Electronic Supplementary Material (ESI) for Nanoscale.

Time-evolution of *in vivo* protein corona onto blood-circulating PEGylated liposomal doxorubicin (DOXIL) nanoparticles

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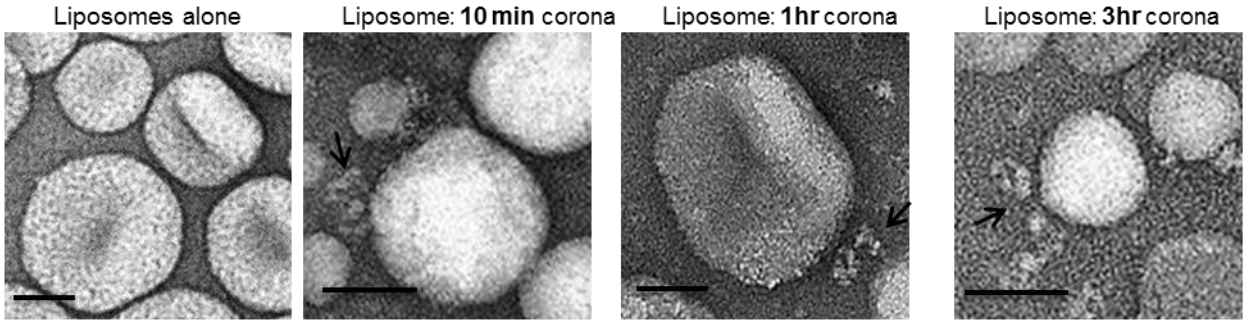
Supporting Table

Table S1: **The physicochemical characteristics of PEGylated liposomal doxorubicin before and after extraction from blood circulation.** Mean vesicle diameter (nm) and ζ-potential (mV) data from DLS and surface charge electrophoresis are shown.

Liposome type	Size (nm)	ζ-potential (mV)	PDI
Liposomes alone (HSPC:CHOL:DSPE-PEG2000) (56.3:38.2:5.5)	114.6 ± 1.752	-36.2 ± 0.85	0.056 ± 0.018
Liposome: **10min** corona	102.0 ± 3.107	-35.5 ± 1.20	0.123 ± 0.012
Liposome: **1hr** corona	104.0 ± 1.662	-33.5 ± 3.16	0.127 ± 0.032
Liposome: **3hr** corona	103.1 ± 4.152	-34.1 ± 2.37	0.104 ± 0.015

Supporting Figures



FigureS1: Negative stain TEM imaging of liposomes before their interaction with plasma proteins and **10 min**, **1h** and **3h** after their i.v. injection and recovery from CD-1 mice. Arrows show the presence of proteins around the surface of liposomes. All scale bars are 50nm.

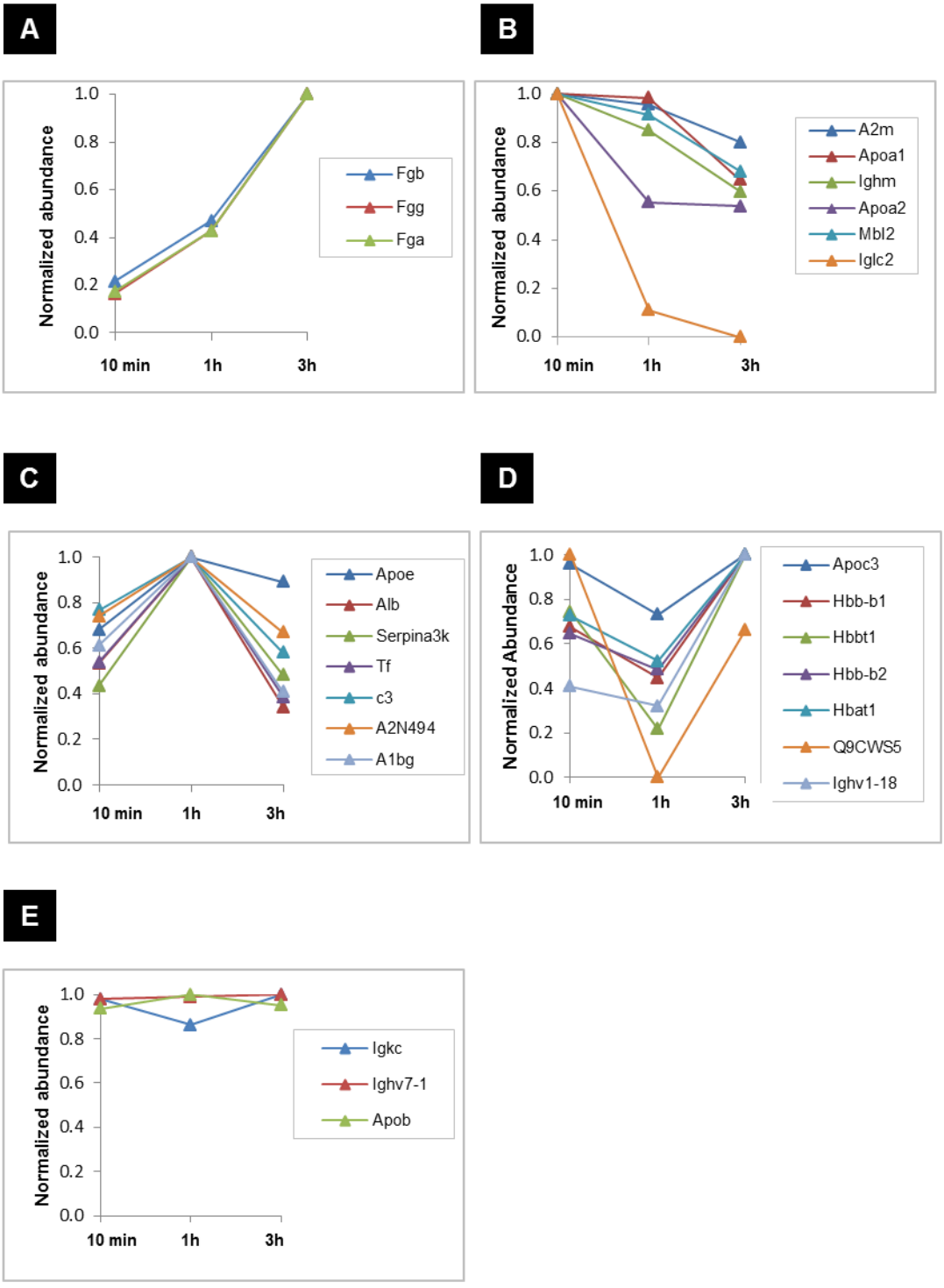


Figure S2: Protein binding kinetics during corona evolution. Relative values were normalized to the maximum amount (set to 1) across the three time points for each of the top-20 proteins. Corona proteins were classified into five groups: **(A)** Proteins displaying increased binding over time; **(B)** Proteins displaying reduced binding over time **(C)** Proteins characterized by low abundance at the early (t=10min) and late time points (t=3h) and higher abundance at intermediate time point (t=1h); **(D)** Proteins characterized by high abundance at the early (t=10min) and late time points (t=3h) and lower abundance at intermediate time point (t=1h); **(E)** Proteins with constant abundance over time.