```
        10         20         30         40         50         60
MMKTLLLFVG LLLTWESGQV LGDQTVSDNE LQEMSNQGSK YVNKEIQNAV NGVKQIKTLI

        70         80         90        100        110        120
EKTNEERKTL LSNLEEAKKK KEDALNETRE SETKLKELPG VCNETMMALW EECKPCLKQT

       130        140        150        160        170        180
CMKFYARVCR SGSGLVGRQL EEFLNQSSPF YFWMNGDRID SLLENDRQQT HMLDVMQDHF

       190        200        210        220        230        240
SRASSIIDEL FQDRFFTREP QDTYHYLPFS LPHRRPHFFF PKSRIVRSLM PFSPYEPLNF

       250        260        270        280        290        300
HAMFQPFLEM IHEAQQAMDI HFHSPAFQHP PTEFIREGDD DRTVCREIRH NSTGCLRMKD

       310        320        330        340        350        360
QCDKCREILS VDCSTNNPSQ AKLRRELDES LQVAERLTRK YNELLKSYQW KMLNTSSLLE

       370        380        390        400        410        420
QLNEQFNWVS RLANLTQGED QYYLRVTTVA SHTSDSDVPS GVTEVVVKLF DSDPITVTVP

       430        440
VEVSRKNPKF METVAEKALQ EYRKKHREE
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Figure S-1. The primary structure of human secretory clusterin (sCLU) and the sites of clusterin glycosylation. sCLU is synthesized as a pre-proprotein consisting of 449 amino acids. During the posttranslational maturation the N-terminal signalling peptide composed of 22 amino acids (highlighted yellow) is cleaved off. The amino acid region 23-227 comprises the α-subunit of the mature protein, while the region 228-449 is known as β-subunit. The two subunits are connected to each other via disulphide bonds. Asparagine residues (N) of the protein (marked as pink) are heavily glycosylated. Data from UniProt Protein Database (Protein ID P10909).

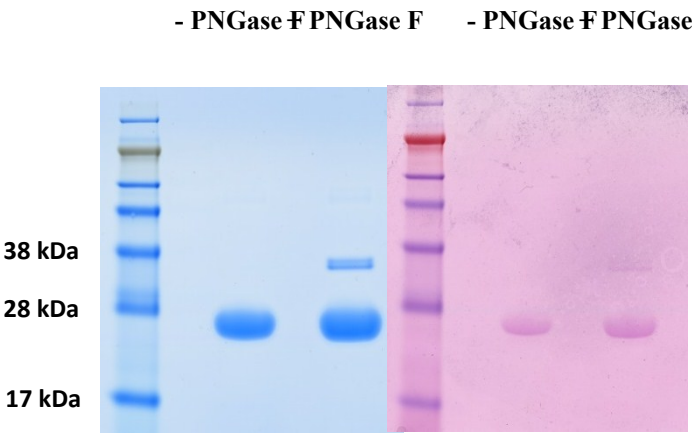

Figure S-2. PNGase F treatment of Apo AI. The PNGase F treatment of Apo AI did not cause a visible shift and the band remained at ca. 28 kDa. Glycoprotein staining kit additionally showed that the PNGase F treated Apo AI still contains sugar molecule (right gel). The band at ca. 35 kDa height corresponds to the enzyme PNGase F. 15 µg protein was loaded onto the gel.

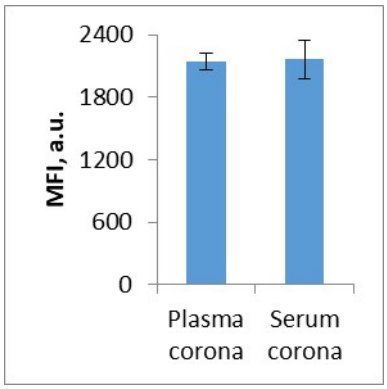

Figure S-3. Comparison of macrophage uptake for plasma-covered and serum-covered nanoparticles.

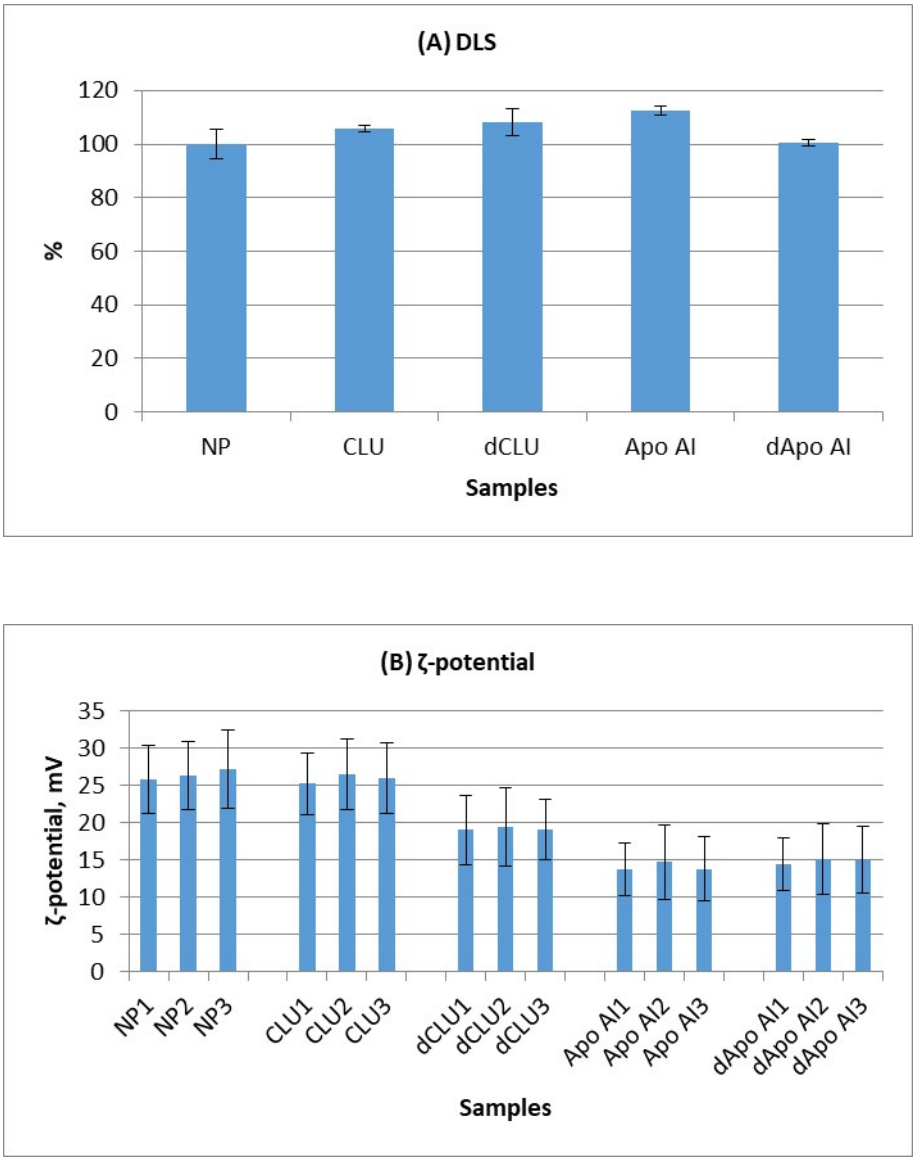

Figure S-4. (A) Dynamic Light Scattering (DLS) and (B) ζ-potential measurements of glycosylated and deglycosylated coronas of clusterin and Apo AI. For DLS measurements the data are normalized to pristine nanoparticles' size (set as 100%). The values are expressed as mean ± Standard Deviation (n=3). For ζ-potential measurements triplicates were used, each of them representing an average of 12 measurements. NP - nanoparticle (KK132a); CLU - clusterin corona, Apo AI - apolipoprotein AI corona; dCLU - deglycosylated clusterin corona; dApo AI - deglycosylated apolipoprotein AI corona.

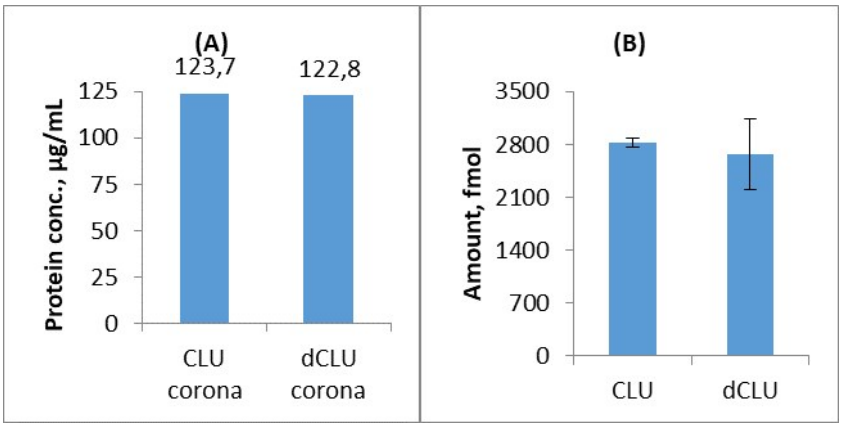

Figure S-5. (A) Total protein and (B) the amount of clusterin covering the surface of TW192 nanoparticles upon incubation with ordinary clusterin (CLU) or deglycosylated clusterin (dCLU). The data in the (A) chart shows the protein concentration of coronas (each 100 µL) measured by Pierce assay. The data in the (B) chart corresponds to the amount contained in 2 µL corona sample that was injected into the LC-MS.