

## Summary of integrative structure determination of model of Cullin4 (PDB ID: 9A40, PDB-Dev ID: PDBDEV\_00000221)

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- CUL4A_HUMAN: chain(s) A (739 residues)</li> <li>- DCAF1_HUMAN: chain(s) B (373 residues)</li> <li>- DDB1_HUMAN: chain(s) C (1142 residues)</li> <li>- RBX1_HUMAN: chain(s) D (98 residues)</li> <li>- G7N4W9_MACMU: chain(s) E (628 residues)</li> <li>- A4UDG5_SIV: chain(s) F (138 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	- Crosslinking-MS data, PRIDE: <a href="#">PXD020453</a>
<b>2. Representation</b>	
<a href="#">Number of representations</a>	1
<a href="#">Scale</a>	Atomic
<a href="#">Number of <i>rigid</i> and <i>flexible</i> segments</a>	0, 6
<b>3. Restraints</b>	
<a href="#">Physical principles</a>	Information about physical principles was not provided
<a href="#">Experimental data</a>	- 1 unique CrossLinkRestraint: SDA, 1534 crosslinks
<b>4. Validation</b>	
<a href="#">Number of ensembles</a>	0
<a href="#">Number of models in ensembles</a>	Not applicable
<a href="#">Number of deposited models</a>	1
<a href="#">Model precision (uncertainty of models)</a>	Not available
<a href="#">Data quality</a>	Data quality has not been assessed
<a href="#">Model quality: assessment of atomic segments</a>	<ul style="list-style-type: none"> <li>- Clashscore: 0.32</li> <li>- Ramachandran outliers: 20</li> <li>- Sidechain outliers: 30</li> </ul>
<a href="#">Fit to data used for modeling</a>	Satisfaction of crosslinks: 70.14%
<a href="#">Fit to data used for validation</a>	Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<a href="#">1. Name</a>	AlphaLink2

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<a href="#"><i>Method</i></a>	AlphaLink2
<a href="#"><i>Description</i></a>	No starting models were used in the modeling
<a href="#"><i>Number of computed models</i></a>	1
<a href="#"><i>Software</i></a>	<a href="#">AlphaLink2</a> (version 1.0)