Table S1 Molodtsov and Murakami

Complex	Binary (SeMet)**	Binary***	EC– RNA12***	EC – RNA8***
PDB code		6DT7	6DT8	6DTA
Data collection				
Space group	C2	I4	I4	I4
Cell dimensions				
a (Å)	241.270	173.321	174.76	175,049
b (Å)	75.056	173.321	174.76	175,049
c (Å)	170.705	76.316	76.404	76,598
β (°)	134.66	90.0	90.0	90.0
Resolution (Å)	50 – 2.3	50 – 2.5	50 – 3.2	30 – 2.7
Total reflections	288,554	173,823	81,031	142,760
Unique reflections	94,476	39,317	19,223	31,537
Redundancy	3.1 (2.4)	4.4 (4.1)	4.1 (4.0)	4.5 (4.3)
Completeness (%)*	97.7 (89.7)	99.87 (100)	99.9 (99.9)	97.9 (96.8)
I / σ*	10.4 (1.1)	15.4 (1.4)	13.7 (1.4)	32.6 (1.7)
R_{sym} (%)*	9.4 (73.4)	7.8 (89.8)	10 (88.6)	5 (87.1)
$CC^{1/2}$*		(0.437)	(0.380)	(0.594)
Refinement				
Resolution (Å)	42.6 – 2.35	43.3 – 2.5	41.1 – 3.2	29.9 – 2.7
R_{work}	0.2092	0.1892	0.1900	0.1909
R_{free}	0.2277	0.2141	0.2428	0.2226
No. of atoms	11,707	5,638	5,672	5,692
R.m.s deviations				
Bond length (Å)	0.003	0.009	0.011	0.010
Bond angles (°)	0.653	1.232	1.386	1.357
Clashscore	5.17	5.17	7.51	6.35
Ramachandran favored, %	95.97	96.68	97.8	96.91
Ramachandran outliers, %	0.84	0	0	0

Table S1. Collection of crystallographic data and refinement statistics.
*Highest resolution shells are shown in parentheses
**Data set collected at NSLS X29 line, Upton, NY
***Data sets collected at MacCHESS F1 line, Ithaca, NY