Electronic Supplementary Material (ESI) for ChemComm.

Supporting Information

Amphiphilic Dendrimers Control Protein Binding and Corona Formation on Liposome Nanocarriers

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1 Synthesis of dendrimers with different surface patterns

1.1 Materials and Instruments

Chemicals and Solvents. All chemicals were obtained from commercial suppliers such as Sigma Aldrich, TCI, Acros Organics, Fisher Scientific, etc., and were utilized without further purification. The solvents (HPLC grade) were purchased from Fisher Scientific or Acros Organics. Chloroform (Rotisolv®, HPLC grade) for the *recycling*-gel permeation chromatography (GPC) system was purchased from Carl Roth. The deuterated solvents were purchased from Sigma Aldrich. Argon (Westfalen AG) was used for reactions under inert gas.

Silica Gel Chromatography. For thin-layer chromatography (TLC) Alugram Sil G/UV254 plates from Macherey-Nagel were used and the detection of substances was performed under UV light at 254 nm or 366 nm. Macherey-Nagel silica gel with particle size of 0.04–0.063 mm or 0.063–0.2 mm was used for preparative silica gel chromatography.

Gel Permeation Chromatography (GPC). Dendrimers with peripheral neopentyl-protected sulfonic acid groups were purified on a *recycling*-GPC purification system from Shimadzu. Dendrimers with deprotected peripheral sulfonic acid groups were purified by size exclusion chromatography using Sephadex® LH-20 in DMF.

Nuclear Magnetic Resonance Spectroscopy (NMR). All ^{1}H NMR and ^{13}C NMR spectra were recorded on a Bruker Avance III 300 MHz, Avance III 500 MHz, Avance III 700 MHz or Bruker Avance III 850 MHz spectrometer in deuterated solvents such as CD_2Cl_2, THF-d_8 and DMSO-d_6 at 298 K. ^{13}C NMR were recorded in j-modulated spin-echo (JMOD) mode. Spectra were analyzed by applying the software MestReNova.

Matrix-assisted Laser Desorption/Ionization–Time of Flight (MALDI-TOF) Mass Spectrometry. MALDI-TOF mass spectra were measured on a Waters MALDI Synapt G2-SI or Bruker rapifleX MALDI-TOF/TOF. Precursors and uncharged dendrimers were dissolved in THF and measured by applying *trans*-2-[3-(4-*tert*-butylphenyl)-2-methyl-2-propenylidene]-malononitrile (DCTB) or dithranol as matrix. Deprotected sulfonic acid based dendrimers were solvated in DMF and diluted in a saturated α-cyano-4-hydroxycinnamic acid (CHCA) solution in water:acetonitrile (1:1) + 0.1% TFA. All dendrimers with peripheral pyridine groups were measured in tetrahydrofuran (THF) with tetracyanoquinodimethane (TCNQ) as matrix. Processing of data was performed in mMass.

Electrospray Ionization (ESI) Spectrometry. ESI spectra were measured on a Waters Synapt G2-SI. The samples were dissolved in methanol.

Atmospheric Pressure Chemical Ionization Mass Spectrometry (APCI-MS). APCI mass spectra of building blocks and intermediates were measured on an Advion expression-L Compact Mass Spectrometer (CMS) (Advion Inc. 61 Brown Rd, Suite 100, Ithaca, NY 14850, USA) by either applying the sample (solid) as an atmospheric solid analysis probe (ASAP) or measuring directly from TLC plates by an automated TLC plate reader (Plate express).

Field Desorption Mass Spectrometry (FD-MS). FD mass spectra of intermediates were measured on a VG Instruments ZAB 2-SE-FPD using an 8 kV accelerating voltage.

Nomenclature for Polyphenylene Dendrimers.

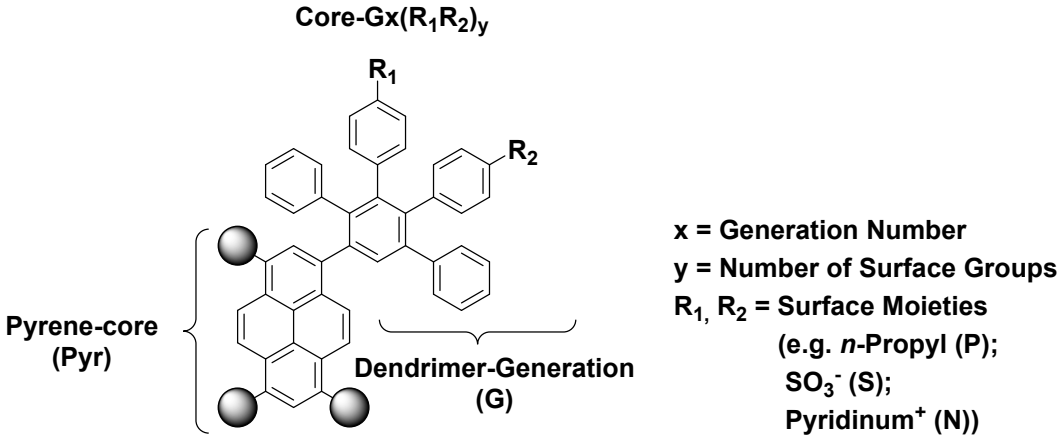

Figure S1. Systematic designation of polyphenylene dendrimers (PPDs)

1.2 Synthesis of a first-generation negatively charged amphiphilic polyphenylene dendrimer – $(PS)_4$

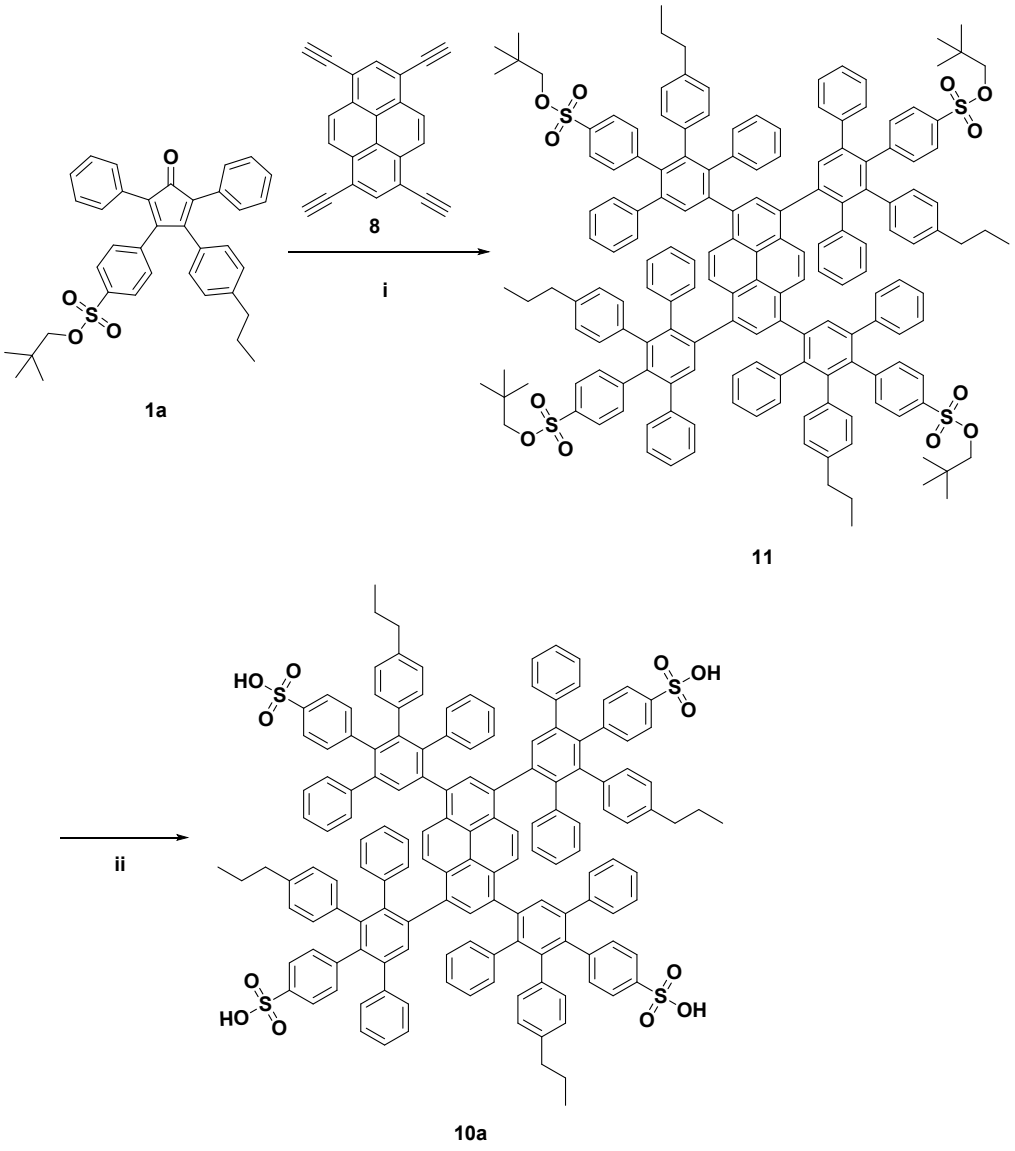

Figure S2. Synthesis of first-generation amphiphilic dendrimer **10a** with alternating sulfonic acid and *n*-propyl groups according to Stangenberg *et al*.[1] i) *o*-xylene, 145 °C, 48 h, 45% yield; ii) DMF, 180 °C, 48 h, 85% yield.

*Neopentyl 4-(3-oxo-2,4-diphenyl-5-(4-propylphenyl)cyclopenta-1,4-dien-1-yl)benzenesulfonate (**1a**)*

Surface building block **1a** was synthesized according to the literature in a four-step synthesis.[2, 3] All spectral data were in agreement with the literature.[2, 3]

^{1}H NMR (300 MHz, CD_2Cl_2): δ(ppm) = 7.70 (d, *J* = 8.5 Hz, 2H), 7.31–7.22 (m, 8H), 7.20–7.12 (m, 4H), 7.01 (d, *J* = 8.3 Hz, 2H), 6.83 (d, *J* = 8.2 Hz, 2H), 3.64 (s, 2H), 2.54 (t, *J* = 7.8, 7.2 Hz, 2H), 1.61 (dt, *J* = 13.7, 7.4 Hz, 2H), 0.92 (t, *J* = 7.3 Hz, 3H), 0.87 (s, 9H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ(ppm) = 200.22, 155.08, 152.76, 144.50, 139.78, 135.83, 131.36, 130.72, 130.66, 130.32, 129.56, 128.84, 128.74, 128.56, 128.09, 127.61, 125.62, 80.56, 38.26, 32.05, 26.27, 24.77, 14.02.

FD-MS: *m/z* calcd. for $C_{37}H_{36}O_4S$: 576.7, found 576.8 $[M]^{\bullet+}$.

*1,3,6,8-Tetraethynylpyrene (**8**)*

Pyrene core **8** was synthesized in three steps according to the literature.[4]

*Pyr-G1-(PSpen)$_4$ **11***

The synthesis of neopentyl-protected dendrimer **11** was modified from the previously reported method.[1] 1,3,6,8-Tetraethynylpyrene (**8**) (10 mg, 33.5 µmol) and building block **1a** (116 mg, 201 µmol, 6 equiv) were dissolved in 3 mL *o*-xylene. The mixture was degassed with argon and stirred at 145 °C for 48 h in a sealed microwave tube. The product was precipitated in methanol, filtered off and purified by silica gel chromatography using a mixture of cyclohexane and THF (3:1). The product was further purified by *recycling*-GPC in chloroform to obtain dendrimer **11** as a yellow solid (38 mg, 45%).

^{1}H NMR (700 MHz, CD_2Cl_2): δ (ppm) = 7.98–7.73 (m, 5H), 7.60–7.31 (m, 11H), 7.26–6.23 (m, 66H), 3.54–3.30 (m, 8H), 2.50–2.27 (m, 8H), 1.52–1.38 (m, 8H), 0.88–0.66 (m, 48H).

^{13}C NMR (176 MHz, CD_2Cl_2): δ(ppm) = 147.44, 147.16, 142.17, 141.36, 141.06, 140.65, 140.53, 140.10, 139.77, 138.10, 137.26, 137.01, 136.65, 136.32, 132.99, 132.81, 131.67, 130.37, 130.28, 128.20, 128.15, 127.92, 127.79, 127.45, 126.99, 126.72, 80.04, 37.68, 26.10, 24.67, 13.49.

MALDI-TOF: *m/z* calcd. for $C_{168}H_{154}O_{12}S_4$ 2491.03, found 2492.98 $[M+H]^+$.

Pyr-G1-(PS)$_4$ ***10a***

Negatively charged amphiphilic dendrimer **10a** was synthesized according to the literature[1] with a modified purification protocol. Briefly, neopentyl-protected dendrimer **11** (12.0 mg, 4.81 µmol) was dissolved in 2 mL dry DMF, the resulting solution was degassed with argon and stirred at 180 °C for 48 h in a sealed microwave tube. Subsequently, DMF was removed *in vacuo*. The residue was dissolved in methanol and precipitated in diethyl ether. The resulting product was further purified by gel permeation chromatography (GPC) applying Sephadex LH-20 in DMF to obtain Pyr-G1-(PS)$_4$ **10a** as a light yellow solid (9 mg, 85%).

^{1}H NMR (700 MHz, DMSO): δ (ppm) = 8.02–6.20 (m, 82H), 2.44–2.28 (m, 8H), 1.52–1.31 (m, 8H), 0.79–0.58 (m, 12H).

^{13}C NMR (176 MHz, DMSO): δ (ppm) = 145.51, 145.41, 141.11, 141.02, 139.64, 139.27, 137.01, 130.93, 130.36, 129.61, 129.54, 127.74, 127.70, 127.46, 127.43, 127.12, 126.72, 125.09, 124.18, 123.89, 36.54, 23.50, 13.12.

MALDI-TOF: *m/z* calcd. for $C_{148}H_{114}O_{12}S_4$ 2210.72, found 2210.73 $[M]^{\bullet+}$.

1.3 Synthesis of a first-generation negatively charged polyphenylene dendrimer – S_8

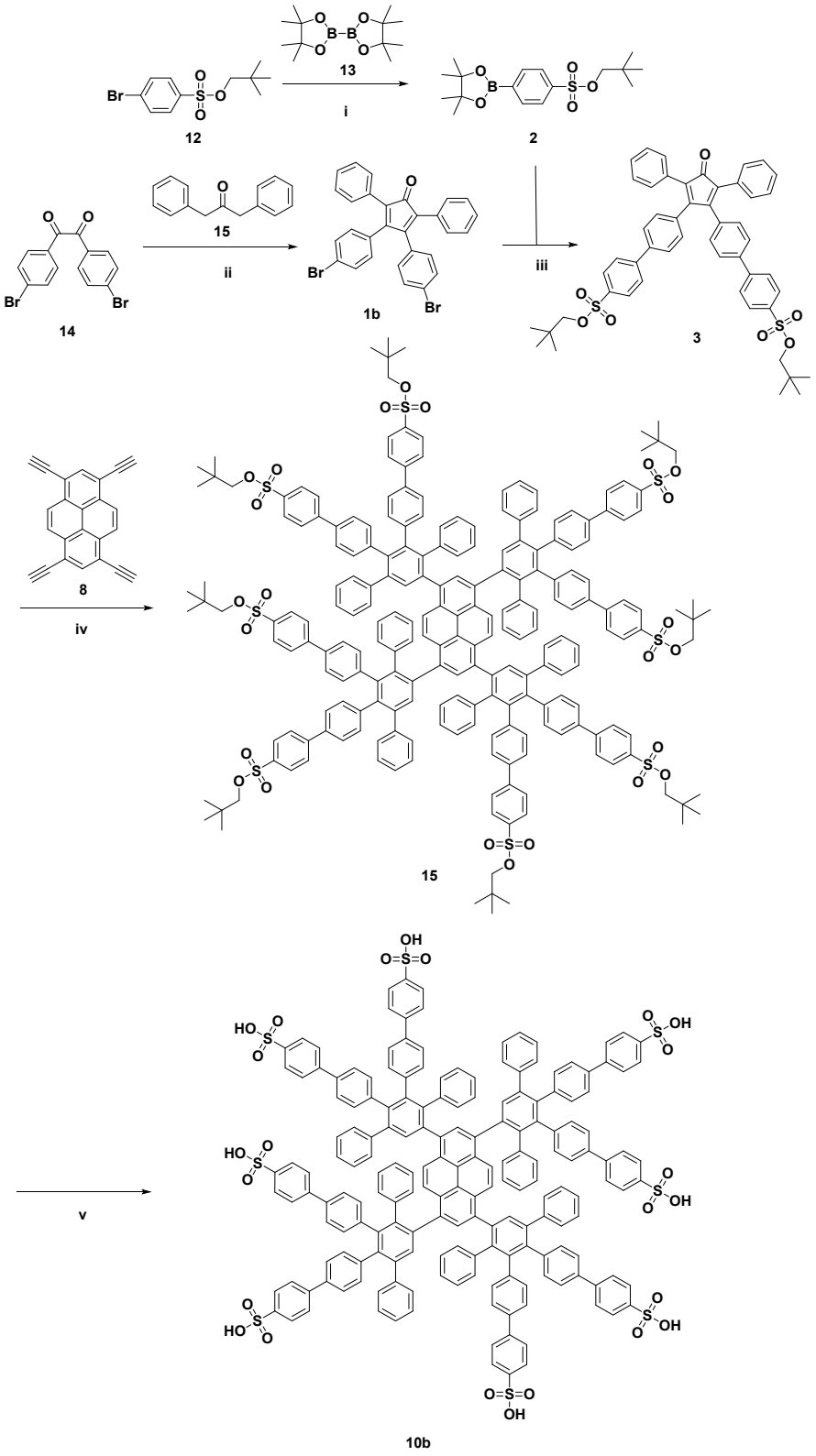

Figure S3. Synthesis of first-generation negatively charged dendrimer **10b**. i) KOAc, $Pd(dppf)Cl_2$, 1,4-dioxane, 90 °C, 6 h, 99% yield; ii) TBAH, ethanol, 85 °C, 0.5 h, 85% yield; iii) $Pd(PPh_3)_4$, K_2CO_3 (aq), 1,4-dioxane, 90 °C, 15 h, 34% yield; iv) *o*-xylene, 145 °C, 36 h, 27% yield; v) DMF, 180 °C, 48 h, 88% yield.

*Neopentyl 4-bromobenzenesulfonate (**12**)*

Compound **17** was synthesized according to the literature.[2, 3] All spectral data were in agreement with the literature.[2]

^{1}H NMR (300 MHz, CD_2Cl_2): δ(ppm) = 7.79–7.70 (m, 4H), 3.67 (s, 2H), 0.89 (s, 9H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ(ppm) = 135.64, 133.12, 129.95, 129.27, 80.63, 32.08, 26.22.

FD-MS: *m/z* calcd. for $C_{11}H_{15}BrO_3S$: 307.2, found 308.7 $[M+H]^+$.

*Neopentyl 4-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)benzenesulfonate (**2**)*

In a dry Schlenk flask neopentyl 4-bromobenzenesulfonate (**12**) (1.00 g, 3.26 mmol), bis(pinacolato)diboron (**13**) (1.24 g, 4.88 mmol, 1.5 equiv) and potassium acetate (703 mg, 7.16 mmol, 2.2 equiv) were dissolved in 15 mL dry 1,4-dioxane. After degassing with argon [1,1′-bis(diphenylphosphino)ferrocene]dichloropalladium(II) ($Pd(dppf)Cl_2$) (53.2 mg, 65.1 µmol, 0.02 equiv) was added under argon atmosphere. The reaction mixture was stirred at 90 °C for 6 h under argon atmosphere. Subsequently, ethyl acetate was added and the organic layer was washed with water. The organic layer was dried over magnesium sulphate. After removing the solvent *in vacuo* the crude product was purified by silica gel column chromatography using a mixture of cyclohexane and ethyl acetate (10:1) to obtain compound **2** as a colourless solid (1.14 g, 99%).

^{1}H NMR (300 MHz, CD_2Cl_2): δ (ppm) = 7.95 (d, *J* = 8.1 Hz, 2H), 7.86 (d, *J* = 8.1 Hz, 2H), 3.65 (s, 2H), 1.35 (s, 12H), 0.88 (s, 9H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ (ppm) = 138.47, 135.62, 127.23, 122.32, 84.95, 83.63, 79.89, 31.89, 26.50, 25.26, 25.06.

APCI-MS: *m/z* calcd. for $C_{17}H_{27}BO_5S$: 354.2, found 371.7 $[M+NH_4]^+$.

*3,4-Bis(4-bromophenyl)-2,5-diphenylcyclopenta-2,4-dien-1-one (**1b**)*

1,2-Bis(4-bromophenyl)ethane-1,2-dione (**14**) (1.5 g, 4.08 mmol) and 1,3-diphenylacetone (**15**) (857 mg, 4.08 mmol) were dissolved in 150 mL ethanol and heated up to 85 °C. Subsequently, 1 M methanolic tetrabutylammonium hydroxide (TBAH) solution (1.06g, 4.08 mL, 4.08 mmol) was added. After stirring at 85 °C for 0.5 h, the reaction mixture was diluted in ethyl acetate. The organic layer was washed with water, dried over sodium sulphate and concentrated *in vacuo*. The product was precipitated in an ethanol water mixture to afford building block **1b** as a dark red solid (1.89 g, 85%).

^{1}H NMR (300 MHz, CD_2Cl_2): δ (ppm) = 7.41–7.32 (m, 4H), 7.32–7.25 (m, 6H), 7.24–7.15 (m, 4H), 6.90–6.77 (m, 4H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ (ppm) = 153.28, 132.24, 131.81, 131.38, 130.85, 130.49, 128.54, 128.18, 126.38, 123.35.

APCI-MS: *m/z* calcd. for $C_{29}H_{18}Br_2O$ 539.97, found 540.7 $[M+H]^+$.

*Dineopentyl 4',4'''-(4-oxo-3,5-diphenylcyclopenta-2,5-diene-1,2-diyl)bis-([1,1'-biphenyl]-4-sulfonate) (**3**)*

Building block **1b** (700mg, 1.29 mmol) and neopentyl 4-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)benzenesulfonate (**2**) were dissolved in 40 mL 1,4-dioxane. Then, an aqueous 2 M potassium carbonate solution (2.68 g, 9.68 mL, 19.4 mmol) was added and the mixture was degassed with argon. Tetrakis(triphenylphosphine)palladium(0) ($Pd(PPh_3)_4$) was added and the reaction mixture was stirred at 90 °C overnight under argon atmosphere. The crude mixture was diluted with dichloromethane and the organic layer was washed with water and dried over sodium sulfate. After removing the solvent *in vacuo* the crude product was purified by silica gel column chromatography using a mixture of cyclohexane and THF (5:1) to obtain building block **3** as a red solid (340 mg, 34%).

^{1}H NMR (300 MHz, CD_2Cl_2): δ (ppm) = 7.85 (dd, J = 48.4, 8.3 Hz, 8H), 7.52 (d, J = 8.1 Hz, 4H), 7.33–7.22 (m, 10H), 7.12 (d, J = 8.2 Hz, 4H), 0.89 (s, 18H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ = 200.21, 153.98, 145.80, 139.36, 135.30, 133.95, 131.15, 130.58, 128.84, 128.52, 128.11, 127.98, 127.30, 126.54, 80.23, 31.92, 26.10.

MALDI-TOF: *m/z* calcd. for $C_{51}H_{48}O_7S_2$ 3531.24, found 836.39 $[M]^{\bullet+}$.

*Pyr-G1-(Spen)$_8$ (**15**)*

1,3,6,8-Tetraethynylpyrene (**8**) (6 mg, 20.1 µmol) and building block **3** (101 mg, 121 µmol, 6 equiv) were dissolved in 3 mL *o*-xylene, degassed with argon and stirred at 145 °C for 36 h in a sealed microwave tube. The solvent was removed *in vacuo* and the crude product was purified by silica gel chromatography using a mixture of cyclohexane and THF (2:1). The product was further purified by *recycling*-GPC in chloroform to obtain dendrimer **15** as a yellow solid (19 mg, 27%).

^{1}H NMR (700 MHz, CD_2Cl_2): δ (ppm) = 8.03 – 7.80 (m, 21H), 7.71 – 7.48 (m, 19H), 7.38 – 6.38 (m, 75H), 3.71 – 3.57 (m, 16H), 0.93 – 0.81 (m, 72H).

^{13}C NMR (176 MHz, CD_2Cl_2): δ(ppm) = 146.12, 141.80, 141.54, 141.24, 140.17, 138.98, 136.90, 136.54, 136.19, 134.78, 132.82, 130.42, 130.33, 128.72, 128.68, 128.12, 128.07, 127.70, 127.61, 126.88, 126.28, 125.94, 80.12, 31.89, 26.09.

MALDI-TOF: *m/z* calcd. for $C_{224}H_{202}O_{24}S_8$ 3531.24, found 3532.72 $[M+H]^+$.

*Pyr-G1-S$_8$ (**10b**)*

Pyr-G1-(Spen)$_8$ **15** (7.00 mg, 1.98 µmol) was dissolved in 2 mL dry DMF, the resulting solution was degassed with argon and stirred at 180 °C in a sealed microwave tube for 48 h. The solvent was evaporated *in vacuo* and the product was precipitated in diethyl ether. The product was further purified by gel permeation chromatography (Sephadex LH-20) in DMF. Dendrimer **10b** was obtained as a slight yellow solid (5.2 mg, 88%).

^{1}H NMR (700 MHz, DMSO): δ (ppm) = 7.98–7.86 (m, 2H), 7.85–7.75 (m, 2H), 7.65–6.31 (m, 110H).

^{13}C NMR (176 MHz, DMSO): δ (ppm) = 147.06, 146.43, 141.53, 140.92, 139.74, 139.06, 138.45, 136.59, 136.14, 131.79, 129.62, 127.63, 126.61, 125.99, 125.94, 125.43, 125.35, 125.01, 124.96, 124.51.

MALDI-TOF: *m/z* calcd. for $C_{184}H_{122}O_{24}S_8$ 2970.61, found 2971.59 $[M+H]^+$, 2994.56 $[M+Na]^+$, 3009.56 $[M+K]^+$.

1.4 Synthesis of a first-generation positively charged amphiphilic polyphenylene dendrimer –$(PN)_4$

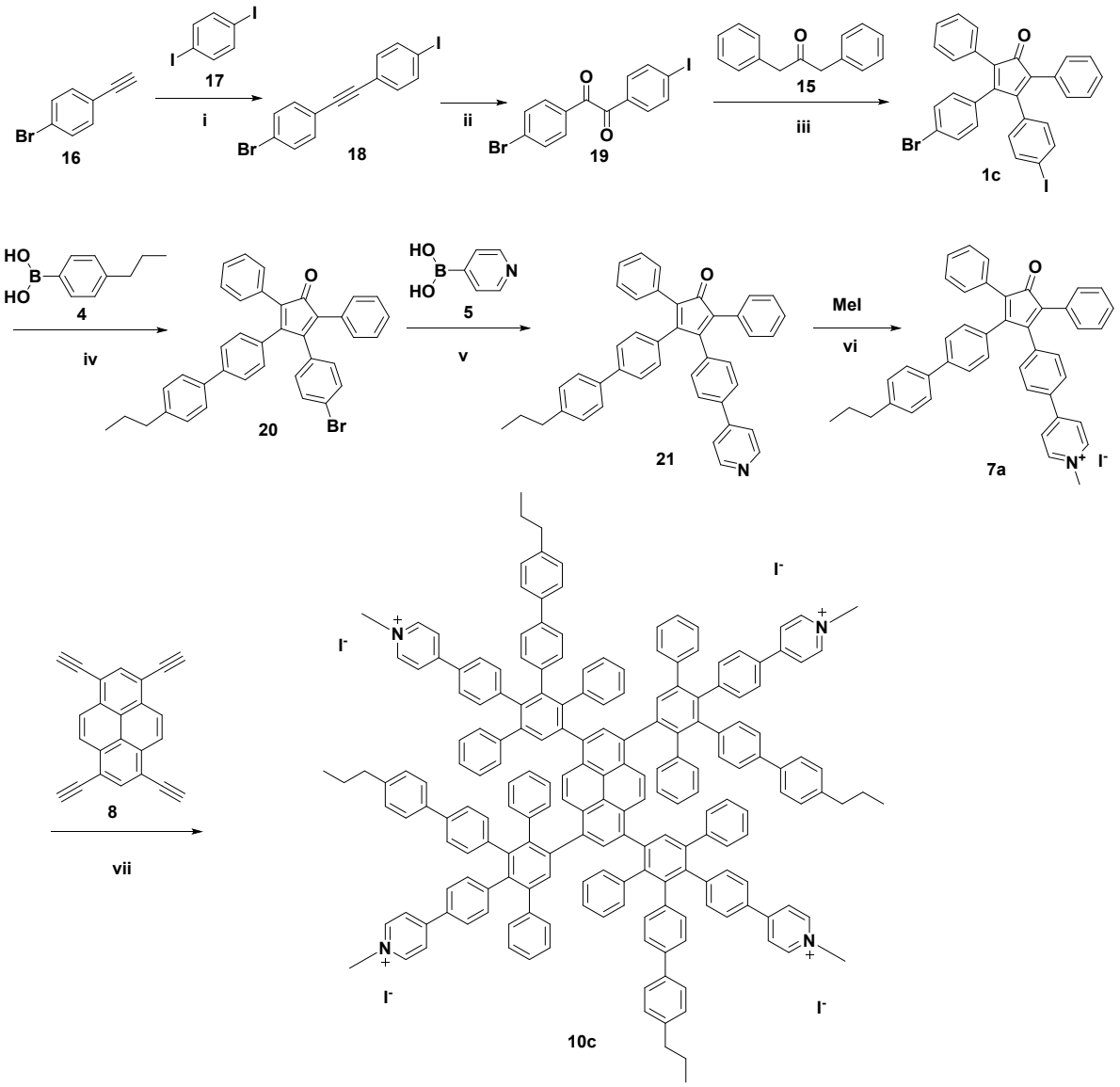

Figure S4. Synthesis of positively charged first-generation dendrimer **10c** with alternating pyridinium and *n*-propyl groups. i) CuI, PPh_3, $PdCl_2(Ph_3P)_2$, 1,4-dioxane, 40 °C, 15 h, 60% yield; ii) I_2, $[Ru(p\text{-cymene})Cl_2]_2$, *tert*-butyl hydroperoxide (70% in H_2O), 1,4-dioxane, 50 °C, 15 h, 86% yield; iii) TBAH, ethanol, 85 °C, 20 min, 60% yield; iv) $Pd(PPh_3)_4$, K_2CO_3 (aq), 1,4-dioxane, 40 °C, 15 h; v) $Pd(PPh_3)_4$, K_2CO_3 (aq), 1,4-dioxane, 80 °C, 15 h, 60 % yield; vi) methanol, RT, 48 h, 70% yield; vii) DMSO, 140 °C, 3 d, 47% yield.

*1-Bromo-4-((4-iodophenyl)ethynyl)benzene (**18**)*

4-Bromophenylacetylene (2.0 g, 11.05 mmol) (**16**), 1,4-diiodobenzene (**17**) (7.29 g, 22.10 mmol, 2 equiv), copper(I) iodide (210 mg, 1.1 mmol, 0.1 equiv) and triphenylphosphine (579 mg, 2.21 mmol, 0.2 equiv) were dissolved in 200 mL 1,4-dioxane in a 500 mL flask. To this mixture 50 mL triethylamine was added and the solution was degassed with argon. Bis(triphenylphosphine)palladium(II) dichloride ($PdCl_2(Ph_3P)_2$) (338 mg, 0.552 mmol) was added and the solution was stirred at 40 °C under argon atmosphere overnight. Then, the solution was filtered and the solvent was removed *in vacuo* followed by an extraction with dichloromethane. The organic layer was dried over magnesium sulphate and purified by silica gel flash chromatography using hexane as eluent to obtain compound **18** as a bright yellow solid (2.54 g, 60 %).

^{1}H NMR (300 MHz, THF-d_8): δ (ppm) = 7.75 (d, J = 7.9 Hz, 2 H), 7.55 (d, J = 8.0 Hz, 2 H), 7.42 (d, J = 8.1 Hz, 2 H), 7.27 (d, J = 8.0 Hz, 2 H).

^{13}C NMR (75 MHz, THF-d_8): δ (ppm) = 138.44, 134.62, 133.71, 133.62, 132.64, 132.43, 123.31, 123.17, 122.81, 95.06, 90.08.

APCI-MS: *m/z* calcd. for $C_{14}H_8BrI$: 381.9, found 383.9 $[M+2H]^+$.

*1-(4-Bromophenyl)-2-(4-iodophenyl)ethane-1,2-dione (**19**)*

Tolane **18** (1.0 g, 2.61 mmol), iodine (132 mg, 0.522 mmol, 0.2 equiv) and dichloro(*p*-cymene)ruthenium(II) dimer (16 mg, 0.026 mmol, 0.01 equiv) were added to a 50 mL flask and dissolved in as little 1,4-dioxane as possible. 1.5 mL (10.44 mmol, 4 equiv) of a 70 % *tert*-butyl hydroperoxide solution was slowly added to the solution. The mixture was stirred at 50 °C overnight. After evaporation of the solvent and purification via silica gel flash column chromatography using hexane as eluent followed by THF benzil **19** was obtained as a yellow solid (931 mg, 86 %).

^{1}H NMR (300 MHz, THF-d_8): δ (ppm) = 7.97 (d, J = 8.5 Hz, 2H), 7.88 (d, J = 8.6 Hz, 2H), 7.75 (d, J = 8.5 Hz, 2H), 7.70 (d, J = 8.5 Hz, 2H).

^{13}C NMR (75 MHz, THF-d_8): δ (ppm) = 193.57, 193.21, 139.43, 138.19, 133.33, 132.99, 132.27, 131.86, 130.91, 128.89, 125.95, 121.07, 104.30.

*3-(4-Bromophenyl)-4-(4-iodophenyl)-2,5-diphenylcyclopenta-2,4-dien-1-one (**1c**)*

Benzil **19** (500 mg, 1.2 mmol) and 1,3-diphenylacetone **3** (279 mg, 1.33 mmol, 1.1 equiv) were dissolved in 15 mL ethanol in a 50 mL flask. The solution was heated under reflux and 0.24 mL tetrabutylammonium hydroxide (1M in THF) were added. After 20 min the reaction was stopped by cooling in an ice bad. After cooling at –20 °C for a few hours the product was filtered off. Building block **1c** was received as a purple solid (424 mg, 60 %).

^{1}H NMR (300 MHz, CD_2Cl_2): δ (ppm) = 7.56 (d, J = 8.3 Hz, 2 H), 7.35 (d, J = 8.5 Hz, 2 H), 7.31–7.24 (m, 6 H), 7.24–7.17 (m, 4 H), 6.82 (d, J = 8.5 Hz, 2 H), 6.68 (d, J = 8.5 Hz, 2 H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ (ppm) = 200.17, 153.53, 153.42, 137.91, 132.92, 132.38, 131.96, 131.59, 131.53, 131.02, 131.01, 130.64, 128.70, 128.33, 126.57, 126.50, 123.50, 95.41.

APCI-MS: *m/z* calcd. for $C_{29}H_{18}BrIO$: 588.0, found 589.1 $[M+H]^+$.

*3-(4-Bromophenyl)-2,5-diphenyl-4-(4'-propyl-[1,1'-biphenyl]-4-yl)cyclopenta-2,4-dien-1-one (**20**)*

Building block **1c** (230 mg, 0.390 mmol) and 4-propylbenzeneboronic acid (**4**) (83 mg, 0.507 mmol, 1.3 equiv) were added to a 50 mL flask and were dissolved in 25 mL 1,4-dioxane. To this solution 0.97 mL of a 2 M potassium carbonate solution were added and degassed with argon. Then, $Pd(PPh_3)_4$ (27 mg, 0.023 mmol, 0.06 equiv) was added and the reaction mixture was stirred at 40 °C overnight. The reaction mixture was filtered and extracted with DCM followed by a filtration over a silica gel flash column using a mixture of THF and hexane (1:19). Product **20** was used without further purification.

APCI-MS: *m/z* calcd. for $C_{38}H_{29}BrO$: 580.1, found 581.5 $[M+H]^+$.

*2,5-Diphenyl-3-(4'-propyl-[1,1'-biphenyl]-4-yl)-4-(4-(pyridin-4-yl)phenyl)cyclopenta-2,4-dien-1-one (**21**)*

Building block **20** (380 mg, 0.653 mmol) and 4-pyridineboronic acid (**5**) (321 mg, 2.61 mmol, 4 equiv) were dissolved in 25 mL 1,4-dioxane in a 50 mL flask. 3.27 mL of a 2M potassium carbonate solution were added and the mixture was degassed. After adding $Pd(PPh_3)_4$ (45 mg, 0.038 mmol, 0.06 equiv) the mixture was stirred at 80 °C for two days under argon atmosphere. The solvent was removed followed by an extraction with DCM. The purification was performed by silica gel flash chromatography using a mixture of THF and hexane (1:2). Building block **21** was received as a violet solid (236 mg, 60%).

^{1}H NMR (300 MHz, CD_2Cl_2): δ (ppm) = 8.64–8.57 (m, 2 H), 7.58–7.43 (m, 8 H), 7.32–7.20 (m, 12 H), 7.12 (d, J = 8.4 Hz, 2 H), 7.03 (d, J = 8.4 Hz, 2 H), 2.66–2.55 (m, 2 H), 1.70–1.56 (m, 2 H), 0.94 (t, J = 7.3 Hz, 3 H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ (ppm) = 200.53, 154.81, 154.22, 152.06, 150.89, 150.83, 148.64, 147.60, 143.18, 141.65, 138.71, 138.51, 137.80, 136.47, 134.64, 132.17, 131.58, 131.44, 130.83, 130.78, 130.50, 129.66, 129.60, 129.58, 129.17, 128.87, 128.68, 128.65, 128.21, 128.12, 127.53, 127.15, 127.03, 126.80, 126.70, 126.13, 125.99, 122.09, 121.78, 38.16, 25.15, 14.17.

APCI-MS: *m/z* calcd. for $C_{43}H_{33}NO$: 579.3, found 580.4 $[M+H]^+$.

*1-Methyl-4-(4-(3-oxo-2,4-diphenyl-5-(4'-propyl-[1,1'-biphenyl]-4-yl)cyclopenta-1,4-dien-1-yl)phenyl)pyridin-1-ium (**7a**)*

Building block **21** (220 mg, 0.38 mmol) was dissolved in 1 mL methyl iodide in a 10 mL Schlenk tube followed by the addition of 1 mL methanol. After two days, the product was precipitated by the addition of diethyl ether. After filtration, compound **7a** was obtained as a red-brown solid (192 mg, 70%).

^{1}H NMR (300 MHz, DMSO-d_6): δ (ppm) = 8.96 (d, J = 6.6 Hz, 2 H), 8.46 (d, J = 7.1 Hz, 2 H), 8.00 (d, J = 8.5 Hz, 2 H), 7.59 (d, J = 2.7 Hz, 2 H), 7.56 (d, J = 2.5 Hz, 2 H), 7.35–7.16 (m, 14 H), 7.08 (d, J = 8.4 Hz, 2 H), 4.29 (s, 3 H), 2.56 (t, J = 7.5 Hz, 2 H), 1.58 (h, J = 7.4 Hz, 2 H), 0.87 (t, J = 7.3 Hz, 3 H).

^{13}C NMR (75 MHz, DMSO-d_6): δ (ppm) = 199.29, 154.27, 153.12, 153.03, 145.53, 141.99, 139.93, 136.65, 136.13, 133.09, 131.26, 130.43, 130.31, 130.20, 129.86, 129.59, 128.16, 128.11, 127.79, 127.60, 126.29, 126.11, 125.82, 124.93, 123.88, 47.04, 36.74, 23.91, 13.52.

ESI-MS: *m/z* calcd. for $C_{44}H_{36}NO^+$: 594.28, found 592.22 $[M+H]^+$.

*Pyr-G1(PN)$_4$ (**10c**)*

Building block **7a** (100 mg, 0.17 mmol) and 1,3,6,8-tetraethynylpyrene (**8**) (6.9 mg, 0.023 mmol, 0.14 equiv) were dissolved in 5 mL DMSO in a 10 mL Schlenk tube. After degassing with argon, the mixture was heated up to 140 °C for three days. After the addition of diethyl ether product **10c** precipitated and was filtered off. Purification was performed applying dialyses (1000 MWCO) in methanol. Dendrimer **10c** was received as yellow crystals (33.3 mg, 47 %).

^{1}H NMR (300 MHz, DMSO-d_6): δ (ppm) = 8.90 (d, J = 6.7 Hz, 8 H), 8.47–6.04 (m, 106 H), 4.25 (s, 12 H), 1.65–1.42 (m, 8 H), 0.86 (t, J = 6.5 Hz, 12 H).

^{13}C-NMR (126 MHz, DMSO-d_6): δ (ppm) = 153.09, 145.46, 141.13, 140.68, 136.32, 132.60, 131.58, 130.31, 129.66, 128.88, 127.88, 126.60, 125.91, 124.83, 123.33, 46.88, 36.71, 24.64, 13.53.

ESI-MS: *m/z* calcd. for $(C_{196}H_{154}N_4)^{4+}$: 641.31, found 641.14; *m/z* calcd. for $(C_{196}H_{154}N_4)^{3+}$: 897.38, found 897.31; *m/z* calcd. for $(C_{196}H_{154}N_4)^{2+}$: 1409.52, found 1409.44.

1.5 Synthesis of a second-generation positively charged amphiphilic polyphenylene dendrimer – $(PN)_8$

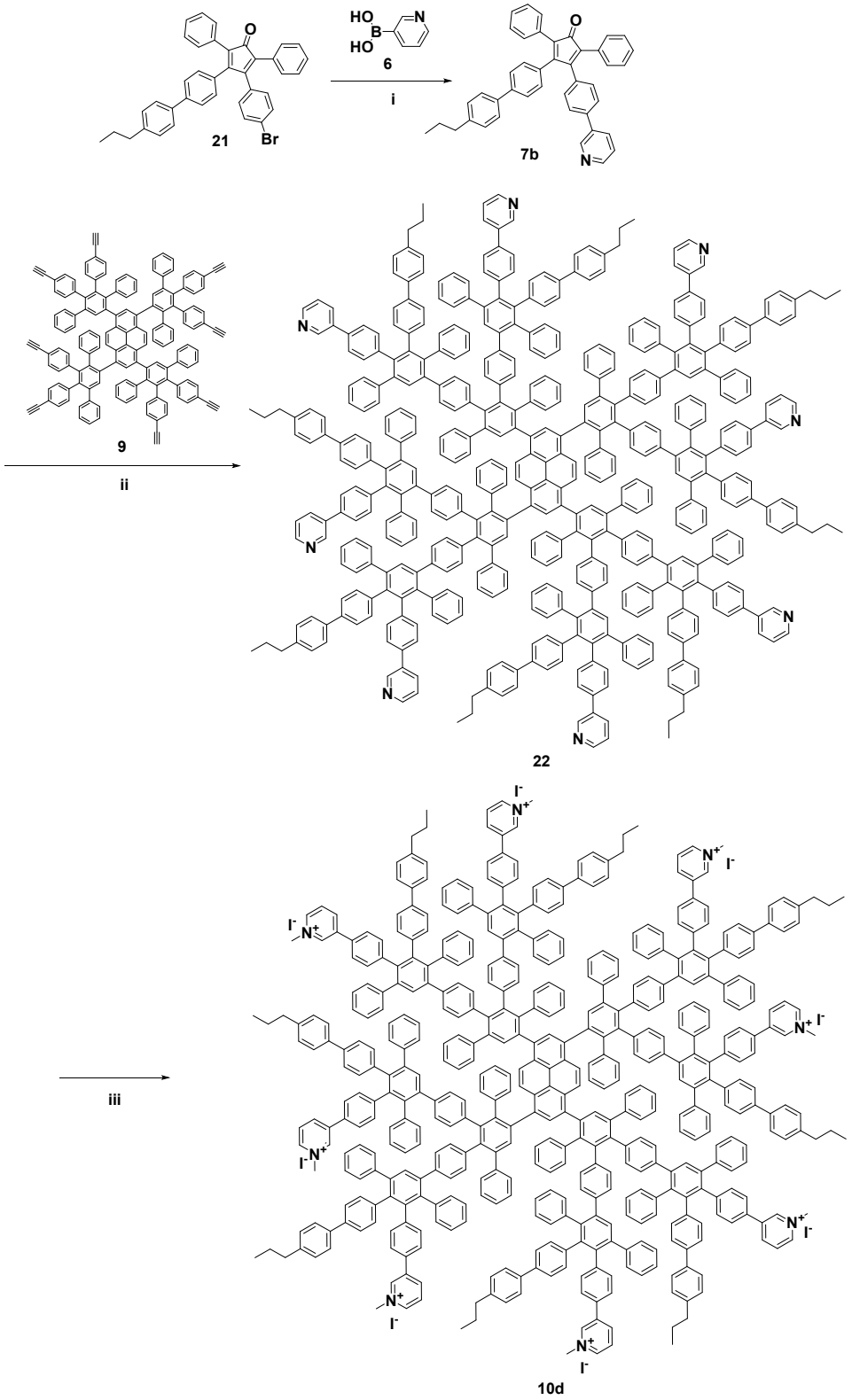

Figure S5. Synthesis of second-generation dendrimer **15d** with alternating pyridinum and *n*-propyl groups. i) $Pd(PPh_3)_4$, K_2CO_3 (aq), 1,4-dioxane, 80 °C, 15 h, 50 % yield; ii) *o*-xylene, 160 °C, 3 d, 64% yield; iii) methanol, RT, 15 h, 92% yield.

*2,5-Diphenyl-3-(4'-propyl-[1,1'-biphenyl]-4-yl)-4-(4-(pyridin-3-yl)phenyl)cyclopenta-2,4-dien-1-one (**7b**)*

Compound **21** (380 mg, 0.653 mmol) and 4-pyridineboronic acid (**6**) (321 mg, 2.61 mmol, 4 equiv) were dissolved in 25 mL 1,4-dioxane in a 50 mL flask. 3.27 mL of a 2M potassium carbonate solution were added and the mixture was degassed with argon. After adding $Pd(PPh_3)_4$ (45 mg, 0.038 mmol, 0.06 equiv) the mixture was stirred at 80 °C for two days under argon atmosphere. The solvent was removed *in vacuo* followed by an extraction with dichloromethane (DCM). The purification was performed by silica gel flash chromatography using a mixture of THF and hexane (1:2). Building block **7b** was received as a violet solid (112 mg, 50%).

^{1}H NMR (300 MHz, CD_2Cl_2): δ (ppm) = 8.82 (d, J = 2.4 Hz, 1 H), 8.55 (dd, J = 4.9, 1.6 Hz, 1 H), 7.88 (dt, J = 8.1, 2.1 Hz, 1 H), 7.55–7.43 (m, 5 H), 7.27 (d, J = 9.3 Hz, 14 H), 7.11 (d, J = 8.2 Hz, 2 H), 7.04 (d, J = 8.3 Hz, 2 H), 2.61 (t, J = 7.6 Hz, 2 H), 1.74–1.54 (m, 2 H), 0.94 (t, J = 7.3 Hz, 3 H).

^{13}C NMR (75 MHz, CD_2Cl_2): δ (ppm) = 200.61, 154.85, 154.44, 149.31, 148.66, 143.16, 141.61, 138.41, 137.82, 136.12, 134.58, 133.56, 132.22, 131.62, 131.52, 130.79, 130.76, 130.50, 129.55, 128.63, 128.61, 128.14, 128.07, 127.14, 127.06, 126.76, 126.53, 126.13, 125.97, 124.08, 38.14, 25.12, 14.12.

APCI-MS: *m/z* calcd. for $C_{43}H_{33}NO$: 579.3, found 580.4 $[M+H]^+$.

*Pyr-G1-(ethynyl)$_8$ **9***

First generation dendrimer **9** was synthesized according to the literature.[1]

^{1}H NMR (300 MHz, THF-d_8): δ (ppm) = 8.05–7.31 (m, 8 H), 7.29–7.02 (m, 28 H), 7.02–6.71 (m, 34 H), 6.71–6.43 (m, 12 H), 3.47–3.32 (m, 8 H).

^{13}C NMR (126 MHz, THF-d_8): δ (ppm) = 142.00, 141.69, 132.76, 131.84, 131.49, 131.42, 130.98, 130.85, 128.69, 128.61, 121.22, 120.89, 78.90.

MALDI-TOF: m/z calcd. for $C_{152}H_{90}$: = 1914.70, found 1914.62 $[M]^{\bullet+}$.

*Pyr-G2-(PN)$_8$ uncharged **22***

First generation dendrimer core **9** (50 mg, 0.0261 mmol) and building block **7b** (242 mg, 0.418 mmol, 16 equiv) were dissolved in 1 mL *o*-xylene in a 10 mL Schlenk tube. After degassing, the reaction mixture was heated up to 160 °C for three days. Subsequently, dendrimer **22** was precipitated in methanol and purified by GPC in THF. Dendrimer **22** was obtained as a yellow solid (106 mg, 64%).

^{1}H NMR (500 MHz, THF-d_8): δ (ppm) = 8.67 (d, *J* = 12.4 Hz, 8H), 8.40 (s, 8H), 7.80–7.72 (m, 8H), 7.56–6.30 (m, 274H), 1.60 (h, *J* = 6.1, 5.7 Hz, 16H), 0.90 (t, *J* = 7.3 Hz, 24H).

^{13}C NMR (126 MHz, THF-d_8): δ (ppm) = 149.21, 148.92, 142.99, 142.59, 142.41, 142.35, 142.33, 142.17, 142.10, 141.75, 141.66, 141.39, 141.25, 141.17, 140.37, 140.27, 139.97, 139.81, 139.74, 139.42, 139.05, 138.89, 138.85, 138.77, 136.66, 136.63, 135.99, 135.71, 134.19, 134.16, 133.43, 133.09, 130.88, 129.61, 129.59, 128.58, 127.95, 127.26, 127.24, 126.68, 126.27, 125.99, 125.72, 124.10, 68.07, 67.92, 67.75, 67.57, 38.53, 25.94, 25.79, 25.64, 25.48, 14.15.

MALDI-TOF: *m/z* calcd. for $C_{488}H_{354}N_8$ 6324.79, found 6325.89 $[M+H]^+$.

*Pyr-G2-(PN)$_8$ **10d***

Dendrimer **22** (106 mg, 0.017 mmol) was dissolved in 1 mL methyl iodide in a 10 mL Schlenk tube followed by the addition of 1 mL methanol. After 24 h diethyl ether was added leading to precipitation of the product which was filtered off to obtain dendrimer **10d** as a yellow-brown solid (116 mg, 92 %).

^{1}H NMR (300 MHz, DMSO-d_6): δ (ppm) = 9.22 (s, 8 H), 8.81 (s, 8 H), 8.68 (s, 8 H), 8.03 (s, 8 H), 7.63–6.38 (m, 266 H), 4.27 (s, 24 H), 1.60–1.44 (m, 16 H), 0.83 (t, J = 7.0 Hz, 24 H).

^{13}C NMR (126 MHz, DMSO-d_6): δ (ppm) = 153.21, 143.25, 140.89, 140.25, 137.99, 136.30, 132.30, 131.63, 130.83, 129.95, 129.48, 128.87, 127.78, 127.57, 125.88, 125.53, 124.62, 124.23, 47.95, 40.02, 39.86, 39.69, 39.52, 39.35, 39.19, 39.02, 36.69, 23.99, 13.52.

ESI-MS: *m/z* calcd. for $(C_{496}H_{378}N_8)^{8+}$: 806.37, found 806.24; *m/z* calcd. for $(C_{496}H_{378}N_8I)^{7+}$: 939.56, found 939.55; *m/z* calcd. for $(C_{496}H_{378}N_8I_2)^{6+}$: 1117.30, found 1117.29; *m/z* calcd. for $(C_{496}H_{378}N_8I_3)^{5+}$: 1366.14, found 1366.15; *m/z* calcd. for $(C_{496}H_{378}N_8I_4)^{4+}$: 1739.40, found 1739.39.

2 Protein corona on dendrimer-coated liposomes and polystyrene nanoparticles

2.1 Material and methods

Liposome synthesis. Based on previous reports,[5] amine functionalized liposomes were synthesized using 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE), L-*α*-phosphatidylcholine (egg PC) and cholesterol (Chol) with a molar ratio of egg PC:DOPE:Chol = 1:1:1 by film hydration followed by extrusion. Cholesterol and the lipids were dissolved in chloroform at a concentration of 10 mg mL^{-1}. All components (Egg PC = 835 µL, DOPE = 767 µL and Cholesterol = 398 µL) were mixed with 2 mL of chloroform containing 1 vol% EtOH in a 50 mL round-bottomed flask. The mixture was dried using a rotary evaporator at room temperature (30 min, 450 mbar) and further at 42°C (30 min, 3 mbar). To remove organic solvent residuals the flask was placed into a vacuum oven for 1 hour. (Diameter Ø: 242 ± 6 nm, ζ – Potential: - 52 ± 6 mV)

Polystyrene nanoparticle synthesis. According to previous reports,[6] amine functionalised polystyrene nanoparticles were prepared via direct miniemulsion. For colloidal stability, the ionic surfactant cetyl trimethyl ammonium chloride was used. To generate amino groups, 2-aminoethyl methacrylate hydrochloride (2 wt% to styrene) was copolymerized with styrene. Excessive surfactant was removed via dialysis. A detailed protocol is given in previous reports.[7] (Diameter Ø: 98 ± 10 nm, ζ – Potential: + 34 ± 12 mV)

Coating of nanoparticles and liposomes with dendrimers. All dendrimers were dissolved in DMSO at a concentration of 10 mg mL^{-1}. PS-NH_2 nanoparticles (10 mg mL^{-1}, 100 µL) and liposomes-NH_2 (3 mg mL^{-1}, 333 µL) were mixed with the dendrimers (10 mg mL^{-1}, 100 µL) and incubated at room temperature for 1 h. To remove unbound dendrimers, the liposome dispersion was diluted with 1 mL of PBS and the PS-nanoparticle dispersion with 1 mL of water. Afterwards, the mixture was centrifuged (20 000 g, 15 min, 4°C). Finally, polystyrene nanoparticles were resuspended in 100 µL of water and liposomes were resuspended in 100 µL of PBS.

Zeta Potential. Measurements were performed using a Nano Z Zetasizer (Malvern Instruments GmbH, Herrenberg, Germany). Uncoated and coated liposomes/PS-

nanoparticles (20 µL) were diluted with 1 mL of a 1 mM KCl solution and measured instantly at 25 °C. Each measurement was repeated in technical triplicate.

Human serum/plasma. Human blood serum and plasma was obtained from healthy donors from the Transfusion Center of the University Clinic of Mainz, Germany. For plasma preparation, citrate was used as an anticoagulant. Six serum batches and ten plasma batches were pooled together and stored at −20 °C. All experiments were performed in compliance with the relevant laws and institutional guidelines. The institutional ethics committee had approved the study (Landesärztekammer Rheinland-Pfalz, 837.439.12 (8540-F)). Written informed consent was obtained for any experimentation with human subjects.

Protein corona analysis. Uncoated and coated liposomes or polystyrene nanoparticles (10 mg mL^{-1}, 100 µL) were incubated with 1 mL of human serum or human plasma at 37 °C for 1 h. The protein corona coated liposomes and nanoparticles were centrifuged (20 000 g, 15 min, 4 °C) and washed with 1 mL PBS solution to remove unbound and loosely bound proteins. Overall, this step was repeated three times. The adsorbed corona proteins were detached from the surface by resuspending the liposome/nanoparticle pellet in 100 µL of an aqueous solution containing 2% SDS supplemented with 62.5 mM Tris-HCL (Sigma Aldrich, Germany). Afterwards, the dispersion was incubated for 5 min at 95 °C and centrifuged as described above. The supernatant contained the detached corona proteins.

Protein Assay. The protein concentration was determined by Pierce 660 nm Protein Assay (Thermo Fisher, Germany) according to manufacturer's instructions.

In solution digestion. Prior to LC-MS analysis, proteins were digested according to former protocols.[7, 8] Briefly, SDS was removed via Pierce detergent removal columns (Thermo Fisher, Germany) according to the manufacture's instruction. Afterwards, proteins were precipitated using ProteoExtract protein precipitation kit (Merck Millipore, Germany) overnight and the protein pellet was isolated via centrifugation (14 000 g, 10 min). Precipitated proteins were resuspended in RapiGest SF (Waters, USA) dissolved in 50 mM ammonium bicarbonate (Sigma Aldrich, Germany) and incubated at 80 °C for 15 min. Further, proteins were reduced with dithithreitol at 56 °C for 45 min (5 mM, Sigma Aldrich, Germany) and alkylated with idoacetoamide at room temperature in the dark for 1 h (15 mM, Sigma Aldrich, Germany). Digestion was carried out using a protein:trypsin ratio of 50:1 for 14–18 h at 37 °C and stopped by adding 2 µL hydrochloric acid (Sigma Aldrich, Germany). To remove degradation products of RapiGest SF, the peptide sample was centrifuged (14 000 g, 15 min, 4 °C).

Liquid chromatography-high resolution mass spectrometry (LC-MS). The peptide samples were spiked with 50 fmol of Hi3 EColi Standard (Waters, USA) for absolute protein quantification. Peptides were separated using a nanoACQUITY UPLC system equipped with a C18 nanoACQUITY Trap Column (5 µm, 180 µm x 20 mm, Waters, USA) and C18 analytic reversed phase column (1.7 µm, 75 µm x 150 mm, Waters, USA). The UPLC system was coupled to a Synapt G2-Si mass spectrometer (Waters, USA) and electrospray ionization (ESI) was carried in positive ion with a nanoLockSpray source. The high-resolution mass spectrometer was operated in resolution mode performing data-independent experiments (MS^E). Data was processed with MassLynx 4.1 and all proteins were identified with Progenesis QI. A reviewed human data base downloaded from Uniprot and the peptide sequence of Hi3 Ecoli standard (Chaperone protein CLpB, Water, USA) was added for absolute protein quantification. Based on the TOP3/Hi3 approach[9] all proteins were quantified and the absolute amount in fmol is calculated.

Statistical Analysis. GraphPad Prism 8.4.2 Software was used for statistical analysis applying a one-way ANOVA followed by Tukey's post-hoc multiple comparisons test for all protein corona results in the main text and Figure S11 in order to compare the difference between both uncoated liposome/ PS nanoparticle and lipo-dendrimers/PS-dendrimers as well as between the different dendrimer-coatings. For zeta-potential and Pierce Assay and concentration dependency measurements a one-way ANOVA followed by Dunnett's post-hoc multiple comparisons test was used to compare the coatings with the uncoated liposomes/PS nanoparticles. Significance was considered at *p*-values such as not significant (ns) for $p > 0.05$, and significant * for $p \leq 0.05$, ** for $p \leq 0.01$, *** for $p \leq 0.001$, **** for $p \leq 0.0001$).

2.2 Supplementary figures: Coating of liposomes and polystyrene nanoparticles and their respective protein corona

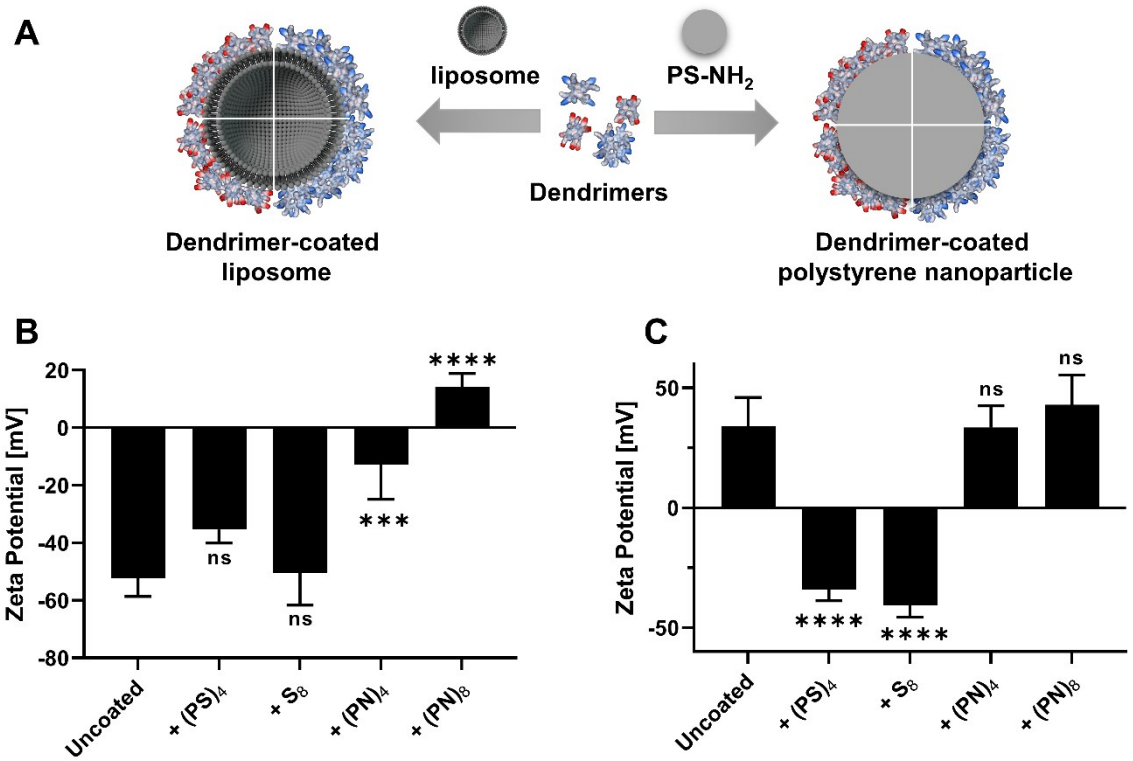

Figure S6. Verification of dendrimer-coating on liposomes and polystyrene nanoparticles (PS-NH_2). (**A**) Dendrimers were mixed with liposomes and ζ-potentials of (**B**) lipo-dendrimers and (**C**) PS-dendrimers were measured. $(PN)_4$ and S_8 did not show a clear change in ζ-potential values when mixed with liposomes indicating an insufficient coating. The same was observed for $(PN)_4$ and $(PN)_8$ when mixed with PS nanoparticles (n = minimum 2; one-way ANOVA, Dunnett's post-hoc multi-comparisons test; ns for $p > 0.05$, *** for $p \leq 0.001$, **** for $p \leq 0.0001$).

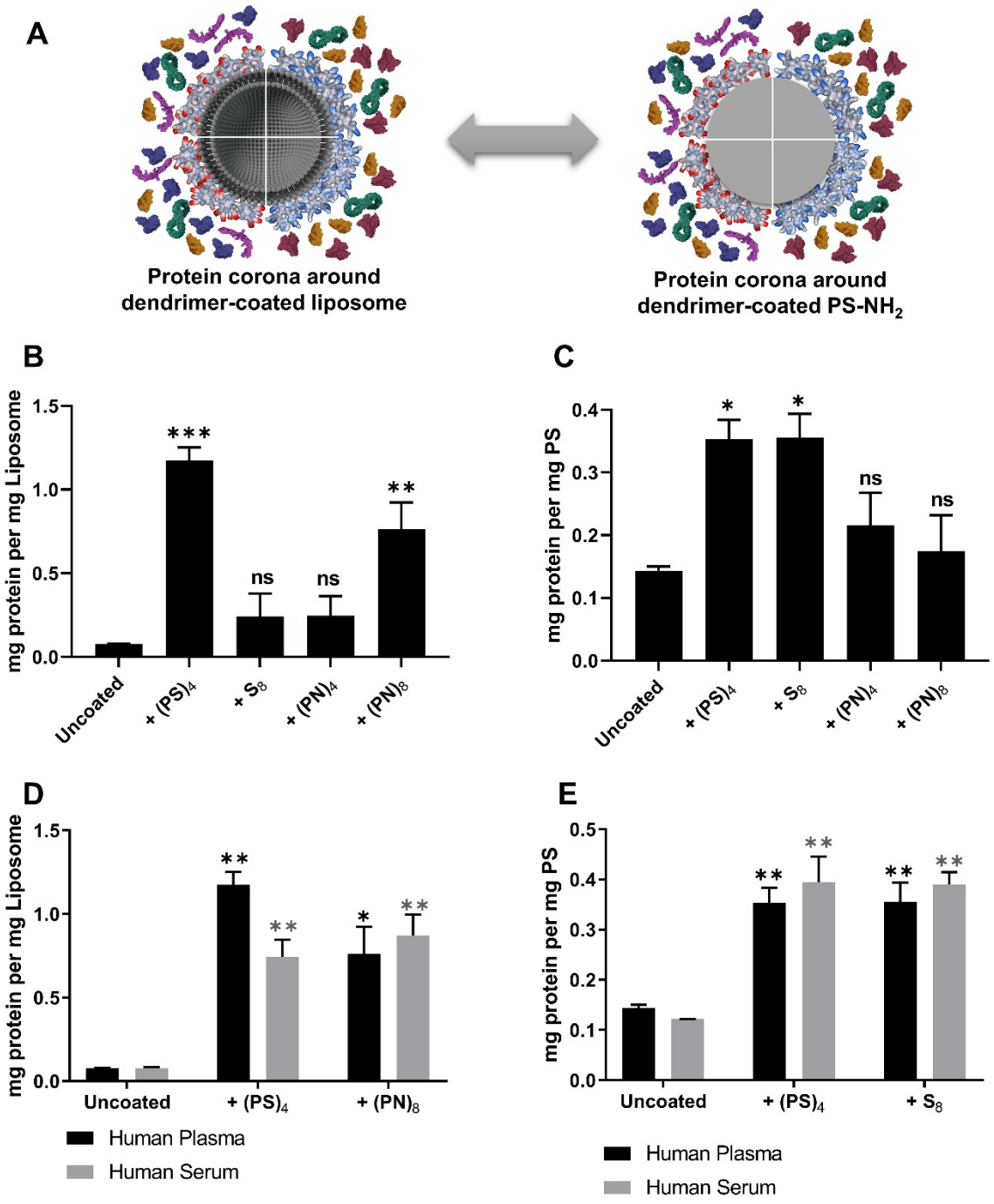

Figure S7. Verification of protein adsorption on lipo-dendrimers and PS-dendrimers: (**A**) Comparison of protein adsorption on lipo-dendrimers and PS-dendrimers. Quantification of protein adsorption by Pierce Assay for (**B**) lipo-dendrimers and (**C**) PS-dendrimers in blood plasma. Liposomes and PS nanoparticles with insufficient dendrimer binding did not show significant differences in protein quantities. Protein quantification by Pierce Assay for efficient dendrimer-coatings in human plasma and serum for (**D**) lipo-$(PS)_4$ and lipo-$(PN)_8$ as well as (**E**) PS-$(PS)_4$ and PS-S_8 (n = minimum 2; one-way ANOVA, Dunnett's post-hoc multi-comparisons test; ns for $p > 0.05$, * for $p \leq 0.05$, ** for $p \leq 0.01$, *** for $p \leq 0.001$).

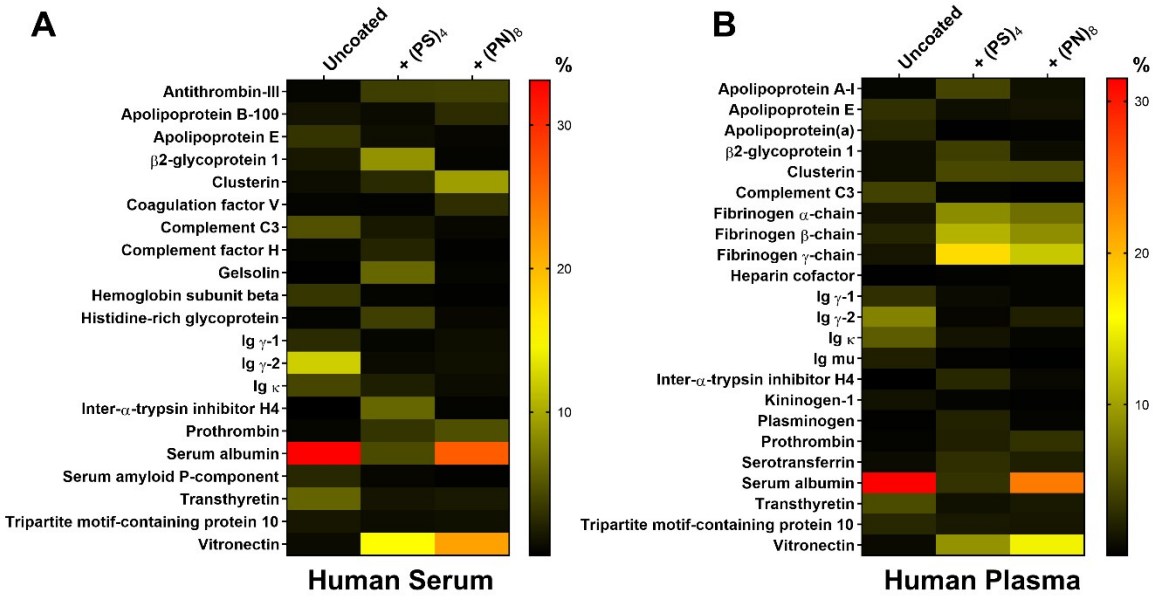

Figure S8. Heatmaps of adsorbed proteins to dendrimer-coated liposomes lipo-$(PS)_4$ and lipo-$(PN)_8$ in (**A**) blood serum and (**B**) blood plasma. A list of all identified proteins is provided in Table S1.

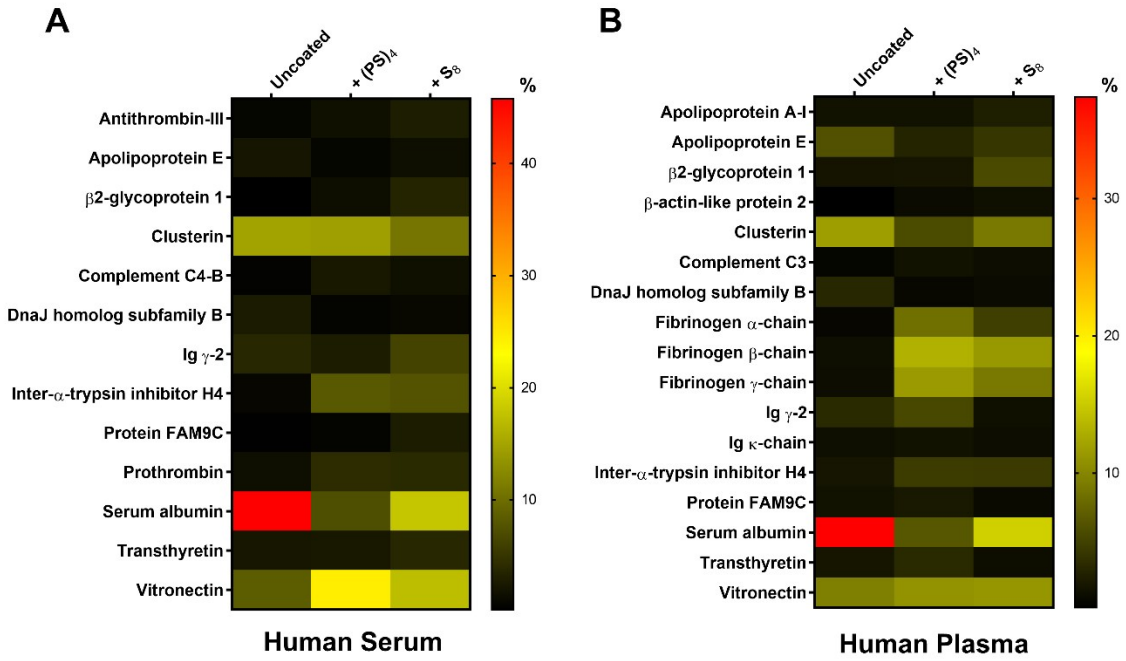

Figure S9. Heatmaps of adsorbed proteins to dendrimer-coated polystyrene nanoparticles PS-$(PS)_4$ and PS-S_8 in (**A**) blood serum and (**B**) blood plasma. A list of all identified proteins is provided in Table S2.

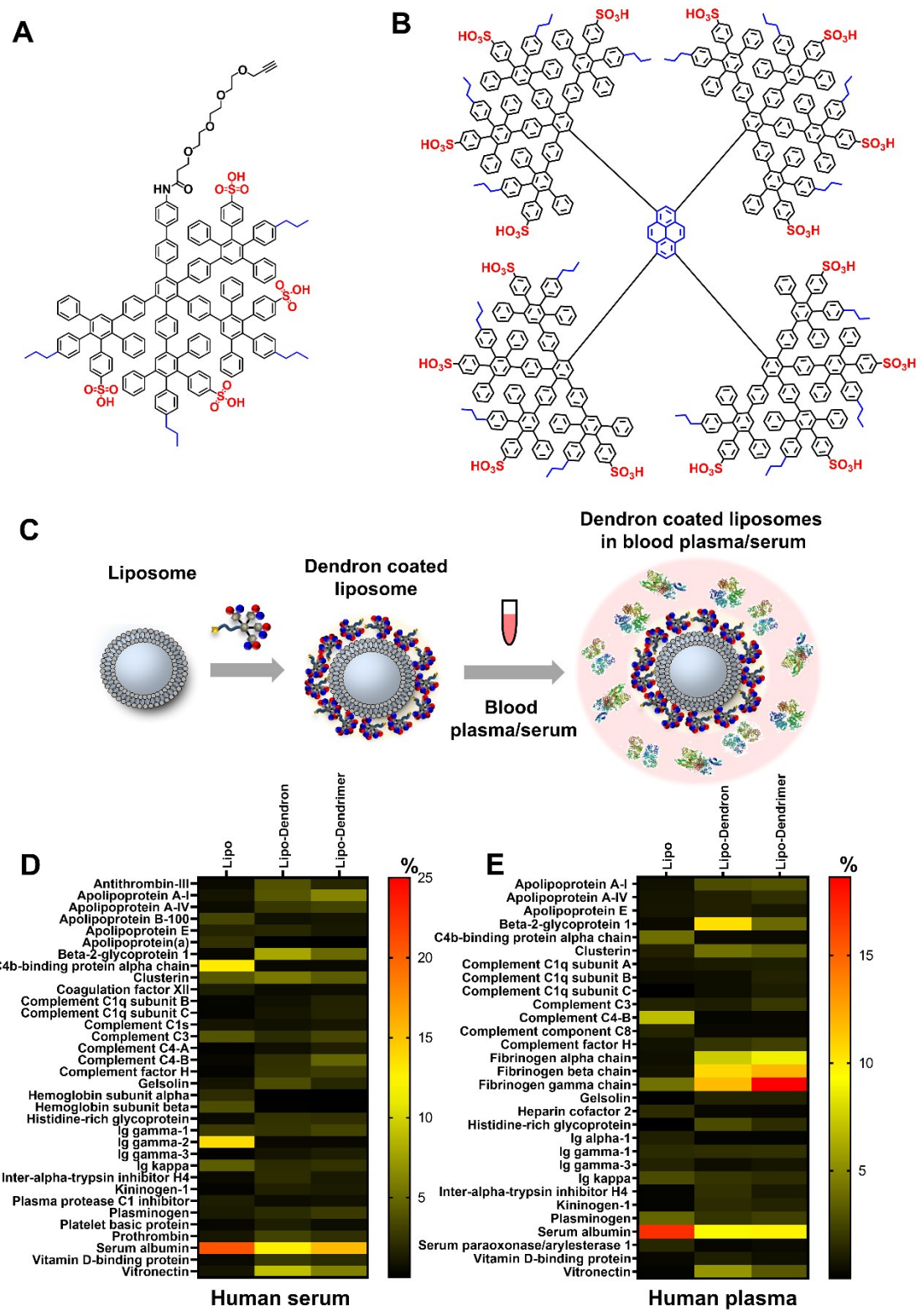

Figure S10. Protein corona on dendron- and dendrimer-coated liposomes. (**A**) Amphiphilic polyphenylene dendron[3] and (**B**) amphiphilic polyphenylene dendrimer[1] with high density of surface pattern. (**C**) Coating of liposomes and addition of human serum and plasma. Heat map of adsorbed proteins on lipo-dendron and lipo-dendrimer in (**D**) human serum and (**E**) human plasma. (**C**-**E**). Reproduced from Wagner *et al.*[3] (https://doi.org/10.1002/anie.201913708). Licensed under a Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).

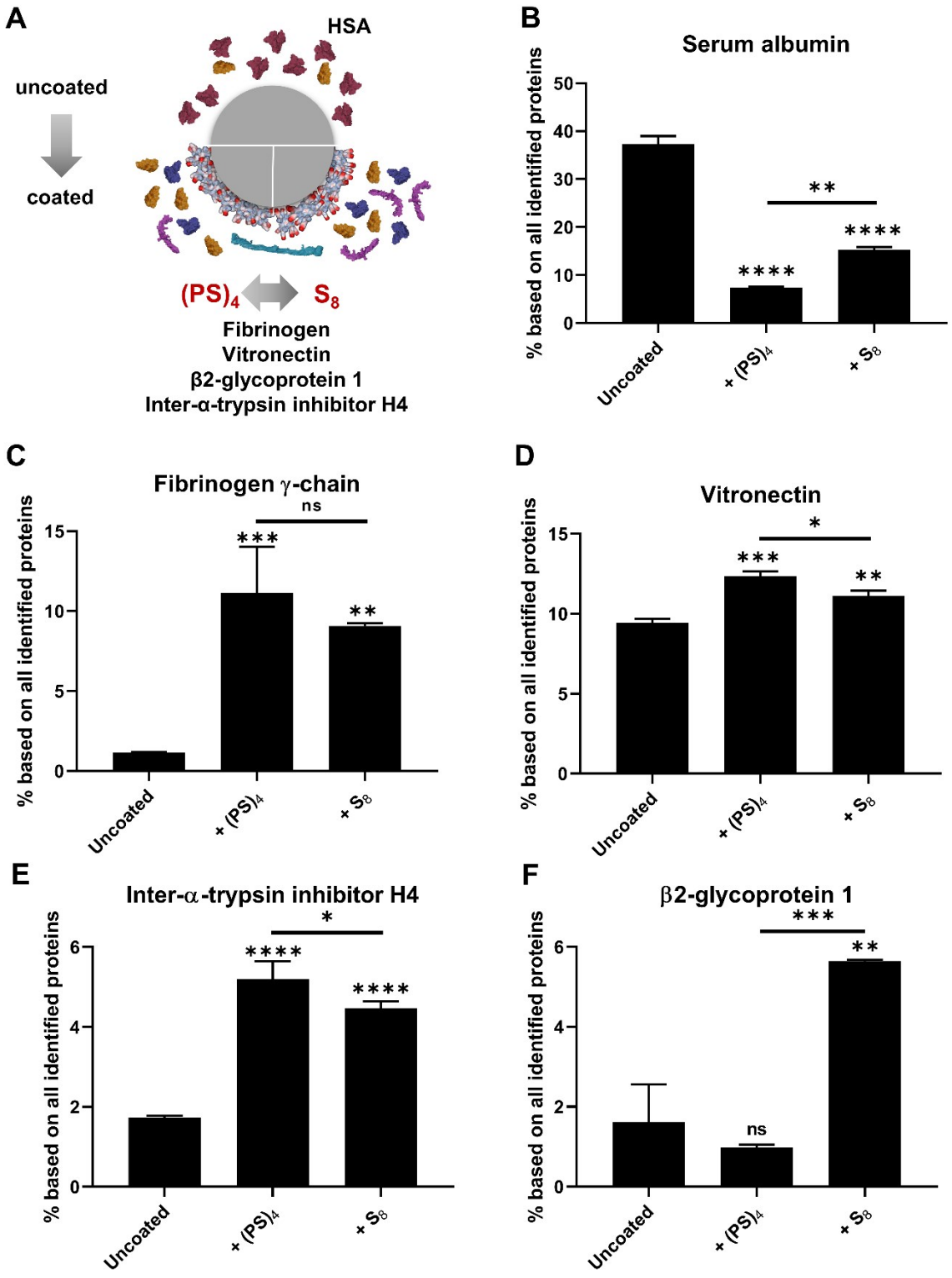

Figure S11. Comparison of adsorbed proteins between uncoated polystyrene nanoparticles (PS-NH_2) and PS-dendrimers (PS-$(PS)_4$ and PS-S_8). (**A**) Coating of PS-NH_2 lead to a different protein corona: Reduction of (**B**) serum albumin adsorption and enhancement of (**C**) fibrinogen, (**D**) vitronectin, (**E**) inter-α-trypsin inhibitor H4 and (**F**) β-2 glycoprotein 1 (n = minimum 2; one-way ANOVA, Tuckey's post-hoc multi-comparisons test; ns for $p > 0.05$, * for $p \leq 0.05$, ** for $p \leq 0.01$, *** for $p \leq 0.001$, **** for $p \leq 0.0001$).

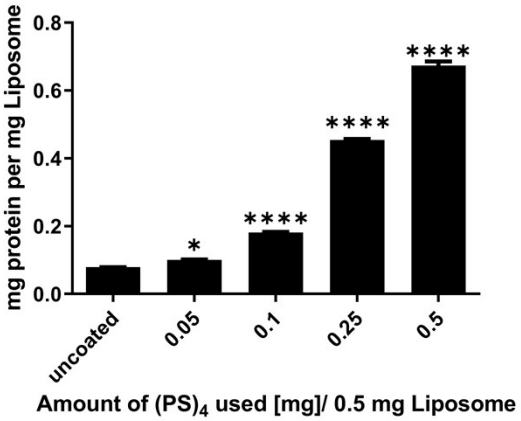

Figure S12. Quantification of protein adsorption in human plasma by Pierce Assay for different $(PS)_4$ concentrations used for the coating to liposomes. The amount of proteins adsorbed increases with higher dendrimer concentrations. (n = 2; one-way ANOVA, Dunnett's post-hoc multi-comparisons test; * for $p \leq 0.05$, **** for $p \leq 0.0001$).

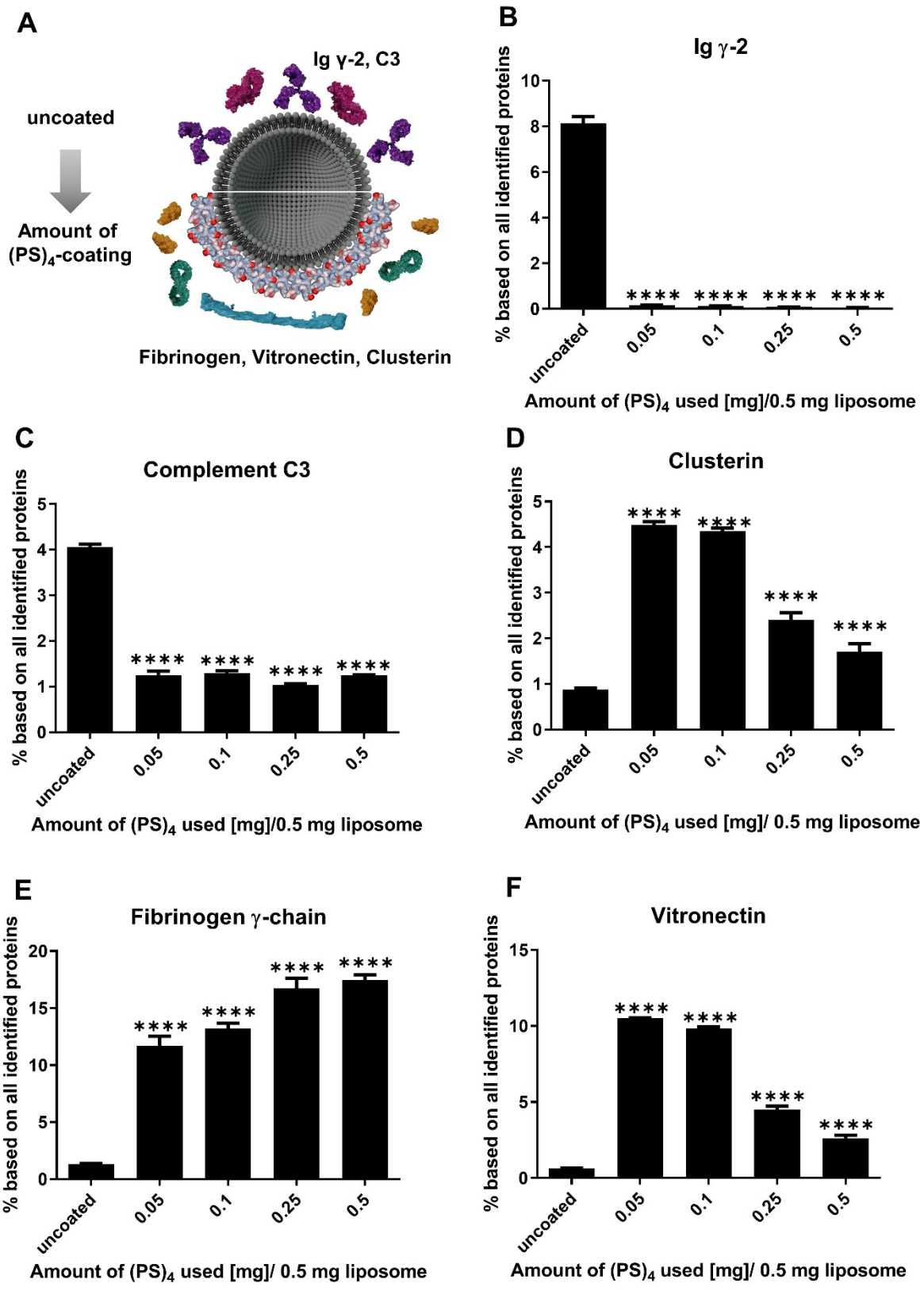

Figure S13. Concentration dependency of dendrimer-coatings on protein adsorption in human plasma. (**A**) Comparison between uncoated liposomes and lipo-$(PS)_4$ at different dendrimer concentrations used for the liposome coating. The adsorption of the opsonins (**B**) Ig γ-2 and (**C**) complement C3 is significantly reduced even at low dendrimer concentrations, whereas the adsorption of (**D**) Clusterin, (**E**) Fibrinogen and (**F**) Vitronectin is significantly enhanced (n = 3; one-way ANOVA, Dunnett's post-hoc multi-comparisons test; * for $p \leq 0.05$, **** for $p \leq 0.0001$). A list of all identified proteins is provided in Table S3.

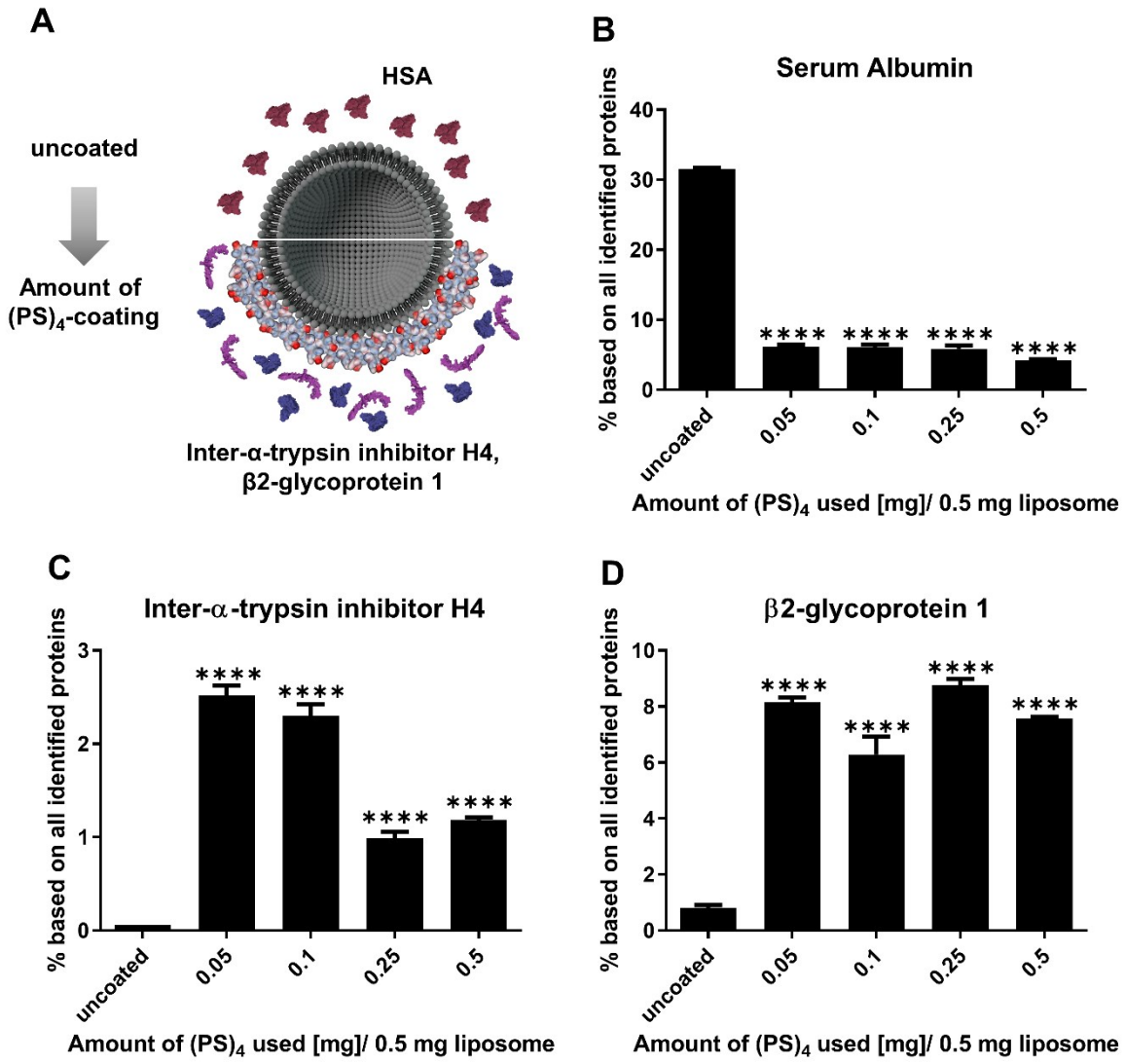

Figure S14. Concentration dependency of dendrimer-coatings specific for $(PS)_4$ on protein adsorption in human plasma. (**A**) Comparison between uncoated liposomes and lipo-$(PS)_4$ at different dendrimer concentrations used for the liposome coating. The adsorption of (**B**) serum albumin is significantly reduced even at low dendrimer concentrations, whereas the adsorption of (**C**) Inter-α-trypsin inhibitor H4 and (**D**) β2-glycoprotein 1 is significantly enhanced (n = 3; one-way ANOVA, Dunnett's post-hoc multi-comparisons test; * for $p \leq 0.05$, **** for $p \leq 0.0001$). A list of all identified proteins is provided in Table S3.

Table S1. List of all identified corona proteins on lipo-dendrimers lipo-$(PS)_4$ and lipo-$(PN)_8$ in human serum and plasma.

				Average in %						Standard deviation					
				Plasma			Serum			Plasma			Serum		
Accession	Peptide count	Unique peptides	Description	Uncoated	(PS)4	(PN)8	Uncoated	(PS)4	(PN)8	Uncoated	(PS)4	(PN)8	Uncoated	(PS)4	(PN)8
63267;P68032	6	3	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	0.42	0.01	0.01	0.13	0.07	0.24	0.00	0.01	0.00	0.01	0.05	0.20
63261;Q562R	9	3	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	0.58	0.08	0.12	1.85	0.48	0.32	0.01	0.03	0.00	0.06	0.36	0.11
P02763	3	3	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	0.28	0.01	0.00	0.35	0.10	0.03	0.01	0.00	0.00	0.01	0.14	0.02
P01011	2	2	Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	0.04	0.00	0.01	0.03	0.07	0.01	0.00	0.01	0.00	0.01	0.08	0.01
P01009	14	12	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	0.67	0.11	0.16	0.54	0.24	0.27	0.04	0.01	0.00	0.01	0.17	0.16
P04217	4	4	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	0.01	0.20	0.05	0.02	0.06	0.37	0.01	0.02	0.01	0.00	0.04	0.51
P08697	10	10	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	0.09	0.26	0.14	0.54	0.25	0.37	0.01	0.00	0.01	0.01	0.24	0.34
P02765	11	11	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	0.04	0.46	0.04	0.02	0.90	0.09	0.00	0.04	0.01	0.00	0.70	0.05
P01023	11	9	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	0.21	0.02	0.01	0.11	0.04	0.05	0.00	0.00	0.00	0.01	0.04	0.03
P01019	8	7	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	0.00	0.02	0.00	0.15	0.21	0.05	0.00	0.00	0.00	0.01	0.22	0.04
P16157	4	2	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	0.22	0.00	0.01	0.10	0.01	0.02	0.01	0.00	0.00	0.01	0.00	0.01
P01008	38	37	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	0.80	0.90	0.82	0.38	5.23	4.84	0.03	0.07	0.04	0.01	5.66	5.16
P02647	32	32	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	0.42	4.65	1.02	0.21	1.16	2.05	0.02	0.12	0.02	0.00	0.94	1.75
P02652	8	8	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	0.04	0.17	0.13	0.03	0.21	0.19	0.01	0.07	0.00	0.00	0.17	0.23
P06727	41	41	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	0.15	0.63	0.91	0.12	1.07	0.86	0.03	0.15	0.07	0.01	0.38	0.72
P04114	155	131	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	1.43	0.14	0.25	1.12	0.73	6.38	0.02	0.01	0.02	0.03	0.33	10.38
P02656	2	2	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	0.08	0.26	0.15	0.05	1.50	1.14	0.01	0.01	0.00	0.01	1.93	1.53
P05090	8	7	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	0.49	0.13	0.16	0.05	0.16	0.43	0.53	0.02	0.00	0.00	0.03	0.17
P02649	28	27	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	2.96	0.84	1.08	3.01	0.88	0.41	0.05	0.06	0.04	0.02	0.32	0.06
P08519	12	10	Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1	2.40	0.11	0.21	0.80	0.49	0.08	0.04	0.00	0.01	0.00	0.44	0.07
P02730	14	11	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	1.63	0.02	0.02	1.11	0.06	0.20	0.15	0.01	0.00	0.16	0.04	0.32
P02749	21	20	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	0.81	4.30	0.88	1.48	6.86	0.40	0.09	0.13	0.26	0.01	5.69	0.57
P04003	19	17	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	0.58	0.07	0.12	1.09	0.35	0.93	0.03	0.01	0.00	0.04	0.42	0.83
Q96IY4	3	3	Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2	0.03	0.02	0.00	0.02	0.11	0.10	0.01	0.01	0.00	0.01	0.06	0.09
P15169	3	3	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	0.10	0.02	0.00	0.07	0.09	0.02	0.00	0.00	0.00	0.00	0.13	0.03
Q5VT06	5	5	Centrosome-associated protein 350 OS=Homo sapiens GN=CEP350 PE=1 SV=1	0.00	0.01	0.00	0.00	0.30	0.00	0.00	0.00	0.00	0.00	0.51	0.00
P10909	29	29	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	0.88	4.64	4.27	0.72	2.14	4.28	0.03	0.13	0.19	0.03	1.67	6.58
P00740	20	20	Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2	0.07	0.92	0.68	0.01	0.31	1.80	0.00	0.02	0.01	0.00	0.28	2.92
P12259	42	34	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	0.16	0.19	0.06	0.23	0.21	7.11	0.01	0.02	0.01	0.00	0.14	11.55
P08709	6	5	Coagulation factor VII OS=Homo sapiens GN=F7 PE=1 SV=1	0.05	0.44	0.26	0.00	0.14	0.01	0.01	0.03	0.03	0.00	0.19	0.01
P00742	5	4	Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2	0.01	0.01	0.06	0.00	0.04	0.05	0.00	0.00	0.01	0.00	0.02	0.03
P03951	17	16	Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1	0.03	0.26	0.21	0.02	0.34	0.19	0.01	0.04	0.02	0.00	0.14	0.06
P00748	12	11	Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3	0.02	0.03	0.02	0.02	0.71	0.20	0.00	0.00	0.00	0.01	0.59	0.14
P00736	12	12	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	0.03	0.09	0.04	0.01	0.58	3.09	0.00	0.07	0.01	0.00	0.42	4.64
P09871	5	4	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	0.00	0.09	0.07	0.00	0.13	3.29	0.00	0.02	0.01	0.00	0.10	5.55
P06681	7	6	Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2	0.00	0.03	0.01	0.00	0.38	0.01	0.00	0.02	0.00	0.00	0.47	0.01
P01024	106	100	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	4.05	0.32	0.07	4.82	1.37	0.31	0.07	0.03	0.00	0.02	0.87	0.22
P0C0L4	65	3	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	1.25	0.06	0.12	0.88	0.22	0.23	0.08	0.00	0.01	0.05	0.17	0.21
P0C0L5	66	3	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	1.07	0.05	0.11	0.75	0.19	0.20	0.06	0.00	0.01	0.03	0.15	0.18
P13671	17	13	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	0.06	0.01	0.00	0.01	0.18	0.02	0.00	0.01	0.00	0.00	0.17	0.03
P10643	10	9	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	0.28	0.16	0.03	0.05	0.25	0.52	0.01	0.03	0.00	0.01	0.08	0.51
P07358	11	11	Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3	0.03	0.13	0.05	0.03	0.16	0.06	0.00	0.01	0.00	0.00	0.18	0.06
P02748	14	11	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	0.81	0.05	0.02	0.76	0.27	0.41	0.01	0.00	0.00	0.00	0.15	0.27
P00751	22	19	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	0.04	0.07	0.02	0.05	1.18	0.16	0.00	0.01	0.00	0.01	1.15	0.12
P00746	5	5	Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5	0.01	0.02	0.01	0.00	0.22	0.01	0.01	0.00	0.00	0.00	0.20	0.01
08603;Q02985	65	59	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	0.22	0.10	0.05	0.33	3.42	0.21	0.01	0.01	0.01	0.01	3.77	0.17
Q03591	15	3	Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	0.12	0.59	0.06	0.10	1.91	0.33	0.01	0.02	0.00	0.01	1.96	0.30
P36980	8	2	Complement factor H-related protein 2 OS=Homo sapiens GN=CFHR2 PE=1 SV=1	0.01	0.04	0.00	0.00	0.14	0.03	0.00	0.00	0.00	0.00	0.16	0.04
Q9BXR6	16	12	Complement factor H-related protein 5 OS=Homo sapiens GN=CFHR5 PE=1 SV=1	0.26	0.35	0.33	0.30	0.14	1.10	0.01	0.01	0.01	0.01	0.12	1.65
P02671	47	46	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	1.19	9.63	5.90	0.47	0.64	0.69	0.04	0.10	0.38	0.01	0.05	0.41
P02675	53	50	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	2.23	12.22	7.74	0.72	1.48	0.73	0.01	0.45	0.01	0.02	1.57	0.51
P02679	40	38	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	1.32	19.69	12.06	0.14	0.59	0.49	0.06	0.53	0.10	0.00	0.08	0.20
P02751	30	24	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	0.15	0.11	0.06	0.04	0.23	0.63	0.01	0.00	0.00	0.01	0.07	0.99
P06396	44	42	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	0.13	0.91	0.20	0.06	5.21	0.40	0.00	0.08	0.00	0.02	4.47	0.13
P14136	6	3	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	0.19	0.01	0.04	0.11	0.20	0.36	0.04	0.01	0.00	0.04	0.24	0.33
P22352	2	2	Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	0.00	0.01	0.00	0.00	0.20	0.03	0.00	0.01	0.00	0.00	0.33	0.06
P00738	13	8	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	0.46	0.09	0.24	0.39	0.07	0.64	0.10	0.02	0.01	0.10	0.04	0.92
P00739	7	4	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	0.04	0.02	0.06	0.03	0.05	0.02	0.00	0.00	0.00	0.00	0.04	0.02
P69905	2	2	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	0.15	0.06	0.03	1.53	0.24	0.07	0.01	0.02	0.00	0.09	0.15	0.05
42;P02100;P68	4	4	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	0.39	0.03	0.00	3.10	0.32	0.13	0.00	0.00	0.00	0.04	0.22	0.05
P02790	15	12	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	0.54	0.35	0.30	0.44	1.42	0.69	0.00	0.04	0.05	0.04	1.30	0.33
P05546	18	16	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	0.10	0.14	0.27	0.08	0.55	0.93	0.00	0.01	0.01	0.00	0.55	0.87
Q04756	6	6	Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1	0.00	0.04	0.00	0.00	0.41	0.02	0.00	0.00	0.00	0.00	0.49	0.03
P04196	24	22	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	0.24	1.45	0.13	0.22	3.14	1.16	0.02	0.57	0.02	0.02	2.60	1.06
Q14520	17	17	Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1	0.21	0.39	1.27	0.07	0.93	0.81	0.00	0.04	0.11	0.01	0.75	0.34
01876;P01877	10	9	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	0.63	0.13	0.08	0.40	0.26	0.12	0.02	0.02	0.00	0.00	0.14	0.01
P01857	13	7	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	2.92	0.78	0.27	2.50	0.29	1.00	0.01	0.04	0.02	0.09	0.20	0.57
P01859	7	4	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	8.13	0.47	1.79	12.17	0.46	0.69	0.31	0.02	0.13	0.21	0.42	0.36
P01860	12	5	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	0.30	0.18	0.01	0.10	0.22	0.09	0.04	0.07	0.00	0.01	0.05	0.06
P01861	5	2	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	0.06	0.05	0.03	0.04	0.08	0.03	0.00	0.00	0.00	0.01	0.06	0.03
P01834	7	6	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	5.75	1.08	0.32	4.10	1.54	1.32	0.28	0.01	0.02	0.35	1.18	1.53
9AD64;P0CF74	5	5	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	0.97	0.32	0.06	0.43	0.78	0.28	0.12	0.09	0.01	0.08	0.68	0.20
01871;P04220	15	12	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	2.04	0.16	0.09	1.23	0.28	0.43	0.06	0.02	0.01	0.04	0.21	0.43
A0A075B6Q5	2	2	Immunoglobulin heavy variable 3-64 OS=Homo sapiens GN=IGHV3-64 PE=3 SV=1	0.43	0.04	0.06	0.52	0.19	0.30	0.04	0.02	0.00	0.01	0.25	0.30
P17936	6	6	Insulin-like growth factor-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=1 SV=2	0.02	0.00	0.00	0.00	0.28	0.01	0.00	0.00	0.00	0.00	0.30	0.01
P35858	2	2	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	0.03	0.42	0.39	0.00	0.23	0.22	0.02	0.42	0.01	0.00	0.33	0.11
P19827	7	6	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	0.00	0.04	0.01	0.00	0.04	0.01	0.00	0.00	0.00	0.00	0.05	0.01
P19823	21	19	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	0.14	0.43	0.33	0.12	0.40	0.23	0.01	0.02	0.01	0.01	0.34	0.26
Q14624	50	50	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	0.06	2.53	0.55	0.01	5.40	0.47	0.00	0.20	0.01	0.01	5.48	0.56
P01042	29	27	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	1.12	0.10	0.12	0.79	2.21	1.02	0.01	0.02	0.00	0.03	1.98	1.49
P18428	10	9	Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3	0.16	0.17	0.00	0.10	0.73	0.23	0.00	0.04	0.00	0.02	0.74	0.35
O75145	5	3	Liprin-alpha-3 OS=Homo sapiens GN=PPFIA3 PE=1 SV=3	1.25	0.11	0.32	0.66	0.33	0.38	0.06	0.00	0.02	0.04	0.14	0.41
P51884	17	15	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	0.08	0.09	0.36	0.21	0.12	0.56	0.01	0.00	0.05	0.01	0.06	0.22
P36955	14	13	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	0.05	0.02	0.01	0.02	1.26	0.14	0.00	0.01	0.00	0.00	1.32	0.12
P03952	19	17	Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1	0.00	0.03	0.01	0.00	1.35	0.30	0.00	0.01	0.00	0.00	1.13	0.44
P05155	14	11	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	0.04	0.12	0.06	0.04	0.26	0.16	0.01	0.01	0.00	0.00	0.18	0.12
P05154	14	12	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	0.19	0.09	0.13	0.04	0.43	0.27	0.00	0.01	0.02	0.00	0.39	0.28
47;Q02325;Q1	53	51	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	0.14	2.01	0.31	0.07	0.92	1.02	0.00	0.19	0.00	0.01	0.54	1.02
P02775	5	5	Platelet basic protein OS=Homo sapiens GN=PPBP PE=1 SV=3	0.04	0.15	0.07	0.03	1.35	0.42	0.00	0.01	0.00	0.00	0.69	0.33
02776;P10720	5	5	Platelet factor 4 OS=Homo sapiens GN=PF4 PE=1 SV=2	0.09	0.06	0.00	0.06	2.19	0.42	0.01	0.05	0.00	0.00	3.10	0.61
Q15113	9	6	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2	0.00	0.48	0.77	0.00	0.39	0.41	0.00	0.01	0.07	0.00	0.41	0.29
P27918	9	9	Properdin OS=Homo sapiens GN=CFP PE=1 SV=2	0.91	0.08	0.05	1.13	0.81	0.13	0.04	0.00	0.01	0.05	1.24	0.12
P02760	7	6	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	0.03	0.04	0.03	0.01	0.09	0.05	0.01	0.03	0.00	0.01	0.09	0.03
Q9UK55	2	2	Protein Z-dependent protease inhibitor OS=Homo sapiens GN=SERPINA10 PE=1 SV=1	0.00	0.03	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.03	0.00
Q92954	14	11	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2	0.06	0.05	0.01	0.02	0.29	0.03	0.01	0.01	0.00	0.00	0.33	0.03
P00734	46	43	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	0.31	2.26	3.56	0.32	2.05	2.25	0.03	0.10	0.24	0.00	2.80	3.15
P49908	5	4	Selenoprotein P OS=Homo sapiens GN=SELENOP PE=1 SV=3	0.01	0.03	0.02	0.00	0.97	0.07	0.02	0.01	0.00	0.00	0.64	0.06
P02787	22	19	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	0.71	3.04	1.61	0.52	1.22	1.85	0.03	0.35	0.08	0.01	0.65	2.68
P02768	67	66	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	31.51	3.50	25.53	33.12	3.15	13.66	0.16	0.13	2.27	0.81	3.56	17.17
P02743	8	7	Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	0.21	0.05	0.04	2.24	0.72	0.17	0.34	0.02	0.01	0.24	1.13	0.19
P27169	9	9	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	1.02	0.19	0.41	0.19	0.39	0.61	0.01	0.04	0.05	0.01	0.50	0.47
P11277	6	5	Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5	0.99	0.10	0.33	0.67	0.04	0.11	0.04	0.06	0.09	0.04	0.03	0.08
Q9H2K2	2	2	Tankyrase-2 OS=Homo sapiens GN=TNKS2 PE=1 SV=1	0.10	0.03	0.00	0.10	0.06	0.01	0.00	0.02	0.00	0.01	0.09	0.01
P05452	5	3	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	0.02	0.04	0.02	0.00	0.12	0.68	0.00	0.00	0.00	0.00	0.09	1.08
P07996	9	3	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	0.01	0.00	0.00	0.00	0.13	0.01	0.00	0.00	0.00	0.00	0.05	0.01
P02766	10	10	Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	4.70	0.64	1.39	5.93	1.25	2.39	0.17	0.02	0.09	0.11	0.70	2.26
Q9UDY6	2	2	Tripartite motif-containing protein 10 OS=Homo sapiens GN=TRIM10 PE=1 SV=3	2.40	1.34	1.27	1.34	0.82	2.37	0.59	0.20	0.04	0.05	0.77	1.96
P02774	36	36	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	0.35	0.52	0.14	0.28	1.11	1.05	0.03	0.02	0.01	0.00	0.76	0.95
P04070	9	8	Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1	0.03	0.09	0.24	0.01	2.19	0.26	0.00	0.05	0.03	0.00	3.61	0.30
P07225	13	12	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	0.04	0.45	0.32	0.03	0.30	0.08	0.00	0.04	0.01	0.01	0.15	0.04
P22891	8	8	Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2	0.00	0.01	0.09	0.00	0.04	0.03	0.00	0.00	0.00	0.01	0.00	0.05	0.01
04004;Q99542	29	28	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	0.64	10.20	17.61	0.64	10.26	12.36	0.02	0.08	1.23	0.00	14.31	12.27

Table S2. List of all identified corona proteins on PS nanoparticles coated with $(PS)_4$ and S_8.

				Average in %						Standard deviation					
				Plasma			Serum			Plasma			Serum		
Accession	Peptide coun	nique peptide	Description	Uncoated	(PS)4	S8	Uncoated	(PS)4	S8	Uncoated	(PS)4	S8	Uncoated	(PS)4	S8
6;P68032;P63267;P	9	4	Actin_ aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	0.91	0.11	0.36	0.24	0.14	0.26	0.16	0.01	0.03	0.06	0.01	0.00
i0709;P63261;Q658	13	5	Actin_ cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	0.95	1.47	0.57	0.33	0.80	1.08	0.02	0.08	0.01	0.02	0.06	0.74
P02763;P19652	4	4	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	0.02	0.05	0.01	0.02	0.03	0.03	0.00	0.01	0.00	0.00	0.00	0.00
;Q5TYW2;Q5VUR7;	3	3	Ankyrin repeat domain-containing protein 20A2 OS=Homo sapiens GN=ANKRD20A2 PE=4 SV=1	0.08	0.08	0.05	0.06	0.08	0.09	0.00	0.01	0.00	0.00	0.01	0.07
P01008	32	31	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	0.02	0.05	0.02	0.70	1.58	2.72	0.00	0.02	0.00	0.07	0.03	1.54
P02647	25	25	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	1.49	1.47	2.33	0.44	1.84	0.41	0.03	0.16	0.01	0.02	0.02	0.36
P02652	2	2	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	0.16	0.02	0.09	0.04	0.03	0.03	0.03	0.00	0.03	0.04	0.00	0.01
P06727	28	25	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	1.39	0.69	0.67	0.93	1.43	0.57	0.04	0.12	0.03	0.16	0.07	0.46
P04114	40	34	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	0.12	0.12	0.09	0.08	0.10	0.18	0.01	0.01	0.00	0.01	0.00	0.10
P02649	26	25	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	6.19	3.34	4.11	2.05	0.71	1.52	0.39	0.28	0.06	0.07	0.01	0.31
Q96P47	3	3	Arf-GAP with GTPase_ ANK repeat and PH domain-containing protein 3 OS=Homo sapiens GN=AGAP3 PE=1 SV=2	0.14	0.29	0.10	0.11	0.13	0.18	0.01	0.06	0.01	0.08	0.01	0.11
O95817	2	2	BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P02730	8	8	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	0.00	0.03	0.04	0.02	0.10	0.05	0.00	0.02	0.00	0.00	0.00	0.00
P02749	15	15	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	1.61	0.98	5.64	0.21	1.41	3.49	0.95	0.07	0.04	0.00	0.03	0.42
Q562R1	8	3	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	0.22	1.04	1.34	0.07	0.06	0.04	0.05	0.01	0.04	0.05	0.02	0.03
Q9Y2P5	3	2	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1	0.03	0.09	0.05	0.03	0.31	0.10	0.01	0.00	0.02	0.01	0.02	0.08
P80723	2	2	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	1.35	0.22	0.60	0.69	0.18	0.40	0.05	0.01	0.02	0.41	0.03	0.27
P04003	18	16	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	0.38	1.20	0.52	0.20	0.19	0.08	0.03	0.10	0.02	0.01	0.03	0.06
Q96IY4	3	3	Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2	0.00	0.00	0.00	0.02	0.11	0.05	0.00	0.00	0.00	0.00	0.01	0.02
P10909	28	25	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	11.74	5.90	9.09	14.63	14.37	10.69	0.23	0.26	0.09	0.84	0.18	2.05
P00740	7	7	Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2	0.19	0.18	0.05	0.09	0.14	0.11	0.01	0.02	0.00	0.00	0.00	0.00
P12259	28	23	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	0.15	0.35	0.33	0.16	0.34	0.35	0.01	0.03	0.01	0.02	0.02	0.18
P03951	10	10	Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1	0.14	0.31	0.16	0.13	0.19	0.17	0.00	0.01	0.00	0.01	0.00	0.12
P02747	4	4	Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	0.05	0.04	0.04	0.07	0.17	0.05	0.00	0.01	0.01	0.01	0.01	0.04
P00736	16	14	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	0.02	0.04	0.06	0.06	0.29	0.11	0.00	0.00	0.00	0.00	0.01	0.01
P09871	14	13	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	0.05	0.14	0.12	0.07	0.17	0.08	0.00	0.02	0.00	0.01	0.01	0.00
P01024	107	100	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	0.63	1.09	1.13	0.76	0.41	0.82	0.03	0.18	0.04	0.06	0.07	0.45
P0C0L4	45	2	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	0.01	0.02	0.01	0.14	0.18	0.11	0.00	0.00	0.00	0.00	0.04	0.04
P0C0L5	46	3	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	0.07	1.03	0.66	0.39	2.26	1.58	0.02	0.06	0.02	0.04	0.25	0.46
P13671	8	6	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	0.08	0.15	0.20	0.08	0.53	0.22	0.02	0.00	0.03	0.02	0.03	0.06
P10643	5	3	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	0.00	0.01	0.02	0.00	0.08	0.03	0.00	0.00	0.00	0.00	0.01	0.02
P02748	11	11	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	0.10	0.07	0.12	0.17	0.38	0.22	0.01	0.00	0.01	0.00	0.02	0.10
P00751	2	2	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	0.00	0.01	0.02	0.01	0.11	0.03	0.00	0.01	0.00	0.00	0.01	0.00
P08603;Q02985	47	42	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	0.06	0.35	0.13	0.10	0.92	0.19	0.01	0.05	0.00	0.01	0.02	0.12
Q03591;P36980	11	6	Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	0.01	0.28	0.73	0.05	0.78	0.58	0.00	0.04	0.07	0.03	0.03	0.03
Q98XR6	13	12	Complement factor H-related protein 5 OS=Homo sapiens GN=CFHR5 PE=1 SV=1	0.13	0.11	0.15	0.06	0.29	0.19	0.01	0.00	0.00	0.00	0.02	0.05
Q16555	3	3	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	0.24	0.11	0.16	0.12	0.24	0.15	0.01	0.00	0.00	0.01	0.01	0.02
Q7Z6W7	2	2	Dnaj homolog subfamily B member 7 OS=Homo sapiens GN=DNAJB7 PE=2 SV=2	3.06	0.55	0.97	2.89	0.55	0.93	0.10	0.02	0.02	2.13	0.04	0.76
Q8TE02	2	2	Elongator complex protein 5 OS=Homo sapiens GN=ELP5 PE=1 SV=2	0.37	0.46	0.20	0.32	0.36	0.49	0.01	0.02	0.01	0.02	0.01	0.42
P02671	43	42	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	0.72	7.17	4.80	0.22	0.16	0.21	0.04	0.77	0.15	0.13	0.03	0.15
P02675	48	48	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	1.25	15.17	11.27	0.08	0.10	0.07	0.09	0.21	0.13	0.00	0.01	0.04
P02679	37	35	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	1.15	11.15	9.06	0.06	0.21	0.07	0.04	2.87	0.18	0.00	0.02	0.02
P47929	2	2	Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P06396	27	27	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	0.23	0.28	0.27	0.21	0.58	0.20	0.08	0.07	0.00	0.13	0.02	0.16
P14136	8	5	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	0.23	0.14	0.12	0.22	0.09	0.23	0.01	0.01	0.00	0.13	0.00	0.01
P22352	4	3	Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	0.01	0.04	0.07	0.02	0.18	0.05	0.00	0.01	0.00	0.00	0.00	0.01
P04406	4	4	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	0.01	0.05	0.02	0.04	0.09	0.05	0.00	0.00	0.00	0.00	0.01	0.04
P00738	6	2	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	0.07	0.09	0.04	0.13	0.08	0.09	0.01	0.00	0.00	0.01	0.02	0.01
P00739	4	2	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	0.05	0.04	0.02	0.05	0.04	0.03	0.00	0.00	0.00	0.00	0.00	0.02
P69905	4	4	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	0.00	0.01	0.01	0.13	0.15	0.06	0.00	0.00	0.00	0.02	0.00	0.04
1;P02100;P69891;P	5	3	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	0.00	0.10	0.01	0.17	0.18	0.08	0.00	0.00	0.00	0.01	0.01	0.05
P02790	7	6	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	0.04	0.16	0.20	0.04	0.14	0.16	0.00	0.04	0.01	0.00	0.02	0.02
Q04756	2	2	Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1	0.00	0.04	0.03	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P04196	11	11	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	0.00	0.16	0.25	0.03	0.67	0.33	0.00	0.01	0.02	0.02	0.04	0.08
P01876	7	3	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	0.17	0.18	0.14	0.17	0.17	0.08	0.01	0.03	0.00	0.02	0.01	0.05
P01857	15	5	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	0.49	0.77	0.48	0.94	1.50	0.84	0.02	0.03	0.01	0.06	0.01	0.67
P01859	11	3	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	3.27	3.84	1.38	3.65	2.68	6.16	0.22	0.07	0.04	0.18	0.22	1.31
P01860	14	4	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	0.02	0.06	0.05	0.06	0.13	0.04	0.00	0.00	0.00	0.00	0.01	0.03
P01834	7	7	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	1.29	1.32	1.14	1.05	1.72	1.20	0.04	0.08	0.06	0.21	0.06	0.05
;P0CF74;P0CG04;P	5	3	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	0.09	0.18	0.25	0.15	0.44	0.32	0.02	0.01	0.02	0.04	0.07	0.02
P01871	16	7	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	0.37	0.29	0.22	0.49	0.56	0.30	0.01	0.01	0.01	0.03	0.03	0.10
P04220	11	2	Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1	0.04	0.06	0.09	0.05	0.11	0.10	0.01	0.04	0.01	0.00	0.00	0.01
5;A0A0C4DH42;P01	2	2	Immunoglobulin heavy variable 3-23 OS=Homo sapiens GN=IGHV3-23 PE=1 SV=2	0.02	0.03	0.02	0.07	0.07	0.04	0.00	0.00	0.00	0.00	0.00	0.03
Q6UXX2	4	4	Immunoglobulin superfamily containing leucine-rich repeat protein 2 OS=Homo sapiens GN=ISLR2 PE=2 SV=1	0.07	0.49	0.39	0.03	0.04	0.21	0.01	0.00	0.01	0.00	0.00	0.05
P19823	7	7	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	0.16	0.18	0.14	0.13	0.18	0.07	0.01	0.02	0.01	0.00	0.00	0.05
Q14624	59	58	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	1.73	5.20	4.46	0.77	8.28	7.51	0.04	0.44	0.18	0.08	0.54	1.54
P01042	21	20	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	0.22	0.16	0.22	0.42	1.61	0.77	0.01	0.00	0.01	0.01	0.06	0.17
Q6PIL6	2	2	Kv channel-interacting protein 4 OS=Homo sapiens GN=KCNIP4 PE=1 SV=1	0.23	0.14	0.33	0.21	0.39	0.26	0.01	0.00	0.00	0.00	0.02	0.03
P18428	12	12	Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3	0.02	0.18	0.04	0.02	0.48	0.36	0.00	0.01	0.00	0.00	0.02	0.23
P51884	9	8	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	0.12	0.03	0.04	0.12	0.01	0.01	0.00	0.00	0.00	0.01	0.00	0.00
Q13201	7	7	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	0.75	0.20	0.40	0.72	0.62	0.49	0.04	0.02	0.04	0.06	0.07	0.07
Q86WJ24	5	4	NACHT _LRR and PYD domains-containing protein 14 OS=Homo sapiens GN=NLRP14 PE=1 SV=1	1.09	1.28	0.48	1.38	1.05	1.61	0.24	0.05	0.08	0.21	0.02	0.23
Q96NY8	4	4	Nectin-4 OS=Homo sapiens GN=NECTIN4 PE=1 SV=1	0.03	0.09	0.04	0.02	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P03952	14	14	Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1	0.03	0.13	0.82	0.02	0.35	0.40	0.00	0.01	0.00	0.01	0.03	0.27
P05155	8	8	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	0.05	0.09	0.08	0.12	0.47	0.18	0.01	0.01	0.01	0.01	0.01	0.06
P05154	7	7	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	0.00	0.03	0.01	0.02	0.17	0.08	0.00	0.00	0.01	0.00	0.01	0.00
P00747	14	14	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	0.00	0.04	0.03	0.01	0.30	0.06	0.00	0.00	0.00	0.00	0.00	0.03
P02775	5	4	Platelet basic protein OS=Homo sapiens GN=PPBP PE=1 SV=3	0.00	0.00	0.00	0.00	0.07	0.03	0.00	0.00	0.00	0.00	0.00	0.01
P02776;P10720	4	4	Platelet factor 4 OS=Homo sapiens GN=PF4 PE=1 SV=2	0.00	0.07	0.11	0.01	1.16	0.27	0.00	0.01	0.01	0.00	0.04	0.24
A5A3E0	6	2	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	1.66	0.52	0.62	1.27	0.61	0.72	0.04	0.02	0.02	0.05	0.05	0.58
P07737	2	2	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	0.00	0.02	0.01	0.02	0.13	0.06	0.00	0.00	0.00	0.00	0.00	0.01
P27918	7	6	Properdin OS=Homo sapiens GN=CFP PE=1 SV=2	0.04	0.05	0.10	0.11	0.52	0.23	0.00	0.04	0.01	0.02	0.04	0.19
Q8IZT9	2	2	Protein FAM9C OS=Homo sapiens GN=FAM9C PE=1 SV=1	1.48	2.34	0.90	0.27	0.56	2.71	0.06	0.16	0.03	0.02	0.03	0.08
P05109	2	2	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	0.03	0.16	0.14	0.20	0.07	0.01	0.00	0.00	0.00	0.01	0.01	0.01
P06702	3	3	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	0.05	0.29	0.36	0.29	0.35	0.15	0.03	0.09	0.04	0.05	0.30	0.08
Q92954	10	10	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2	0.94	0.82	0.24	0.76	0.78	1.23	0.05	0.08	0.01	0.05	0.02	0.87
P00734	37	35	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	0.06	0.14	0.12	1.49	4.14	3.96	0.00	0.00	0.01	0.12	0.19	0.02
P0C7X3	2	2	Putative cyclin-Y-like protein 3 OS=Homo sapiens GN=CCNY13 PE=3 SV=1	0.02	0.10	0.03	0.02	0.01	0.03	0.01	0.01	0.00	0.00	0.00	0.00
Q99969	3	2	Retinoic acid receptor responder protein 2 OS=Homo sapiens GN=RARRES2 PE=1 SV=1	0.00	0.03	0.06	0.00	0.03	0.01	0.00	0.01	0.01	0.00	0.00	0.01
Q8IZV5	2	2	Retinol dehydrogenase 10 OS=Homo sapiens GN=RDH10 PE=1 SV=1	0.02	0.08	0.06	0.03	0.20	0.14	0.00	0.00	0.00	0.00	0.02	0.01
Q13103	3	3	Secreted phosphoprotein 24 OS=Homo sapiens GN=SPP2 PE=1 SV=1	0.11	0.02	0.03	0.04	0.04	0.01	0.02	0.00	0.00	0.00	0.01	0.00
P49908	2	2	Selenoprotein P OS=Homo sapiens GN=SELENOP PE=1 SV=3	0.00	0.03	0.04	0.01	0.12	0.03	0.00	0.00	0.00	0.01	0.01	0.02
P02787	9	8	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	0.11	0.56	0.56	0.09	0.15	0.10	0.01	0.04	0.01	0.00	0.01	0.02
P02768	67	67	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	37.31	7.44	15.33	45.57	7.18	17.88	1.65	0.14	0.52	1.78	0.37	1.09
P02743	7	6	Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	0.00	0.02	0.02	0.00	0.23	0.17	0.00	0.00	0.00	0.00	0.02	0.08
P27169	6	4	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	0.18	0.02	0.04	0.01	0.02	0.01	0.02	0.00	0.00	0.00	0.00	0.01
Q96DN5	2	2	TBC1 domain family member 31 OS=Homo sapiens GN=TBC1D31 PE=1 SV=2	0.13	0.07	0.07	0.14	0.07	0.15	0.01	0.00	0.01	0.01	0.00	0.03
P07996	8	8	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	0.12	0.27	0.18	0.18	0.53	0.27	0.01	0.00	0.01	0.02	0.06	0.21
P02766	11	10	Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	1.78	2.37	1.20	2.17	2.28	3.61	0.05	0.21	0.05	0.20	0.10	0.85
P02774	20	20	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	0.30	0.24	0.26	0.31	0.39	0.16	0.02	0.00	0.01	0.00	0.14	0.11
P04004	28	28	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	9.43	12.34	11.12	8.30	24.29	16.98	0.26	0.31	0.32	0.92	1.61	3.97

Table S3. List of all identified corona proteins on lipo-$(PS)_4$ in human plasma applying different dendrimer amounts.

				Average in %				Standard deviation			
				Amount Dendrimer [mg]				Amount Dendrimer [mg]			
				n=3	n=3	n=3	n=3				
Accession	Peptide count	Unique peptides	Description	0.5	0.25	0.1	0.05	0.5	0.25	0.1	0.05
P02730	8	8	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	0.01689706	0.02334408	0.05950601	0.12323086	0.00149152	0.00123881	0.00380345	0.00497245
Q92696	3	3	Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens GN=RABGGTA PE=1 SV=2	0.71593041	0.11633758	0.11099014	0.08870386	0.02537714	0.00809266	0.01039934	0.00631582
P04004	21	20	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	2.61621035	4.49355647	9.8432212	10.5030001	0.19632669	0.2339972	0.1113526	0.02820207
P02671	55	51	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	12.6128433	11.0492687	7.42876573	6.3568448	0.18578229	0.16358085	0.01802835	0.10160731
P08697	12	12	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	1.46620385	0.58859918	0.60708084	0.53672878	0.04204691	0.04406477	0.02526978	0.02191196
P01859	6	2	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	0.0570516	0.07610793	0.12606853	0.16023325	0.00256228	0.00127081	0.0022423	0.00428111
P22352	3	3	Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	0.03743359	0.05785592	0.1135287	0.12336943	0.00373591	0.00221532	0.00275734	0.00414055
P01023	18	17	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	0.08375203	0.05376149	0.09382822	0.11998797	0.00049734	0.00189113	0.00403643	0.00362802
P02751	60	52	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	0.57868631	0.33923781	0.24545587	0.25224773	0.01014003	0.00650392	0.00607379	0.01738048
Q9BXR6	14	12	Complement factor H-related protein 5 OS=Homo sapiens GN=CFHR5 PE=1 SV=1	0.07290999	0.09718585	0.16110797	0.17446656	0.00630945	0.00354996	0.0055798	0.00840534
P00738	16	9	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	0.16210704	0.22448115	0.26720294	0.27469488	0.00622597	0.00805067	0.01556167	0.00804511
P02765	14	13	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	2.41049562	1.47697963	1.60167713	1.06861451	0.09491196	0.13424621	0.06863666	0.02353633
Q99969	3	3	Retinoic acid receptor responder protein 2 OS=Homo sapiens GN=RARRES2 PE=1 SV=1	0.01025139	0.00991817	0.03193048	0.05181746	0.00122238	0.00060706	0.00152326	0.00517599
P01019	8	8	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	0.20663555	0.16854789	0.1308342	0.1127002	0.01004552	0.00638945	0.00615027	0.00149482
Q7Z5Q1	2	2	Cytoplasmic polyadenylation element-binding protein 2 OS=Homo sapiens GN=CPEB2 PE=2 SV=3	0.03024327	0.05171295	0.08467073	0.0982388	0.00268791	0.00123022	0.00486943	0.00248735
P03950	2	2	Angiogenin OS=Homo sapiens GN=ANG PE=1 SV=1	0.03457441	0.05053615	0.12948308	0.15297786	0.00353075	0.00353602	0.00231504	0.00645584
P01834	5	5	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	0.81092834	1.01101255	1.74171849	2.16678958	0.05922793	0.10910821	0.04479627	0.04105914
P02747	7	7	Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	0.37687082	0.22735334	0.19945107	0.19898215	0.00484563	0.01945441	0.00978353	0.00624156
Q14624	52	50	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	1.18474708	0.98782063	2.29933092	2.51988744	0.02708899	0.0674759	0.1252438	0.10602918
P02766	11	11	Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	0.1439157	0.25215136	0.3765968	0.38907946	0.00481699	0.01717617	0.00278445	0.0119711
P04003	17	15	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	0.15859543	0.21575953	0.24679932	0.28744353	0.00471119	0.01150386	0.00838267	0.00187257
P04196	20	19	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	1.5098255	2.08719334	2.4161981	2.35625971	0.06519936	0.19736139	0.05345164	0.0651156
P19827	12	12	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	0.1630198	0.13708383	0.30321668	0.30346427	0.00387944	0.00803767	0.00432545	0.01333936
Q03591	16	3	Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	0.47170624	0.69416016	1.00039793	1.00748835	0.02589545	0.06323134	0.01735261	0.0529882
P10909	26	26	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	1.70213632	2.40402967	4.35258286	4.48551293	0.17919434	0.15604558	0.066049	0.07595851
P06396	42	40	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	2.48904478	2.08576336	1.49771086	1.29573167	0.0895163	0.15700522	0.07228916	0.04721548
P18428	13	13	Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3	0.1476349	0.21251798	0.25170351	0.27688587	0.00781216	0.02851302	0.00847545	0.00831553
P01876;P01877	8	8	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	0.13359189	0.13329059	0.17865486	0.22123758	0.00671348	0.01134741	0.01088698	0.00888062
P00747	60	53	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	2.83385469	2.70734672	1.87983331	1.81981217	0.08305235	0.23170924	0.0464916	0.04916012
Q04756	4	3	Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1	0.05168923	0.07433671	0.13766185	0.16119391	0.01141516	0.00505051	0.00682391	0.00550703
P01008	21	20	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	0.30242272	0.26528726	0.21263828	0.18994728	0.01467999	0.01246892	0.00793888	0.00695791
P03952	21	20	Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1	0.13806749	0.18585173	0.28932841	0.38325441	0.00535319	0.02206945	0.03806903	0.02648168
P02774	39	36	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	1.72444466	1.65911354	1.29967586	0.99264604	0.04602358	0.03991976	0.11932767	0.0414988
P15169	2	2	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	0.1818917	0.17756868	0.26782649	0.2653259	0.00336966	0.01512492	0.00409354	0.0116737
P02649	24	22	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	0.9238183	0.7168897	1.05656929	1.11756329	0.01359168	0.04409195	0.03981678	0.03404351
P04220	11	2	Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1	0.89397698	0.80793498	0.61205681	0.5447833	0.01747804	0.09562495	0.00552732	0.01424769
P05452	7	6	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	0.08870051	0.05586599	0.05023185	0.04093707	0.00307442	0.00205108	0.00132212	0.00359867
P05154	13	13	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	0.41714988	0.18931508	0.20334111	0.20360763	0.03028776	0.00616582	0.01156769	0.00947297
P01871	12	3	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	0.6110741	0.58265612	0.44959973	0.4319126	0.00873013	0.06000401	0.00406104	0.00914893
P02675	58	53	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	9.44596683	9.0628383	6.6754533	6.63161727	0.08206924	0.13453753	0.44585982	0.10012517
P35858	7	7	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	0.07055625	0.05093932	0.05383788	0.05050882	0.00260214	0.00304103	0.00265867	0.00282788
P49747	4	3	Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2	0.4711	0.59477344	0.69005777	0.7480974	0.00426954	0.07034751	0.03644782	0.04851716
P02776;P10720	3	3	Platelet factor 4 OS=Homo sapiens GN=PF4 PE=1 SV=2	0.59501421	0.23996641	0.28817978	0.34631335	0.03197061	0.01852544	0.04004158	0.00633333
P06727	31	31	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	0.84393857	1.22004209	1.01343462	1.10655368	0.0551395	0.11554096	0.07785851	0.06701966
P07360	4	4	Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3	0.03295717	0.03570771	0.05385831	0.05561421	0.00228776	0.00217735	0.00426823	0.0022399
P01857	9	3	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	0.95204447	1.25168942	1.4579445	1.72302598	0.01879344	0.04543826	0.16785334	0.17906051
P13671	30	29	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	0.47446176	0.54428947	0.49021261	0.53815045	0.01430008	0.01282204	0.00767384	0.01061598
Q15113	10	9	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2	0.19444805	0.24154414	0.18092367	0.19794838	0.01460986	0.02277837	0.00462302	0.00469559
P02790	17	15	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	0.50535402	0.56846952	0.79928405	0.66399422	0.03384357	0.016749	0.03705232	0.01886974
P05155	16	16	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	0.16700356	0.23949943	0.19703284	0.23307188	0.0136845	0.01895309	0.00622411	0.00789117
P02652	6	6	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	0.34234117	0.22531624	0.24063297	0.21269458	0.0113327	0.017813	0.01948378	0.01301247
P29622	4	4	Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3	0.08210865	0.04869602	0.06467541	0.06198813	0.00833514	0.00172905	0.00375066	0.00387003
P10643	10	9	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	0.12368874	0.1173945	0.15333231	0.16403195	0.00484725	0.01150353	0.00566891	0.00507464
P01861	9	4	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	0.32405931	0.40739448	0.43765947	0.45161738	0.02159932	0.01961741	0.01944097	0.01809518
P08603	68	58	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	1.08200684	1.31169017	1.39264469	1.66385608	0.02742439	0.09653225	0.08263564	0.02866491
P02768	60	54	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	4.20375498	5.8386098	6.06981425	6.12024102	0.14064368	0.47926637	0.4031686	0.32619286
P02679	35	35	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	17.44946	16.703158	13.2144832	11.6938736	0.45366663	0.92644755	0.47981686	0.85342963
P02647;Q9HB71	33	32	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	3.41926183	3.39117075	5.04087912	4.47532589	0.01160755	0.28062297	0.06468756	0.06610493
P09871	8	8	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	0.11253815	0.12390018	0.09978223	0.10481417	0.00303187	0.01442929	0.00054261	0.00228166
O14791	4	3	Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5	0.04988289	0.03470572	0.03943779	0.03769327	0.00178313	0.00295777	0.00419425	0.00221659
P02748	13	12	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	0.3661132	0.31371503	0.4481027	0.41686217	0.01137251	0.0116763	0.00493701	0.02109751
P27169	14	14	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	0.39286717	0.309742	0.36808372	0.37026184	0.01611334	0.01497733	0.01586552	0.00679515
P02749	19	18	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	7.56769686	8.75097494	6.28597195	8.149292	0.07360599	0.2244413	0.63884989	0.16844124
P17936	5	5	Insulin-like growth factor-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=1 SV=2	0.36744862	0.24187706	0.26373622	0.23985397	0.03848039	0.00404687	0.01269944	0.00827533
P01011	6	6	Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	0.17735797	0.17261485	0.14239756	0.14263752	0.01286504	0.0207418	0.0014576	0.001139
P36980	10	5	Complement factor H-related protein 2 OS=Homo sapiens GN=CFHR2 PE=1 SV=1	0.53361414	0.42517818	0.4878339	0.49725371	0.00508919	0.01381234	0.01020677	0.01292245
Q9UK55	4	4	Protein Z-dependent protease inhibitor OS=Homo sapiens GN=SERPINA10 PE=1 SV=1	0.07653505	0.0757115	0.06526816	0.0662652	0.00014568	0.00558249	0.00203317	0.00266983
P00746	4	3	Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5	0.04707106	0.06093371	0.05506731	0.06946564	0.00345442	0.00316375	0.00539677	0.00365977
P02760	15	14	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	0.25724573	0.14754057	0.18096721	0.19518	0.01090484	0.01398056	0.0188497	0.0100467
P07358	15	14	Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3	0.1978408	0.16130111	0.19684372	0.22668844	0.02487054	0.01359987	0.0047816	0.00331732
P00736	17	17	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	0.12564737	0.17775549	0.1658926	0.14597081	0.00912477	0.01261244	0.02969056	0.00178559
P02746	5	5	Complement C1q subcomponent subunit B OS=Homo sapiens GN=C1QB PE=1 SV=3	0.15392239	0.17413302	0.13863004	0.14051066	0.0190166	0.02103677	0.00598566	0.00708584
P00734	17	15	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	0.13403162	0.18547575	0.21251131	0.19405413	0.00665795	0.02536725	0.0023778	0.01150548
O43866	3	3	CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	0.02620514	0.03143267	0.03042378	0.03616211	0.00257435	0.00333444	0.00087767	0.00305335
P01042	28	28	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	1.21347107	1.41777108	1.35562995	1.29104223	0.05170315	0.05176817	0.12918769	0.04029737
P0C0L5	62	3	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	0.31407562	0.35434275	0.38492493	0.35878904	0.01062954	0.00730774	0.03139205	0.01849924
P0C0L4	62	3	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	0.24422719	0.27553917	0.29932006	0.27899663	0.0082656	0.00568255	0.02441065	0.01438512
P01009	14	14	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	0.18700983	0.20212135	0.19205249	0.2074926	0.00452977	0.00730682	0.01250997	0.00998746
P0CG05;P0CG06	7	6	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	1.20770389	0.96870895	0.99591232	1.16276655	0.05106677	0.0642798	0.03621363	0.05798487
P24071	2	2	Immunoglobulin alpha Fc receptor OS=Homo sapiens GN=FCAR PE=1 SV=1	0.03050643	0.0281942	0.02509897	0.02792152	0.00075806	0.00134571	0.0005692	0.00133518
Q96PD5	5	5	N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1	0.03517954	0.03313835	0.03279857	0.02918194	0.00104162	0.00349285	0.00208548	0.00116466
P36955	17	16	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	0.4300038	0.38251541	0.35086205	0.38384471	0.02285883	0.03239166	0.01928868	0.01567609
Q8WWA0	2	2	Intelectin-1 OS=Homo sapiens GN=ITLN1 PE=1 SV=1	0.03661873	0.02297807	0.02191098	0.01941327	0.00950343	0.00230952	0.00429507	0.00186801
P00740	8	8	Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2	0.08151545	0.08094968	0.06877153	0.06456289	0.00689	0.00640872	0.01053018	0.00433146
P12259	27	25	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	1.06869072	1.0728709	0.8363373	0.80541505	0.14841846	0.15216206	0.01152496	0.02512285
P19823	33	30	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	0.39666301	0.33150814	0.34698253	0.31961239	0.00585128	0.01404315	0.01030533	0.02390921
P04217	8	6	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	0.13795734	0.14553184	0.13876046	0.12446234	0.00469062	0.01267883	0.00397504	0.00284227
Q6ZWK4	2	2	Uncharacterized protein C1orf186 OS=Homo sapiens GN=C1orf186 PE=2 SV=1	0.0447242	0.0526427	0.0454755	0.04426543	0.00020658	0.00280422	0.0071625	0.00214547
Q14520	13	12	Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1	0.46674707	0.49131001	0.47631956	0.51529714	0.01908416	0.04963741	0.00384253	0.01577812
P01024	103	100	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	1.24317874	1.03602941	1.29343069	1.24451031	0.01220744	0.02806992	0.05081137	0.09526962
P02656	2	2	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	0.31194815	0.33075479	0.37559015	0.3840302	0.03809001	0.01134767	0.02327007	0.02742631
P49908	6	6	Selenoprotein P OS=Homo sapiens GN=SELENOP PE=1 SV=3	0.38145359	0.40890312	0.44152587	0.41463907	0.05640701	0.01728999	0.02917149	0.00623846
Q5TAB7	2	2	Protein ripply2 OS=Homo sapiens GN=RIPPLY2 PE=1 SV=1	0.05825167	0.0570042	0.06014659	0.06340941	0.0012833	0.00169724	0.00241341	0.00151987
P02787	24	23	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	0.72699262	0.76486183	0.80145594	0.81708967	0.03207043	0.04792846	0.04106951	0.06093394
P01860	11	4	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	0.64570985	0.53220334	0.57383478	0.65295985	0.02276524	0.04268161	0.08784418	0.06190566
P00748	12	11	Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3	0.20966048	0.20207159	0.21234211	0.21747437	0.00946773	0.01234431	0.00401689	0.00936537
P03951	12	12	Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1	0.14994623	0.1437313	0.11418307	0.06165379	0.02644127	0.02014236	0.01421048	
P00751	17	17	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	0.26834532	0.27487553	0.33763838	0.26175095	0.087736	0.09125743	0.05817281	0.03905605
P05546	16	16	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	0.17254203	0.1615275	0.16492811	0.16689089	0.02554911	0.01587485	0.00426214	0.00445427

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