

Crystal condition	Apo CPSF4YTH	CPSF4YTH / m6A	CPSF4YTH / m6A 7 mer RNA
Beamline	i04 (Diamond Light Source)	ID30-A1 (ESRF)	i04 (Diamond Light Source)
Wavelength	0.9795	0.9660	0.9795
Resolution range	34.53 - 1.23 (1.274 - 1.23)	30.76 - 1.349 (1.397 - 1.349)	31.04 - 1.38 (1.45 - 1.38)
Space group	P 41 21 2	P 1	P 1
Unit cell	40.18 40.18 202.6 90 90 90	32.47 35.22 38.18 114.51 100.44 97.77	32.44 35.15 38.35 114.68 100.70 97.65
Total reflections	544909 (14247)	49449 (3627)	65418 (506)
Unique reflections	49444 (4552)	30036 (2887)	19181 (288)
Multiplicity	11.0 (4.3)	1.6 (1.7)	3.4 (1.8)
Completeness (%)	99.32 (93.70)	92.64 (88.38)	62.86 (6.5)
Mean I/sigma(I)	20.3 (1.0)	6.6 (2.1)	17.3 (3.1)
Wilson B-factor	16.70	9.18	10.99
R-merge	0.045 (1.000)	0.092 (0.338)	0.025 (0.123)
CC1/2	1.0 (0.427)	0.956 (0.496)	0.999 (0.989)
Reflections used in refinement	49441 (4550)	30007 (2876)	19180 (153)
Reflections used for R-free	2500 (232)	1532 (144)	1918 (16)
R-work	0.1769 (0.3296)	0.1825 (0.2413)	0.1430 (0.1611)
R-free	0.2034 (0.3267)	0.1966 (0.2556)	0.1684 (0.1854)
Number of non-hydrogen atoms	1447	1408	1324
macromolecules	1293	1237	1232
ligands	4	23	31
solvent	150	148	61
Protein residues	158	150	149
RMS(bonds)	0.005	0.005	0.005
RMS(angles)	0.77	0.82	0.76
Ramachandran favored (%)	99.35	99.32	98.64
Ramachandran allowed (%)	0.65	0.68	1.36
Ramachandran outliers (%)	0.00	0.00	0.00
Rotamer outliers (%)	0.00	0.72	1.49
Clashscore	3.47	3.19	2.01
Average B-factor	22.56	13.21	14.72
macromolecules	21.50	11.61	14.11
ligands	26.98	17.20	20.91
solvent	31.58	25.93	23.89
PDB id	7NG2	7NH2	7NJC