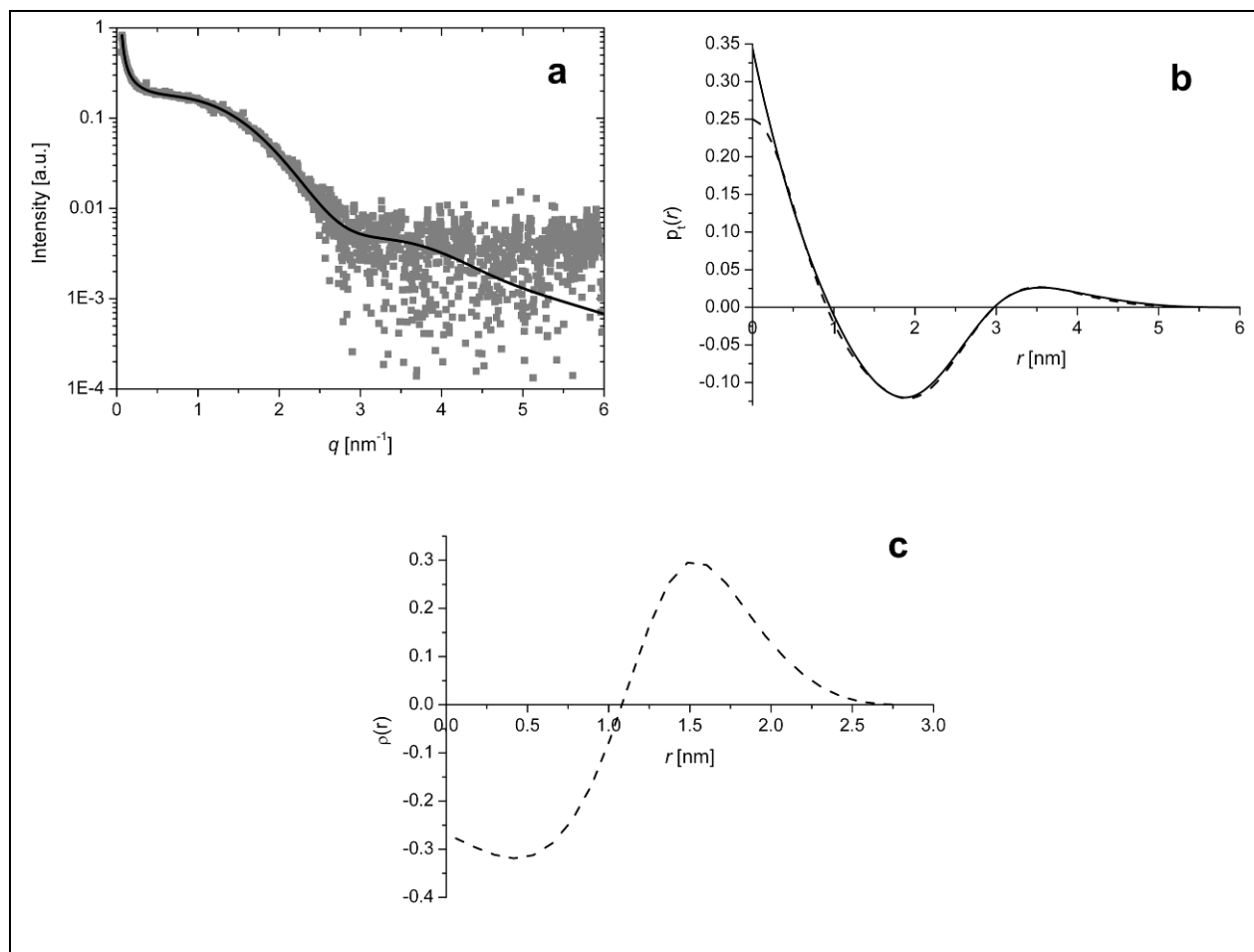
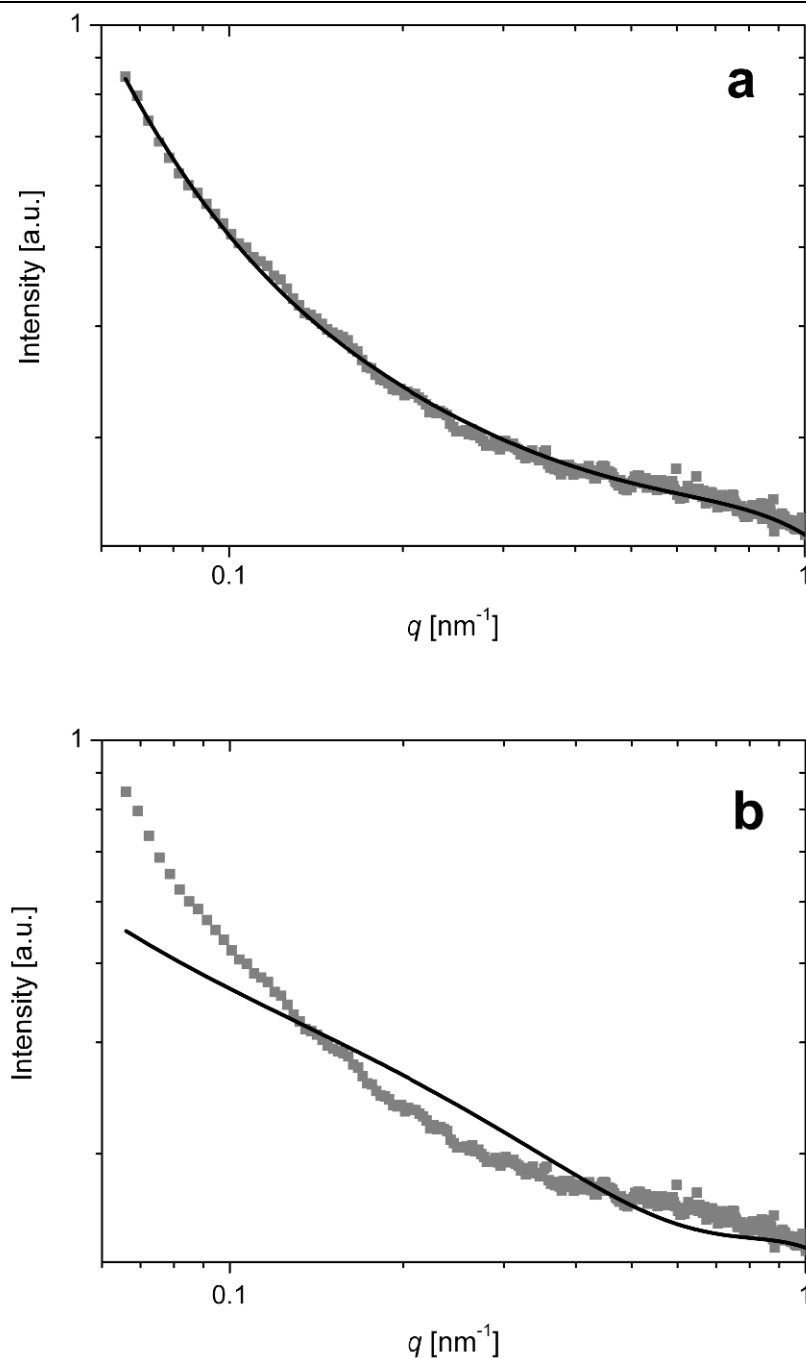


## Electronic Supporting Information



**Figure SI-1:** Model dependent fitting of the SAXS data obtained from the in-vitro digestion of a BCN/BLG (1/1) stabilized triolein emulsions,  $\beta = 0.4$ , at oil/P = 1.1 and oil/BS = 1.7 after 189 min of lipase action. **(a)** Measured SAXS data (filled gray squares) and the model-dependent IFT fit for lamellar structures (solid line). **(b)** The resulting  $p_t(r)$  for lamellar structures (solid line) and the fit calculated by deconvolution square root operation (dashed line), and **(c)** the corresponding  $\rho_t(r)$ , of the half bilayer, showing negative electron density for the carbon chains and positive electron density for hydrated head groups. The half bilayer thickness is 2.6 nm.



**Figure SI-2:** Model-dependent IFT fitting of the low  $q$ -part of the SAXS data presented in Figure SI-1 presented in a log-log plot: (a) Fit for lamellar structure (e.g. vesicles or bicelles), and (b) the attempt to fit the measured data with a model for cylinder cross-sections. The filled gray squares are the measured data points while the solid lines are the calculated model-dependent fittings.