Supporting Information

Dual-Metal Centered Zirconium-Organic Framework: A

Metal-Affinity Probe for Highly Specific Interaction with

Phosphopeptides

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Table S1. Contact angles of UiO-66-NH₂, UiO-66-NH-PO₃, and DZMOF.

Materials	Contact angle / degree	Images
UiO-66-NH ₂	35.7	
UiO-66-NH-PO ₃	29.1	
DZMOF	20.2	

Table S2. ICP-OES results of UiO-66-NH₂, UiO-66-NH-PO₃, and DZMOF.

Materials	Zr (wt%)
UiO-66-NH ₂	22.2
UiO-66-NH-PO ₃	20.0
DZMOF	24.3

Table S3. Comparison of our proposed DZMOF to the reported MOF based affinity probes in the past three years.

MOF Affinity Probes	Year of	Sensitivity	Selectivity	Ref
	Publication		β-casein:BSA(n:n)	
Fe ₃ O ₄ @PDA@Zr-MOF	2014	1 fmol	1:500	1
magG@PDA@Zr-MOFs	2015	100 fmol	1:1000	2
Fe ₃ O ₄ @MIL-100 (Fe)	2015	0.5 pmol	1:500	3
UiO-66 and UiO-67	2015	15 fmol	1:200	4
MIL-101(Cr)-UR ₂	2016	20 fmol	1:200	5
Fe ₃ O ₄ @PDA@Er(btc)	2016	4 fmol	1:500	6
UiO-66-(OH) ₂	2016	10 pmol	1:100	7
DZMOF	Proposed	10 fmol	1:5000	Our
	Probe			work

Table S4. Identification of phosphopeptides from tryptic digests of β -casein by MALDI-TOF MS with enrichment of DZMOF.

Protein	Peak	Amino Acid Sequence	No. of	$[M+H]^+$
			Phosphorylation	
			Sites	
β-casein	β_1	FQ[pS]EEQQQTEDELQDK	1	2061.7798
	β_2	FQ[pS]EEQQQTEDELQDKIHPF	1	2556.0596
	β_3	RELEELNVPGEIVE[pS]L[pS][pS][pS]EESITR	4	3122.2236

Table S5. Recovery of a standard phosphopeptide (GRRNpSIGK) treated by DZMOF. The recovery of standard phosphopeptide was calculated by the peak intensity ratio of eluted light isotope-labeled standard phosphopeptides to subsequently added heavy isotope-labeled standard phosphopeptides.

PFF		
Repeated	Intensity Ratio	Average Recovery ± SD
Experiments	(L/H)	(%, n=5)
1	95.6%	
2	89.5%	
3	93.6%	91.4±3.2
4	87.4%	
5	90.8%	

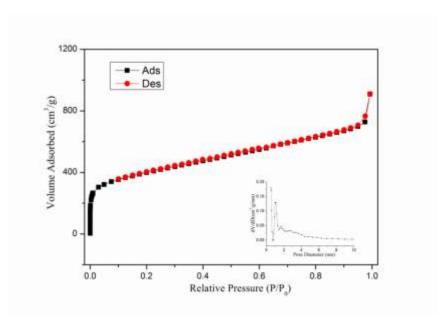


Figure S1. The nitrogen sorption/desorption isotherms of UiO-66-NH₂. The inset shows the pore distribution obtained by DFT.

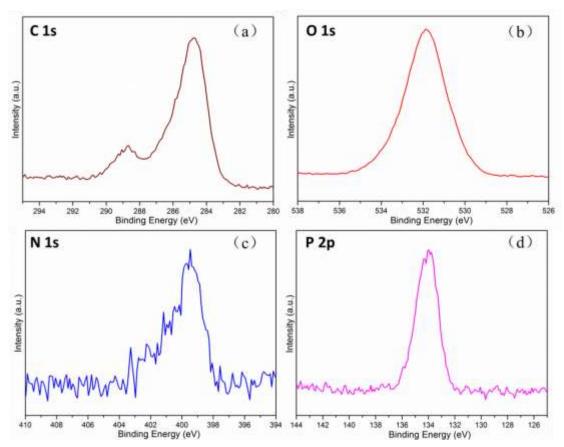


Figure S2. High-resolution XPS spectra of (a) C 1s, (b) O 2p, (c) N 1s, and (d) P 2p regions taken from DZMOF.



Figure S3. Digital photograph of a homemade pipette tip column.

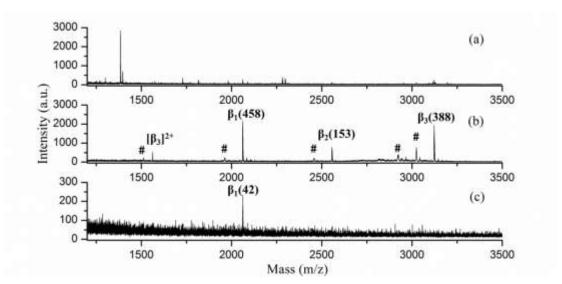


Figure S4. MALDI-TOF mass spectra of 10 pmol of β-casein tryptic digests (a) before and after enrichment by (b) DZMOF and (c) UiO-66-NH₂. The numbers in parentheses represent the S/N of the peaks; "#" denoted dephosphorylated fragments.

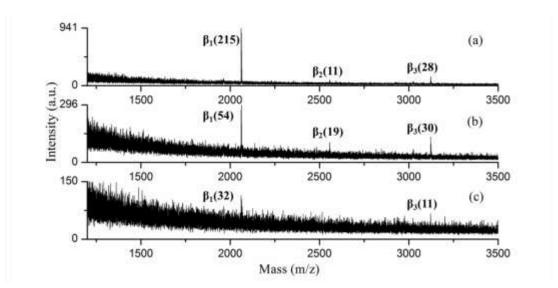


Figure S5. MALDI-TOF mass spectra of the tryptic digests of β-casein with a concentration of (a) 1.3 fmol/ μ L, (b) 0.67 fmol/ μ L, and (c) 0.07 fmol/ μ L, treated by DZMOF respectively. The numbers in parentheses represent the S/N of the peaks.

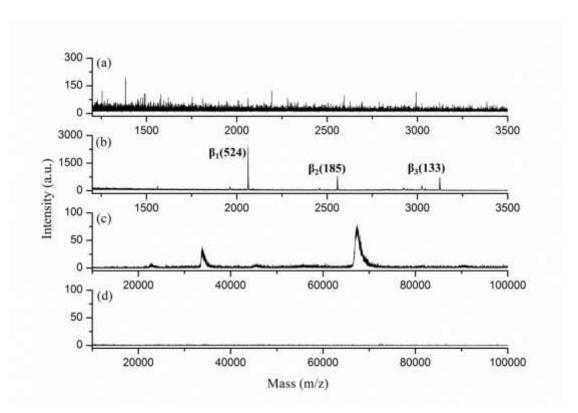
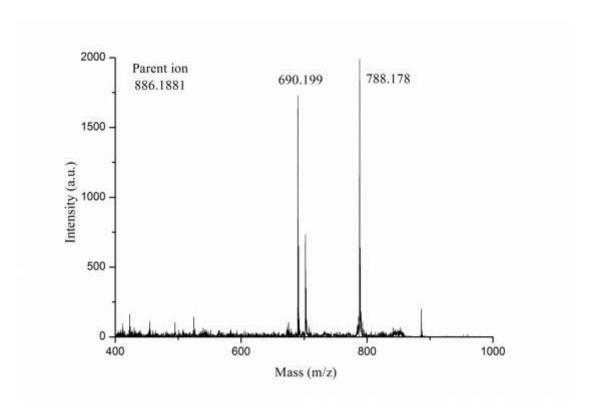
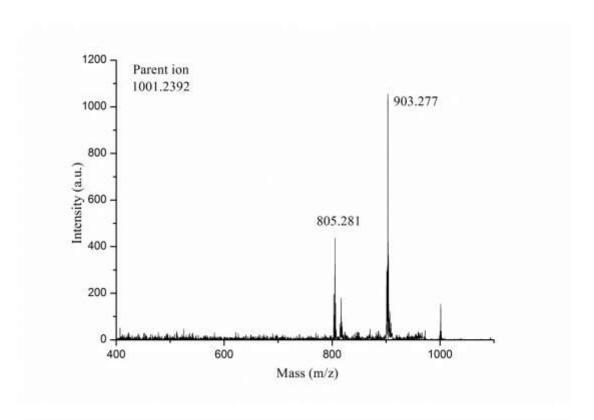
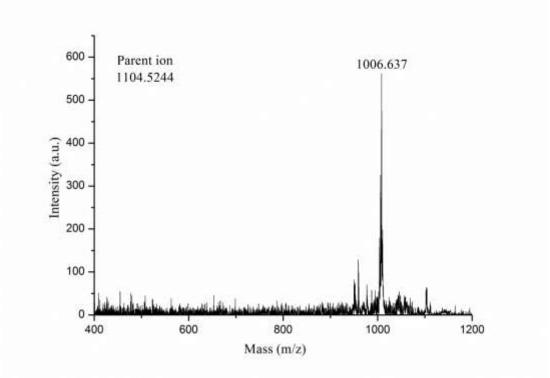
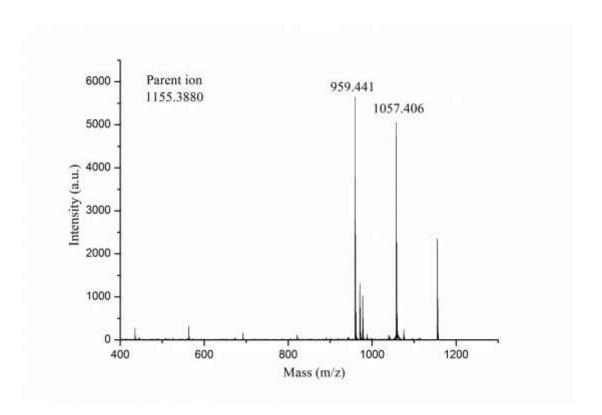


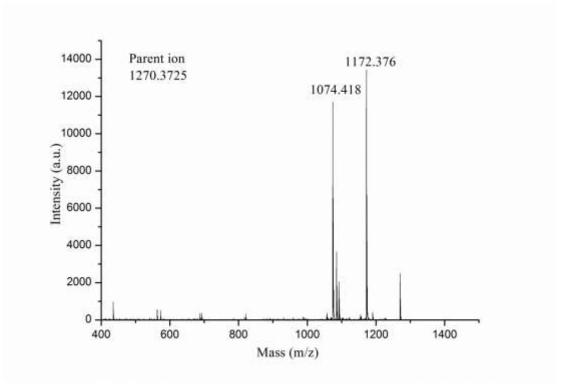
Figure S6. MALDI-TOF mass spectra of β -casein tryptic digests and BSA standard protein with a molar ratio of 1:1000 by direct analysis at (a) low molecular weight region, (c) high molecular weight region and enrichment with DZMOF at (b) low molecular weight region, (d) high molecular weight region. The numbers in parentheses represent the S/N of the peaks.

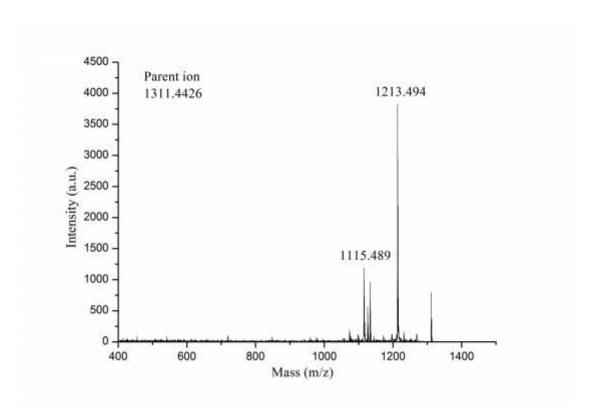


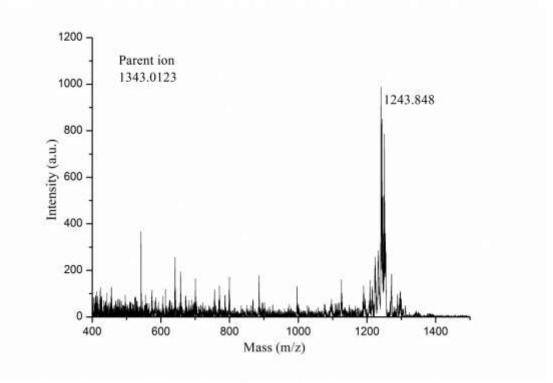


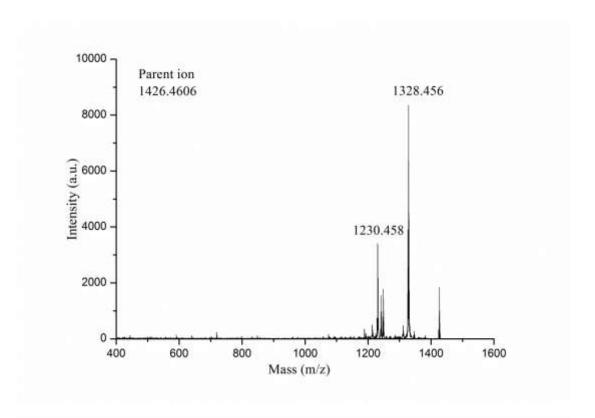


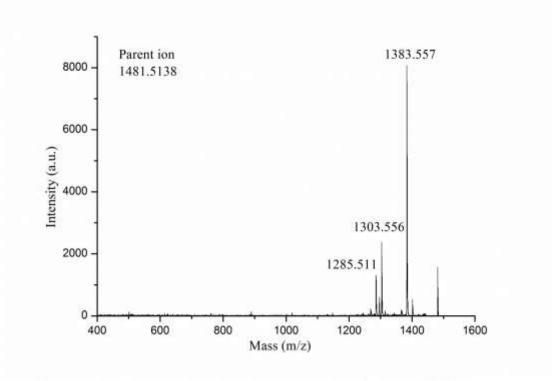


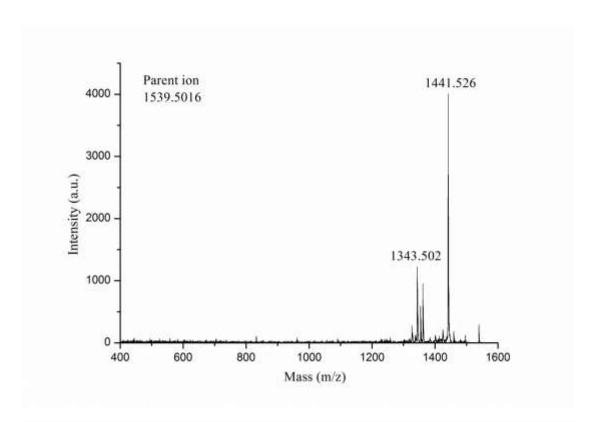


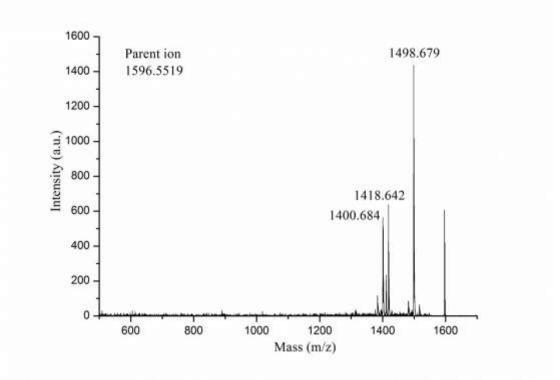


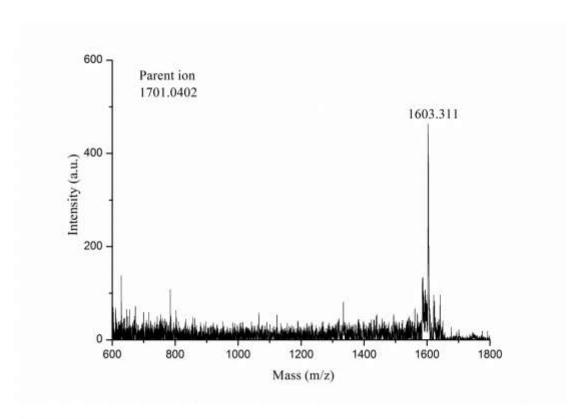


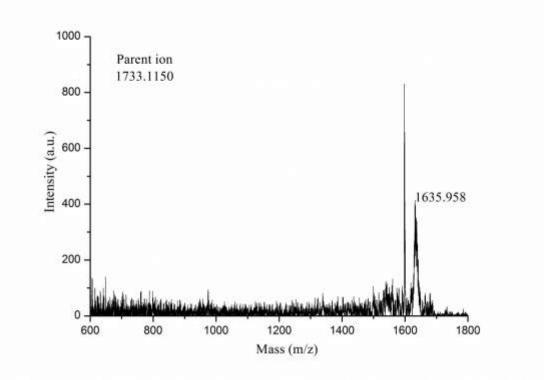


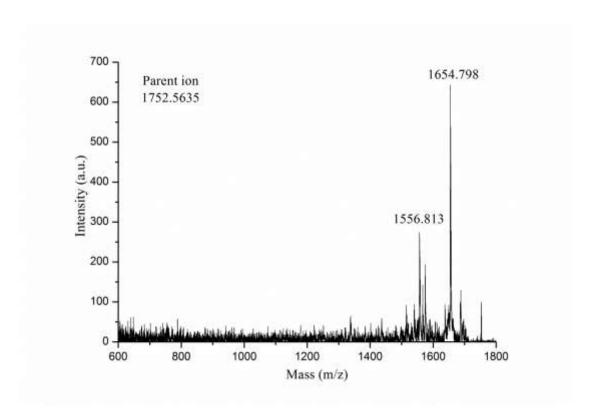


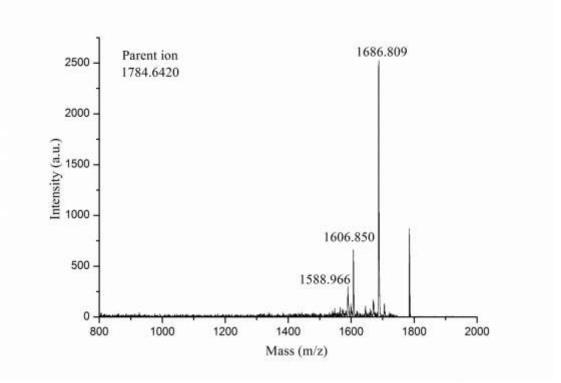


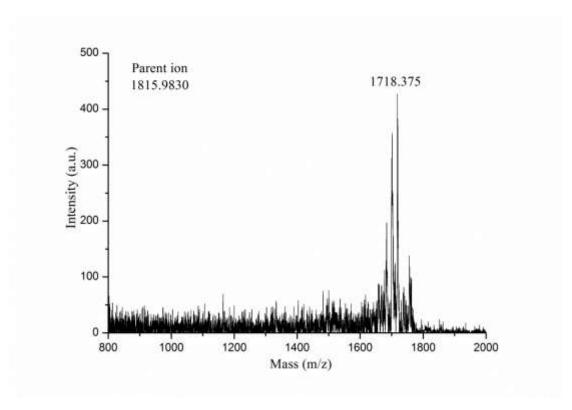












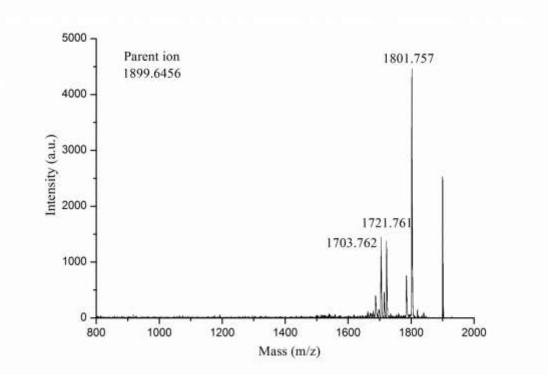


Figure S7. MALDI-TOF MS/MS spectra of phosphorylated peptides in human saliva after enrichment with DZMOF (dephosphorylated fragments about [M-98]⁺, [M-98-80]⁺ or [M-98×2]⁺).

References

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