Increasing the length of poly-pyrimidine bulges broadens RNA conformational ensembles with minimal impact on stacking energetics

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ABSTRACT
Helical elements separated by bulges frequently undergo transitions between unstacked and coaxially stacked conformations during the folding and function of noncoding RNAs. Here, we examine the dynamic properties of poly-pyrimidine bulges of varying length (n = 1–4, 7) across a range of Mg2+ concentrations using HIV-1 TAR RNA as a model system and solution NMR spectroscopy. In the absence of Mg2+, helices linked by bulges with n ≥ 3 residues adopt predominantly unstacked conformations (stacked population <15%), whereas one-bulge and two-bulge motifs adopt predominantly stacked conformations (stacked population >74%). In the presence of 3 mM Mg2+, the helices predominantly coaxially stack (stacked population >84%), regardless of bulge length, and the midpoint for the Mg2+-dependent stacking transition is within threefold regardless of bulge length. In the absence of Mg2+, the difference between free energy of interhelical coaxial stacking across the bulge variants is estimated to be ~2.9 kcal/mol, based on an NMR chemical shift mapping with stacking being more energetically disfavored for the longer bulges. This difference decreases to ~0.4 kcal/mol in the presence of Mg2+. NMR RDCs and resonance intensity data show increased dynamics in the stacked state with increasing bulge length in the presence of Mg2+. We propose that Mg2+ helps to neutralize the growing electrostatic repulsion in the stacked state with increasing bulge length thereby increasing the number of coaxial conformations that are sampled. Energetically compensated interhelical stacking dynamics may help to maximize the conformational adaptability of RNA and allow a wide range of conformations to be optimally stabilized by proteins and ligands.

Keywords: NMR; RNA folding; HJH motifs; RNA dynamics; RNA bulges; HIV

INTRODUCTION

Studies over the past two decades have established a plethora of functions for noncoding RNAs (ncRNAs) (Eddy 2001; Gesteland et al. 2006; Wahl et al. 2009; Cech and Steitz 2014). The biological mechanisms of many ncRNAs require highly coordinated conformational changes that are not only essential for the proper folding and assembly of RNA and ribonucleoprotein (RNP) complexes but also provide the basis for RNA-based molecular machines and switches (Cruz and Westhof 2009; Dethoff et al. 2012; Mustoe et al. 2014b). A common RNA conformational transition involves changing the orientation of helical domains linked by bulges, internal loops, and higher order junctions from linear coaxially stacked conformations to what can be a broad range of bent interhelical conformations. Such transitions can help orient motifs involved in tertiary contacts (Kim et al. 1974; Robertus et al. 1974; Jack et al. 1976; Murphy et al. 1994) or optimize intermolecular interactions with ligands (Duchardt-Ferner et al. 2010; Stelzer et al. 2010), proteins (Leulliot and Varani 2001; Noller 2005), and metal ions (Bassi et al. 1995; Ippolito and Steitz 1998) that bind interhelical junctions.
Indeed, a survey of the Protein Data Bank (PDB) (Berman et al. 2000) shows that RNA helices linked by bulges tend to predominantly adopt near coaxially stacked conformations whereas kinked conformations are more often observed in RNA–protein and RNA–ligand complexes, particularly for longer bulges (Fig. 1A). A deep understanding regarding the dynamic behavior of helices across junctions is key for advancing RNA structure prediction (Somarowthu 2016; Miao and Westhof 2017), RNA-targeted drug discovery (Stelzer et al. 2011; Hermann 2016), the design of RNA-based devices (Arakiannis et al. 2016; Ohno and Saito 2016) as well as for understanding and manipulating biological RNA and RNA/protein machines.

The most common RNA interhelical junction is the bulge motif, a single asymmetric strand that adjoins two helical domains (Fig. 1B; Ignacio Tinoco et al. 1989; Turner 1992; Hermann and Patel 2000). Studies using transient electric birefringence (TEB) have shown that at low salt concentrations (2 mM NaCl), poly(A) and poly(U) bulges induce kinks that increase as the bulge length increases from 1 to 6 nucleotides (nts) (Zacharias and Hagerman 1995a). Additional studies using Föster resonance energy transfer (FRET) show that in 100 mM NaCl the average bend angle between RNA helices increases up to 7 nts, but that further addition of bulge nucleotides results in more linear conformations, likely because the bulge nucleotides can pair up to form helical stems that impose unique topological constraints (Gohlke et al. 1994). This increase in average kink angle with bulge length can be explained by simple topological models in which helices sample wider interhelical distributions as connectivity constraints are weakened (Chu et al. 2009; Mustoe et al. 2014a). For $A_n$ bulges (where $n$ is equal to the number of bulge nucleotides), addition of divalent metal ions, such as Mg$^{2+}$ or Ca$^{2+}$, helps to neutralize electrostatic charge repulsion and promote interhelical coaxial stacking through a process that likely requires the flipping out of the bulge nucleotides (Zacharias and Hagerman 1995a; Ippolito and Steitz 1998; Casiano-Negroni et al. 2007). However, for $A_n$ bulges, a greater tendency to stack intrahelically hinders interhelical coaxial stacking even in the presence of Mg$^{2+}$ (Kalnik et al. 1990; Zacharias and Hagerman 1995a).

Together, these studies show that many competing factors, including the length and sequence of the bulge as well as the concentration and identity of metal ions present in solution, can influence the dynamic behavior of bulges (Bhattacharyya and Lilley 1989; Hsieh and Griffith 1989; Bhattacharyya et al. 1990; Tang and Draper 1990; Riordan et al. 1992; Gohlke et al. 1994; Zacharias and Hagerman 1995a).

The trinucleotide (UCU) bulge in the transactivation response element (TAR) RNA from the human immunodeficiency type-1 virus (HIV-1) has served as a model system for studying the behavior of poly-pyrimidine bulges (Fig. 1B; Riordan et al. 1992; Hermann and Westhof 2000; Pitt et al. 2004; Casiano-Negroni et al. 2007; Dethoff et al. 2008; Do et al. 2012; Jalalirad et al. 2012; Shi et al. 2017). Stacking of helices across the TAR bulge is proposed to play important roles in the assembly of a RNP complex that activates transcription (Roy et al. 1990; Calnan et al. 1991). In addition, the TAR helices sample a variety of unstacked conformations (Faber et al. 2000; Davis et al. 2004; Murchie et al. 2004; Zhang et al. 2006; Frank et al. 2009; Stelzer et al. 2010; Shi et al. 2017), which can be stabilized when bound to different small molecules (Jones and Peterlin 1994; Hermann 2016).

Biophysical studies using a variety of techniques (Zacharias and Hagerman...
Poly(U) bulges have similar Mg stacking energetics

1995b; Ippolito and Steitz 1998; Zhang et al. 2003, 2006; Casiano-Negroni et al. 2007; Stelzer et al. 2010; Lu et al. 2011; Salman et al. 2013; Dickson et al. 2014; Mustoe et al. 2014a; Shi et al. 2017) have shown that at low salt concentrations (25 mM NaCl) and in the absence of divalent cations, the two TAR helices are unstacked and on average kinked by 45° relative to one another, forming a highly dynamic ensemble of interhelical conformations (Zacharias and Hagerman 1995b; Aboul-el et al. 1996; Al-Hashimi et al. 2002; Dethoff et al. 2008). The bulge residues U23 stacks on the junctional A22, while bulge residues C24 and U25 are looped out and highly flexible (Fig. 1B, left). The stacked state is thought to be disfavored in low concentrations of monovalent metal ions and in the absence of divalent metal ions due to electrostatic repulsion at the bulge (Casiano-Negroni et al. 2007). In contrast, in the presence of divalent cations (Mg2+ or Ca2+), the two TAR helices adopt a coaxially stacked and more rigid conformation in which all three bulge nucleotides are flipped out (Fig. 1B, right; Ippolito and Steitz 1998; Al-Hashimi et al. 2003; Casiano-Negroni et al. 2007). A crystal structure of the coaxially stacked TAR conformation (interhelical bend angle is 5°) shows four Ca2+ ions that help neutralize electrostatic repulsion through a network of inner- and outer-sphere interactions (Fig. 1B, right; Ippolito and Steitz 1998). NMR studies of TAR in the presence of Mg2+ (Al-Hashimi et al. 2003; Casiano-Negroni et al. 2007) show that it adopts a stacked conformation with flipped out bulge nucleotides similar to that observed in a high resolution X-ray structure of TAR in the presence of Ca2+ (Ippolito and Steitz 1998), suggesting the interactions with Ca2+ are likely similar to those observed with Mg2+. NMR studies indicate that there exists a two-state dynamic equilibrium between the rigid coaxial and flexible unstacked conformations (Al-Hashimi et al. 2003; Casiano-Negroni et al. 2007). Increasing the concentration of Mg2+ or Na+ (Casiano-Negroni et al. 2007) shortening the bulge from 3 to 2 nts (Merriman et al. 2016), or replacing A22-U40 with G22-C40 shifts the equilibrium in favor of the coaxial conformation (Stelzer et al. 2010).

It is interesting to note that while the sequence of HIV-1 TAR is highly conserved, TAR variants with UU bulges exist in HIV-1 isolates (HIV-1mal and HIV-1U455), Simian immuno-deficiency virus (SIV) (Berkhout, 1992), and in the twofold TAR hairpins of HIV type 2 (HIV-2) (Berkhout 1992). Cell-based assays show that while the two bulge (U) TAR variants supports transcriptional activation, single bulge or TAR variants lacking the bulge significantly inhibit transcriptional activation (Roy et al. 1990). This effect could be due to disruption of the U23-A27-U38 base-triple which is thought to be important for Tat binding (Puglisi et al. 1992; Brodsky and Williamson 1997; Hennig and Williamson 2000) and/or because a degree of interhelical kinking across the bulge is important for transcriptional activation.

Here, we build on prior studies of HIV-1 TAR and use NMR spectroscopy to investigate how systematically varying the bulge length impacts the dynamic properties of unstacked and stacked states as well as their relative energetics. Specifically, we investigate various length uridine bulges (n = 1, 2, 4, and 7) as compared to the wild-type HIV-1 TAR UCU bulge, which has been shown to behave similarly to the UUU bulge based on biophysical and functional studies (Roy et al. 1990; Sumner-Smith et al. 1991; Berkhout 1992; Riordan et al. 1992). We find that apart from the n = 1 bulge, all U bulge variants [n = 2,3(UCU), 4, and 7] exhibit a two-state Mg2+-dependent stacking transition. Increasing the bulge length leads to broader conformational distributions in both the stacked and unstacked ensemble but has a limited effect on the energetics of coaxial interhelical stacking in the presence of Mg2+. Energetically compensated stacking dynamics may help to maximize the conformational adaptability of RNA, allowing a wide range of conformations to be optimally stabilized by proteins and ligands, and sampled during folding of large RNAs.

RESULTS

Mg2+-dependent interhelical stacking transition monitored by NMR chemical shift mapping

We used NMR chemical shift mapping experiments to examine whether four poly(U) variants of wtTAR containing one, two, four, and seven uridine bulges (U,TAR, where n denotes the number of uridines in the bulge motifs, Fig. 2A) also undergo Mg2+-dependent interhelical stacking transitions. Prior studies showed that coaxial stacking of wtTAR induced by increasing the concentration of either Mg2+ or Na+ (Al-Hashimi et al. 2003; Casiano-Negroni et al. 2007) or through replacement of A22-U40 with G22-C40 (Stelzer et al. 2010) results in specific chemical shift perturbations (CSPs) at nucleotides in and around the bulge, specifically residues A22, U23, and C24 (Fig. 2A). These CSPs report on conformational differences between the unstacked and stacked states with U23 being partially flipped in and the unstacked state but flipped out in the stacked conformation (Fig. 1B).

In prior studies of wtTAR (UCU-TAR), 2D HSQC spectra were collected following incremental addition of Mg2+ (Casiano-Negroni et al. 2007). Here, we carried out analogous experiments by dialyzing each TAR NMR samples into the desired Mg2+ concentration. This equilibration was important to properly account for the free [Mg2+] when deriving thermodynamic parameters of interest. We also used lower RNA concentrations (25 µM) to facilitate comparison to other biophysical studies that use lower RNA concentrations and in which the free concentration of Mg2+ is assumed to be known. For each TAR variant, NMR spectra were recorded at eleven different Mg2+ concentrations.
concentrations at 25°C using aromatic SOFAST-HMQCs
(Sathyamoorthy et al. 2014) for optimal data collection.

In the absence of Mg²⁺, shortening or elongating the
wtTAR bulge resulted in large CSPs at the same residues
in and around the bulge that experience CSPs in wtTAR
upon coaxial interhelical stacking (Fig. 2B; Supplemental
Fig. 1A). Relative to wtTAR, shortening the bulge resulted
in CSPs that are similar to those observed upon addition of
Mg²⁺ or Na⁺, whereas elongating the bulge leads to oppo-
sitely shifted CSPs (Fig. 2B; Supplemental Fig. 1B), similar
to the low-salt form of wtTAR. Additionally, normalized
resonance intensity analysis reveals that the local bulge dy-
namics at picosecond-to-nanosecond timescales increases
as the bulge is elongated (Supplemental Fig. 2A). These
results indicate that shortening/elongating the bulge leads
to an increase/decrease in the fractional population of the
stacked state.

Increasing the concentration of Mg²⁺ resulted in CSPs
for all TAR variants, with the largest CSPs generally ob-
served in and around the bulge as reported previously
for wtTAR (Fig. 2C; Supplemental Fig. 1D). The directions
of the CSPs in the TAR variants were also similar to those
observed for wtTAR and are consistent with an increase
in the fractional population of the stacked state. U₇TAR ex-
periences smaller CSPs and does not reach the chemical
shift positions observed for the other variants, indicating
that it does not undergo an Mg²⁺-dependent stacking
transition. The NMR spectra of the TAR variants recorded
at low salt differ significantly (Fig. 2B), reflecting differenc-
es in the relative populations of stacked and unstacked
states as well as potential differences in the stacked and
unstacked ensemble. Conversely, the spectra recorded
at saturating Mg²⁺ concentration are much more similar,
consistent with stabilization of more similar coaxially
stacked conformations (Fig. 2D; Supplemental Fig. 1C).

**Similar midpoints for the Mg²⁺-dependent stacking transition**

With a few exceptions noted below, all Mg²⁺-dependent
CSPs measured for the TAR variants could be satisfactorily
fit to a two-state model, suggesting that all TAR variants exist in a dynamic equilibrium between unstacked and stacked conformations (Fig. 3A; Supplemental Fig. 3; Supplemental Table 1). We analyzed the fitted Mg1/2 values representing the midpoint for the Mg2+-dependent conformational transition. Because the stacked conformation is significantly populated for many of the variants in 25 mM NaCl even in the absence of Mg2+, the midpoints do not necessarily represent the concentration at which stacked and unstacked populations are 50%. Rather, the Mg1/2 values report on the energetics of Mg2+ association, which in turn depends on the energetics of coaxial stacking as well as the strength of the metal-RNA interactions.

The Mg1/2 values tend to be higher (~0.4 mM) for resonances within helices that are far from the bulge and that are not sensitive to the stacking transition (Fig. 3B, top). These Mg1/2 values vary insignificantly across the different bulge variants and likely report small local conformational changes due to interactions with ion atmosphere. In contrast, smaller Mg1/2 values (0.1–0.4 mM) were observed for resonances A22-C8 and U23-C6, which are sensitive to the stacking transition (Fig. 3A). These values do differ across the TAR variants, and tend to be smaller for shorter bulge variants, reflecting increased tendencies to form the stacked conformation that is stabilized by Mg2+ (Fig. 3B, bottom).

For U1TAR, all of the measured Mg1/2 values were ~0.4 mM, consistent with the absence of a metal-dependent stacking transition (Fig. 3B, top). Additionally, Mg2+ midpoints for G26 and A22-C2 were ~0.4 mM, consistent with the nonspecific Mg2+ binding rather than interhelical stacking. Finally, we note that the CSPs for A22-C8 in U2TAR deviate from two-state behavior (Fig. 3A; Supplemental Fig. 4; Supplemental Table 2). Fitting to a two-site binding equation (see Materials and Methods) resulted in a low Mg1/2 value of 0.10 mM consistent with Mg2+-dependent coaxial interhelical stacking and a higher Mg1/2 that is consistent with nonspecific interactions with the ion atmosphere (Supplemental Fig. 4; Supplemental Table 2).

**Similar stacking energetics in the presence but not absence of Mg2+**

We used NMR chemical shifts of A22-C8 and U23-C6, which are uniquely sensitive to coaxial stacking, to estimate the relative population of the unstacked and stacked states for the TAR variants in the absence and presence of Mg2+. The observed chemical shifts (δobs) for a given TAR variant is assumed to represent a population weight-averaged over the chemical shifts of the stacked (δstack) and unstacked (δunstack) conformations, such that δobs = Pstack δstack + Punstack δunstack and Pstack + Punstack = 1, where Pstack and Punstack are the fractional populations of stacked and unstacked states, respectively. δstack was obtained from fitting Mg2+-dependent CSPs in U7TAR while δunstack was obtained from prior work based on fitting both Mg2+ and Na+ CSPs in wtTAR (Casiano-Negroni et al. 2007). We then used the values of δobs, δstack, and δunstack to solve for Pstack and Punstack for each TAR variant. Similar results were obtained when using δstack obtained from fitting CSPs to other bulge variants or the chemical shifts measured at 25 mM NaCl with 25.6 mM Mg2+ for any bulge variant and when using the observed chemical shifts at 25 mM NaCl directly for wt, U4, and U7TAR to represent δunstack (data not shown).

Similar populations were obtained when using U23-C6 or A22-C8 chemical shifts to estimate the populations, indicating that these resonances report on the same two-state conformational equilibrium. Based on these chemical shifts, the average population of the stacked state in 25 mM NaCl without Mg2+ is estimated to be 72, 73, 21, 9, and 3% for U1, U2, wt, U4, and U7TAR, respectively. These values correspond to free energy
differences of coaxial stacking ($\Delta G = G_{\text{stack}} - G_{\text{unstack}}$) ranging between $-0.61$ and $2.25$ (Fig. 4A). The differences in interhelical stacking energetics relative to wtTAR ($\Delta \Delta G = \Delta G(\text{variant}) - \Delta G(\text{wtTAR})$) are $-1.39$, $-1.43$, $0.61$, $1.18$ kcal/mol for U1, U2, U4, and U7TAR, respectively (Fig. 4B). As expected, the population of the stacked state decreases for longer bulges. This is most likely due to (i) growing electrostatic repulsion in and around the bulge with increasing bulge length in the stacked conformation, and (ii) there is a greater entropic penalty accompanying stacking with increasing bulge length as the number of unstacked conformations is expected to grow more rapidly than the number of stacked conformation with increasing bulge length (Bailor et al. 2011b; Mustoe et al. 2012). However, there are complexities in the changes in stacking energetics. We observe little to no change in the stacking energetics between U1 and U2TAR ($\Delta \Delta G = 0.04$ kcal/mol), and removing a single nt from wtTAR stabilizes stacking to an extent ($\Delta \Delta G = -1.43$ kcal/mol) that is greater than the destabilizing effects observed when adding four bulgents to wtTAR ($\Delta \Delta G = 1.18$ kcal/mol).

The same analysis based on a two-state model reveals that the population of the stacked state in the presence of 3 mM Mg$^{2+}$ increases to 88%, 82%, 86%, 91% for U2, wt, U4, and U7TAR, respectively (Fig. 4A). This lowers the difference in interhelical stacking energetics relative to wtTAR ($\Delta \Delta G$) to $-0.29$, $-0.21$, $-0.45$ kcal/mol for U2, U4, and U7TAR (Fig. 4B). Therefore, Mg$^{2+}$ significantly reduces the dependence of stacking energetics on bulge length. It is likely that Mg$^{2+}$ effectively diminishes electrostatic repulsion in the stacked state for the various conformations of the bulge residues, thereby lowering the energetic differences with different length bulges. In addition, Mg$^{2+}$ may also help increase the number of conformations of the helices that are sampled in the stacked state with increasing bulge length, as we show below.

**FIGURE 4.** Energetics of interhelical coaxial stacking the TAR bulge variants. (A) Free energy differences between the stacked and unstacked states for each bulge variant ($\Delta G = G_{\text{stack}} - G_{\text{unstack}}$) and (B) the relative free energy as compared to wtTAR where $\Delta \Delta G = \Delta G(\text{variant}) - \Delta G(\text{wtTAR})$ at 25 mM NaCl (gray) and 25 mM NaCl + 3.2 mM Mg$^{2+}$ (gold). Error bars represent an estimated error due to imprecise chemical shift measurements, which was estimated to be $\sim 0.02$ ppm for $^{13}$C.

**NMR RDCs and resonance intensities support Mg$^{2+}$-dependent interhelical stacking**

We used NMR residual dipolar couplings (RDCs) (Tjandra and Bax 1997; Tolman et al. 2001) to further test and characterize the Mg$^{2+}$-dependent stacking transition in the TAR variants. RDCs measured between two nuclei provide long-range information regarding the orientation of the internuclear vector and the applied magnetic field as given by

$$\frac{1 - 3 \cos^2 \theta}{2},$$

where $\theta$ is the angle between internuclear bond vector and the applied magnetic field, and the angular bracket denotes a time average over all orientations sampled in solution (Fürtig et al. 2003; Pitt et al. 2005; Bailor et al. 2010; Zhao and Zhang 2015). RDCs can be used to obtain information regarding the orientation and dynamics of molecular fragments such as the A-form helices in RNA over a broad range of timescales (<msec) (Tolman et al. 2001; Al-Hashimi et al. 2002; Musselman et al. 2006; Bailor et al. 2007; Getz et al. 2007). They can also provide insights into the local dynamics of bulges (Getz et al. 2007; Sun et al. 2007) and other RNA motifs (Eichhorn and Al-Hashimi 2014). We previously reported the RDC-based conformational analysis of wtTAR (Dethoff et al. 2008) and U2TAR (Merriman et al. 2016) at 25 mM NaCl, in the absence of Mg$^{2+}$ and for wtTAR in the presence of Mg$^{2+}$ (Al-Hashimi et al. 2003; Casiano-Negroni et al. 2007). Here, we measured RDCs for U1 and U7TAR in 25 mM NaCl, in the absence of Mg$^{2+}$ and U1, wt, and U7TAR in 25 mM NaCl and 3 mM Mg$^{2+}$ (Supplemental Fig. 5A; Supplemental Tables 3, 4). Measurements under saturating Mg$^{2+}$ concentrations were not feasible due to the incompatibility of these conditions with the Pf1-phage alignment medium used to measure RDCs. Based on the Mg$^{2+}$-dependent CSPs for U23-C6 and A22-C8, the population of the stacked state is predicted to be 88%–90%, for both wt, and U7TAR at 25 mM NaCl and 3 mM Mg$^{2+}$. This can be compared to ~20%, ~3% for wt and U7, respectively, in the absence of Mg$^{2+}$. Such a significant Mg$^{2+}$-dependent shift toward the stacked ensemble should be readily measurable using RDCs, which are exquisitely sensitive to global interhelical conformation (Tolman et al. 1997; Casiano-Negroni et al. 2007; Zhang et al. 2007).

In the absence of Mg$^{2+}$, bulge residues exhibited small RDCs (Supplemental Fig. 5B) and high resonance intensities in 2D HSQC spectra (Supplemental Fig. 2A) consistent with a high degree of local flexibility, with U1TAR and U7TAR exhibiting greater flexibility than the longer bulges most likely due to the flipping out of U23 (Merriman et al. 2016). The RDCs measured throughout wt and U7TAR in the presence of 3 mM Mg$^{2+}$ differed significantly from counterparts measured in the absence of Mg$^{2+}$, consistent
with Mg$^{2+}$ inducing a global change in the structure and/or dynamics of these TAR variants (Fig. 5A). In contrast, similar RDCs were measured for U1TAR in the presence or absence of Mg$^{2+}$, strongly suggesting Mg$^{2+}$ does not significantly alter the U1TAR conformation (Fig. 5A). In all other cases, we observed a decrease in the magnitude of bulge RDCs in 3 mM Mg$^{2+}$ as compared to bulge RDCs at 25 mM NaCl, which is consistent with a shift toward the flipped out flexible conformation expected in the stacked state (Supplemental Fig. 5C; Tolman et al. 2001; Merriman et al. 2016). This conclusion is also supported by another independent measurement of flexibility at the bulge resonances using intensity measurements on 2D NMR spectra (Zhang et al. 2006; Getz et al. 2007; Sun et al. 2007) (see Materials and Methods). Higher resonance intensities, which are indicative of extensive motions on the picosecond to nanosecond timescale, are observed for the bulge residues in the presence of Mg$^{2+}$.

**FIGURE 5.** Characterizing the interhelical structure and dynamics of the TAR bulge variants using NMR. (A) Comparison of RDCs measured at 25 mM NaCl and 25 mM NaCl + 3 mM Mg$^{2+}$ for wt, U2, and U1TAR. RDCs were normalized to the alignment of wtTAR at 25 mM NaCl (see Materials and Methods). RDC values are color coded to represent the part of the molecule measurements that were made: helix 1 (red), helix 2 (blue), apical loop (green), and bulge (orange), whereas symbols represent the bond vector: C8H8/C6H6 (square), C2H2 (circle), C1′H1′ (diamond), C5H5 (triangle), and N1H1/N3H3 (downward triangle). Error bars represent the estimated error of RDC measurements (see Materials and Methods). (B) Normalized peak intensities (see Materials and Methods) measured in U1, wt, and U7TAR at 25 mM NaCl (bottom) and 25 mM NaCl + 25.6 mM Mg$^{2+}$ (top). See inset for legend. The average interhelical conformation of wtTAR, U1, U2, and U7 bulge variants with helix 1 in red, and helix 2 in blue measured at (C) 25 mM NaCl without Mg$^{2+}$ and (D) 25 mM NaCl and 3 mM Mg$^{2+}$. The average bend angle (⟨|βh|⟩) and θint is shown for each structure. (E) ⟨|βh|⟩ and θint as a function of bulge length for TAR variants in 25 mM NaCl without Mg$^{2+}$ (gray) and 25 mM NaCl + 3 mM Mg$^{2+}$ (gold). RDC derived values of ⟨|βh|⟩ and θint for the interhelical coaxially stacked (red) and unstacked (blue) state of wt and U7TAR are also shown. Error bars represent the propagated error in ⟨|βh|⟩ and θint as determined using AFORM-RDC (see Table 1; Musselman et al. 2006).
as compared to resonance intensities at 25 mM NaCl (Fig. 5B; Supplemental Fig. 2B).

**Insights into interhelical ensembles from order tensor analysis of RDCs**

To characterize the interhelical ensemble in the presence and absence of Mg\(^{2+}\), RDCs measured in each helix were subjected to an order tensor analysis (Losonczi et al. 1999; Tolman et al. 2001; Hansen and Al-Hashimi 2006). In this analysis, the average orientation of helices is obtained by superimposing the order tensor frame of each helix, which describes how the helix aligns relative to the applied magnetic field in the presence of an ordering medium (Table 1; Supplemental Fig. 6A–C). The amplitude of interhelical motions is computed from the ratio of the generalized degree of order (\(\theta_{\text{int}} = \theta_i/\theta_j; \theta_i < \theta_j\)) describing the degree of helix alignment relative to the applied magnetic field (Tolman et al. 2001). The \(\theta_{\text{int}}\) value ranges between 1 for interhelical rigidity and 0 for maximum interhelical motions. Because of possible coupling between helix motions and overall alignment (Zhang et al. 2006), the \(\theta_{\text{int}}\) value will generally underestimate the motional amplitudes (Al-Hashimi et al. 2002; Zhang et al. 2003).

Figure 5C shows the RDC-derived average interhelical orientation for bulge variants in the absence of Mg\(^{2+}\). Consistent with prior studies using TEB (Zacharias and Hagerman 1995a) and FRET (Gohlke et al. 1994), increasing the bulge length from 1 to 7 nts resulted in a gradual increase in the interhelical bend angle (\(\beta_{ij}\)) from \(17 \pm 7^\circ\) to \(75 \pm 10^\circ\) (Table 1). Consistent with the CSP data (Fig. 2B), a sharp transition was observed between U2 and wtTAR, which is again biased toward the interhelical coaxial conformation (\(\beta_{ij} = 8\) and \(45^\circ\) for U2 and wtTAR, respectively). The increase in the average bend angle with bulge length was accompanied by an increase in the amplitude of interhelical motions as the RDC-derived \(\theta_{\text{int}}\) decreased from 0.90 ± 0.05 in U1TAR to 0.34 ± 0.06 in U7TAR. Here, U2TAR follows the linear trend formed by the other TAR variants. Therefore, in the absence of Mg\(^{2+}\), increasing the bulge length increases the interhelical flexibility and biases the ensemble toward more kinked conformations.

A similar order analysis of the RDCs (Table 1; Supplemental Fig. 6D) shows that for both wtTAR and U2TAR, Mg\(^{2+}\) shifts the equilibrium toward the more linear and rigid stacked state (Fig. 5D). The average bend angle decreased from \(45 \pm 7^\circ\) and \(75 \pm 10^\circ\) in the absence of Mg\(^{2+}\) to \(22 \pm 13^\circ\) and \(21 \pm 14^\circ\) in the presence of 3 mM Mg\(^{2+}\), respectively. Similarly, the \(\theta_{\text{int}}\) value increased from 0.54 ± 0.07 and 0.34 ± 0.06 in the absence of Mg\(^{2+}\) to 0.95 ± 0.06 and 0.81 ± 0.12 in the presence of 3 mM Mg\(^{2+}\) (Fig. 5E). In contrast, similar order tensor parameters were obtained for U1TAR under the different salt conditions, again supporting the absence of an Mg\(^{2+}\)-induced conformational transition. The fact that the RDC derived interhelical behavior tracks with the CSPs helps to confirm that the A22 and U23 CSPs faithfully report on the stacking transition.

**TABLE 1.** Order tensor analysis statistics for U1TAR, U2TAR (Merriman et al. 2016), wtTAR (Dethoff et al. 2008), and U7TAR

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<td>0.19 ± 0.1</td>
<td>1.14 ± 0.04</td>
<td>0.90 ± 0.05</td>
<td>-17 ± 7</td>
<td>6 ± 50</td>
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<td>2.4</td>
<td>3.6</td>
<td>0.99</td>
<td>0.18 ± 0.08</td>
<td>1.27 ± 0.04</td>
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<tr>
<td><strong>U2TAR(^a)</strong></td>
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<tr>
<td>Helix 1</td>
<td>11</td>
<td>2.5</td>
<td>4.4</td>
<td>0.99</td>
<td>0.59 ± 0.15</td>
<td>1.4 ± 0.1</td>
<td>0.75 ± 0.07</td>
<td>-8 ± 3</td>
<td>23 ± 50</td>
</tr>
<tr>
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<td>11</td>
<td>1.5</td>
<td>5.9</td>
<td>0.99</td>
<td>0.14 ± 0.09</td>
<td>1.9 ± 0.1</td>
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<tr>
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<td>Helix 1</td>
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<td>1.2</td>
<td>5.7</td>
<td>0.99</td>
<td>0.36 ± 0.10</td>
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<td>1.7</td>
<td>3.0</td>
<td>0.99</td>
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<td>1.19 ± 0.05</td>
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<tr>
<td><strong>U7TAR</strong></td>
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<td>0.77 ± 0.22</td>
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<td>7.0</td>
<td>0.99</td>
<td>0.75 ± 0.07</td>
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<td><strong>U7TAR 3mM Mg(^{2+})</strong></td>
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<td>0.99</td>
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<td>1.05 ± 0.04</td>
<td>0.90 ± 0.07</td>
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<td>Helix 2</td>
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<td>4.2</td>
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<td>0.20 ± 0.07</td>
<td>1.16 ± 0.06</td>
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<tr>
<td><strong>TAR 3mM Mg(^{2+})</strong></td>
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<tr>
<td>Helix 1</td>
<td>13</td>
<td>2.7</td>
<td>2.9</td>
<td>0.99</td>
<td>0.16 ± 0.08</td>
<td>1.15 ± 0.06</td>
<td>0.95 ± 0.06</td>
<td>22 ± 13</td>
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<td>Helix 2</td>
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<td>3.2</td>
<td>0.99</td>
<td>0.13 ± 0.09</td>
<td>1.22 ± 0.05</td>
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<tr>
<td><strong>7U-TAR 3mM Mg(^{2+})</strong></td>
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<tr>
<td>Helix 1</td>
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<td>2.2</td>
<td>3.0</td>
<td>0.99</td>
<td>0.86 ± 0.1</td>
<td>0.72 ± 0.08</td>
<td>0.81 ± 0.12</td>
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<td>0.47 ± 0.07</td>
<td>0.88 ± 0.08</td>
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</table>

\(^a\)Previously reported RDC measurements.
\(^b\)Error could not be accurately reported from AFORM-RDC and was estimated from Sanson-Flamsteed projections of helical order tensors (Supplemental Fig. 6C).

Reported parameters are the number of input RDCs (\(N\)), root-mean-square deviation (RMSD) and Pearson’s correlation coefficient (\(R\)) between measured and back-calculated RDCs; condition number (\(CN\)) describing the independents of the RDC data; degree of asymmetry (\(\eta = |S_{yy} - S_{zz}| / S_{zz}\)); generalized degree of order (\(\theta = \sqrt{2/3}[S_{yy} + S_{zz} + S_{xx}]\)) (Tolman et al. 2001). Also shown are the internal generalized degree of order (\(\theta_{\text{int}} = \theta / \theta_{ij}\), \(\theta_i < \theta_j\)), and the average interhelical bend (\(\beta_{ij}\)) and twist (\(\xi\)) (see Materials and Methods). Errors were estimated using AFORM-RDC (Musselman et al. 2006).
U2TAR is biased toward linear conformations in the presence and absence of Mg$^{2+}$

The average bend angle for U2TAR in the presence or absence of Mg$^{2+}$ is lower than that of any other bulge variant, including U1TAR (Table 1). Such a bias toward more linear conformations was not observed in prior TEB studies of A and U dinucleotide bulges, indicating that it is potentially unique to TAR (Zacharias and Hagerman 1995a). We observe unique NOEs between G26-H1’ and U23-H6, A22-H8, and U25-H6 in U2TAR, but not wtTAR, which suggests a potentially unique bulge conformation in which U23 forms a U23•A27•U38 base triple (Supplemental Fig. 7A). This base triple is observed in U2 and wtTAR when complexed with mimics of the HIV viral protein Tat (Puglisi et al. 1992; Brodsky and Williamson 1997; Hennig and Williamson 2000). Indeed, a molecular dynamics (MD) simulation and a structure-based survey suggest that such an interaction could occur in U2TAR (Supplemental Material Discussion, Supplemental Fig. 7). Thus, the 2 nt bulge in U2TAR may be short enough to promote stacking but long enough to allow base triple formation.

To test this hypothesis, we collected H6(C5)NN NMR spectra (Pitt et al. 2004) to directly probe for H-bonding between U23-N3 and A22-N7 in U2TAR at 25 mM NaCl in the absence or presence of 3 mM Mg$^{2+}$ (Supplemental Fig. 7F). Results revealed that U23-N3 is not hydrogen bonded to A27-N7, and thus is not stably forming a base triple under either buffer condition. However, weak hydrogen bonding between A22 and U40 was observed at 25 mM NaCl (Supplemental Fig. 7F). This H-bond is not observed in wtTAR (Pitt et al. 2004). Stronger hydrogen bonding of the flanking A22-U40 base pair, as compared to wtTAR, coupled with conformational changes in the bulge may result in stronger stacking interactions between helices and thus a smaller interhelical bend in U2TAR. Assuming negligible line broadening due to conformational exchange, it should have been possible to detect a base triple using the H6(C5)NN NMR experiment even if its population was as low as ~10%. On the other hand, the base triple may be forming with significant population >10% but is not detectable because of unfavorable exchange kinetics that may lead to unfavorable line broadening. Future studies could explore other trans-hydrogen bond scalar coupling experiments (Hennig and Williamson 2000) to examine whether such lowly populated base triple species form and to examine how their stability and dynamics vary across bulge lengths.

Evidence for increased dynamics in the stacked state with longer bulges

We can estimate βh values of 0.98 ± 0.15/20 ± 12° and 0.90 ± 0.20/15 ± 10° for the stacked state of wt and U2TAR based on the population of the stacked (pstack) and unstacked (punstack) state derived from the Mg1/2 values, approximate interhelical parameters for the unstacked states deduced at low salt concentration, and assuming that the measured bend angles and βh values correspond to population-weighted averages (i.e., $\beta_{h,obs} = p_{stack}\beta_{h,stacked} + p_{unstack}\beta_{h,unstacked}; \beta_{h,obs} = p_{stack}\beta_{h,stacked} + p_{unstack}\beta_{h,unstacked}$). This can be compared to 0.51 ± 0.08/46 ± 28°and 0.31 ± 0.07/78 ± 53° for the corresponding unstacked state, respectively. Interestingly, we find a greater degree of interhelical flexibility in the stacked state of U2TAR as compared to wtTAR although these differences are within error. Additional evidence for increased flexibility in stacked state in the presence of Mg$^{2+}$ with increasing bulge length comes from the higher resonance intensities at both base and sugar resonances belonging to residues in and around the bulge (Fig. 5B; Supplemental Fig. 2B).

Taken together, these NMR data provide strong evidence that U2, wt, and U7TAR but not U1TAR undergo an Mg$^{2+}$-dependent stacking transition and that elongating the bulge results in an increase in the dynamics in both the unstacked and coaxially stacked conformations.

DISCUSSION

Early studies showed that the kinks introduced by bulges decrease with decreasing bulge length and increasing salt concentration (Lilley 1995; Zacharias and Hagerman 1995a). Subsequent NMR studies on HIV-1 TAR (Al-Hashimi et al. 2003; Casiano-Negroni et al. 2007) as well as the two bulge variant (Merriman et al. 2016) indicated that poly-pyrimidine bulges exist in a dynamic equilibrium between stacked and unstacked conformations with Mg$^{2+}$ favoring the stacked state. Our results show that other TAR variants with n ≥ 2 can be described by a similar two-state dynamic equilibrium. Conversely, U1TAR did not undergo an Mg$^{2+}$-induced transition. Prior RDC studies showed that Mg$^{2+}$ minimally affects the global conformation of RNase P P4 RNA containing a single bulge (Getz et al. 2007). This similarity indicates that the absence of an Mg$^{2+}$-dependent transition is not unique to U1TAR and may be a general feature of single-pyrimidine bulges.

In the X-ray structure of wtTAR (Ippolito and Steitz 1998), some of the metal interactions rely on contacts with more than one bulge nt, interactions that could not be supported in U1TAR. Indeed, unlike wt and U7TAR, U1TAR did not exhibit large Mg$^{2+}$ CSPs at purine-N7, which frequently forms contacts with metals (Supplemental Fig. 8). The shorter bulge in U1TAR may also preclude optimal interhelical stacking and/or may form more stable alternative structures. A crystal structure of an RNA duplex containing a single uridine bulge shows a highly stable structure, in which the uridine bulge folds back to hydrogen bond to flanking residues in the minor groove (Xiong et al. 2001).
The uridine bulge causes over-twisting between flanking bps and the single bound Ca2+ ions near the bulge appear to be disordered. Together these works support our findings of a highly stable structure of U1TAR that is minimally perturbed by divalent metal ions.

Increasing the bulge length from 1 to 7 nts resulted in an increase in both the average kink angle as well as the degree of interhelical flexibility in both the stacked and unstacked conformations. Yet despite this significant difference, the TAR variants showed similar energetics for the stacking transition in the presence of Mg2+, with differences of ∼0.4 kcal/mol, compared to differences upwards of ∼2.9 kcal/mol in low monovalent salt. One plausible explanation supported by our NMR data is that in the presence of Mg2+, the stacked state is not rigid, but rather retains a degree of conformational flexibility, possibly involving twisting motions and bending motions that maintain stacking as well as localized flexibility within the bulge itself. Indeed, prior studies have shown that Mg2+ activates dynamics (Chu et al. 2009; Herschlag et al. 2010; Chen et al. 2012; Shi et al. 2015; Bao et al. 2016). These motions could be restricted in the absence of Mg2+ because electrostatic repulsion between the closely stacked helices limits the range of conformations sampled. However, we cannot rule out other contributions. For example, longer bulges may provide more flexibility to form optimal stacking interactions that are otherwise topologically inaccessible to shorter bulges. While the different bulge variants show similar helical chemical shifts at saturating Mg2+ conditions, there are notable differences at residues near the bulge that suggest differences in the stacked ensemble. The longer bulges may also interact more favorably with Mg2+ ions. Further studies are needed to dissect these different energetic contributions. Finally, while unlikely given prior studies showing that UCU and UUU bulge behave similarly (Roy et al. 1990; Sumner-Smith et al. 1991; Riordan et al. 1992; Carter-O’Connell et al. 2008), we cannot rule out sequence effects on the behavior of wtTAR relative to poly(U) bulge variants. Future studies should also examine how sequence composition affects the conformational behavior of bulge motifs (Eichhorn and Al-Hashimi 2014).

Our work provides detailed conformational, dynamic and energetic information yet there are, as we note, atomic-level uncertainties. We previously showed that the interhelical behavior of the TAR ensemble is difficult to model using MD simulations (Eichhorn et al. 2012; Salmon et al. 2013; Yang et al. 2014). The rich data set obtained in this work can provide powerful opportunities to develop and test atomic-level MD force field energetics. Systematic data sets such as the one presented here will ultimately be needed to fully understand the forces underlying RNA energetics and dynamics.

The picture that emerges from this study is that under near-physiological (3 mM) Mg2+, poly-pyrimidine bulges exist predominantly (population >90%) in the stacked state, with the population of stacked state decreasing minimally between 1 and 7 bulge motifs. However, the interhelical flexibility of the stacked state ensemble increases with increasing bulge length, possibly allowing a broader range of conformations to be sampled while simultaneously compensating for the entropy loss accompanying stacking. This ability to sample unstacked conformations is important when considering that most helices are coaxially stacked in naked RNA structures but deviate significantly from coaxial when in complex with proteins and ligands (Fig. 1A). Energetically compensated transitions between states that retain varying degrees and/or types of flexibility may be a common feature of RNA junctions that helps to maximize adaptability and malleability of these motifs for optimally effecting changes in response to cellular cues.

**MATERIALS AND METHODS**

**Sample preparation**

**In vitro transcription**

RNA NMR samples were prepared by in vitro transcription using T7 RNA polymerase (Fisher Scientific), uniformly labeled 15C/15N nucleotides (Cambridge Isotopes Laboratories, Inc.), and synthetic DNA templates (Integrated DNA Technologies), which contain the T7 promoter sequence (TTAATACGACTCACTATAG) and RNA sequence. Samples were purified with denaturing, 8 M Urea and 1× tris-borate-EDTA, polyacrylamide gel electrophoresis (PAGE). RNA was excised after briefly shadowing the gel at 365 nm using a UV handlamp, followed by electro elution (Whatman, GE Healthcare) in 1× tris-acetic acid-EDTA. The eluted RNA was concentrated after briefly shadowing the gel at 365 nm using a UV handlamp, followed by electro elution (Whatman, GE Healthcare) in 1× tris-acetic acid-EDTA. The eluted RNA was concentrated followed by ethanol precipitation. The RNA was then annealed by heating to 95°C for 5–10 min and snap-cooled on ice for 1 h. Finally, samples were buffer exchanged using centrifugal concentration into NMR buffer (15 mM sodium phosphate, 25 mM NaCl, 0.1 mM EDTA and pH’d to 6.4 using concentrated 12 M HCl or 5 M NaOH). 10% D2O was added to each sample before data were collected.

**Solid-phase oligonucleotide synthesis**

Unlabeled U2TAR used in 2D NOESY NMR experiments was synthesized with the MerMade 6 DNA/RNA synthesizer (Bioautomation) using standard phosphoramidite chemistry and base and 2′-hydroxyl deprotection protocols. Samples were purified using Glen-Pak RNA purification cartridges following product protocol which can be found online (www.glenresearch.com). After purification the RNA was ethanol precipitated, and buffer exchanged as described above.

**NMR experiments**

**Resonance assignments**

Resonance assignments for TAR variants were obtained by overlaying 2D HSQC spectra of TAR variants with spectra of...
wtTAR (Dethoff et al. 2008) and U7TAR (Merriman et al. 2016) as well as HCN experiments to confirm sugar and aromatic assignments (Supplemental Fig. 9). Experiments were processed using NMRPipe (Delaglio et al. 1995), and visualized in SPARKY (Goddard and Kneller, SPARKY 3, University of California, San Francisco).

**Measuring residual dipolar couplings**

One-bond C-H splittings (1DCH) in base (C2H2, C6H6, and C8H8) and sugar (C1'H1) moieties were measured with 2D 13C-1H 5T E HSQC experiments, which encode splittings in either the 1H or 13C dimension (Meissner and Sorensen 1999; Pitt et al. 2005). N-H splittings (1DNH) were measured using 2D 1H/15N HSQC experiments using spin-state selection, which encode splittings in the 1H dimension (Parella 2006), and a decoupled 2D 1H/15N HSQC was used to measure splittings in the 15N dimension. RDCs were calculated by taking the difference between splittings measured in the absence (I) and presence (I + D) of 15-23 mg/mL of Pt1 phage (Asla Biotech, Ltd.) aligning medium. The RDCs measured from the two sets of experiments were averaged and used in subsequent analyses (Supplemental Fig. 5A; Supplemental Tables 3, 4). The root-mean-square deviation (RMSD) between RDCs measured using splittings encoded in 1H versus 13C/15N dimension was used to estimate the RDC measurement uncertainty (Supplemental Fig. 5A). Data were collected on a 600 MHz Bruker NMR spectrometer equipped with an HCN cryogenic probe for U1 and U7TAR in NMR buffer, and U7TAR in NMR buffer with 3 mM Mg2+, and on a 700 MHz Bruker NMR spectrometer equipped with a 5 mM QXI room temperature quadrupolar probe (1H/19F/13C/15N) with Z-axis pulse field gradients for U1 and wtTAR in NMR buffer with 3 mM Mg2+.

**Order tensor analysis of RDCs**

RDCs measured in nonterminal Watson–Crick base pairs (G18-C44, C19-G43,A20-U42 in helix 1 and G26-C39, A27-U38, G29-C37 in helix 2) were subjected to an order tensor analysis (Losonczi et al. 1999) using the program RAMAH (Hansen and Al-Hashimi 2006) as described previously (Losonczi et al. 1999; Bailor et al. 2007). The analysis used idealized A-form helices as the input structure for the two helices. The helices were created in Insight II (Molecular Simulations) correcting the propeller twist to 15°. Uncertainties in the best-fit order tensor were estimated with the program AFORM-RDC (Musselman et al. 2006). Average interhelical orientations were determined by rotating the input idealized A-form helix into the principal axis system (PAS) of the best-fit order tensor frame. Degeneracies in the structures (Pretestegard et al. 2007) were then determined by visualizing helices in PyMOL (http://www.pymol.org) where helix 2 was superimposed onto helix 1. Helices were then rotated by 180° in S22, Syy, and Sxz axes of the PAS. Selected poses were chosen such that the distances from U40(P)-C39(O3) and A22(O3)-G26 (P) were <1.59 Å and <4.9 Å x by the number of bulge residues. This eliminated degeneracies for all molecules except U7TAR measured in NMR buffer and 3 mM Mg2+ (the degenerate solution can be found in Supplemental Fig. 6B). Interhelical Euler angles for the allowed orientations were then calculated using an in-house C program based on Euler-RNA (Bailor et al. 2007). RDCs for TAR variants were normalized relative to wtTAR using a normalization factor that is based on the ratio of helix 2 φ values. In all cases, RDCs measured in the A-form helices showed an excellent fit to the idealized A-form geometry (Supplemental Fig. 6A, D), as described previously for wtTAR (Dethoff et al. 2008) and U7TAR (Merriman et al. 2016).

**Chemical shift titrations and determination of Mg1/2**

Aromatic SOFAST-HMQCs (Sathyamoorthy et al. 2014) were collected on a 600 MHz Bruker NMR spectrometer equipped with an HCN cryogenic probe. 12 13C/15N labeled samples of wtTAR and each bulge mutant was diluted to 25 μM RNA at 500 μL in NMR buffer after sample preparation (see above). Each sample was then subjected to 18 h of dialysis against 500× the sample volume of NMR buffer containing 0, 0.025, 0.05, 0.01, 0.2, 0.4, 0.8, 1.6, 3.2, 6.4, 12.8, 25.6 mM Mg2+ using a 1 kDa molecular weight cut off Tube-O-DIALYZER Medi unit (G-Biosciences). Buffer was changed after 3 h, 12 h, and an additional 3 h to ensure complete thermodynamic equilibration. Additional dialysis titration experiments on wtTAR were conducted using the same dialysis protocol and Tube-O-DIALYZER Medi units. In one case, EDTA was removed from the NMR buffer and all subsequent buffers containing Mg2+ (Supplemental Fig. 1B). In the other, the [wtTAR] was 0.3 mM and additional titration points were added (0.075, 0.15, 0.25, 0.3, 0.6, 1.2, 2.4, and 32 mM Mg2+) (Supplemental Fig. 1F).

Chemical shift values were measured using SPARKY (Goddard and Kneller, SPARKY 3, University of California, San Francisco) after processing in NMRPipe (Delaglio et al. 1995). Chemical shifts were fit to an expression (Equation 1) describing one site binding using an in-house python script available online (https://github.com/DrComFlakes/ChemicalShiftTitrations).

\[
\delta_{obs} = \delta_i + \Delta \delta \left( \frac{[Mg^{2+}]_{free}}{Mg^{1/2} + [Mg^{2+}]_{free}} \right)
\]

where \(\delta_{obs}\) is the observed chemical shift, \(\delta_i\) is the fitted chemical shift of the unstacked state, \(\Delta \delta\) is the difference between the chemical shift of the unstacked and the stacked state, and \(Mg^{1/2}\) is apparent equilibrium constant for Mg2+ binding. In the case of resonances that report on stacking, it is assumed to be the concentration of Mg2+ in which the RNA has a 50% population between stacked and unstacked states. The expression assumes that any chemical shift is only sensitive to one Mg2+-dependent transition. Note that carrying out the titrations using buffer exchange simplifies this expression since the concentration of free [Mg2+] is known, one does not have to solve for total and free concentrations of [Mg2+]. Fits are shown in Supplemental Figure 3, with listed fitted parameters in Supplemental Table 2.

The uncertainty in the fitted parameters was estimated using Monte-Carlo simulations. Briefly, for a given TAR variant, all CSPs were fit to Equation 1. The differences between the measured CPSs and values back-calculated from a fit to Equation 1 were then fit to a Gaussian distribution to obtain a standard deviation \(\sigma_1\). Simulations were then performed in which each CSP data point was perturbed by an amount determined by selecting values from the Gaussian distribution, and the noise corrupted data was then refit to Equation 1. Simulations were repeated 2000 times and the standard deviation in each fitted parameter was used to approximate the uncertainty in the fitted parameter (Supplemental Tables 1, 5), which are shown in Supplemental Figure 3.
The nonlinear CSP trajectory of A22-C8 in U2TAR was fitted (Supplemental Fig. 4) to a more complex model (Equation 2) that assumes two independent binding sites (Arai et al. 2012),

\[
\delta_{\text{obs}} = \delta_0 \Delta \text{Mg}_{1/2(1)} (\text{Mg}_{1/2(2)}) + \delta_0 \Delta \text{Mg}_{1/2(1)} + (\text{Mg}_{1/2(1)} + \text{Mg}_{1/2(2)}) + \delta_0 (\text{Mg}_{2(0)})^2 + \text{Mg}_{1/2(1)} + (\text{Mg}_{1/2(1)} + \text{Mg}_{1/2(2)}) + [\text{Mg}_{2(0)}]^2
\]

where \(\delta_0\) is the chemical shift of the unstacked state, \(\delta_\text{Mg}_{1/2}\) is the chemical shift of the unknown helical \text{Mg}_{2(0)}-dependent event, \(\delta_0\) is the chemical shift of the stacked state, and \(\text{Mg}_{1/2(1)}\) and \(\text{Mg}_{1/2(2)}\) are the fitted equilibrium constants. Supplemental Table 2 lists fitted parameters with the standard error between measured and fitted data.

PDB survey of RNA two-way junction structure

All available nucleic acid X-ray structures in the PDB (Berman et al. 2000) released before August 16, 2017 were downloaded as biological assemblies. An in-house Python script based on previous work (Zhou et al. 2015) was adopted to search and extract coordinates of all two-way junctional motifs. DSSR (Lu et al. 2015) was used to parse sequence and structural information into a complete database using an in-house python code (https://github.com/alhashimilab/RNAJunction). Euler angles were computed using an in-house python script based on Euler RNA (https://github.com/alhashimilab/ABG_calc) (Bailor et al. 2010, 2011a).

Molecular dynamics simulations

U2TAR molecular dynamics simulation

A 3.3 msec continuous MD simulation was run using AMBER 12 (Case et al. 2017) and the ff99bsc0 force field (Zgarbová et al. 2017). Starting coordinates were obtained from model 1 of the NMR solved structure of U2TAR (Brodsky and Williamson 1997) (PDBID: 1ANR) after removing the small molecule arginine. A total of 33,000 conformers were utilized in the distance measurements (Supplemental Fig. 7).

SUPPLEMENTAL MATERIAL

Supplemental material is available for this article.

COMPETING INTEREST STATEMENT

H.M.A. is an advisor to and holds an ownership interest in Nymirum, an RNA-based drug discovery company.

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