Summary of integrative structure determination of PTX3 hybrid cryoEM and AlphaFold model (PDB ID: 9A24, PDB-Dev ID: PDBDEV_00000141)

1. Model Composition	
Entry composition	- PTX3 (protein complex): chain(s) A [B], B [A], C [D], D [C], E [F], F [E], G [H], H [G] (364 residues) - N-ACETYL-D-GLUCOSAMINE: chain(s) I [B], J [B], N [A], O [A], S [D], W [D], X [C], Y [C], CA [F], DA [F], HA [E], IA [E], MA [H], NA [H], RA [G], SA [G] - BETA-D-MANNOSE: chain(s) K [B], P [A], T [D], Z [C], EA [F], JA [E], OA [H], TA [G] - ALPHA-D-MANNOSE: chain(s) L [B], M [B], Q [A], R [A], U [D], V [D], AA [C], BA [C], FA [F], GA [F], KA [E], LA [E], PA [H], QA [H], UA [G], VA [G] - water: chain(s) WA [B], XA [F], YA [I]
Datasets used for modeling	- De Novo model, Not available - 3DEM volume, EMDB: EMD-14774 - Mass Spectrometry data, PRIDE: PXD034602 - 2DEM class average, Not available - Other, Not available - Experimental model, PDB: 7ZL1
2. Representation	
Number of representations	1
Scale	Atomic
Number of *rigid* and *flexible* segments	0, 16
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique EM3DRestraint: None
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	1
Model precision (uncertainty of models)	Not available
Data quality	Data quality has not been assessed

Model quality: assessment of atomic segments	- Clashscore: 5.64 - Ramachandran outliers: 33 - Sidechain outliers: 8
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. _Name_	None
Software	- EMAN2 (version Not available) - IMOD (version Not available) - Relion (version Not available) - AlphaFold (version Not available)