

## Supplementary Information

### Protein binding on acutely toxic and non-toxic polystyrene nanoparticles during filtration by *Daphnia magna*

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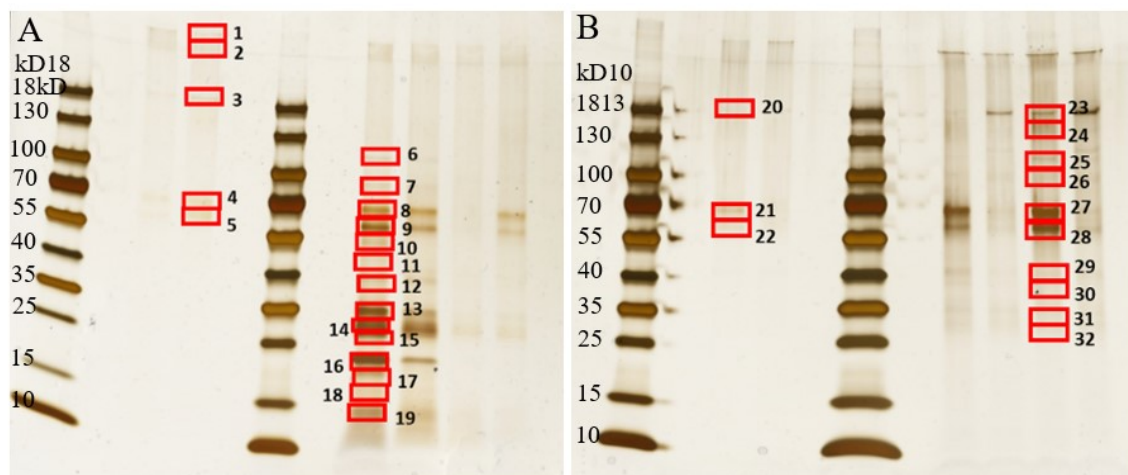
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**Supplementary Table 1.** The size of PS particles before and after filtration by *D. magna*. All measurements are at least in triplicate.

| Particle | Before filtration |                    | After filtration |                    |
|----------|-------------------|--------------------|------------------|--------------------|
|          | Diameter (nm)     | Polydispersity (%) | Diameter (nm)    | Polydispersity (%) |
|          |                   |                    |                  |                    |

|                           |         |        |          |            |
|---------------------------|---------|--------|----------|------------|
| 53 nm PS-NH <sub>2</sub>  | 47 ± 1  | 10 ± 2 | 215 ± 12 | multimodal |
| 200 nm PS-NH <sub>2</sub> | 179 ±   | 1 ± 1  | 180 ± 2  | 6 ± 2      |
| 62 nm PS-COOH             | 61 ± 1  | 14 ± 2 | 95 ± 6   | multimodal |
| 200 nm PS-COOH            | 180 ± 4 | 8 ± 3  | 191 ± 6  | 7 ± 2      |



**Supplementary Figure 1. SDS gels with silver staining.** The numbers represent the bands used for mass spectrometry analyses for the different conditions. (A) Control group (1-5 bands) and 53 nm PS-NH<sub>2</sub> incubated with *D. magna* (6-19 bands). (B) Control group (20-22 bands) and 200 nm PS-NH<sub>2</sub> incubated with *D. magna* (23-32 bands).

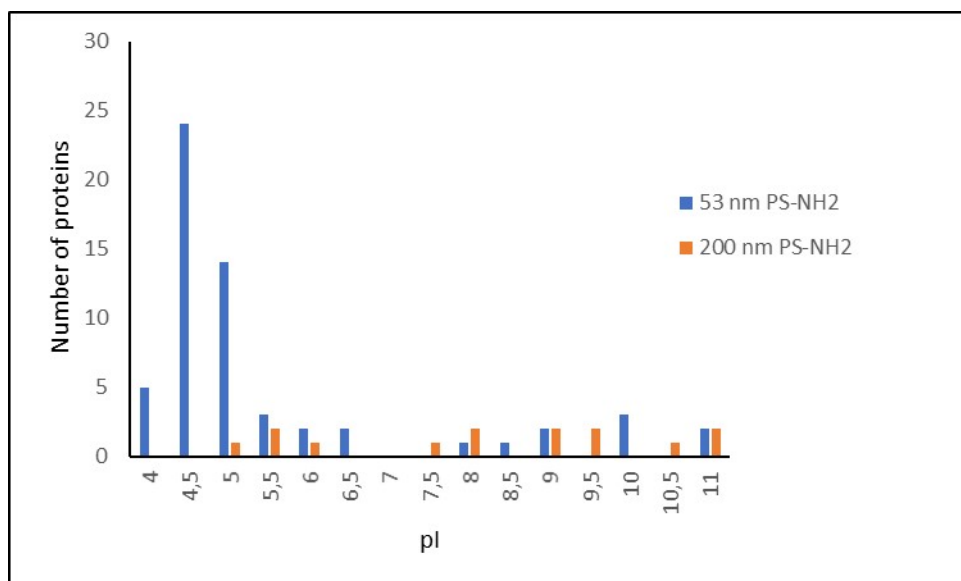
**Supplementary Table 2.** All identified proteins with a score number of 50 or larger and at least two identified unique peptides. (“NA” – Pi was not available as the sequence contains several consecutive undefined amino acids).

| Treatment                | Band | MW  | Protein name                     | Accession number | MW         | pI   |       |
|--------------------------|------|-----|----------------------------------|------------------|------------|------|-------|
| 53 nm PS-NH <sub>2</sub> | 6    | 121 | Protease m1 zinc metalloprotease | A0A0P5E8H8       | 109        | 4.59 |       |
|                          |      |     |                                  | A0A0P6JK73       | 109        | 4.61 |       |
|                          |      |     |                                  | A0A0N8AXC2       | 85         | 4.66 |       |
|                          |      |     |                                  | Histone H4       | A0A0N8AML8 | 11   | 11.33 |
|                          | 7    | 90  | Neutral endopeptidase (Fragment) | A0A0N8A4R4       | 82         | 4.67 |       |
|                          |      |     | Putative Neutral endopeptidase   | A0A0P5QHD4       | 35         | 4.83 |       |
|                          |      |     | Beta-galactosidase-1 protein 2   | A0A0P4WLE9       | 63         | 4.53 |       |

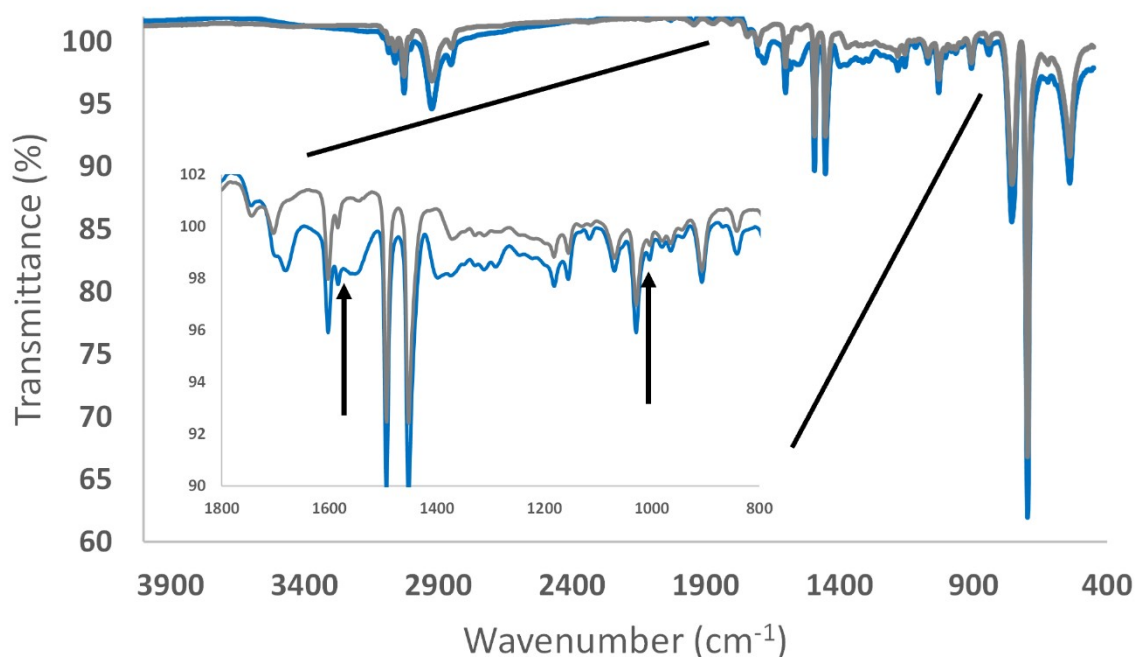
|  |    |    |  |            |    |       |
|--|----|----|--|------------|----|-------|
|  |    |    | Protease m1 zinc metalloprotease       | A0A0N8B8B4 | 89 | 4.58  |
|  |    |    | Lamin-A                                | A0A0P6IZ96 | 58 | 5.64  |
|  | 8  | 70 | Actin, alpha skeletal muscle           | A0A0N8AKX4 | 41 | 5.49  |
|  |    |    |  | A0A0N7ZFH2 | 49 | NA    |
|  |    |    | Tubulin beta chain                     | A0A0P6CCV0 | 49 | 4.78  |
|  |    |    |  | A0A0N7ZH16 | 52 | 4.75  |
|  |    |    | Tubulin alpha chain                    | A0A0P5ZYN7 | 50 | 4.94  |
|  |    |    | Fructose-bisphosphate aldolase         | A0A0N8DTE5 | 39 | 8.30  |
|  |    |    | Heat shock 70 kDa protein cognate      | A0A0P6DCT5 | 70 | 5.37  |
|  |    |    | Histone H2A (Fragment)                 | A0A0P6A1I4 | 14 | 11.23 |
|  |    |    | ATP synthase subunit beta              | A0A0P6CBB6 | 56 | 5.19  |
|  |    |    | Eukaryotic initiation factor 4A-II     | A0A0P6CFN1 | 46 | 5.32  |
|  |    |    | Histone H2B (Fragment)                 | A0A0P6A3S1 | 13 | 10.32 |
|  |    |    | Elongation factor 1-alpha              | A0A0P5WWR3 | 50 | 9.10  |
|  |    |    | Armadillo segment polarity protein     | A0A0P6IJT4 | 90 | 5.18  |
|  |    |    | ATP synthase subunit alpha (Fragment)  | A0A0N8AAM5 | 51 | NA    |
|  | 9  | 55 | Beta-klotho                            | A0A0N7ZV82 | 48 | NA    |
|  |    |    | Glucosylceramidase                     | A0A0N8A576 | 61 | 4.66  |
|  |    |    | Adenosine deaminase CECR1-A            | A0A0N7ZT57 | 53 | 4.75  |
|  |    |    | Alkaline phosphatase (Fragment)        | A0A0N8B5J6 | 34 | 4.80  |
|  | 10 | 55 | Lamin-A                                | A0A0P6IZ96 | 58 | 5.64  |
|  | 11 | 43 | Actin, alpha skeletal muscle           | A0A0N8AKX4 | 42 | 5.5   |
|  |    |    | Uncharacterized protein                | A0A0N8E6U4 | 43 | 4.74  |
|  |    |    | Chymotrypsin elastase family member 2A | A0A0N7ZRR8 | 20 | 4.3   |
|  |    |    | Ubiquitin-40S ribosomal protein S27a   | A0A0N7ZFP2 | 13 | 10.13 |
|  |    |    | Elongation factor 1-alpha              | A0A0N7ZL24 | 49 | 8.81  |
|  |    |    | Calmodulin                             | A0A0P6C8L3 | 17 | 4.04  |
|  | 12 | 38 | Mannan endo-1                          | A0A0N8AWI2 | 49 | 5.7   |
|  |    |    | Putative Brain chitinase and chia      | A0A0N8AJS7 | 31 | 4.4   |
|  | 13 | 35 | Carboxypeptidase B                     | A0A0P6GRN0 | 47 | 5.0   |
|  |    |    |  | A0A0N8A0G8 | 47 | 4.7   |
|  |    |    |  | A0A0N8DXD3 | 51 | 5.2   |
|  |    |    | Poly(U)-specific endoribonuclease      | A0A0N8AU82 | 41 | 4.5   |
|  |    |    | Serine protease                        | A0A0N7ZYN7 | 32 | 4.9   |

|                           |    |     |  |            |     |       |
|---------------------------|----|-----|--|------------|-----|-------|
|                           |    |     | Zinc carboxypeptidase  | A0A0N8ASM6 | 49  | 5.3   |
|                           |    |     | Pancreatic triacylglycerol lipase  | A0A0N8A9Z9 | 38  | NA    |
|                           |    |     | Uncharacterized protein  | A0A0N7ZR74 | 50  | 4.56  |
|                           | 14 | 30  | Serine protease  | A0A0N7ZYN7 | 32  | 4.9   |
|                           |    |     | Chymotrypsin elastase family member 2A                                   | A0A0N7ZN74 | 33  | 5.4   |
|                           |    |     | Neurexin IV  | A0A0N8BJ04 | 32  | 4.2   |
|                           | 15 | 27  | Chymotrypsin elastase family member 2A                                   | A0A0N7ZN74 | 33  | 5.4   |
|                           |    |     | Uncharacterized protein  | A0A0N7ZEA0 | 20  | 4.53  |
|                           |    |     | Metalloendopeptidase (Fragment)  | A0A0N8BGG7 | 33  | 6.1   |
|                           | 16 | 22  | Chymotrypsin elastase family member 2A                                   | A0A0N7ZRR8 | 20  | 4.6   |
|                           | 17 | 19  | Chymotrypsin elastase family member 2A                                   | A0A0N7ZRR8 | 20  | 4.6   |
|                           | 19 | 15  | Elongation factor 1-alpha  | A0A0N7ZYV1 | 50  | 9.0   |
|                           |    |     | Heat shock 70 kDa protein  | A0A0N8AGX4 | 67  | 5.29  |
|                           |    |     |  | A0A0N8CD53 | 71  | 5.14  |
|                           |    |     | C-type lectin domain family 6 member A                                   | A0A0N7ZMI0 | 17  | 4.9   |
|                           |    |     | Actin, alpha skeletal muscle (Fragment)                                  | A0A0P5ZI52 | 31  | 4.94  |
|                           |    |     | Putative Chymotrypsin elastase family member 2A                          | A0A0N7ZSD8 | 28  | NA    |
|                           |    |     | Uncharacterized protein  | A0A0N8AVI2 | 40  | 5.33  |
|                           |    |     | ADP-ribosylation factor (Fragment)                                       | A0A0N8BN21 | 19  | 6.4   |
|                           |    |     | 60S ribosomal protein L23 (Fragment)                                     | A0A164I9D0 | 22  | 10.2  |
|                           |    |     | Histone H4   | A0A0N8AML8 | 11  | 11.3  |
|                           |    |     | ATP synthase subunit beta  | A0A0N7ZMA0 | 57  | 5.14  |
| 200 nm PS-NH <sub>2</sub> | 23 | 190 | Vitellogenin-1   | A0A0N8ERH4 | 171 | 9.0   |
|                           | 24 | 170 | Vitellogenin-1   | A0A0N8ERH4 | 171 | 9.0   |
|                           |    |     | Actin, alpha skeletal muscle   | A0A0N7ZDS7 | 37  | 5.7   |
|                           | 25 | 120 | Hemocyte protein-glutamine gamma-glutamyltransferase                     | A0A0N8CBE8 | 105 | 7.9   |
|                           |    |     |  | A0A0P5CTZ7 | 109 | NA    |
|                           |    |     |  | A0A0P5CW37 | 101 | 8.4   |
|                           |    |     |  | A0A0N8AI27 | 105 | 8.2   |
|                           |    |     | Putative Hemocyte protein-glutamine gamma-glutamyltransferase (Fragment) | A0A0P5MNQ2 | 45  | 5.90  |
|                           |    |     | Histone H4   | A0A0N8AML8 | 11  | 11.33 |
|                           |    |     | Elongation factor 1-alpha  | A0A0P5WWR3 | 50  | 9.10  |
|                           |    |     | 40S ribosomal protein S3   | A0A0P6A3F6 | 27  | 9.68  |
|                           |    |     | Actin, alpha skeletal muscle   | A0A0N8AKX4 | 42  | 5.49  |

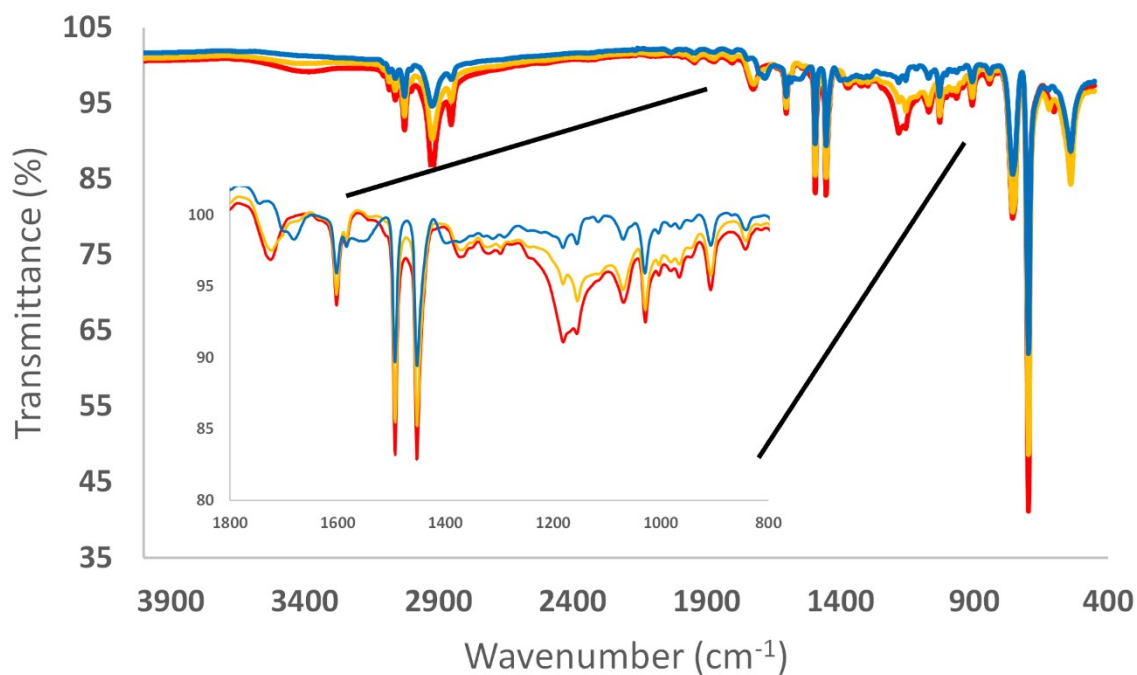
|         |    |     |   |            |     |       |
|---------|----|-----|---|------------|-----|-------|
|         |    |     | 40S ribosomal protein S1                                      | A0A0P6CD52 | 18  | 10.99 |
|         |    |     | Putative Vitellogenin-1 (Fragment)                            | A0A0N8ABJ0 | 92  | NA    |
|         |    |     | Eukaryotic initiation factor 4A-II                            | A0A0P6CFN1 | 46  | 5.32  |
|         |    |     | Elongation factor 1-gamma (Fragment)                          | A0A0P6CFP1 | 50  | 6.33  |
|         |    |     | 60S ribosomal protein L8                                      | A0A0P6CEH7 | 28  | 11.04 |
|         |    |     | 40S ribosomal protein S14                                     | A0A0N8B0M4 | 22  | 9.60  |
|         |    |     | Heat shock 70 kDa protein cognate                             | A0A0N7ZMQ1 | 71  | 5.25  |
|         |    |     |   | A0A0P6A337 | 72  | 5.10  |
|         |    |     | 40S ribosomal protein S9                                      | A0A0P6DE13 | 23  | 10.66 |
|         |    |     | 40S ribosomal protein S25                                     | A0A0P6CKS1 | 14  | 10.12 |
|         |    |     | 40S ribosomal protein S26 (Fragment)                          | A0A0N8A385 | 18  | 10.80 |
|         | 26 | 100 | Hemocyte protein-glutamine gamma-glutamyltransferase          | A0A0P5CTZ7 | 109 | NA    |
|         |    |     |   | A0A0N8AI27 | 105 | 8.2   |
|         |    |     |   | A0A0P5C8I4 | 108 | 7.3   |
|         |    |     |   |            |     |       |
|         | 27 | 70  | Putative Hemocyte protein-glutamine gamma-glutamyltransferase | A0A0N8AYD5 | 68  | 6.6   |
|         |    |     | Double oxidase: two peroxidase domains                        | A0A0N8CQ82 | 131 | NA    |
|         |    |     |   | A0A0N7ZFU0 | 54  | 9.2   |
|         | 28 | 60  | Hemocyte protein-glutamine gamma-glutamyltransferase          | A0A0P5PVU7 | 93  | NA    |
|         |    |     |   | A0A0N8AXK8 | 103 | NA    |
|         |    |     |   | A0A0P5MNQ2 | 45  | 5.9   |
|         | 29 | 45  | Uncharacterized protein                                       | A0A0N7ZTW3 | 59  | 5.98  |
|         | 30 | 38  | Uncharacterized protein                                       | A0A0N7ZTW3 | 59  | 5.98  |
|         |    |     | Putative Hemocyte protein-glutamine gamma-glutamyltransferase | A0A0N8AYD5 | 68  | 6.6   |
|         | 31 | 33  | Hemocyte protein-glutamine gamma-glutamyltransferase          | A0A0P5CTZ7 | 109 | NA    |
|         |    |     |   | A0A0N8AI27 | 105 | 8.2   |
|         | 32 | 30  | Hemocyte protein-glutamine gamma-glutamyltransferase          | A0A0P5CTZ7 | 109 | NA    |
|         |    |     |   | A0A0N8AI27 | 105 | 8.2   |
|         |    |     | Chymotrypsin elastase family member 2A                        | A0A0N7ZRR8 | 20  | 4.6   |
| Control | 20 | 190 | Vitellogenin-1  | A0A0N8ERH4 | 171 | 9.0   |



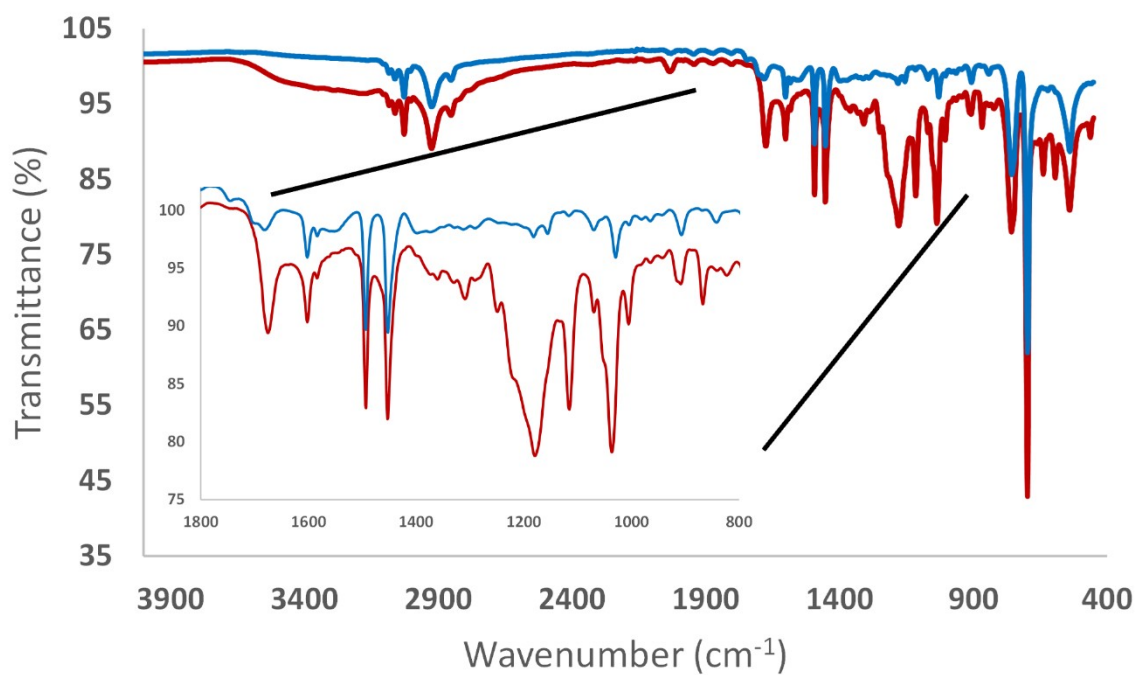
**Supplementary Figure 2.** The distribution of proteins bound to 50 nm and 200 nm PS-NH<sub>2</sub>. The proteins are grouped with pI between 4.0 to 4.5 and so on.



**Supplementary Figure 3.** Comparison between plain and amine polystyrene particles of the size ~200 nm. ATR-FTIR spectrum for PS-NH<sub>2</sub> 200 nm in blue and PS 195 nm in gray. The inset is a zoom-in on the area of wavenumber 800 -1800 cm<sup>-1</sup>. The two arrows point at signals at wavenumber ~1570 cm<sup>-1</sup> which have been assigned to the stretching vibrations of -NH<sub>2</sub> (Ref: 10.1021/acs.est.6b02846) and wavenumber ~1005 cm<sup>-1</sup> which have been assigned to stretching vibrations of C-N bonds (ref:10.1016/j.jcis.2015.03.052).



**Supplementary Figure 4. Comparison between amine polystyrene particles of the size 50, 52, and 200 nm.** ATR-FTIR spectrum for PS-NH<sub>2</sub> 200 nm in blue, PS-NH<sub>2</sub> 50 nm in red, and PS-NH<sub>2</sub> 52 nm in orange. The inset is a zoom-in on the area of wavenumber 800 - 1800 cm<sup>-1</sup>.



**Supplementary Figure 5. Comparison between amine polystyrene particles of the size 180 and 200 nm.** ATR-FTIR spectrum for PS-NH<sub>2</sub> 200 nm in blue and PS-NH<sub>2</sub> 180 nm in dark red. The inset is a zoom-in on the area of wavenumber 800 -1800 cm<sup>-1</sup>.

**Supplementary Table 3.** Proteins were identified in the content of the pellets after nanoparticles were filtrated by the digestive system of *D. magna* for 4 h in comparison with a control group. All proteins with a score number of 50 or larger and at least two identified unique peptides were taken into consideration.

| Treatment                | Accession  | Score | Num. of significant sequences | emPAI | Description   |
|--------------------------|------------|-------|-------------------------------|-------|---|
| 53 nm PS-NH <sub>2</sub> | A0A0N8ERH4 | 1371  | 33                            | 1.74  | Vitellogenin-1  |
|                          | A0A0P5XJT6 | 227   | 5                             | 1.56  | Uncharacterized protein (Fragment)                            |
|                          | A0A164FM53 | 148   | 3                             | 10.53 | Uncharacterized protein (Fragment)                            |
|                          | A0A0P5UGM5 | 115   | 3                             | 0.99  | Uncharacterized protein (Fragment)                            |
|                          | A0A0N8B1S8 | 1006  | 16                            | 1.23  | Hemocyte protein-glutamine gamma-glutamyltransferase          |
|                          | A0A0N8AYD5 | 555   | 9                             | 0.86  | Putative Hemocyte protein-glutamine gamma-glutamyltransferase |
|                          | A0A0P5E182 | 416   | 9                             | 0.74  | Hemocyte protein-glutamine gamma-glutamyltransferase          |
|                          | A0A0N7ZTW3 | 470   | 9                             | 0.91  | Uncharacterized protein (Fragment)                            |
|                          | A0A0N7ZU01 | 372   | 5                             | 0.74  | Di-domain hemoglobin  |
|                          | A0A0P4XQ89 | 336   | 4                             | 0.56  | Di-domain hemoglobin  |
|                          | A0A0P5F3Z1 | 190   | 4                             | 0.68  | Di-domain hemoglobin  |
|                          | A0A0P5D088 | 247   | 4                             | 0.83  | Chymotrypsin elastase family member 2A (Fragment)             |
|                          | A0A0N8BSM2 | 211   | 2                             | 0.3   | Uncharacterized protein                                       |



|                               |            |     |    |      |  |
|-------------------------------|------------|-----|----|------|--|
|                               | A0A0N8AW39 | 194 | 2  | 0.3  | Uncharacterized protein                                  |
|                               | A0A0P5EK64 | 164 | 2  | 0.28 | Uncharacterized protein (Fragment)                       |
|                               | A0A0N7ZE53 | 182 | 2  | 0.18 | Uncharacterized protein                                  |
|                               | A0A0N8BCY1 | 177 | 2  | 0.23 | Chymotrypsin BI  |
|                               | A0A0P5CJN7 | 159 | 2  | 1.25 | Mucin peritrophin  |
|                               | A0A0N7ZDU7 | 155 | 4  | 0.61 | Actin, alpha skeletal muscle<br>(Fragment)               |
|                               | A0A0N7ZYN7 | 149 | 3  | 0.48 | Serine protease  |
|                               | J9R260     | 134 | 3  | 0.61 | Trypsin 152 (Fragment)                                   |
|                               | A0A0N7ZFA7 | 131 | 3  | 0.59 | Serine protease (Fragment)                               |
|                               | A0A0N7ZMQ5 | 134 | 2  | 0.33 | Putative Serine protease P76<br>(Fragment)               |
|                               | A0A0P5HL93 | 123 | 5  | 0.23 | Uncharacterized protein                                  |
|                               | A0A0N7ZUL9 | 118 | 2  | 0.23 | Uncharacterized protein (Fragment)                       |
|                               | A0A0P4Z5S1 | 117 | 2  | 0.5  | Putative Secreted ferritin g subunit                     |
| 200 nm PS-<br>NH <sub>2</sub> | A0A0N8ERH4 | 591 | 19 | 0.64 | Vitellogenin-1   |
|                               | A0A0P6B5M1 | 551 | 12 | 0.33 | Vitellogenin-1   |
|                               | A0A0P6CX53 | 537 | 13 | 0.44 | Vitellogenin-1   |
|                               | A0A0N8A166 | 294 | 3  | 0.27 | Vitellogenin-1-like protein                              |
|                               | A0A0P5D5M6 | 269 | 4  | 0.4  | Vitellogenin-1-like protein                              |
|                               | A0A0N8B626 | 169 | 4  | 0.1  | Vitellogenin-1   |
|                               | A0A0P6HJB7 | 290 | 6  | 0.88 | Actin, alpha skeletal muscle                             |
|                               | A0A0N8A3C7 | 268 | 6  | 0.82 | Actin, alpha skeletal muscle                             |
|                               | A0A0N7ZEH2 | 194 | 3  | 0.13 | Hemocyte protein-glutamine gamma-<br>glutamyltransferase |
|                               | A0A0N7ZYN7 | 188 | 4  | 0.68 | Serine protease  |
|                               | A0A0N7ZSD8 | 162 | 3  | 0.56 | Putative Chymotrypsin elastase family<br>member 2A       |

|                |            |      |    |      |  |
|----------------|------------|------|----|------|--|
|                | A0A0N7ZES6 | 154  | 2  | 0.38 | Obstructor-A   |
|                | A0A0A7CK57 | 149  | 4  | 0.52 | Arginine kinase                                      |
|                | A0A0N7ZEE0 | 113  | 2  | 0.33 | Gly d 3  |
|                | A0A0N7ZUW0 | 111  | 3  | 0.03 | Mucin 5AC, oligomeric mucus/gel-forming              |
|                | A0A0N8AJS9 | 108  | 2  | 0.08 | Uncharacterized protein (Fragment)                   |
| 62 nm PS-COOH  | A0A0N8ERH4 | 1160 | 29 | 1.29 | Vitellogenin-1                                       |
|                | A0A0N8ACD3 | 328  | 5  | 0.3  | Hemocyte protein-glutamine gamma-glutamyltransferase |
|                | A0A0P5CTZ7 | 137  | 3  | 0.13 | Hemocyte protein-glutamine gamma-glutamyltransferase |
|                | A0A0P5PVU7 | 130  | 4  | 0.21 | Hemocyte protein-glutamine gamma-glutamyltransferase |
|                | A0A0N7ZEH2 | 86   | 4  | 0.18 | Hemocyte protein-glutamine gamma-glutamyltransferase |
|                | A0A0N7ZUW0 | 309  | 7  | 0.06 | Mucin 5AC, oligomeric mucus/gel-forming              |
|                | A0A0N8A626 | 285  | 8  | 0.79 | Uncharacterized protein                              |
|                | A0A0N7ZYN7 | 210  | 3  | 0.5  | Serine protease                                      |
|                | A0A0P5LBK9 | 204  | 3  | 0.13 | Uncharacterized protein                              |
|                | A0A0N8AGI9 | 201  | 3  | 0.12 | Tissue factor pathway inhibitor                      |
|                | A0A0N8AJD1 | 131  | 3  | 0.14 | Tissue factor pathway inhibitor                      |
|                | A0A0N8A945 | 197  | 4  | 0.52 | Actin, alpha skeletal muscle                         |
|                | A0A0N7ZTW3 | 136  | 3  | 0.25 | Uncharacterized protein (Fragment)                   |
| 200 nm PS-COOH | A0A0N8ERH4 | 875  | 22 | 0.9  | Vitellogenin-1                                       |
|                | A0A0P5UGM5 | 200  | 3  | 0.99 | Uncharacterized protein (Fragment)                   |
|                | A0A0P5M5E3 | 175  | 4  | 0.67 | Vitellogenin-1-like protein (Fragment)               |

|         |            |     |   |      |   |
|---------|------------|-----|---|------|---|
|         | A0A0P5XJT6 | 160 | 4 | 1.12 | Uncharacterized protein (Fragment)              |
|         | A0A164FM53 | 149 | 3 | 5.26 | Uncharacterized protein (Fragment)              |
|         | A0A164G126 | 138 | 3 | 5.26 | Uncharacterized protein (Fragment)              |
|         | A0A0N8A945 | 220 | 5 | 0.64 | Actin, alpha skeletal muscle                    |
|         | A0A0N8AUD4 | 212 | 3 | 0.11 | Tissue factor pathway inhibitor                 |
|         | A0A0N8AGI9 | 161 | 3 | 0.11 | Tissue factor pathway inhibitor                 |
|         | A0A0N7ZYN7 | 180 | 4 | 0.68 | Serine protease                                 |
|         | A0A0N7ZSD8 | 154 | 3 | 0.56 | Putative Chymotrypsin elastase family member 2A |
|         | A0A0N7ZTW3 | 141 | 2 | 0.15 | Uncharacterized protein (Fragment)              |
|         | A0A0N7ZUW0 | 112 | 4 | 0.03 | Mucin 5AC, oligomeric mucus/gel-forming         |
| Control | A0A0N7ZYN7 | 242 | 4 | 0.68 | Serine protease                                 |
|         | A0A0N7ZSD8 | 200 | 3 | 0.56 | Putative Chymotrypsin elastase family member 2A |
|         | A0A0P6H0J1 | 148 | 3 | 0.44 | Uncharacterized protein (Fragment)              |
|         | A0A0P5CAU9 | 125 | 2 | 0.59 | Uncharacterized protein (Fragment)              |
|         | A0A0N7ZE19 | 117 | 2 | 0.52 | Uncharacterized protein (Fragment)              |
|         | A0A0N8BCY1 | 148 | 2 | 0.23 | Chymotrypsin BI                                 |
|         | A0A0N8AZL9 | 130 | 2 | 0.3  | Trypsin serine protease                         |
|         | A0A0N7ZUL9 | 129 | 2 | 4.69 | Uncharacterized protein (Fragment)              |
|         | A0A0P4WVW2 | 102 | 2 | 7.58 | Uncharacterized protein                         |
|         | A0A0N7ZMQ5 | 101 | 2 | 5.92 | Putative Serine protease P76 (Fragment)         |