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Supplemental Information

Refolding of SDS-Unfolded Proteins by Nonionic Surfactants

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Supplementary Information

Refolding of SDS-unfolded proteins by non-ionic surfactants

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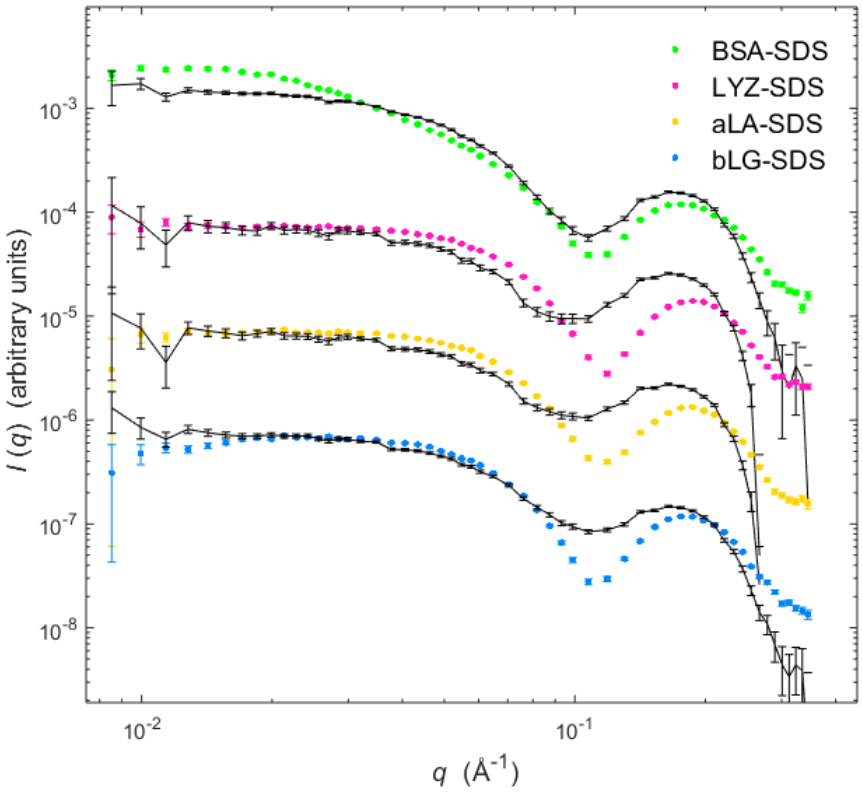

Fig. S1: Best fits of the four different protein-SDS complexes using linear combinations of data from the pure protein species and SDS micelles as basis functions. The poor fit quality demonstrates that the samples do not consist of native protein and SDS micelles, so protein-SDS complexes must have been formed.

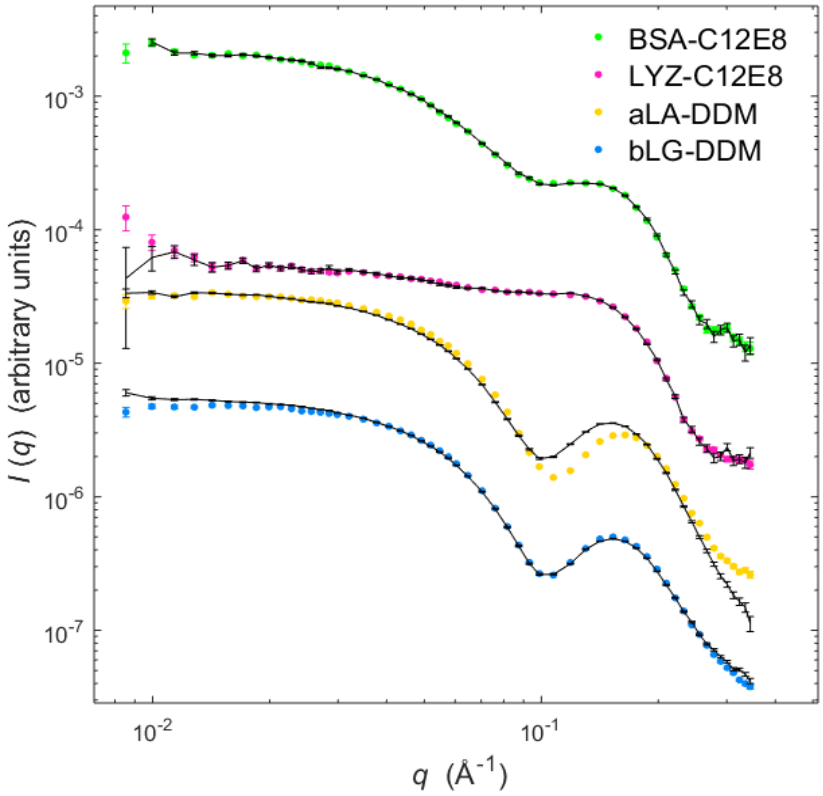

Fig. S2: Best fits of four different protein-NIS complexes using linear combinations of data from the pure protein species and NIS micelles as basis functions. The good fit quality demonstrates that most samples consist of native protein and SDS micelles, while additional changes have occurred in the αLA-DDM sample.

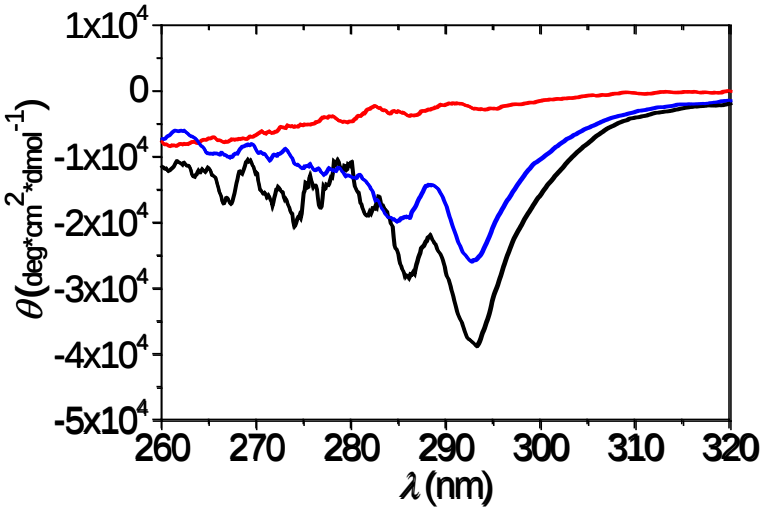

Fig. S3: Near-UV CD data for pure β-LG (black), βLG mixed with SDS and C12E8 at SDS mole fractions of 0.8 (red) and 0.35 (blue), respectively

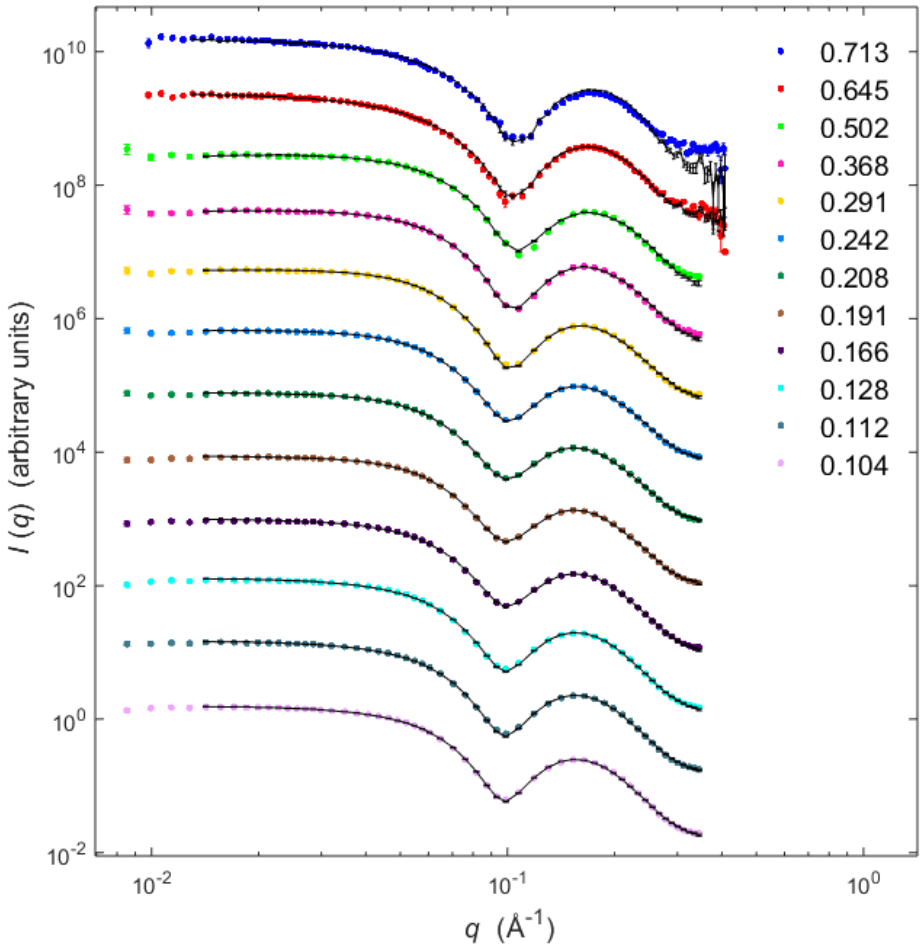

Fig. S4: Fits of β-LG and different χ_{SDS} in DDM. Data were fit with a linear combination of folded protein in presence of mixed micelles and SDS-unfolded protein in presence of pure NIS micelles, as described in materials and methods. Decreasing χ_{SDS} from top to bottom.

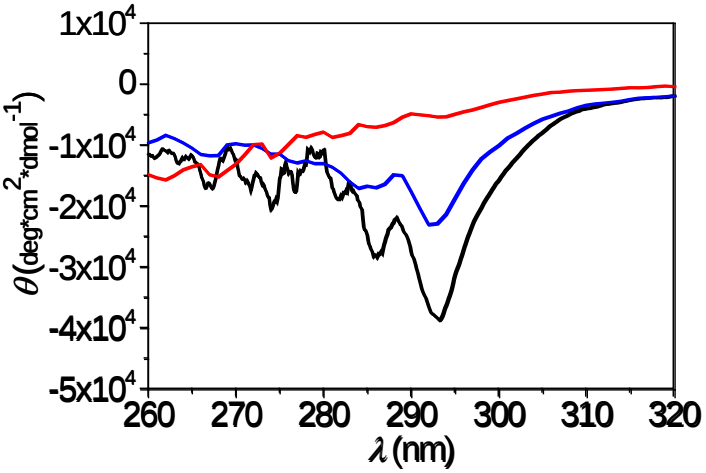

Fig. S5: Near-UV CD spectra for pure βLG (black), βLG mixed SDS and DDM with SDS mole fraction of 0.5 (red) and 0.1 (blue), respectively

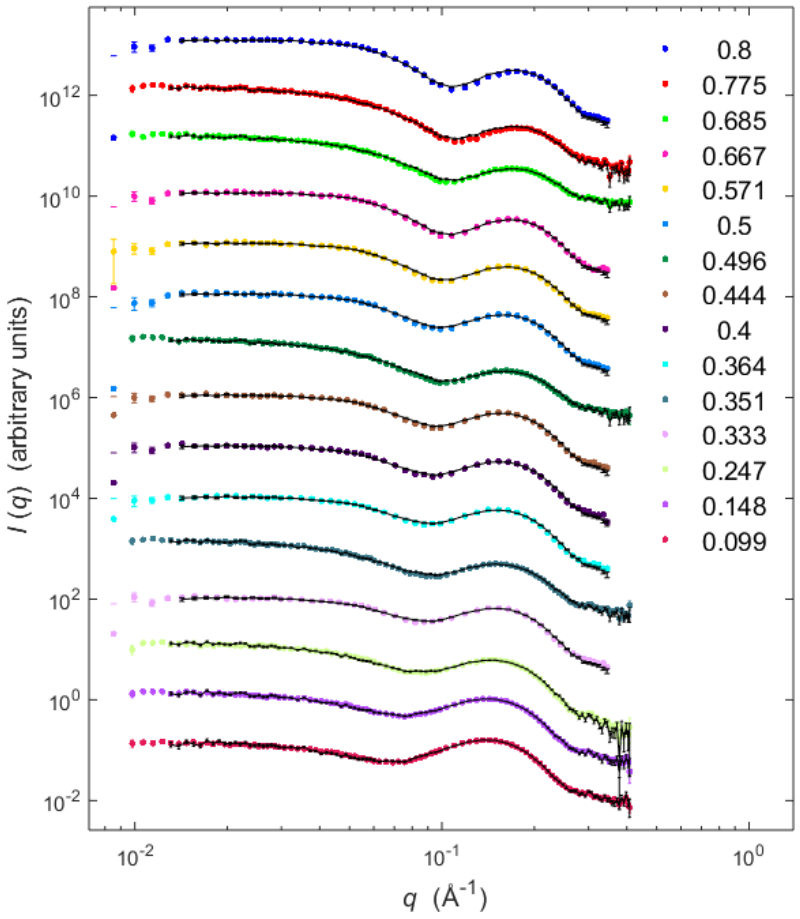

Fig. S6: Fits of αLA and different χ_{SDS} in $C_{12}E_8$. Data were fit with a linear combination of folded protein in presence of mixed micelles and SDS-unfolded protein in presence of pure NIS micelles, as described in materials and methods. Decreasing χ_{SDS} from top to bottom. The basis function for the SDS-unfolded state of αLA was in the fitting procedure replaced by αLA-SDS with a small amount of $C_{12}E_8$ as this gives better fits than for the pure SDS-protein complex as basis function.

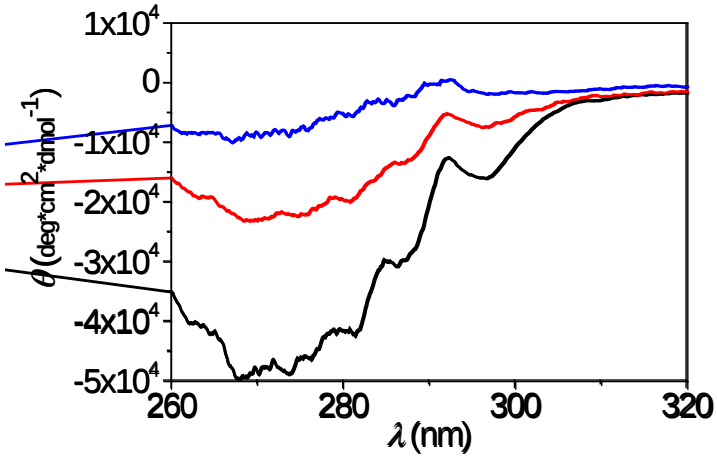

Fig. S7: Near-UV CD data for pure αLA (black), and αLA mixed SDS and C12E8 with SDS mole fractions of 0.5 (blue) and 0.1 (red), respectively.

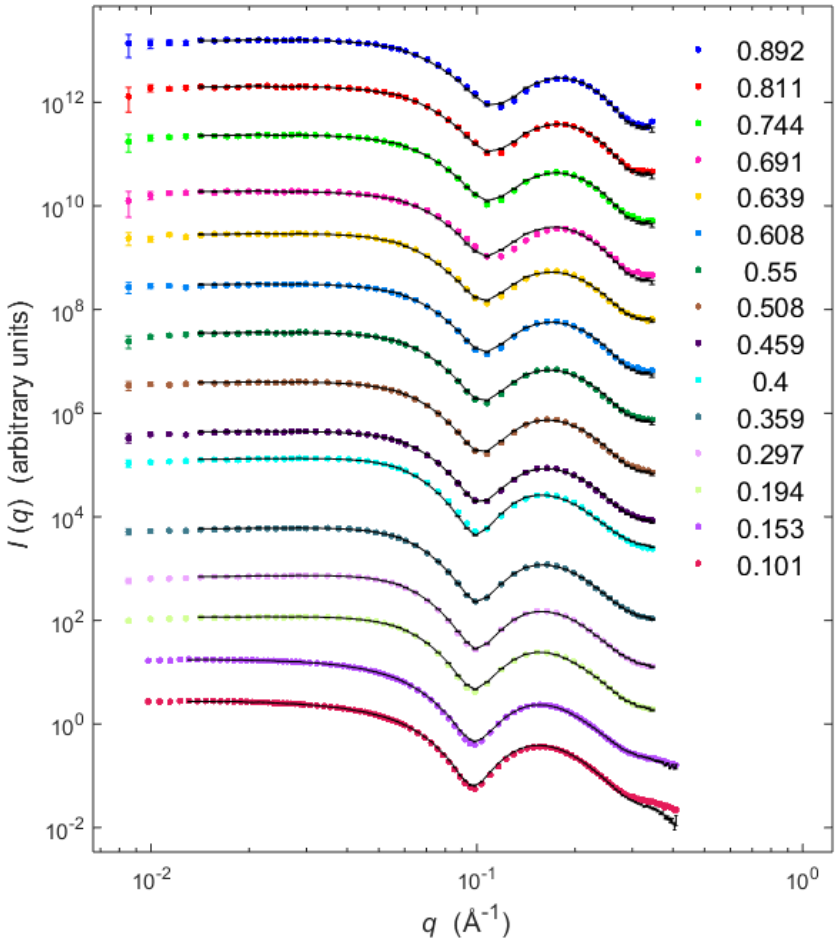

Fig. S8: Fits of αLA and different χ_{SDS} in DDM. Data were fit with a linear combination of folded protein in presence of mixed micelles and SDS-unfolded protein in presence of pure NIS micelles, as described in materials and methods. Decreasing χ_{SDS} from top to bottom.

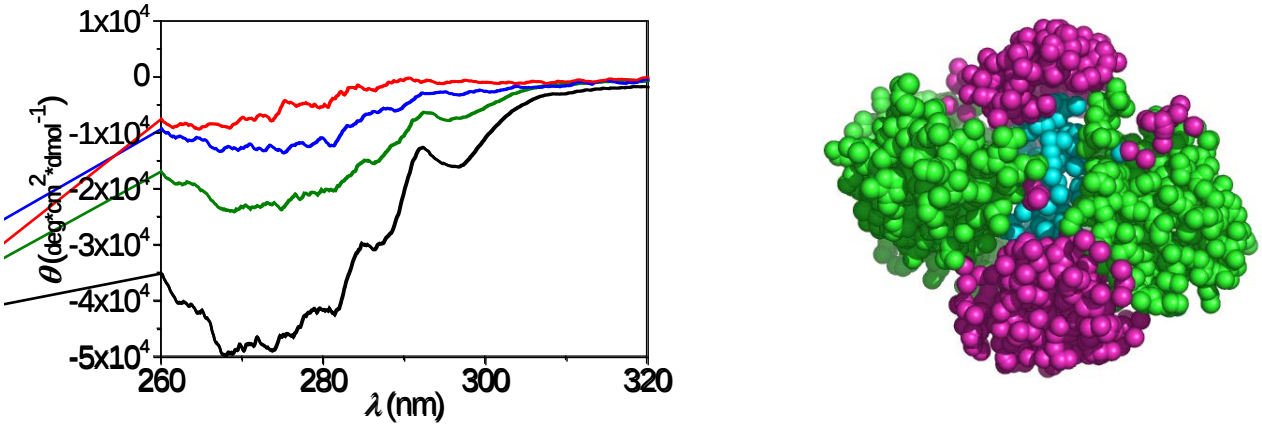

Fig. S9: Left-hand side:Near-UV CD data for pure αLA (black), αLA mixed with DDM (green), and αLA mixed with SDS and DDM to SDS mole fractions of 0.5 (red) and 0.1 (blue), respectively. Right-hand side: Model of DDM- αLA derived from SAXS data. The partly unfolded protein is shown as green spheres, the hydrocarbon of DDM as light blue spheres and the DDM headgroups as purple spheres.

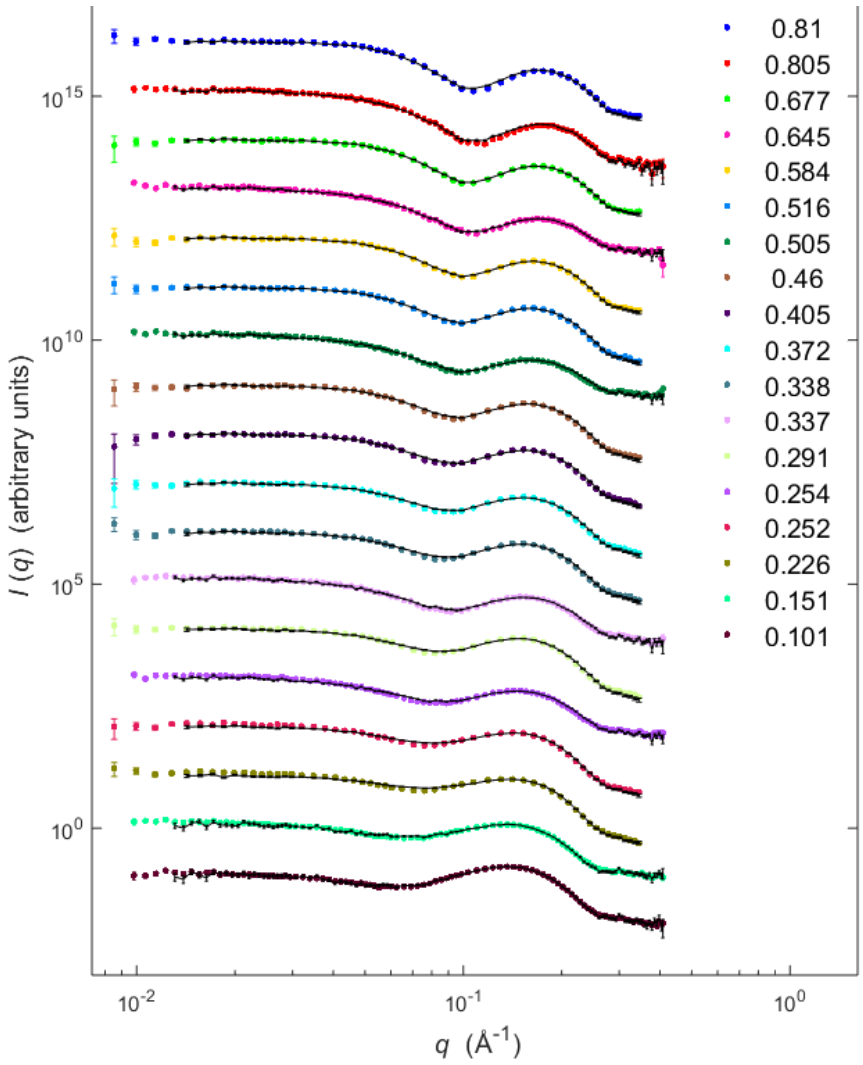

Fig. S10: Fits of LYZ and different χ_{SDS} in $C_{12}E_8$. Data were fit with a linear combination of folded protein in presence of mixed micelles and SDS-unfolded protein in presence of pure NIS micelles, as described in materials and methods. Decreasing χ_{SDS} from top to bottom.

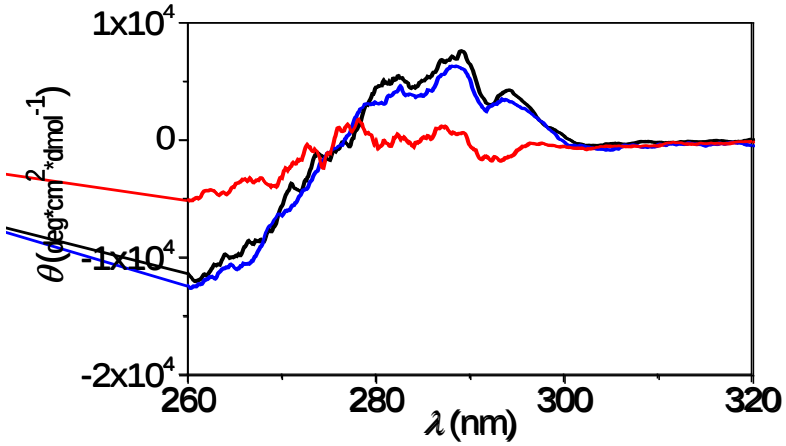

Fig. S11: Near-UV CD data for pure LYZ (black), LYZ mixed SDS and C12E8 with SDS mole fractions of 1 (red) and 0.1 (blue), respectively

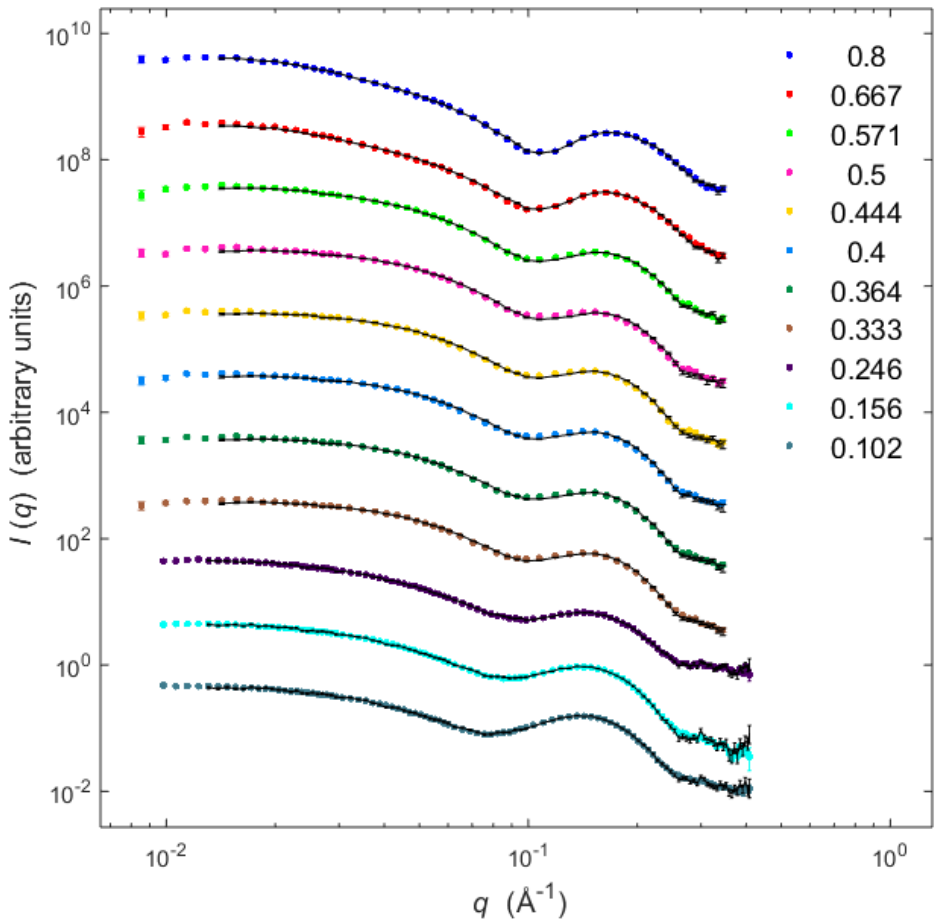

Fig. S12: Fits of BSA and different χ_{SDS} in $C_{12}E_8$. Data were fit with a linear combination of folded protein in presence of mixed micelles and SDS-unfolded protein in presence of pure NIS micelles, as described in materials and methods. Decreasing χ_{SDS} from top to bottom.