## Supplementary Information

# Bacteriophage T4 capsid as a nanocarrier for Peptide-N-Glycosidase F immobilization through self-assembly

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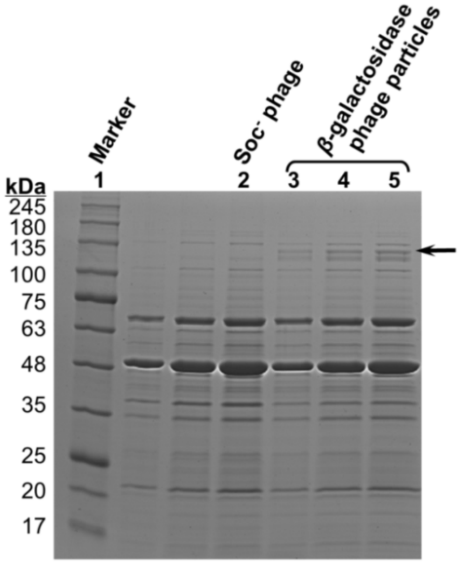

**Figure S1.**

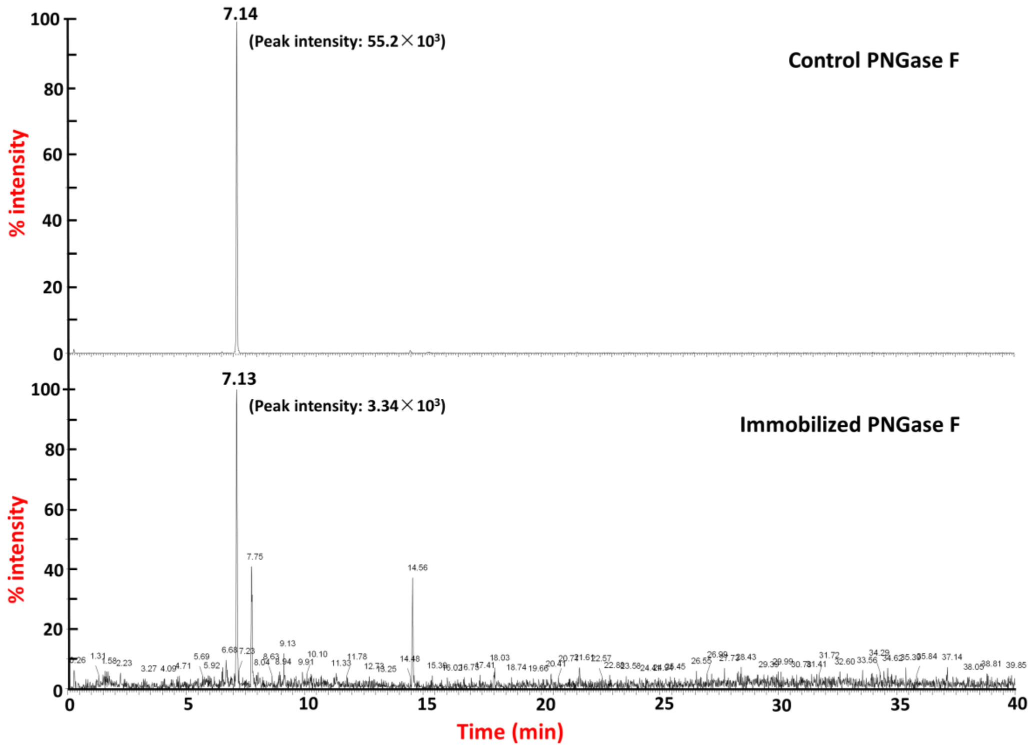

**Figure S2.** LC-MS data extracted for 511.73 (m/z) peptides.

Signals of peptides with 511.73±0.5 (m/z) (representing the peptide 4, refer to Tables S2 and S3 for m/z calculation) were extracted from the total ion chromatograms. Spectra of the extracted signals from the trypsin digested control PNGase F (top) and phage particles immobilized with PNGase F (bottom) are presented. Signals at the retention time of ~7.1 min were identified as from the peptide 4. This is one representative figure of three replicates.

**Table S1.** Protein detected and sequence coverages

| Sample | Sequence coverage | Accession No. | Name | Species | Peptides (95%) |
|---|---|---|---|---|---|
| **Control PNGase F** | 75.7% | sp\|P21163\|PNGF_ELIMR | Peptide-N(4)-(N-acetyl-beta-D-glucosaminyl) asparagine amidase F | ELIMR | 142 |
| **Phage particles** | 44.9% | sp\|P21163\|PNGF_ELIMR | Peptide-N(4)-(N-acetyl-beta-D-glucosaminyl) asparagine amidase F | ELIMR | 10 |

**Table S2**. Peptides with highest contribution and confidence scores (Phage particle sample)

| No. | Contribution | Confidence | Sequence | Precise molecular weight | z |
|---|---|---|---|---|---|
| 1 | 2 | 99 | AGWCPGMAVPTR | 1301.623 | 2 |
| 2 | 2 | 99 | NIQLPTNTEK | 1156.607 | 2 |
| 3 | 2 | 99 | SLLSGNTELK | 1060.575 | 2 |
| 4 | 2 | 99 | SSIDGVPYGK | 1021.517 | 2 |
| 5 | 2 | 99 | YANVYVK | 855.4571 | 2 |
| 6 | 2 | 99 | TCDEWDRYANVYVKNK | 2060.856 | 2 |
| 7 | 2 | 99 | TEKAYLRTTISGWGHAK | 1917.929 | 4 |

**Table S3.** Peptides with highest contribution and confidence scores (Control PNGase F sample)

| No. | Contribution | Confidence | Sequence | Precise molecular weight | z |
|---|---|---|---|---|---|
| 1 | 2 | 99 | AGWCPGMAVPTR | 1301.598 | 2 |
| 2 | 2 | 99 | NIQLPTNTEK | 1156.589 | 2 |
| 3 | 2 | 99 | SLLSGNTELK | 1060.564 | 2 |
| 4 | 2 | 99 | SSIDGVPYGK | 1021.507 | 2 |
| 5 | 2 | 99 | YANVYVK | 855.4483 | 2 |
| 6 | 2 | 99 | ADNTVNIK | 873.4775 | 2 |
| 7 | 2 | 99 | AISSFVIAK | 934.55 | 2 |
| 8 | 2 | 99 | FDIVYGTPDYK | 1316.64 | 2 |
| 9 | 2 | 99 | FITPYWVGTEK | 1339.673 | 2 |
| 10 | 2 | 99 | GCAEWCFR | 1084.41 | 2 |
| 11 | 2 | 99 | GLEIDVTDFK | 1135.575 | 2 |
| 12 | 2 | 99 | IQLPTNTEK | 1042.566 | 2 |
| 13 | 2 | 99 | IVYGTPDYK | 1054.536 | 2 |
| 14 | 2 | 99 | IYTETWLAK | 1123.589 | 2 |
| 15 | 2 | 99 | KNIQLPTNTEK | 1284.706 | 3 |
| 16 | 2 | 99 | NAFGDGLSQSAEGT | 1352.601 | 2 |
| 17 | 2 | 99 | NAFGDGLSQSAEGTF | 1499.659 | 2 |
| 18 | 2 | 99 | NKTTGEWYEIGR | 1452.7 | 3 |
| 19 | 2 | 99 | SIDGVPYGK | 934.4803 | 2 |
| 20 | 2 | 99 | SNTPISAPVVT | 1084.576 | 2 |
| 21 | 2 | 99 | SNTPISAPVVTN | 1198.627 | 2 |
| 22 | 2 | 99 | SSIDGVPY | 836.3905 | 2 |
| 23 | 2 | 99 | SVDFDIVYGTPDYK | 1617.77 | 2 |
| 24 | 2 | 99 | TCDEWDR | 980.3639 | 2 |
| 25 | 2 | 99 | TFQHQLGALGC | 1230.586 | 2 |
| 26 | 2 | 99 | TTGEWYEIGR | 1210.549 | 2 |
| 27 | 2 | 99 | TTISGWGH | 857.4033 | 2 |
| 28 | 2 | 99 | TTISGWGHAK | 1056.535 | 2 |
| 29 | 2 | 99 | TTISGWGHAKPYDAGSR | 1802.875 | 4 |
| 30 | 2 | 99 | YAISSFVIAK | 1097.609 | 2 |