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 distinct, and the corresponding characteristic size can be roughly estimated from an additional Guinier-type term as ~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 ~ 2 nm\(^{-1}\) (corresponding correlation length ~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, “Institute of Crystallography of the Russian Academy of Sciences, Leninsky pr. 59, Moscow, 119333, (Russia), A.N. Belozersky Institute of Physico-Chemical biology, Moscow State University, Vorobiovy Gory, Build. ‘A’, Moscow, 119991, (Russia), EMBL, Hamburg Outstation, Notkestraße 85, D-22603 Hamburg, (Germany), E-mail: viwopixs@yahoo.co.uk

**Keywords:** SANS, surfactant solutions, liquid crystalline phase

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

E. V. Shtrykova, L. A. Baratova, D. I. Svergun, Institute of Crystallography of the Russian Academy of Sciences, Leninsky pr. 59, Moscow, 119333, (Russia), A.N. Belozersky Institute of Physico-Chemical biology, Moscow State University, Vorobiovy Gory, Build. ‘A’, Moscow, 119991, (Russia), EMBL, Hamburg Outstation, Notkestraße 85, D-22603 Hamburg, (Germany), E-mail: viwopixs@yahoo.co.uk

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.

**Keywords:** protein, modelling, structure

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**SAXS study of phase separation process in the SiO\(_2\)-SnO\(_2\) nanostructured materials**

René Guinebretière, Matthieu Dumoulin, Elsa Thune, Cyrille Rochas, ESPCT USMR CNRS 6638, ENSCI, Centre Européen de la Céramique, 12 rue Atlantis, 87068 Limoges, (France), CERMAV, Notkestraße 85, D-22603 Hamburg, (Germany), E-mail: viwopixs@yahoo.co.uk

SAXS study of phase separation process in the SiO\(_2\)-SnO\(_2\) nanostructured materials

Poster Sessions