Experimental report

Proposal:	8-04-7	60	Council: 4/2015				
Title:	Real ti	eal time study of protein dynamics during a one-step and a two-step crystallization process					
Research area: Biology							
This proposal is a continuation of 8-05-420							
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Samples: Bovine Beta-Lactoglobulin, ZnCl2, CdCl2, D2O							
Instrument			Requested days	Allocated days	From	То	
IN11			4	5	29/10/2015	03/11/2015	
IN16B			2	2	25/06/2015	27/06/2015	
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Protein crystallization is of great interest due to its crucial role for the determination of protein structures, as well as in other fields such as drug engineering by pharmaceutical industries [J. Gunton et al. Protein Condensation: Kinetic Pathways to Crystallization and Disease. CUP, (2007)]. Despite its importance, a fundamental understanding of the mechanisms underlying such a process is still missing. Recently, both experimental [F. Zhang et al. Journal of Applied Crystallography 44, (2011); A.Sauter et al., J.Am.Chem.Soc. 137, 1485 (2015)] and theoretical [P. G. Vekilov, Nanoscale 2, (2010)] studies have shown that, under certain conditions, crystallization follows a multi-step mechanism, rather than the classical nucleation pathway. In order to gain a better understanding of such processes, an in situ study of the dynamics of two suitable crystallizing systems by QENS at IN16B and IN11 may provide new extremely useful information, thus potentially significantly improving the general physical picture. This proposal continues the IN16B work and adds IN11 to measure on and off the correlation peak found in SANS.

Real-time study of protein dynamics during a one-step and a two-step crystallization process

experiment 8-04-760 on IN16B and IN11

experimentlists M.Grimaldo, F.Roosen-Runge, C.Beck, B.Sohmen, M.Braun, O.Czakkel, T.Seydel; co-proposers A.Sauter, F.Zhang, F.Schreiber; ILL and University of Tübingen



Solutions of bovine β -lactoglobulin (BLG) proteins in D₂O with added ZnCl₂ salt were investigated on both IN11 and IN16B. The investigated samples slowly crystallized on time scales of several hours to days during the experiment, as became apparent by visual inspection of the samples at the start and at the end of each measurement (figure 1).

The IN16B data were described by the scattering function *S* depending on the scattering vector q and energy transfer ω ,

$$S(q,\omega) = \beta \{ L_{\gamma}(\omega) \otimes [A_0 \delta(\omega) + (1 - A_0) L_{\Gamma}(\omega)] \} , \qquad (1)$$

where $\delta(\omega)$ and $L_{\Gamma}(\omega)$ denote, respectively, the Dirac function and Lorentzian linewidth due to the elastic scattering and internal relaxations of the proteins and $A_0=A_0(q)$ the elastic incoherent structure factor. These internal motions are convoluted with the global center-of-mass diffusion of the proteins associated with a Lorentzian with the linewidth γ .

When fitting the model in equation (1) to the IN16B data, a clear time-dependence of the linewidth γ associated with the global diffusion of the proteins becomes apparent (figure 2). This trend indicates a slowing-down of the protein diffusion with time. The observed trend is consistent with a slow crystallization process on a time scale of several hours and an associated immobilization of the global motion of the proteins. The deviation of the q-dependence of the width γ from simple Brownian diffusion indicates a confined or jump-like behavior at already at an early stage of the process.

A similar trend of an *in situ* crystallization was observed during the IN11 experiment with a timeand *q*-dependent change in the intermediate scattering function (figure 3 and 4).

