Table S1: Summary of Integrative Structure Determination of Structural dynamics of the E6AP/UBE3A-E6-p53 enzyme-substrate complex (PDBDEV00000023)

1. Model Composition	
Entry composition	- E6AP HECT Domain: Chain A (350 residues) - E6: Chain B (143 residues) - p53: Chain C (199 residues)
Datasets used for modeling	- CX-MS data, Linker name: D, Number of cross-links: S - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 1C4Z - Experimental model, PDB ID: 4XR8
2. Representation	
Atomic structural coverage	100%
Number of rigid bodies, flexible units	3, 0
Rigid regions	- A: 497-846:Comparative model/None. - B: 1-143:Comparative model/None. - C: 94-292:Comparative model/None.
Flexible units	- A: - - B: - - C: -
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: 50 residues per bead.
3. Restraints	
Physical principles	Excluded volume and Sequence connectivity.
Experimental data	- 1 unique CrossLinkRestraint: DSS, 127 cross-links
4. Validation	
Sampling validation	1. Information related to sampling validation has not been provided
Clustering algorithm ,clustering feature	distance threshold-based clustering, RMSD
Number of ensembles	1
Number of models in ensembles	500
Model precision (uncertainty of models)	NoneÅ
Quality of data	1. Quality of input data has not be assessed
Assessment of atomic regions	

Assessment of excluded volume	
Fit of the model to information used to compute it	1. Fit of model to information used to compute it has not been determined
Fit of the model to information not used to compute it	1. Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
Method	MC based Bayesian sampling using crosslinks
Name	IMP
Details	- Method details unspecified
Software	- Integrative Modeling Platform (IMP) (version git checkout 2018/01/08 (commit 5eb8151c651256d50bbcd847932bc913df94090c)) - No location specified