

Abstract Submitted  
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**Universality in the timescales of internal loop formation in unfolded proteins and single-stranded oligonucleotides**<sup>1</sup> RYAN CHENG, UT Austin, TAKANORI UZAWA, Hokkaido University, Japan, KEVIN PLAXCO, UC Santa Barbara, DMITRII MAKAROV, UT Austin — Understanding the rate at which various parts of a molecular chain come together to facilitate the folding of a biopolymer (e.g., a protein) into its functional form remains an elusive goal. Here we use experiments, simulations, and theory to study the kinetics of internal loop closure in disordered biopolymers such as single-stranded DNA and unfolded proteins. We present theoretical arguments and computer simulation data to show that the relationship between the timescale of internal loop formation and the positions of the monomers enclosing the loop can be recast in a form of a universal master dependence. Our measurements of the loop closure times in single-stranded oligonucleotides, as well the internal loop closure kinetics in unfolded proteins reported by others, are all well described by this theoretically predicted dependence. Experimental deviations from the master dependence can then be used as a sensitive probe of dynamical and structural order in unfolded proteins and other biopolymers.

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