Summary of integrative structure determination of Hybrid NMR-SAXS structure of a trans-cleaving VS ribozyme (PDB ID: 9A0V, PDB-Dev ID: PDBDEV_00000067)

1. Model Composition	
Entry composition	Neurospora Varkud Satellite Ribozyme: chain(s) A (101 residues)
Datasets used for modeling	- NMR data, BMRB: 25654 - NMR data, BMRB: 25163 - NMR data, BMRB: 17292 - NMR data, BMRB: 50637 - SAS data, SASBDB: SASDKU3 - SAS data, SASBDB: SASDKV3 - SAS data, SASBDB: SASDKW3 - SAS data, SASBDB: SASDKY3 - Experimental model, PDB: 2N3Q - Experimental model, PDB: 2MTJ - Experimental model, PDB: 2L5Z - Experimental model, PDB: 1YN1
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 15
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 4 unique SASRestraint: Assembly name: Complete assembly Fitting method: Crysol Multi-state: False
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	10
Model precision (uncertainty of models)	Not available
Data quality	
Model quality: assessment of atomic segments	- Clashscore: 0.62-0.62 - Ramachandran outliers: 0-0 - Sidechain outliers: 0-0

Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. Name	?
Method	fragment assembly
Description	?
Number of computed models	?
2. Name	?
Method	refinement
Description	?
Number of computed models	?
Software	- QRNAS (version Not available) - Pymol (version Not available) - Crysol (version Not available)