Summary of integrative structure determination of A structural model of the endogenoushuman SWI/SNF (BAF) complex bound to the nucleosome informs disease mechanisms (PDB ID: 9A0K, PDB-Dev ID: PDBDEV_00000056)

1. Model Composition	
Entry composition	- SMARCC1: chain(s) 1 (1105 residues) - SMARCC2: chain(s) 2 (1214 residues) - SMARCA4: chain(s) 4 (1647 residues) - ACTL6A: chain(s) 6 (429 residues) - ARID1A: chain(s) A (2285 residues) - ACTB: chain(s) B (375 residues) - SMARCD1: chain(s) D (515 residues) - SMARCE1: chain(s) E (411 residues) - DPF2: chain(s) P (391 residues) - H2A: chain(s) V, v (130 residues) - H2B: chain(s) W, w (126 residues) - H3: chain(s) X, x (136 residues) - H4: chain(s) Y, y (103 residues) - SMARCB1: chain(s) b (385 residues) - 601 dna fwd: chain(s) p (196 residues) - 601 dna rev: chain(s) q (196 residues)
Datasets used for modeling	- 3DEM volume, Zenodo: 10.5281/zenodo.3998811 - Crosslinking-MS data, PRIDE: PXD020992 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo: 10.5281/zenodo.3998811 - Comparative model, Zenodo:

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2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	23, 0
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: BS3, 1261 crosslinks - 1 unique EM3DRestraint: None
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	1
Model precision (uncertainty of models)	Not available
Data quality	Data quality has not been assessed

Model quality: assessment of atomic segments	- Clashscore: 0.00 - Ramachandran outliers: 27 - Sidechain outliers: 10
Fit to data used for modeling	Satisfaction of crosslinks: 58.13%
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. Name	Production sampling
2. Name	trRosetta
3. Name	Rosetta Hybridize
Software	- Rosetta (version Rosetta version unknown:ff8ee24ee5f65423d5064cba818ede41d012fa8 2020-08-10 10:39:53 -0700 from git@github.com:RosettaCommons/main.git) - trRosetta (version 1.0.0) - HHpred (version website)