

## Cryo-EM data collection, refinement and validation statistics

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	CPSF-AAUAAA (EMD-4225) (PDB 6FBS)
<b>Data collection and processing</b>	
Magnification	47259
Voltage (kV)	300
Electron exposure (e-/Å <sup>2</sup> )	80
Defocus range (µm)	1.0-2.2
Pixel size (Å)	1.058
Symmetry imposed	C1
Initial particle images (no.)	263000
Final particle images (no.)	137000
Map resolution (Å)	3.1
FSC threshold	0.143
<b>Refinement</b>	
Initial model used (PDB code)	6F9N
Model resolution (Å)	3.1
FSC threshold	0.143
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-94.21
Model composition	
Non-hydrogen atoms	13421
Protein residues	1631
RNA residues	10
<i>B</i> factors (Å <sup>2</sup> )	
Protein	37.17
RNA	55.38
R.m.s. deviations	
Bond lengths (Å)	0.010
Bond angles (°)	0.968
Validation	
MolProbity score	2.15
Clashscore	10.75
Poor rotamers (%)	0.00
Ramachandran plot	
Favored (%)	88.2
Allowed (%)	11.8
Disallowed (%)	0.00

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