Supplementary Information:

Secondary structure and rigidity in model proteins

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Table S1: Refractive index of proteins measured in our experiments. A comparison with literature values is also provided.

n	**dry**	**wet**	**literature**
GFP	1.473	1.475	1.34 -1.46[1]
LYS	1.472	1.484	1.48[2] 1.51[3] 1.538 – 1.575[4] 1.45[5]
BSA	1.480	1.487	1.582[6] 1.4[7]
MYO	1.478	1.483	1.549[6]
proteins			1.35-1.55[8] 1.45[5]

In agreement with terahertz (THz) time domain spectroscopy data reported for Cytocrome C samples[9] the refractive index of hydrated proteins is slightly higher than that of the dry system. The variation of *n* with temperature can be neglected[10, 11]

Table S2. Density values used to calculate the Young's modulus of hydrated samples. Variation of density of protein crystals as a function of hydration and temperature (literature data) used to calculate density of dry samples and the temperature dependence of ρ.

ρ	**ρ wet [g/cm^3]**	**% Δρ dry to wet**	**% Δρ T_r (room) to T_c (cryogenic)**
GFP	1.220	7.3%	T_r=300K, T_c=100K -4.5%[12]
LYS	1.227[13]	(298K) 7.3% [13]	T_r=298K, T_c=100K -1.8%[14]
BSA	1.170[15]	7.3%	T_r=300K, T_c=100K -1.8%[16]
MYO	0.976[17]	7.3%	T_r=277K, T_c=77K -2.9%[17]

Table S3 Poisson's ratio σ reported in literature for different proteins

protein	**technique**	**σ**
Tetragonal lysozyme	Brillouin spectroscopy	**0.33** as observed in many polymers[3, 18]
Tetragonal lysozyme	Ultrasonic pulse-echo	0.37[13]
Collagen	Brillouin spectroscopy	II 0.42 ; ⊥ 0.26[19]
lysozyme	Derived from X-Ray	0.25[20]
Tetragonal lysozyme	Ultrasonic pulse-echo	0.42[21]
Lysozyme, haemoglobin, myoglobin	ultrasound	0.47[22]

Table S4 Literature data at room temperature (~295K) for longitudinal sound velocity c_L and Young's modulus E of biological systems with different secondary structures. c_L or E values for dry and hydrated proteins are reported in separated columns. Data in each column refer to samples with comparable hydration levels. For the hydrated samples the hydration ratio h=g water/g protein (similar to our samples) is given in parenthesis.

protein	Secondary structure	technique	c_L ,[m/s]		Young's modulus E [GPa]	
			DRY	***HYDR.***	***DRY***	***HYDR.***
Bombyx mori silk (dry, in oil)	30% pleated β-sheet	Brillouin scattering	4700[19]		30.9[19]	
β-Keratin 28% from feather rachis (dry in oil)	β structure	Brillouin scattering	3710[19]		19.3[19]	
β-lactoglobulin	β barrel	X-ray scattering		2900 ±160 (h=0.5) 2860 ± 110[23] (h=1)		
Maltose Binding Protein (MBP)	α/β	Brillouin neutron scattering	3780 ± 130[24]			
Tetragonal lysozyme	α/β	Ultrasonic pulse-echo method	[110] ν1 3097 [001] ν4 3149[21]	ν1 2070 ± 34 ν4 2001 ± 33 [21] (h=0.47)	7.25[21]	3.21[21] (h=0.47)
Triclinic lysozyme	α/β	Resonance method			[011] 10 ± 1.1 [01$\bar{1}$] 11.2±1.3[25]	
monoclinic P2, lysozyme						[010] 2.5-3.5 [26] (h=0.3)
Ribonuclease crystal	α/β	Ultrasound		1784 ± 72[22] (h~0.5)		
α-Keratin 25% from Porcupine quill (dry in oil)	α-helix	Brillouin scattering	3660 [19]		18.8[19]	
Cytochrome C	α-helix	X-ray scattering	3458 ± 42 [27]			
Paramyosin from Molluscan catch muscle	supercoiled α-helix	Brillouin scattering	3530 [28]		17.4[28]	
Hemoglobin crystal	α-helix	Ultrasound[22] / Resonance method [25]		1828[22] (h~0.5)		[110] or [$\bar{1}$10] 5±1[25] (h=0.3)
myoglobin monoclinic	α-helix	Resonance method				[001] 3.6±1.3[25] (h=0.3)
Whale myoglobin amorphous films	α-helix	Resonance method				2-3.6[26] (h=0.3)

Morozov et al.[26] reported also measurements of E at low temperature for hydrated samples of amorphous whale myoglobin and cross-linked BSA amorphous films. Their results are in agreement with our estimates: at 150K MYO systems (E=7.8 GPa) are softer than the BSA (E=13.2 GPa) ones.

Table S5 Number of HBs per residue in the secondary structural units for MYO, BSA (helices) as well as for GFP (β-barrel)

	Number of residues in helices	**Total HBs in helices**	**Number of HBs/residues in helices**
BSA	450	375	0.83
MYO	123	102.5	0.83
	Number of residues in β-barrel	**Total HBs in β-barrel**	**Number of HBs/residues in β-barrel**
GFP	121	109 [29]	0.9

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