Supplementary Table 1: Crystallographic data and refinement

RNA construct	ss-HP92 (7PLI)	ds-HP92 (7PMM)	hp-HP92 (7PMQ)
Space group	P1	$P4_22_12$	$P4_32_12$
Cell dimensions (a, b, c (Å))	58.643 121.599 122.417	169.69 169.69 111.99	159.644 159.644 204.682
α, β, γ (°)	97.16 92.43 103.44	90.00 90.00 90.00	90.00 90.00 90.00
Resolution (Å)	2.50	3.00	3.22
R merge	0.113 (0.640)	0.1214 (1.043)	0.246 (1.793)
I/σ(I)	7.25 (1.75)	24.40 (3.05)	10.72 (1.42)
CC 1/2	0.990 (0.75)	0.998 (0.914)	0.998 (0.553)
Completeness (%)	96.62 (96.52)	99.93 (99.97)	99.72 (99.65)
Redundancy	3.6 (3.6)	36.2 (15.2)	13.6 (14.0)
Refinement			
Resolution (Å)	56.9 – 2.50 (2.59 - 2.50)	48.39 – 3.0 (3.11 – 3.0)	49.33 – 3.22 (3.33 – 3.22)
Unique reflections	108844 (10869)	33295 (3268)	43424 (4266)
R work / R free	0.2133 / 0.2469	0.1971 / 0.2246	0.2276 / 0.2637
No. atoms	23591	8687	17493
Protein	23321	8601	17345
ligands	246	78	146
Water	24	8	0
B factors	69.07	116.82	86.14
Protein	69.18	116.99	86.22
ligands	61.63	101.51	76.47
Water	46.95	82.26	-
R.m.s. deviations			
Bond lengths (Å)	0.003	0.005	0.004
Bond angles (°)	0.83	0.85	0.71
Ramachandran statistics			
Favored regions (%)	98.37	97.63	95.66
Allowed regions (%)	1.55	2.26	4.01
Outliers (%)	0.07	0.11	0.33

The highest resolution shell values are indicated in parenthesis.