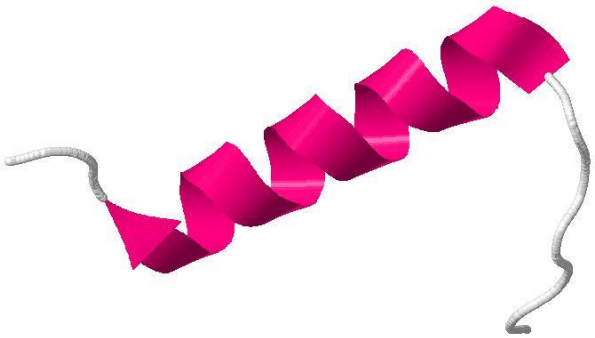
Electronic Supplementary Material (ESI) for Nanoscale.



Amino acid sequence:

Synthetic Human N-Terminal SP-B_{1-25}

FPIPLPYCWLCRALIKRIQAMIPKG

Figure S1. Cartoon of SP-B N-Terminal 1-25 structure [PDB: 1DFW, visualised using Jmol (Jmol: an open-source Java viewer for chemical structures in 3D http://www.jmol.org/)] and amino acid sequence in one letter code.

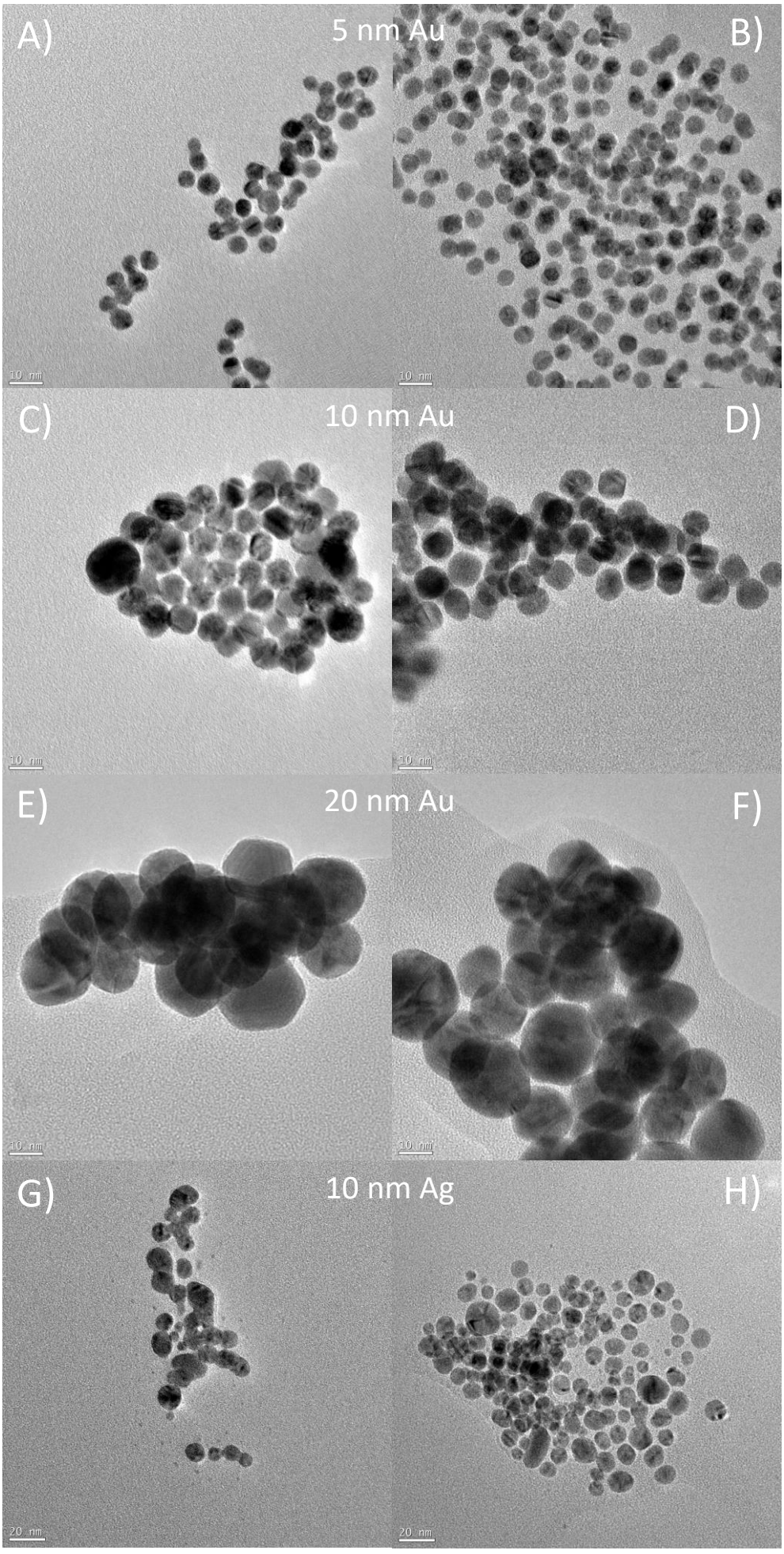


Figure S2. TEM images of 5nm AuNPs A) without and B) with 4 $\mu g.ml^{-1}$ SP-B_{1-25}; 10nm AuNPs C) without and D) with 4 $\mu g.ml^{-1}$ SP-B_{1-25}; 20nm AuNPs E) without and F) with 4 $\mu g.ml^{-1}$ SP-B_{1-25}; 10nm AgNPs G) without and H) with 4 $\mu g.ml^{-1}$ SP-B_{1-25}. AuNP and AgNP concentrations 5 $\mu g.ml^{-1}$ and 2.5 $\mu g.ml^{-1}$ respectively in TFE/4nM PB, 1:4 v:v. All images were taken at magnification 150000X.

NP mass conc. (µg.ml^{-1})	0.3125		0.625		1.25		2.5		5		10	
B= buffer (TFE/PB) S=sample (SP-B$_{1-25}$/TFE/PB)	B	S	B	S	B	S	B	S	B	S	B	S
5nm Au			355	377	77	1058	184	1192	72	1025		
10nm Au					100	838	101	1133	104	1127	85	1159
20nm Au					913	1009	863	1162	159	1301	131	1090
10nm Ag	163	208	131	826	629	922	25	1370				

Table S1. Mean, number-based, hydrodynamic diameter measured using dynamic light scattering (Zetasizer Nano-ZS), results presented are the average of 3 consecutive runs.

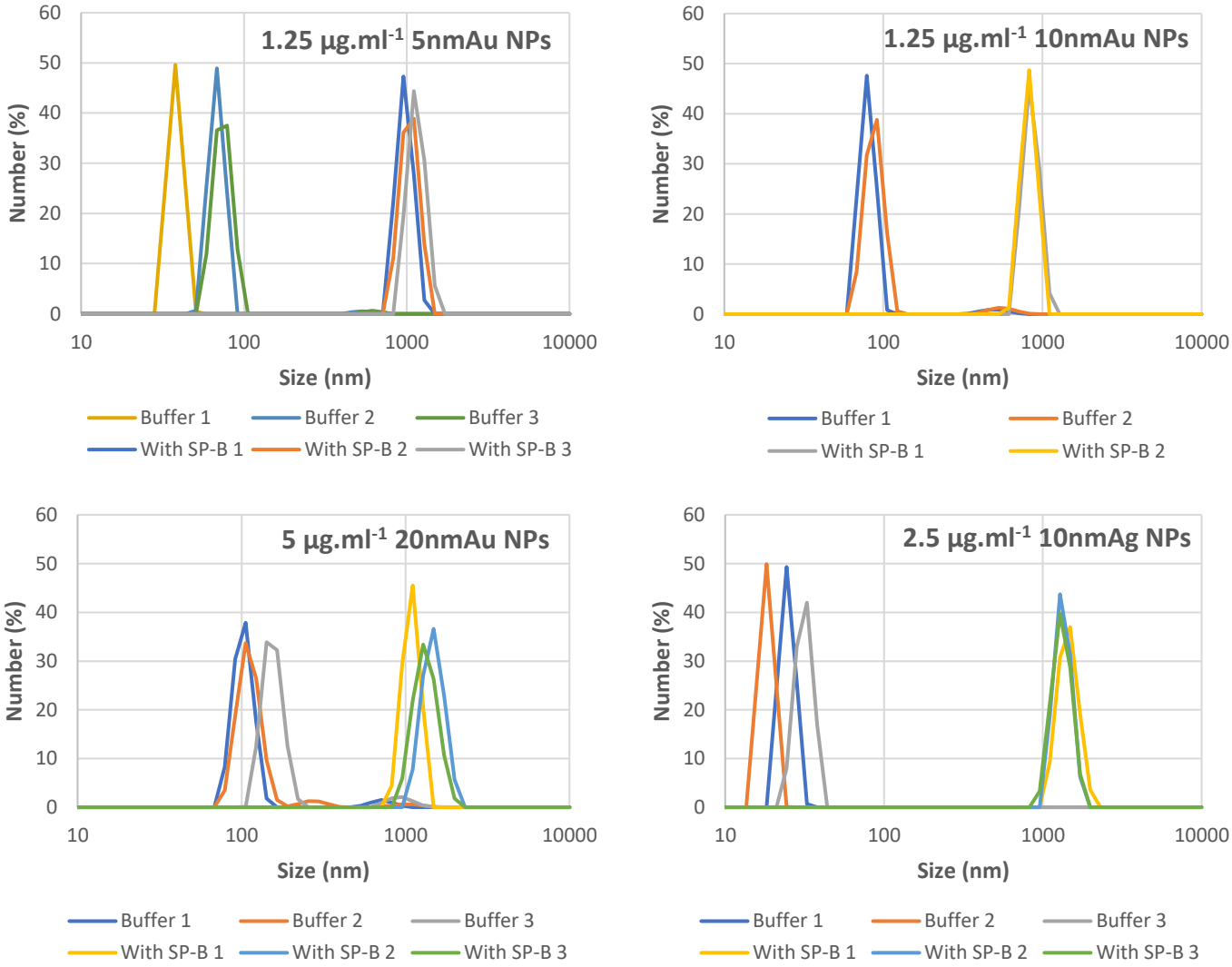


Figure S3. Example number-weighted hydrodynamic diameter distributions as measured by dynamic light scattering for each nanoparticle investigated. Buffer refers to NPs suspended in TFE/PB and With SP-B refers to NPs suspended in SP-B$_{1-25}$/TFE/PB. Repeat measurements were made consecutively.

Sample	Mode Zeta Potential (mV)		
	Stock NP Solution	Buffer	With SP-B_{1-25}
SP-B_{1-25} in TFE/PB	-	-	4.1
7.59 µg.ml^{-1} 5 nm Au	-	-17.9	-11.7
3.79 µg.ml^{-1} 10 nm Au	-	-13.6	5.1
7.59 µg.ml^{-1} 10 nm Au	-17.5	-15	-0.8
7.59 µg.ml^{-1} 20 nm Au	-	-14.5	9.5
2.5 µg.ml^{-1} 10 nm Ag	-	-9.3	2.0

Table S2. Average (mode) zeta potential results for a selection of buffers (no SP-B_{1-25}) and samples (with SP-B_{1-25}) similar to those used in the CD study. As for the CD study, all samples were made in TFE/4 mM PB, 1:4 v:v, with SP-B_{1-25} concentration 4 µg.ml^{-1} where used. All results are the average of 3 consecutive measurements. Zeta Potential measurement of stock NP solution diluted with mQ water was only made for 10nmAuNPs.

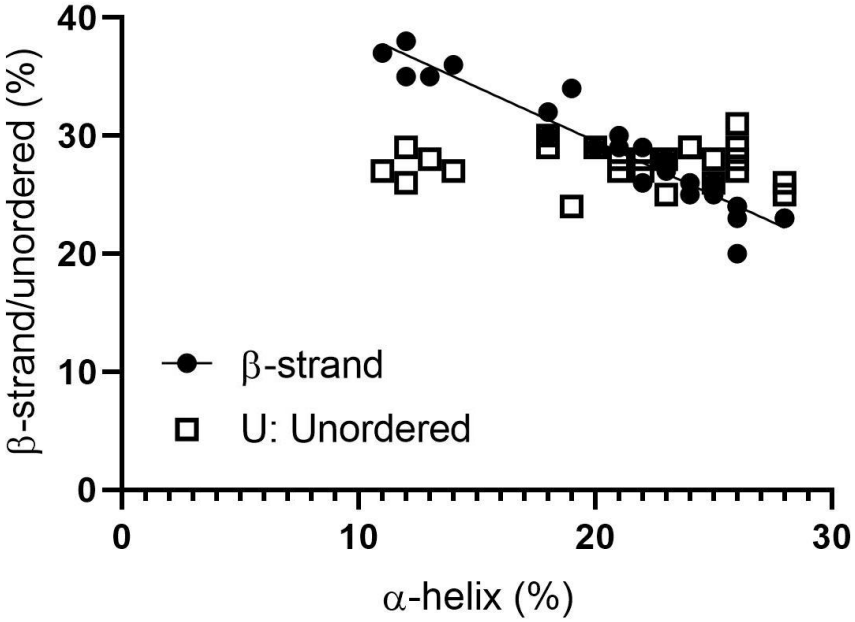


Figure S4. Relationship between alpha-helix component and beta-strand and unordered components for all the NP + SP-$B_{1\text{-}25}$ + TFE/PB dispersions with Au and Ag NPs where secondary structure analysis was possible.

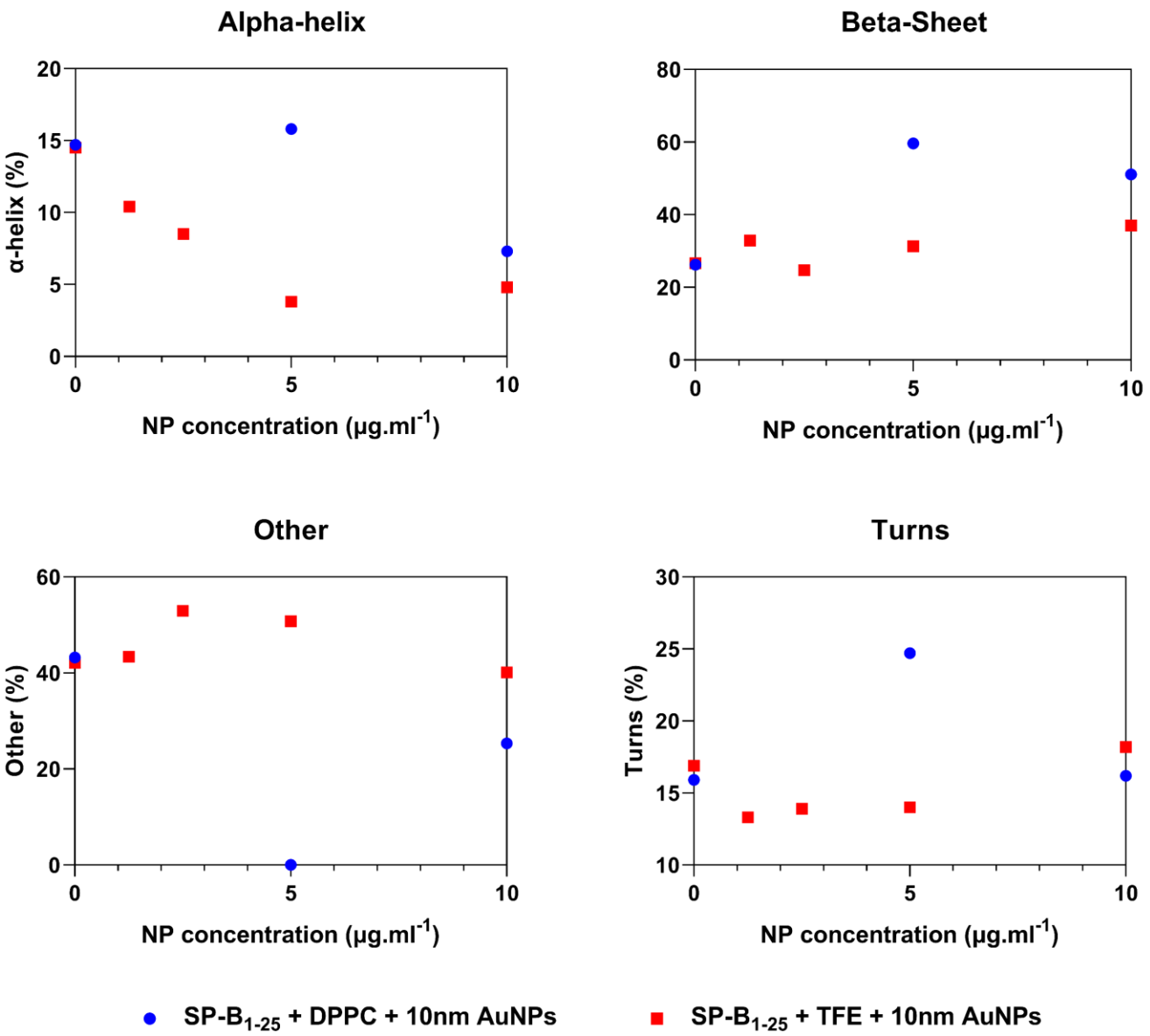


Figure S5. BeStSel analysis of the secondary structure of SP-B_{1-25} suspended in DPPC (50:1 mol:mol) at a range of 10 nm AuNP concentrations (**blue** data points). For comparison, BeStSel analysis was also carried out for the equivalent CD spectra of SP-B_{1-25} in TFE (**red** data points). The intensity of the CD spectra obtained for SP-B_{1-25} in DPPC (see Figure 5) was considerably lower than for the equivalent spectra obtained for SP-B_{1-25} in TFE (Figure 3A), suggesting that the concentration of SP-B_{1-25} assumed in the data analysis was incorrect. CD spectra measurements of proteins in lipid systems such as DPPC are known to be difficult due to various effects including micelle formation, which can result in a lack of uniformity in concentration across the sample and the increased potential for losses to surfaces, such that the effective concentration of SP-B_{1-25} "seen" by the system is lower than that in the original solution. To be able to compare the trends observed on the secondary structure of SP-B_{1-25} in DPPC and TFE with increasing concentration of 10 nm AuNPs, prior to BeStSel analysis, the DPPC CD spectra were scaled by a factor of 1.77. This corresponds to the scaling factor required to match the CD spectra troughs at 208 nm for SP-B_{1-25} only in DPPC and TFE. A general trend of decreasing alpha helix and increasing beta sheet with increasing concentration of 10 nm AuNPs can be seen for SP-B in DPPC, similar to that for TFE, albeit not as consistently. Turns and Other show no obvious trend as for TFE. Other than for SP-B_{1-25} in DPPC with no NPs, the CD spectra were really too noisy and the variability between runs was too high to carry out secondary structure fitting analysis accurately. While the secondary structure results for SP-B_{1-25} in DPPC with no NPs and the highest NP concentration show a clear match to the TFE results, this can only be taken as an indication of a similar effect of NPs on the secondary structure of SP-B_{1-25} when suspended in the more biologically relevant DPPC compared to TFE. Further work would be required to investigate the actual peptide concentration and potential reasons for the reduced intensity and to reduce the noise of and stability between consecutive CD scans before firm conclusions can be drawn.