Table S2. Sharp Backbone Kinks in RNA Structures

PDB ID	Chain	Nucleotide Number	Nucleotide Name	Angle[a]	Molecule
1ET4	A	214	A	47.77	vitamin B(12) RNA aptamer
1SDS	D	210	U	50.44	protein L7Ae bound to a K-turn derived from an archaeal box H/ACA sRNA
1MMS	C	1071	G	42.36	ribosomal protein L11-RNA complex
1S72	0	1105	C	46.29	*H. marismortui* large ribosomal subunit
1S72	0	1369	A	46.57	*H. marismortui* large ribosomal subunit
1S72	0	1533	A	49.82	*H. marismortui* large ribosomal subunit
1S72	0	174	A	50.64	*H. marismortui* large ribosomal subunit
1S72	0	1776	A	48.93	*H. marismortui* large ribosomal subunit
1S72	0	2007	A	47.82	*H. marismortui* large ribosomal subunit
1S72	0	212	A	50.76	*H. marismortui* large ribosomal subunit
1S72	0	357	A	49.23	*H. marismortui* large ribosomal subunit
1S72	0	893	C	49.73	*H. marismortui* large ribosomal subunit
1XMQ	A	508	C	49.27	t6A37-ASLLysUUU AAA-mRNA bound to the decoding center
1MSY	A	2654	A	50.58	GUAA tetraloop mutant of Sarcin/Ricin domain from *E. coli* 23 S rRNA
4FAQ	A	1	G	50.12	*O. iheyensis* group II intron before 5'exon hydrolysis
4E8K	B	6	U	137.6	*O. iheyensis* group II intron before SER

[a]: defined as the angle formed by three consecutive phosphorus atoms.

Table S3. Properties of the Different Metal Ions Used in This Work

metal class	ion	cationic radius (Å)[a]	hydration energy (kJ/mol)[b, d]	Lewis acid strength[a]	absolute hardness (η)[b, c, e]	absolute electronegativity (χ)[b, e]
alkaline metal ions	Li^+	0.60	-514.10	0.188	35.12	40.52
	Na^+	0.95	-405.40	0.148	26.21	21.08
	K^+	1.33	-334.72	0.112	17.99	13.64
	Rb^+	1.48	-310.50	0.102	11.70	15.77
	Cs^+	1.69	-278.00	0.094	10.60	14.50
other monovalent metal ions	Tl^+	1.49	-325.90	0.120	7.16	13.27
alkali earth metal ions	Mg^{2+}	0.65	-1922.10	0.334	47.59	32.55
	Ca^{2+}	0.99	-1592.40	0.274	19.52	31.39
	Ba^{2+}	1.35	-1303.70	0.195	12.80	na

a: (Brown, 1988); b: (Feig and Uhlenbeck, 1999); c: (Essington, 2005); d : (Payzant et al., 1973); e: absolute hardness (η) and absolute electronegativity (χ) are defined according to Pearson (Pearson, 1988); na = not available ; dark green indicates strong and light green weak X-ray anomalous scattering properties.

References

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Table S4. Kinetic Parameters of the Wild-Type Intron and Mutants

Construct	k_1[a]	k_2[a]
wt	100	100
G288A	0.79 ± 0.08	1.49 ± 0.29
G288C	1.87 ± 1.08	1.22 ± 0.42
G288U	10.1 ± 1.75	4.96 ± 1.33
C377A	69.4 ± 7.14	38.4 ± 16.6
C377G	9.53 ± 1.28	2.66 ± 0.01
C377U	214 ± 35.4	105 ± 15.8

[a]: first (k_1) and second (k_2) splicing step rates for the indicated mutants relative to wild type (wt, k_1 = 0.011 ± 0.003 min^{-1}, k_2 = 0.094 ± 0.012 min^{-1}, set to 100 %). The standard deviation was calculated from three independent experiments.