

SUPPORTING DATA FOR WORLD WIDE WEB EDITION

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“Achieving specificity in selected and wild-type N peptide–RNA complexes: The importance of discrimination against noncognate RNA targets”

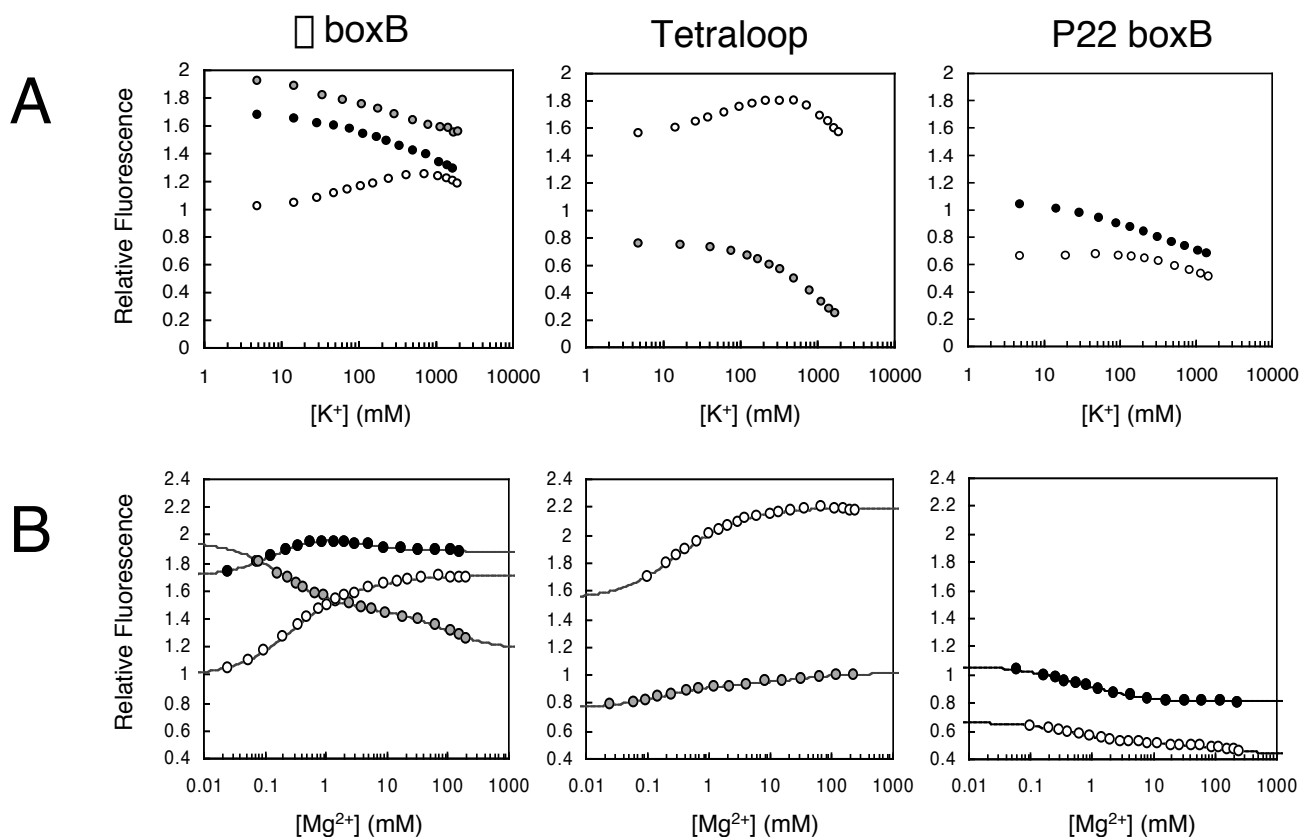


Figure S1. (A) K⁺ and (B) Mg²⁺ binding to GNRA-folded loops. Concentrated solutions of the acetate salts of each cation were added to 2AP labeled RNA loops in 20 mM Tris•Cl (pH 7.5). K⁺ and Mg²⁺ titrations used 200 nM and 800 nM of each RNA target, respectively. Experimental fluorescence values are shown as circles shaded to represent the position of 2AP labeling in the titration: 2AP-2 (white), 2AP-3 (gray), and 2AP-4 (black). All fluorescence values are relative to free □ boxB 2AP-2 in 20 mM Tris•Cl buffer. K⁺ binding could not be fit to a simple binding model. The curves for Mg²⁺ titrations represent least squares fits to a two independent binding site model.

Table S1. Mg²⁺ Binding to Hairpins ^a

RNA Loop	BoxB			Tetraloop		P22 BoxB	
	2AP-2	2AP-3	2AP-4	2AP-2	2AP-3	2AP-2	2AP-4
K ₁ (mM ⁻¹)	3.8 ± 0.3	4.8 ± 0.4	5.4 ± 0.9	4.2 ± 0.5	5.4 ± 0.5	1.88 ± 0.07	3.5 ± 0.9
K ₂ (mM ⁻¹)	0.16 ± 0.09	0.012 ± 0.002	0.6 ± 0.2	0.4 ± 0.2	0.04 ± 0.01	0.006 ± 0.001	0.5 ± 0.2
q ₁	1.62 ± 0.02	0.76 ± 0.01	1.23 ± 0.02	1.34 ± 0.02	1.22 ± 0.01	0.77 ± 0.01	0.86 ± 0.03
q ₂	1.04 ± 0.01	0.75 ± 0.02	0.92 ± 0.01	1.04 ± 0.01	1.07 ± 0.01	0.80 ± 0.01	0.86 ± 0.03
q ₁₂	1.71 ± 0.06	0.61 ± 0.02	1.11 ± 0.05	1.42 ± 0.07	1.32 ± 0.02	0.65 ± 0.01	0.76 ± 0.06

^a The data in Figure S1 for Mg²⁺ titrations were fit to a two independent site binding model (Menger and Porschke, 2000). K₁ and K₂ are the empirical binding constants, and q₁ and q₂ are the quantum yields of the RNA with one magnesium bound at the respective sites relative to RNA fluorescence in the absence of magnesium. q₁₂ is the relative quantum yield with both sites occupied.