Supplementary material

Modulation of the stability of the *Salmonella* fourU-type RNA thermometer

*Jörg Rinnenthal*¹, *Birgit Klinkert*², *Franz Narberhaus*² and *Harald Schwalbe*¹*

¹Institute for Organic Chemistry and Chemical Biology, Center for Biomolecular Magnetic Resonance, Johann Wolfgang Goethe-University, Max-von-Laue-Strasse 7, D-60438 Frankfurt/Main, Germany.

²Microbial Biology, Ruhr-Universität Bochum, Universitätsstrasse 150, NDEF06/783, 44780 Bochum, Germany.

**E-mail**: schwalbe@nmr.uni-frankfurt.de
CD unfolding and refolding curves

CD unfolding and refolding curves of the wt (Figure S1), A8C-mutant (Figure S2) and G14A-C25U-mutant (Figure S3) were analyzed to investigate the reversibility of the global unfolding process. All three RNAs show unfolding and refolding curves that are very similar indicating that the unfolded RNA is able to refold to its native fold under the given buffer conditions (15 mM K₅H₇PO₄, pH 6.5, 25 mM KCl). However, unfolding and refolding curves are slightly shifted. This shift is due to incomplete equilibration of the RNA at the given temperature since the shift is dependent on the temperature slope used in the temperature scan. For the analysis of the melting point Tₘ and the extraction of the thermodynamic parameters of the global unfolding transition ΔGₜₐₜ, ΔHₜₐₜ and ΔSₜₐₜ unfolding and refolding curves were averaged.

![CD unfolding and refolding curves of the wildtype](image)

Figure S1: CD unfolding (red line) and refolding (blue line) curves of the 4U-hp2-wt RNA recorded at a wavelength of 258 nm with a temperature slope of 1°C/min and -1°C/min for unfolding and refolding, respectively.
Figure S2: CD unfolding (red line) and refolding (blue line) curves of the 4U-hp2-A8C-mutant RNA recorded at a wavelength of 258 nm with a temperature slope of 1°C/min and -1°C/min for unfolding and refolding, respectively.
Figure S3: CD unfolding (red line) and refolding (blue line) curves of the 4U-hp2-G14A-C25U-mutant RNA recorded at a wavelength of 258 nm with a temperature slope of 1°C/min and -1°C/min for unfolding and refolding, respectively.
Monophasic CSP fitting results of the imino resonances of the 4U-hp2-wt RNA

Mg\(^{2+}\) titrations of the 4U-hp2-wt RNA were performed and the resulting CSP curves of the imino group resonances were fitted as described (main article, materials and methods, Mg\(^{2+}\) titration experiments). Table S1 illustrates the values for the respective maximum CSP and dissociation constant \(K_{\text{diss}}\) for each analyzed imino signal obtained from the monophasic fit according to equation (2) (main article).

### Table S1: CSPs of the imino groups of the nucleobases of the 4U-hp2-wt RNA caused by the addition of MgCl\(_2\). CSP\(_{\text{max}}\) and \(K_{\text{diss}}\)-values were derived by fitting of the CSP curves by equation (2) (main article). CSP\(_{\text{max}}\): CSP at infinite Mg\(^{2+}\)-concentration; \(K_{\text{diss}}\): dissociation constant.

<table>
<thead>
<tr>
<th></th>
<th>CSP(_{\text{max}}) [ppm]</th>
<th>(K_{\text{diss}}) [mM]</th>
</tr>
</thead>
<tbody>
<tr>
<td>U4</td>
<td>0.057 ± 0.003</td>
<td>0.85 ± 0.18</td>
</tr>
<tr>
<td>U5</td>
<td>0.119 ± 0.004</td>
<td>2.51 ± 0.19</td>
</tr>
<tr>
<td>G6</td>
<td>0.045 ± 0.002</td>
<td>2.12 ± 0.21</td>
</tr>
<tr>
<td>U33</td>
<td>./c</td>
<td>./c</td>
</tr>
<tr>
<td>U32</td>
<td>./a</td>
<td>./a</td>
</tr>
<tr>
<td>G30</td>
<td>./a</td>
<td>./a</td>
</tr>
<tr>
<td>U10</td>
<td>./b</td>
<td>./b</td>
</tr>
<tr>
<td>U11</td>
<td>./b</td>
<td>./b</td>
</tr>
<tr>
<td>G27/G28</td>
<td>./c</td>
<td>./c</td>
</tr>
<tr>
<td>U12</td>
<td>./c</td>
<td>./c</td>
</tr>
<tr>
<td>U13</td>
<td>0.250 ± 0.008</td>
<td>2.38 ± 0.16</td>
</tr>
<tr>
<td>G14</td>
<td>0.030 ± 0.001</td>
<td>1.17 ± 0.12</td>
</tr>
<tr>
<td>U24</td>
<td>0.045 ± 0.003</td>
<td>3.77 ± 0.42</td>
</tr>
<tr>
<td>U23</td>
<td>0.085 ± 0.005</td>
<td>3.34 ± 0.36</td>
</tr>
</tbody>
</table>

*a: imino signal too weak or not detectable  
b: no CSP  
c: no valid fit*
Cooperativity of the two Mg\(^{2+}\) binding sites

According to the CSP curves, the 4U-hp2-wt RNA has two distinct Mg\(^{2+}\) binding sites. Binding of the Mg\(^{2+}\) ions shows positive cooperative effects. These effects can be quantified by the Hill coefficient. To quantify the extent of cooperativity the fraction of occupied Mg\(^{2+}\) binding sites as a function of the Mg\(^{2+}\) concentration was simulated according to the determined macroscopic dissociation constants K\(_1\) and K\(_2\) (Table 3, main article). Subsequently, the \(\theta([\text{Mg}^{2+}])\) curve was fitted according to a four parameter Hill equation (equation S1).

\[
\theta([\text{Mg}^{2+}]) = y_0 + \frac{a*[\text{Mg}^{2+}]^b}{c^b + [\text{Mg}^{2+}]^b}
\]  

(S1)

In equation (S1) \(\theta([\text{Mg}^{2+}])\) is the fraction of occupied Mg\(^{2+}\) binding sites, \(y_0\) is the ordinate intercept, \(a\) is the amplitude, \(c\) the concentration at which 50\% of the Mg\(^{2+}\) binding sites are occupied and \(b\) is the Hill coefficient.

The simulated \(\theta([\text{Mg}^{2+}])\) curve and the sigmoidal fit are illustrated in Figure S4. Apparently, the simulated curve can be fitted by equation (S1). The extracted Hill coefficient is equal to \(b=1.47\). For RNA molecules with two Mg\(^{2+}\) binding sites the Hill coefficient has to be in the range between 1-2. A factor \(b=1\) indicates uncooperative binding while \(b=2\) indicates maximum cooperativity. Factors of \(b<1\) indicate negative cooperativity. Apparently, the observed \(b\) factor is directly in between uncooperative binding and maximum cooperativity. Thus, the two Mg\(^{2+}\) binding sites of the 4U-hp2-wt RNA exhibit intermediate cooperativity.
Figure S4: Plot of the fraction of occupied Mg\textsuperscript{2+} binding sites in the 4U-hp2-wt RNA versus the Mg\textsuperscript{2+} concentration. Parameters used for the simulated curve (blue line): $K_1 = 3.58$ mM, $K_2 = 2.06$ mM. The simulated curve was fitted according to a four parameter Hill equation (red line).
Enthalpy-entropy correlations and implications

In Figure S5 the enthalpy-entropy correlation for the base-pair opening event is illustrated for the 4U-hp2-wt RNA in the absence and in the presence of 1.5 mM MgCl₂. $\Delta H_{\text{diss}}$ and $\Delta S_{\text{diss}}$ are correlated linearly. Linear correlations are very similar in the absence and in the presence of 1.5 mM Mg$^{2+}$. While the Mg$^{2+}$-effect on the slope of the enthalpy-entropy correlation is not significant, the y-axis intercept in the presence of 1.5 mM MgCl₂ ($y0=9.19\text{kJ/mol}$ ± 0.66kJ/mol) is slightly higher than in the absence of MgCl₂ ($y0=8.33\text{kJ/mol}$ ± 0.75kJ/mol). Consequently, Mg$^{2+}$ has a stabilizing effect on the native RNA-RNA interactions involved in base pairing.

![Enthalpy-Entropy correlation](image)

Figure S5: Enthalpy-entropy correlation for the base-pair opening event of individual nucleobases in the 4U-hp2-wt RNA in the absence (blue) and in the presence of 1.5 mM MgCl₂ (orange). Plots were fitted according to the linear equation $f = y0 + mx$. Linear fitting results are illustrated within the figures.
**Mg\(^{2+}\) binding model for one binding site but different conformations of the [RNA*\(\text{Mg}^{2+}\)] complex**

A Mg\(^{2+}\) binding model assuming an [RNA*\(\text{Mg}^{2+}\)]-complex with only one Mg\(^{2+}\) binding site but three different Mg\(^{2+}\) bound states is given in Figure S6.

![Figure S6: Mg\(^{2+}\) binding model assuming one single Mg\(^{2+}\) binding site but three different conformations of the [RNA*\(\text{Mg}^{2+}\)] complex. In this model, the free form is indicated as I (green) and the three different [RNA*\(\text{Mg}^{2+}\)] complexes are indicated as II (blue), III (yellow) and IV (red).](image)

In this model (Figure S6), the free form of the RNA is in equilibrium with the three different Mg\(^{2+}\)-bound forms (II, III, IV). The Mg\(^{2+}\)-bound forms [II, III and IV] are either directly connected to each other or via the free form of the RNA so that the complexes II, III, and IV are in equilibrium to each other, too. The equilibria can be described by the following equations:

\[ K_{\text{II,III}} = \frac{[\text{III}]}{[\text{II}]} \quad (S2) \]

\[ K_{\text{II,IV}} = \frac{[\text{IV}]}{[\text{II}]} \quad (S3) \]

\[ K_{\text{III,IV}} = \frac{[\text{IV}]}{[\text{III}]} \quad (S4) \]
Note that the equilibria in the equations S2, S3 and S4 are not dependent on the Mg\(^{2+}\) concentration. In contrast, the equilibria of the state I with the states II, III and IV (equations (S5), (S6) and (S7)) are dependent on the Mg\(^{2+}\) concentration.

\[
K_{I,II} = \frac{[I][Mg^{2+}]}{[II]} \quad (S5)
\]

\[
K_{I,III} = \frac{[I]/[Mg^{2+}]}{[III]} \quad (S6)
\]

\[
K_{I,IV} = \frac{[I][Mg^{2+}]}{[IV]} \quad (S7)
\]

Insertion of the equations (S2) and (S3) into the equations (S6) and (S7) leads to equation (S8)

\[
K_{I,II} = K_{I,III} \cdot K_{II,III} = K_{I,IV} \cdot K_{II,IV} = \frac{[I][Mg^{2+}]}{[II]} \quad (S8)
\]

From equation (S8) a monophasic hyperbolic binding curve can be deduced. Thus, the binding model in Figure S6 leads to monophasic and hyperbolic CSP curves with the same apparent binding constant for all curves.

Significantly varying \(K_{\text{diss}}\) values for different imino signals (Figure 8, main article; Table S1) and the biphasic CSP curve of nucleotide U12 (Figure 8, main article) cannot be explained by a model assuming only one Mg\(^{2+}\) binding site but different conformations for the [RNA*\(Mg^{2+}\)] complex (Figure S6).

**Evidence for defined Mg\(^{2+}\) binding**
The $\text{Mg}^{2+}$ dependence of the melting point $T_m$ is described in the main manuscript (Figure 5, Table 2). In Figure 5, the $T_m$ values are plotted against the $\text{Mg}^{2+}$ concentration and the free energy values for $\text{Mg}^{2+}$ binding are derived from the hyperbolic fit according to equation (14).

The same data can also be plotted differently. According to (1,2) a plot of $(1/T_m)$ against $\ln[\text{Mg}^{2+}]$ should be sigmoidal in case of diffuse binding but should reveal a linear dependency in case of specific $\text{Mg}^{2+}$ binding. The corresponding plot is given in Figure S7.

![Figure S7](image_url)

Figure S7 $(1/T_m)$ on $\ln[\text{Mg}^{2+}]$ dependence of the 4U-hp2-wt RNA as derived from CD melting curves. The curve can be fitted linearly according to the equation $f = y_0 + mx$. Fitting results are $y_0 = 2.8612 \times 10^{-3} \pm 8.62 \times 10^{-6}$, $m = 3.3126 \times 10^{-5} \pm 0.1304 \times 10^{-5}$ and $r^2 = 0.9893$.

 Apparently, the plot in Figure S7 reveals a linear dependency. Therefore, the observed $\text{Mg}^{2+}$ dependence of $T_m$ is caused by specific $\text{Mg}^{2+}$ binding. Consequently, the CSP curves of the imino region (Figure 8, main article) are caused by specific $\text{Mg}^{2+}$ binding. The plot of $1/T_m$ vs. $\ln[\text{Mg}^{2+}]$ would exhibit a superposition of a sigmoidal curve for diffuse binding and a linear curve for defined binding, if diffuse binding effects would cause significant $T_m$ variations. According to Figure S7 the
The plot is purely linear and does not show any sigmoidal curvature in the concentration range investigated. Thus, the effects of specific Mg\(^{2+}\) binding clearly dominate over diffuse binding effects, at least in the concentration range (0-7mM) observed here.

**Qualitative explanation of the observed CSP curves using a two binding site model**

The different monophasic CSP curves can be described by a model with two Mg\(^{2+}\) binding sites (Figure 1, main article) as follows. While some imino groups sense the binding of a Mg\(^{2+}\) ion to the first binding site, other imino groups experience a CSP upon binding of a Mg\(^{2+}\) ion to the second binding site. A few imino signals might sense only the formation of the binary or only the formation of the ternary complex, others might experience different CSPs for the different Mg\(^{2+}\) binding sites. Due to the observed cooperativity, the model predicts two dissociation constants for a particular Mg\(^{2+}\) binding site which lead to two superimposing curves. However, the respective dissociation constants (K\(_{2,4}\); K\(_{1,2}\)) are very different so that only the small dissociation constant K\(_{2,4}\) is observable. The same is true for the second Mg\(^{2+}\) binding site (dissociation constants K\(_{3,4}\); K\(_{1,3}\)) where only K\(_{3,4}\) is observable. The signals U23 and U24 exhibit a dissociation constant of approximately 3.56 mM, which is within the margin of error of the macroscopic dissociation constant K\(_{1}\). Thus, a scenario, in which U23 and U24 experience the transition between free RNA and binary complex, no matter which binding site is occupied, but do not exhibit a CSP upon transition between binary and ternary complex might explain the observed CSP curves. Monophasic CSP curves that show dissociation constants between 2.12 mM and 2.51 mM (G6, U13, U5) might result from overlapping biphasic CSP curves with equal signs for the CSPs of both transitions. Such curves might appear as monophasic curves with dissociation constants between K\(_{1}\) (3.58 mM) and K\(_{2}\) (2.06 mM), which is the case for G6 (2.12 mM), U13 (2.38 mM) and U5 (2.51 mM).
Literature
