

Summary of integrative structure determination of Driving Integrative Structural Modeling with Serial Capture Affinity Purification (PDB ID: 9A0P, PDB-Dev ID: PDBDEV_00000061)

1. Model Composition	
Entry composition	- SPIN1: chain(s) A (203 residues) - SPINDOC: chain(s) B, C (381 residues)
Datasets used for modeling	- Crosslinking-MS data, MASSIVE: MSV000084719 - Experimental model, PDB: 4MZF - De Novo model, Not available
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 3
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSSO, 21 crosslinks
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	1
Model precision (uncertainty of models)	Not available
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	- Clashscore: 20.06 - Ramachandran outliers: 92 - Sidechain outliers: 197
Fit to data used for modeling	Satisfaction of crosslinks: 80.95%
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	ab initio modeling of SPINDOC

2. Name	integrative modeling of SPIN1-SPINDOC complex
Software	<ul style="list-style-type: none">- HADDOCK (version Not available)- I-TASSER (version Not available)