MAR08-2007-007516

Abstract for an Invited Paper
for the MAR08 Meeting of
the American Physical Society

Single-Molecule Dynamics of a DNA Aptamer Targeting VEGF Protein

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Single-molecule fluorescence resonance energy transfer (SMFRET) and SMFRET autocorrelation analysis were used to examine structural fluctuations in a DNA aptamer that binds and exhibits inhibition activity towards the vascular endothelial growth factor (VEGF) protein, a protein that is involved in macular degeneration. The aptamer's most stable conformation contains 4 Watson-Crick base pairs, resulting in only a shallow negative potential relative to the unfolded state. The weakly stable folded state and the manifold of unfolded structures quickly interconvert. In contrast, in the presence of the VEGF target, the aptamer folding rate constant decreases and the fluctuations in both the unfolded and folded states decrease in frequency, but are not eliminated. A possible relationship between activity and aptamer flexibility is discussed