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Dynamics of Partially Folded and Unfolded Proteins Investigated with Quasielastic Neutron Scattering

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Protein folding is a fundamental process in molecular biology. Apomyoglobin (apo-Mb) –myoglobin without the heme group –is less stable than Mb and can be trapped in different folded, partially folded molten globules and unfolded states under equilibrium conditions depending on the chosen solvent conditions. I will present an investigation on the dynamics of the protein in its different folded states by quasielastic neutron backscattering (IN16, IRIS) and time-of-flight (IN5, IN6) spectroscopy [1,2]. The samples have been measured in the solution state to allow for solvent induced effects and to enable reversible thermodynamic properties. Global protein diffusion and internal macromolecular dynamics could be separated from the recorded spectra. Detailed insight into the properties of the internal dynamics of the different folded states of the protein was obtained. Our results point out the relevance of protein dynamics for stability and folding of Mb.

1. Stadler, Koza, Fitter; Determination of Conformational Entropy of Fully and Partially Folded Conformations of Holo- and Apomyoglobin; *Journal of Physical Chemistry B*, 119, 72-82 (2015)
2. Stadler, Demmel, Ollivier, Seydel; Picosecond to Nanosecond Dynamics Provide a Source of Conformational Entropy for Protein Folding; submitted

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