

Summary of integrative structure determination of Complex of UbchH5c, RNF168-RING domain and the nucleosome (PDB ID: 8ZZT, PDB-Dev ID: PDBDEV_00000029)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - H3: chain(s) A, E (99 residues) - H4: chain(s) B, F (80 residues) - H2A N18S mutant: chain(s) C, G (107 residues) - H2B S121A mutant: chain(s) D, H (95 residues) - DNA strand 1: chain(s) I (147 residues) - DNA strand 2: chain(s) J (147 residues) - RNF168 RING domain: chain(s) K (91 residues) - UbchH5c: chain(s) L (153 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Integrative model, PDB-Dev: PDBDEV_00000028 - Experimental model, PDB: 1X23 - Other, Not available: 10.1038/s41467-019-09756-z
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 12
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 12 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0 - 1 unique DerivedDistanceRestraint: Upper Bound Distance: 2.5 - 1 unique DerivedDistanceRestraint: Upper Bound Distance: 4.0 - 2 unique DerivedDistanceRestraint: Upper Bound Distance: 9.0
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	10
Model precision (uncertainty of models)	Not available
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	<ul style="list-style-type: none"> - Clashscore: 9.38-10.63 - Ramachandran outliers: 3-9 - Sidechain outliers: 41-61

<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>	None
<i>Software</i>	HADDOCK (version 2.2)