



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 05:19 PM UTC

PDB ID : 8EVG / pdb_00008evg
EMDB ID : EMD-28628
Title : 162bp CX3CR1 nucleosome (further classified with better nucleosome end)
Authors : Tengfei, L.; Ruifang, G.; Yawen, B.
Deposited on : 2022-10-20
Resolution : 2.75 Å (reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

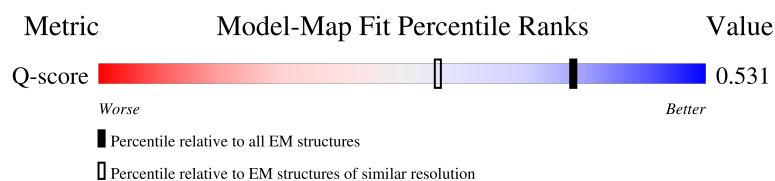
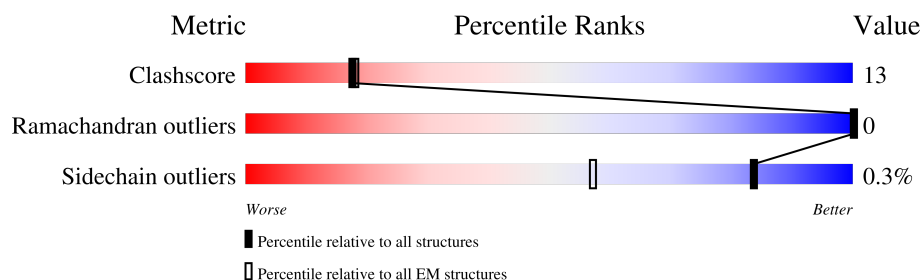
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

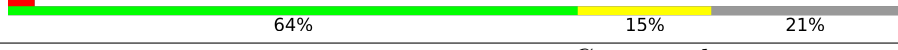
The reported resolution of this entry is 2.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10570 (2.25 - 3.25)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	136	
1	E	136	
2	B	103	
2	F	103	

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Mol	Chain	Length	Quality of chain
3	C	129	
3	G	129	
4	D	126	
4	H	126	
5	I	162	
6	J	162	
7	M	265	
7	N	265	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15577 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	98	Total	C	N	O	S	0	0
			810	511	157	138	4		
1	E	96	Total	C	N	O	S	0	0
			790	499	151	136	4		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	82	Total	C	N	O	S	0	0
			653	413	127	112	1		
2	F	81	Total	C	N	O	S	0	0
			648	410	126	111	1		

- Molecule 3 is a protein called Histone H2A type 2-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O	S	0	0
			820	518	159	142	1		
3	G	108	Total	C	N	O	S	0	0
			829	524	161	143	1		

- Molecule 4 is a protein called Histone H2B type 2-E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	94	Total	C	N	O	S	0	0
			731	459	131	139	2		
4	H	94	Total	C	N	O	S	0	0
			731	459	131	139	2		

- Molecule 5 is a DNA chain called DNA (162-MER).

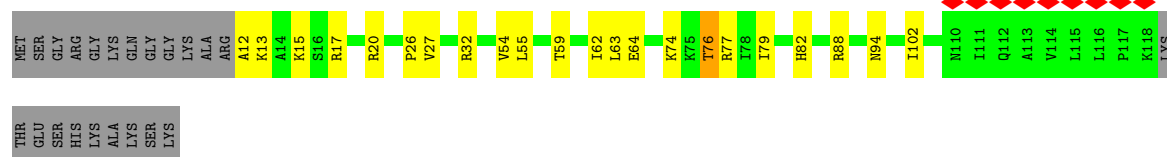
Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	147	Total	C	N	O	P	0	0
			3015	1434	540	894	147		

- Molecule 6 is a DNA chain called DNA (162-MER).

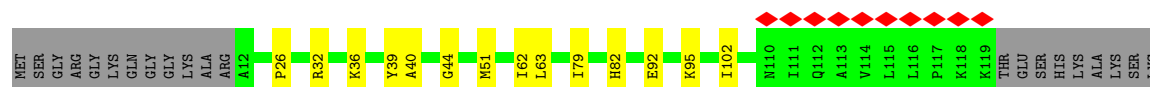
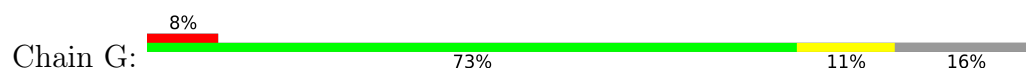
Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	147	Total	C	N	O	P	0	0
			3012	1429	566	870	147		

- Molecule 7 is a protein called Single-chain variable fragment.

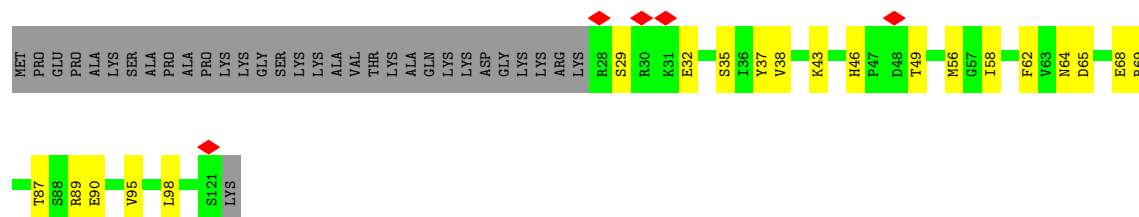
Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	226	Total	C	N	O	S	0	0
			1769	1115	289	357	8		
7	N	226	Total	C	N	O	S	0	0
			1769	1115	289	357	8		



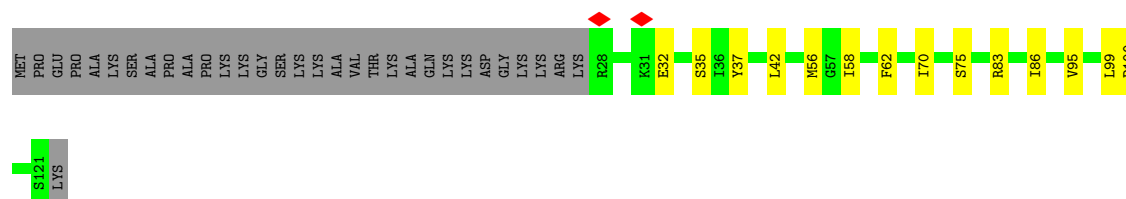
• Molecule 3: Histone H2A type 2-C



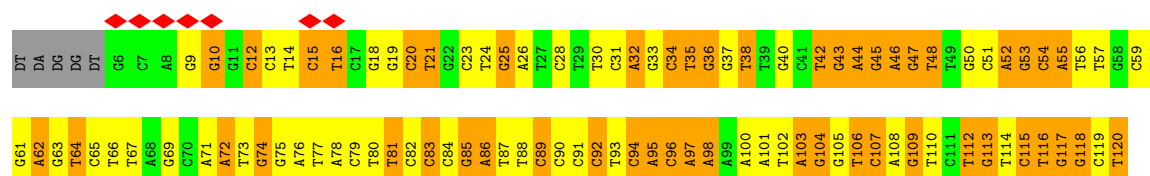
• Molecule 4: Histone H2B type 2-E



• Molecule 4: Histone H2B type 2-E

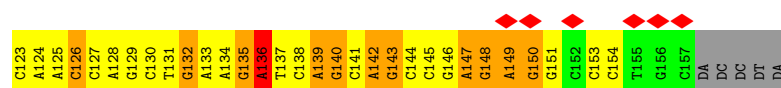
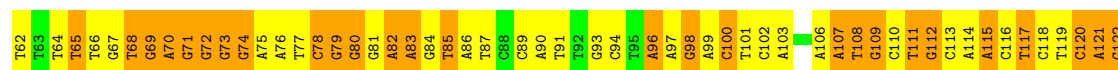
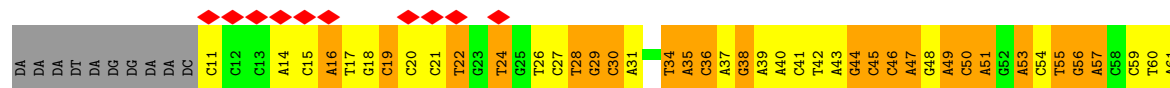


• Molecule 5: DNA (162-MER)

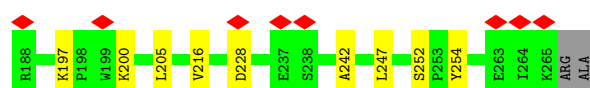
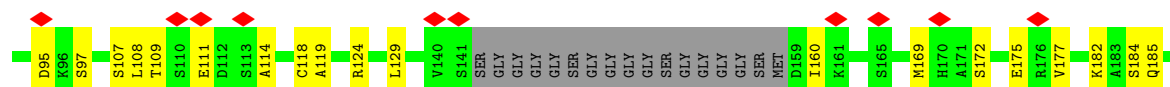
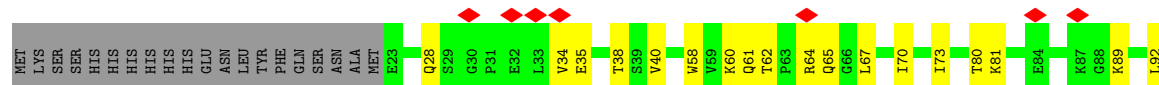




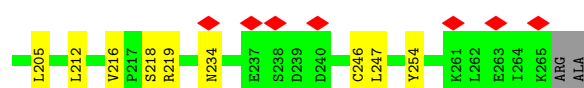
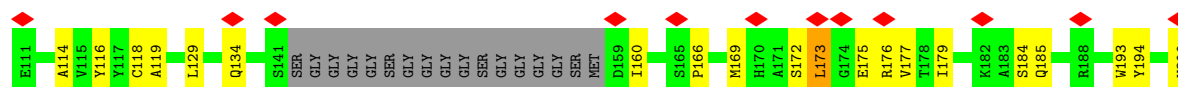
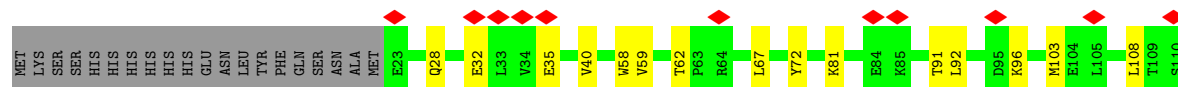
• Molecule 6: DNA (162-MER)



• Molecule 7: Single-chain variable fragment



• Molecule 7: Single-chain variable fragment



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46748	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.137	Depositor
Minimum map value	-0.872	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.078	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	253.44, 253.44, 253.44	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.056, 1.056, 1.056	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.14	0/822	0.27	0/1102
1	E	0.14	0/802	0.26	0/1076
2	B	0.32	1/660 (0.2%)	0.36	0/885
2	F	0.14	0/655	0.32	0/878
3	C	0.14	0/830	0.27	0/1118
3	G	0.14	0/839	0.26	0/1129
4	D	0.32	0/742	0.48	1/998 (0.1%)
4	H	0.15	0/742	0.30	0/998
5	I	1.74	77/3378 (2.3%)	1.76	149/5214 (2.9%)
6	J	1.65	71/3382 (2.1%)	1.67	129/5215 (2.5%)
7	M	0.14	0/1811	0.33	0/2454
7	N	0.15	0/1811	0.35	0/2454
All	All	1.10	149/16474 (0.9%)	1.17	279/23521 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	I	0	1
6	J	0	1
All	All	0	2

All (149) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	117	DG	O3'-P	-17.86	1.34	1.61
6	J	80	DG	O3'-P	-16.51	1.36	1.61
5	I	85	DG	O3'-P	-16.18	1.36	1.61
5	I	107	DC	O3'-P	-15.77	1.37	1.61
5	I	35	DT	O3'-P	-15.43	1.38	1.61
6	J	96	DA	O3'-P	-14.65	1.39	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	87	DT	O3'-P	-14.35	1.39	1.61
5	I	106	DT	O3'-P	-14.31	1.39	1.61
6	J	132	DG	O3'-P	-13.84	1.40	1.61
5	I	44	DA	O3'-P	-13.62	1.40	1.61
6	J	34	DT	O3'-P	-13.47	1.41	1.61
5	I	55	DA	O3'-P	-13.03	1.41	1.61
6	J	81	DG	P-OP1	-12.92	1.22	1.48
6	J	134	DA	O3'-P	-12.72	1.42	1.61
5	I	118	DG	P-OP1	-12.66	1.23	1.48
5	I	45	DG	P-OP1	-12.54	1.23	1.48
6	J	125	DA	O3'-P	-12.17	1.42	1.61
5	I	107	DC	P-OP1	-12.01	1.24	1.48
6	J	122	DG	O3'-P	-12.00	1.43	1.61
5	I	66	DT	O3'-P	-12.00	1.43	1.61
6	J	50	DC	P-OP1	-12.00	1.24	1.48
6	J	29	DG	O3'-P	-11.96	1.43	1.61
6	J	112	DG	P-OP1	-11.91	1.24	1.48
6	J	100	DC	O3'-P	-11.76	1.43	1.61
6	J	131	DT	O3'-P	-11.71	1.43	1.61
5	I	65	DC	O3'-P	-11.53	1.43	1.61
5	I	118	DG	O3'-P	-11.44	1.44	1.61
5	I	95	DA	O3'-P	-11.06	1.44	1.61
6	J	38	DG	O3'-P	-10.97	1.44	1.61
6	J	83	DA	O3'-P	-10.92	1.44	1.61
6	J	101	DT	O3'-P	-10.86	1.44	1.61
5	I	64	DT	O3'-P	-10.59	1.45	1.61
5	I	45	DG	O3'-P	-10.37	1.45	1.61
6	J	93	DG	O3'-P	-10.21	1.45	1.61
5	I	56	DT	P-OP1	-10.16	1.28	1.48
6	J	132	DG	P-OP1	-10.08	1.28	1.48
6	J	121	DA	O3'-P	-10.01	1.46	1.61
6	J	102	DC	P-OP2	-9.88	1.28	1.48
5	I	36	DG	P-OP2	-9.85	1.28	1.48
5	I	105	DG	O3'-P	-9.83	1.46	1.61
5	I	87	DT	P-OP1	-9.74	1.28	1.48
5	I	87	DT	P-OP2	-9.68	1.29	1.48
5	I	67	DT	O3'-P	-9.59	1.46	1.61
5	I	86	DA	O3'-P	-9.47	1.47	1.61
6	J	81	DG	O3'-P	-9.38	1.47	1.61
5	I	56	DT	O3'-P	-9.34	1.47	1.61
6	J	30	DC	O3'-P	-9.28	1.47	1.61
5	I	66	DT	P-OP1	-9.19	1.30	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	70	DA	O3'-P	-9.19	1.47	1.61
6	J	93	DG	P-OP1	-9.18	1.30	1.48
6	J	69	DG	O3'-P	-9.13	1.47	1.61
6	J	112	DG	P-OP2	-9.11	1.30	1.48
6	J	39	DA	O3'-P	-9.10	1.47	1.61
6	J	79	DG	O3'-P	-9.01	1.47	1.61
5	I	86	DA	P-OP2	-8.99	1.30	1.48
6	J	133	DA	P-OP1	-8.71	1.31	1.48
6	J	111	DT	O3'-P	-8.50	1.48	1.61
5	I	36	DG	P-OP1	-8.47	1.31	1.48
5	I	88	DT	P-OP1	-8.41	1.31	1.48
6	J	142	DA	P-OP1	-8.33	1.31	1.48
6	J	82	DA	O3'-P	-8.26	1.48	1.61
6	J	101	DT	P-OP1	-8.20	1.32	1.48
6	J	81	DG	P-OP2	-8.18	1.32	1.48
5	I	37	DG	P-OP1	-8.11	1.32	1.48
5	I	56	DT	P-OP2	-8.11	1.32	1.48
6	J	147	DA	O3'-P	8.10	1.73	1.61
5	I	36	DG	O3'-P	-8.08	1.49	1.61
6	J	118	DC	O3'-P	-8.08	1.49	1.61
5	I	88	DT	P-OP2	-8.02	1.32	1.48
5	I	45	DG	P-OP2	-8.01	1.32	1.48
6	J	133	DA	P-OP2	-7.84	1.32	1.48
5	I	86	DA	P-OP1	-7.81	1.32	1.48
5	I	145	DC	O3'-P	7.79	1.72	1.61
6	J	84	DG	O3'-P	-7.78	1.49	1.61
5	I	74	DG	O3'-P	-7.68	1.49	1.61
5	I	107	DC	P-OP2	-7.66	1.33	1.48
6	J	77	DT	O3'-P	-7.48	1.50	1.61
6	J	37	DA	O3'-P	-7.48	1.50	1.61
6	J	49	DA	O3'-P	-7.47	1.50	1.61
6	J	102	DC	P-OP1	-7.35	1.33	1.48
5	I	67	DT	P-OP2	-7.33	1.33	1.48
5	I	118	DG	P-OP2	-7.32	1.33	1.48
5	I	54	DC	O3'-P	-7.27	1.50	1.61
6	J	90	DA	O3'-P	-7.27	1.50	1.61
6	J	139	DA	O3'-P	-7.22	1.50	1.61
6	J	122	DG	P-OP1	-7.21	1.34	1.48
6	J	98	DG	O3'-P	-7.11	1.50	1.61
6	J	133	DA	O3'-P	-6.93	1.50	1.61
5	I	128	DT	P-OP1	-6.91	1.34	1.48
5	I	112	DT	O3'-P	-6.86	1.50	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	148	DG	O3'-P	-6.85	1.50	1.61
5	I	89	DC	P-OP1	-6.84	1.34	1.48
5	I	67	DT	P-OP1	-6.74	1.34	1.48
5	I	121	DA	O3'-P	-6.69	1.51	1.61
6	J	127	DC	O3'-P	-6.68	1.51	1.61
5	I	25	DG	O3'-P	-6.66	1.51	1.61
5	I	25	DG	P-OP1	-6.64	1.35	1.48
5	I	116	DT	O3'-P	-6.60	1.51	1.61
5	I	96	DC	P-OP2	-6.39	1.35	1.48
6	J	101	DT	P-OP2	-6.37	1.35	1.48
5	I	75	DG	O3'-P	-6.35	1.51	1.61
5	I	24	DT	O3'-P	-6.30	1.51	1.61
5	I	35	DT	P-OP1	-6.29	1.35	1.48
5	I	73	DT	O3'-P	-6.27	1.51	1.61
6	J	135	DG	O3'-P	-6.24	1.51	1.61
6	J	122	DG	P-OP2	-6.22	1.36	1.48
5	I	95	DA	P-OP1	-6.20	1.36	1.48
5	I	66	DT	P-OP2	-6.17	1.36	1.48
6	J	73	DG	O3'-P	-6.15	1.51	1.61
6	J	115	DA	O3'-P	-6.12	1.51	1.61
5	I	78	DA	O3'-P	-6.11	1.51	1.61
5	I	35	DT	P-OP2	-6.05	1.36	1.48
5	I	127	DG	P-OP1	-6.03	1.36	1.48
6	J	142	DA	O3'-P	-6.03	1.52	1.61
6	J	50	DC	P-OP2	-5.85	1.36	1.48
5	I	34	DC	P-OP2	-5.78	1.36	1.48
5	I	37	DG	P-OP2	-5.73	1.36	1.48
5	I	117	DG	P-OP2	-5.72	1.37	1.48
5	I	50	DG	O3'-P	-5.66	1.52	1.61
6	J	132	DG	P-OP2	-5.63	1.37	1.48
5	I	10	DG	O3'-P	5.61	1.69	1.61
5	I	81	DT	O3'-P	-5.60	1.52	1.61
6	J	55	DT	O3'-P	-5.59	1.52	1.61
6	J	91	DT	O3'-P	-5.57	1.52	1.61
5	I	129	DA	P-OP1	-5.55	1.37	1.48
5	I	94	DC	O3'-P	-5.50	1.52	1.61
5	I	128	DT	O3'-P	-5.48	1.52	1.61
6	J	128	DA	O3'-P	-5.46	1.52	1.61
5	I	126	DT	O3'-P	-5.44	1.52	1.61
6	J	134	DA	P-OP1	-5.44	1.37	1.48
6	J	134	DA	P-OP2	-5.43	1.37	1.48
5	I	117	DG	C2'-C1'	-5.41	1.42	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	40	DA	O3'-P	-5.39	1.53	1.61
6	J	60	DT	O3'-P	-5.38	1.53	1.61
5	I	76	DA	O3'-P	-5.37	1.53	1.61
6	J	142	DA	P-OP2	-5.34	1.37	1.48
5	I	66	DT	O4'-C1'	-5.32	1.31	1.41
6	J	94	DC	P-OP1	-5.29	1.37	1.48
6	J	61	DA	O3'-P	-5.28	1.53	1.61
5	I	55	DA	C2'-C1'	-5.23	1.42	1.52
6	J	94	DC	P-OP2	-5.22	1.38	1.48
6	J	30	DC	P-OP1	-5.19	1.38	1.48
6	J	130	DC	O3'-P	-5.18	1.53	1.61
6	J	76	DA	O3'-P	-5.13	1.53	1.61
5	I	128	DT	P-OP2	-5.12	1.38	1.48
2	B	95	ARG	C-O	-5.02	1.18	1.23
5	I	23	DC	O3'-P	5.02	1.68	1.61
5	I	25	DG	P-OP2	-5.02	1.38	1.48
6	J	30	DC	P-OP2	-5.01	1.38	1.48

All (279) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	96	DC	C2'-C3'-O3'	-14.11	90.34	111.50
6	J	82	DA	C2'-C3'-O3'	-13.86	90.71	111.50
6	J	97	DA	C2'-C3'-O3'	12.97	130.96	111.50
5	I	131	DT	C4'-C3'-O3'	12.72	129.07	110.00
6	J	19	DC	C2'-C3'-O3'	12.71	130.56	111.50
5	I	98	DA	C2'-C3'-O3'	-12.48	92.78	111.50
6	J	28	DT	C4'-C3'-O3'	-12.18	91.73	110.00
5	I	21	DT	C2'-C3'-O3'	-12.12	93.31	111.50
5	I	117	DG	C2'-C3'-O3'	-11.79	93.82	111.50
5	I	117	DG	N9-C1'-C2'	-11.69	95.96	113.50
5	I	20	DC	C4'-C3'-O3'	11.68	127.52	110.00
6	J	26	DT	C2'-C3'-O3'	-11.67	94.00	111.50
5	I	19	DG	C2'-C3'-O3'	-11.43	94.35	111.50
5	I	46	DA	C4'-C3'-O3'	-11.41	92.88	110.00
5	I	44	DA	C2'-C3'-O3'	11.34	128.50	111.50
5	I	65	DC	C4'-C3'-O3'	-11.28	93.09	110.00
5	I	112	DT	C4'-C3'-O3'	-11.08	93.38	110.00
5	I	147	DT	C2'-C3'-O3'	-10.98	95.02	111.50
5	I	24	DT	C4'-C3'-O3'	-10.84	93.74	110.00
6	J	38	DG	C4'-C3'-O3'	-10.83	93.76	110.00
6	J	110	DC	C4'-C3'-O3'	-10.80	93.80	110.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	53	DA	C2'-C3'-O3'	-10.79	95.32	111.50
6	J	81	DG	C2'-C3'-O3'	-10.59	95.62	111.50
5	I	53	DG	C2'-C3'-O3'	10.59	127.38	111.50
6	J	34	DT	P-O3'-C3'	10.28	135.62	120.20
5	I	90	DC	C4'-C3'-O3'	-10.05	94.93	110.00
6	J	110	DC	C2'-C3'-O3'	10.02	126.53	111.50
5	I	107	DC	O5'-P-OP1	-9.79	79.64	109.00
6	J	57	DA	C4-N9-C1'	-9.58	112.68	127.05
5	I	118	DG	C2'-C3'-O3'	-9.58	97.13	111.50
6	J	74	DG	C2'-C3'-O3'	-9.56	97.15	111.50
6	J	36	DC	C4'-C3'-O3'	-9.43	95.85	110.00
6	J	83	DA	C4-N9-C1'	-9.43	112.91	127.05
6	J	45	DC	C2'-C3'-O3'	-9.39	97.41	111.50
5	I	23	DC	C2'-C3'-O3'	-9.27	97.59	111.50
5	I	92	DC	C2'-C3'-O3'	9.22	125.33	111.50
5	I	95	DA	P-O5'-C5'	-9.04	106.44	120.00
6	J	50	DC	C4'-C3'-O3'	-9.01	96.48	110.00
6	J	77	DT	C4'-C3'-O3'	-8.90	96.64	110.00
6	J	51	DA	O5'-P-OP1	-8.88	82.35	109.00
5	I	73	DT	C4'-C3'-O3'	-8.88	96.69	110.00
6	J	102	DC	O5'-P-OP1	-8.78	82.66	109.00
5	I	130	DC	C2'-C3'-O3'	8.75	124.62	111.50
6	J	57	DA	C5'-C4'-O4'	8.71	122.46	109.40
6	J	36	DC	O5'-P-OP1	-8.67	82.99	109.00
6	J	85	DT	C2'-C3'-O3'	-8.67	98.50	111.50
6	J	78	DC	C4'-C3'-O3'	-8.67	97.00	110.00
6	J	83	DA	C8-N9-C1'	8.65	140.03	127.05
4	D	29	SER	N-CA-C	8.61	125.52	109.24
6	J	71	DG	C2'-C3'-O3'	-8.56	98.66	111.50
6	J	140	DG	C4'-C3'-O3'	8.53	122.80	110.00
6	J	134	DA	N9-C1'-C2'	-8.48	100.78	113.50
6	J	147	DA	C2'-C3'-O3'	8.46	124.19	111.50
5	I	82	DC	C4'-C3'-O3'	-8.45	97.32	110.00
6	J	140	DG	C2'-C3'-O3'	-8.41	98.89	111.50
5	I	46	DA	C2'-C3'-O3'	-8.33	99.00	111.50
5	I	127	DG	P-O3'-C3'	8.29	132.63	120.20
6	J	112	DG	O5'-P-OP1	-8.28	84.16	109.00
5	I	61	DG	N9-C1'-C2'	8.27	125.91	113.50
6	J	57	DA	C8-N9-C1'	8.27	139.46	127.05
6	J	101	DT	C4'-C3'-O3'	-8.27	97.59	110.00
6	J	29	DG	C4'-C3'-O3'	-8.22	97.67	110.00
5	I	121	DA	C4'-C3'-O3'	-8.19	97.71	110.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	19	DG	C4'-C3'-O3'	8.17	122.25	110.00
5	I	48	DT	C2'-C3'-O3'	8.16	123.74	111.50
6	J	22	DT	P-O3'-C3'	8.12	132.38	120.20
5	I	97	DA	C2'-C3'-O3'	-8.07	99.39	111.50
6	J	115	DA	N9-C1'-C2'	8.06	125.60	113.50
5	I	56	DT	C4'-C3'-O3'	-8.00	98.00	110.00
6	J	80	DG	C2'-C3'-O3'	-7.98	99.53	111.50
6	J	115	DA	C4-N9-C1'	-7.89	115.22	127.05
5	I	52	DA	C4'-C3'-O3'	-7.82	98.27	110.00
6	J	36	DC	O5'-P-OP2	7.81	131.43	108.00
5	I	122	DG	C4'-C3'-O3'	-7.81	98.29	110.00
6	J	150	DG	N9-C1'-C2'	7.79	125.19	113.50
5	I	25	DG	C4'-C3'-O3'	-7.77	98.34	110.00
6	J	67	DG	C4'-C3'-O3'	-7.63	98.55	110.00
5	I	72	DA	C4-N9-C1'	-7.62	115.61	127.05
5	I	86	DA	P-O3'-C3'	7.62	131.63	120.20
5	I	34	DC	C4'-C3'-O3'	-7.57	98.64	110.00
5	I	56	DT	C2'-C3'-O3'	7.55	122.83	111.50
6	J	46	DC	C2'-C3'-O3'	7.45	122.67	111.50
5	I	103	DA	C4'-C3'-O3'	-7.44	98.84	110.00
5	I	40	DG	C2'-C3'-O3'	-7.42	100.37	111.50
5	I	115	DC	C4'-C3'-O3'	-7.41	98.88	110.00
5	I	95	DA	C5'-C4'-C3'	-7.41	103.79	114.90
6	J	133	DA	C2'-C3'-O3'	-7.40	100.40	111.50
5	I	86	DA	C2'-C3'-O3'	-7.37	100.45	111.50
6	J	115	DA	C8-N9-C1'	7.34	138.06	127.05
5	I	38	DT	C4'-C3'-O3'	-7.33	99.00	110.00
6	J	55	DT	C4'-C3'-O3'	-7.30	99.05	110.00
5	I	129	DA	C2'-C3'-O3'	-7.29	100.56	111.50
5	I	116	DT	C4'-C3'-O3'	-7.25	99.13	110.00
5	I	109	DG	C2'-C3'-O3'	-7.24	100.64	111.50
6	J	16	DA	C4-N9-C1'	-7.23	116.20	127.05
5	I	81	DT	C4'-C3'-O3'	-7.23	99.16	110.00
6	J	149	DA	C2'-C3'-O3'	-7.21	100.69	111.50
5	I	121	DA	C4-N9-C1'	-7.20	116.25	127.05
6	J	133	DA	N9-C1'-C2'	-7.18	102.73	113.50
5	I	147	DT	N1-C1'-C2'	7.16	124.24	113.50
6	J	79	DG	C2'-C3'-O3'	-7.15	100.77	111.50
5	I	106	DT	C4'-C3'-O3'	-7.13	99.30	110.00
5	I	124	DT	C2'-C3'-O3'	-7.13	100.81	111.50
6	J	120	DC	C2'-C3'-O3'	-7.12	100.81	111.50
5	I	66	DT	P-O5'-C5'	7.11	130.66	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	46	DC	C4'-C3'-O3'	-7.11	99.34	110.00
5	I	144	DG	N9-C1'-C2'	7.10	124.15	113.50
5	I	93	DT	C4'-C3'-O3'	-7.07	99.40	110.00
5	I	104	DG	C2'-C3'-O3'	-7.05	100.92	111.50
6	J	109	DG	C2'-C3'-O3'	-7.05	100.92	111.50
6	J	72	DG	C2'-C3'-O3'	-7.04	100.94	111.50
5	I	12	DC	C2'-C3'-O3'	-7.02	100.97	111.50
6	J	16	DA	C8-N9-C1'	7.00	137.56	127.05
5	I	72	DA	C8-N9-C1'	7.00	137.55	127.05
5	I	121	DA	C8-N9-C1'	7.00	137.55	127.05
6	J	56	DG	C4'-C3'-O3'	-6.99	99.52	110.00
5	I	80	DT	C4'-C3'-O3'	-6.98	99.52	110.00
5	I	120	DT	C2'-C3'-O3'	-6.97	101.05	111.50
5	I	147	DT	C4'-C3'-O3'	6.96	120.43	110.00
6	J	124	DA	C2'-C3'-O3'	-6.93	101.11	111.50
6	J	57	DA	C2'-C3'-O3'	6.93	121.89	111.50
5	I	66	DT	O5'-P-OP1	-6.88	88.35	109.00
5	I	88	DT	O5'-P-OP1	-6.87	88.38	109.00
5	I	64	DT	P-O3'-C3'	6.86	130.49	120.20
6	J	47	DA	C2'-C3'-O3'	-6.83	101.26	111.50
6	J	59	DC	C2'-C3'-O3'	-6.80	101.30	111.50
6	J	150	DG	C2'-C3'-O3'	6.73	121.59	111.50
5	I	32	DA	C2'-C3'-O3'	-6.71	101.44	111.50
5	I	45	DG	O5'-P-OP1	-6.68	88.95	109.00
6	J	108	DT	C4'-C3'-O3'	-6.67	100.00	110.00
6	J	17	DT	C4'-C3'-O3'	-6.66	100.00	110.00
5	I	126	DT	C2'-C3'-O3'	-6.65	101.52	111.50
6	J	143	DG	C2'-C3'-O3'	-6.65	101.53	111.50
5	I	71	DA	C4-N9-C1'	-6.59	117.17	127.05
5	I	38	DT	N1-C1'-C2'	6.53	123.30	113.50
6	J	147	DA	P-O3'-C3'	6.53	130.00	120.20
6	J	53	DA	C4'-C3'-O3'	6.48	119.72	110.00
5	I	36	DG	C2'-C3'-O3'	-6.48	101.78	111.50
5	I	53	DG	O3'-P-O5'	6.45	113.68	104.00
5	I	144	DG	C2'-C3'-O3'	6.40	121.10	111.50
6	J	78	DC	N1-C1'-C2'	6.40	123.10	113.50
5	I	89	DC	O5'-P-OP2	6.36	127.09	108.00
5	I	148	DG	C2'-C3'-O3'	6.36	121.03	111.50
6	J	107	DA	C4'-C3'-O3'	-6.36	100.47	110.00
5	I	71	DA	N9-C1'-C2'	6.35	123.03	113.50
5	I	71	DA	C8-N9-C1'	6.35	136.57	127.05
5	I	30	DT	C2'-C3'-O3'	-6.34	101.99	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	117	DT	O5'-P-OP2	6.34	127.03	108.00
6	J	139	DA	C4'-C3'-O3'	-6.32	100.52	110.00
6	J	57	DA	C4'-C3'-O3'	-6.32	100.53	110.00
6	J	139	DA	C2'-C3'-O3'	-6.31	102.03	111.50
5	I	75	DG	C4'-C3'-O3'	-6.30	100.55	110.00
5	I	107	DC	P-O3'-C3'	6.29	129.64	120.20
5	I	88	DT	O5'-P-OP2	6.27	126.82	108.00
6	J	80	DG	N9-C1'-C2'	-6.24	104.15	113.50
6	J	66	DT	C2'-C3'-O3'	6.22	120.83	111.50
5	I	43	DG	N9-C1'-C2'	6.19	122.78	113.50
5	I	114	DT	C2'-C3'-O3'	-6.18	102.22	111.50
6	J	78	DC	C2'-C3'-O3'	6.17	120.76	111.50
5	I	83	DC	C4'-C3'-O3'	6.11	119.17	110.00
5	I	71	DA	C3'-C2'-C1'	-6.08	92.48	101.60
5	I	57	DT	C4'-C3'-O3'	-6.08	100.88	110.00
6	J	137	DT	C2'-C3'-O3'	-6.07	102.39	111.50
6	J	125	DA	C4-N9-C1'	-6.07	117.95	127.05
5	I	107	DC	O3'-P-O5'	-6.05	94.92	104.00
6	J	96	DA	C4-N9-C1'	-6.04	117.99	127.05
5	I	123	DT	C4'-C3'-O3'	-5.99	101.02	110.00
6	J	19	DC	N1-C1'-C2'	5.99	122.48	113.50
6	J	87	DT	C4'-C3'-O3'	-5.98	101.03	110.00
6	J	153	DC	P-O3'-C3'	5.97	129.15	120.20
6	J	42	DT	C4'-C3'-O3'	-5.96	101.06	110.00
5	I	86	DA	C4'-C3'-O3'	-5.96	101.07	110.00
5	I	96	DC	P-O3'-C3'	5.95	129.12	120.20
6	J	153	DC	C2'-C3'-O3'	-5.94	102.58	111.50
5	I	86	DA	N9-C1'-C2'	-5.92	104.62	113.50
6	J	81	DG	O5'-P-OP1	-5.91	91.26	109.00
5	I	147	DT	C1'-O4'-C4'	-5.91	100.83	109.70
6	J	37	DA	C2'-C3'-O3'	-5.90	102.65	111.50
5	I	55	DA	N9-C1'-C2'	-5.89	104.67	113.50
5	I	65	DC	C2'-C3'-O3'	5.89	120.33	111.50
5	I	148	DG	C4'-C3'-O3'	-5.87	101.20	110.00
5	I	92	DC	C4'-C3'-O3'	5.86	118.79	110.00
6	J	68	DT	P-O5'-C5'	-5.86	111.21	120.00
5	I	76	DA	C4'-C3'-O3'	-5.81	101.28	110.00
5	I	127	DG	C4'-C3'-O3'	-5.80	101.29	110.00
5	I	86	DA	C5'-C4'-O4'	-5.80	100.70	109.40
5	I	137	DA	O5'-P-OP1	-5.80	91.61	109.00
6	J	102	DC	C4'-C3'-O3'	-5.79	101.32	110.00
6	J	112	DG	C2'-C3'-O3'	-5.76	102.85	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	90	DC	P-O5'-C5'	-5.75	111.37	120.00
5	I	91	DC	C4'-C3'-O3'	-5.75	101.38	110.00
5	I	89	DC	O5'-P-OP1	-5.74	91.79	109.00
6	J	135	DG	C2'-C3'-O3'	-5.73	102.90	111.50
5	I	45	DG	O5'-P-OP2	5.71	125.14	108.00
5	I	79	DC	C4'-C3'-O3'	-5.70	101.44	110.00
5	I	37	DG	C2'-C3'-O3'	-5.69	102.97	111.50
5	I	85	DG	C2'-C3'-O3'	-5.68	102.98	111.50
5	I	88	DT	C2'-C3'-O3'	-5.67	102.99	111.50
5	I	67	DT	C2'-C3'-O3'	-5.67	103.00	111.50
6	J	57	DA	C3'-C2'-C1'	-5.67	93.10	101.60
5	I	113	DG	C2'-C3'-O3'	5.66	119.99	111.50
5	I	90	DC	O5'-P-OP2	5.66	124.97	108.00
6	J	136	DA	C5'-C4'-C3'	-5.65	106.43	114.90
5	I	67	DT	O3'-P-O5'	-5.64	95.54	104.00
6	J	112	DG	O5'-P-OP2	5.64	124.91	108.00
6	J	142	DA	O5'-P-OP1	-5.63	92.12	109.00
5	I	118	DG	C4-N9-C1'	-5.61	118.58	127.00
5	I	113	DG	C4'-C3'-O3'	-5.60	101.60	110.00
6	J	55	DT	C2'-C3'-O3'	-5.60	103.10	111.50
5	I	47	DG	C2'-C3'-O3'	5.57	119.85	111.50
5	I	43	DG	C4'-C3'-O3'	-5.55	101.67	110.00
6	J	111	DT	C4'-C3'-O3'	-5.55	101.67	110.00
6	J	100	DC	C5'-C4'-C3'	5.55	123.22	114.90
6	J	133	DA	C4'-C3'-O3'	-5.53	101.71	110.00
6	J	27	DC	O5'-P-OP2	-5.49	91.52	108.00
6	J	148	DG	C2'-C3'-O3'	-5.48	103.28	111.50
5	I	37	DG	C4'-C3'-O3'	-5.46	101.82	110.00
5	I	149	DT	C4'-C3'-O3'	-5.45	101.83	110.00
6	J	120	DC	O5'-P-OP1	-5.43	92.70	109.00
6	J	66	DT	C4'-C3'-O3'	-5.42	101.87	110.00
6	J	44	DG	C2'-C3'-O3'	-5.40	103.39	111.50
5	I	10	DG	P-O3'-C3'	5.40	128.29	120.20
6	J	61	DA	C4'-C3'-O3'	-5.40	101.90	110.00
5	I	121	DA	N9-C1'-C2'	5.38	121.58	113.50
6	J	41	DC	C4'-C3'-O3'	-5.38	101.92	110.00
5	I	72	DA	C3'-C2'-C1'	-5.38	93.53	101.60
5	I	83	DC	C2'-C3'-O3'	-5.37	103.44	111.50
5	I	127	DG	C2'-C3'-O3'	5.36	119.54	111.50
6	J	27	DC	N1-C1'-C2'	5.35	121.53	113.50
6	J	24	DT	C2'-C3'-O3'	-5.35	103.48	111.50
5	I	62	DA	C2'-C3'-O3'	5.33	119.50	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	84	DG	C4'-C3'-O3'	-5.33	102.00	110.00
6	J	68	DT	C5'-C4'-O4'	-5.33	101.41	109.40
5	I	43	DG	O5'-P-OP1	-5.32	93.05	109.00
6	J	37	DA	O5'-P-OP1	-5.32	93.06	109.00
6	J	65	DT	C4'-C3'-O3'	-5.32	102.03	110.00
6	J	94	DC	C4'-C3'-O3'	-5.31	102.03	110.00
5	I	16	DT	C2'-C3'-O3'	-5.29	103.56	111.50
6	J	67	DG	C2'-C3'-O3'	5.29	119.43	111.50
5	I	14	DT	C2'-C3'-O3'	5.28	119.43	111.50
5	I	128	DT	C2'-C3'-O3'	5.27	119.41	111.50
5	I	45	DG	C2'-C3'-O3'	-5.25	103.63	111.50
6	J	125	DA	C3'-C2'-C1'	-5.25	93.73	101.60
6	J	68	DT	C2'-C3'-O3'	-5.24	103.64	111.50
5	I	96	DC	O5'-P-OP1	5.23	124.69	109.00
5	I	106	DT	O5'-P-OP1	-5.21	93.37	109.00
6	J	130	DC	C4'-C3'-O3'	-5.21	102.19	110.00
6	J	35	DA	O5'-P-OP2	5.19	123.58	108.00
5	I	107	DC	C2'-C3'-O3'	5.19	119.28	111.50
5	I	136	DG	C2'-C3'-O3'	-5.18	103.72	111.50
5	I	66	DT	N1-C1'-C2'	5.18	121.28	113.50
5	I	98	DA	N9-C1'-C2'	-5.17	105.75	113.50
5	I	42	DT	C4'-C3'-O3'	5.16	117.74	110.00
6	J	115	DA	C3'-C2'-C1'	-5.16	93.86	101.60
5	I	77	DT	C4'-C3'-O3'	-5.16	102.26	110.00
6	J	117	DT	O5'-P-OP1	-5.15	93.54	109.00
5	I	147	DT	C3'-C2'-C1'	-5.15	93.88	101.60
5	I	130	DC	C4'-C3'-O3'	-5.14	102.29	110.00
6	J	98	DG	C4'-C3'-O3'	-5.14	102.30	110.00
5	I	106	DT	O4'-C1'-C2'	-5.13	98.71	106.40
6	J	142	DA	C4'-C3'-O3'	-5.13	102.31	110.00
6	J	17	DT	N1-C1'-C2'	5.12	121.19	113.50
6	J	127	DC	N1-C1'-C2'	-5.12	105.81	113.50
5	I	131	DT	P-O3'-C3'	5.12	127.88	120.20
6	J	123	DC	C2'-C3'-O3'	-5.12	103.82	111.50
6	J	112	DG	C4'-C3'-O3'	-5.12	102.33	110.00
5	I	93	DT	C2'-C3'-O3'	5.10	119.16	111.50
6	J	60	DT	C2'-C3'-O3'	-5.10	103.85	111.50
5	I	15	DC	O5'-C5'-C4'	5.09	118.43	110.80
5	I	61	DG	C4-N9-C1'	-5.08	119.38	127.00
5	I	132	DT	P-O5'-C5'	-5.08	112.39	120.00
6	J	126	DC	C4'-C3'-O3'	-5.07	102.39	110.00
5	I	113	DG	N9-C1'-C2'	-5.06	105.90	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	56	DG	O3'-P-O5'	-5.06	96.41	104.00
6	J	50	DC	C5'-C4'-C3'	5.05	122.48	114.90
5	I	54	DC	N1-C1'-C2'	5.05	121.08	113.50
6	J	68	DT	C5'-C4'-C3'	-5.04	107.33	114.90
5	I	85	DG	O5'-P-OP1	-5.04	93.88	109.00
6	J	82	DA	N9-C1'-C2'	-5.04	105.94	113.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	I	98	DA	Sidechain
6	J	136	DA	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	810	0	851	12	0
1	E	790	0	826	10	0
2	B	653	0	695	9	0
2	F	648	0	693	18	0
3	C	820	0	880	22	0
3	G	829	0	893	17	0
4	D	731	0	747	20	0
4	H	731	0	747	16	0
5	I	3015	0	1659	137	0
6	J	3012	0	1647	154	0
7	M	1769	0	1708	30	0
7	N	1769	0	1708	32	0
All	All	15577	0	13054	362	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (362) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:109:DG:N2	6:J:54:DC:O2	1.79	1.14
5:I:25:DG:N2	6:J:138:DC:O2	1.82	1.10
5:I:151:DG:H8	5:I:151:DG:H5''	1.16	1.06
5:I:151:DG:H5''	5:I:151:DG:C8	1.94	1.02
5:I:139:DA:C8	5:I:139:DA:H5'	1.97	0.99
7:M:81:LYS:HZ1	7:M:252:SER:HB3	1.34	0.90
1:A:41:TYR:HA	5:I:149:DT:H5''	1.55	0.88
5:I:51:DC:H42	6:J:112:DG:H1	1.18	0.88
5:I:134:DC:O2	6:J:29:DG:N2	2.07	0.85
5:I:89:DC:H42	6:J:74:DG:H1	1.23	0.85
5:I:89:DC:N4	6:J:74:DG:H1	1.76	0.84
4:D:35:SER:HA	4:D:56:MET:HE2	1.59	0.83
6:J:44:DG:H5'	6:J:44:DG:H8	1.42	0.83
5:I:100:DA:H1'	5:I:101:DA:H5'	1.62	0.82
5:I:144:DG:O6	6:J:19:DC:N4	2.14	0.80
7:M:81:LYS:NZ	7:M:252:SER:HB3	1.94	0.80
5:I:51:DC:N4	6:J:112:DG:H1	1.80	0.78
5:I:74:DG:H1	6:J:89:DC:H42	1.30	0.78
6:J:115:DA:OP2	6:J:115:DA:H2'	1.84	0.78
5:I:96:DC:H2''	5:I:97:DA:H5'	1.64	0.77
2:F:31:LYS:HE3	2:F:51:TYR:CZ	2.21	0.76
5:I:18:DG:H2'	5:I:18:DG:OP2	1.85	0.76
7:N:62:THR:HG22	7:N:114:ALA:HB2	1.68	0.76
5:I:16:DT:C2	6:J:148:DG:N2	2.56	0.74
2:F:70:VAL:HA	2:F:73:THR:HG22	1.68	0.74
5:I:84:DC:H42	6:J:79:DG:H1	1.37	0.73
2:F:31:LYS:HG3	2:F:51:TYR:CE1	2.24	0.72
5:I:15:DC:H42	6:J:148:DG:H1	1.35	0.72
2:F:31:LYS:HE3	2:F:51:TYR:CE2	2.25	0.71
5:I:125:DC:H42	6:J:38:DG:H1	1.37	0.71
5:I:53:DG:N2	6:J:111:DT:O2	2.23	0.71
5:I:110:DT:OP2	5:I:110:DT:H2'	1.90	0.70
6:J:148:DG:OP2	6:J:148:DG:H2'	1.92	0.70
6:J:44:DG:H5'	6:J:44:DG:C8	2.26	0.69
5:I:13:DC:C2	6:J:151:DG:N2	2.61	0.69
5:I:89:DC:N3	6:J:74:DG:N2	2.41	0.68
5:I:12:DC:H42	6:J:151:DG:H1	1.42	0.68
3:C:62:ILE:HD12	4:D:62:PHE:CE2	2.30	0.67
3:G:62:ILE:HD12	4:H:62:PHE:CE2	2.31	0.66
6:J:44:DG:H8	6:J:44:DG:C5'	2.08	0.66
7:M:28:GLN:NE2	7:M:118:CYS:SG	2.68	0.65
7:M:81:LYS:NZ	7:M:252:SER:CB	2.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:55:DT:OP2	6:J:55:DT:H2'	1.96	0.65
6:J:15:DC:H1'	6:J:16:DA:H5'	1.80	0.64
6:J:14:DA:O5'	6:J:14:DA:H8	1.80	0.64
5:I:148:DG:C6	6:J:14:DA:C6	2.85	0.64
3:C:76:THR:OG1	6:J:141:DC:H5''	1.98	0.64
5:I:59:DC:H2'	5:I:59:DC:OP2	1.97	0.63
1:E:121:PRO:HB3	2:F:53:GLU:HG3	1.80	0.63
6:J:14:DA:H8	6:J:14:DA:C5'	2.11	0.63
1:A:99:TYR:HB2	2:B:95:ARG:NH2	2.14	0.62
7:N:62:THR:CG2	7:N:114:ALA:HB2	2.29	0.62
7:M:109:THR:HG22	7:M:111:GLU:H	1.63	0.62
5:I:139:DA:H5'	5:I:139:DA:H8	1.61	0.61
5:I:15:DC:N4	6:J:148:DG:H1	1.98	0.61
1:A:41:TYR:HA	5:I:149:DT:C5'	2.28	0.61
5:I:121:DA:H2'	5:I:121:DA:OP2	2.00	0.61
6:J:107:DA:H1'	6:J:108:DT:H5'	1.81	0.60
5:I:59:DC:H1'	5:I:60:DT:H5'	1.84	0.60
5:I:148:DG:O6	6:J:14:DA:N6	2.35	0.59
6:J:14:DA:C5'	6:J:14:DA:C8	2.85	0.59
6:J:115:DA:H2'	6:J:115:DA:P	2.41	0.59
7:N:176:ARG:NH2	7:N:234:ASN:OD1	2.34	0.59
5:I:16:DT:N3	6:J:148:DG:N2	2.49	0.59
5:I:32:DA:C2	6:J:132:DG:N2	2.70	0.59
7:M:119:ALA:HB3	7:M:129:LEU:HD22	1.84	0.59
6:J:136:DA:C5'	6:J:136:DA:C8	2.85	0.59
3:G:102:ILE:HG23	4:H:58:ILE:HD13	1.84	0.59
6:J:44:DG:C8	6:J:44:DG:C5'	2.85	0.59
5:I:18:DG:H2'	5:I:18:DG:P	2.41	0.59
7:M:40:VAL:HG12	7:M:108:LEU:HD11	1.84	0.59
7:M:205:LEU:HA	7:M:216:VAL:HG21	1.85	0.59
5:I:143:DG:H1	6:J:20:DC:H42	1.49	0.59
5:I:109:DG:N2	6:J:54:DC:C2	2.48	0.58
6:J:11:DC:P	6:J:11:DC:H3'	2.44	0.58
6:J:53:DA:H2'	6:J:53:DA:O5'	2.04	0.58
5:I:131:DT:H2''	5:I:132:DT:H72	1.85	0.58
6:J:136:DA:C8	6:J:136:DA:H5''	2.39	0.57
7:N:176:ARG:HH21	7:N:234:ASN:HA	1.68	0.57
4:D:64:ASN:O	4:D:68:GLU:HG3	2.04	0.57
5:I:85:DG:H1	6:J:78:DC:H42	1.51	0.57
5:I:12:DC:N4	6:J:151:DG:H1	2.01	0.57
5:I:42:DT:O4	6:J:121:DA:N1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:148:DG:O6	6:J:14:DA:C6	2.58	0.57
6:J:83:DA:O5'	6:J:83:DA:H2'	2.05	0.57
2:F:31:LYS:HE3	2:F:51:TYR:OH	2.05	0.57
5:I:125:DC:N4	6:J:38:DG:H1	2.03	0.57
5:I:118:DG:H1	6:J:45:DC:H42	1.52	0.56
3:C:55:LEU:O	3:C:59:THR:HG22	2.05	0.56
7:N:219:ARG:HG3	7:N:234:ASN:H	1.69	0.56
1:A:120:MET:N	1:A:123:ASP:OD2	2.34	0.56
7:N:119:ALA:HB3	7:N:129:LEU:HD22	1.86	0.56
3:G:51:MET:HE1	4:H:70:ILE:HB	1.87	0.56
3:C:102:ILE:HG23	4:D:58:ILE:HD13	1.86	0.56
5:I:43:DG:O5'	5:I:43:DG:H2'	2.06	0.56
3:G:62:ILE:CD1	4:H:62:PHE:CZ	2.89	0.56
4:D:38:VAL:HB	4:D:56:MET:HE1	1.89	0.55
7:M:197:LYS:HD3	7:M:242:ALA:HB2	1.89	0.55
5:I:148:DG:C6	6:J:14:DA:N6	2.75	0.55
2:F:31:LYS:HG3	2:F:51:TYR:CZ	2.41	0.55
7:N:169:MET:HE1	7:N:177:VAL:HB	1.88	0.55
1:A:40:ARG:O	5:I:149:DT:H4'	2.07	0.55
5:I:72:DA:H2'	5:I:72:DA:P	2.47	0.55
6:J:96:DA:O5'	6:J:96:DA:H2'	2.07	0.55
6:J:62:DT:O5'	6:J:62:DT:H2'	2.07	0.54
6:J:136:DA:C5'	6:J:136:DA:H8	2.19	0.54
1:E:120:MET:N	1:E:123:ASP:OD2	2.37	0.54
6:J:132:DG:O5'	6:J:132:DG:H2'	2.07	0.54
5:I:109:DG:N1	6:J:54:DC:N3	2.51	0.54
5:I:63:DG:H2''	5:I:64:DT:H71	1.88	0.54
5:I:108:DA:N1	6:J:55:DT:C4	2.76	0.54
1:E:68:GLN:O	1:E:72:ARG:HG3	2.07	0.54
5:I:16:DT:O2	6:J:148:DG:N2	2.40	0.54
5:I:89:DC:N4	6:J:74:DG:N1	2.43	0.54
6:J:56:DG:H1'	6:J:57:DA:H5'	1.90	0.53
5:I:136:DG:H1'	5:I:137:DA:H5'	1.89	0.53
6:J:29:DG:H2'	6:J:29:DG:O5'	2.08	0.53
7:N:205:LEU:HA	7:N:216:VAL:HG21	1.90	0.53
5:I:25:DG:N2	6:J:139:DA:C2	2.76	0.53
7:N:172:SER:HB3	7:N:175:GLU:HG3	1.90	0.53
6:J:14:DA:C8	6:J:14:DA:H5''	2.44	0.53
6:J:103:DA:H2'	6:J:103:DA:O5'	2.09	0.53
6:J:73:DG:H2'	6:J:73:DG:O5'	2.09	0.53
7:M:62:THR:HG22	7:M:114:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:119:DC:H42	6:J:44:DG:H1	1.58	0.52
5:I:127:DG:H2'	5:I:128:DT:H72	1.91	0.52
7:N:59:VAL:HG11	7:N:67:LEU:HD22	1.91	0.52
5:I:108:DA:H2'	5:I:108:DA:O5'	2.10	0.52
5:I:18:DG:H2'	5:I:18:DG:O5'	2.10	0.52
7:N:28:GLN:HE22	7:N:118:CYS:H	1.57	0.52
2:B:75:HIS:O	4:D:89:ARG:NH2	2.40	0.52
5:I:137:DA:H2'	5:I:137:DA:O5'	2.09	0.52
2:B:78:ARG:NH2	2:B:85:ASP:OD2	2.43	0.52
6:J:19:DC:H2'	6:J:19:DC:O5'	2.10	0.52
5:I:83:DC:H42	6:J:80:DG:H1	1.57	0.52
7:M:34:VAL:HG11	7:M:108:LEU:HD13	1.92	0.52
7:N:35:GLU:N	7:N:35:GLU:OE2	2.43	0.52
6:J:16:DA:H2'	6:J:16:DA:O5'	2.10	0.51
5:I:28:DC:H42	6:J:135:DG:H1	1.58	0.51
3:G:92:GLU:OE1	7:M:124:ARG:NH1	2.33	0.51
6:J:147:DA:H2'	6:J:147:DA:O5'	2.11	0.51
7:N:212:LEU:HD11	7:N:218:SER:HA	1.91	0.51
4:D:87:THR:OG1	4:D:90:GLU:OE2	2.29	0.51
5:I:94:DC:H42	6:J:69:DG:H1	1.57	0.51
6:J:34:DT:H2''	6:J:35:DA:C8	2.46	0.51
7:N:247:LEU:HD11	7:N:254:TYR:HB3	1.92	0.51
1:E:100:LEU:HD11	2:F:58:LEU:HD13	1.93	0.51
5:I:72:DA:H2'	5:I:72:DA:OP2	2.11	0.51
3:C:12:ALA:N	5:I:38:DT:OP1	2.43	0.51
3:G:32:ARG:NH1	4:H:32:GLU:OE2	2.41	0.51
5:I:112:DT:H2'	5:I:112:DT:O5'	2.11	0.50
7:N:40:VAL:HG12	7:N:108:LEU:HD11	1.93	0.50
6:J:75:DA:O5'	6:J:75:DA:H2'	2.11	0.50
7:N:62:THR:HG22	7:N:114:ALA:CB	2.40	0.50
6:J:136:DA:C8	6:J:136:DA:H5'	2.47	0.50
6:J:136:DA:H8	6:J:136:DA:H5'	1.76	0.50
7:N:103:MET:HE1	7:N:116:TYR:CD2	2.46	0.50
5:I:63:DG:H2''	5:I:64:DT:C7	2.41	0.50
6:J:35:DA:H1'	6:J:36:DC:H5'	1.93	0.50
3:C:62:ILE:CD1	4:D:62:PHE:CZ	2.94	0.50
5:I:108:DA:N1	6:J:55:DT:O4	2.45	0.50
7:M:89:LYS:NZ	7:M:107:SER:O	2.45	0.50
3:C:88:ARG:NH1	3:C:94:ASN:OD1	2.36	0.50
7:M:35:GLU:O	7:M:38:THR:OG1	2.30	0.50
1:A:86:SER:O	1:A:90:MET:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:25:DG:H2''	5:I:26:DA:C8	2.46	0.49
5:I:108:DA:N6	6:J:54:DC:N4	2.60	0.49
6:J:65:DT:H2'	6:J:65:DT:O5'	2.12	0.49
7:M:61:GLN:HB2	7:M:67:LEU:HD23	1.93	0.49
6:J:86:DA:H2'	6:J:86:DA:O5'	2.11	0.49
6:J:138:DC:H2''	6:J:139:DA:C8	2.48	0.49
5:I:45:DG:H2'	5:I:45:DG:O5'	2.12	0.49
5:I:115:DC:H42	6:J:48:DG:H1	1.60	0.49
5:I:116:DT:O4	6:J:47:DA:N1	2.46	0.49
2:F:30:THR:HB	2:F:32:PRO:HD2	1.95	0.49
5:I:20:DC:H2''	5:I:21:DT:C6	2.48	0.49
5:I:54:DC:H42	6:J:109:DG:H1	1.61	0.49
6:J:109:DG:H2'	6:J:109:DG:O5'	2.13	0.49
5:I:62:DA:H2'	5:I:62:DA:O5'	2.13	0.48
1:A:68:GLN:O	1:A:72:ARG:HG3	2.12	0.48
3:G:63:LEU:HD13	4:H:42:LEU:HB2	1.94	0.48
5:I:102:DT:H2'	5:I:102:DT:O5'	2.13	0.48
5:I:139:DA:H2'	5:I:140:DC:C6	2.49	0.48
5:I:31:DC:H2''	5:I:32:DA:C8	2.48	0.48
2:F:70:VAL:HA	2:F:73:THR:CG2	2.42	0.48
5:I:35:DT:H2''	5:I:36:DG:C8	2.49	0.48
5:I:69:DG:H2'	5:I:69:DG:O5'	2.13	0.48
7:N:160:ILE:HG12	7:N:185:GLN:HB2	1.95	0.48
3:C:13:LYS:HA	3:C:13:LYS:HD3	1.68	0.48
5:I:47:DG:H1	6:J:116:DC:H42	1.62	0.48
5:I:74:DG:H1	6:J:89:DC:N4	2.06	0.48
6:J:70:DA:H2''	6:J:71:DG:C8	2.49	0.48
6:J:148:DG:H2'	6:J:148:DG:P	2.54	0.48
7:N:96:LYS:HE3	7:N:96:LYS:HB2	1.53	0.48
7:N:160:ILE:HG23	7:N:184:SER:HB3	1.95	0.47
7:M:160:ILE:HG12	7:M:185:GLN:HB2	1.96	0.47
5:I:20:DC:H42	6:J:143:DG:H1	1.62	0.47
3:C:63:LEU:HD11	4:D:38:VAL:HG13	1.96	0.47
3:G:95:LYS:HD3	4:H:100:PRO:HB3	1.96	0.47
7:M:247:LEU:HD11	7:M:254:TYR:HB3	1.97	0.47
5:I:144:DG:H2'	5:I:144:DG:O5'	2.14	0.47
3:C:26:PRO:HG3	4:D:37:TYR:CE2	2.49	0.47
4:D:46:HIS:HB3	4:D:49:THR:HG22	1.97	0.47
6:J:46:DC:H2''	6:J:47:DA:C8	2.50	0.47
6:J:69:DG:H2''	6:J:70:DA:C8	2.50	0.47
6:J:113:DC:H2'	6:J:114:DA:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:64:ARG:HG3	7:M:65:GLN:HG2	1.97	0.47
1:E:79:LYS:HB3	1:E:82:LEU:HG	1.95	0.47
5:I:139:DA:N1	6:J:24:DT:O4	2.48	0.46
6:J:78:DC:H1'	6:J:79:DG:H5'	1.96	0.46
5:I:129:DA:C2	6:J:35:DA:C2	3.03	0.46
1:E:65:LEU:HB3	1:E:66:PRO:HD3	1.97	0.46
3:G:26:PRO:HG3	4:H:37:TYR:CE2	2.50	0.46
5:I:35:DT:O2	6:J:129:DG:N2	2.48	0.46
5:I:106:DT:H2''	5:I:107:DC:C6	2.51	0.46
5:I:44:DA:H2''	5:I:45:DG:C8	2.51	0.46
7:M:73:ILE:HG13	7:M:80:THR:HG22	1.96	0.46
3:G:62:ILE:CD1	4:H:62:PHE:CE2	2.98	0.46
3:G:62:ILE:HD11	4:H:62:PHE:CZ	2.50	0.46
5:I:139:DA:H2''	5:I:140:DC:H5'	1.97	0.46
5:I:46:DA:N1	6:J:117:DT:O4	2.48	0.46
7:M:95:ASP:OD1	7:M:97:SER:OG	2.33	0.46
7:N:28:GLN:NE2	7:N:118:CYS:H	2.13	0.46
1:A:65:LEU:HB3	1:A:66:PRO:HD3	1.99	0.45
5:I:13:DC:O2	6:J:151:DG:N2	2.49	0.45
5:I:51:DC:N3	6:J:112:DG:N2	2.62	0.45
5:I:55:DA:C2	6:J:109:DG:N2	2.85	0.45
5:I:149:DT:O5'	5:I:149:DT:H2'	2.16	0.45
6:J:74:DG:H8	6:J:74:DG:H2'	1.64	0.45
6:J:85:DT:H6	6:J:85:DT:H2'	1.53	0.45
5:I:85:DG:O5'	5:I:85:DG:H2'	2.16	0.45
3:C:32:ARG:NH1	4:D:32:GLU:OE2	2.46	0.45
5:I:42:DT:C4	6:J:121:DA:N1	2.85	0.45
5:I:103:DA:H2''	5:I:104:DG:C8	2.50	0.45
6:J:80:DG:H8	6:J:80:DG:H2'	1.56	0.45
7:N:81:LYS:HE3	7:N:81:LYS:HB2	1.64	0.45
3:C:79:ILE:HG12	3:C:82:HIS:ND1	2.32	0.45
5:I:63:DG:H1	6:J:100:DC:H42	1.65	0.45
6:J:30:DC:H2''	6:J:31:DA:C8	2.52	0.45
7:N:194:TYR:HE2	7:N:247:LEU:HB3	1.82	0.45
3:C:64:GLU:HA	4:D:46:HIS:CE1	2.52	0.45
7:N:193:TRP:CZ3	7:N:246:CYS:HB3	2.52	0.45
3:G:79:ILE:HG12	3:G:82:HIS:CE1	2.52	0.45
6:J:98:DG:H1'	6:J:99:DA:H5'	1.98	0.44
6:J:106:DA:H2'	6:J:106:DA:O5'	2.17	0.44
7:M:28:GLN:HE22	7:M:118:CYS:H	1.65	0.44
6:J:64:DT:H1'	6:J:65:DT:H5'	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:149:DA:C8	6:J:149:DA:OP2	2.70	0.44
7:M:60:LYS:HB3	7:M:70:ILE:HD11	1.98	0.44
4:H:95:VAL:HG13	4:H:99:LEU:HD12	2.00	0.44
6:J:121:DA:H2''	6:J:122:DG:C8	2.52	0.44
5:I:134:DC:H2''	5:I:135:DA:C8	2.53	0.44
6:J:21:DC:H2'	6:J:22:DT:H71	1.99	0.44
3:C:17:ARG:HB2	3:C:27:VAL:HB	2.00	0.43
2:F:30:THR:HG22	6:J:72:DG:OP1	2.18	0.43
5:I:139:DA:C8	5:I:139:DA:C5'	2.84	0.43
7:M:89:LYS:HA	7:M:89:LYS:HD3	1.89	0.43
7:M:58:TRP:CD1	7:M:92:LEU:HD21	2.53	0.43
1:A:118:THR:OG1	2:B:45:ARG:HD3	2.19	0.43
3:C:54:VAL:HG21	4:D:95:VAL:HG21	1.99	0.43
6:J:136:DA:H5'	6:J:136:DA:H2'	1.68	0.43
5:I:145:DC:H2''	5:I:146:DA:N7	2.33	0.43
6:J:68:DT:H6	6:J:68:DT:H2'	1.57	0.43
6:J:115:DA:H2'	6:J:115:DA:O5'	2.18	0.43
1:E:41:TYR:HA	6:J:154:DC:H5''	2.01	0.43
6:J:140:DG:H2''	6:J:141:DC:C5	2.53	0.43
7:M:182:LYS:HG2	7:M:228:ASP:OD1	2.18	0.43
7:N:166:PRO:HG2	7:N:179:ILE:HG23	2.01	0.43
5:I:46:DA:N1	6:J:117:DT:C4	2.87	0.43
5:I:92:DC:H6	5:I:92:DC:H2'	1.52	0.43
7:N:28:GLN:NE2	7:N:118:CYS:SG	2.76	0.43
3:C:74:LYS:HB2	3:C:74:LYS:HE2	1.86	0.43
6:J:149:DA:OP2	6:J:149:DA:H8	2.02	0.43
5:I:95:DA:C8	5:I:95:DA:H5''	2.54	0.43
5:I:131:DT:H2'	5:I:131:DT:O5'	2.19	0.43
6:J:119:DT:H2''	6:J:120:DC:C5	2.54	0.43
6:J:148:DG:OP2	6:J:148:DG:C8	2.71	0.43
1:E:126:LEU:O	1:E:130:ILE:HG12	2.19	0.42
2:F:35:ARG:O	2:F:39:ARG:HG2	2.19	0.42
5:I:52:DA:C2	6:J:112:DG:N2	2.87	0.42
7:N:134:GLN:H	7:N:134:GLN:CD	2.27	0.42
3:C:15:LYS:O	3:C:20:ARG:NH1	2.52	0.42
3:C:79:ILE:HG12	3:C:82:HIS:CE1	2.53	0.42
3:G:40:ALA:HB2	4:H:86:ILE:HG13	2.02	0.42
5:I:9:DG:H2''	5:I:10:DG:C8	2.55	0.42
6:J:144:DC:H6	6:J:144:DC:H2'	1.71	0.42
6:J:144:DC:H2''	6:J:145:DC:C6	2.54	0.42
3:C:62:ILE:CD1	4:D:62:PHE:CE2	3.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:39:TYR:O	4:H:75:SER:HB2	2.19	0.42
6:J:43:DA:H1'	6:J:44:DG:H5''	2.02	0.42
6:J:68:DT:H5'	6:J:68:DT:C6	2.53	0.42
5:I:115:DC:N4	6:J:48:DG:H1	2.17	0.42
7:N:172:SER:OG	7:N:173:LEU:N	2.52	0.42
7:M:169:MET:HE1	7:M:177:VAL:HB	2.01	0.42
3:G:63:LEU:HD23	3:G:63:LEU:HA	1.94	0.42
5:I:13:DC:H42	6:J:150:DG:H1	1.68	0.42
3:C:64:GLU:O	4:D:46:HIS:HE1	2.02	0.42
5:I:94:DC:N4	6:J:69:DG:H1	2.17	0.42
3:G:44:GLY:HA2	5:I:117:DG:H5''	2.02	0.42
2:B:92:ARG:HH22	4:D:98:LEU:HD23	1.85	0.42
1:E:108:ASN:O	1:E:112:ILE:HG13	2.20	0.42
4:H:83:ARG:NH2	6:J:51:DA:OP2	2.53	0.42
5:I:33:DG:H4'	5:I:34:DC:OP1	2.20	0.42
7:N:200:LYS:HB3	7:N:200:LYS:HE3	1.87	0.42
1:E:85:GLN:HG3	2:F:82:THR:HA	2.01	0.41
5:I:113:DG:H8	5:I:113:DG:H2'	1.63	0.41
7:N:32:GLU:OE2	7:N:32:GLU:HA	2.19	0.41
1:A:50:GLU:HB2	2:B:39:ARG:HD2	2.02	0.41
2:B:23:ARG:HD3	2:B:23:ARG:HA	1.61	0.41
2:F:47:SER:HA	5:I:86:DA:H5''	2.02	0.41
2:F:73:THR:HG21	2:F:81:VAL:HG22	2.02	0.41
4:H:35:SER:HA	4:H:56:MET:SD	2.61	0.41
5:I:128:DT:H2''	5:I:129:DA:C8	2.55	0.41
5:I:51:DC:H2''	5:I:52:DA:C8	2.55	0.41
5:I:120:DT:H6	5:I:120:DT:H2'	1.56	0.41
6:J:53:DA:O5'	6:J:53:DA:C2'	2.68	0.41
6:J:107:DA:C1'	6:J:108:DT:H5'	2.48	0.41
5:I:62:DA:O5'	5:I:62:DA:C2'	2.68	0.41
5:I:113:DG:H1	6:J:50:DC:H42	1.68	0.41
7:N:72:TYR:CE1	7:N:81:LYS:HB3	2.56	0.41
2:F:70:VAL:CA	2:F:73:THR:HG22	2.44	0.41
6:J:56:DG:C1'	6:J:57:DA:H5'	2.49	0.41
4:D:43:LYS:HA	4:D:43:LYS:HD3	1.72	0.41
4:H:32:GLU:HA	5:I:128:DT:OP1	2.21	0.41
6:J:145:DC:H2''	6:J:146:DG:H5'	2.01	0.41
7:M:197:LYS:HB2	7:M:200:LYS:HE2	2.01	0.41
2:F:32:PRO:HG2	6:J:71:DG:H2'	2.03	0.41
5:I:121:DA:H2'	5:I:121:DA:P	2.61	0.41
6:J:28:DT:H6	6:J:28:DT:H2'	1.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:N:58:TRP:CD1	7:N:92:LEU:HD21	2.56	0.41
1:A:61:LEU:HD22	2:B:36:ARG:HB3	2.02	0.41
5:I:20:DC:H6	5:I:20:DC:H2'	1.78	0.41
5:I:140:DC:H1'	5:I:141:DA:H5'	2.03	0.41
6:J:49:DA:O5'	6:J:49:DA:H2'	2.21	0.41
6:J:96:DA:O5'	6:J:96:DA:C2'	2.69	0.41
7:M:160:ILE:HG23	7:M:184:SER:HB3	2.02	0.41
7:M:172:SER:HB2	7:M:175:GLU:HG3	2.01	0.41
1:A:63:ARG:HA	1:A:63:ARG:HD2	1.95	0.41
3:C:62:ILE:HD11	4:D:62:PHE:CZ	2.56	0.41
6:J:68:DT:H1'	6:J:69:DG:C8	2.55	0.41
6:J:126:DC:H6	6:J:126:DC:H2'	1.50	0.41
7:M:200:LYS:HB3	7:M:200:LYS:HE3	1.88	0.41
5:I:45:DG:O5'	5:I:45:DG:C2'	2.69	0.40
5:I:149:DT:O5'	5:I:149:DT:C2'	2.69	0.40
6:J:82:DA:H8	6:J:82:DA:H2'	1.59	0.40
3:C:77:ARG:HB2	6:J:142:DA:OP1	2.21	0.40
2:F:34:ILE:HD13	2:F:54:THR:HB	2.02	0.40
5:I:81:DT:O4	6:J:82:DA:N1	2.54	0.40
5:I:134:DC:H6	5:I:134:DC:H2'	1.77	0.40
5:I:150:DG:N2	6:J:14:DA:C2	2.89	0.40
6:J:146:DG:H2''	6:J:147:DA:C8	2.56	0.40
4:D:65:ASP:O	4:D:69:ARG:HG3	2.21	0.40
5:I:13:DC:N3	6:J:151:DG:N2	2.68	0.40
5:I:48:DT:O5'	5:I:48:DT:H2'	2.21	0.40
5:I:146:DA:C2	6:J:18:DG:N2	2.90	0.40
3:G:36:LYS:HA	3:G:36:LYS:HD3	1.89	0.40
5:I:89:DC:N3	6:J:74:DG:C2	2.88	0.40
6:J:83:DA:O5'	6:J:83:DA:C2'	2.69	0.40
6:J:103:DA:O5'	6:J:103:DA:C2'	2.70	0.40
2:B:91:LYS:HB2	2:B:91:LYS:HE3	1.78	0.40
5:I:69:DG:O5'	5:I:69:DG:C2'	2.70	0.40
5:I:144:DG:N2	6:J:20:DC:O2	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	E	94/136 (69%)	94 (100%)	0	0	100	100
2	B	80/103 (78%)	78 (98%)	2 (2%)	0	100	100
2	F	79/103 (77%)	77 (98%)	2 (2%)	0	100	100
3	C	105/129 (81%)	105 (100%)	0	0	100	100
3	G	106/129 (82%)	105 (99%)	1 (1%)	0	100	100
4	D	92/126 (73%)	89 (97%)	3 (3%)	0	100	100
4	H	92/126 (73%)	89 (97%)	3 (3%)	0	100	100
7	M	222/265 (84%)	213 (96%)	9 (4%)	0	100	100
7	N	222/265 (84%)	210 (95%)	12 (5%)	0	100	100
All	All	1188/1518 (78%)	1155 (97%)	33 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	86/111 (78%)	86 (100%)	0	100	100
1	E	84/111 (76%)	84 (100%)	0	100	100
2	B	67/79 (85%)	67 (100%)	0	100	100
2	F	67/79 (85%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	83/99 (84%)	82 (99%)	1 (1%)	63	78
3	G	84/99 (85%)	84 (100%)	0	100	100
4	D	80/106 (76%)	80 (100%)	0	100	100
4	H	80/106 (76%)	80 (100%)	0	100	100
7	M	199/224 (89%)	199 (100%)	0	100	100
7	N	199/224 (89%)	197 (99%)	2 (1%)	68	81
All	All	1029/1238 (83%)	1026 (100%)	3 (0%)	84	93

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	76	THR
7	N	91	THR
7	N	173	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
3	C	38	ASN
3	C	73	ASN
4	D	46	HIS
1	E	39	HIS
3	G	73	ASN
4	H	64	ASN
7	N	170	HIS
7	N	249	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	I	6
6	J	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	132:DG	O3'	133:DA	P	1.40
1	I	87:DT	O3'	88:DT	P	1.39
1	I	106:DT	O3'	107:DC	P	1.39
1	J	96:DA	O3'	97:DA	P	1.39
1	I	35:DT	O3'	36:DG	P	1.38
1	I	107:DC	O3'	108:DA	P	1.37
1	I	85:DG	O3'	86:DA	P	1.36
1	J	80:DG	O3'	81:DG	P	1.36
1	I	117:DG	O3'	118:DG	P	1.34

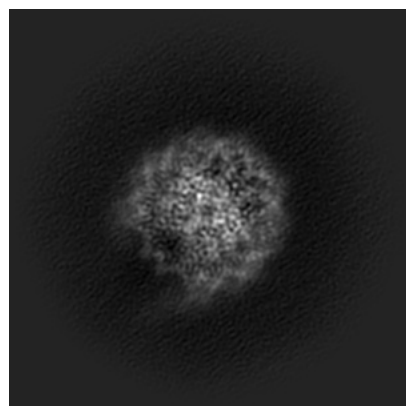
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28628. These allow visual inspection of the internal detail of the map and identification of artifacts.

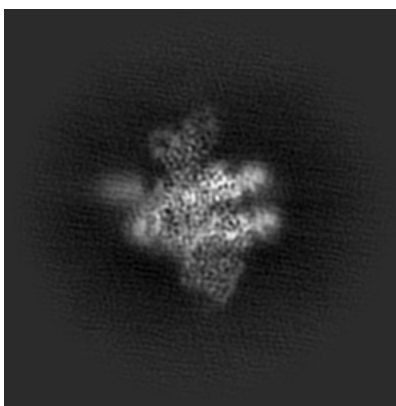
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

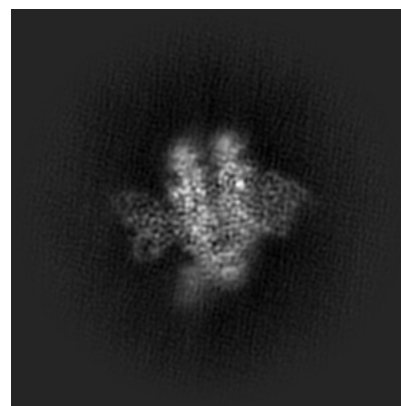
6.1.1 Primary map



X

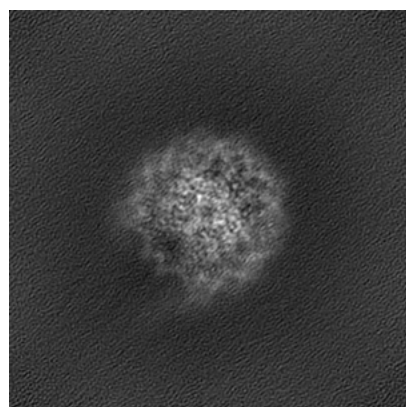


Y

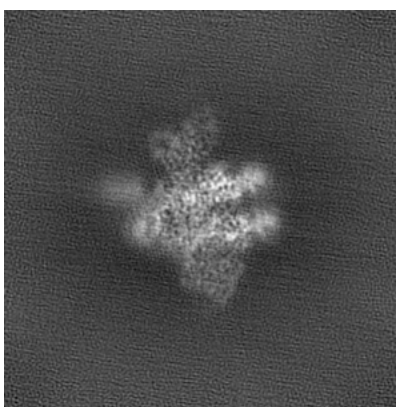


Z

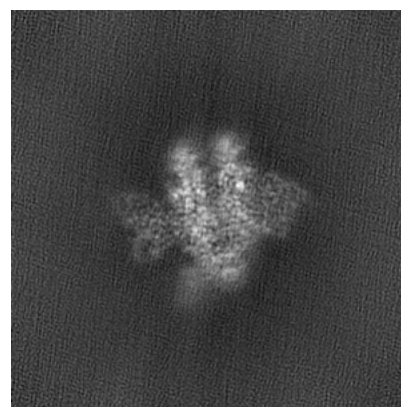
6.1.2 Raw map



X



Y

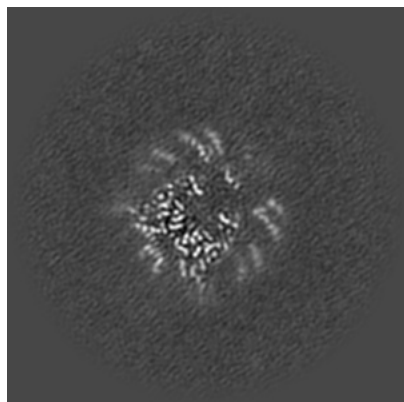


Z

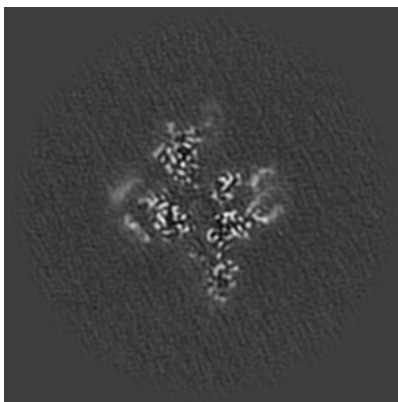
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

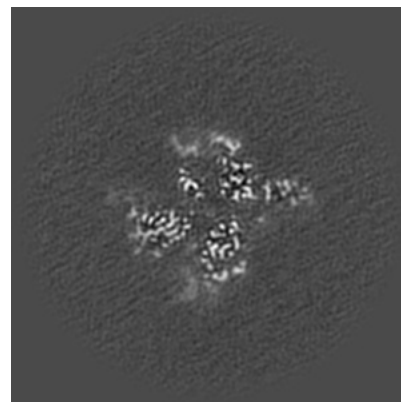
6.2.1 Primary map



X Index: 120

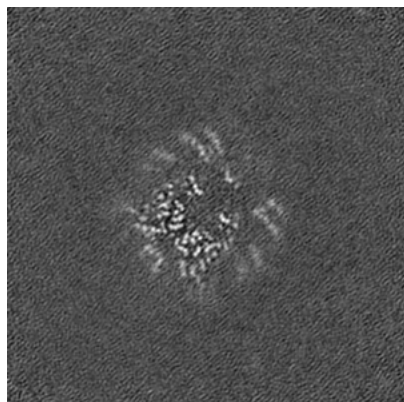


Y Index: 120

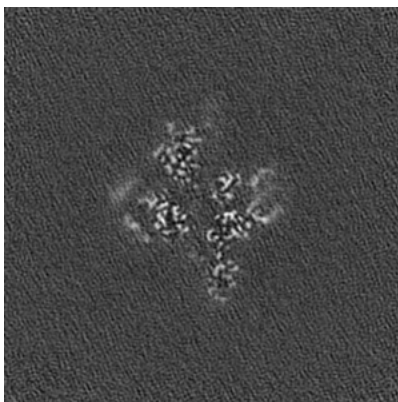


Z Index: 120

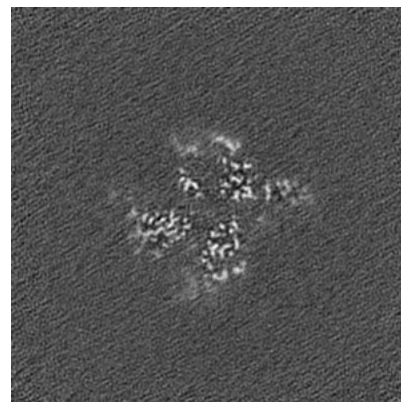
6.2.2 Raw map



X Index: 120



Y Index: 120

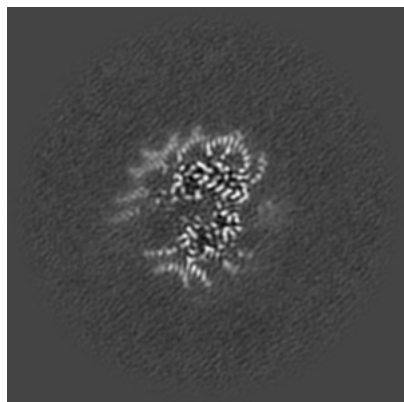


Z Index: 120

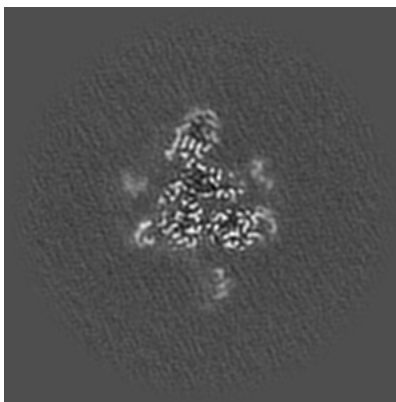
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

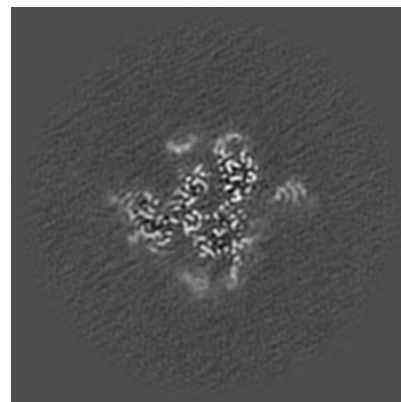
6.3.1 Primary map



X Index: 112

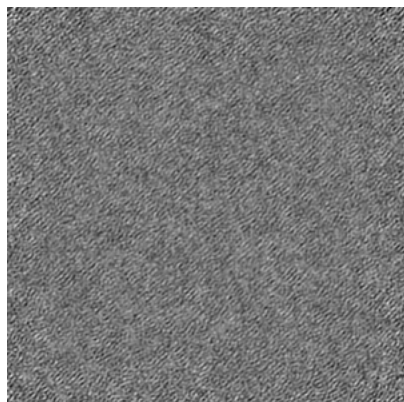


Y Index: 129

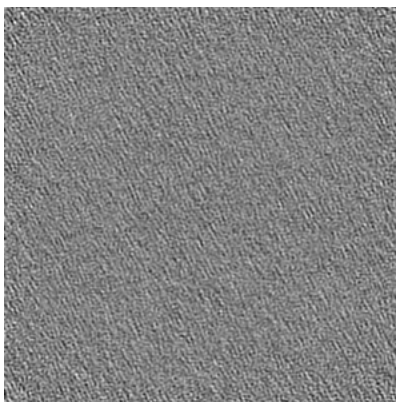


Z Index: 125

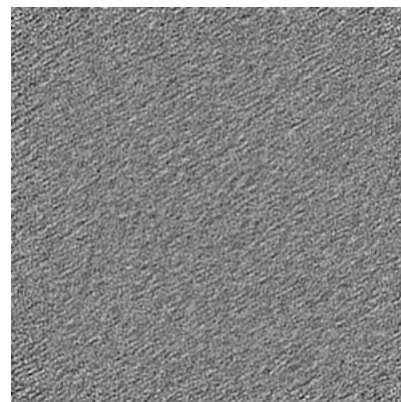
6.3.2 Raw map



X Index: 0



Y Index: 0

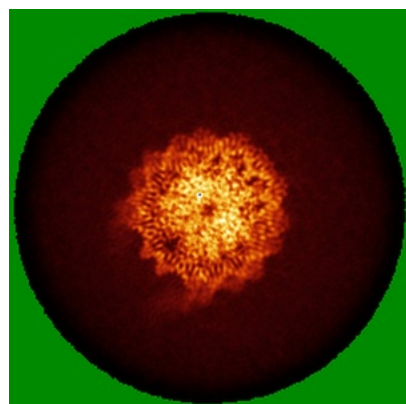


Z Index: 0

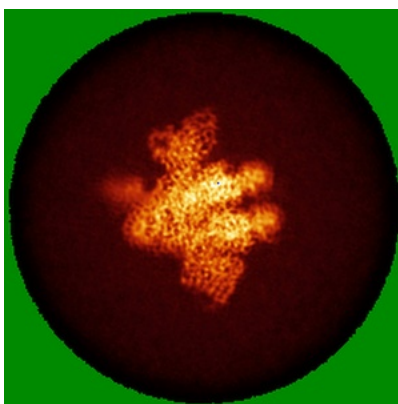
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

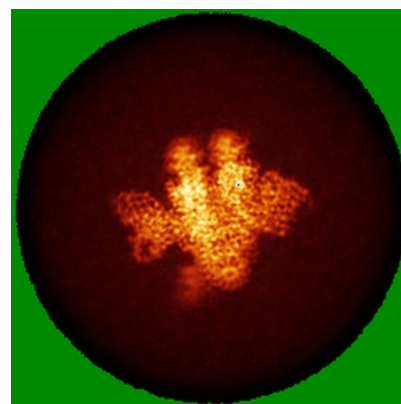
6.4.1 Primary map



X

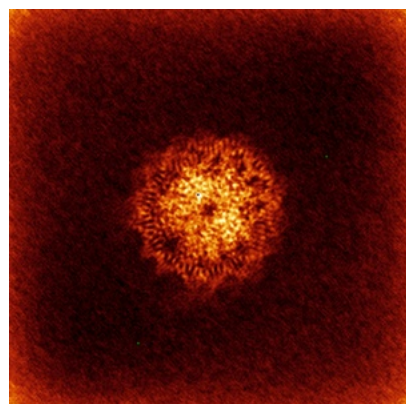


Y

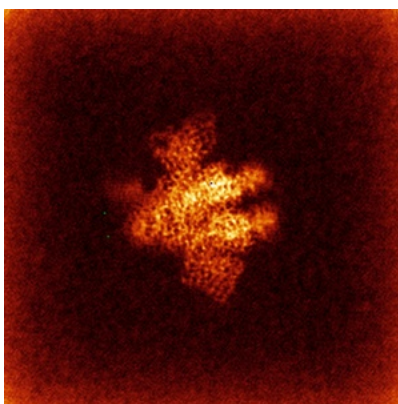


Z

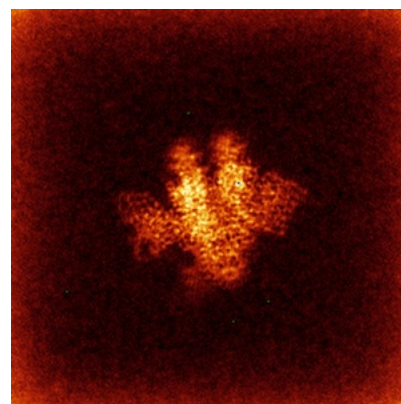
6.4.2 Raw map



X



Y

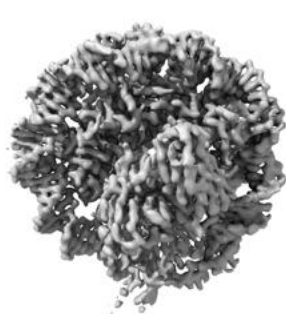


Z

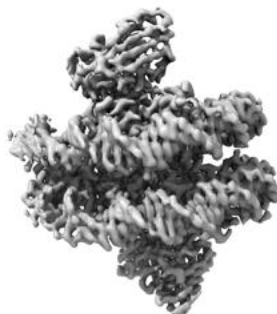
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

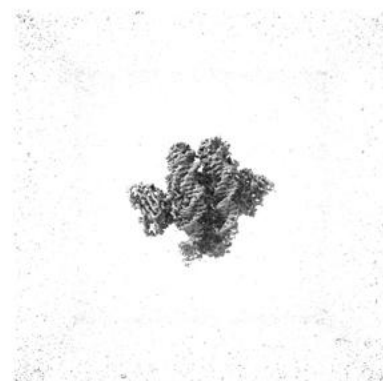
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

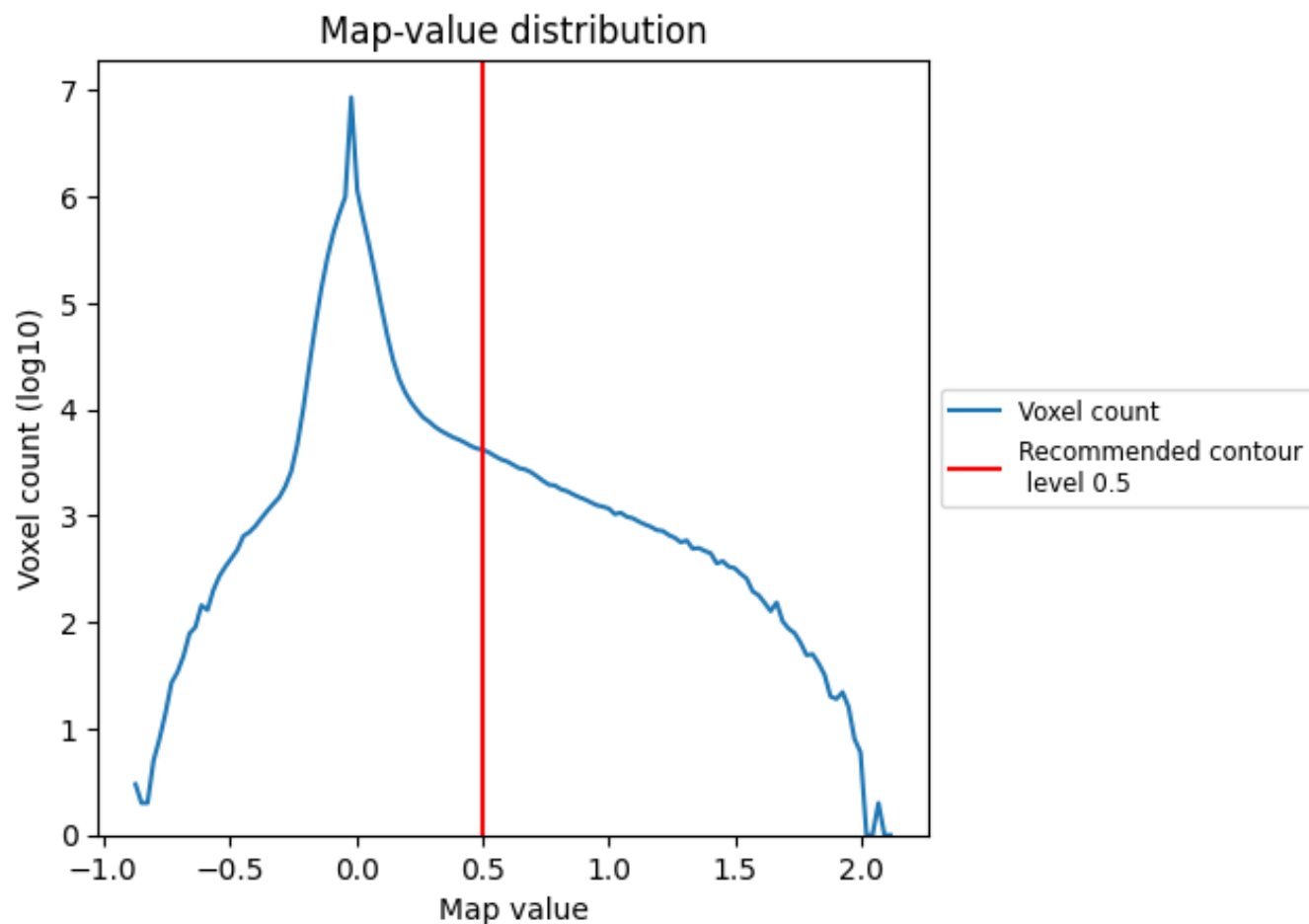
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

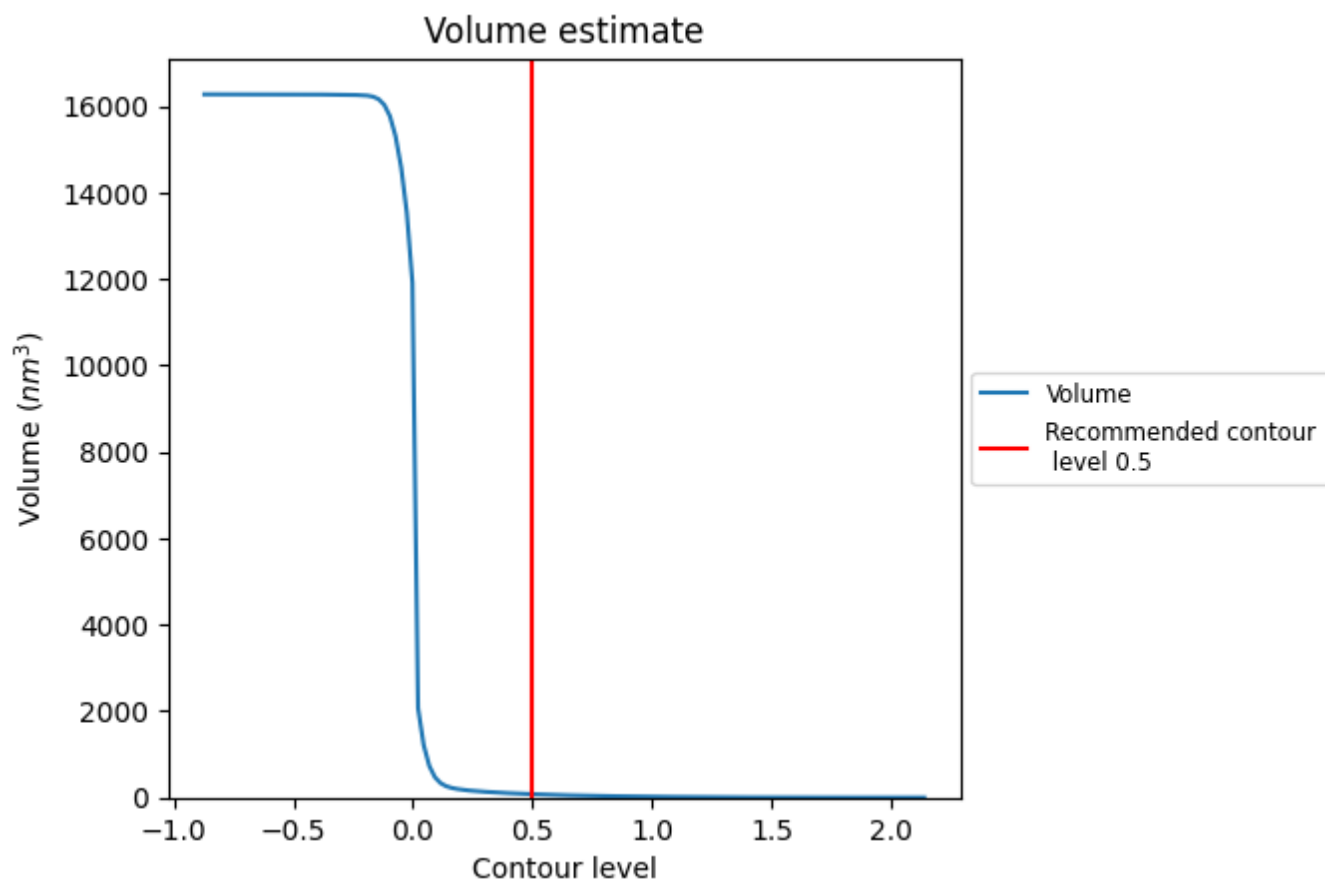
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

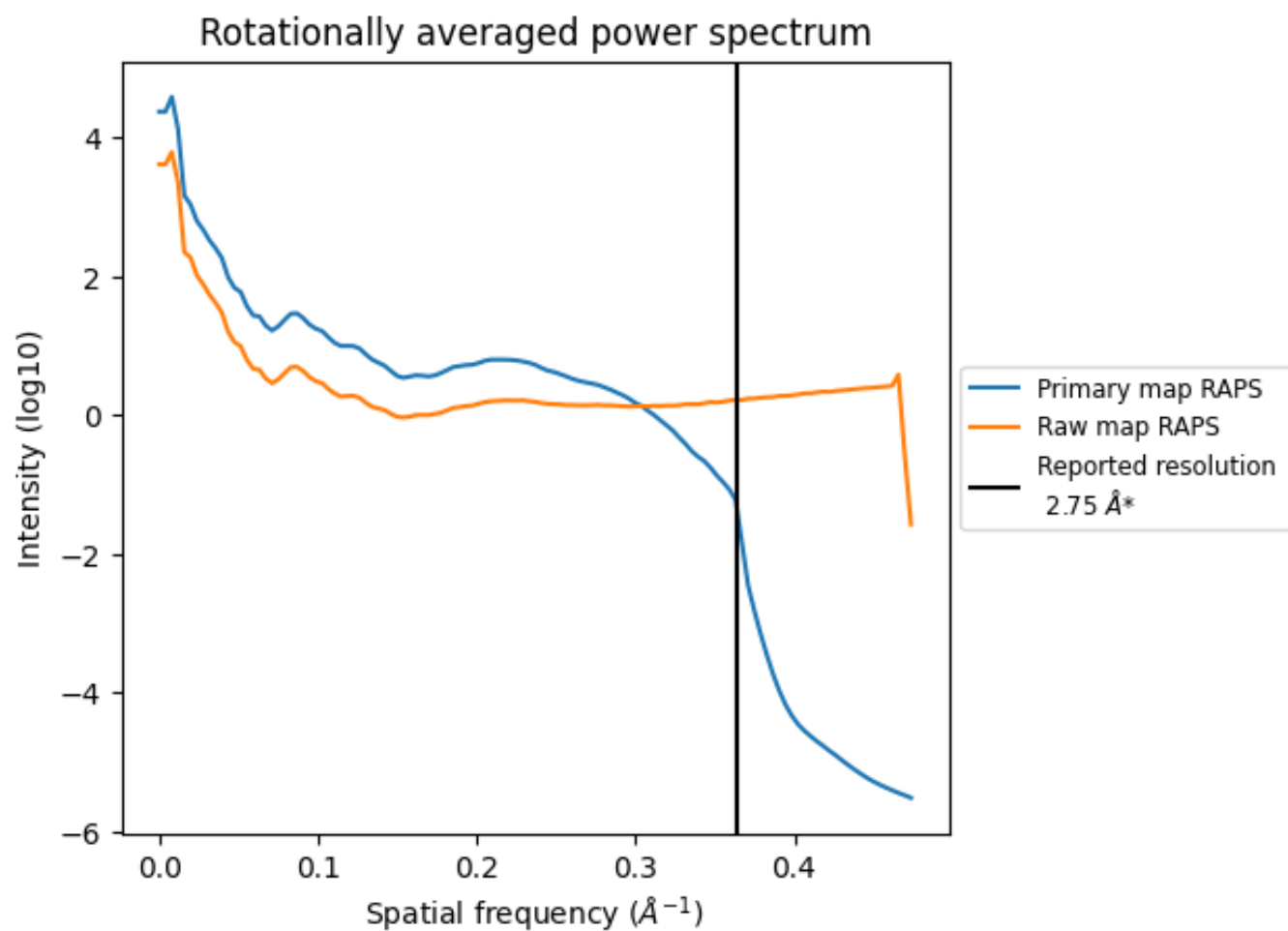
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 79 nm³; this corresponds to an approximate mass of 71 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

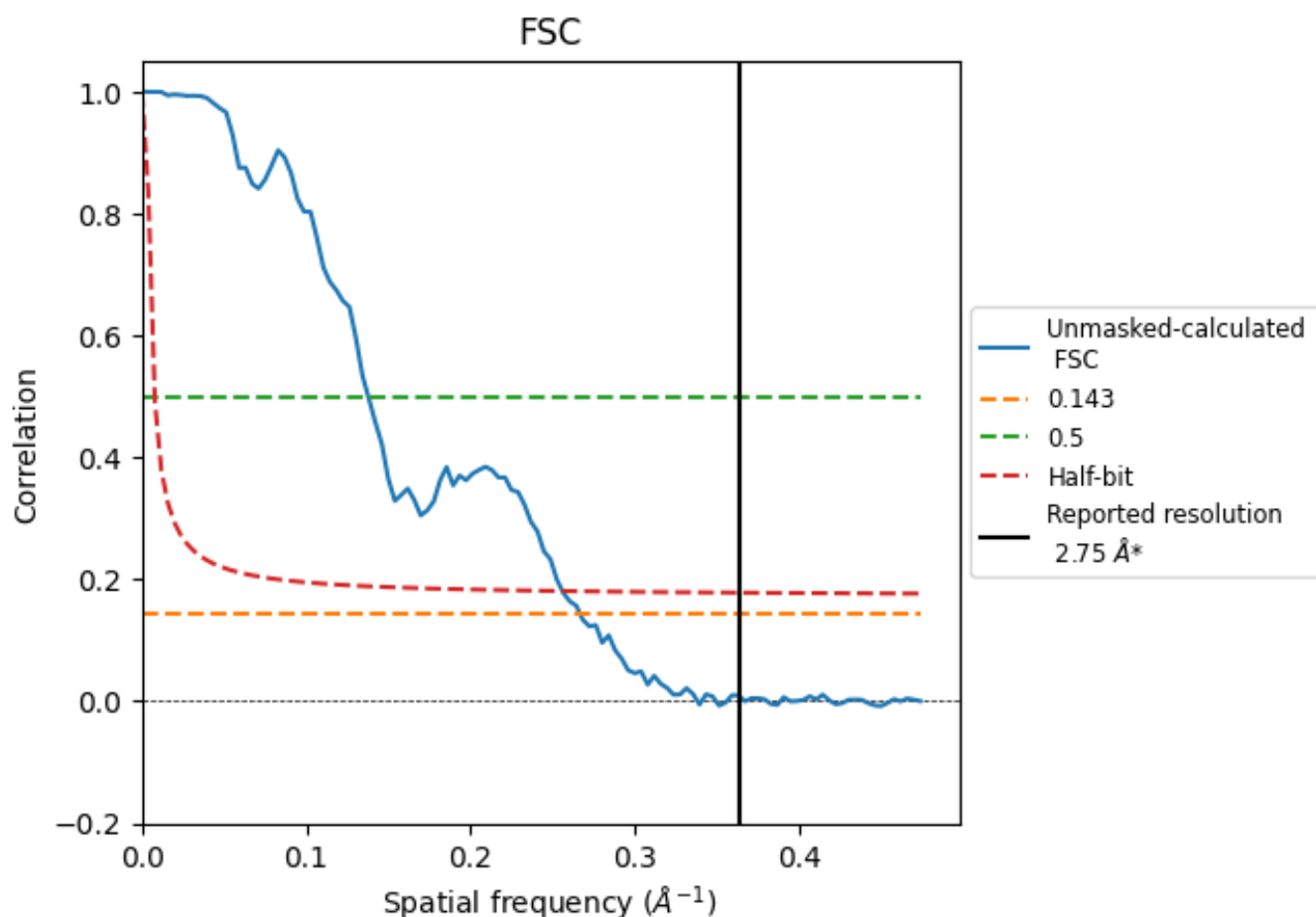


*Reported resolution corresponds to spatial frequency of 0.364 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.364 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

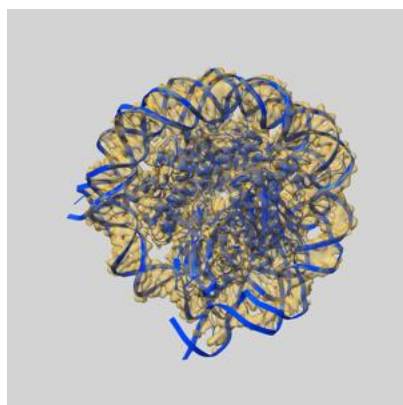
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.75	7.26	3.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.75 differs from the reported value 2.75 by more than 10 %

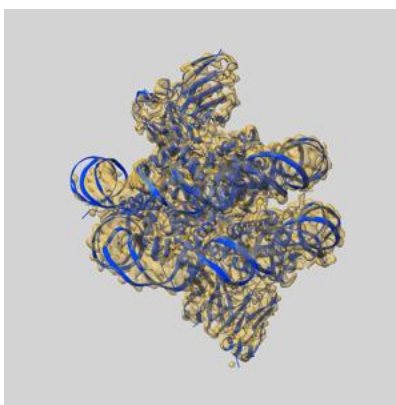
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28628 and PDB model 8EVG. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

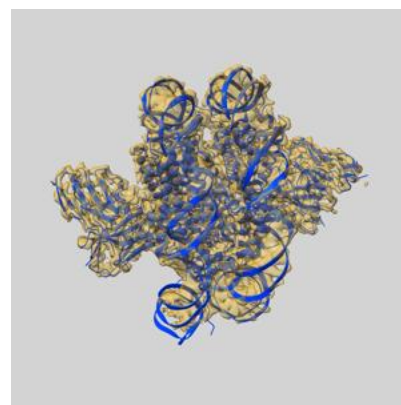
9.1 Map-model overlay [i](#)



X



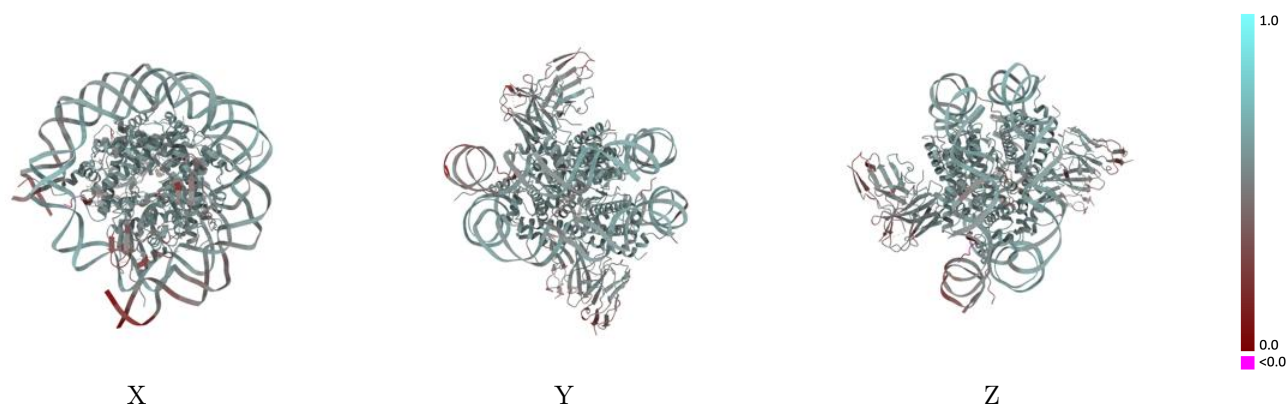
Y



Z

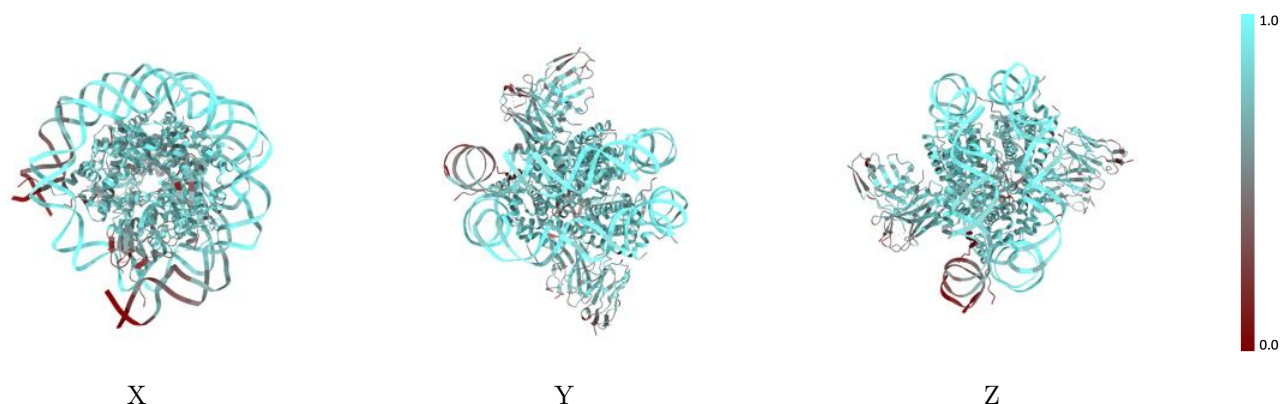
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



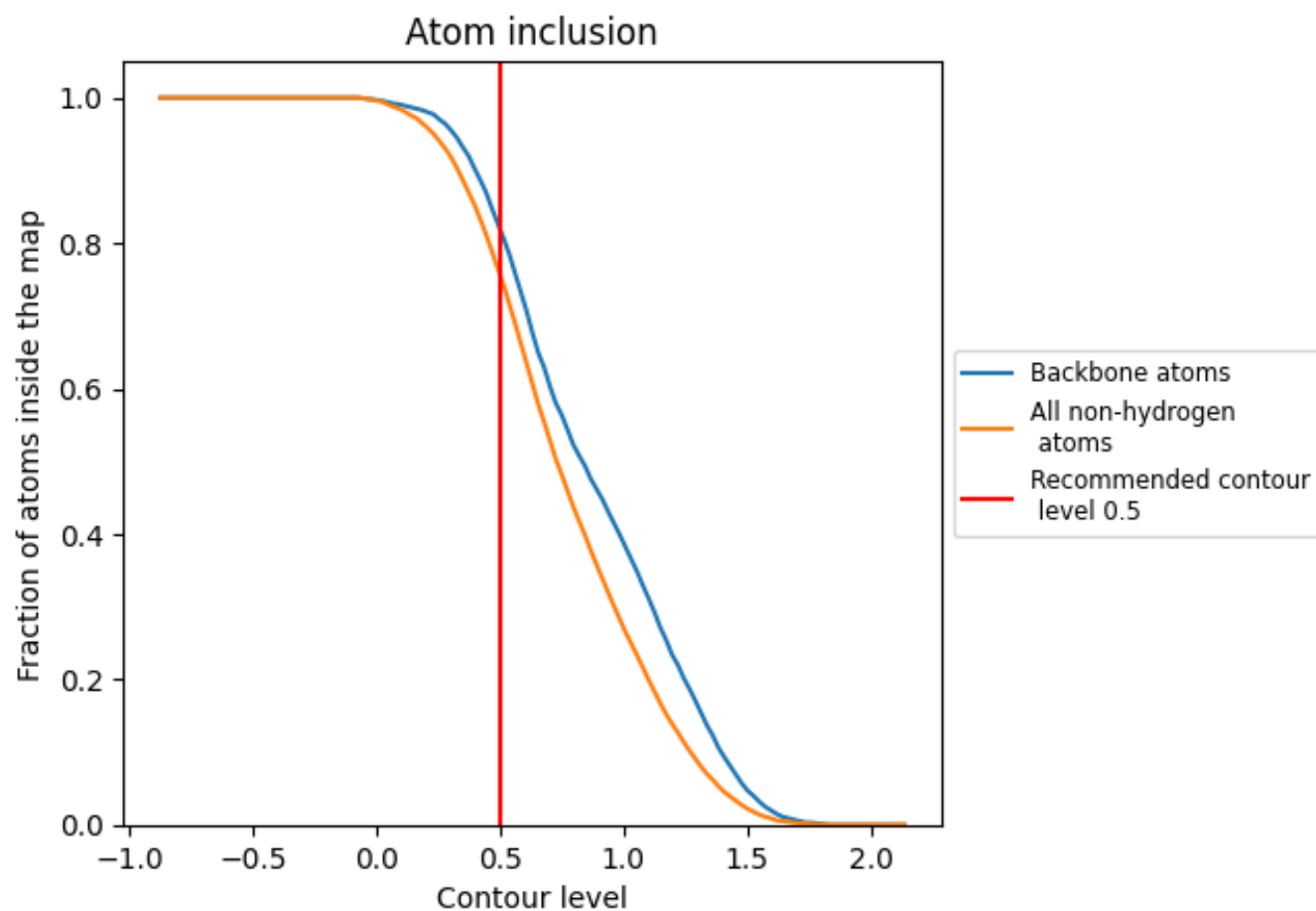
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7570	0.5310
A	0.7610	0.5580
B	0.8280	0.5730
C	0.7520	0.5400
D	0.8140	0.5550
E	0.7630	0.5490
F	0.8230	0.5680
G	0.7420	0.5250
H	0.8240	0.5630
I	0.7790	0.5390
J	0.7850	0.5390
M	0.6610	0.4710
N	0.6700	0.4900

