

Table S1: Summary of Integrative Structure Determination of Genetic interaction mapping informs integrative determination of biomolecular assembly structures (PDBDEV000000XX)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - h3: Chain A (136 residues) - h4: Chain B (103 residues) - h3: Chain A (136 residues) - h4: Chain B (103 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB ID: 1TZY - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - unspecified, Not listed - unspecified, Not listed
2. Representation	
Atomic structural coverage	100%
Number of rigid bodies , flexible units	2, 0
<i>Rigid bodies</i>	<ul style="list-style-type: none"> - A: 39-136:Comparative model/None. - B: 20-103:Comparative model/None.
— <i>Flexible units</i>	<ul style="list-style-type: none"> - A: - - B: -
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: 10 residues per bead.
3. Restraints	
Physical principles	Excluded volume and Sequence connectivity.
Experimental data	
4. Validation	
Sampling validation	
Clustering algorithm , clustering feature	None, dRMSD
Number of ensembles	2
Number of models in ensembles	20000, 10000
Model precision (uncertainty of models)	1.04Å, 1.2Å
Quality of data	-
Assessment of atomic segments	-
Fit of the model to information used to compute it	

<i>Fit of the model to information not used to compute it</i>	
5. Methodology and Software	
<i>Method</i>	Sampling
<i>Name</i>	Replica exchange Monte Carlo
<i>Details</i>	
<i>Software</i>	<ul style="list-style-type: none"> - IMP PMI module (version develop-9c8707cfc5) - Integrative Modeling Platform (IMP) (version develop-9c8707cfc5) - MODELLER (version 9.21)