

Summary of integrative structure determination of Predicted model of tissue transglutaminase 2 (TG2) in complex with plasma fibronectin type I modules 2 and 3 (FN12-3) (PDB ID: 9A3X, PDB-Dev ID: PDBDEV_00000218)

1. Model Composition	
<i>Entry composition</i>	<ul style="list-style-type: none"> - Protein-glutamine gamma-glutamyltransferase 2: chain(s) A (687 residues) - Fibronectin: chain(s) B (90 residues)
<i>Datasets used for modeling</i>	<ul style="list-style-type: none"> - Crosslinking-MS data, PRIDE: PXD043976 - Experimental model, PDB: 4PYG - Experimental model, PDB: 2CG7
2. Representation	
<i>Number of representations</i>	1
<i>Scale</i>	Atomic
<i>Number of rigid and flexible segments</i>	0, 2
3. Restraints	
<i>Physical principles</i>	Information about physical principles was not provided
<i>Experimental data</i>	<ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: DMTMM, 1 crosslinks - 1 unique CrossLinkRestraint: DSS, 0 crosslinks - 1 unique CrossLinkRestraint: PDH, 0 crosslinks
4. Validation	
<i>Number of ensembles</i>	0
<i>Number of models in ensembles</i>	Not applicable
<i>Number of deposited models</i>	1
<i>Model precision (uncertainty of models)</i>	Not available
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of atomic segments</i>	<ul style="list-style-type: none"> - Clashscore: 11.96 - Ramachandran outliers: 10 - Sidechain outliers: 86
<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 100.00%
<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. <u>Name</u>	Refinement
<u>Description</u>	structural refinement of starting models guided by experimental crosslinks
2. <u>Name</u>	satisfied/violated crosslinks identification
<u>Description</u>	calculation of Euclidean distances between crosslinked residues
3. <u>Name</u>	calculation of accessible area
<u>Description</u>	calculation of accessible area
4. <u>Name</u>	accessible interaction space
<u>Description</u>	determine the number of complexes consistent with the restraints
5. <u>Name</u>	docking
<u>Description</u>	generates predicted model of a protein complex
<u>Software</u>	<ul style="list-style-type: none"> - I-TASSER (version Not available) - Xwalk (version Not available) - NACCESS (version Not available) - DisVis (version Not available) - HADDOCK (version Not available)