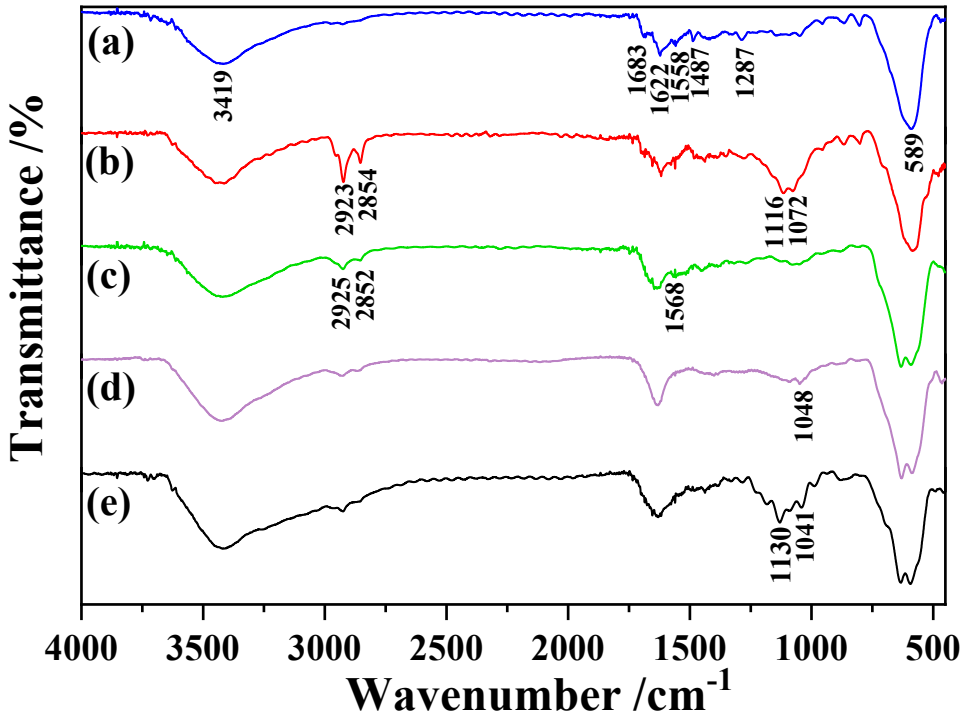

Fig. S2 FT-IR spectra of (a) mCOF, (b) mCOF-GLYMO, (c) mCOF@ε-PL, (d) mCOF@ε-PL@THBA, and (e) mCOF@ε-PL@THBA-Ti^{4+}.

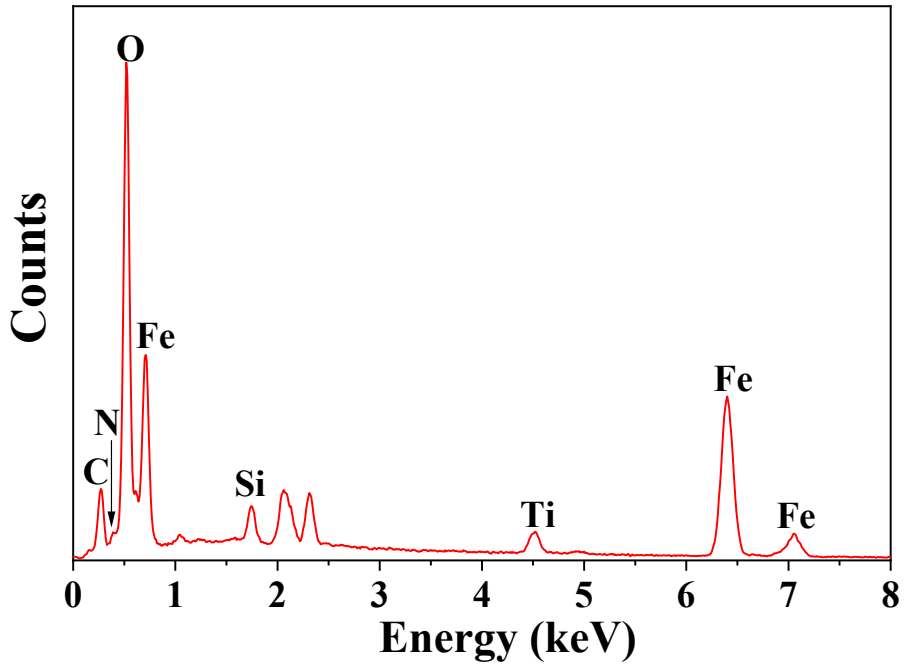

Fig. S3 EDX spectrum of mCOF@ε-PL@THBA-Ti^{4+}.

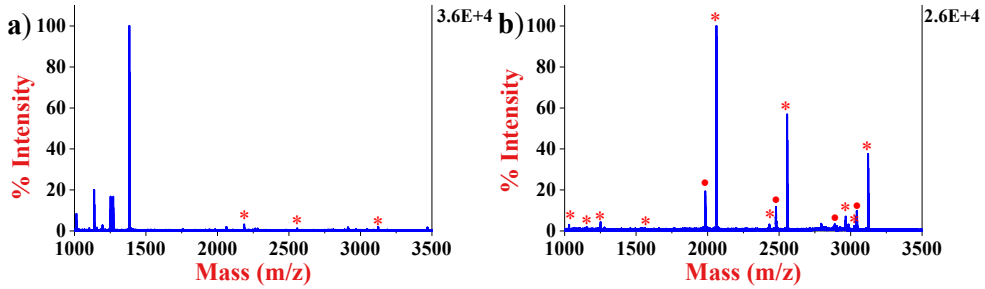

Fig. S4 Mass spectra of β-casein digests: (a) direct analysis, (b) after enrichment with mCOF@ε-PL@THBA-Ti^{4+}. Peaks of phosphopeptide and dephosphorylated are signed as "∗" and "●", respectively.

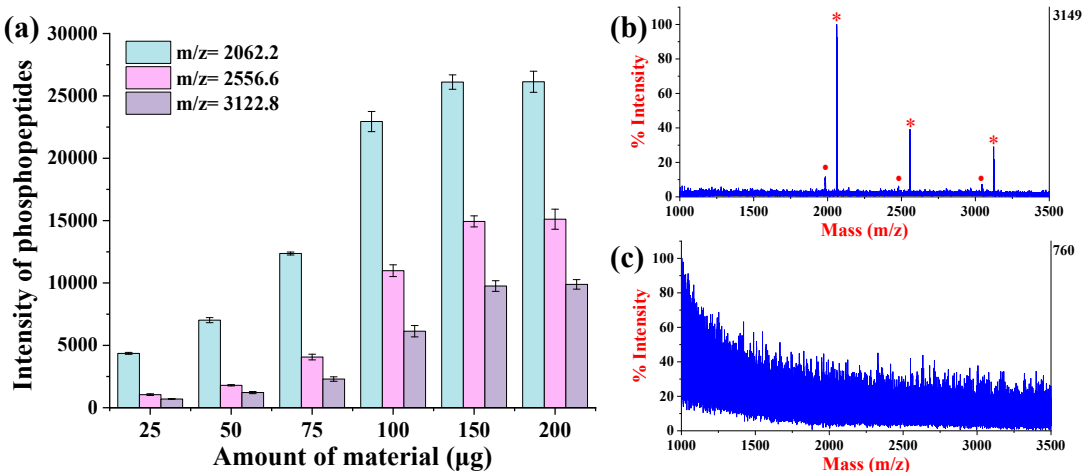

Fig. S5 (a) The loading capacity of mCOF@ε-PL@THBA-Ti^{4+}: different amounts of material (25, 50, 75, 100, 150, 200 μg) were used to enrich phosphopeptides from the a certain β-casein digests (10 μg). MALDI-TOF MS spectra of the supernatant of material with (b) 100 μg, (c)150 μg after enriched by mCOF@ε-PL@THBA-Ti^{4+}.

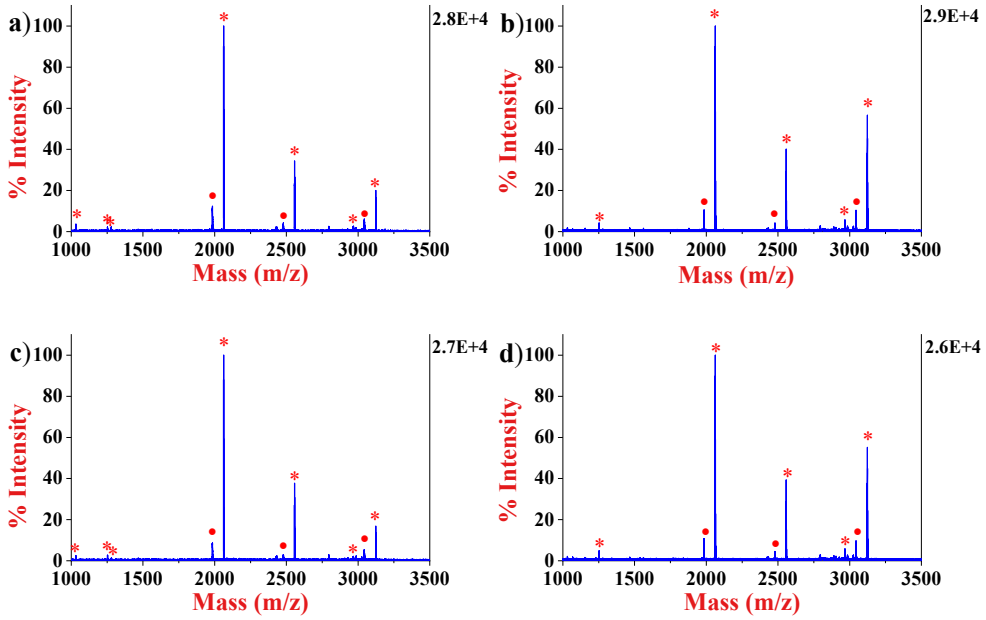

Fig. S6 Mass spectra of phosphopeptides from β-casein digests enriched with mCOF@ε-PL@THBA-Ti^{4+} at pH=2: (a) 24 hours, (c) 48 hours; pH=12: (b) 24 hours, (d) 48 hours.

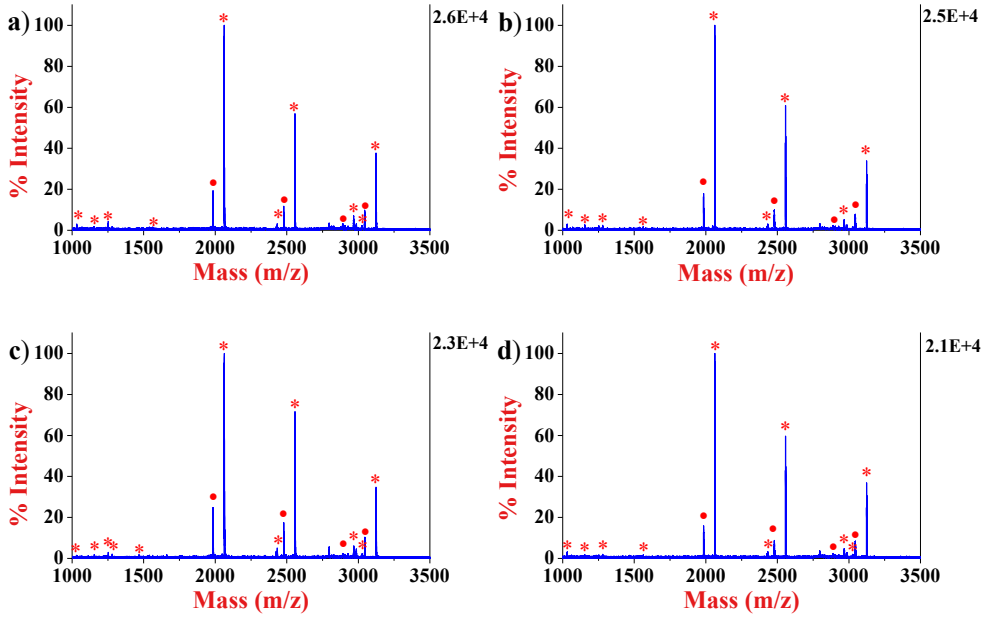

Fig. S7 Mass spectra of phosphopeptides from β-casein digests after enriched with mCOF@ε-PL@THBA-Ti^{4+}: (a) the first time, (b) the fourth time, (c) the seventh time, and (d) the tenth time. Peaks of phosphopeptide and dephosphorylated are signed as "∗" and "•", respectively.

Table S1. The detailed information of phosphopeptides assigned to β-casein after enrichment by mCOF@ε-PL@THBA-Ti^{4+}. ([pS], [pT] and [pY] represent phosphorylation on serine, threonine, and tyrosine, respectively. [Mo] represents oxidation on methionine, # indicates doubly charged peak dephosphorylated peptide).

No.	m/z	Amino acid sequence	Phosphorylation sites
1	1031.0	FQ[pS]EEQQQTEDELQDK	1
2	1155.7	[pS] [pS]EEKFLR	2
3	1252.7	TVD[Mo]ME[pS]TEVF	1
4	1562.0	RELEELNVPGEIVESL[pS] [pS] [pS]EE[pS] ITR	4
5	1983.8	FQ[pS]EEQQQTEDELQDK	1 #
6	2062.0	FQ[pS]EEQQQTEDELQDK	1
7	2432.3	IEKFQ[pS]EEQQQTEDELQDK	1
8	2477.9	FQ[pS]EEQQQTEDELQDKIHPF	1#
9	2556.4	FQ[pS]EEQQQTEDELQDKIHPF	1
10	2889.8	ELEELNVPGEIVE[pS]L[pS][pS][pS]EESITR	4 #
11	2966.4	ELEELNVPGEIVE[pS]L[pS][pS][pS]EESITR	4
12	3024.6	FPQYLQ[pY]L[pY]QGPIVLNPWDQVKR	2
13	3043.6	RELEELNVPGEIVE[pS]L[pS][pS][pS]EESITR	4#
14	3122.6	RELEELNVPGEIVE[pS]L[pS][pS][pS]EESITR	4

Table S2. Comparison of the enrichment performance of mCOF@ε-PL@THBA-Ti^{4+} with other recently published materials for enriching phosphopeptides. ('/' not given)

Materials	Sensitivity (LOD)	Selectivity	Practical Samples (MALDI-TOF)	Adsorption capacity	Reusability	Ref.
MCNC@COF@Zr^{4+}	10 fmol	β-casein: BSA 1:200	Defatted milk-14 Serum-5	46.48 $\mu g \cdot mg^{-1}$	/	[1]
Fe_3O_4@iCOFs	0.4 fmol	β-casein: OVA: BSA 1:200:200	Non-fat milk-13	/	7/7 cycles	[2]
Fe_3O_4@SiO_2@TpPa-Ti^{4+}	0.2 fmol μl^{-1} (100 μl)	α-casein: BSA 1:5000	Serum-4	200 mg g^{-1}	/	[3]
SPIO@COF-guanidyl	5×10^{-11}M (200 μL)	β-casein: BSA 1:1000	Non-fat milk-17 Saliva-63	/	5/5 cycles	[4]
Fe_3O_4@TAPTDHTA-Ti^{4+}	0.05 fmol μl^{-1} (100 μl)	β-casein: BSA 1:5000	Serum-4 Saliva-12	62.9 $\mu g \cdot mg^{-1}$	4/4 cycles	[5]
mCOF@ε-PL@THBA-Ti^{4+}	2 fmol	β-casein: BSA 1:5000	Serum-4 Saliva-16	66.7 $mg \cdot g^{-1}$	10/10 cycles	This work

Table S3. The detailed information of endogenous phosphopeptides assigned to the human saliva enriched by mCOF@ε-PL@THBA-Ti^{4+}. ([pS] and [pT] represent phosphorylation on serine and threonine, respectively.

No.	m/z	Amino acid sequence	Phosphorylation sites
1	1116.7	D[pS][pS]EEKFL	2
2	1155.5	[pS][pS]EEKFLR	2
3	1193.0	D[pS]SEEKFLR	1
4	1230.6	[pS]HEKRHHGY	1
5	1270.5	D[pS] [pS]EEKFLR	2
6	1305.5	D[pS]HAKRHHGY	1
7	1345.6	D[pS]HEKRHHGY	1
8	1426.7	D[pS][pS]EEKFLRR	2
9	1501.7	DVPLVISDGGD[pS]EQ	1
10	1539.8	FGQG[pS]GPIVLDDVR	1
11	1597.7	NEDV[pS]QEESPSLIA	1
12	1752.9	QPQITPNPV[pT]QHVQS	1
13	1862.7	AGPPGPPG[pS]VGPRGPEGLQG	1
14	1900.0	GPPGSRG[pS]PGAPGPPGPPGSH	1
15	2119.8	LVISDGGD[pS]EQFIDEERQ	1
16	2224.8	NEDV[pS]QEESPSVISGKPEGR	1

Table S4. The detailed information of endogenous phosphopeptides assigned to the healthy human serum enriched by mCOF@ε-PL@THBA-Ti^{4+}. ([pS] shows phosphorylation on serine).

No.	m/z	Amino acid sequence	Phosphorylation sites
1	1389.5	AD[pS]GEGDFLAEGGGV	1
2	1460.5	D[pS]GEGDFLAEGGGV	1
3	1545.6	D[pS]GEGDFLAEGGGVR	1
4	1616.6	AD[pS]GEGDFLAEGGGVR	1

Table S5. The detailed information of phosphopeptides assigned to the tryptic digests of uremia patients serum enriched by mCOF@ε-PL@THBA-Ti^{4+}.

No.	Annotated Sequence	Modifications	Master Protein Accessions	Theo. MH+ [Da]
1	[K].SSSQELGLK.[D]	1xPhospho [S3(100)]	Q14515	1028.46598
2	[R].ISASAEELR.[Q]	1xPhospho [S4(100)]	P06727	1055.47688
3	[R].LQSESLVNR.[R]	1xPhospho [S3(100)]	Q9GZX5	1125.52998
4	[K].SKEQLTPLIK.[K]	1xPhospho [S1(100)]	P02652	1236.65993
5	[K].AAISGENAGLVR.[A]	1xPhospho [S4(100)]	P19827	1237.59364
6	[K].TLEELSHTLK.[H]	1xPhospho [T8(100)]	Q494V2	1250.60281
7	[K].IKDSMPLLEK.[N]	1xPhospho [S4(100)]	Q9ULT0	1253.6211
8	[K].VKSPELQAEAK.[S]	1xPhospho [S3(100)]	P02652	1279.62936
9	[K].SGELEQEEER.[L]	1xPhospho [S1(100)]	P10645	1285.49438
10	[K].MKSEVKSLVNR.[S]	1xPhospho [S3(100)]	O60282	1370.68616
11	[R].THLAPYSDELR.[Q]	1xPhospho [S7(100)]	P02647	1381.61477
12	[R].FIANSQEPEIR.[L]	1xPhospho [S5(100)]	Q9BUN1	1383.63042
13	[K].QLGAGSIEECAAK.[C]	1xCarbamidomethyl [C10]; 1xPhospho [S6(100)]	P00747	1413.60797
14	[R].VRESDEETQIK.[V]	1xPhospho [S4(100)]	P04114	1413.62573
15	[K].CDSSPDSAEDVR.[K]	1xCarbamidomethyl [C1]; 1xPhospho [S7(100)]	P02765	1417.49373
16	[R].MPEPTSSPTIGPR.[K]	1xPhospho [T/S]	Q96NA8	1449.64436
17	[R].DYVSQFEGSALGK.[Q]	1xPhospho [S4(100)]	P02647	1480.63557
18	[R].EDSLEAGLPLQVR.[G]	1xPhospho [S3(100)]	P10645	1506.71996
19	[K].CDSSPDSAEDVRK.[V]	1xCarbamidomethyl [C1]; 1xPhospho [S7(100)]	P02765	1545.58869
20	[R].IPIEDGSGEVVLSR.[K]	1xPhospho [S7(100)]	P01024	1550.74618
21	[R].SPPLIHCSGEMLK.[F]	1xCarbamidomethyl [C7];	Q8TC20	1564.68993

		1xOxidation [M11]; 1xPhospho [S8(100)]		
22	[R].SAGSVESPSVSSTHR.[V]	1xPhospho [S4(99.4)]	P17936	1567.67481
23	[K].TCVADESAENCDK.[S]	2xCarbamidomethyl [C2; C11]; 1xPhospho [S7(100)]	P02768	1578.54478
24	[K].ESNEELTESCETK.[K]	1xCarbamidomethyl [C10]; 1xPhospho [S2(100)]	P01042	1635.60915
25	[R].VTEPISAESGEQVER.[V]	1xPhospho [S9(100)]	O14791	1710.7582
26	[R].SSSPELSEMLEYDR.[S]	1xPhospho [S3(99.1)]	P12259	1722.69282
27	[R].DELTKNQVSLTCLVK.[G]	1xCarbamidomethyl [C12]; 1xPhospho [T4(100)]	P01857	1827.89219
28	[R].IFTVAQMDDNSIQMK.[K]	1xOxidation [M7]; 1xPhospho [T3(100)]	Q9H2X9	1836.79076
29	[R].INQELSSKENIVQER.[K]	1xPhospho [S7(99.6)]	Q9NQ76	1866.8957
30	[K].SYFEKSKEQLTPLIK.[K]	1xPhospho [S6(100)]	P02652	1890.96126
31	[K].ATEDEGSEQKIPEATNR.[R]	1xPhospho [S7(100)]	P01008	1954.83897
32	[R].GSVQYLPDLDDKNSQEK.[G]	1xPhospho [S14(100)]	Q9UGM5	2015.89576
33	[R].CAIQLTQSPSSLSASVGDR.[V]	1xCarbamidomethyl [C1]; 1xPhospho [S/T]	A0A0B4J2D9	2056.93691
34	[R].HTFMGVVSLGSPSGEVSHPR.[K]	1xPhospho [S13(100)]	P02765	2160.98961
35	[K].IYEYVEDVLNVCDNEK.[W]	1xCarbamidomethyl [C12]; 2xPhospho [Y2(100); Y4(100)]	P35424	2161.84366
36	[K].VHTECCHGDLLECADDR.[A]	3xCarbamidomethyl [C5; C6; C13]; 1xPhospho [T3(100)]	P02768	2166.80386
37	[R].HTFMGVVSLGSPSGEVS	1xOxidation [M4]; 1xPhospho	P02765	2176.98453

	HPR.[K]	[S13(100)]		
38	[K].SVTMDSAPKPFTDVSIVMR.[S]	2xOxidation [M4; M18]; 1xPhospho [S15(99.2)]	Q96RL7	2192.99673
39	[K].FSVVYAKCDSSPDSAEDVR.[K]	1xCarbamidomethyl [C8]; 1xPhospho [S14(100)]	P02765	2211.92641
40	[R].DIPTNSPELEETLTHTITK.[L]	1xPhospho [S6(99.2)]	P01042	2219.0479
41	[R].ETTCSKESNEELTESCETK.[K]	2xCarbamidomethyl [C4; C16]; 1xPhospho [S8(100)]	P01042	2341.90474
42	[R].QVEKEETNEIQVVNEEPQR.[D]	1xPhospho [T7(100)]	Q8NBJ4	2378.08714
43	[R].VTTVASHTSDSDVPSGVTEVVVK.[L]	1xPhospho [T/S]	P10909	2394.14359
44	[R].YKVDYESQSTDTQNFSSESK.[R]	1xPhospho [S/Y/T]	P17936	2422.99224
45	[R].ETTCSKESNEELTESCETKK.[L]	2xCarbamidomethyl [C4; C16]; 1xPhospho [T3(99.5)]	P01042	2469.99971
46	[K].TSESGELHGLTTEEEFVEGIYK.[V]	1xPhospho [S/T/Y]	P02766	2535.11744
47	[R].LGPLSAEGTTGLAPAGQTSEESRPR.[L]	1xPhospho [T/S]	Q16473	2562.21955
48	[K].SHCIAEVENDEMPADLPSLAADFVESK.[D]	1xCarbamidomethyl [C3]; 1xOxidation [M12]; 1xPhospho [S18(100)]	P02768	3070.30572
49	[R].TNTNVNCPIECFMPLDVQADREDSRE.[-]	2xCarbamidomethyl [C7; C11]; 1xPhospho [S24(100)]	P02751	3190.32754
50	[R].VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK.[D]	3xCarbamidomethyl [C7; C18; C28]; 1xPhospho [S3(99.4)]	P00747	3317.39087

Table S6. The detailed information of phosphopeptides assigned to the tryptic digests of normal controls human serum enriched by mCOF@ε-PL@THBA-Ti^{4+}.

No.	Annotated Sequence	Modifications	Master Protein Accessions	Theo. MH+ [Da]
1	[R].GSESGIFTNTK.[E]	1xPhospho [S2(99.7)]	P02671	1220.51947
2	[K].SKEQLTPLIK.[K]	1xPhospho [S1(100)]	P02652	1236.65993
3	[K].TLEELSHTLK.[H]	1xPhospho [T8(100)]	Q494V2	1250.60281
4	[K].VKSPELQAEAK.[S]	1xPhospho [S3(100)]	P02652	1279.62936
5	[K].ITLLSALVETR.[T]	1xPhospho [S5(100)]	P01011	1295.69704
6	[R].FIANSQEPEIR.[L]	1xPhospho [S5(100)]	Q9BUN1	1383.63042
7	[K].QLGAGSIEECAAK.[C]	1xCarbamidomethyl [C10]; 1xPhospho [S6(100)]	P00747	1413.60797
8	[R].VRESDEETQIK.[V]	1xPhospho [S4(100)]	P04114	1413.62573
9	[K].CDSSPDSAEDVR.[K]	1xCarbamidomethyl [C1]; 1xPhospho [S7(100)]	P02765	1417.49373
10	[K].CDSSPDSAEDVRK.[V]	1xCarbamidomethyl [C1]; 1xPhospho [S7(100)]	P02765	1545.58869
11	[R].IPIEDGSGEVVLSR.[K]	1xPhospho [S7(100)]	P01024	1550.74618
12	[K].TCVADESAENCDK.[S]	2xCarbamidomethyl [C2; C11]; 1xPhospho [S7(100)]	P02768	1578.54478
13	[R].TKNLMWYGVLGTR.[E]	1xPhospho [Y7(99.2)]	Q86XP1	1618.78113
14	[R].TPGPYAGALREAVSR.[I]	1xPhospho [Y5(99.1)]	O94850	1624.7843
15	[R].HPDEAAFFDTASTGK.[T]	1xPhospho [S12(99.3)]	P02671	1673.68431
16	[R].VTEPISAESGEQVER.[V]	1xPhospho [S9(100)]	O14791	1710.7582

17	[K].ESSSHHPGIAEFPSR.[G]	1xPhospho [S]	P02671	1717.73299
18	[R].GAEEDFKELQTQGIK.[L]	1xPhospho [T11(100)]	Q9UQQ1	1772.81024
19	[R].TGAEWNPPLSFSLASR.[G]	1xPhospho [S/T]	Q8N6Y1	1812.83164
20	[R].IFTVAQMDDNSIQMK.[K]	1xOxidation [M7]; 1xPhospho [T3(100)]	Q9H2X9	1836.79076
21	[K].SYFEKSKEQLTPLIK.[K]	1xPhospho [S6(100)]	P02652	1890.96126
22	[K].MADEAGSEADHEGTHSTK.[R]	1xPhospho [S7(100)]	P02671	1952.73279
23	[K].ATEDEGSEQKIPEATNR.[R]	1xPhospho [S7(100)]	P01008	1954.83897
24	[R].HRHPDEAAFFDTASTGK.[T]	1xPhospho [S14(99.7)]	P02671	1966.84433
25	[K].AEQCCEETASSISLHGK.[G]	2xCarbamidomethyl [C4; C5]; 1xPhospho [S/T]	P02748	1986.79328
26	[R].NPSSAGSWNSGSSGPGSTGNR.[N]	1xPhospho [S/T]	P02671	2043.81521
27	[R].KSTHAEDSSLFPLSIQNR.[V]	1xPhospho [S/T]	Q8B0H0	2109.99647
28	[R].HTFMGVVSLGSPSGEVSHPR.[K]	1xPhospho [S13(100)]	P02765	2160.98961
29	[R].HTFMGVVSLGSPSGEVSHPR.[K]	1xOxidation [M4]; 1xPhospho [S13(100)]	P02765	2176.98453
30	[R].DIPTNSPELEETLTHTITK.[L]	1xPhospho [S6(99.1)]	P01042	2219.0479
31	[K].ATKEQLKAVMDDFAAFVEK.[C]	1xPhospho [T2(100)]	P02768	2221.06105
32	[R].ETTCSKESNEELTESCETK.[K]	2xCarbamidomethyl [C4; C16]; 1xPhospho [S8(100)]	P01042	2341.90474
33	[R].QVEKEETNEIQVVNEEPQR.[D]	1xPhospho [T7(100)]	Q8NBJ4	2378.08714
34	[R].VTTVASHTSDSDVPSGVTE	1xPhospho [S/T]	P10909	2394.14359

	VVVK.[L]			
35	[R].ETTCSKESNEELTESCETKK.[L]	2xCarbamidomethyl [C4; C16]; 1xPhospho [S5(99.5)]	P01042	2469.99971
36	[K].QVRPEHPAETEYDSLYPEDDL.[-]	1xPhospho [S14(100)]	P02679	2583.09228
37	[R].GSESGIFTNTKESSSHHPGIAEFPSR.[G]	1xPhospho [S2(99.9)]	P02671	2839.26829
38	[R].TNTNVNCPIECFMPLDVQADREDSRE.[-]	2xCarbamidomethyl [C7; C11]; 1xPhospho [S24(100)]	P02751	3190.32754
39	[K].EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.[H]	1xCarbamidomethyl [C11]; 1xOxidation [M15]; 1xPhospho [T/S]	P02671	3224.3647

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