Supplementary material:

Single VS ribozyme molecules reveal dynamic and hierarchical folding toward catalysis

Miguel J. B. Pereira[1], Evgenia N. Nikolova[1,2] , Shawna L. Hiley[3], Dominic Jaikaran[3], Richard A. Collins[3], and Nils G. Walter[1,*]

[1]*Department of Chemistry, Single Molecule Analysis Group, 930 N. University Ave., University of Michigan, Ann Arbor, MI 48109-1055, USA*

[2]*Chemical Biology Doctoral Program, 930 N. University Ave., University of Michigan, Ann Arbor, MI 48109-1055, USA*

[3]*Department of Molecular and Medical Genetics, University of Toronto, Toronto, ON M5S 1A8, Canada*

[*]*Corresponding author*. Department of Chemistry, Single Molecule Analysis Group, 930 N. University Ave., University of Michigan, Ann Arbor, MI 48109-1055, USA. E-mail address: nwalter@umich.edu.

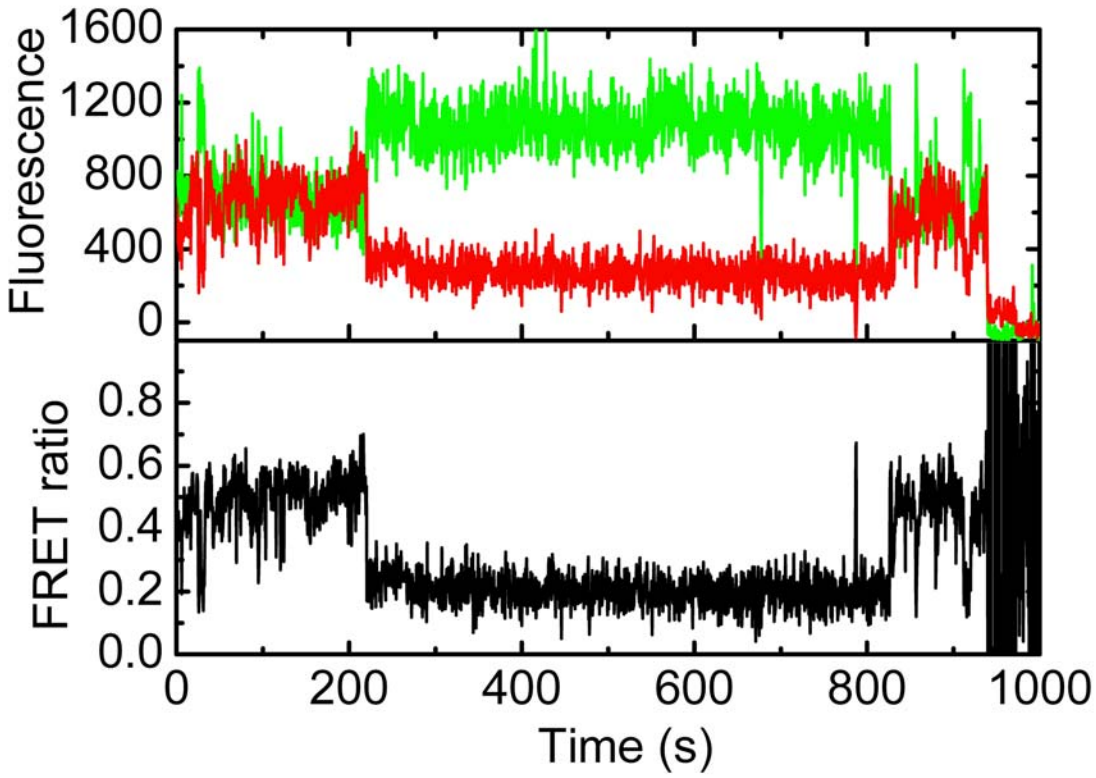

Figure S1: Raw fluorescence and FRET signals of a misfolded wild-type VS ribozyme molecule; the catalytically competent H state of FRET ≈ 0.76 is never occupied. 10% of all WT time traces show this behavior, at least partially explaining the typically ~30% of inactive ribozyme in our ensemble cleavage assays (Fig. 1c).