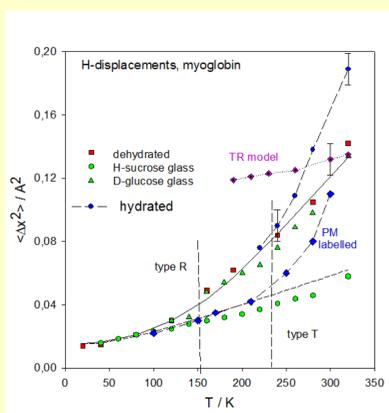


A new rotation-translation model of hydrated protein dynamics, combining elastic, time domain and multiple neutron scattering

Beyond phenomenological energy landscape models, we propose a two component analytical model of the neutron intermediate scattering function of dry and hydrated proteins: **rotational transitions of side chains** (methyl groups) and **local translational diffusion of non-methyl residues**. Spectra of three spectrometers with overlapping range are Fourier transformed to the time domain based on an exceptionally wide time and Q-range.

Elastic scattering: two dynamical transitions, R (rot) and T:



Results for various solvents:

Hydrated: two transitions R (180 K) and T (240 K)

Dehydrated: a single transition R (180 K)

D-vitrified: a single transition R (180 K)

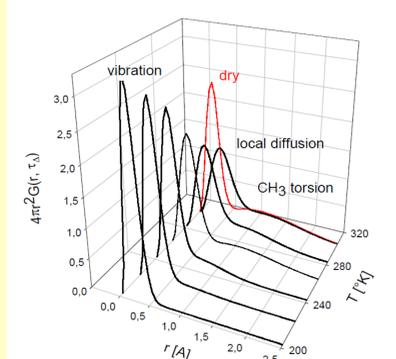
H-vitrified: no transition, only elastic glassy matrix

Deuterated methyl groups: single transition: T 240 K

Data corrected for resolution: TR model: no transition

Two solvent dependent components R, T

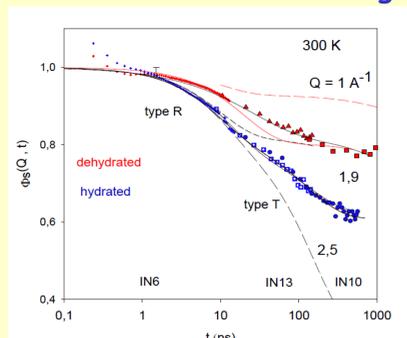
Displacement Distribution versus T at 50 ps (D-hyd myoglobin)



Three elastic components: Vib, Trans, Rot

- 1) vibrations, below 180 K
- 2) local translational diffusion requires hydration >200 K
- 3) CH₃-torsion also in the dehydrated state

Intermediate Scattering function of dry/hydrated protein

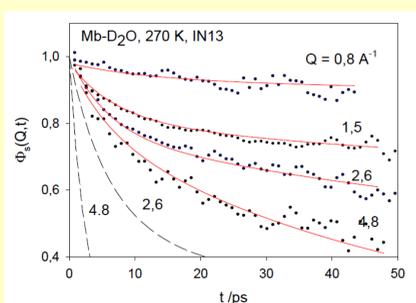


$\Phi_s(Q, t)$

at 300 K and $Q = 1,9 \text{ Å}^{-1}$
 R-T model fits versus Q:
 Methyl rotation is exponential in the hydrated state, but becomes distributed upon dehydration, while the T-component disappears

Time domain back-scattering $\Phi_s(Q, t)$: much wider Q-range than ever published before

RT model fits work remarkably well



Rotation-Translation Model

$$\Phi_s(Q, t) = \sigma_R \cdot \Phi_R(Q, t) + (1 - \sigma_R) \cdot \Phi_T(Q, t)$$

σ_R denotes the fractional cross section of the type R sites.

$$\Phi_R(Q, t) = \frac{1}{3} \{ 1 + 2j_0(Q) + 2 \cdot (1 - j_0(Q)) \cdot \exp(-t/\tau_{rot}) \}$$

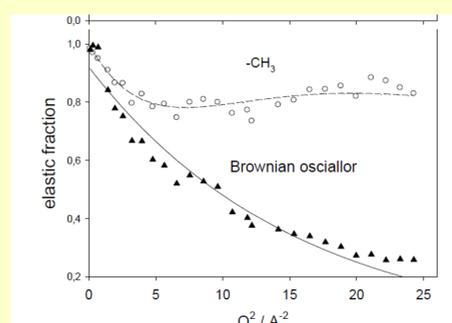
$$j_0(Q) = \sin(Q\sqrt{3} \cdot r) / (Q\sqrt{3} \cdot r)$$

Side chain torsion

$$\Phi_T(Q, t) = \exp\{-Q^2 \delta^2 \cdot (1 - \exp(-t/\tau_{trans}))\}$$

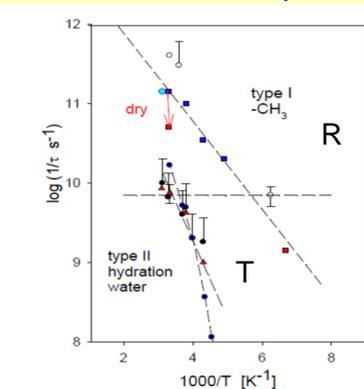
Brownian oscillator (6)

$\delta^2 = \langle \Delta x^2 \rangle$ denotes the translational mean square displacement of local diffusion



EISF(Q) of R-T Model components data and simulation

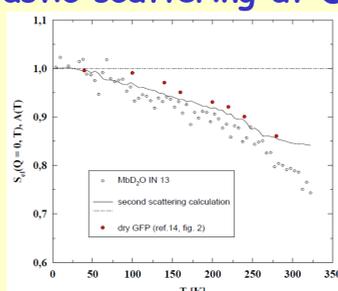
Arrhenius Analysis of R-T Model



Type R: coincides with methyl rotational transitions

Type T: coincides with hydration water relaxation times of NMR and n-scattering

Elastic scattering at $Q = 0$ decreases with temperature $S_{el}(Q=0, T)$: Multiple scattering



our MS calculations (second scattering) compare well with IN13 data and the Frauenfelder analysis (GFP, PNAS 2017)

MS explains the anomaly attributed erroneously to energy landscapes

- Conclusions:**
- 1) The R-T model unifies the description of elastic and inelastic neutron scattering spectra of solvated proteins, covering a wide range in time and momentum exchange. Accounting for resolution effects the „dynamical transition“ disappears. This result demonstrates the validity of scattering theory even for complex systems like proteins.
 - 2) Heterogeneity does not play a dominant role in neutron spectra of proteins, two slightly distributed components cover the full parameter range.

Reference : Doster W, Int J Mol Theor Phys. (2018) 2(1):1-14.