

[illegible]

	10.5281/zenodo.1209565 - 2DEM class average, Zenodo: 10.5281/zenodo.1209565 - 2DEM class average, Zenodo: 10.5281/zenodo.1209565 - 2DEM class average, Zenodo: 10.5281/zenodo.1209565 - 2DEM class average, Zenodo: 10.5281/zenodo.1209565 - 2DEM class average, Zenodo: 10.5281/zenodo.1209565 - 2DEM class average, Zenodo: 10.5281/zenodo.1209565 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.1209565 - Experimental model, PDB: 3I4R - Experimental model, PDB: 3KFO - Experimental model, PDB: 4Q9T - Experimental model, PDB: 2JO8 - Experimental model, PDB: 2QIW - Experimental model, PDB: 3CIG - Experimental model, PDB: 2ELO - Experimental model, PDB: 3GUZ - Experimental model, PDB: 2CIW - Experimental model, PDB: 1A92 - Experimental model, PDB: 1GDJ - Experimental model, PDB: 1X4O - Comparative model, Zenodo: 10.5281/zenodo.1209565
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 1
3. Restraints	
Physical principles	Information about physical principles was not provided

Experimental data	<ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: DSS, 18 crosslinks - 1 unique CrossLinkRestraint: EDC, 23 crosslinks - 1 unique EM2DRestraint: Number of micrographs: 103, Image resolution: 15.0 - 2 unique EM2DRestraint: Number of micrographs: 100, Image resolution: 15.0 - 3 unique EM2DRestraint: Number of micrographs: 88, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 64, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 60, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 111, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 51, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 70, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 49, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 32, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 76, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 77, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 44, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 56, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 86, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 120, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 16, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 34, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 6, Image resolution: 15.0 - 1 unique EM2DRestraint: Number of micrographs: 11, Image resolution: 15.0 - 19 unique SASRestraint: Assembly name: SAXS assembly Fitting method: FoXS Multi-state: True
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	4
Model precision (uncertainty of models)	Not available
Data quality	
Model quality: assessment of atomic segments	<ul style="list-style-type: none"> - Clashscore: 0.00-0.00 - Ramachandran outliers: 127-170 - Sidechain outliers: 61-76

<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 87.80-92.68%
<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>Name</i>	MD-based conformational sampling
<i>Method</i>	AllosMod
<i>Number of computed models</i>	7000
2. <i>Name</i>	Minimal Ensemble Search
<i>Method</i>	MES
<i>Number of computed models</i>	4
<i>Software</i>	<ul style="list-style-type: none"> - HHpred (version 2.0.16) - PSIPRED (version 4.0) - DISOPRED (version 3) - Integrative Modeling Platform (IMP) (version 2.2) - MODELLER (version 9.13) - AllosMod (version Not available)