

## Supplementary Tables

**Table S1. Cryo-electron microscopy data collection summary, processing statistics and model quality indicators**

<b>Data collection parameters and processing</b>	
Dataset	<b>mPSF + PAPOA<sub>c</sub></b>
Microscope	FEI Titan Krios G2
Voltage [kV]	300
Camera	Gatan K3
Energy Filter	Gatan Quantum-LS (GIF)
Magnification	105,000x
Pixel Size [Å]	0.8512
Electron exposure [e <sup>-</sup> /Å <sup>2</sup> ]	60.6
Target defocus range [μm]	-0.6 to -2.2
Number of movies	24,972
Initially selected particles	2,478,308
Final number of particles	186,241
Resolution [Å]	2.79
Local resolution range [Å]	2.5-3.5
Sharpening B-factor [Å <sup>2</sup> ]	-116.4
<b>Refinement</b>	
Number of atoms	13,089
Residues (protein/RNA)	1,683/6
Ligands	Zn: 3
CC <sub>box</sub> , CC <sub>mask</sub> , CC <sub>volume</sub>	0.75, 0.91, 0.88

CC for individual chains (CPSF160 = A, WDR33 = B, CPSF30 = C, PAPOA <sub>C</sub> = D, RNA = E)	A = 0.866, B = 0.873, C = 0.795, D = 0.585, E = 0.718
Resolution <small>FSC map vs. model (0/0.143/0.5)</small> [Å]	2.6/2.6/2.8
r.m.s. deviations	
Bond lengths [Å]	0.002
Bond angles [°]	0.5
Ramachandran favored [%]	96.67
Ramachandran allowed [%]	3.33
Ramachandran outliers [%]	0.00
MolProbity score	1.19
Clash score	2.10
Rotamer outliers [%]	0.00