

Supplementary Information

Painting Biological Low-Frequency Vibrational Modes: from Small Peptides to Proteins

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1)-Additional details on MD simulations

MD simulations

Molecular dynamics (MD) simulations have been performed on NALMA powders, using the COMPASS27 force field and the FORCITE module inside the Materials Studio Modelling Environment (v. 5.0) from Accelrys, Inc.¹. This model has recently been shown to reproduce many of the structural and dynamical properties of a wide variety of small inorganic and organic molecules, including amides²⁻³. The peptide structure was initialized using atomic positions reported in crystallographic studies⁴. Seven water molecules were gradually added and the optimized geometry of the single unit peptide:H₂O was calculated. Then an amorphous packing of these peptide units was constructed using the Theodorou/Suter method as implemented in the Amorphous-Cell module, employing 72 peptide molecules in cubic boxes. We explored two hydration levels, h=0 (72 NALMA molecules) and h=0.68 by weight (72 NALMA molecules / 504 water molecules). The h=0.68 hydration level corresponds to a ratio NALMA/water molecules 1 to 7 and represents a single full hydration layer around the peptide⁵. The density values used in the MD simulations were 1.11667 and 1.08711 g/cm³ for the dry and the hydrated system, respectively. The density of the hydrated sample was extrapolated with a polynomial form, given the values of the neat peptide⁴ and those of concentrated aqueous solutions⁶. Before performing MD simulations the geometry of the cubic boxes was optimized. We investigated temperatures between 50–298K. The initial systems were equilibrated in the NVT ensemble for 260 ps

(employing a time step of 1.0 fs), using Berendsen's thermostat with a relaxation time constant of 1.0 ps and fixing the Cartesian positions of the central carbon atom C_α . After the removal of this constraint, production runs of 1 ns duration were carried out in the NVT ensemble using again Berendsen's thermostat with a relaxation time constant of 1.0 ps. The time step chosen to integrate the equations of motions was 0.5 fs. Three-dimensional cubic periodic boundary conditions were applied. Electrostatic and van der Waals interactions were evaluated using the standard Ewald summation method (with a cutoff radius $R=10$ Å). Additional simulations of 50 ps (time step of 0.5 fs) at the same conditions have been performed to calculate VDOS. The program package nMOLDYN⁷ (v.3.0.9) was used for the analysis of VDOS. nMOLDYN calculates the power spectrum of the velocity autocorrelation function (VACF), which in case of the mass-weighted VACF defines the phonon discrete VDOS, summed over all α atoms, defined as:

$$VDOS(n\Delta\nu) = \sum_{\alpha} \omega_{\alpha} C_{VV;\alpha\alpha}(n\Delta\nu), \quad n = 0 \dots N_t - 1 \quad (5)$$

where N_t is the total number of time steps and $\Delta\nu = 1/(2N_t\Delta t)$ is the frequency step. $VDOS(n\Delta\nu)$ is smoothed by applying a Gaussian window in the time domain⁸. In the time domain the width is $\sigma_t = \alpha/T$ where T is the length of the simulation. We note that the diffusion constant obtained from VDOS is biased due to the spectral smoothing procedure, since the VACF is weighted by the window Gaussian function. nMOLDYN computes the density of states starting from both atomic velocities and atomic coordinates. In this way the velocities are computed by numerical differentiation of the coordinate trajectories, correcting first for possible jumps due to periodic boundary conditions.

2) Static structure factor of NALMA

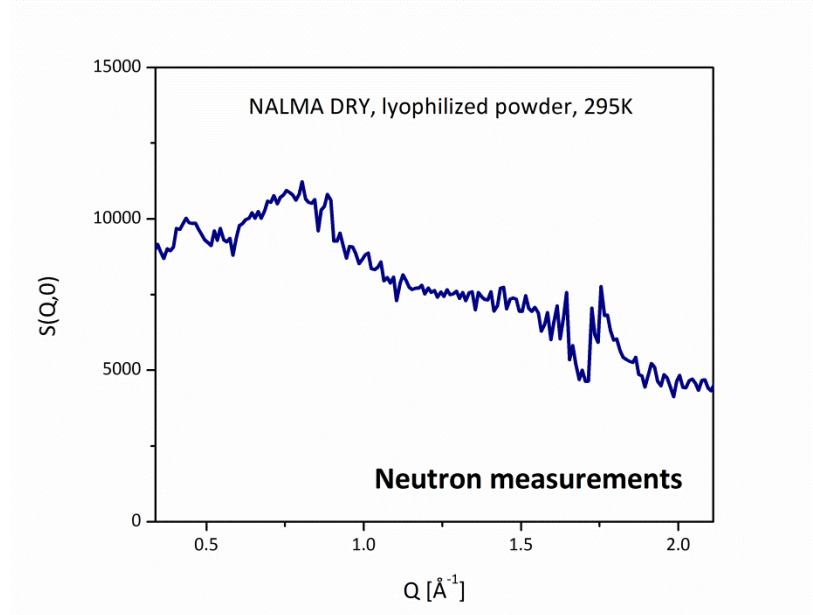


Figure S1 Static structure factor of NALMA obtained from our measurements on CNCS spectrometer. The absence of sharp Bragg peaks indicates that the sample was an amorphous powder.

3) Integrated intensity of SF_{DLS} spectra of lysozyme

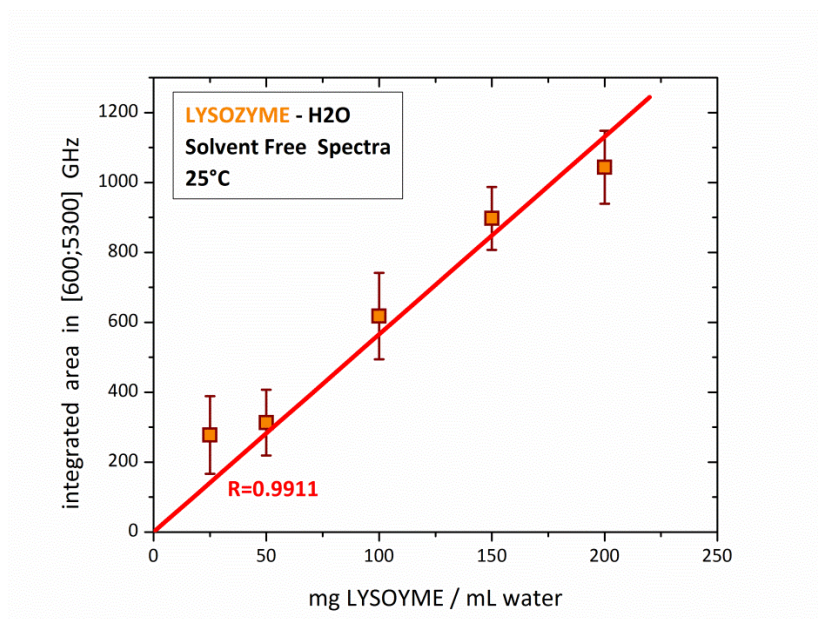


Figure S2 The integrated intensity of SF_{DLS} spectra between 600 and 5300 GHz linearly increases with solute concentration.

4)-Graphical summary of methyl groups' dynamics of hydrated NALMA powders from MD simulations

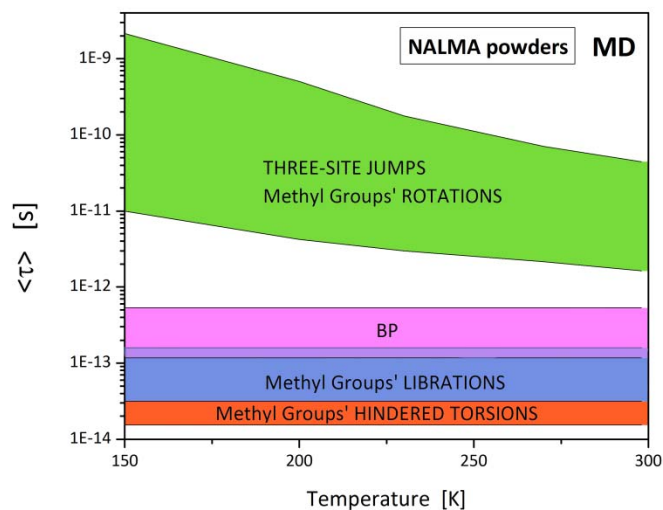


Figure S3 Schematic representation of methyl groups' dynamics of hydrated NALMA powders obtained from our MD simulations. The time scale relative to the BP, derived from our INS and DLS experiments on NALMA powders, is also shown. Three-site jumps rotations of NALMA methyl groups were described in ref. ⁹ Experimental information concerning diffusion-like motions of NALMA powders (not shown here) can be found in ref. ⁵.

NMR experiments have shown that the so called three-site jump methyl relaxations are due mainly to either the reorientational dynamics of the symmetry axis or rotation of C–H vectors about the symmetry axis¹⁰. Neutron scattering experiments^{5, 11-12} and MD simulations describe these dynamics as jump-like motions of a tagged methyl hydrogen around the methyl carbon from one site of probability density to another¹³. Neutron scattering experiments^{5, 11-12} and MD simulations describe these dynamics as jump-like motions of a tagged methyl hydrogen around the methyl carbon from one site of probability density to another¹³.

Supplementary References

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