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Supplementary Table 1. Cryo-EM data collection, refinement and validation statistics.

Data collection and processing		
Structure name	PPV	
Microscope	TALOS	Arctica
Voltage (kV)	200	
Camera	Falcon 3	
Magnification	× 120,000	
Total electron dose (e-/Å²)	40.0	
Defocus range (µm)	-0.5 and -2.2 µm	
Pixel size (Å)	0.889	
Micrographs	2508	
Manually picked filaments	29892	
Initial segments	406769	
Final segments	357073	
Helical Symmetry		
Rise ΔZ (Å)	4.08	
Twist ΔΦ (°)	-40.89	
Resolution (Å)	2.89	
(FSC threshold)	(0.143)	
Sharpening B-factor (Å²)	-139.7	
EMDB code	EMD-53450	
Model refinement		
CP molecules	45	
Protein residues	9090	
RNA nucleotides	225	
r.m.s. deviations		
Bond lengths (Å)	0.006	
Bond angles (°)	0.641	
Ramachandran plot		
Favored (%)	95.02	
Allowed (%)	4.98	
Disallowed (%)	0.00	
Validation		
Molprobity score	1.47	
Clashscore	3.33	
Poor rotamers (%)	0.00	
Map-model correlation (CCmask)	0.92	
PDB code	9QY3	