

Table 1 The divergence of the α A-crystallin genes of the human, hamster and blind mole rat relative to that of the mouse gene

	Exon 1	Intron 1	Insert exon
Human	94	47	86
Hamster	95	59	99
Mole rat	90	49	93

Divergence is shown by comparing nucleotide sequences for the coding region of the first exon, the IE and the intervening sequence between them. Values given for coding regions represent the percentage of positions at which the nucleotides are identical; values for intron sequences represent the percentage of matched residues after alignment by the NUCALN program²² using default values for all parameters.

accumulating changes at the same rate as pseudogenes (4.5×10^{-9} substitutions per site per year)¹⁷, we estimate that the human gene stopped using the IE some 30 to 40 million years ago. Interestingly, the human genome contains pseudogenes for two other lens proteins, both γ -crystallins with functional counterparts in rats¹⁸. This silencing of genes and an exon may have been triggered by similar environmental changes resulting in altered requirements for lens proteins.

The IE was acquired by an extremely well conserved, tissue-specific gene, either by exon shuffling or by the development of functional splicing signals within an intron. Its transformation into a pseudo-exon shows that part of a functional gene can be released from evolutionary pressures while the rest remains stringently conserved. This process may have occurred many

times in the evolutionary history of modern proteins, but is only rarely glimpsed now.

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Dynamical transition of myoglobin revealed by inelastic neutron scattering

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Structural fluctuations in proteins on the picosecond timescale have been studied in considerable detail by theoretical methods such as molecular dynamics simulation^{1,2}, but there exist very few experimental data with which to test the conclusions. We have used the technique of inelastic neutron scattering to investigate atomic motion in hydrated myoglobin over the temperature range 4-350 K and on the molecular dynamics timescale 0.1-100 ps. At temperatures below 180 K myoglobin behaves as a harmonic solid, with essentially only vibrational motion. Above 180 K there is a striking dynamic transition arising from the excitation of non-vibrational motion, which we interpret as corresponding to torsional jumps between states of different energy, with a mean energy asymmetry of 12 kJ mol⁻¹. This extra mobility is reflected in a strong temperature dependence of the mean-square atomic displacements, a phenomenon previously observed specifically for the heme iron by Mössbauer spectroscopy³⁻⁵, but on a much slower timescale (10⁻⁷ s). It also correlates with a glass-like transition in the hydration shell of myoglobin⁶ and with the temperature-dependence of ligand-binding rates at the heme iron, as monitored by flash photolysis⁷. In contrast, the crystal structure of myoglobin determined down to 80 K shows no significant structural transition⁸⁻¹⁰. The dynamical behaviour we find for myoglobin (and other

globular proteins) suggests a coupling of fast local motions to slower collective motions, which is a characteristic feature of other dense glass-forming systems.

Inelastic neutron scattering is a spectroscopic technique which can be used to study protein motions on exactly the same timescale (0.1-100 ps) as is now widely accessible by computer simulation¹¹. Because of the anomalously large incoherent neutron cross-section of the ¹H nucleus, the method specifically probes the motion of hydrogen atoms. As hydrogens are abundant and are uniformly distributed in proteins, the method gives a global view of protein dynamics. The quantity measured experimentally is the incoherent dynamic structure factor $S(q, \omega)$, where $\hbar q$ and $\hbar \omega$ are respectively the momentum and energy transfers between system and incident neutron. $S(q, \omega)$ is the Fourier transform of the time-correlation function of the density fluctuations in a system and can be directly calculated from the results of a molecular dynamics simulation. For samples of myoglobin hydrated with D₂O, we have measured as a function of temperature both the elastic intensity $S(q, \omega = 0)$, which gives information on the geometry of motions, and $S(q, \omega > 0)$, which gives the timescale (or spectrum) of the corresponding diffusive and vibrational motion^{12,13}.

Between 4 K and 180 K the elastic intensity of myoglobin has the gaussian form expected for a harmonic solid whose vibrational motion can be described by a Debye-Waller factor, that is, $S(q, \omega = 0) = \exp(-q^2 \langle \Delta x^2 \rangle)$, where the mean-square displacement (Δx^2) is proportional to temperature (except for quantum effects at very low temperatures). But near 200 K an extra decrease in the elastic intensity at low q is observed, indicating the excitation of new degrees of freedom. The geometry of these motions gives rise to a transition to a non-gaussian elastic intensity (Fig. 1). As the deviation from gaussian behaviour increases with temperature, we can conclude that the motion involves jumping of hydrogens to distinct sites of different energy. The simplest model accounting for these observations involves jumps between two sites separated by a distance d and free energy ΔG (Fig. 2). The powder-averaged normalized elastic

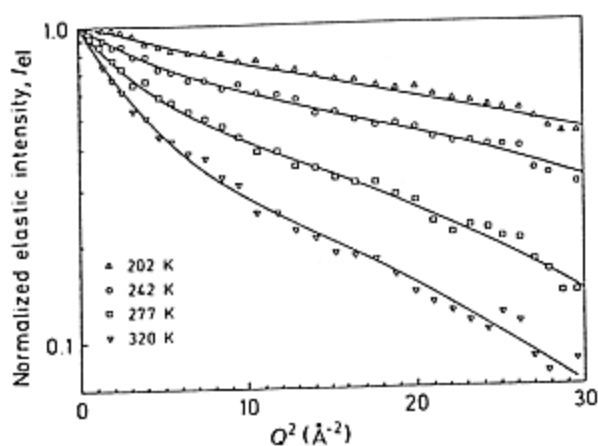


Fig. 1 The elastic intensity $I_e(q) = S(q, \omega = 0)$ was determined with a fixed window method at a resolution of $10 \mu\text{eV}$ (FWHM) using the backscattering spectrometer²⁶ IN13 at the Institut Laue-Langevin in Grenoble, France with an incident wavelength of 2.23 \AA . The sample was continuously heated from 4 K to 320 K over a period of 24 h. Raw data were corrected for cell scattering and detector response and normalized to unity at $q = 0$. The lines are fits to equation (1). The sample was $\sim 400 \text{ mg}$ sperm-whale myoglobin powder (Sigma) hydrated to $0.38 \text{ g D}_2\text{O}$ per g protein, at which level the protein is essentially fully hydrated. The D_2O contributes $\sim 5\%$ to the total scattering cross-section; the neutron spectrum is thus dominated by scattering from unexchanged protons in the protein (CH , CH_2 and CH_3 and a few inaccessible NH) which reflect internal and surface protein motions.

intensity is then given by¹⁴

$$S(q, 0) = e^{-q^2 \langle \Delta x^2 \rangle_G} \left\{ 1 - 2p_1 p_2 \left(1 - \frac{\sin(qd)}{qd} \right) \right\} \quad (1)$$

The first term describes the gaussian contribution to the mean-square displacement (below 180 K $\langle \Delta x^2 \rangle_G = \langle \Delta x^2 \rangle_{\text{vib}}$) and the term in brackets denotes the elastic incoherent structure factor of the two-state model. The variables p_1 and p_2 denote the probability of finding a hydrogen in the ground or excited state respectively, with $p_2/p_1 \propto \exp(-\Delta G/RT)$. The second factor contributes to the q -dependence of $S(q, 0)$ essentially only for $qd < 1$. The hydrogen mean-square displacement is given by

$$\begin{aligned} \langle \Delta x^2 \rangle &= - \left(\frac{d \ln(S(q, 0))}{d(q^2)} \right)_{q=0} \\ &= \langle \Delta x^2 \rangle_G + \frac{p_1 p_2 d^2}{3} \end{aligned} \quad (2)$$

which is the initial slope of the curves in Fig. 1. Least-squares fits of equation (1) to the data (Fig. 1) give $p_1 p_2$, $\langle \Delta x^2 \rangle_G$ and $\langle \Delta x^2 \rangle_G$ as a function of temperature (Fig. 2). A van't Hoff plot of p_2/p_1 gives an energy asymmetry of $\Delta H = 12(\pm 2) \text{ kJ mol}^{-1}$ and entropy $\Delta S/R = 3.0(\pm 0.1)$. The value of the jump distance d is found to be $1.5(\pm 0.1) \text{ \AA}$. The magnitude of this value would indicate the involvement of torsional degrees of freedom and large amplitude, fast dihedral angle fluctuations are indeed observed in molecular dynamics simulations of proteins¹⁵. As discussed more fully elsewhere, the parameters given above are dependent on hydration. In particular, the excess entropy of the excited state is significantly reduced on dehydration and the distance d drops to 1.1 \AA . Furthermore at low and intermediate levels of hydration, $\langle \Delta x^2 \rangle_G$ is dominated by the vibrational contribution $\langle \Delta x^2 \rangle_{\text{vib}}$, whereas in the high-hydration data presented here there is an additional gaussian process, $\langle \Delta x^2 \rangle_G = \langle \Delta x^2 \rangle_{\text{vib}} + \langle \Delta x^2 \rangle_a$. The resulting $\langle \Delta x^2 \rangle_a$ is also shown in Fig. 2.

The extra loss in elastic intensity is compensated by neutrons scattered into a broad quasielastic spectrum between 0 and 3 meV . To derive the actual shape of this spectrum requires a careful subtraction of the vibrational background (manuscript

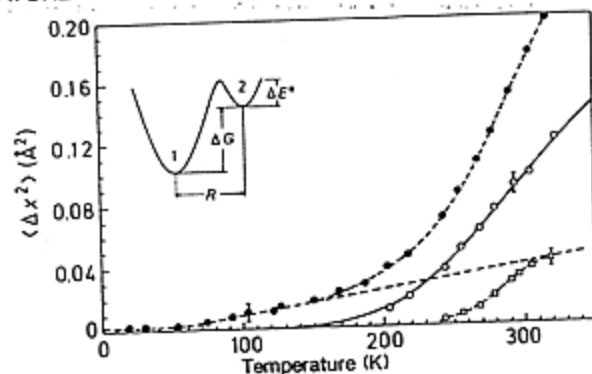


Fig. 2 Average mean-square hydrogen displacements obtained from the analysis of $I_e(q)$ assuming an asymmetric two-state model. The full circles give the total mean-square displacement $\langle \Delta x^2 \rangle$ defined by equation (2). The solid line shows $\langle \Delta x^2 \rangle_G = p_1 p_2 d^2/3$ obtained using the parameters in the text and the open circles give the corresponding experimental points. The squares show $\langle \Delta x^2 \rangle_a$ (see text). The dashed straight line is the vibrational contribution $\langle \Delta x^2 \rangle_{\text{vib}}$ extrapolated linearly from low temperature. A symmetrical model with two excited states may be more appropriate for torsional motion. Such a model does indeed fit the data equally well, but the derived parameters (apart from the entropy, which is lower) are not significantly different. Jump models with multiple ground states are excluded by the data. Quantum effects are important below 50 K , leading to a temperature-independent $\langle \Delta x^2 \rangle$ of $0.005 (\pm 0.005) \text{ \AA}^2$.

in preparation; see also ref. 16). In Fig. 3 we show the resultant quasielastic spectra combining data from two spectrometers with different energy resolutions and the inset shows the corresponding correlation functions. Two spectral components with different shape and temperature dependence can clearly be recognized, a fast β -process and a slower α -process. The increase with temperature of the intensity of the broad β -line is consistent with local jumps between two states of energy asymmetry of 12 kJ mol^{-1} . Surprisingly however, the linewidth is temperature-independent with a value of $1.5\text{--}2 \text{ meV}$ (corresponding to a correlation time of $\sim 0.3\text{--}0.5 \text{ ps}$, see inset to Fig. 3). Within the framework of the two-state model, this would imply that the activation energy ΔE^* , essentially the depth of the well in the excited state, is smaller than RT ($< 1.6 \text{ kJ mol}^{-1}$). Qualitatively similar behaviour of the quasielastic spectrum has been obtained with the polymeric glass polybutadiene¹⁷.

The linewidth of the α -relaxation by contrast broadens with increasing temperature. Below 240 K this component is not well resolved and therefore contributes to the elastic intensity. The gaussian mean-square displacement $\langle \Delta x^2 \rangle_a$ (Fig. 2) is related to this process. The shape of the α -relaxation is clearly not lorentzian but is reasonably well fitted by a Cole-Davidson function¹⁸ often used to parameterize the α -process in liquids and polymers:

$$S(q, \omega) = -A_1(q) \text{Im} \{ (1 + i\omega\tau_0)^{-b} \} / \omega \quad (3)$$

This formula implies a power-law dependence at high frequencies with exponent $-(1+b)$, (a lorentzian has $b = 1$). We find a value for b of $0.25(\pm 0.1)$, which is temperature independent between 250 K and 350 K (Fig. 3). The temperature-independent shape essentially excludes an explanation of this component in terms of a distribution of correlation times unless we assume that the corresponding distribution of activation energies varies with temperature in a unique way. The shape of the total spectrum (α and β) however is qualitatively consistent with the results derived from a mode-coupling theory of the liquid-glass transition in a hard core liquid¹⁹⁻²². The α -process in this theory is a collective effect, its shape arising as a result of non-linear coupling between density fluctuations. The β -process corresponds to local motions of atoms in the cage formed by their neighbours. Our data therefore demonstrate that diffusive motions in a protein resemble those in other close-packed sys-

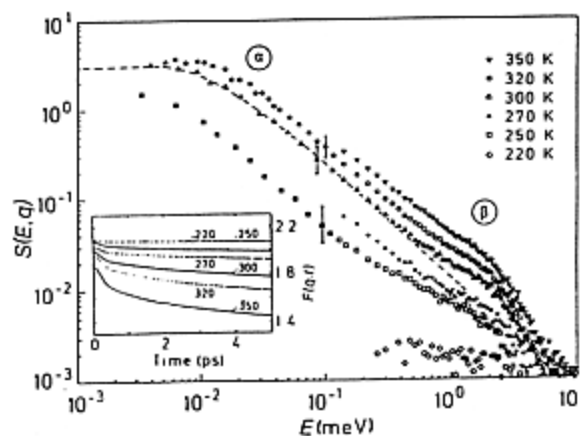


Fig. 3 Log/log plot of quasielastic neutron spectra obtained by combining the results of IN13 (filled symbols) and the time-of-flight spectrometer IN6 (open symbols)²⁶. IN6 has a gaussian resolution function ($\sigma = 50 \mu\text{eV}$) and an incident wavelength of 5.1 \AA . In addition to the usual corrections, a vibrational background has been subtracted at each temperature; this was obtained by scaling the inelastic scattering measured at 180 K or 100 K, assuming harmonic behaviour. The IN6 data represent a single scattering angle (58.5°); the IN13 data have been averaged over the q -range of IN6 (2 \AA^{-1}) to improve the statistics. Shape and linewidth of the spectra are roughly independent of q . The data from the spectrometers were matched at the overlap energy of 0.1 meV . Spectra are not corrected for multiple scattering. The effect of instrumental resolution is small within the energy range presented here. The dashed line represents equation (3) convoluted with the resolution function of IN13, with $b = 0.25$ and $\langle \tau \rangle = b\tau_0 = 2.10^{-11} \text{ s}$. The β -process has a shape intermediate between gaussian and lorentzian and an estimated correlation time of 0.35 ps . Inset: correlation functions obtained from the IN6 quasielastic spectra by Fourier transform and deconvolution of the instrumental resolution function. The overall decrease in intensity with increasing temperature is due to the decrease in the elastic peak which was not subtracted out and contributes a flat background to the correlation functions.

tems dominated by hard-core interactions. But some unique features have to be explained in terms of protein structure: the exponent 0.25 is unusually small (close to $1/f$ noise) and the non-gaussian scattering law, indicating jumps between distinct sites of different energy, suggests that the geometry of the local motion is highly constrained by strong interactions along the chain. A similar asymmetric two-state model has been proposed to explain the microwave absorption of the main-chain in lysozyme and haemoglobin²³. The corresponding energy asymmetry is almost identical to our result. In this connection we remark that neutron data on hydrated lysozyme powders (not shown) behave very similarly to those from myoglobin, suggesting that the dynamic phenomena described here are a general property of globular proteins. The temperature dependence of the hydrogen mean-square displacement (Fig. 2) resembles that derived for the heme iron by Mössbauer spectroscopy³⁻⁵. This correlation indicates that the picosecond fluctuations observed with neutron scattering could couple to the heme group and are likely to be an important component in the decrease of the Lamb-Mössbauer factor above 200 K (ref. 5), as well as in the slower motions resolved in the Mössbauer spectrum (down to 10^{-7} s). Further discussion of this point awaits the current re-evaluation of new and more accurate Mössbauer data²⁴.

Finally we suggest that an important test of the molecular dynamics simulation technique would be to reproduce the temperature dependence of the picosecond protein dynamics reported here. This would also provide insight into the specific atomic motions involved. A step in this direction is the recent theoretical analysis of multiple conformational states in myoglobin²⁵.

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