

**Table S1: Summary of Integrative Structure Determination of Structure of K63-linked Diubiquitin (PDBDEV00000004)**

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- Ubiquitin: Chain A (76 residues)</li> <li>- Ubiquitin: Chain B (76 residues)</li> <li>- Ubiquitin: Chain A (76 residues)</li> <li>- Ubiquitin: Chain B (76 residues)</li> <li>- Ubiquitin: Chain A (76 residues)</li> <li>- Ubiquitin: Chain B (76 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- SAS data, SASDCG7</li> <li>- Experimental model, PDB ID: 1UBQ</li> <li>- Experimental model, PDB ID: 2N2K</li> <li>- CX-MS data, Linker name: E, Number of cross-links: G</li> <li>- Single molecule FRET data, Not listed</li> </ul>
<b>2. Representation</b>	
<a href="#">Atomic structural coverage</a>	100%
Number of <a href="#">rigid bodies</a> , <a href="#">flexible units</a>	0, 2
<i>Rigid regions</i>	<ul style="list-style-type: none"> <li>- A: -</li> <li>- B: -</li> </ul>
<i>Flexible units</i>	<ul style="list-style-type: none"> <li>- A: 1-76.</li> <li>- B: 1-76.</li> </ul>
<a href="#">Resolution</a>	Rigid bodies: 1 residue per bead. Flexible regions: 50 residues per bead.
<b>3. Restraints</b>	
<a href="#">Physical principles</a>	Excluded volume and Sequence connectivity.
<a href="#">Experimental data</a>	<ul style="list-style-type: none"> <li>- 1 unique CrossLinkRestraint: EGS, 1 cross-links</li> <li>- 1 unique CrossLinkRestraint: BS3, 1 cross-links</li> <li>- 1 unique CrossLinkRestraint: BS2G, 1 cross-links</li> <li>- 1 unique CrossLinkRestraint: DST, 1 cross-links</li> </ul>
<b>4. Validation</b>	
<a href="#">Sampling validation</a>	1. Information related to sampling validation has not been provided
<a href="#">Clustering algorithm</a> , <a href="#">clustering feature</a>	distance threshold-based clustering, Not applicable
<a href="#">Number of ensembles</a>	0
<a href="#">Number of models in ensembles</a>	Not applicable
<a href="#">Model precision (uncertainty of models)</a>	Model precision can not be calculated with one structure

<a href="#"><i>Quality of data</i></a>	1. Quality of input data has not be assessed
<a href="#"><i>Assessment of atomic regions</i></a>	Clashscore: 4.07, Ramachandran outliers: 0.68, Sidechain outliers: 6.13
<a href="#"><i>Assessment of excluded volume</i></a>	1. Not applicable
<a href="#"><i>Fit of the model to information used to compute it</i></a>	1. Fit of model to information used to compute it has not been determined
<a href="#"><i>Fit of the model to information not used to compute it</i></a>	1. Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<a href="#"><i>Method</i></a>	None
<a href="#"><i>Name</i></a>	None
<a href="#"><i>Details</i></a>	- Method details unspecified
<a href="#"><i>Software</i></a>	- Software details not provided - No location specified