

Supplement to:

Molecular dynamics suggest multifunctionality of an adenine imino group in acid-base catalysis of the hairpin ribozyme

Mark A. Ditzler^{1,2}, Jiří Šponer³ and Nils G. Walter^{2,*}

¹Biophysics, University of Michigan, 930 N. University Ave., Ann Arbor, MI 48109-1055,
USA

²Department of Chemistry, University of Michigan, 930 N. University Ave., Ann Arbor, MI
48109-1055, USA

³Institute of Biophysics, Academy of Sciences of the Czech Republic, Kralovopolska
135, 612 65 Brno, Czech Republic

*To whom correspondence should be addressed. Tel: +1 734 615 2060; Email:
nwalter@umich.edu.

SUPPLEMENTAL FIGURE 1. Force-field parameters for adenosine protonated at N1. The atom types and partial charges are indicated on the atoms, whereas nonstandard equilibrium angles and distances are boxed.

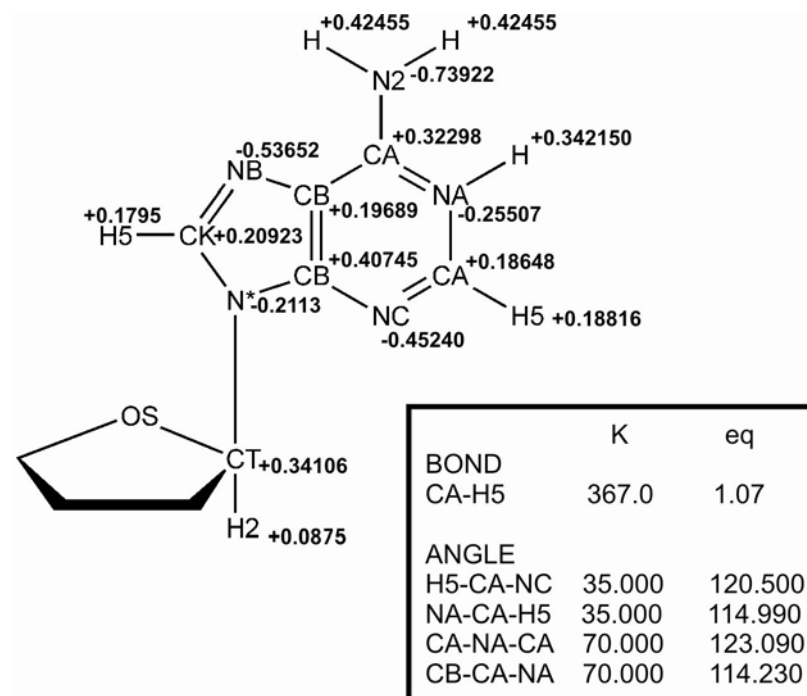
SUPPLEMENTAL FIGURE 2. Backbone analysis of the entire backbone. **(A)** Secondary structure schematic of the minimal hairpin ribozyme used in our simulations. **(B)** Analysis of the complete domain A using the software Suitename {Davis, 2007 #65; Richardson, 2008 #64}. Regions of the backbone that fall within one of the inferred low energy conformations are identified by their corresponding two character codes; outliers are identified by !!. Crystal structures and corresponding simulations are aligned to compare backbone conformations. **(C)** Analysis of the complete domain B using Suitename.

SUPPLEMENTAL FIGURE 3. Inter-atomic distances involved in the key inter-domain hydrogen bonds of Figures 1C and 1E, tracked for all of our simulations. Distances are color coded as indicated in Figure 1E. **(A)** Inter-domain distance for all simulations with C39 and **(B)** all simulations with U39. Simulations in which the ribose zipper is disrupted are indicated by blue boxes.

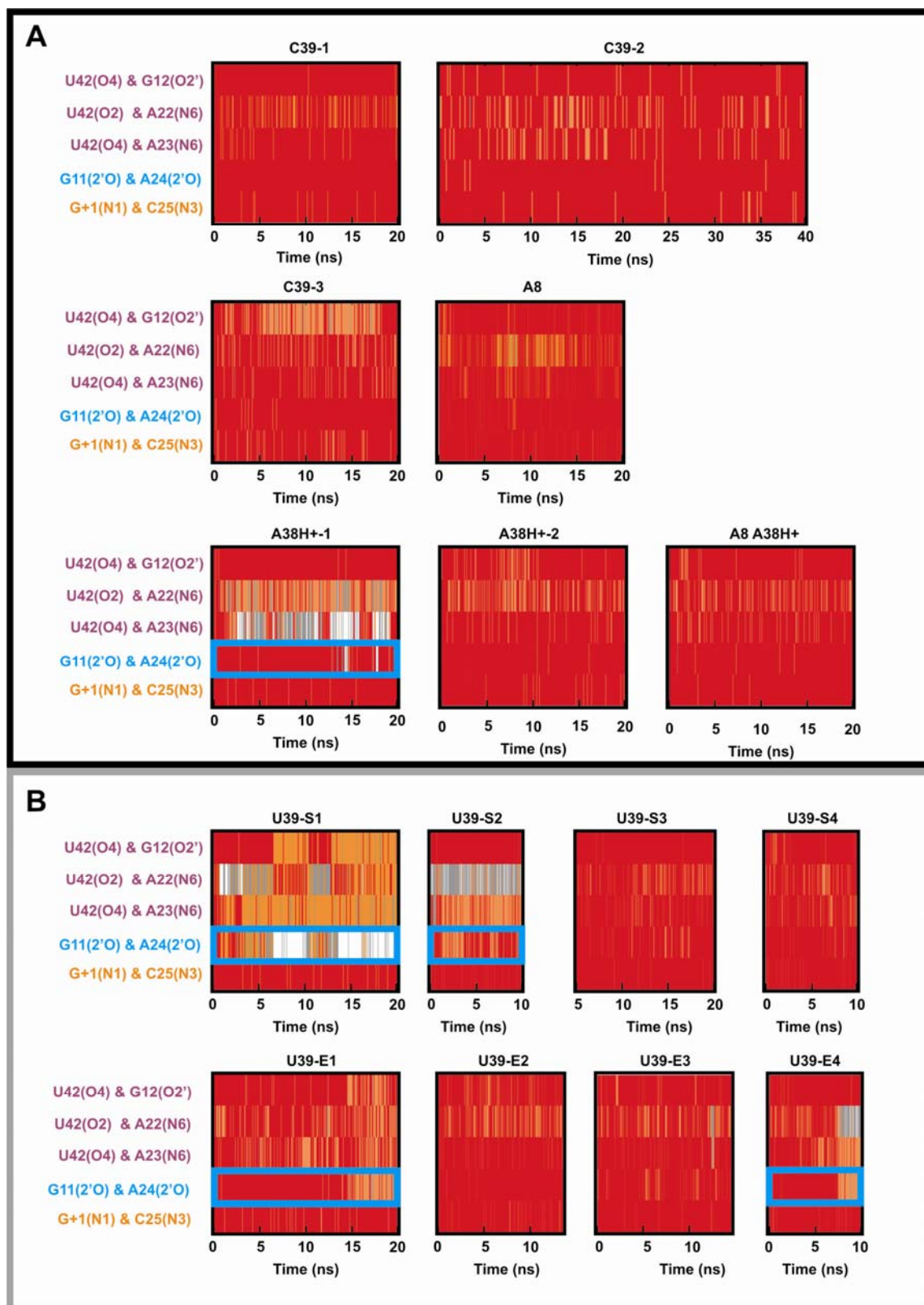
SUPPLEMENTAL FIGURE 4. The U37 conformation transitions from the sequestered to the exposed conformation 19 ns into simulation U39-S1 (red), whereas simulation U39-E1 begins and stays in the exposed conformation (black). The U37 conformation is monitored by tracking the inter-atomic distance between O2 of U37 and C1' of G+1.

SUPPLEMENTAL FIGURE 5. In-line attack angle and important inter-atomic distances are tracked over the course of all additional simulations not shown in the main text; distances and angles are color-coded as in Figure 5. Hydrogen bonding partners observed in TSA crystal structures are indicated in green, but generally not observed to form in these simulations. Simulations in which the A-1(2'OH) to A38(N1) hydrogen bond is observed are indicated by yellow boxes.

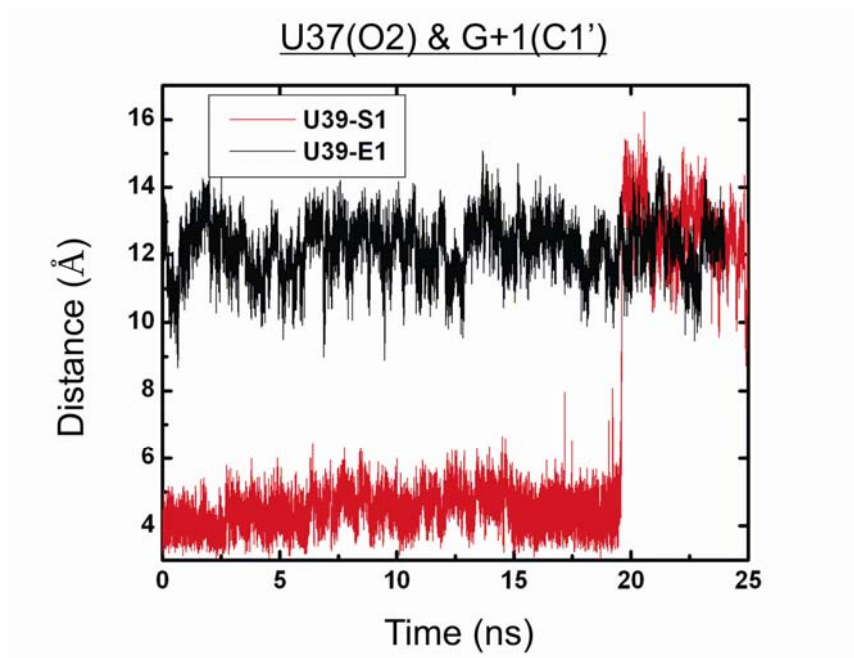
Ditzler, Šponer and Walter, Supplemental Figure 1



Ditzler, Šponer and Walter, Supplemental Figure 3



Ditzler, Šponer and Walter, Supplemental Figure 4



Ditzler, Šponer and Walter, Supplemental Figure 5

