

Correction to “Unfolded Protein and Peptide Dynamics Investigated with Single-Molecule FRET and Correlation Spectroscopy from Picoseconds to Seconds”

Daniel Nettels, Armin Hoffmann, and Benjamin Schuler*

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In this work, we reported, among other aspects, results on the chain dynamics in the unfolded state of the small cold shock protein from *Thermotoga maritima* (Csp), determined using nanosecond fluorescence correlation spectroscopy (FCS) in combination with Förster resonance energy transfer (FRET). Recent experiments in our laboratory have now shown that some of the correlation times given in Figure 6b are not only due to fluctuations in the FRET rate but contain a contribution from static quenching of the donor and/or acceptor fluorophores by the tryptophan residues within the chain.¹ As a result, for some of the variants, the conversion of the reported decay times of the intensity correlation functions, τ_{CD} , to decay times of the intramolecular distance correlation time, τ_r , and to intramolecular diffusion coefficients, D (Figure 6c), are affected significantly by this additional quenching component. Recent measurements on Csp without tryptophan residues show that τ_{CD} and τ_r increase with increasing sequence separation,¹ as expected for a Rouse chain,² but additional effects from internal friction have to be taken into account to explain the behavior quantitatively.¹ None of the other results are affected. Note also that fluorophores positioned at the chain termini of Csp (position 2 and 67) are not influenced by tryptophan quenching, and the values of τ_r reported for this variant are unaffected, both here and in earlier work.³ In that case, and in all other published work where we use nanosecond FCS, the absence of quenching by tryptophan was verified in experiments employing, e.g., direct excitation of the acceptor and samples labeled only with donor dye.

■ REFERENCES

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