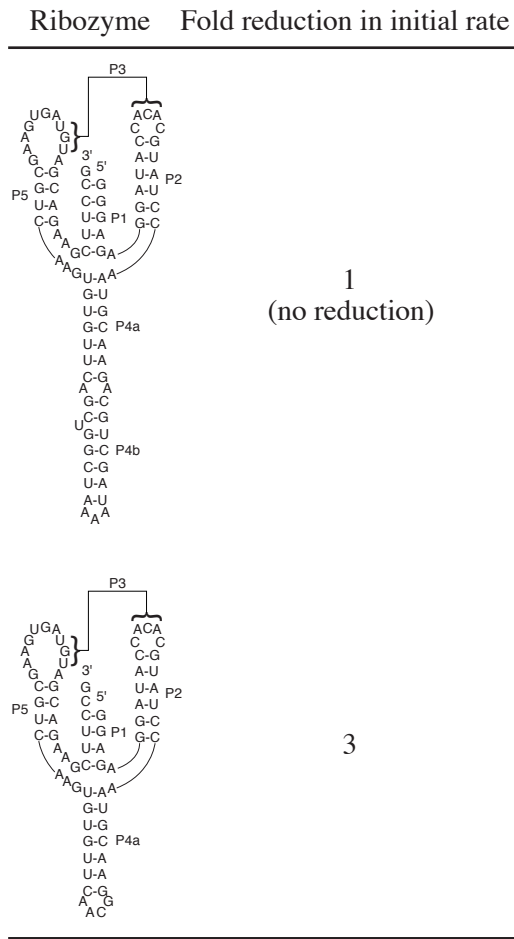


Supplementary Figure 3

a



b

Helix	Base pair	Sequence	Fold reduction in initial rate
P1	4-86	A-U	1 (no reduction)
		U U	> 50
		A A	> 50
		U-A	4
P2	8-22	G-C	1
		C C	> 50
		G G	7
P3	15-75	C-G	1
		G G	> 50
		C C	> 50
P4	26-58	G-C	1
		U-G	1
		G G	5
P5	63-81	U C	2
		G-C	1
		C-G	1
		U-G	3
P5	65-79 66-78	C A	10
		U-A	1.4
		G-C	1
		C-G	1
P5	65-79 66-78	A C	> 50
		U-G	> 50
		G-U	> 50
		C A	> 50
P5	65-79 66-78	U-A	1
		A-U	1

Supplementary Figure 3 Testing the secondary structure model of kinase ribozyme 7-16 by site-directed mutagenesis. **(a)** Identification of the minimized catalytic core of kinase 7-16 by deletion analysis. Initial rates were typically measured at several different GTP γ S concentrations between 10 μ M and 1 mM. Time points were taken within the first 70 minutes of the reaction, and analyzed by APM polyacrylamide gel electrophoresis. **(b)** Testing proposed base pairs with compensatory mutations. Initial rates were measured as described. All mutations were tested in the context of the ribozyme's minimized catalytic core. Numbering of base pairs according to alignment in **Fig. 5**.