Experimental report

20/01/2017

Proposal: TEST-2593 **Council:** 4/2016

Title: Dynamics of Unfolded Bovine serum albumin

Research area:

This proposal is a new proposal

Main proposer: Felix AMESEDER

Experimental team: Andreas STADLER
Felix AMESEDER

Local contacts: Peter FALUS

Samples: protein (Bovine Serum Albumin) in 4M and 6M GndDCl D2O ((CHNO)x, CD6CN3)

Instrument	Requested days	Allocated days	From	To
IN15	5	5	27/06/2016	02/07/2016

Abstract:

The secondary structure of proteins is shaped by the presence of covalent sulfur bonds cross-linking distinct domains. Here, we investigate the influence of sulfur bonds on the internal dynamics of the denatured Bovine Serum Albumin BSA protein. Naturally with more degrees of freedom we expect an increase of dynamics when no sulfur bonds are present.

We measured two BSA samples 30mg/ml in D20 buffer solution (50mMol H3PO4) with 6M Guanidine Hydrochloride GndHCl and 150mMol beta-Mercaptoethanol as additional solvents, and two respective buffer solutions alike.

The q-range was 0,0287 to 0,179 $Å^{-1}$. The neutron wavelength used were 10, 8, and 6 Å and Fourier times up 200ns were measured. The temperature was set at 22°C.

The dynamics structure factor DSF S(q,t)/S(q,t=0) of the first q values for the two protein samples is shown below. Solid circles represent the DSF of the sample A with **active** sulfur bonds, hollow squares represent the DSF of the sample B with **no active** sulfur bonds, later one is decaying faster at longer Fourier times indicating the presence of additional internal dynamics as expected.
Straight lines are fits with a diffusion model for each single q. Respective effective diffusion coefficients are displayed (black symbols for sample A, red symblos for sample B). The fit with a stretched exponential model $e^{(\Gamma * t)^b}$ for each q of sample B gives values for the stretching exponent b close to 0.85, which is characteristic for ZIMM like dynamics.