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

1. Model Composition	
Entry composition	- h3: Chain A (136 residues) - h4: Chain B (103 residues) - h3: Chain A (136 residues) - h4: Chain B (103 residues)
Datasets used for modeling	- Experimental model, PDB ID: 1TZY - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - set 1, Not listed - set 2, Not listed
2. Representation	
Atomic structural coverage	100%
Number of rigid bodies, flexible units	2, 0
Rigid bodies	- A: 39-136:Comparative model/None. - B: 20-103:Comparative model/None.
Flexible units	- 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	- DerivedDistanceRestraint: 946 distinct restraints, set 1 dataset - DerivedDistanceRestraint: 757 distinct restraints, set 2 dataset
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	
Fit of the model to information not used to compute it	
5. Methodology and Software	
Method	Sampling
Name	Replica exchange Monte Carlo
Details	
Software	- IMP PMI module (version develop-9c8707cfc5) - Integrative Modeling Platform (IMP) (version develop-9c8707cfc5) - MODELLER (version 9.21)