

	Overall C6 Reconstruction	Tal-focused C3 reconstruction	RBP-focused reconstruction	FibL-focused reconstruction	FibU-focused reconstruction
Data Collection					
Microscope			Titan Krios 300 keV		
Detector			Direct Electron DE-20		
Pixel Size (Å)			1.21		
Defocus range (µm)			0.42-4.9		
Reconstruction					
Number of particles	74,294	43,601	66,861	73,384	58,716
Software	RELION-2.1.0		RELION-3.0-beta-2		
Symmetry	C6	C3	C6	C6	C6
Final resolution (FSC=0.143, Å)*	3.45	3.96	3.60	3.69	4.14
Atomic model refinement					
Software			PHENIX v1.15.2; Coot v0.8.9		
Resolution limit (Å)**	3.75	4.08	3.64	3.62	3.85
Model-map correlation (FSC=0.5, Å)	3.86	4.21	3.89	3.94	4.15
Proteins included	MTP _U and MTP _L	Dit, Tal, and TMP	RBP	FibL	FibU
Chains	12	12	24	18	12
Residues	1878	3105	11,418	3222	1464
Number of atoms					
Protein atoms	28,866	50,376	183,498	50,550	23,916
Hydrogens	13,956	25,086	89,970	25,008	12,084
Metal ions	0	0	6	0	0
Map CC _{box}	0.39	0.52	0.61	0.48	0.59
Map CC _{mask}	0.79	0.77	0.76	0.77	0.77
RMS bond length (Å)	0.008	0.007	0.006	0.002	0.002
RMS bond angles (°)	1.042	1.190	1.118	0.959	1.014
Validation					
Ramachandran plot (%)					
Favored	93.53	88.77	90.99	86.82	85.69
Allowed	6.47	11.23	8.96	13.15	14.31
Outliers	0	0	0.05	0.03	0
Rotamers outliers (%)	0	1.07	0	0.03	0
Clashscore	10.39	4.63	4.07	8.88	8.45
EMRinger score	2.68	1.39	1.49	2.19	2.57

*Between half-maps resolution reported by Phenix Comprehensive Validation after automated masking

**Between half-maps resolution reported by RELION-2/3 Postprocessing after masking and FSC correction