

crystalline state towards smaller concentrations as compared to the MA case. At some concentration of SA/MA a partial aggregation (regions with liquid crystals of acid molecules in the solution) is observed as a deviation of the scattering curves from the Guinier law at the smallest  $q$ -values. As the concentration increases, the SANS signal from these aggregates becomes rather distinguishable, and the corresponding characteristic size can be roughly estimated from an additional Guinier-type term as  $\sim 10$  nm. The further increase in SA/MA concentration leads to the alignment of these aggregates (transition to a smectic phase), which is reflected in the appearance of the diffraction peak at  $q \sim 2 \text{ nm}^{-1}$  (corresponding correlation length  $\sim 3.2$  nm). The position of the peak shifts to higher  $q$ -values (smaller distance between aggregates) with an increase in the acid concentration. The possibilities of the wide-angle diffraction for the study of the observed liquid crystalline phase in solutions of linear molecules with comparatively short alkane chains are considered.

The formation of the found LC-phase in bulk solutions of mono-carboxylic acids is an important factor, which influences the stabilization efficiency of the studied acids in colloidal solutions of magnetic nanoparticles.

[1] M.V. Avdeev, D. Bica, L. Vekas, V.L. Aksenov, A.V. Feoktystov, O. Marinica, L. Rosta, V.M. Garamus, R. Willumeit *J. Coll. Inter. Sci.* **2009**, *334*, 37-41. [2] V.I. Petrenko, M.V. Avdeev, L. Almasy, L.A. Bulavin, V.L. Aksenov, L. Rosta, V.M. Garamus *J. Col. Surf. A* **2009**, *337*, 91-95. [3] T. Shimada, M. Doi, K. Okano *J. Chem. Phys.* **1988**, *88*, 2815-2821.

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### Nanostructures in a supramolecular side-chain liquid crystalline block copolymer

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Hydrogen-bonding amphiphilic nonmesogen 4'-(3,4,5-trioctyloxybenzoyloxy)benzoic acid (TOB), of a wedge shape, is bound to P4VP block for supramolecular side-chain liquid crystalline blocks in polystyrene-*block*-poly(4-vinylpyridine) (PS-*b*-P4VP). We have demonstrated that rich phase transitions of hierarchical structures can be manipulated by adjusting the mesomorphic ordering of P4VP(TOB)<sub>x</sub> block via the TOB grafting fraction ratio,  $x$ , in the PS-*b*-P4VP(TOB)<sub>x</sub> thin films under solvent-casting and stretch-annealing treatments. Using synchrotron-based small- and wide- angle X-ray scattering and transmission electron microscopy (SAXS, WAXS and TEM), we observed global phase transitions of the PS-*b*-P4VP(TOB)<sub>x</sub> compound from lamellar (LAM), hexagonal-packed cylinder (HC), undulating hexagonal-packed cylinder (UHC), face-centered cubic sphere (FCC), to tetragonally perforated layer (TPL) structures, upon increasing the TOB content for an increasingly ordered mesomorphic phase of the hydrogen-bonded complex of P4VP(TOB)<sub>x</sub>, from nematic (N), smectic A (SmA), hexagonal columnar disordered (Col<sub>hd</sub>), to hexagonal columnar ordered (Col<sub>ho</sub>) phases. The mechanism of stretch-induced phase transition from FCC to TPL in the PS-*b*-P4VP(TOB)<sub>0.7</sub> thin film was also investigated by simultaneous SAXS and in-situ stretching mechanical measurement. When the SAXS patterns from the stretching film of PS-*b*-P4VP(TOB)<sub>0.7</sub> were examined, we found that the FCC spheres become oblate ellipsoids by the initial deformation and than merging of each oblate ellipsoids along  $\langle 110 \rangle$  direction of FCC form TPL mesophase by thermal annealing. The TPL, a kinetic trapped phase, is directed by strong local ordering columns of TOB with  $\pi$ - $\pi$  interactions at a sufficient grafting density. The FCC-to-TPL phase

transition is described for the first time in block copolymers.

[1] W.T. Chuang, H.S. Sheu, U.S. Jeng, H.H. Wu, P.D. Hong, J.J. Lee *Chem. Mater.* **2009**, *21*, 975-978.

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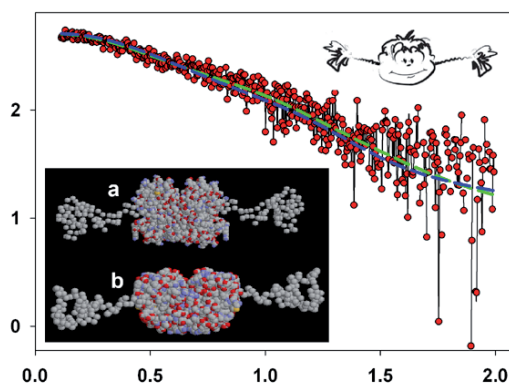
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### Virus matrix protein M1: SAXS data analysis and modeling

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Structural analysis of the influenza A virus full-length matrix M1 protein was performed using small-angle X-ray scattering (SAXS). The structure of the M1 protein macromolecules in solution was for the first time reconstructed using advanced methods of SAXS data analysis and interpretation [1-6]. The detailed analysis of the scattering data and modeling revealed a structurally polarized molecule with a compact NM-fragment and weakly ordered C-terminal domain. These structural peculiarities explain the ability of the matrix M1 protein to mediate the multistep process of cell infection due to flexibility of the C-terminal regions.



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### SAXS study of phase separation process in the SiO<sub>2</sub>-SnO<sub>2</sub> nanostructured materials

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