Glasslike Structure of Globular Proteins and the Boson Peak

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Vibrational spectra of proteins and topologically disordered solids display a common anomaly at low frequencies, known as boson peak. We show that such feature in globular proteins can be deciphered in terms of an energy landscape picture, as it is for glassy systems. Exploiting the tools of Euclidean random matrix theory, we clarify the physical origin of such anomaly in terms of a mechanical instability of the system. As a natural explanation, we argue that such instability is relevant for proteins in order for their molecular functions to be optimally rooted in their structures.

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Proteins are characterized by mechanically stable, unique native structures that bear a precise relation with their biological functions. Yet, in most cases, specific functionality is accompanied by large-amplitude dynamical conformational changes that require high flexibility [1]. Protein structures are complex, hierarchical ones, characterized by short-range order and overall spatial correlations that bear strong similarities with those of glassy materials [2]. In actual fact, proteins and glasses share many physical properties, such as peculiar relaxation processes [3] and the occurrence of a dynamical transition as revealed by the temperature dependence of the atomic mean square displacements (MSD) [1,4,5].

Interestingly, there exists a remarkable similarity of the Raman and neutron-scattering spectra of proteins with those of glasses and supercooled liquids [4], i.e., a peak that develops at low temperatures in the low-frequency regions. Such anomaly, known as boson peak (BP), also shows up in the experimentally determined density of states when divided by the Debye law, i.e., $g(\omega)/\omega^2$ [6]. Several models have been proposed for the explanation of the BP in proteins, among which the phonon-fracton model [7], and the log-normal distribution model [8].

The BP is, on the other hand, a universal feature of many glassy systems [9]. In this context, several possible explanations have been proposed, from the two-level system scenario [10] to localized modes arising from a strong scattering of the phonons by the disorder [11], from "glassy" van Hove singularities [12] to a mechanical instability [13]. Recently, the possibility that a BP may be a general feature of weakly connected systems has also been investigated [14,15].

In a different analytical framework [16], the excess of low-energy modes with respect to the Debye behavior is viewed as a symptomatic effect of the topological phase transition which is conjectured to happen in glasses at low temperatures [13]. Recently, a quantitative description of the BP phenomenology has been given within the formalism of the Euclidean Random Matrix (ERM) theory [16], whose predictions have been confirmed by numerical simulations on realistic glass-forming systems, emphasizing its universal character [17].

In this Letter, we show that the emergence of a BP in globular proteins is the signature of a structural instability of the saddle-phonon kind akin to that predicted within the ERM theory of glasses. Remarkably, our explanation allows for a natural interpretation of such instability in proteins in terms of the mutual relations among their structure, dynamics, and biological function.

To investigate the vibrational properties of a given globular protein, we coarse grain its structure at the amino-acid level and build the associated elastic network (EN). The application of EN models to proteins is relatively recent [18], since it has commonly been assumed that little structural detail could be given up in order to model their complex energy landscapes. However, there is now strong evidence that most features of the large- and medium-scale dynamics of proteins' fluctuations around their native states, related to function and stability, can be successfully reproduced by simple harmonic interactions between amino acids [19–23]. In view of the BP phenomenology, it is important to mention the growing consensus that an explanation in glasses could be found within a purely harmonic context [24].

In the framework of EN models, the potential energy is written as a sum of pairwise harmonic potentials,

$$\mathcal{V}(\{\vec{r}\}) = \sum_{i<j} V(\vec{r}_i, \vec{r}_j) = \sum_{i<j} \frac{k_{ij}}{2} (|\vec{r}_{ij}| - |\vec{r}_{ij}^{(0)}|)^2, \qquad (1)$$

where $\vec{r}_{ij} = \vec{r}_i - \vec{r}_j$, $\vec{r}_i$ being the position of the ith particle, $\vec{r}_i^{(0)}$ its equilibrium position, and k_{ij} the stiffness of the spring connecting particles i and j. More precisely, the vector $\vec{r}_i$ represents the instantaneous position of the α carbon of the ith amino acid, $\vec{r}_i^{(0)}$ its position in the native state as determined from x-ray crystallography or nuclear magnetic resonance, and k_{ij} can take different functional forms, such as $k_{ij} = \kappa\theta(r_c - |\vec{r}_i^{(0)} - \vec{r}_j^{(0)}|)$ [sharp cutoff model [20]] or $k_{ij} = \kappa \exp(-|\vec{r}_i^{(0)} - \vec{r}_j^{(0)}|^2/r_c^2)$ [Gaussian

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model [21]], which is the one we adopt here. The parameter κ sets the physical units for force constants, and can be fixed by requiring the theoretical MSDs to match the experimental ones as determined from x-ray spectra [19].

In the harmonic approximation, the total potential energy (1) is the quadratic form $\mathcal{V}(\{\vec{r}\}) = \frac{1}{2}\vec{r}^T\mathbb{K}\vec{r}$, where the contact matrix $\mathbb{K}_{i\alpha,j\beta}$ ($\alpha, \beta = 1, 2, 3$) is the Hessian of the function (1) evaluated at the equilibrium structure. Were the position vectors in the native structure $\vec{r}_i^{(0)}$ arranged at random, $\mathbb{K}$ would exactly fall in the class of Euclidean Random Matrices. Even if protein structures are surely not random, an analysis of the pair correlation function $g(r)$ reveals interesting features. In Fig. 1 we plot $g(r)$ for serum albumin, a relatively large globular protein whose equivalent ellipsoid [25] has principal radii measuring 2.3, 3.7, and 4 nm, and for an identical number of residues uniformly distributed within such ellipsoid. The comparison shows that the protein structure is characterized by two well-defined coordination shells, namely, the nearest neighbors at fixed distance along the chain and the next-nearest off-chain neighbors, including the pairs belonging to alpha helices and those lying at turning regions, such as loops. After a third, less resolved shell all pairwise spatial correlations are lost. We repeated this analysis for several proteins and always found that the second and the third peaks are always related to the presence of secondary motifs as well as to the intrinsic flexibility of the peptide chain, while beyond such range spatial correlations are absent. This fact is a clear indication that, as far as large-scale structural properties are involved, proteins are well approximated by random assemblies of amino acids with specified density.

The analogy between protein structures and disordered systems with no long-range order suggests that a common

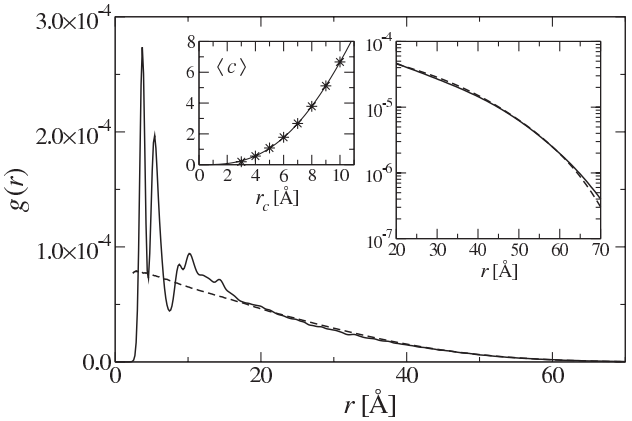

FIG. 1. Plot of the pair correlation function for serum albumin ($N = 578$, solid line) and for a collection of an equal number of residues uniformly distributed in its equivalent ellipsoid (dashed line). Right inset: a magnification of the tails in lin-log scale. Left inset: average connectivity vs cutoff distance (symbols) and cubic fit (solid line).

mechanism might be responsible for the emergence of the BP in both cases. In topologically disordered solids, this anomaly appears upon increasing the temperature or, as observed, for example, in silica, upon lowering the density. In the present case, we are dealing with proteins, i.e., objects whose equilibrium structure is fixed by the biological function. However, changes in the particle density may still be simulated by resorting to the free parameter r_c. In the framework of EN models, r_c sets the range of interparticle interactions and should in principle be tuned by fitting the low-frequency portion of experimental spectra at temperatures below the dynamical transition, where the protein vibrates harmonically within a local minimum. The usual alternative is to compare with spectra as determined by all-atom force fields [21]. By doing this, one obtains $\rho_c \approx 3$ Å in an all-atom representation [21], which coarse grains to $r_c \approx \langle N_a\rangle^{1/3}\rho_c \approx 8$ Å when the average number of atoms per amino acid $\langle N_a\rangle \approx 18$ is introduced. Interestingly, by its very definition, the parameter r_c also allows to regulate an effective *local density* of the system by tuning the average connectivity $\langle c\rangle \equiv \frac{1}{3N} \times \sum_{i=1}^{N}\sum_{\alpha=1}^{3}\mathbb{K}_{i\alpha,i\alpha}$. By decreasing the cutoff r_c, the average number of neighbors per residue diminishes accordingly. Thus, a measure of compactness may be introduced that is proportional to $\langle c\rangle$. It can be shown that varying r_c induces a change in the connectivity that scales with the interaction volume r_c^3 up to finite-size $\mathcal{O}(r_c)$ corrections (see left inset in Fig. 1). This means that we can study the spectral features of a given protein structure with the additional degree of freedom of varying density by simply changing the interaction cutoff r_c, which thus plays in this context the role of a control parameter.

The vibrational spectrum of a protein for a certain value of the parameter r_c is obtained by diagonalizing the contact matrix. However, especially for small proteins, the finite number of residues makes it difficult to analyze the low-frequency features of the spectra. In order to circumvent this problem, we generated a number of different conformers for each of the analyzed structures such that all of them are by construction compatible with the atomic MSDs as specified by the native contact matrices. More precisely, if we write the coordinates of a given conformer as $\vec{\rho}^{(0)} = \vec{r}^{(0)} + \delta\vec{r}$, then it is sufficient to take $\delta\vec{r} = \mathbb{U}\vec{c}$, where $\mathbb{U}$ is the matrix of eigenvectors of $\mathbb{K}$ and the $3N - 6$ coefficients c_k are drawn from as many one-dimensional Gaussian distributions with zero mean and standard deviations $\sigma_k = \sqrt{-k_BT/\lambda_k}$, $\lambda_k = -\omega_k^2$ being the eigenvalues of the contact matrix $\mathbb{K}$. This procedure provides a simple means to construct an arbitrary number of conformations that are dynamically equivalent to the native one in the harmonic approximation.

In Fig. 2 we plot $g(\omega)$ and $g(\omega)/\omega^2$ for several values of the cutoff r_c for two representative proteins of different size. Similar results were obtained for a choice of other proteins. A shoulder manifestly appears in the low-

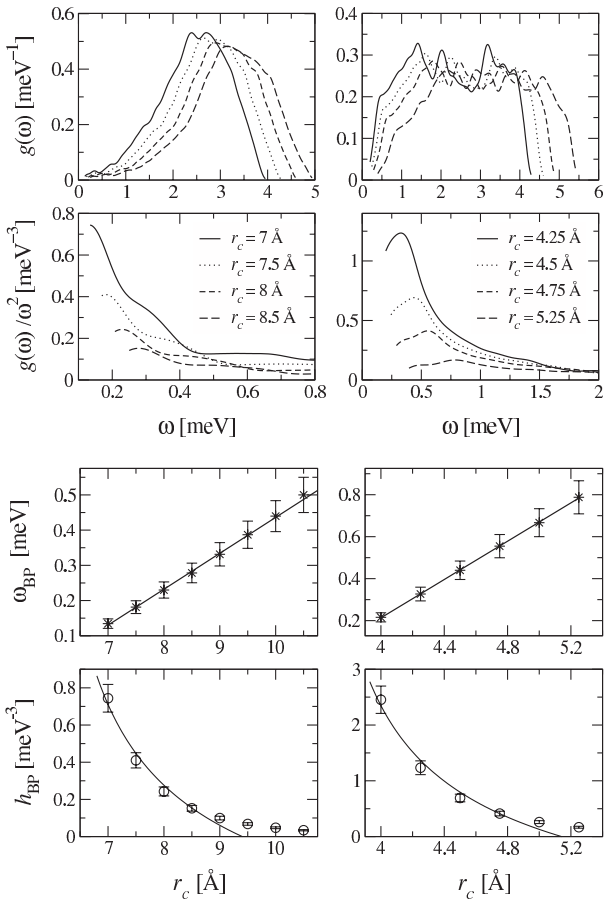

FIG. 2. Boson peak analysis for two globular proteins of different size. Left panels: serum albumin (1AO6), $N = 578$ residues. Right panels: ubiquitin (1UBI), $N = 76$ residues. The four upper panels show the density of states for different values of r_c (for 1000 thermal replicas). In the four lower ones, we show the fits to the BP frequency and height with the mean-field expressions (2). The best-fit results are: $r_c^* = 5.7$ Å (serum albumin) and $r_c^* = 3.5$ Å (ubiquitin). The physical units for frequencies were obtained with $r_c = 8$ Å.

frequency region as r_c is reduced (see upper panels in Fig. 2), and eventually a divergence develops if r_c is decreased below a critical value. The origin of such peak can be uncovered by tracking its position ω_{BP} and height h_{BP} as r_c, i.e., our effective density, decreases. From the lower panels of Fig. 2 one can clearly appreciate that the scaling followed by ω_{BP} and h_{BP} is very well interpolated by the analytical functional forms predicted by the ERM theory in the mean-field approximation [16], i.e.,

$$\omega_{\mathrm{BP}} \sim (r_c - r_c^*)^{\alpha}, \qquad h_{\mathrm{BP}} \sim (r_c - r_c^*)^{-\beta} \tag{2}$$

with $\alpha = 1$ and $\beta = 1/2$. Therefore, our analysis strongly suggests that the BP in protein structures at low densities can be interpreted in terms of a topological instability utterly analogous to the one found in glasses and glass-forming liquids [17]. More rigorously, as it is the case for the Gaussian model in glasses, the BP should be interpreted as a precursor of the transition within a model that by definition becomes meaningless at the critical point. This is precisely what happens in our case, at an interaction range below which protein structures start unfolding. We also stress that the shift of ω_{BP} towards zero frequency and the divergence of the BP height as the systems lose rigidity is a spectral feature equally unveiled within different theoretical approaches [12–15].

It is also instructive to study the localization properties of typical ensembles of spectra through the level-spacing statistics $P(s)$ [26]. As an example, we plot the results obtained for ubiquitin in Fig. 3. Overall, the distribution is very well described by a Wigner law, which holds for fully extended spectra. As we decrease the cutoff, a small contribution from localized modes is observed, as the measure of $J_0 \equiv \langle s^2 \rangle / 2$ shows (upper inset of Fig. 3). Otherwise, J_0 should be close to 1 in the case of a localized spectrum, which is never the case. A more refined analysis [27] performed on several proteins clearly shows that the only localized modes are due to the tail of the spectrum at large frequencies, much alike structural glasses [12,28]. This conclusion, further confirmed by the level-spacing statistics from the low-frequency portion of the spectra (lower inset of Fig. 3), rules out the presence of localized modes in the BP region.

The origin of a precursory feature of a topological instability in proteins can be formally understood by recalling that their structures are those of folded polymers. If the interaction cutoff r_c is lowered below the first off-chain coordination shell, native conformations lose their folded nature and become more and more akin to liquids. In fact, we argue that the appearance of the BP precisely antici-

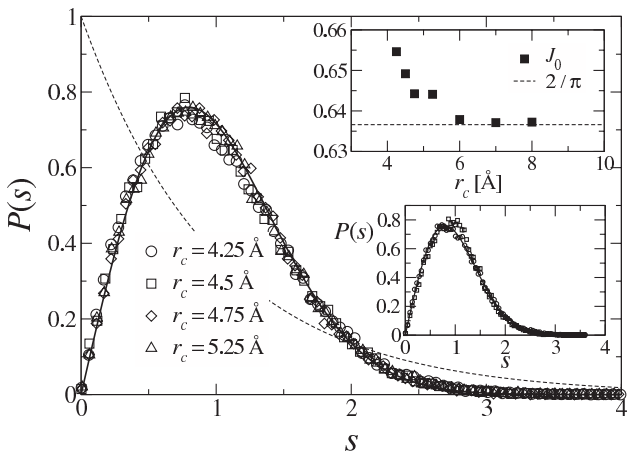

FIG. 3. Plot of the level-spacing statistics of ubiquitin for different values of the cutoff r_c. The Wigner-Dyson (thick solid line) and Poisson (dashed line) statistics, which describe totally uncorrelated spectra, are also shown for comparison. Upper inset: $J_0 \equiv \langle s^2 \rangle / 2$ is plotted vs r_c. The dashed line represents the value expected for a fully extended spectrum. Lower inset: level-spacing statistics for frequencies $\omega < 2.5$ meV. The solid line is a plot of the Wigner surmise.

TABLE I. Correlation of r_c^* with structural parameters.

Protein	N	p	$(\alpha+\beta)$	r_c^* (Å)
Insulin	51	0.20	0.53	4.57
Protein G	56	0.21	0.70	3.64
Ubiquitin	71	0.20	0.46	3.53
PDZ binding domain	85	0.21	0.55	4.03
Lysozyme	162	0.17	0.74	4.27
Adenylate kinase	214	0.12	0.64	7.85
LAO	238	0.16	0.60	5.44
CYSB	260	0.17	0.59	4.70
PBGD	296	0.16	0.60	3.70
Thermolysin	316	0.18	0.53	4.55
HSP70 ATP-binding domain	382	0.15	0.66	5.28
Fab-fragment	437	0.13	0.48	5.70
Serum albumin	578	0.12	0.70	5.70
Correlation with r_c^*	**0.45**	**−0.82**	**0.17**	1

pates such inherent instability before the critical cutoff is reached. Accordingly, the best-fit values of r_c^* for all the analyzed structures never does exceed the first off-chain coordination shell (see Fig. 2). Keeping in mind that the optimal value of r_c is around 8 Å, i.e., above its critical value, our results suggest that protein structures express an inherent trade off between spatial properties of liquids, i.e., increased degree of mobility, and the necessity of maintaining a certain structural stability. Interestingly, from an extensive analysis on a selection of 13 proteins, we find that r_c^* is substantially anticorrelated with the packing fraction $p = 4/3(N/V)(d_0/2)^3$, i.e., a measure of global compactness, whereas weak correlation is found with indicators of local stability, such as the content of α helices and β sheets. Here N and V are the number of residues and the volume, while $d_0 \simeq 3.83$ Å is the inter-residue distance along the main chain. Moreover, we also find a positive correlation between r_c^* and N, which may signal the larger mechanical stability of smaller proteins (see Table I).

The above conclusions may be interpreted by regarding proteins as molecular machines bound to keep a specified geometry in order to perform their biological function, yet preserving a high degree of structural flexibility in order to efficiently explore different conformational states. In this sense, the mechanical instability underlying the emergence of a BP appears to be a universal signature of their engineered ability to easily travel between adjacent local minima in their native states. We note that our results agree with recent estimates of the spectral dimension of globular proteins, whose non-Debye behavior has been interpreted in terms of a vibrational instability of the Peierls-Landau type [29].

Summarizing, in this Letter we have provided compelling evidence of the equivalence of the boson peak phenomenon in globular proteins and glasses. Our analysis suggests that a topological instability of the saddle-phonon type in proteins reflects the balance imprinted in their structures between being capable of rapidly accessing different minima in the native energy landscape while keeping a relative mechanical rigidity.

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