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ARTICLE TYPE

Efficient enrichment of glycopeptides using phenylboronic acid polymer brush modified silica microspheres

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Abstract

For the development of rapid glycopeptide enrichment materials, conventional monolayer phenylboronic acid (PBA) based ¹⁰ materials inevitably encounter many puzzle problems, such as low loading efficiency, long incubation time, and unsatisfied

- selectivity. Expanding the materials from 1D monolayer to 3D polymeric matrix will be one of best candidates tackling these problems. In this work, a PBA-based polymer material (denoted as ask/DBA (SiQ)) was developed in which flowible DBA
- ¹⁵ as polyPBA@SiO₂) was developed, in which flexible PBA polymer brushes were immobilized on the surface of silica microspheres, constructing an ideal platform for the efficient enrichment of glycopeptides. This material exhibits strong interaction with glycopeptides in higher concentration of organic
- ²⁰ solvent than in aqueous solution, resulting in the maxium binding capacity of 60 mg/g. Moreover, higher selectivity for glycopeptides can be achieved with polyPBA@SiO₂ than with both monolayer PBA modified silica and commercial PBAagarose. These unique features of PB-PBA@SiO₂ could be
- 25 attributed to the synergistic effect of polyvalent interaction provided by polymer brush, specific interaction between PBA and glycopeptides and suppression of the non-specific binding of non-glycopeptides under high ACN concentration.

30 Introduction

Glycosylation is one of the most important post translational modifications of proteins^{1, 2} and aberrant protein glycosylation has been associated with various diseases including cancer.³⁻⁵

- ³⁵ Enrichment of N-linked glycopeptides has been significantly important because they are crucial to further structural determination and functional elucidation of N-linked glycoproteins. Conventional approaches for glycopeptide enrichment are mainly based on lectin affinity chromatography,⁶⁻⁹
- ⁴⁰ hydrazide chemistry¹⁰⁻¹³ or hydrophilic interaction affinity chromatography (HILIC).¹⁴⁻¹⁷ These conventional methods, however, are limited by either low coverage of glycopeptides, loss of glycan information or medium specificity. Recently, phenylboronic acid (PBA) functionalized materials have attracted
- ⁴⁵ much attention in various biological applications due to reversible diester bonds between PBA and *cis*-diol-containing

compounds.¹⁸⁻²³ Especially, PBA-containing materials have been utilized for glycopeptide enrichment in basic buffer solution.²⁴⁻²⁷ However, these PBA-based methods suffer from non-specific ⁵⁰ binding resulting from hydrophobic interactions of nonglycopeptides in aqueous solution,^{27, 28} leading to limited selectivity. Moreover, PBA-based method requires long incubation time because of slow formation of diesters between glycans and boronic acid. In order to improve the selectivity and ⁵⁵ fasten the binding of glycopeptides, it is of urgent need to develop novel method, which can strongly enhance the interaction between PBA glycopeptides and notably reduce the non-specific binding of non-glycopeptides.

Polymer brushes contain end-tethered polymer chains ⁶⁰ grafted on the support.²⁹ These flexible polymer chains stretch away from the substrate and facilitate multiple interactions between materials and targets.^{21, 30} Moreover, some polymer brushes respond to various stimuli including solvent and pH. ³¹Nlinked glycopeptides contain branched, bulky, mobile ⁶⁵ oligosaccharide clusters,³² and have higher hydrophilicity than their counterparts.³³ In HILIC mode, hydrophilic glycopeptides generally retain stronger on the polar matrix than the corresponding non-glycopeptides. Hydrophobic peptides tend to be eluted in the flowthrough and earlier fractions. ^{14, 34}

Herein, we designed and prepared PBA polymer brush modified silica microsphere materials (polyPBA@SiO₂). Furthermore, polyPBA@SiO₂ was used to separate glycopeptides from non-glycopetpides in HILIC mode. Improving retention of target glycopeptides and reduced binding of non-glycopeptides 75 would be acchieved in HILIC mode. By combining the synergistic effect of polyvalent interaction between polymer brush and glycan, specific recognition of PBA toward saccharide residues and hydrophilic interaction of glycopeptides (Fig. 1A), highly selective and rapidly enrichment of glycopeptides would 80 be obtained with polyPBA@SiO₂.

Experimental Materials

85 All chemicals unless otherwise mentioned were purchased form Sigma-Aldrich (St. Louis, MO, USA). Sequencing grade modified trypsin was obtained from Promega (Madison, WI, 75

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USA). Acetonitrile (ACN) was purchased from Merck (Darmstadt, Germany). Formic acid (FA) was purchased from Acros Organics (Geel, Belgium). Water was purified with a Milli-Q system (Millipore, Bedford, MA, USA). Commercial ⁵ phenylboronate agarose (PBA-agarose) was purchased from Sigma-Aldrich (St. Louis, MO, USA).

Preparation of polyPBA@SiO₂

- ¹⁰ PolyPBA@SiO₂ was prepared via typical chain-transfer radical polymerization.³⁵ Porous silica microspheres with 30 nm pore size (1 g) were dispersed in anhydrous methanol (10 ml) containing 5 wt% 3-mercaptopropyltrimethoxysilane at room temperature for 24 h, generating chemically bonded -SH groups
- ¹⁵ as the chain-transfer agent. After rinsing with methanol and 1,4-dioxane, polymerization of PBA was performed by dispersing the -SH bonded silica microspheres into a degassed solution of PBA (0.2 g) in 1,4-dioxane (10 mL) containingα, α'-azodiisobutyronitrile (10 mg) for 1 h at 80 °C. After washing with ²⁰ acetone, the polyPBA@SiO₂ were obtained through
- centrifugation (12000 r/min for 5 min), and then dried at 60 $^{\circ}$ C for 5 days.

Characterization of polyPBA@SiO2

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- Characterization of prepared polyPBA@SiO₂ materials was performed for morphology and composition analysis. Fourier transform infrared (FTIR) spectrum was recorded with Vertex 80. The X-ray photoelectron spectroscopy (XPS) was performed with
- ³⁰ an ESCALab220i-XL electron spectrometer from VG Scientific using 300W AlK α radiation. The base pressure was about 3×10^{-9} mbar. The binding energies were referenced to the C1s line at 284.8 eV from adventitious carbon. High-resolution scanning electron microscopy (HRSEM) was taken on a Hitachi-S5500. N₂
- ³⁵ adsorption-desorption experiments were measured on an automatic TriStar II 3020. Brunauer-Emmett-Teller (BET) surface areas were calculated from adsorption data in the relative pressure range from 0.01 to 0.2. Pore size distributions were analyzed from the adsorption branches of the isotherms. Thermo-
- $_{40}$ gravimetric analysis (TGA) carried out on Perkin Elmer Pyris Diamond. 10 mg sample was analysed with a 10 °C/min heating rate from 50 to 750 °C under N_2 atmosphere.

Trypsin digestion of glycoproteins

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- Horseradish peroxidase (HRP) (1 mg) was dissolved with 100 μ L 6 M urea in 50 mM ammonium bicarbonate (NH₄HCO₃). The protein solution was treated with 4 μ L 50 mM dithiothreitol for 45 min at 56 °C. Then 5 μ L 50 mM iodoacetamide was added and
- $_{50}$ the mixture was incubated in the dark for 30 min at the room temperature. The mixture was diluted to 10 folds with 50 mM NH₄HCO₃ and digested with trypsin at an enzyme to protein ratio of 1:30.

55 Enrichment of glycopeptides

For glycopeptide enrichment from tryptic digests of standard glycoproteins, 1 mg of polyPBA@SiO2 materials suspended in

ACN was loaded into 20 μL GELoader tips (Eppendorf AG, ⁶⁰ Hambrug, Germany). After conditioning and equilibrating with 30 μL 50 mM NH₄HCO₃ and 85% ACN/50 mM NH₄HCO₃, 5 μL glycoprotein (12.5 pmol) tryptic digests were dried and redissolved with 30 μL 85% ACN/50 mM NH₄HCO₃. The redissolved peptides were loaded into the packed polyPBA@SiO₂
⁶⁵ microcolumn. The microcolumn was washed twice with 30 μL 72% ACN/50 mM NH₄HCO₃. Glycopeptides were detached from column with 20 μL 50% ACN/0.1% FA. For comparison, commercial PBA-agarose and monolayer PBA@SiO₂ (See supporting information (SI)) were used to enrich glycopeptides ⁷⁰ under same condition applied to polyPBA@SiO₂ using HRP digests as samples. For C18 desalting, the performance was according to previous report. ³⁶

Nano-ESI-MS analysis

Peptide fractions eluted from polyPBA@SiO₂, PBA-agarose, C18 and monolayer PBA@SiO₂ were analyzed directly with a nano electrospray ionization-quadrupole time-of-flight mass spectrometer (ESI Q-TOF MS) (Waters, Milford, MA, USA) The 80 MS analysis was under positive ion mode. Full scan MS data and MS/MS data were acquired at m/z 600-2000 and 100-2000, respectively. Collision energy was set in the range from 30-45 eV.



Fig. 1 Schematic illustration of multiple sites interaction between polyPBA@SiO₂ and glycopeptides (A), synthesis route of polyPBA@SiO₂ (B), chemical structures of two reference materials: ⁹⁰ PBA@SiO₂ and PBA-agarose (C).

Enrichment capacity

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To determine the enrichment capacity of polyPBA@SiO₂, various amounts of HRP digests in fixed volume (50 μ L) were loaded into 1 mg materials packed GELoader tips. The flow-through was analyzed with Q-TOF MS until the glycopeptide 5 signals were observed. The experiments were repeated triple times.

Results and discussion Synthesis and characterization of polyPBA@SiO₂

The synthesis procedure of polyPBA@SiO₂ was illustrated in Fig. 1B. PolyPBA@SiO₂ was prepared via typical chain-transfer radical polymerization.³⁵ HRSEM images (Fig. 2) and N₂ adsorption (Fig. S1) results revealed that polyPBA@SiO₂ ¹⁵ materials preserve similar morphology to that of silica microspheres and the pores in polyPBA@SiO₂ were not blocked. BET surface area of 70 m²/g and pore volume of 0.55 cm³/g were derived from N₂ adsorption experiment. These data proved that polyPBA@SiO₂ materials were not degraded after coating with ²⁰ polymers on the silica surface.

FTIR spectrum of polyPBA@SiO₂ exhibits obvious bands at about 1630 cm⁻¹ and 1450 cm⁻¹, which corresponds to the characteristic groups in polyPBA. By comparison, no obvious ²⁵ bands can be found in the spectrum of SiO₂ (Fig. 3A). The XPS spectrum of polyPBA@SiO₂ shows four peaks with binding energies at about 173.3, 285.3, 400.3 and 533.8 eV, which can be ascribed to the B1s, C1s, N1s and O1s, respectively (Fig. 3B). Carbon content of 5.4% was measured from elemental analysis.

³⁰ TGA was used to further measure the relative composition of polyPBA@SiO₂ (Fig. S2). The sharp decline above 350 °C was resulted from the weight loss of polymer layer. The calculated surface coverage of polyPBA@SiO₂ was 0.12 µmol/m². These data suggested that PBA polymer brush was successfully grafted ³⁵ on the silica microspheres.



Fig. 2 High resolution scanning electron microscopy (HRSEM) images of polyPBA@SiO₂ (A) X 20 000, (C) X 100 000 and SiO₂ ⁵⁵ (B) X 20 000, (D) X 100 000.



Fig. 3 Fourier transform infrared spectrum (A) and X-ray photoelectron spectroscopy of polyPBA@SiO₂ (B).

Retention of peptides on polyPBA@SiO2

To test whether polyPBA@SiO₂ can retain glycopeptides, HRP digests in different concentration of ACN was loaded into the 1 ⁷⁵ mg polyPBA@SiO₂ packed solid phase extraction (SPE) microcolumns. The peptide sequence and glycan composition of HRP glycopeptides were listed in Table 1.³⁷ When 90% ACN/50 mM NH₄HCO₃ and 80% ACN/50 mM NH₄HCO₃ were used as loading buffer, only several non-glycopeptides were detected in ⁸⁰ their flowthrough. With the decrease of ACN concentration, 3 glycopeptides were found in 70% ACN flowthrough (Fig. S3C). When 50 mM NH₄HCO₃ solution was applied as loading buffer, 5 glycopeptides were detected in the flowthrough (Fig. S3D). These data suggested that strong interaction might be involved ⁸⁵ between glycopeptides and polyPBA@SiO₂. We speculated that the polyPBA@SiO₂ might be more lyophobic in 50 mM NH₄HCO₃ solution.

Table 1 Information of identified HRP glycopeptides

		Observed m/z	
Amino acid sequence	Glycans	and charge	Position
NVGLNR	Man3GlcNAc2Fuc1Xyl1	921.85 (2+)	184-189
GLIQSDQELFSSPNATDTIP LVR	Man3GlcNAc2Fuc1	1175.33(3+)	272-294
NQCR			205-208,
GLCPLNGNLSALVDFDLR	Man3GlcNAc2Fuc1Xyl1	1202.23(3+)	237-254
		1224.55(3+),	
GLIQSDQELFSSPNATDTIP LVR	Man3GlcNAc2Fuc1Xyl1	1836.07(2+)	272-294
NQCR			205-208,
GLCPLNGNLSALVDFDLR	Man4GlcNAc2Fuc1Xyl1	1256.23(3+)	237-254
LYNFSNTGLPDPTLNTTYLQ TLR	Man3GlcNAc2Fuc1Xyl1	1272.2(3+)	214-236
LHFHDCFVNGCDA SILLDNTTSFR	Man3GlcNAc2Fuc1Xyl1	1299.36(3+)	69-92
MGNITPLTGTQGQIR	Man3GlcNAc2Fuc1Xyl1	1306.2(2+)	314-328
AAVESACPR			115-123,
QLTPTFYDNSCPNVSNIVR	Man3GlcNAc2Fuc1Xyl1	1407.59(3+)	31-49
LYNFSNTGLPDPTLNTTYLQ TLR	Man ₆ GlcNAc ₄ Fuc ₂ Xyl ₂	1662.06(3+)	214-236
SFANSTQTFFNAFVEAMDR	Man3GlcNAc2Fuc1Xyl1	1677.55(2+)	295-313

N*: Glycosylation site. C: disulfide bonds formed by the oxidation of two cysteine amino acids

To confirm our speculation, contact angles were measured on ⁹⁵ polyPBA grafted silicon wafer by using different liquid probes. Fig. 4 shows contact angles were about 67° and 65° when using 50 mM NH₄HCO₃ and 50 mM NH₄HCO₃/10 mM mannose as the probes, implying higher lyophobicity of polyPBA in aqueous solution. In contrast, the contact angle was about 33° when 85% ¹⁰⁰ ACN/50 mM NH₄HCO₃ was used, which indicates that the polymer surface became more lyophilic under the treatment of



Fig. 4 Contact angle of polyPBA grafted silicon wafer under different conditions

- high concentration of organic solvent. The presence of 10 mM 5 mannose in the 85% ACN/50 mM NH₄HCO₃ buffer could induce more obvious change in the contact angle, which further decreased to 25°. This extra change can be attributed to the stronger interaction between monosaccharide (e.g. mannose) and PBA functional units, as well as the better compatibility of 10 polyPBA@SiO2 in high concentration of ACN. Considering Nlinked glycopeptides comprise a large number of pentasaccharides in their glycans, which are supposed to exhibit much higher hydrophilicity than their counterparts, nonglycopeptides. The above results inspired us to deduce that 15 polyPBA@SiO2 had stronger binding to glycopeptides under higher concentration of organic solvent, while more lyophilic characteristic of materials can help to reduce the undesirable adsorption of non-glycopeptides.
- The effect of acidic, neutral and basic solution to the retention of glycopeptides was also investigated. HRP digests dissolved with 75% ACN of pH 3, 7 and 9 were loaded into polyPBA @SiO₂ packed SPE microcolumns, respectively. It was found that glycopeptides were eluted with 75% ACN under both neutral and
- ²⁵ acidic solution (Fig. S4). On the contrary, the glycopeptides were well captured with 75% ACN in basic solution. This result demonstrated that polyPBA@SiO₂ bound strongly with glycopeptides in the higher pH solution even under high concentration of organic solvent, indicating affinity interaction
- ³⁰ existing between glycopeptides and boronate groups. Taken these results together, we concluded that both affinity interaction and hydrophilic interaction might be synergistically involved in the interaction between glycopeptides and the as-prepared polyPBA@SiO₂.
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Enrichment of glycopeptides with polyPBA@SiO2

The enrichment of glycopeptides was carried out under SPE mode because of microsphere morphology and flowthrough pore ⁴⁰ size of polyPBA@SiO₂. Tryptic HRP digests were used to qualitatively evaluate the enrichment selectivity. The captured peptides were characterized with ESI Q-TOF MS. Before enrichment, a large number of high-intensity non-glycopeptides

dominated the mass spectrum and severely suppressed the signals ⁴⁵ of glycopeptides, leading to only 4 observed glycopeptide signals (Fig. 5A). After enrichment with polyPBA@SiO₂ materials, up to 27 HRP glycopeptide signals covering all known glycosylation sites were readily detected because the high-abundance nonglycopeptides and ion suppression effect were efficiently 50 removed (Fig. 5D). HRP glycopeptides were characterized by comparing their molecular weights and fragment ion mass spectrum with those of literature. MS/MS mass spectra of the identified glycopeptides all had at least three indicator fragment ions of glycopeptides including oxonium ions m/z 163 (Hex+), 55 m/z 204 (HexNAc+) and m/z 366 (Fig. S5 in SI). For comparison, commercial PBA-agarose and monolayer PBA modified SiO₂ (PBA@SiO₂, the synthesis and characterization of PBA@SiO₂ see SI) were used to bind HRP glycopeptides under the same condition as polyPBA@SiO2. Enrichment selectivity of 60 PBA@SiO2 toward glycopeptides was impaired by several nonglycopeptides in the m/z range between 700-900 (Fig. 5B) even though incubation of PBA@SiO2 and HRP digests for 30 min. PBA-agarose showed nonspecific adsorption toward nonglycopeptides, leading to co-elution of non-glycopeptides at m/z 65 959.5344, 1185.6184 and 1573.8035 with HRP glycopeptides (Fig. 5C). The above data demonstrated polyPBA@SiO₂ had higher enrichment efficiency for glycopeptides than commercial PBA-agarose and monolayer PBA@SiO2.

When PBA@SiO₂, PBA-agarose and polyPBA@SiO₂ were ⁷⁰ used to enrich glycopeptides, they showed varied glycopeptides selectivity. We speculate that PBA@SiO₂ has low-density and close PBA groups modified on SiO₂, which to large extent leads to weak interaction with glycopeptides. For PBA-agarose, PBA on the rigid polysaccharide structures restricts the effective ⁷⁵ interaction between glycopeptides and materials, resulting in the limited selectivity. Compared with PBA-agarose and PBA@SiO₂, flexible PBA polymer chains on polyPBA@SiO₂ extend from the SiO₂ surface and provide multiple interactions between PBA and glycopeptides. Moreover, the end-grafted flexible chains might

- ³⁰ be more reactive than monolayer PBA close to SiO₂ surface.³⁰ These multiple interaction sites and more reactive end-grafted chains facilitate strong and selective interaction between glycopeptides and polyPBA@SiO₂. Meanwhile, the hydrophilic interactions of polyPBA@SiO₂ with non-glycopeptides were ⁸⁵ much weaker than that with glycopeptides containing multiple hydroxyl groups. Therefore, the enhanced affinity interactions and hydrophilic interaction provided by polyPBA@SiO₂ contributed to the isolation of glycopeptides and the improved selectivity of materials.
- ⁹⁰ In order to test our speculation, flowthrough fractions from PBA@SiO₂ and polyPBA@SiO₂ were analyzed with MS. No HRP glycopeptide signals could be found in the mass spectra of flowthrough fractions from polyPBA@SiO₂ (Fig. S6 in SI). However, 3 HRP glycopeptides and a number of non-⁹⁵ glycopeptides could be detected in the flowthrough fraction from PBA@SiO₂ (Fig. S6 in SI). This result further proved polyPBA@SiO₂ bound stronger and faster than momolayer PBA@SiO₂. ³⁰

Due to the multiple interactions between glycopeptides and 100 polyPBA@SiO₂, we assumed that polyPBA@SiO₂ had high capacity toward glycopeptides. To determine the adsorption



Fig. 5 Nano-ESI-Q-TOF mass spectra of tryptic HRP digests before enrichment (A) and after enrichment with monolayer PBA modified SiO_2 (B), commercial PBA-agarose(C) and (D) polyPBA@SiO₂ under the same conditions. Glycopeptides are labelled with *. The non-glycopeptides were labelled with their m/z values. polyPBA@SiO₂ showed much higher selectivity for glycopeptides than monolayer PBA modified SiO₂, commercial PBA-agarose.

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capacity of PB-PBA@SiO₂, 1 mg materials were employed to bind various concentration of HRP digests in a fixed volume (50 μL). The flowthrough fraction was characterized with Q-TOF MS.
¹⁰ Before reaching the adsorption capacity of PB-PBA@SiO₂, no glycopeptide signals were detected. When the loading mass of glycopeptides was overweighed the adsorption capacity of binding materials, the glycopeptide signals were observed. The binding capacity of PB-PBA@SiO₂ toward HRP glycopeptides
¹⁵ were measured as was 60 mg/g, compared to 20 mg/g of monolayer PBA@SiO₂ (Fig. 6). The high binding capacity was attributed to the multiple sites interaction provided by polymer brush.



Fig. 6 Determination of adsorption capacity of polyPBA@SiO₂ and ²⁰ monolayer BA@SiO₂.

Conclusions

³⁰ In summary, we developed a new strategy based on PBA polymer brush modified silica microspheres (i.e., polyPBA@SiO₂) to efficiently enrich glycopeptides. Our strategy demonstrated much higher enrichment selectivity and adsorption capacity toward glycopeptides than PBA@SiO₂ and PBA-agarose. We anticipate ³⁵ this new kind of glycopeptides capturing method may become a useful tool for glycoproteome. Further studies will introduce more functional groups including small peptides and oligosaccharides to polymer chains and enhance the interaction between glycopeptides and materials.

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Notes and references

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- W. Yi, P. M. Clark, D. E. Mason, M. C. Keenan, C. Hill, W. A. Goddard, E. C. Peters, E. M. Driggers and L. C. Hsieh-Wilson, *Science*, 2012, **337**, 975.
- 2. M. Kowarik, S. Numao, M. F. Feldman, B. L. Schulz, N. Callewaert, E. Kiermaier, I. Catrein and M. Aebi, *Science*, 2006, **314**, 1148.
- M. Demetriou, M. Granovsky, S. Quaggin and J. W. Dennis, *Nature*, 2001, 409, 733.
- 20 4. R. Saldova, L. Royle, C. M. Radcliffe, U. M. A. Hamid, R. Evans, J. N. Arnold, R. E. Banks, R. Hutson, D. J. Harvey, R. Antrobus, S. M. Petrescu, R. A. Dwek and P. M. Rudd, *Glycobiology*, 2007, **17**, 1344.
- F. G. Hanisch, T. R. E. Stadie, F. Deutzmann and J. PeterKatalinic, *Eur. J. Biochem.*, 1996, 236, 318.
- 25 6. H. Kaji, H. Saito, Y. Yamauchi, T. Shinkawa, M. Taoka, J. Hirabayashi, K. Kasai, N. Takahashi and T. Isobe, *Nat. Biotechnol.*, 2003, 21, 667.
 - 7. R. Q. Qiu and F. E. Regnier, Anal. Chem., 2005, 77, 2802.
- 8. G. Alvarez-Manilla, N. L. Warren, J. Atwood, R. Orlando, S. Dalton and M. Pierce, *J. Proteome Res.*, 2010, **9**, 2062.
- M. C. Galan, P. Dumy and O. Renaudet, *Chem. Soc. Rev.*, 2013, 42, 4599.
- H. Zhang, X. J. Li, D. B. Martin and R. Aebersold, *Nat. Biotechnol.*, 2003, **21**, 660.
- ³⁵ 11. T. Liu, W. J. Qian, M. A. Gritsenko, D. G. Camp, M. E. Monroe, R. J. Moore and R. D. Smith, *J. Proteome Res.*, 2005, **4**, 2070.
 - Y. Tian, F. J. Esteva, J. Song and H. Zhang, *Mol. Cel. Proteomics*, 2012, **11**, (doi: 10.1074/mcp.M111.011403).
 - L. Zhang, H. Jiang, J. Yao, Y. Wang, C. Fang, P. Yang and H. Lu, *Chem. Commun.*, 2014, **50**, 1027.
- S. Mysling, G. Palmisano, P. Hojrup and M. Thaysen-Andersen, Anal. Chem., 2010, 82, 5598.
- L. Yu, X. L. Li, J. Dong, X. L. Zhang, Z. M. Guo and X. M. Liang, *Anal. Methods*, 2010, 2, 1667.
- ⁴⁵ 16. P. H. Jensen, S. Mysling, P. Hojrup and O. N. Jensen, *Methods Mol. Bio.*, 2013, **951**, 131.
 - 17. A. Shen, Z. Guo, L. Yu, L. Cao and X. Liang, *Chem. Commun.*, 2011, **47**, 4550.
 - M. Zhang, G. Qing, C. Xiong, R. Cui, D.-W. Pang and T. Sun, *Adv. Mater.*, 2013, 25, 749.
 - G. Qing, X. Wang, H. Fuchs and T. Sun, J. Am. Chem. Soc., 2009, 131, 8370.
 - F. Xia, H. Ge, Y. Hou, T. Sun, L. Chen, G. Zhang and L. Jiang, *Adv. Mater.*, 2007, **19**, 2520.
- 55 21. H. L. Liu, Y. Y. Li, K. Sun, J. B. Fan, P. C. Zhang, J. X. Meng, S. T. Wang and L. Jiang, *J. Am. Chem. Soc.*, 2013, **135**, 7603.
 - X. Zhang, X. He, L. Chen and Y. Zhang, J. Mater. Chem., 2012, 22, 16520.

- 23. Z.-A. Lin, J.-N. Zheng, F. Lin, L. Zhang, Z. Cai and G.-N. Chen, J. *Mater. Chem.*, 2011, 21, 518.
 - 24. M. Y. Li, N. Lin, Z. Huang, L. P. Du, C. Altier, H. Fang and B. H. Wang, J. Am. Chem. Soc., 2008, 130, 12636.
 - L. J. Zhang, Y. W. Xu, H. L. Yao, L. Q. Xie, J. Yao, H. J. Lu and P. Y. Yang, *Chem.- Eur. J.*, 2009, 15, 10158.
- 65 26. Y. W. Xu, Z. X. Wu, L. J. Zhang, H. J. Lu, P. Y. Yang, P. A. Webley and D. Y. Zhao, *Anal. Chem.*, 2009, **81**, 503.
 - L. B. Ren, Z. Liu, Y. C. Liu, P. Dou and H. Y. Chen, *Angew. Chem. Int. Ed*, 2009, 48, 6704.
- 28. L. B. Ren, Z. Liu, M. M. Dong, M. L. Ye and H. F. Zou, J. *Chromatogr. A*, 2009, **1216**, 4768.
- 29. S. T. Milner, Science, 1991, 251, 905.
- A. E. Ivanov, H. A. Panahi, M. V. Kuzimenkova, L. Nilsson, B. Bergenstahl, H. S. Waqif, M. Jahanshahi, I. Y. Galaev and B. Mattiasson, *Chem.- Eur. J.*, 2006, **12**, 7204.
- 75 31. T. S. Kelby, M. Wang and W. T. S. Huck, *Adv. Funct. Mater.*, 2011, 21, 652.
 - 32. A. Helenius and M. Aebi, Science, 2001, 291, 2364.
 - Y. Wada, M. Tajiri and S. Yoshida, Mol. Cel. Proteomics, 2005, 4, S267.
- 80 34. Y. Wada, M. Tajiri and S. Yoshida, Anal. Chem., 2004, 76, 6560.
- 35. D. L. Huber, R. P. Manginell, M. A. Samara, B. I. Kim and B. C. Bunker, *Science*, 2003, **301**, 352.
- L. Yu, X. L. Li, Z. M. Guo, X. L. Zhang and X. M. Liang, *Chem.-Eur. J.*, 2009, **15**, 12618.
- 85 37. M. Wuhrer, C. H. Hokke and A. M. Deelder, *Rapid Commun. Mass Spectrom.*, 2004, 18, 1741.