

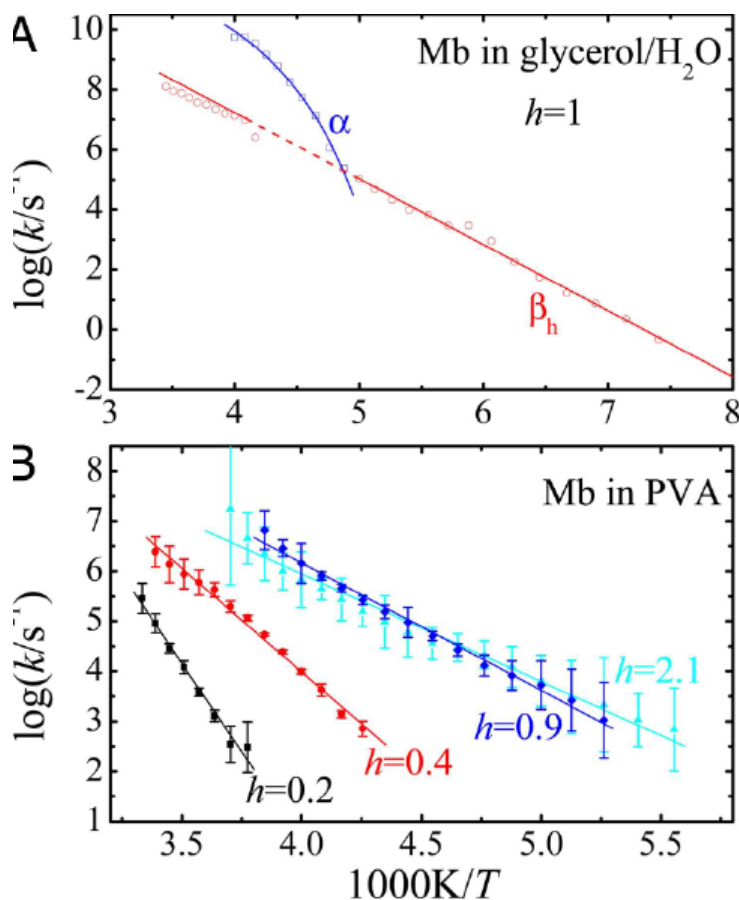
## A unified model of protein dynamics

### H. Frauenfelder, Swenson et al. PNAS 2008

This paper is based on the dielectric relaxation work of Swenson on myoglobin in various solvents.

Their unified model is based on distinguishing between two processes the alpha relaxation of bulk water and the beta relaxation of protein hydration water.

The latter is independent of the solvent viscosity (see figure, A) . In our previous work we have identified an alpha relaxation in the protein hydration water phase, different from bulk water. The discrepancy is resolved by the work of Lunkenheimer and Loidl, who show, that the so- called alpha relaxation reflect the protein rotation and is termed beta relaxation. See below. The relaxation processes all depend on the solvent viscosity. A Frauenfelder-Swenson beta-relaxation thus does not exist.



Relaxation dynamics of a protein solution investigate by dielectric spectroscopy

Fig.1.Schematic view of the dielectric loss spectrum of a typical protein solution close to room temperature(circles).The shaded areas show the contributions of the  $\beta$ -, $\delta$ -,and  $\gamma$ -relaxations,which arise from reorientational motion of the proteins molecules (beta), and bound and free water molecules delta, gamma).

