Some major achievements of the Doster group (Bioneutron Scattering)

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Many neutron scattering experiments of proteins, were first performed by the Munich bioneutron group. In the list I omit the word "first", which could be nearly always added.

1986: low temperature study of the glass transition of protein hydration water by IR spectroscopy and calorimetry. First assignment of anharmonic onsets of displacements (Mössbauer) to the cross-over of two time scales: water relaxation time and instrumental observation time. Emphasis on the role of protein-water hydrogen bonds: O-H stretching vibration for frozen in conformational substates. Lit. (Doster et al. Biophys.J. 50, 213, 1986).

1988-1989: First wide temperature-, wide frequency-, wide Q- range inelastic neutron scattering study of globular proteins (myoglobin, lysozyme, dry hydrated).

a) Definition of the **Protein Dynamical Transition** as a two-step feature: onset of fast H-bond fluctuations above T_g and slow protein-water structural relaxation with onset depending on the instrumental time window
b) analysis of the elastic scattering function of a protein in terms of rotational transition of side chains and Gaussian protein-water librational displacements. (Lit. Doster et al. Nature 1989).

1990: Analysis of the vibrational density of states including multiple scattering corrections with S. Cusack, definition of the protein Boson peak and its relation to fractal behavior.

Comparison of experimental DOS with MD simulations of myoglobin with M. Karplus and J. Smith.

Susceptibility analysis of protein spectra, Mode Coupling approach of the liquid-glass transition to hydrated protein spectra (Doster et al. PRL 1990)

1992: Spectral Analysis and the elastic scattering function of alanine peptide and MD simulations (with Smith Kneller)

Dynamic neutron scattering experiments with hydrated tRNa in comparison with simulations. "Dynamics of tRNA: Experimental Neutron Spectra Compared with a Normal Mode Analysis F. Nardi, W. Doster, B. Tidor, M. Karplus, S. Cusack,J.C. Smith" Lit. Isr. J. Chem. (1994) 34,233

1995: Solvent Effects on internal dynamics of proteins, dry/hydrated (Lit. Protein Solvent Interactions Ed. Gregory

1996: Time-Resolved displacements of protein hydration water with M. Settles, model independent moment analysis of neutron spectra. (Lit. Faraday Disc. 103), Iterative calculation of the protein vibrational density of states from incoheren neutron scattering data with account of double scattering, with M. Settles.

1997: water coupled low frequency modes of proteins, hydration dependent Boson peak, structure independence of the Boson peak (Diehl et al. Bioph J. 73) and Vibrational frequency shifts as a probe of protein-water hydrogen bonds (with F. Demmel) EBJ 26, 327

1999: heme-solvent coupling, a Mössbauer study with H. Lichtenegger and G. Vogel. Anharmonic onset varies with viscosity and molecular time scale (BJ 76,414)

Boson peak oscillations and far infrared emission (with H. Leyser) PRL 82, 2987.

2000: Time resolved mean square displacements in proteins, first assignment of one dynamic component to methyl group rotation. Abstract. Eur.Biophys. Conf. in Munich:

12H-3
TIME-RESOLVED MEAN SQUARE DISPLACEMENTS OF PROTEIN – WATER HYDROGENS

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The potential of inelastic neutron scattering to explore structural fluctuations and hydration dynamics of proteins and its relation to computer simulations is discussed. The method probes the single particle motions of the nonexchangeable hydrogens. The exchangeable hydrogens can be masked by deuterium which exhibits a much lower scattering cross-section. Dihedral torsional transitions, rotational jumps of side-chain methyl groups and water-plasticized collective displacements comprise the most important contributions to the fluctuation spectrum of myoglobin and other proteins. The assignment is based on the elastic scattering function, reflecting the spatial distribution of accessible states. Temperature-dependent studies of hydrated proteins reveal a dynamical transition, connected with the onset of collective motions. The transition is triggered by fast fluctuations of protein-water hydrogen bonds, which can be suppressed by dehydration or vitrification in a glassy matrix. Using a moment analysis of the density correlation function we obtain time-resolved mean square displacements of protein and hydration water hydrogens.

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2001: Elastic Resolution Spectroscopy of Proteins, with M. Diehl how to derive dynamic information from elastic scattering functions, varying the instrumental resolution, Physica B 301, 56.
2002 First neutron scattering **high pressure study** of a protein and hydration water across pressure denaturation, with R. Gehardt.
Neutron spin echo studies of crowded protein solutions (with S. Longeville)

2003 Extended TOF analysis of "Elastic Resolution Spectroscopy" with R. Lechner Chem.Phys. 292, 383

2004 Moment Analysis of Protein-Water Dynamics
in: Neutrons in Biology, Springer Verlag (2004) Ed. R. Gutberlet

2005 Protein-water displacement distributions with M. Settles, profound theoretical and experimental analysis of protein dynamics using neutron scattering: moment analysis of protein spectra, time resolved displacements, first detailed account of methyl group rotation,

multi-component displacements derived from dynamic analysis. Demonstration, that methyl group rotational transition in proteins are independent of the protein environment, hydrated, dry, glassy (BBA 2005).

2008: Concepts and Misconceptions of the protein dynamical transition, EBJ 37,591. Static displacements are derived from dynamics, discussion of various models of the protein dynamical transition using two state models (Eur.Biophys.J. 37,591)

First comparison of protein dynamics with different structures:
Dynamics of well folded and natively disordered proteins in solution a TOF study with Gaspar et al. Eur. Biophys. J. 37, 573. It is shown that the neutron scattering spectra of hydrated proteins of different structure are nearly identical, but differ significantly in solution.

2010: Protein-Solvent Glass Transition (Review) Doster BBA 1804, 3 (2010).

First polarisation analysis of dry and hydrated protein spectra, separation of coherent and incoherent scattering with A. Gaspar, Bioch. Biophys. Act. (2010) 1804, 76.

Disprove of the Fragile-Strong Cross-Over model of Chen et al. with backscattering of hydrated, perdeuterated CPC, effect of resolution, with J. Wuttke, PRL (2010) 104, 198101

2011: Two step scenario of the protein dynamical transition, new analysis of elastic scattering data, first demonstration of a pre-transition with hydration water, (J.Noncryst. Sol. (2011), 357, 622.

2012: Review: Protein Dynamics and Function: Model of Protein Dynamics based on neutron scattering data, with S. Longeville ch. 8 in Dynamics of Soft Matter, Neutron Applications, Springer 2012.

2013: Scaling Analysis of biomolecular motions from elastic incoherent neutron scattering, with M.S. Appavou and H. Nakagawa, J. Chem. Phys.(2013) 139, 45105
First detailed investigation of elastic neutron scattering of biomolecular dynamics.

2018: A new principle component model of protein dynamics is proposed: methyl group rotation combined with local residue displacements supported by water. The model unifies elastic and inelastic scattering and accounts even for multiple scattering. Experiments are displayed in the time domain, covering a huge Q-range.
W. Doster, Are proteins dynamically heterogeneous? Int. J. Mol. Theo. Phys.2(1): 1-14, 2018, open access