Supporting Information for

Abasic Site-Containing DNAzyme and Aptamer for Label-free Fluorescent Detection of Pb^{2+} and Adenosine with High Sensitivity, Selectivity and Tunable Dynamic Range

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Content

Figure S1. Activity assay of the 8-17 DNAzyme and its abasic-site containing variants using denatured PAGE (20 % acrylic amide). The 24 base pair (bp) substrate 17S ((1 μM) was fluorescein-labeled at 3′- end. The assay was carried out in the presence of 2 μM DNAzymes and 1 μM Pb^{2+} in 25 mM HEPES pH 7.0, 100 mM NaCl, at 5 °C for 10 minutes. 1: no DNAzyme; 2,3: $17E_{ab}$; 4,5: $17E_G$–G; 6: Mutant $17E_{ab}$; 7,8: $17E_{ab}$ with 2 μM ATMND; 9,10: $17E_G$.

Sequences:

$17E_G$–G ($17E_G$ with G base removed from 3′- end):

5′-ACAGACATCTCTTCTCCGAGCCGGTCGAAATAGGGA-3′

Mutant $17E_{ab}$ ($17E_{ab}$ with T replaced by underlined C):

5′-ACAGACATCTCTTCCCCGAGCCGGTCGAAATAGXGAG-3′

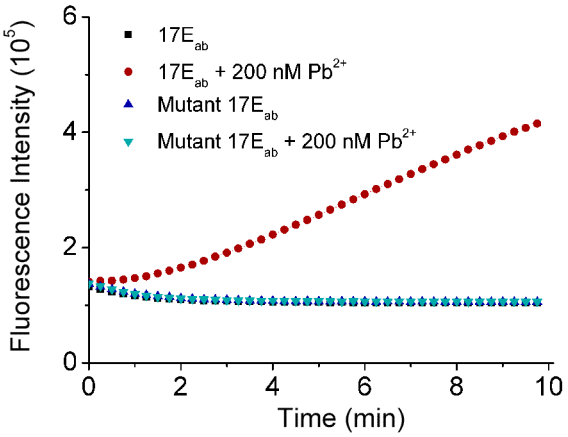

Figure S2. Effect of mutation in abasic-site containing $17E_{ab}$ on the kinetics of fluorescence enhancement by Pb^{2+}-catalyzed cleavage of 17S. Condition: 1 μM ATMND, 1 μM 17S, 2 μM DNAzyme, 0 or 200 nM Pb^{2+}, 25 mM HEPES pH 7.0, 100 mM NaCl, at 5 °C. $\lambda_{ex}/\lambda_{em}$ = 358/405 nm.

Sequences:

Mutant $17E_{ab}$ ($17E_{ab}$ with T replaced by underlined C):

5′-ACAGACATCTCTTCCCCGAGCCGGTCGAAATAGXGAG-3′

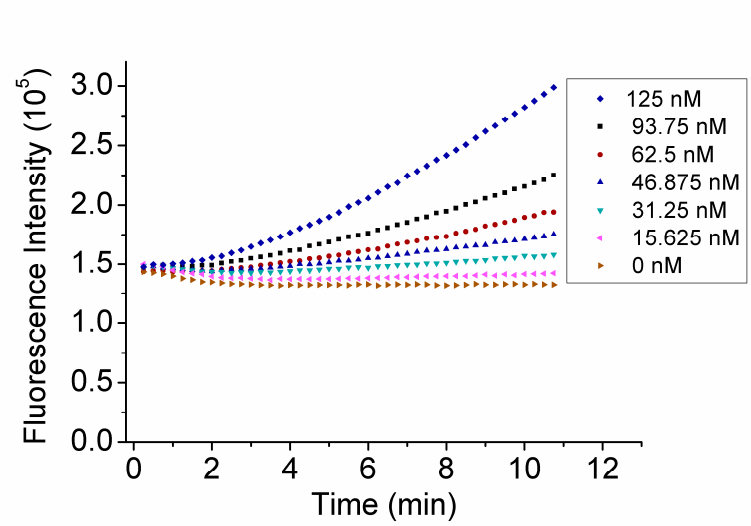

Figure S3. Kinetics of fluorescence enhancement by Pb^{2+}-catalyzed cleavage at lower Pb^{2+} concentration range. $\lambda_{ex}/\lambda_{em}$ = 358/405 nm. Condition: 1 μM ATMND, 2.14 μM $17E_{ab}$, 1.02 μM 17S in 25 mM HEPES pH 7.0, 100 mM NaCl at 5 °C. The decrease of fluorescence during the first 2 minutes is because the Pb^{2+} stock solution added at 0 minute is at room temperature and 2 minutes is required for the equilibrium of temperature.

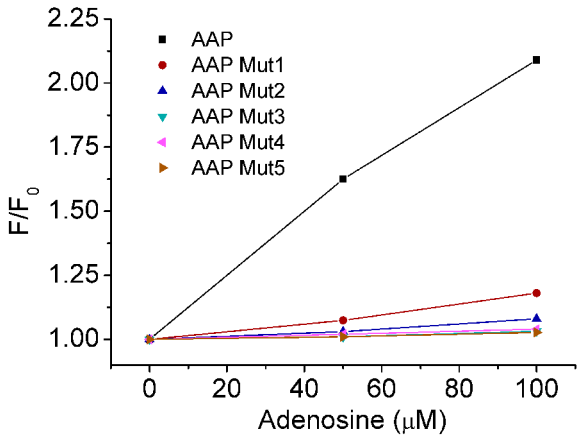

Figure S4. Effect of mutations in adenosine aptamer AAP on the fluorescence enhancement ratio upon binding with different concentrations of adenosine. Condition: 500 nM ATMND, 1 μM APP or APP mutants, 1.25 μM $L1_{ab}$, 0, 50 or 100 μM adenosine, 10 mM HEPES pH 7.0, 100 mM NaCl, 1 mM EDTA, at 5 °C. $\lambda_{ex}/\lambda_{em}$ = 358/405 nm.

Sequences (Mutation sites compared to APP are underlined, where in APP is A base):

APP Mut1: 5′-TGTCGTTGACCTGGGGGAGTATTGCGGAGGGAGGT-3′

APP Mut2: 5′-TGTCGTTGACCTGGGGGCGTATTGCGGAGGAAGGT-3′

APP Mut3: 5′-TGTCGTTGACCTGGGGGAGTATTGCGGAGGCAGGT-3′

APP Mut4: 5′-TGTCGTTGACCTGGGGGAGTATTGCGGAGGTAGGT-3′

APP Mut5: 5′-TGTCGTTGACCTGGGGGTGTATTGCGGAGGAAGGT-3′