**MS44-03** **Crystallization behaviors of protein molecules in high magnetic forces fields.** Nobutaka Numoto,[a] Akiko Kita,[a] [a]*Research Reactor Institute, Kyoto University, Japan*
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X-ray crystallography is one of the most powerful methods for structure determination of biological macromolecules, but researchers have to spend plenty of time for crystallization experiments. There are many biological, chemical, and physical factors that must be optimized to obtain high quality crystals. Gravity is one of such factors, which would affects in crystallization because it causes convection of solution due to a density gradient near the growing crystal. The convection would cause excess provision of solute molecules and prevent accurate arrangement in the crystals. To overcome the gravity-derived convection without using micro gravity environment in space, we have performed crystallization experiments in the magnetic levitation condition achieved by high magnetic forces fields (gradient magnetic fields) from a superconducting magnet system designed for the protein crystallization.

Crystals of several proteins grown in the high magnetic forces fields were obtained within 1-4 weeks. Compared to the reference experiments, crystals of some proteins appeared under higher concentration conditions of both protein and precipitant solutions in the high magnetic forces fields. In addition, there was a tendency that the crystals were obtained in the higher concentration conditions with the increase in the magnetic forces. These facts suggest that in the high magnetic forces fields that oppose the gravity, the convection in the crystallizing solution is suppressed and crystals grow primarily owing to simple diffusion. On the other hand, unit-cell dimensions are decreased for crystals of another protein. The crystal structure indicated that a loop region at the interface of inter molecules are slightly moved in the crystals obtained in the high magnetic forces fields, and this structural change enable the molecule to pack tighter than the crystals of the reference experiments. Finally, crystals of a membrane protein composed of a-helix structures appeared aligning parallel to the magnetic field direction. Self-rotation function of the obtained crystals revealed that the helix axis in the crystals aligned parallel to the magnetic field direction. This is the first observation for magnetic orientation for the crystals of a membrane protein, although it has been proposed that a-helix structure in a protein molecule exhibit some diamagnetic anisotropy and the crystals should orient parallel to the magnetic field. All above observations suggest significant possibilities to improve the quality of crystals grown in the high magnetic forces fields.

**Keywords: crystal growth; magnetic levitation; gravity**

**MS44-04** **Time-resolved Crystallization of Charged Colloidal Silica Spheres.** Wolfgang Hornfeck, Dieter Herlach, *Institut für Materialphysik im Weltraum, Deutsches Zentrum für Luft- und Raumfahrt (DLR), 51170 Köln, Germany*
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Aqueous suspensions of charged colloidal particles have proven to be suitable model systems for metals and alloys in order to study the solidification from their respective melts. A major advantage is due to the fact that the corresponding phenomena occur on spatio-temporal scales which are much more easier to influence and monitor from an experimental point of view.[1-3]

Previous research focused (inter alia) on the phase behaviour and nucleation kinetics of *single-component* samples.

Here we report on experiments particularly devoted to *binary mixtures* of charged colloidal silica spheres, studying their phase behaviour, nucleation kinetics, short-range order, as well as possible compound formation and/or phase transformations.

For this purpose a set of distinct samples were investigated, consisting of a mono- and polydisperse reference and binary mixtures of large and small monodisperse particles (ratio of diameters $d_L$:$d_S$ ~ 2) of varying composition.

The measurements mainly involved time-resolved ultra-small-angle X-ray scattering (USAXS) experiments at the beamline BW4 at HASYLAB/DESY, Hamburg as well as time-resolved in-house Bragg-microscopy. Both methods were used in order to determine the phase behaviour and nucleation kinetics for homo- and heterogeneously nucleated colloidal crystals.

Control parameters were given by the particle number density and the amount of base (NaOH) added to the suspensions.

Preliminary results show a sensitive dependance of the nucleation kinetics, regarding crystal growth and size, on the composition as well as a re-entrant crystallization behaviour while steadily increasing the relative amount of large particles in a suspension of smaller ones.

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**Keywords: USAXS; time-resolved diffraction; colloids**