aequorin luminescence as a fast, sensitive test for presence of Ca^{2+} in biological systems[12–19]. Inclusion of coelenterazine in the test system should prolong considerably the luminescence life of aequorin.

A recent paper[20] contains statements which amount to the suggestion that YC of the present paper is in effect *Renilla* luciferin. We have shown, however, that *Renilla* luciferin is actually identical to coelenterazine[9]. It should be emphasised that the absorption spectrum of YC (ref. 5) is significantly different from that of coelenterazine except for the one peak in the visible region. Moreover, recent mass spectrometric data (O.S. and F.H.J., unpublished) have demonstrated that YC and coelenterazine are in fact different compounds.

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Erratum

In the article "Computer simulation of protein folding" by M. Levitt and A. Warshel (*Nature*, **253**, 694; 1975) the wrong version of Fig. 4 was printed. The correct version is reprinted below.

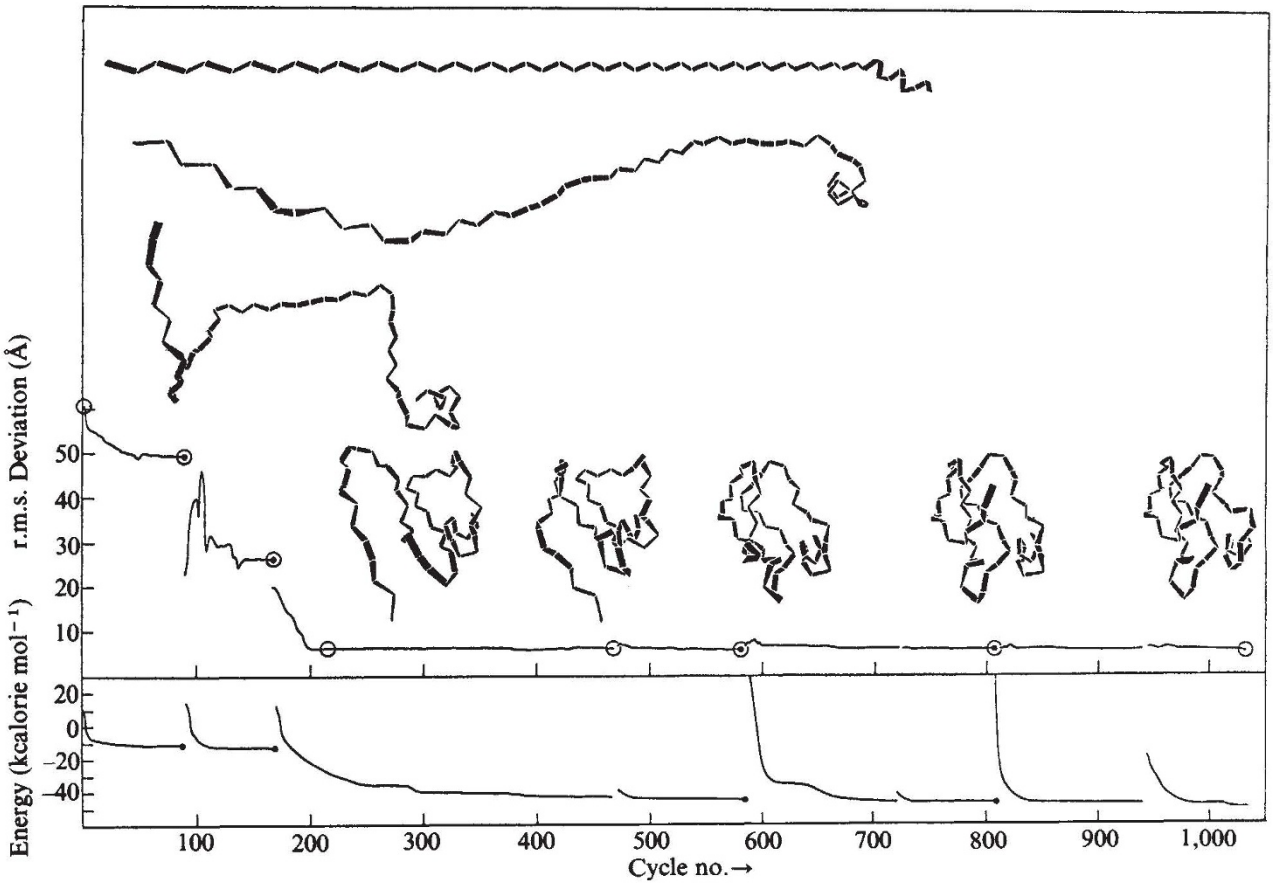

Fig. 4 Simulation of PTI folding from an extended starting conformation with the terminal helix ($\alpha = 180°$ for all except 48 to 58 where $\alpha = 45°$). No knowledge whatsoever about native PTI is used during this simulation (apart from setting the terminal helix). The conformation was thermalised at the end of each minimisation except near cycles 490 and 730 when the energy rises slightly because the minimisation was restarted after rounding the torsion angles to one degree. In the first two thermalisations, each normal mode was perturbed in the plus direction to raise the associated energy to $\bar{R}(n)kT/2$ with $T = 1{,}000$ K. In the other three thermalisations, the perturbations were randomly in the plus and minus directions but always such as to raise the energy by $kT/2$ with $T = 300$ K. (Because the random numbers are distributed uniformly rather than exponentially, these temperatures do not correspond to the macroscopic temperature.) The 8 ribbon diagrams, which show the C^{α} chain path, refer from left to right to the 8 conformations at the circled points on the r.m.s. deviation curve, respectively. The last five conformations have progressively lower energies and are each a little closer to the native structure ($E = -43.3$, -45.7, -46.0, -46.9 and -48.9 kcalorie mol^{-1}, respectively; r.m.s. deviation = 6.08, 5.7, 5.6, 5.4 and 5.3 Å, respectively). The solid dots at the end of a minimisation indicate that a perfect minimum was reached (r.m.s. gradient less than 10^{-6} kcalorie mol^{-1}-rad^{-1}). One cycle takes about 0.6 s on an IBM 370/165 computer.