

Summary of integrative structure determination of Structures of multiple states of the hGBP1 resolved by FRET, SAXS, and EPR (PDB ID: 9A1G, PDB-Dev ID: PDBDEV_00000088)

1. Model Composition	
Entry composition	hGBP1 wildtype: chain(s) A (583 residues)

[Datasets used for modeling](#)

- Experimental model, PDB: [1DG3](#)
- SAS data, SASBDB: [SASDDD6](#)
- Ensemble FRET data, Zenodo: [10.5281/zenodo.6534557](#)
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- EPR data, Zenodo: [10.5281/zenodo.6534557](#)
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- Single molecule FRET data, Zenodo: [10.5281/zenodo.6534557](#)
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2. Representation

<i>Number of representations</i>	1
<i>Scale</i>	Atomic
<i>Number of <i>rigid</i> and <i>flexible</i> segments</i>	0, 1
3. Restraints	
<i>Physical principles</i>	Information about physical principles was not provided
<i>Experimental data</i>	
4. Validation	
<i>Number of ensembles</i>	2
<i>Number of models in ensembles</i>	100, 106
<i>Number of deposited models</i>	206
<i>Model precision (uncertainty of models)</i>	- Not available - Not available
<i>Data quality</i>	SASDDD6: Rg from Gunier is 3.89nm and Rg from p(r) is 4.02nm
<i>Model quality: assessment of atomic segments</i>	- Clashscore: 0.21-5.21 - Ramachandran outliers: 2-19 - Sidechain outliers: 8-123
<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>Name</i>	Rigid body docking
2. <i>Name</i>	Targeted NMSim
3. <i>Name</i>	MD simulation
<i>Software</i>	- FPS (version Not available) - NMSim (version Not available) - Amber 14 (version Not available) - DeerAnalysis2006 (version Not available)