# Electronic Supplementary Information (ESI) 

# Corroboration of $\mathbf{Z n}($ II $)-\mathbf{M g}($ III $)$-tertiary structure interplays essential to optimal catalysis of a phosphorothiolate thiolesterase ribozyme 

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GNRA tetraloop

Running title: Divalent metal ions essential to phosphorothiolate thiolesterase RNA
catalysis

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## Supplemental Figures

(A)

(B)


Fig. S1. Kinetics of TW17 ribozyme catalysis in the presence of $0.5 \mathrm{mM} \mathrm{Zn}^{2+}$ only. (A) Time-course study of catalysis for the ${ }^{32} \mathrm{P}$-labeled GMPS-primed TW17 ribozyme previously conjugated with 18a. The reaction products from each time point were separated by SAv gel shift assay in $8 \%$ urea-PAGE, and analyzed by an Amersham Typhoon PhosphorImager system. The top arrow indicates the location of the SAvretarded ${ }^{32} \mathrm{P}$-labeled TW17 ribozyme-18a conjugate; the bottom arrow represents the migration of the ${ }^{32} \mathrm{P}$-labeled TW17 ribozyme-catalyzed reaction product. (B) Determination of the pseudo-first-order rate constant $k_{\text {obs }}$ for the TW17 ribozyme catalysis in the presence of $0.5 \mathrm{mM} \mathrm{Zn}{ }^{2+}$ only. Data obtained from the ImageQuant software analysis in Figure S1A were fitted into a single-exponential equation for the first-order kinetics, $\mathrm{F}(t)=\mathrm{F}_{0}+\mathrm{F}_{\max }\left(1-\mathrm{e}^{-k_{\text {obst }} t}\right)[\mathrm{F}(t)$, percent cleavage of the reactant at a
specific time point $t$; GraphPad, La Jolla, CA, USA), to obtain the pseudo first-order rate constant $k_{\text {obs }}=0.005 \mathrm{~min}^{-1}$ for TW17 ribozyme catalysis.


Fig. S2. Outer-sphere and inner-sphere $\mathrm{Mg}^{2+}$ all required for optimal TW17 ribozyme catalysis. The ${ }^{32} \mathrm{P}$-body-labeled GMPS-primed TW17 RNA previously conjugated with 18a catalyzed each reaction in the presence of specified metal ions. Reaction products were separated by streptavidin (SAv) gel shift assay in $8 \%$ ureaPAGE and analyzed by an Amersham Typhoon PhosphorImager system. The top arrow in the figure indicates the location of the SAv-retarded ${ }^{32} \mathrm{P}$-labeled TW17 ribozyme-18a conjugate; the bottom arrow represents the migration of the ${ }^{32} \mathrm{P}$-labeled TW17 ribozyme-catalyzed reaction product. The presence of doublet signals in the region indicated by the top arrow was the result of either one (lower band) or at least two (upper band) TW17 ribozyme-18a conjugates adsorbed onto an SAv molecule during the SAv gel shift assay due to significant excess of the TW17 ribozyme-18a conjugates in the samples.


Fig. S3. Constructs of trans-acting TW17 ribozyme systems for studying of base-pairing (bp) effects on degrees of substrate RNA-catalyst RNA adsorption by classical Langmuir isotherm analysis. The black-colored RNA sequences and structures shown here are those for TW17S-1 RNA (named as $\mathrm{S}_{1-18}$ RNA before) \{Wang, 2012 \#527\} and TW17C1 RNA (named as TW17 $2_{22-87}$ RNA before) $\{W a n g, 2012$ \#527\}. The RNA molecules complex to each other through the base pairs in the P1 helix (marked in the light blue box). Additional base-pairings in the P1 helix were acquired by either site-directed mutagenesis or sequence insertions in the RNA molecules to obtain more trans-acting TW17 ribozyme systems for Langmuir isotherm studies. The newly incorporated nucleotides in the RNA were either highlighted in red or shown as the purple arrows. All RNA molecules were acquired by in vitro transcription of the corresponding DNAs synthesized by procedures described on Table S1. Values of $K_{\mathrm{d}}$ (the dissociation constant for the TW17S RNA-TW17C RNA complex at equilibrium) and released binding free energy ( $\Delta G_{\text {binding }}$ ) were obtained from Langmuir isotherm analysis as stated in Experimental.


Figure S4. The secondary structure for the cis-acting GMPS-primed TW17 ribozyme when covalently linked to the substrate $\mathbf{1 8 a}$ (gray color highlighted by a red-color box).
(A)

(B)

(C)

| Reaction Time (min): | $\mathbf{0}$ | $\mathbf{5}$ | $\mathbf{1 0}$ | $\mathbf{2 0}$ | $\mathbf{4 5}$ | $\mathbf{9 0}$ | $\mathbf{1 8 0}$ |
| ---: | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Yield (\%): | 2 | 6 | 18 | 38 | 54 | 57 | 65 |

(D)


## (E)

| Reaction Time (min): | 0 | 5 | 10 | 20 | 45 | 90 | 180 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Yield (\%): | 3 | 13 | 14 | 18 | 26 | 31 | 34 |
|  |  |  |  |  | - | - | - |

## (F) <br> 

Fig. S5. Cis-actingTW17 ribozyme catalysis in the presence of metal concentrations different from those in the standard reaction condition $\left(\left[\mathrm{Zn}^{2+}\right]=0.5 \mathrm{mM}\right.$ and $\left[\mathrm{Mg}^{2+}\right]=$ 100 mM ). Streptavidin (SAv) gel-shift assay in $10 \%$ urea-PAGE was employed to separate products of TW17 ribozyme catalysis when (A) $\left[\mathrm{Zn}^{2+}\right]$ was adjusted to 1.25 mM , (C) $\left[\mathrm{Mg}^{2+}\right]$ was changed to 37.5 mM , or ( E ) both $\left[\mathrm{Zn}^{2+}\right]$ and $\left[\mathrm{Mg}^{2+}\right]$ were adjusted to 1.25 mM and 37.5 mM , respectively. The images of (A), (C) and (E) were acquired from the analyses of an Amersham Typhoon PhosphorImager system. The top blue arrow in each image represents the location of the SAv-retarded ${ }^{32} \mathrm{P}$-labeled TW17 RNA-18a conjugate; the bottom blue arrow indicates the migration of the ${ }^{32} \mathrm{P}$-labeled TW17 ribozyme-catalyzed reaction product. Each data set obtained from the ImageQuant software analysis in Figures S5A, S5C or S5E was plotted as (B), (D) or (F) respectively, and fitted into a single-exponential equation for the first-order kinetics, $\mathrm{F}(t)=\mathrm{F}_{0}+$
$\mathrm{F}_{\max }\left(1-\mathrm{e}^{-k_{\text {olot }}}\right)[\mathrm{F}(t)$, percent cleavage of the reactant at a specific time point $t$; GraphPad, La Jolla, CA, USA), to afford the corresponding pseudo first-order rate constant $k_{\text {obs }}$ of $0.027 \mathrm{~min}^{-1}, 0.041 \mathrm{~min}^{-1}$ or $0.030 \mathrm{~min}^{-1}$ respectively for TW17 ribozyme catalysis.

## (A)



## (B)



$$
\begin{aligned}
V_{i} & =0.15 \mathrm{nM} \cdot \mathrm{~min}^{-1} \\
\text { Four-day } \text { yield } & =24 \%
\end{aligned}
$$

## (C)



## $\mathrm{V}_{i}=0.05 \mathrm{nM} \cdot \mathrm{min}^{-1}$ <br> Four-day yield $=\mathbf{2 1 \%}$

Fig. S6. Multiple substrate turnover of two trans-actingTW17 ribozyme systems in the presence of the optimal metal concentrations determined by the results of Figure S5 $\left(\left[\mathrm{Zn}^{2+}\right]=0.5 \mathrm{mM}\right.$ and $\left.\left[\mathrm{Mg}^{2+}\right]=37.5 \mathrm{mM}\right)$ and of those in the standard reaction condition ( $\left[\mathrm{Zn}^{2+}\right]=0.5 \mathrm{mM}$ and $\left[\mathrm{Mg}^{2+}\right]=100 \mathrm{mM}$ ). SAv gel-shift assay in 20\% urea-PAGE was employed to separate catalytic products of two TW17 ribozyme systems: (A) and (C) of the TW17S ${ }_{1-29}$ RNA-TW17C $\mathrm{Col}_{37}$ RNA pair; (B) of the TW17S $\mathrm{S}_{1-29}$ RNA-TW17C-1 pair. Catalysis under multiple substrate turnover was attained by including 300 nM of the ${ }^{32} \mathrm{P}$ labeled TW17S $\mathrm{S}_{1-29}$ RNA and 30 nM of TW17C $\mathrm{C}_{30-87}$ RNA/TW17C-1 RNA in the reactions. In addition, the TW17 ribozyme systems in (A) and (B) performed catalysis in the presence of 0.5 mM of $\mathrm{Zn}^{2+}$ and 100 mM of $\mathrm{Mg}^{2+}$. On the other hand, TW17 ribozyme catalysis in (C) was carried out in the presence of 0.5 mM of $\mathrm{Zn}^{2+}$ and 37.5 mM of $\mathrm{Mg}^{2+}$. All images were acquired from the analyses of an Amersham Typhoon PhosphorImager system and were quantified by the ImageQuant software. The top blue arrow in each image represents the location of the SAv-retarded ${ }^{32} \mathrm{P}$-labeled TW17S ${ }_{1-29}$ RNA-18a conjugate; the bottom blue arrow indicates the migration of the ${ }^{32} \mathrm{P}$-labeled TW17 ribozyme-catalyzed reaction product. The initial velocities $\left(\mathrm{v}_{i}\right)$ were determined by measuring the slope of the time-course curve from 0 to 1 h in each reaction.

## Supplemental Tables

Table S1. Procedures for construction of the trans-acting TW17 ribozyme systems.

| Biomolecular trans-acting TW17 ribozyme systems | Synthesis of the 5' fragment RNAs | Synthesis of the catalytic core RNAs |
| :---: | :---: | :---: |
| TW17S-1 RNA + <br> TW17C-1 RNA | TW17S-1 RNA: The DNA was acquired by a PCR reaction using Primer TC-20 as the template, and the shortened Normal 5'-primer and Primer TC-21 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C-1 RNA: The DNA was acquired by an extension reaction between Primer TC-2 and Primer TC-3, then a PCR reaction using the extension reaction product as the template, and Primer TC-2 and the normal 3' -35 primer as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} |
| TW17S-2 RNA + <br> TW17C-2 RNA | TW17S-2 RNA: The DNA was acquired by a PCR reaction using the modified 5'-primer as the template, and the shortened Normal 5'-primer and Primer TC-4 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C-2 RNA: The DNA was acquired by a $1^{\text {st }}$ extension reaction between Primer TC-6 and Primer TC-11, a $2^{\text {nd }}$ extension reaction using the $1^{\text {st }}$ extension reaction product as the template and Primer TC-11 and the normal 3' -35 primer as the primer pair, then a PCR reaction using the extension reaction product as the template, and Primer TC-11 and the normal 3' -35 primer as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} |
| TW17S-3 RNA + <br> TW17C-3 RNA | TW17S-3 RNA: The DNA was acquired by an extension reaction between Primer TC-9 and Primer TC10 , then a PCR reaction using the extension reaction product as the template, and the shortened Normal 5'-primer and Primer TC-10 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C-3 RNA: The DNA was acquired by an extension reaction between Primer TC-6 and Primer TC-8, then a PCR reaction using the extension reaction product as the template, and the shortened normal 5'-primer and the normal 3' -35 primer as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} |
| TW17S-4 RNA + <br> TW17C-4 RNA | TW17S-4 RNA: The DNA was acquired by a PCR reaction using Primer TC-12 as the template, and the shortened Normal 5'-primer and Primer TC-13 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C-4 RNA: The DNA was acquired by an extension reaction between Primer TC-6 and Primer TC-14, then a PCR reaction using the extension reaction product as the template, and the shortened normal 5'-primer and the normal 3' -35 primer as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} |


| TW17S-5 RNA + <br> TW17C-5 RNA | TW17S-5 RNA: The DNA was acquired by a PCR reaction using Primer TC-15 as the template, and the shortened Normal 5'-primer and Primer TC-16 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C-5 RNA: The DNA was acquired by a $1^{\text {st }}$ extension reaction between Primer TC-6 and Primer TC-17, a $2^{\text {nd }}$ extension reaction using the $1^{\text {st }}$ extension reaction product as the template and the shortened normal 5'-primer and the normal 3' -35 primer as the primer pair, then a PCR reaction using the extension reaction product as the template, and the shortened normal 5'-primer and the normal 3' -35 primer as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} |
| :---: | :---: | :---: |
| TW17S-6 RNA + <br> TW17C-5 RNA | TW17S-6 RNA: The DNA was acquired by a PCR reaction using Primer TC-18 as the template, and the shortened Normal 5'-primer and Primer TC-19 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C-5 RNA: the same as the above. |
| TW17S-1 RNA + <br> TW17C-5 RNA | TW17S-1 RNA: the same as the above | TW17C-5 RNA: the same as the above. |
| TW17S-2 RNA + <br> TW17C-3 RNA | TW17S-2 RNA: the same as the above | TW17C-3 RNA: the same as the above. |
| TW17S ${ }_{1-29}$ RNA + <br> TW17C ${ }_{30-87}$ RNA | $\mathbf{T W 1 7 S}_{1-29}$ RNA: The DNA was acquired by an extension reaction between Primer TC-9 and Primer TC22 , then a PCR reaction using the extension reaction product as the template, and the shortened Normal 5'-primer and Primer TC-22 as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} | TW17C $_{30-87}$ RNA: The DNA was acquired by a $1^{\text {st }}$ extension reaction between Primer TC-23 and Primer TC-24, a $2^{\text {nd }}$ extension reaction using the $1^{\text {st }}$ extension reaction product as the template and the shortened normal 5'-primer and the normal 3' -35 primer as the primer pair, then a PCR reaction using the extension reaction product as the template, and the shortened normal 5'-primer and the normal 3' -35 primer as the primer pair. The afforded DNA was in vitro transcribed by T7 RNA polymerase. \{Wang, 2012 \#527\} |
| TW17S $_{1-29}$ RNA + <br> TW17C-1 RNA | TW17S $_{1-29}$ RNA: the same as the above | TW17C-1 RNA: The synthesis was reported previously. \{Wang, 2012 \#527\} |

Table S2. Sequences of the primers for construction of the trans-acting TW17 ribozyme systems.

| Primer name | Primer sequence |
| :--- | :--- |


| Shortened <br> Normal 5'primer | 5'-GGTAACACGCATATGTAATACG-3' |
| :---: | :---: |
| Normal 3'-35 primer | 5'-ACCCCTTGGGGATACCACCGGGCCAGCACCACGGA-3' |
| Modified 5'primer | 5'- <br> AACACGCATATGTAATACGACTCACTATAGGGATCGTCAGTGCATT GAG-3' |
| Primer TC-2 | 5'- <br> AACACGCATATGTAATAGGACTCACTATAAGTGCAGTGTCTTGCGC TG-3' |
| Primer TC-3 | 5'-CACCGGGCCAGCACCACGGACCGCTCGAACCCAGCGCAAGAC3' |
| Primer TC-4 | 5'-TCTCAATGCACTGACGATCC-3' |
| Primer TC-6 | 5'CACCGGGCCAGCACCACGGACCGCTCGAACCCAGCGCAAGACACT GCAC-3' |
| Primer TC-8 | 5’- <br> CACGCATATGTAATACGACTCACTATAGGGTGTCAGTGCAGTGTCT TGC-3' |
| Primer TC-9 | 5’-GGTAACACGCATATGTAATACGACTCACTATAGGGATCGTC-3' |
| Primer TC-10 | 5'-GGGTCTCAATGCACTGACGATCCCTATAGTGAGTCG-3' |
| Primer TC-11 | 5’- <br> AACACGCATATGTAATACGACTCACTATAGTCTCAGTGCAGTGTCT TGC-3' |
| Primer TC-13 | 5'-GGAATGCACTGACGATCCC-3' |
| Primer TC-14 | 5'- <br> AACACGCATATGTAATACGACTCACTATAGGAGTGCAGTGTCTTGC GC-3' |
| Primer TC-15 | 5'- <br> AACACGCATATGTAATACGACTCACTATAGGGATCGTCAGTGCAC C-3' |
| Primer TC-16 | 5'-GGTGCACTGACGATCCC-3' |
| Primer TC-17 | 5’- <br> AACACGCATATGTAATACGACTCACTATAGGTGCAGTGTCTTGCGC TGG-3' |
| Primer TC-18 | 5'- <br> AACACGCATATGTAATACGACTCACTATAGGGATCGTCAGTGCATC -3' |


| Primer TC-19 | 5'-GATGCACTGACGATCCC-3' |
| :---: | :---: |
| Primer TC-20 | 5’AACACGCATATGTAATACGACTCACTATAGGGATCGTCGTGCAT TG-3' |
| Primer TC-21 | 5'-CAATGCACTGACGATCCC-3' |
| Primer TC-22 | 5'-ACT GCA CTT CTC AAT GCA CTG ACG ATC CCT ATA GTG AGT CG-3' |
| Primer TC-23 | 5'-GGT AAC ACG CAT ATG TAA TAC GAC TCA CTA TAGT CTT GCG CTG GG-3' |
| Primer TC-24 | 5'-CCG GGC CAG CAC CAC GGA CCG CTC GAA CCC AGC GCA AGA CTA TAG-3' |

Table S3. Compositions of RNA solutions for the Langmuir isotherm analyses of trans-acting TW17 ribozyme systems. 4 X EK buffer: 400 mM EPPS, $4 \mathrm{M} \mathrm{KCl}, \mathrm{pH}$ 7.5.

| TW17S-X <br> RNA: <br> TW17C- <br> Y RNA <br> ratio | TW17S-X <br> RNA <br> solution <br> volume <br> (Stock <br> solution <br> conc.) | $\mathbf{Z n}^{\mathbf{2 +}}$ <br> solution <br> volume <br> (Stock <br> solution <br> conc.) | 4X EK <br> buffer <br> volume | DEPC <br> water <br> volume | TW17C-Y <br> RNA <br> solution <br> volume <br> (Stock <br> solution <br> conc.) | $\mathbf{M g}^{\mathbf{2 +}}$ <br> solution <br> volume <br> (Stock <br> solution <br> conc.) | 4X EK <br> buffer <br> volume | DEPC <br> water <br> volume |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1:0 | $\begin{aligned} & 0.5 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.9 \mu \mathrm{l} \\ & (0.01 \mathrm{M}) \end{aligned}$ | $2 \mu \mathrm{l}$ | $0.6 \mu \mathrm{l}$ | $0 \mu \mathrm{l}$ | $0.188 \mu \mathrm{l}$ (2 M) | $2 \mu \mathrm{l}$ | $\begin{aligned} & 1.812 \\ & \mu 1 \end{aligned}$ |
| 1:0.5 | $\begin{aligned} & 0.5 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.9 \mu \mathrm{l} \\ & (0.01 \mathrm{M}) \end{aligned}$ | $2 \mu \mathrm{l}$ | $0.6 \mu \mathrm{l}$ | $\begin{aligned} & 0.25 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $0.188 \mu \mathrm{l}$ (2 M) | $2 \mu \mathrm{l}$ | $\begin{aligned} & 1.562 \\ & \mu \mathrm{l} \end{aligned}$ |
| 1:1 | $\begin{array}{\|l} 0.5 \mu \mathrm{l} \\ (1.13 \mu \mathrm{M}) \end{array}$ | $\begin{aligned} & 0.9 \mu \mathrm{l} \\ & (0.01 \mathrm{M}) \end{aligned}$ | $2 \mu \mathrm{l}$ | $0.6 \mu \mathrm{l}$ | $\begin{aligned} & 0.5 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $0.188 \mu \mathrm{l}$ (2 M) | $2 \mu 1$ | $1.312$ <br> $\mu 1$ |
| 1:5 | $\begin{aligned} & 0.5 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.225 \mu \mathrm{l} \\ & (0.2 \mathrm{M}) \end{aligned}$ | $2 \mu \mathrm{l}$ | $1.47 \mu \mathrm{l}$ | $\begin{aligned} & 0.17 \mu \mathrm{l} \\ & (16.32 \mu \mathrm{M}) \end{aligned}$ | $0.924 \mu \mathrm{l}$ $(2 \mathrm{M})$ | $2 \mu 1$ | $\begin{aligned} & 0.906 \\ & \mu \mathrm{l} \end{aligned}$ |
| 1:10 | $\begin{aligned} & 0.5 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $0.45 \mu 1$ <br> (0.2 M) | $2 \mu \mathrm{l}$ | $1.45 \mu \mathrm{l}$ | $\begin{aligned} & 0.346 \mu \mathrm{l} \\ & (16.32 \mu \mathrm{M}) \end{aligned}$ | $1.232 \mu \mathrm{l}$ (3 M) | $2 \mu \mathrm{l}$ | $0.41 \mu \mathrm{l}$ |


| 1:20 | $\begin{aligned} & 0.74 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.09 \mu \mathrm{l} \\ & (2 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $2.17 \mu \mathrm{l}$ | $\begin{aligned} & 0.341 \mu \mathrm{l} \\ & (49.16 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 1.56 \mu 1 \\ & (3 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $\begin{aligned} & 1.099 \\ & \mu \mathrm{l} \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1:25 | $\begin{aligned} & 0.74 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.113 \mu \mathrm{l} \\ & (2 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $2.14 \mu \mathrm{l}$ | $\begin{aligned} & 0.427 \mu \mathrm{l} \\ & (49.16 \mu \mathrm{M}) \end{aligned}$ | $1.56 \mu$ <br> (3 M) | $3 \mu \mathrm{l}$ | $\begin{aligned} & 1.013 \\ & \mu 1 \end{aligned}$ |
| 1:40 | $\begin{aligned} & 0.74 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.18 \mu \mathrm{l} \\ & (2 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $2.08 \mu \mathrm{l}$ | $\begin{aligned} & 0.683 \mu \mathrm{l} \\ & (49.16 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 1.56 \mu 1 \\ & (3 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $\begin{aligned} & 0.757 \\ & \mu \mathrm{l} \end{aligned}$ |
| 1:50 | $\begin{aligned} & 0.74 \mu \mathrm{l} \\ & (1.13 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 0.225 \mu \mathrm{l} \\ & (2 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $2.03 \mu \mathrm{l}$ | $\begin{aligned} & 0.854 \mu \mathrm{l} \\ & (49.16 \mu \mathrm{M}) \end{aligned}$ | $\begin{aligned} & 1.56 \mu 1 \\ & (3 \mathrm{M}) \end{aligned}$ | $3 \mu \mathrm{l}$ | $\begin{aligned} & 0.586 \\ & \mu \mathrm{l} \end{aligned}$ |

Table S4. Determination of dissociation constant $K_{\mathrm{d}}(\mathrm{mM})$ and $\Delta G_{\text {binding }}$ ( $\mathrm{kcal} / \mathrm{mol}$ ) of trans-acting TW17 ribozyme systems from Langmuir isotherm analyses.

| Binary Systems | Dissociation <br> Constant <br> $\left(K_{\mathrm{d}}, \mu \mathrm{M}\right)$ | $\begin{gathered} \Delta G_{\text {binding }} \\ (\mathrm{kcal} / \mathrm{mol}) \end{gathered}$ | Notes |
| :---: | :---: | :---: | :---: |
| $\begin{aligned} & \text { TW17S-1 RNA } \\ & +\quad \text { TW17C-1 } \\ & \text { RNA } \end{aligned}$ | 0.18 | -9.19 | TW17S-1 RNA:18-mer RNA ; <br> TW17C-1 RNA:66-mer RNA |
| $\begin{aligned} & \text { TW17S-2 RNA } \\ & +\quad \text { TW17C-2 } \\ & \text { RNA } \end{aligned}$ | 0.81 | -8.30 | TW17S-2 RNA:21-mer RNA ; <br> TW17C-2 RNA:71-mer RNA |
| $\begin{aligned} & \text { TW17S-3 RNA } \\ & +\quad \text { TW17C-3 } \\ & \text { RNA } \end{aligned}$ | 1.61 | -7.89 | TW17S-3 RNA:24-mer RNA ; <br> TW17C-3 RNA:73-mer RNA |
| $\begin{aligned} & \text { TW17S-4 RNA } \\ & +\quad \text { TW17C-4 } \\ & \text { RNA } \end{aligned}$ | 0.51 | -8.57 | TW17S-4 RNA: 19-mer RNA, the 3' terminus ended with two C; TW17C-4 RNA :68-mer RNA, the 5' terminus ended with two G. |
| $\begin{aligned} & \text { TW17S-5 RNA } \\ & +\quad \text { TW17C-5 } \\ & \text { RNA } \end{aligned}$ | 0.19 | -9.16 | TW17S-5 RNA:17-mer RNA, the 3' terminus ended with two C; TW17C-5 RNA:66-mer RNA, the 5, terminus ended with two G. |
| $\begin{aligned} & \hline \text { TW17S-6 RNA } \\ & +\quad \text { TW17C-5 } \end{aligned}$ | 1.13 | -8.10 | TW17S-6 RNA: 17-mer RNA, the 3' terminus ended with U and C . |


| RNA |  |  |  |
| :--- | :---: | :---: | :---: |
| TW17S-1 RNA <br> + <br> TW17C-5 | 0.15 | -9.30 |  |
| RNA |  |  |  |



(s) sequence: dept
$\mathrm{m} / \mathrm{z}$ INT

```
325.1335 16.7563 **********
    325.1335 16.7563
    326.1357 2.3224
    327.1380 0.2325
    328.1403 0.0194
    329.1426 0.0014
```




Theoretical Ion Distribution ]
Molecular Formula : C13 H17 O7 N5 P S Ba (m/z 555.9639, MW 555.6770, U.S. 10.5)
Base Peak : 555.9639, Averaged MW : 555.6729 (a), 555.6757 (w)

[ Elemental Composition ]
Data : EIHR333
Date : 09-Mar-2009 15:55
Sample: $\mathrm{S}-20$
Note : NBA + glycerol
Inlet : Direct
Ion Mode : FAB+
RT : 0.67 min
Scan\#: 5
Elements : C 13/0, H 17/0, O 7/0, N 5/0, P 1/0, S 1/0, Ba 1/0
Mass Tolerance : 5mmu
Unsaturation (U.S.) : 0.5-30.0
Observed m/z Int\% Err[ppm / mmu] U.S. Composition
$555.964020 .0+0.2 /+0.1 \quad 10.5$ C 13 H 1707 N 5 P S Ba


S-21


GMPS

(10
[ Theoretical Ion Distribution
Molecular Formula : C10 H21 07 N7 P S
(m/z 414.0961, MW 414.3592, U.S. 6.5)
Base Peak : 414.0961, Averaged MW : 414.3582 (a), 414.3591 (w)

[ Elemental Composition ]
Data : EIHR334
Date : 09-Mar-2009 16:08
Sample: S-21
Note : NBA + glycerol
Inlet : Direct
Ion Mode : FAB+
RT : 4.17 min Scan\#: 26
Elements : C 10/0, H $21 / 0, \mathrm{O} 7 / 0, \mathrm{~N} 7 / 0, \mathrm{P} 1 / 0, \mathrm{~S} 1 / 0$, Ba $1 / 0$
Mass Tolerance : 5mmu
Unsaturation (U.S.) : 0.5-30.0
Observed m/z Int\% Err[ppm / mmu] U.S. Composition
$414.09621 .0+0.2 /+0.1 \quad 6.5$ C 10 H 2107 N 7 PS




/d=/Data/yu/S5B/1/pdata/1 Administrator Tue Dec 2 11:43:50 2008





/d=/Data/yu/boccystaminebrac/4/pdata/1 Administrator Thu Jul 9 17:13:49 2009







/d=/Data/yu/CYRSTAMINEBRAC/2/pdata/1 Administrator Mon Jun 15 16:14:16 2009








/d=/Data/yu/s8/1/pdata/1 Administrator Wed Jan 21 14:49:06 2009






[ Theoretical Ion Distribution ]
Molecular Formula : C22 H39 O4 N5 Br S
( $\mathrm{m} / \mathrm{z}$ 612.1348, MW 613.6848, U.S. 8.5)
Base Peak : 614.1328, Averaged MW : $613.6814(\mathrm{a}), \quad 613.6843(\mathrm{w})$
m/z
$612.1348 \quad 86.5444$
$\begin{array}{lr}613.1375 & 25.4538 \\ 614.1328 & 100.0000\end{array}$

616.1311 16.5450
617.13263 .9507 **
$618.1298 \quad 1.1769$ *
$619.1305 \quad 0.2293$
620.12910 .0446
$621.1294 \quad 0.0069$
$622.1292 \quad 0.0010$
$623.1297 \quad 0.0001$

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