Bulk-solvent and hydration shell fluctuation, similar to α- and β- fluctuations in glasses, control protein motions and function by Fenimore et al. PNAS 101 (2004)

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This heavily referenced, not peer reviewed paper is probably rarely read or even understood, it contains already several errors in the title:

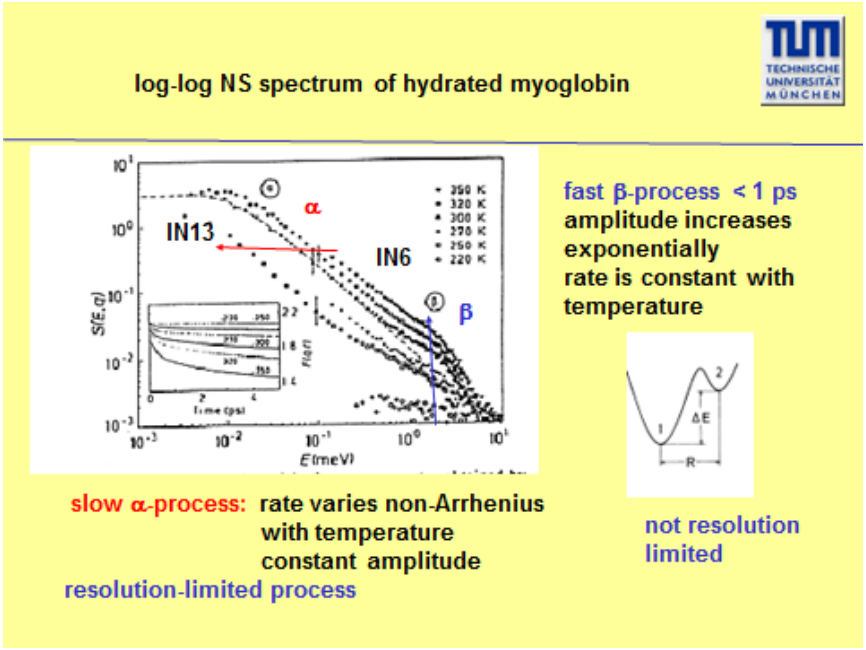
(1) There are no α-fluctuations in glasses, the glassy state is defined by the absence of structural relaxation.

(2) Proteins are not glasses, proteins are equilibrium structures, which is a dogma of molecular biology. The multiminima model of proteins does not allow to classify them as glasses.

(3) The paper does not justify the postulates made in the title. In fact internal motions of the discussed proteins persist even in the absence of bulk and hydration water. The definitions are not precise: especially the Frauenfelder β-relaxation is obscure, it is assigned because of an activation energy falling into the common range of 35 kJ/mol.

(4) Quite arbitrary, solvent fluctuations are split into statistically independent sets of bulk fluctuations (α) and fluctuations of hydration water (β). Numerous experiments have shown that there is a gradual transition from water near the protein surface to the bulk phase.

(5) The terms α- and β-relaxation were already assigned to protein spectral components by us in Doster et al. (Nature, 1989). The goal of Frauenfelder's paper is clearly meant as an attack on our concept, yet our work is not even cited in this context. There is no discussion at all just ignorance. The reader gets the impression, that Frauenfelder is pulling everything out of his own sleeve for the first time.



Doster et al. 1989 Nature see Comment.

6) Frauenfelder is by training a nuclear scientist, he never did experiments on fast dynamics, let alone neutron scattering experiments. Still he wants to control "slave" the field of bio-neutron scattering. He is a master of catch words and of simple concepts. This works since few people in this field can discriminate α- from β-relaxation or even know what they mean. Usually the term α-relaxation is assigned to the viscosity related structural relaxation, the loss of memory of the liquid, it establishes thermal equilibrium. On a short time scale the liquid will thus exhibit the properties of a glass. On a microscopic scale, the α-process denotes the elementary process of translational diffusion. It thus implies long-range transport. β-relaxation by contrast implies a localized molecular process, which can act as a precursor of the α-process. In modern liquid dynamics one views the molecule surrounded by a cage of nearest neighbors. Intra-cage motion would thus classify as β, while escape out of the cage would be the α-relaxation. As a function of temperature the fast β-process reacts with increasing amplitude of the in-cage motion, while the time constant remains constant. The α-process by contrast has a constant amplitude, but the time constant changes super-exponentially with the temperature, the signature of collective (viscosity) motion. In our protein spectra we identified such processes coupled to hydration water and thus we chose these terms. The "dynamical transition" is not a catch word, but has a precise physical meaning related to the glass transition of hydration water, observed on a short time scale. Frauenfelder's concept is completely detached from condensed matter theory: Hydration shell: β, bulk phase α. In this paper it is never demonstrated that large scale protein fluctuations couple to the bulk viscosity, neither it is shown that the hydration shell is completely detached from the solvent viscosity. In fact there are numerous experiments (see also the comment on slaving 2002) and simulations demonstrating that hydration water can perform long range diffusion and that the surface viscosity exists, which can be different from the bulk (see comments on Confined Water and Slaving 2).

/) Hydration shell fluctuations do not control internal motions, the latter persist in the dehydrated state, Doster/Settles BBA 2005. Ligand escape from myoglobin is observed even with the hydrated protein in the absence of bulk water. Internal ligand transfer occurs in dry myoglobin. Doster BBA(2010). The Frauenfelder model is inconsistent with experiment.

8) The model used (equ.3) is too primitive to yield proper results, no worker in the Mössbauer field could publish such stuff without running the risk to ruin his reputation:

"We assume that only a fraction ε in the hydration shell cause the iron to move so that the observed fluctuations are given by:

$$k_c(T) = \varepsilon\, k_\beta(T)$$

Equ. 3 then gives for the MSD seen by the iron atom:

$$\langle x^2(T)\rangle = \varepsilon\, k_\beta/k_m\, s^2$$

By some hand-waving arguments on s, he derives: ε = 0.002, which implies that the solvent fluctuation rate k_β is 500 time faster than the structural relaxation rate of the heme. In 1999 Lichtenegger et al. Biophys. J. 76, 414 had shown that ε ≅ 1, never cited by Frauenfelder.

This new view of the “dynamical transition” as a cross-over of two time scales, originally proposed by Doster BJ (1986) and Doster et al. Nature (1989), is a complete revision of Frauenfelders original landscape detrapping model of the Mössbauer effect. But this revision is not openly discussed. Instead Frauenfelder sells the dynamic cross-over model as his own idea (see Comment to Puzzle of the PDT).