

Summary of integrative structure determination of Integrative structural model of alpha-synuclein compact states bound to membrane mimics (PDB ID: 9A1H, PDB-Dev ID: PDBDEV_00000089)

1. Model Composition	
<u>Entry composition</u>	- alpha-synuclein: Chain B (110 residues) - alpha-synuclein: Chain A (110 residues)
<u>Datasets used for modeling</u>	- Crosslinking-MS data, Linker name and number of cross-links: EDC, 3 cross-links - NMR data, BMRB: 50996
2. Representation	
<u>Resolution</u>	Atomic
<u>Number of rigid bodies, flexible units</u>	0, 2
<u>Flexible units</u>	- A: 1-110 - B: 1-110
<u>Structural coverage (rigid bodies)</u>	100%
3. Restraints	
<u>Physical principles</u>	Information about physical principles was not provided
<u>Experimental data</u>	- 1 unique CrossLinkRestraint: EDC, 3 cross-links
4. Validation	
<u>Number of ensembles</u>	0
<u>Number of models in ensembles</u>	Not applicable
<u>Number of deposited models</u>	5
<u>Model precision (uncertainty of models)</u>	Model precision can not be calculated with one structure
<u>Data quality</u>	Data quality has not been assessed

	<ul style="list-style-type: none"> - Model-1: Clashscore = 9.63, Number of Ramachandran outliers = 5, Number of sidechain outliers = 0 - Model-2: Clashscore = 18.98, Number of Ramachandran outliers = 2, Number of sidechain outliers = 1 - Model-3: Clashscore = 20.54, Number of Ramachandran outliers = 3, Number of sidechain outliers = 0 - Model-4: Clashscore = 18.67, Number of Ramachandran outliers = 2, Number of sidechain outliers = 1 - Model-5: Clashscore = 4.97, Number of Ramachandran outliers = 3, Number of sidechain outliers = 3
<i>Model quality: assessment of atomic segments</i>	
<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>	Simulated annealing of the monomer
<i>Name</i>	Simulated Annealing
<i>Number of computed models</i>	2700
2. <i>Method</i>	Simulated annealing of the dimer
<i>Name</i>	Simulated Annealing
<i>Number of computed models</i>	1500
<i>Software</i>	XPLOR-NIH (version 1.49)