

Summary of integrative structure determination of Structural model of UDP-glucose:glycoprotein glucosyl-transferase bound to Fab (PDB ID: 9A0I, PDB-Dev ID: PDBDEV_00000054)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - TdUGGT: chain(s) A (1368 residues) - Fab Heavy Chain: chain(s) B [L] (214 residues) - Fab Light Chain: chain(s) C [H] (214 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - 3DEM volume, EMDB: EMD-30386 - Other, Not available: 10.1038/s41598-017-12283-w - Experimental model, PDB: 5Y7O - Experimental model, PDB: 5MU1 - Experimental model, PDB: 5H18 - Experimental model, PDB: 1FGN - Other, Not available
2. Representation	
Number of representations	1
Scale	Atomic
Number of <i>rigid</i> and <i>flexible</i> segments	16, 0
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 2 unique DerivedDistanceRestraint: restraint type DistanceRestraintOther - 2 unique EM3DRestraint: None
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	2
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: 110.34-114.27 - Ramachandran outliers: 21-21 - Sidechain outliers: 47-47

<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Name</i>	Fitting the TdUGGT and Fab models in the negative stain EM map
<i>Software</i>	<ul style="list-style-type: none"> - Coot (version Not available) - Modeller (version Not available) - Chimera (version Not available)