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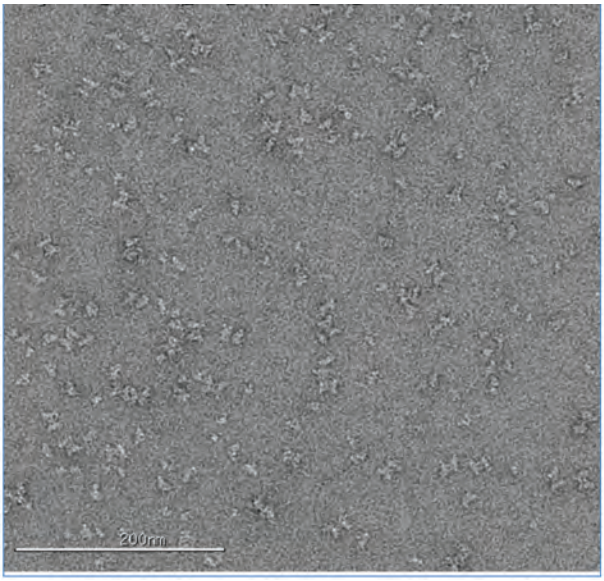
Fig. S1

a.



b.

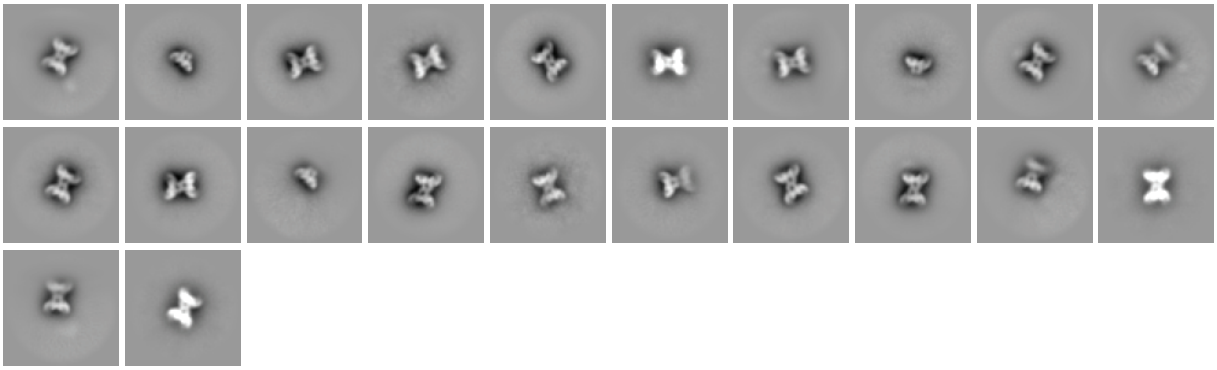


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Fig. S2

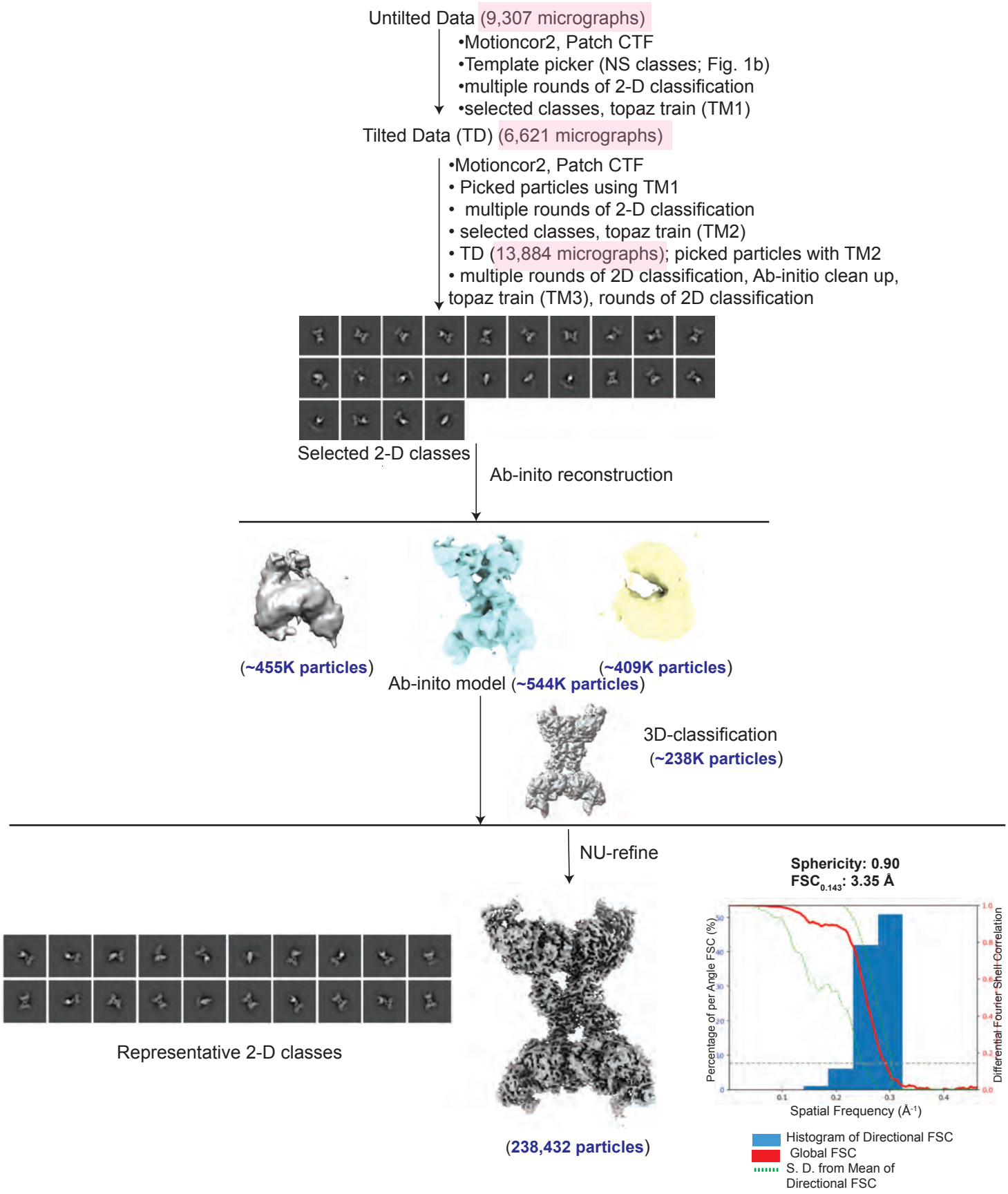

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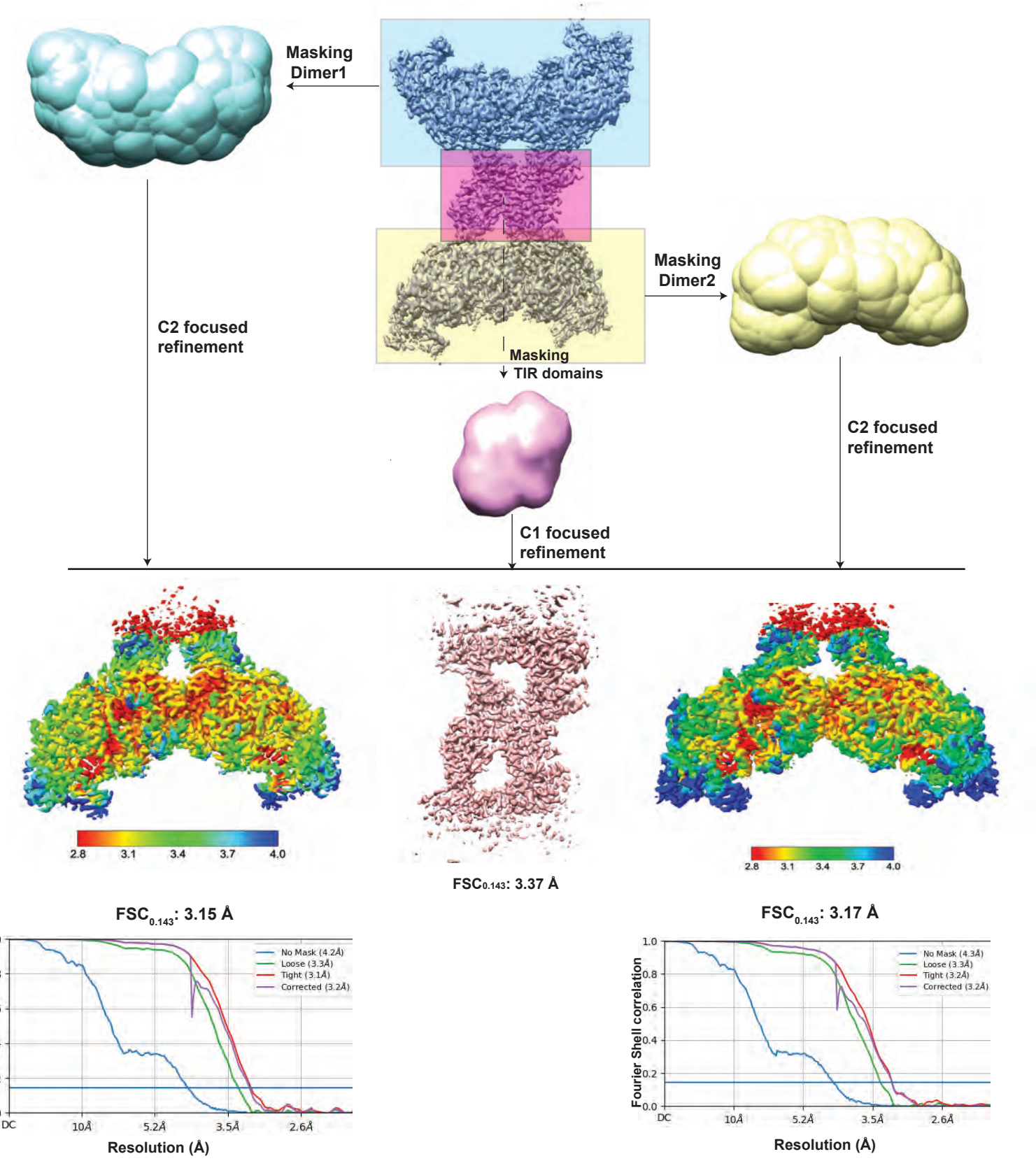
Fig. S3



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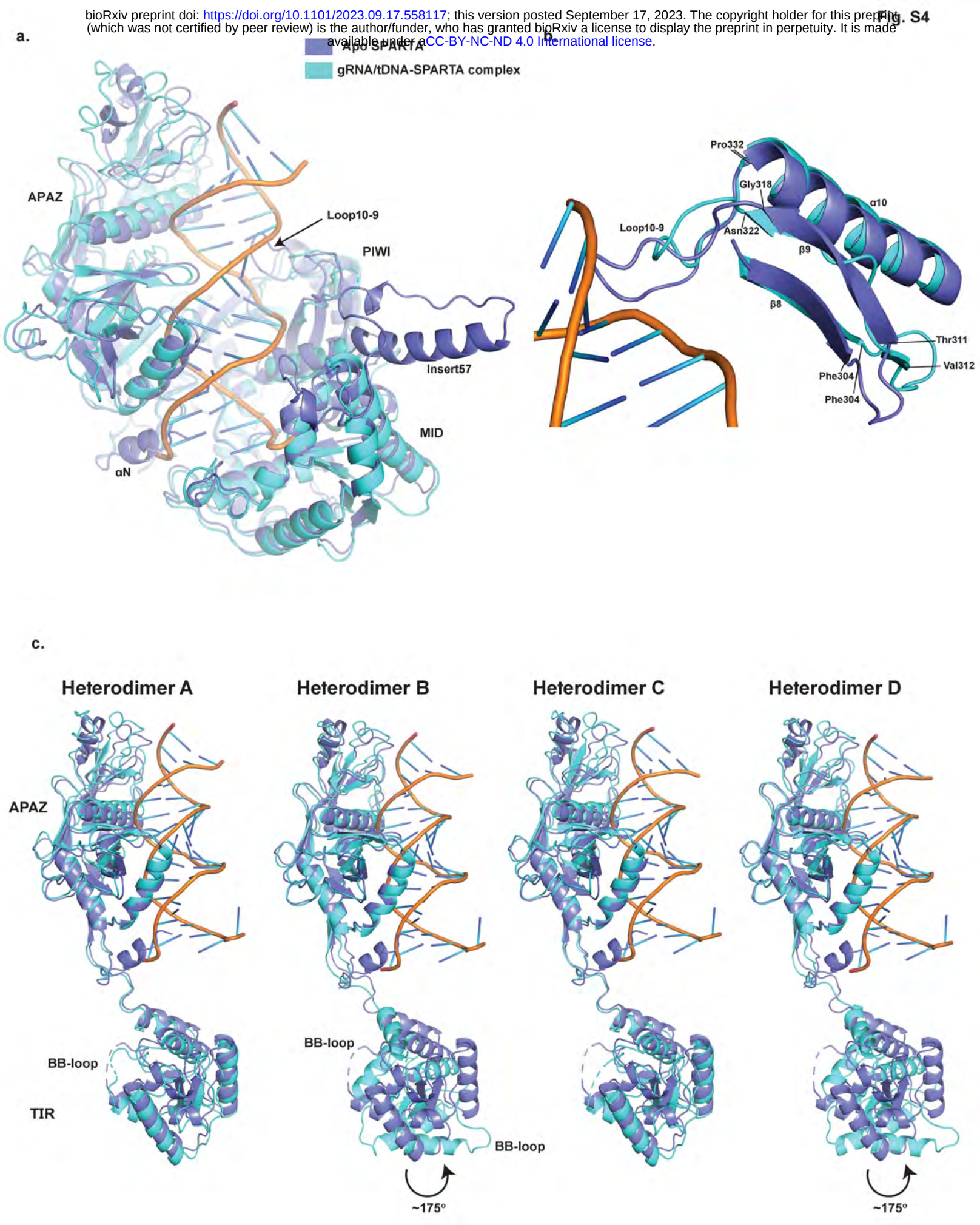

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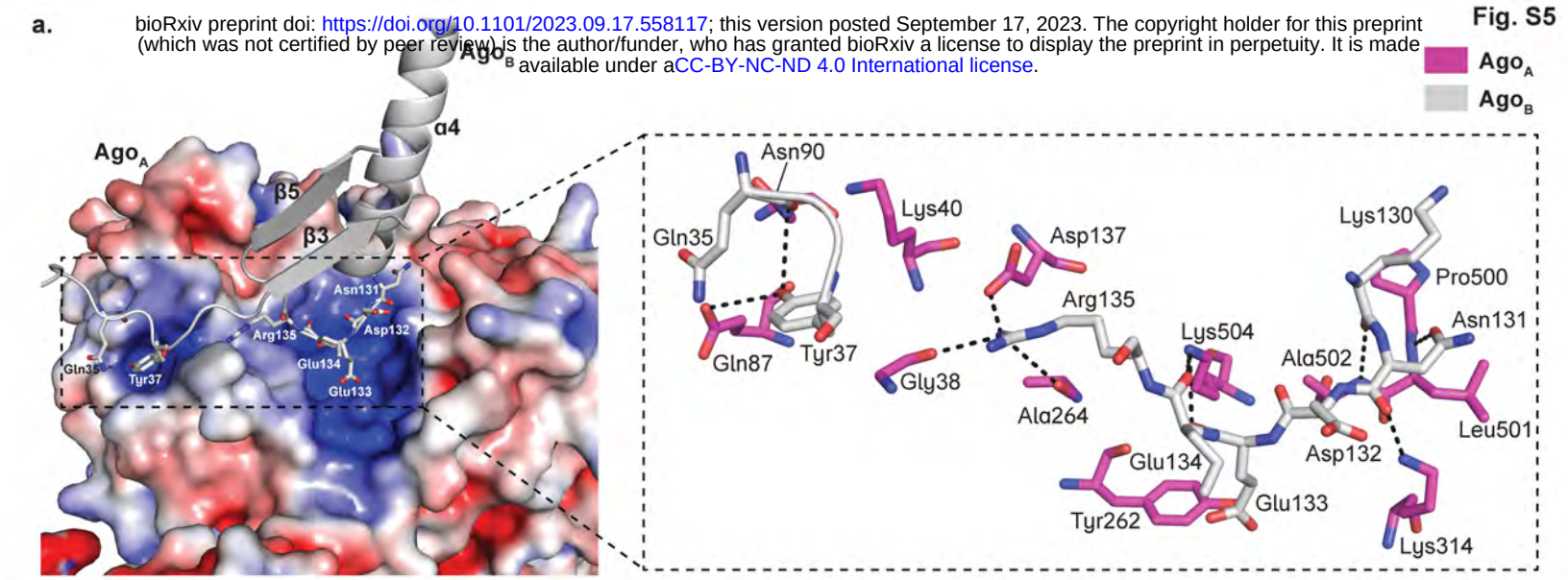
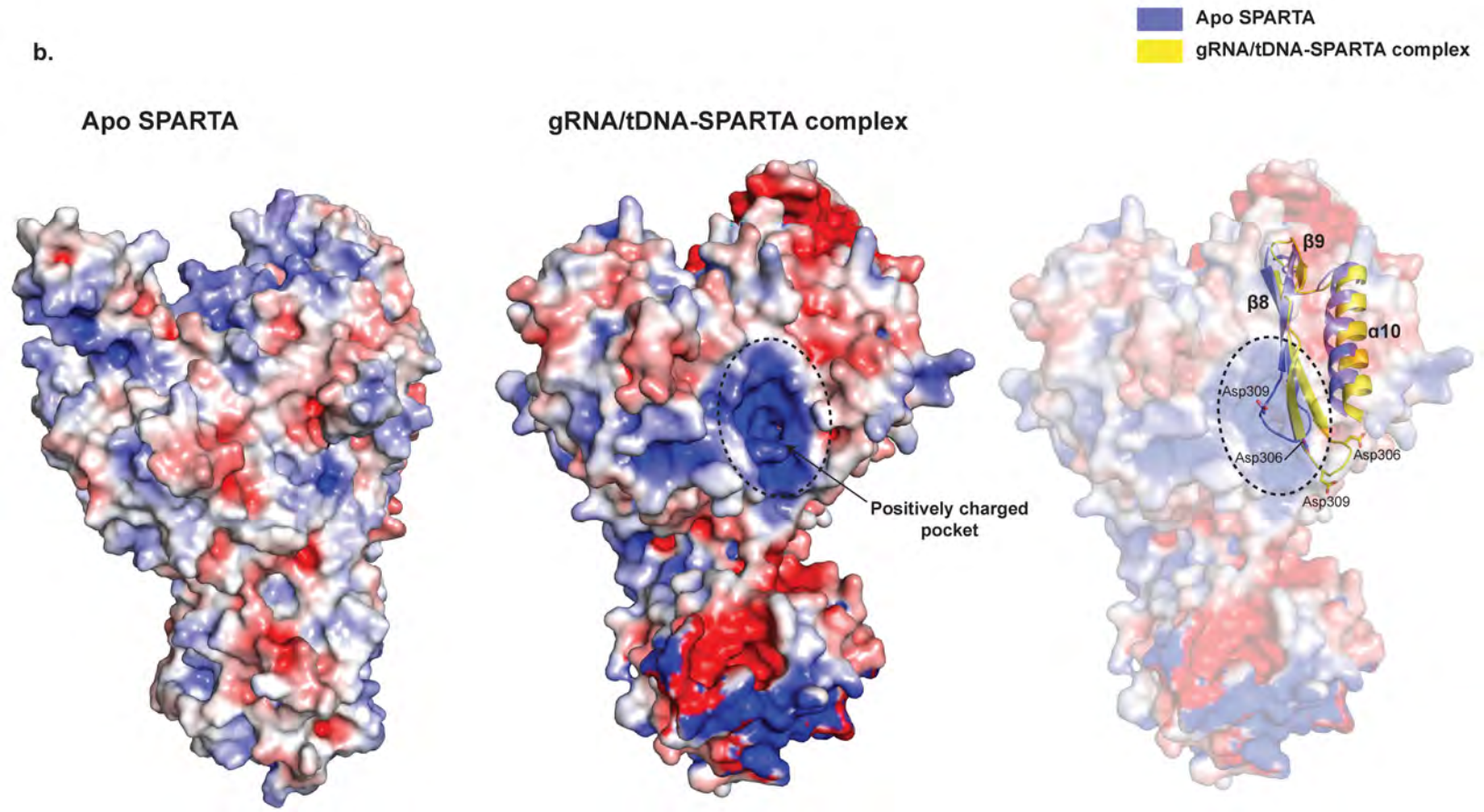
Fig. S5





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	Apo-SPARTA **(PDB: 8U7B)**
Data collection	
Space group	$P6_522$
Cell dimensions	
a, *b*, *c* (Å)	197.18 Å, 197.18 Å 183.4 Å,
α, β, γ (°)	90.00 90.00 120.00
Resolution (Å)	170.76-2.66 (2.99-2.66)*
R_{sym} or R_{merge}	14.8 (176.7)
R_{pim}	4.2 (55.4)
No. of unique reflections	40914
$I / \sigma I$	13.7 (1.7)
Completeness (%) (ellipsoidal)	96.2 (73.9)
Redundancy	13.3 (10.7)
CC(1/2)	1.00 (0.57)
Refinement	
Resolution (Å)	49.71-2.66
No. reflections	40895
R_{work} / R_{free}	18.6/24.0
No. atoms	
Macromolecules	7420
Ligands/Ions	2
Water	91
B-factors	
Macromolecules	69.0
Ligands/Ions	67.0
Water	63.9
R.m.s. deviations	
Bond lengths (Å)	0.003
Bond angles (°)	0.61
Ramachandran Plot	
Favored (%)	93.0
Allowed (%)	6.5
Outliers (%)	0.5

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Table S2: CryoEM data collection, model refinement and validation statistics

	SPARTA-gRNA-tDNA-Mg PDB ID:8U72 EMDB IDs: EMD-41945, EMD-41947, EMD-41948, EMD-41949, EMD-41966
Data collection and processing	
Magnification (kV)	x81000
Voltage (kV)	300
Pixel Size (Å/pixel)	1.083
Electron dose ($e^-/Å^2$)	51.11
Defocus range (μm)	0.8 - 2.5
Number of Micrographs	13,884
Tilt angle	30º, 45º
Number of particles	238,432
Nominal Map resolution (Å)	3.35
FSC threshold	0.143
Refinement (Phenix)	
Model composition	
Non-hydrogen atoms	29715
Protein residues	3469
DNA/other	148/4
R.M.S. deviations	
Bond lengths (Å)	0.003
Bond Angles (°)	0.596
Validation	
Molprobity score	1.90
Clashscore	7.07
Rotamer outliers (%)	0.33
Cβ outliers (%)	0.00
Ramachandran Statistics (%)	
Favored	91.16
Allowed	8.78
Outliers	0.06