

Summary of integrative structure determination of model of Cullin4 (PDB ID: 9A40, PDB-Dev ID: PDBDEV_0000221)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - G7N4W9_MACMU: Chain E (628 residues) - A4UDG5_SIV: Chain F (138 residues) - DDB1_HUMAN: Chain C (1142 residues) - CUL4A_HUMAN: Chain A (739 residues) - DCAF1_HUMAN: Chain B (373 residues) - RBX1_HUMAN: Chain D (98 residues)
Datasets used for modeling	Crosslinking-MS data, Linker name and number of cross-links: SDA, 1534 cross-links
2. Representation	
Resolution	Atomic
Number of rigid bodies, flexible units	0, 6
Flexible units	<ul style="list-style-type: none"> - C: 1-1142 - B: 1-373 - F: 1-138 - A: 1-739 - E: 1-628 - D: 1-98
Structural coverage (rigid bodies)	100%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: SDA, 1534 cross-links
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	1
Model precision (uncertainty of models)	Model precision can not be calculated with one structure
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	Model-1: Clashscore = 0.32, Number of Ramachandran outliers = 20, Number of sidechain outliers = 30

<i>Model quality: assessment of excluded volume</i>	Not applicable
<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Method</i>	AlphaLink2
<i>Name</i>	AlphaLink2
<i>Description</i>	No starting models were used in the modeling
<i>Number of computed models</i>	1
<i>Software</i>	AlphaLink2 (version 1.0)