Helman *et al.* Respond: In the *low*-frequency (ω) limit, where the acoustic phonon density of states is given[1] by $\rho(\omega) \propto \omega^{d_{\mathrm{fr}}-1}$ ($d_{\mathrm{fr}} = 2d_f/d_w$, where d_f is the fractal dimension and d_w is the fractal dimension associated with a random walk restricted to the fractal), the weak cross-links (mainly hydrogen bonds) of the protein are important and may influence the effective values of *both* d_f and d_w as a result of finite-size effects. When cross links are present the fractal dimension should be deduced by counting the alpha carbons which, within successive radii R, are bridged either by the main chain or by cross links. Thus one expects that for a *finite* chain, as a function of the density of cross links (and assuming that the spatial structure of the protein backbone remains invariant), the effective value of d_f increases continuously from the chain fractal dimension[2] d_c (for zero density) up to the reentrant fractal dimension[2] d_r (for high density). However, the effective values of the fractal dimension d_c and d_r should be equal and coincide with the true fractal dimension d_f in the infinite-size limit. Also we expect that for a finite chain d_c approximates d_f better than d_r ($d_c \simeq d_f$). On the other hand, it appears also quite plausible that for a *finite* chain as the density of cross links increases d_w makes a smooth crossover from $2d_c \simeq 2d_f$ down to a value near to 2, while in the infinite-size limit we expect $d_w \simeq 2$ for any nonzero density of cross links. Therefore for a nonzero concentration of cross links and for an *infinite* chain we expect $d_w \simeq 2$ and $d_f \simeq d_c$, which imply the experimentally observed relation $d_{\mathrm{fr}} \simeq d_c$. This corresponds to the case discussed in our paper.[3] On the other hand, for a *finite* chain we expect the effective value of the fractal dimension to be larger than d_c and the effective value of d_w to be larger than 2, still giving the same value $d_{\mathrm{fr}} \simeq d_c$. This is the case discussed by Stapleton.[2]

Computer simulations could be used to study the dependence of d_f and d_w on the density of cross links and to assess the magnitude of the finite-size blurring. The experimental equivalent of such a study (chemical or thermal denaturation of the protein) is hard to perform, because the backbone naturally tends to modify its spatial structure simultaneously.

Like Stapleton,[2] although for different reasons,

Cates[4] argues that the inclusion of short ("local" in his words) cross links (which obviously are the most relevant in the proteins) does not necessarily yield $d_w = 2$. As an example he refers to a work by Banavar, Harris, and Koplik[5] who obtained $x \simeq 0.46$ for $d = 2$ and 0.73 for $d = 3$; hence $d_w = d_f + \bar{z} = d_f + 2x \simeq 2.92$ (or $d_{\mathrm{fr}} = 2d_f/d_w \simeq 1.37$) for $d = 2$ and $d_w \simeq 3.46$ (or $d_{\mathrm{fr}} \simeq 1.15$) for $d = 3$. However, Havlin *et al.*[6] have more recently obtained results which, as they point out, *are at variance* with those of Banavar, Harris, and Koplik[5] for $d = 2$ (the discrepancy disappears for $d = 3$). Havlin *et al.*[6] obtain for both $d = d_f = 1$ and $d = d_f = 2$, $d_w = 2$, thus supporting our model [note a misprint in their Table I: for $d = 1$ it should read $d_f = 1$, in accordance with their statement slightly below their Eq. (13)].

In summary, the fractal conception of a protein first introduced by Stapleton still seems to be adequate *if the cross links are taken into account.*

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