

Supplementary Information

Protein Corona of Anionic Fluid-Phase Liposomes Compromises Their Integrity rather than Uptake by Cells

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Table S1. Liposome diameter before incubation with 50% HP and after incubation followed by separation of the liposome–protein complexes using SEC

Sample ID	$D_H \pm SD, \text{ nm}$	
	Liposomes	Liposome–protein complexes
PC	194.4 \pm 3.8	186.2 \pm 1.8
33CH	199.9 \pm 4.4	190.1 \pm 3.0
CHPG	164.6 \pm 2.6	150.3 \pm 1.4
10PG	153.1 \pm 0.6	160.6 \pm 5.4
40PG	148.7 \pm 1.1	232.2 \pm 9.5

Data obtained for ~200-nm liposomes prepared in 10 mM KCl with 1 mM K₂HPO₄ and 1 mM KH₂PO₄ measured using Litesizer 500 (Anton Paar GmbH, Austria).

Calcein release assay

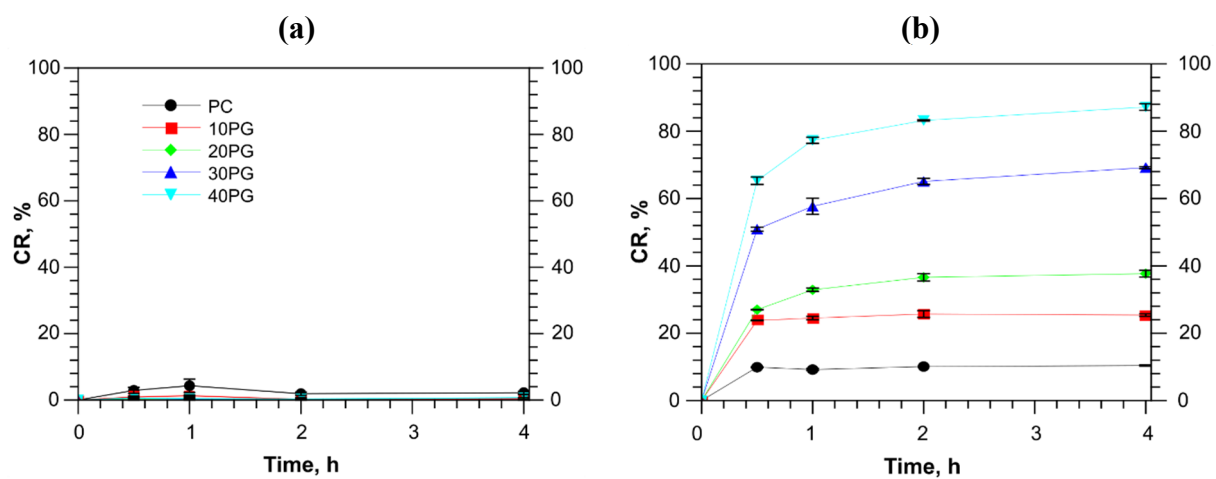


Figure S1. Calcein release assessment in PBS (a) and in 50% human plasma (b) for liposomes with increasing POPG percentage.

Total peptide assay

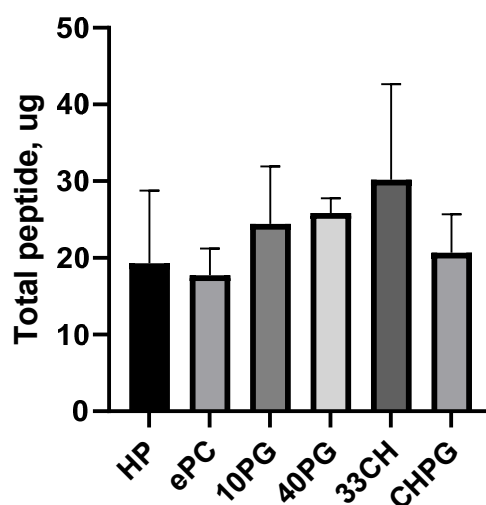


Figure S2. Peptide content in samples after proteolysis and filtration on STrap filters measured using the Pierce™ Quantitative Colorimetric Peptide Assay kit (Thermo Scientific, Waltham, MA, USA). No statistically significant differences according to Welch's ANOVA, $p < 0.05$. Note that HP sample represents combined material of three SEC runs (one SEC run was sufficient for other samples).

Western blotting

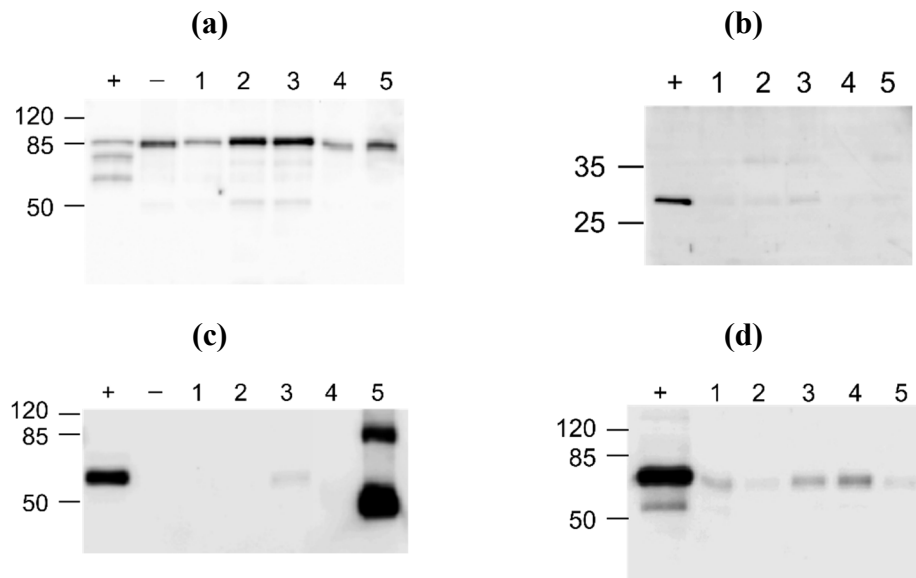


Figure S3. *Western blotting results with (a) anti-IgM, (b) anti-ApoA1, (c) anti-beta-2-glycoprotein 1, and (d) anti-HSA antibodies. Designations: +, diluted HP; -, negative control HP; 1, PC; 2, 33CH; 3, CHPG; 4, 10PG; 5, 40PG*

Western blotting has given us the reassurance of mass spectroscopy data, as we have observed the same patterns of protein adsorption for IgM, ApoA1, beta-2-glycoprotein 1, and albumin (Figs. S2a-d).

Liposome uptake by EA.hy926 cells

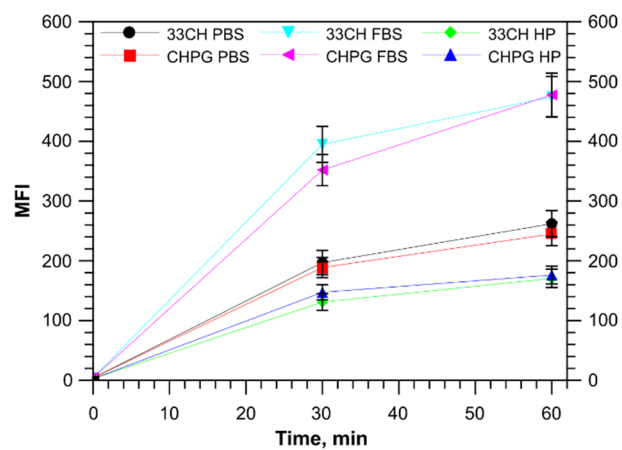


Figure S4. Liposome (33CH and CHPG samples) uptake by EA.hy926 cells without protein corona, with protein corona formed in FBS and with protein corona formed in HP.