

Summary of integrative structure determination of USP7 TRAF domain in complex with DNA polymerase iota peptide 573-584 (PDB ID: 9A0Y, PDB-Dev ID: PDBDEV_00000070)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - DNA polymerase iota peptide 573-584: chain(s) A (12 residues) - USP7 TRAF domain: chain(s) B (145 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Comparative model, Not available - Comparative model, Not available - Experimental model, PDB: 2fop - NMR data, BMRB: 50080 - Mutagenesis data, Not available: 10.1016/j.jmb.2020.166733
2. Representation	
Number of representations	1
Scale	Atomic
Number of <i>rigid</i> and <i>flexible</i> segments	2, 0
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 96 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	20
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: 5.66-13.75 - Ramachandran outliers: 0-3 - Sidechain outliers: 5-19
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined

5. Methodology and Software	
1. <i>Name</i>	None
<i>Method</i>	docking
<i>Number of computed models</i>	?
<i>Software</i>	<ul style="list-style-type: none">- MODELLER (version Not available)- HADDOCK (version Not available)- PYMOL (version Not available)