RNA L [nt]	Buff.	Guinier Fit, PRIMUS			From P(r), GNOM			NSD from DAMSUP Avg.(SD)	NAST R_g Avg.(SD) [Å]
		R_g [Å]	qR_g	Fid.	R_g [Å]	D_{max} [Å]	QoF		
975	TE	172±7.5	0.79–1.38	0.99	182	600	0.69	1.80(0.11)	81.0(5.4)
975	IVA	180±2.5	0.83–1.45	0.70	168	550	0.61	1.21(0.27)	⟨77.7(7.6)⟩
1523	TE	199±6.6	0.91–1.60	0.99	208	620	0.62	2.02(0.14)	94.2(6.6)
1523	IVA	188±2.6	0.86–1.51	0.93	206	700	0.75	1.47(0.11)	
2777	IVA	171±2.0	0.88–1.37	0.94	172	600	0.63	1.43(0.12)	124.7(9.1)

Table ST1: RNA Structural Properties from SAXS Data. Fid. = PRIMUS Fidelity Number, QoF = GNOM Goodness of Fit, NSD = Normalized Spatial Discrepancy, IVA = *in vitro* assembly buffer. R_gs calculated from NAST simulations are typically lower than experimental values because they sample compact structures not seen in cryo-EM studies. Ensemble time-averaged NAST R_g from 10 other secondary structures is shown in ⟨ ⟩