



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:17 PM UTC

PDB ID : 7EU0 / pdb_00007eu0
EMDB ID : EMD-31305
Title : The cryo-EM structure of A. thaliana Pol IV-RDR2 backtracked complex
Authors : Fang, C.L.; Wu, X.X.; Huang, K.; Zhang, Y.
Deposited on : 2021-05-15
Resolution : 3.16 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

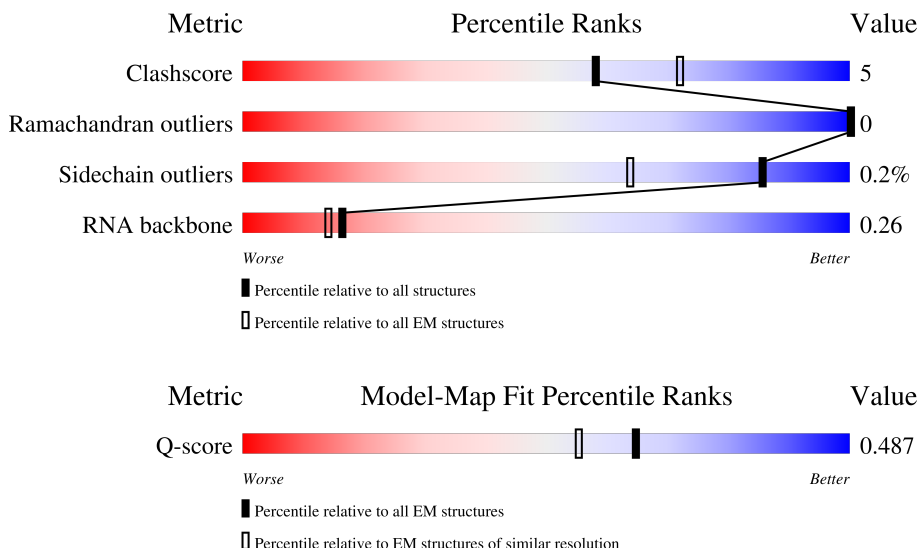
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.16 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.



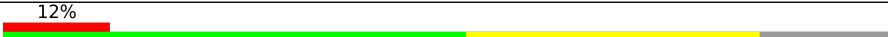
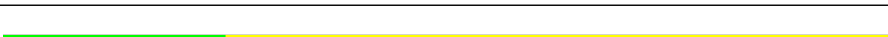
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14474 (2.66 - 3.66)

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	1510	
2	B	1172	
3	C	319	

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Mol	Chain	Length	Quality of chain
4	E	205	
5	F	144	
6	H	146	
7	I	114	
8	J	71	
9	K	116	
10	L	51	
11	M	1133	
12	N	20	
13	O	39	
14	Q	33	
15	R	4	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 32686 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 DNA-directed RNA polymerase IV subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1060	Total	C	N	O	S	0	0
			7722	4901	1341	1434	46		

- Molecule 2 is a protein called DNA-directed RNA polymerases IV and V subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1054	Total	C	N	O	S	0	0
			7861	5020	1418	1379	44		

- Molecule 3 is a protein called DNA-directed RNA polymerases II, IV and V subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	291	Total	C	N	O	S	0	0
			2148	1367	372	395	14		

- Molecule 4 is a protein called DNA-directed RNA polymerases II and IV subunit 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	198	Total	C	N	O	S	0	0
			1458	937	265	250	6		

- Molecule 5 is a protein called DNA-directed RNA polymerases II, IV and V subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	76	Total	C	N	O	S	0	0
			554	355	97	99	3		

- Molecule 6 is a protein called DNA-directed RNA polymerases II, IV and V subunit 8B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	126	Total	C	N	O	S	0	0
			923	606	147	163	7		

- Molecule 7 is a protein called DNA-directed RNA polymerases II, IV and V subunit 9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	113	Total	C	N	O	S	0	0
			819	502	155	150	12		

- Molecule 8 is a protein called DNA-directed RNA polymerases II, IV and V subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	62	Total	C	N	O	S	0	0
			472	308	83	75	6		

- Molecule 9 is a protein called DNA-directed RNA polymerases II, IV and V subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	94	Total	C	N	O	S	0	0
			711	456	130	124	1		

- Molecule 10 is a protein called DNA-directed RNA polymerases II, IV and V subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	42	Total	C	N	O	S	0	0
			293	182	50	57	4		

- Molecule 11 is a protein called RNA-dependent RNA polymerase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	1052	Total	C	N	O	S	0	0
			8055	5144	1383	1476	52		

- Molecule 12 is a DNA chain called DNA (5'-D(*CP*TP*GP*TP*GP*CP*TP*TP*AP*TP*CP*GP*GP*TP*AP*GP*AP*GP*TP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	17	Total	C	N	O	P	0	0
			353	168	63	105	17		

- Molecule 13 is a RNA chain called RNA (39-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	32	Total	C	N	O	P	0	0
			664	297	98	237	32		

- Molecule 14 is a DNA chain called DNA (33-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	28	Total	C	N	O	P	0	0
			561	268	98	167	28		

- Molecule 15 is a RNA chain called RNA (5'-R(*CP*CP*GP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	4	Total	C	N	O	P	0	0
			82	38	16	25	3		

- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

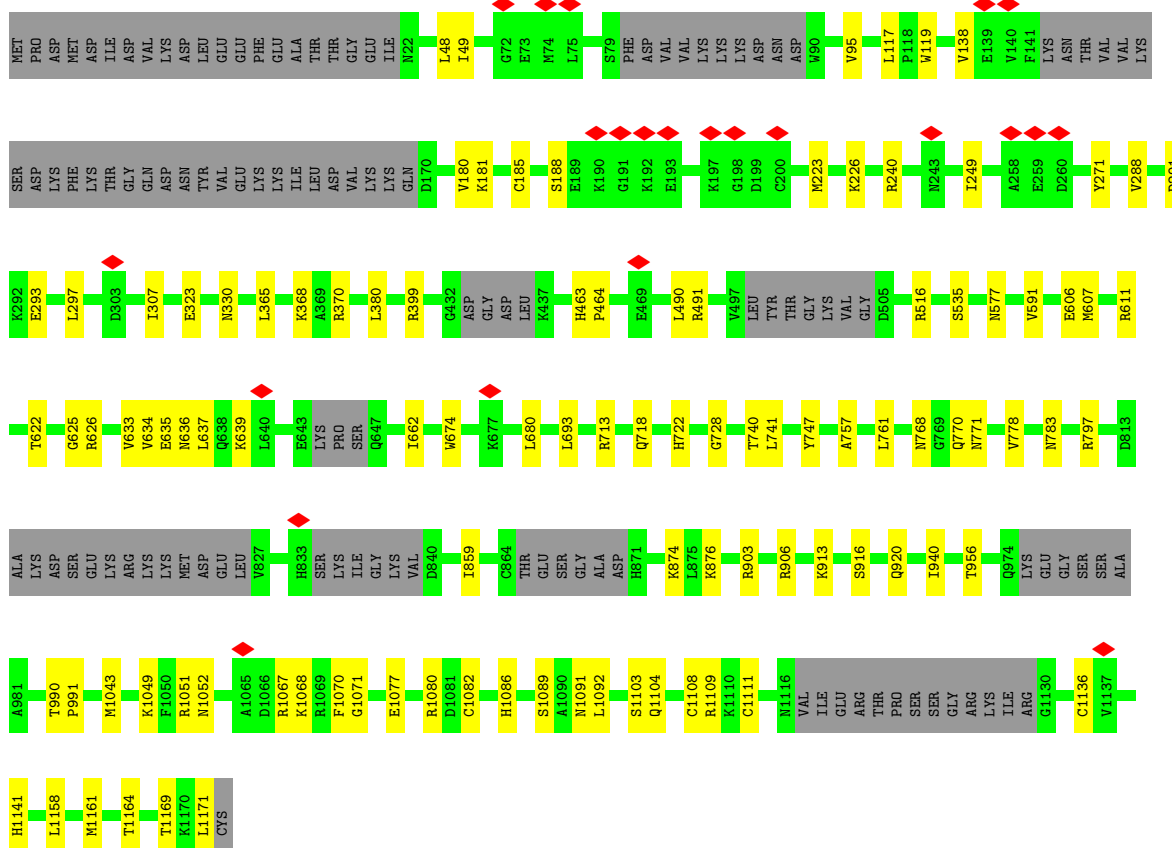
Mol	Chain	Residues	Atoms		AltConf
16	A	2	Total	Zn	0
			2	2	
16	B	1	Total	Zn	0
			1	1	
16	C	1	Total	Zn	0
			1	1	
16	I	2	Total	Zn	0
			2	2	
16	J	1	Total	Zn	0
			1	1	
16	L	1	Total	Zn	0
			1	1	

- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

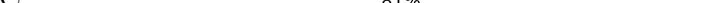
Mol	Chain	Residues	Atoms		AltConf
17	A	1	Total	Mg	0
			1	1	
17	M	1	Total	Mg	0
			1	1	

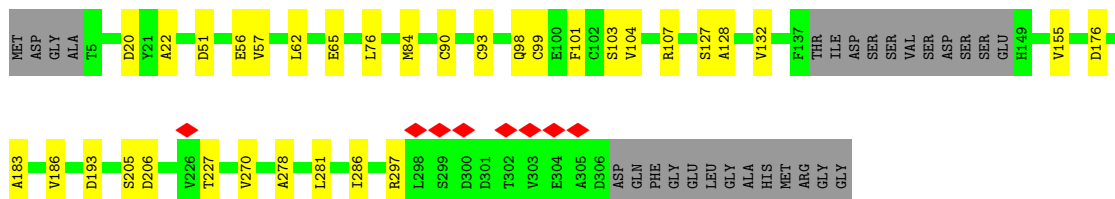
- Molecule 2: DNA-directed RNA polymerases IV and V subunit 2

Chain B: 81% 9% 10%

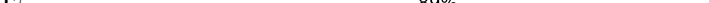


- Molecule 3: DNA-directed RNA polymerases II, IV and V subunit 3

Chain C:  81% 10% 9%

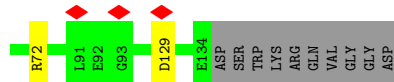
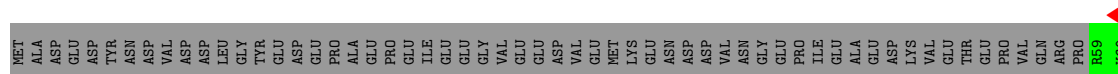


- Molecule 4: DNA-directed RNA polymerases II and IV subunit 5A

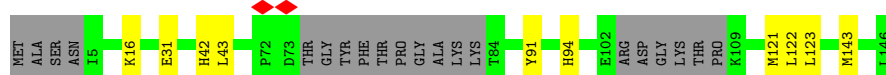
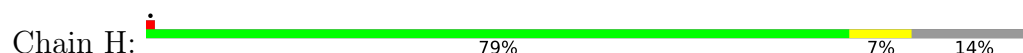
Chain E:  89% 7% .



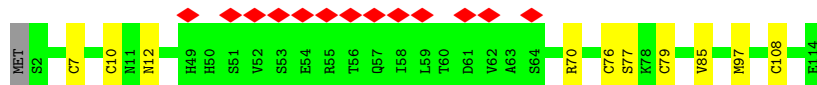
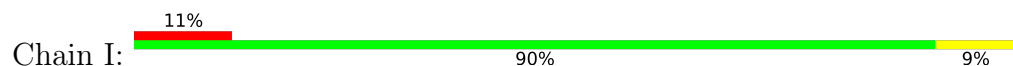
- Molecule 5: DNA-directed RNA polymerases II, IV and V subunit 6A



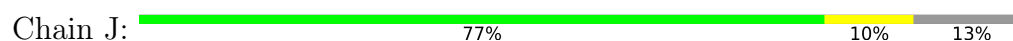
- Molecule 6: DNA-directed RNA polymerases II, IV and V subunit 8B



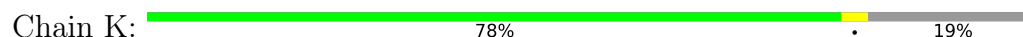
- Molecule 7: DNA-directed RNA polymerases II, IV and V subunit 9A



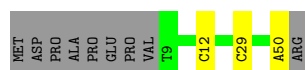
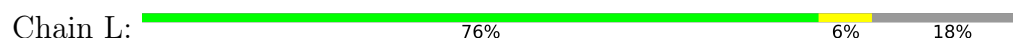
- Molecule 8: DNA-directed RNA polymerases II, IV and V subunit 10



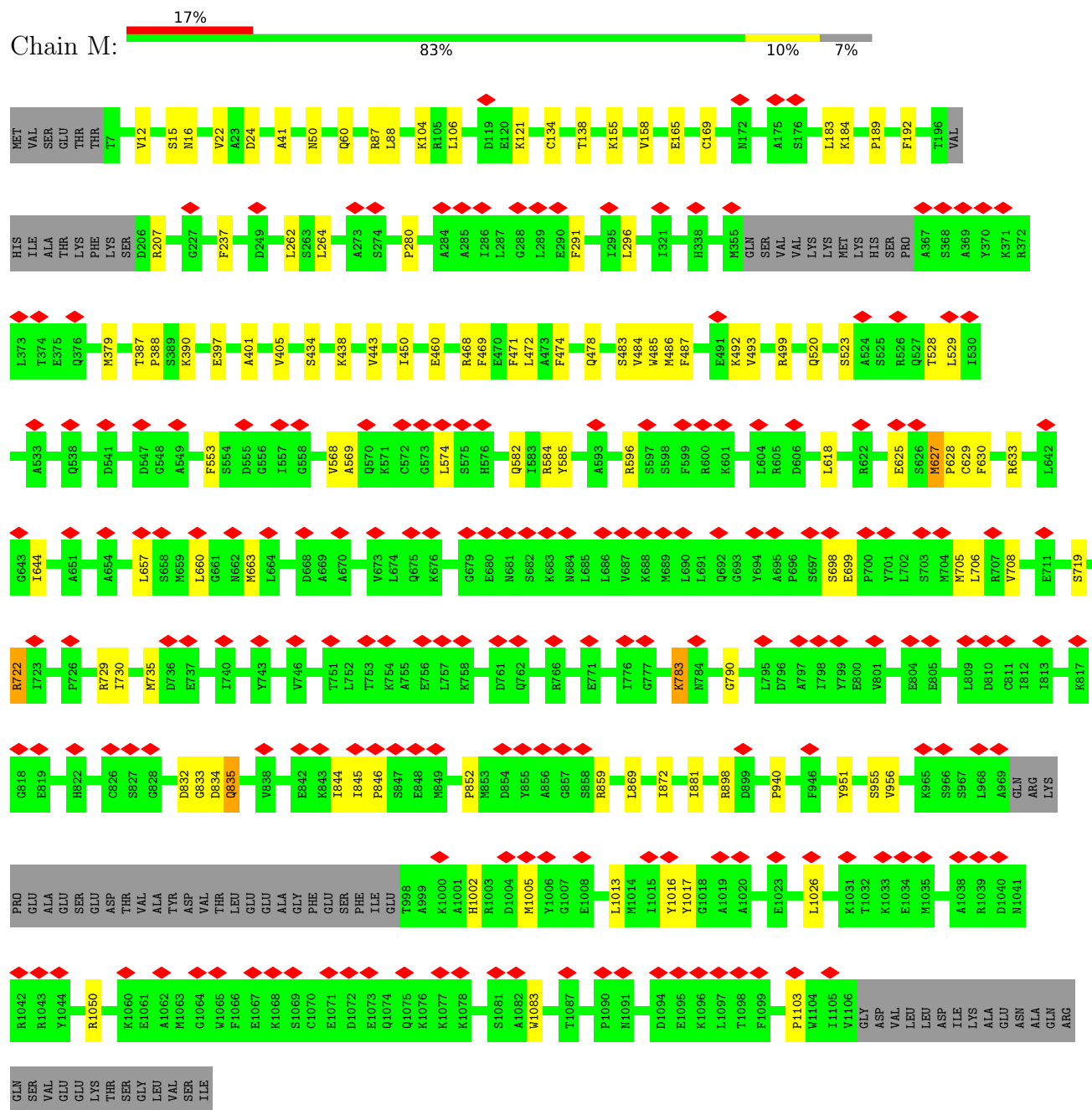
- Molecule 9: DNA-directed RNA polymerases II, IV and V subunit 11



- Molecule 10: DNA-directed RNA polymerases II, IV and V subunit 12

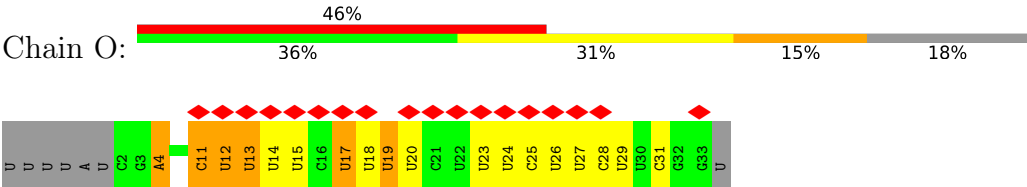


Chain M:

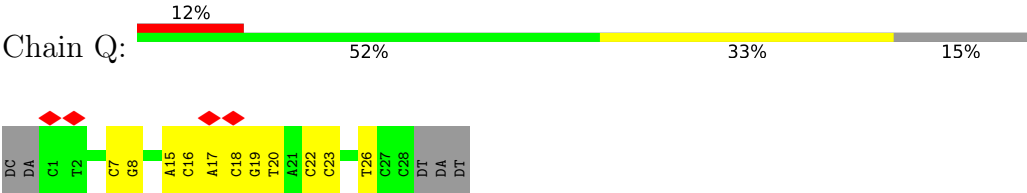


Chain N:





• Molecule 14: DNA (33-MER)



• Molecule 15: RNA (5'-R(*CP*CP*GP*A)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63253	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 ($e^-/\text{\AA}^2$)	1.95	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.188	Depositor
Minimum map value	-0.121	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.019	Depositor
Map size ($\text{\AA}$)	296.8, 296.8, 296.8	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.17	0/7866	0.44	0/10702
2	B	0.14	0/8026	0.40	0/10875
3	C	0.19	0/2178	0.47	0/2954
4	E	0.15	0/1479	0.42	0/2011
5	F	0.17	0/564	0.43	0/767
6	H	0.17	0/938	0.50	0/1267
7	I	0.14	0/835	0.41	0/1135
8	J	0.13	0/479	0.39	0/649
9	K	0.13	0/725	0.38	0/987
10	L	0.16	0/296	0.41	0/401
11	M	0.17	0/8224	0.45	0/11140
12	N	0.22	0/395	0.48	0/609
13	O	0.15	0/736	0.36	0/1141
14	Q	0.34	1/626 (0.2%)	1.05	3/960 (0.3%)
15	R	0.22	0/91	0.38	0/140
All	All	0.17	1/33458 (0.0%)	0.45	3/45738 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	Q	15	DA	O3'-P	5.60	1.69	1.61

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	Q	15	DA	O3'-P-O5'	22.25	137.38	104.00
14	Q	15	DA	P-O3'-C3'	12.80	139.40	120.20
14	Q	15	DA	OP2-P-O3'	-10.34	76.97	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	7722	0	7280	69	0
2	B	7861	0	7490	64	0
3	C	2148	0	2131	23	0
4	E	1458	0	1391	9	0
5	F	554	0	516	2	0
6	H	923	0	860	6	0
7	I	819	0	709	6	0
8	J	472	0	478	7	0
9	K	711	0	675	4	0
10	L	293	0	244	2	0
11	M	8055	0	7752	69	0
12	N	353	0	194	18	0
13	O	664	0	337	10	0
14	Q	561	0	314	42	0
15	R	82	0	45	4	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	A	1	0	0	0	0
17	M	1	0	0	0	0
All	All	32686	0	30416	295	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 5.

All (295) 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)
1:A:56:CYS:HB3	1:A:59:CYS:SG	1.64	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:31:DT:O4	14:Q:17:DA:N6	1.56	1.34
12:N:31:DT:O4	14:Q:17:DA:C6	1.91	1.24
12:N:31:DT:O4	14:Q:17:DA:N1	1.80	1.14
14:Q:19:DG:H2''	14:Q:20:DT:H5'	1.35	1.08
12:N:31:DT:C4	14:Q:17:DA:N1	2.29	1.00
11:M:478:GLN:HE22	11:M:485:TRP:CD1	1.80	0.98
14:Q:19:DG:H2''	14:Q:20:DT:C5'	1.94	0.97
14:Q:19:DG:C2	14:Q:20:DT:C2	2.55	0.94
1:A:56:CYS:HB3	1:A:59:CYS:HG	1.24	0.94
12:N:31:DT:H2''	12:N:32:DG:O5'	1.68	0.93
12:N:32:DG:N1	14:Q:16:DC:N3	2.19	0.89
12:N:32:DG:N2	14:Q:16:DC:O2	2.05	0.89
1:A:307:ARG:NH2	1:A:310:LYS:HE2	1.90	0.86
1:A:56:CYS:CB	1:A:59:CYS:SG	2.59	0.85
12:N:41:DG:H2''	12:N:42:DG:H8	1.41	0.83
3:C:90:CYS:SG	3:C:93:CYS:HB2	2.20	0.81
14:Q:19:DG:N2	14:Q:20:DT:O2	2.15	0.79
12:N:41:DG:H2''	12:N:42:DG:C8	2.19	0.78
13:O:11:C:H3'	13:O:11:C:O2	1.84	0.77
2:B:1108:CYS:SG	2:B:1111:CYS:HB3	2.26	0.75
1:A:413:PRO:HG3	14:Q:19:DG:N2	2.03	0.73
12:N:32:DG:O6	14:Q:16:DC:N4	2.20	0.71
14:Q:17:DA:H2''	14:Q:18:DC:C5'	2.21	0.71
14:Q:19:DG:C2'	14:Q:20:DT:H5'	2.18	0.71
8:J:7:CYS:SG	8:J:10:CYS:HB3	2.32	0.70
14:Q:19:DG:C2	14:Q:20:DT:N3	2.60	0.70
14:Q:17:DA:H1'	14:Q:18:DC:O4'	1.94	0.68
11:M:783:LYS:HZ1	11:M:834:ASP:HB2	1.61	0.65
14:Q:19:DG:N2	14:Q:20:DT:C2	2.64	0.65
14:Q:17:DA:H2''	14:Q:18:DC:O4'	1.95	0.65
2:B:1111:CYS:HB2	2:B:1136:CYS:SG	2.38	0.64
14:Q:19:DG:N3	14:Q:20:DT:C2	2.66	0.64
14:Q:17:DA:H2''	14:Q:18:DC:H5''	1.79	0.64
2:B:771:ASN:HD21	8:J:51:THR:HG21	1.63	0.64
1:A:734:LYS:CD	13:O:13:U:H3	2.10	0.63
13:O:11:C:O2	13:O:11:C:C3'	2.45	0.63
11:M:478:GLN:HE22	11:M:485:TRP:NE1	1.96	0.63
14:Q:17:DA:N9	14:Q:18:DC:C6	2.67	0.62
11:M:280:PRO:HG3	11:M:390:LYS:HB2	1.83	0.61
1:A:734:LYS:HD3	13:O:13:U:H3	1.66	0.61
13:O:11:C:O2	13:O:11:C:C2'	2.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:41:DG:H1'	12:N:42:DG:C8	2.37	0.60
14:Q:17:DA:C4	14:Q:18:DC:C6	2.90	0.59
11:M:582:GLN:HE21	11:M:833:GLY:HA3	1.67	0.59
14:Q:17:DA:C4	14:Q:18:DC:C5	2.90	0.59
14:Q:17:DA:C5	14:Q:18:DC:C5	2.90	0.59
12:N:41:DG:C2'	12:N:42:DG:C8	2.85	0.59
1:A:306:LEU:O	1:A:310:LYS:HG2	2.04	0.58
1:A:1082:ILE:HG12	1:A:1113:MET:HG2	1.86	0.57
12:N:41:DG:C1'	12:N:42:DG:C8	2.87	0.56
11:M:106:LEU:HB2	11:M:134:CYS:HB3	1.87	0.56
1:A:58:THR:HG21	1:A:70:HIS:CE1	2.41	0.56
11:M:625:GLU:O	11:M:627:MET:HE2	2.04	0.56
1:A:59:CYS:SG	1:A:62:LYS:CB	2.94	0.56
1:A:528:ALA:HA	6:H:94:HIS:HB3	1.86	0.56
2:B:365:LEU:HD12	2:B:368:LYS:HD2	1.86	0.56
13:O:4:A:H61	14:Q:26:DT:H3	1.52	0.56
2:B:859:ILE:HG13	2:B:874:LYS:HG2	1.87	0.56
11:M:169:CYS:HB3	11:M:264:LEU:HD22	1.88	0.55
12:N:40:DC:H2''	12:N:41:DG:OP2	2.05	0.55
11:M:835:GLN:OE1	11:M:835:GLN:N	2.40	0.55
1:A:471:VAL:O	1:A:476:GLN:NE2	2.39	0.55
11:M:783:LYS:HZ1	11:M:834:ASP:CG	2.15	0.54
11:M:783:LYS:HZ1	11:M:834:ASP:CB	2.21	0.54
15:R:17:C:HO5'	15:R:17:C:H6	1.54	0.54
2:B:607:MET:HG3	2:B:622:THR:HB	1.89	0.54
14:Q:19:DG:H2'	14:Q:20:DT:C6	2.42	0.54
1:A:514:GLN:NE2	9:K:57:LEU:O	2.41	0.53
2:B:577:ASN:HD21	2:B:622:THR:H	1.56	0.53
4:E:175:ALA:HA	4:E:180:LEU:HD12	1.91	0.53
1:A:442:LEU:O	1:A:445:ARG:NH2	2.42	0.53
3:C:22:ALA:HB3	3:C:270:VAL:HB	1.90	0.53
1:A:562:ASN:ND2	1:A:578:SER:O	2.41	0.53
14:Q:19:DG:H2''	14:Q:20:DT:O5'	2.09	0.53
1:A:317:ARG:NH1	14:Q:22:DC:OP1	2.41	0.53
8:J:10:CYS:SG	8:J:42:ARG:NH2	2.80	0.53
2:B:718:GLN:NE2	2:B:916:SER:O	2.41	0.53
3:C:127:SER:OG	3:C:128:ALA:N	2.42	0.53
3:C:98:GLN:OE1	3:C:98:GLN:HA	2.08	0.52
11:M:569:ALA:HB1	11:M:574:LEU:HB2	1.91	0.52
2:B:491:ARG:NH2	2:B:535:SER:O	2.42	0.52
11:M:155:LYS:HB3	11:M:192:PHE:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:185:CYS:HB3	2:B:188:SER:HB3	1.92	0.52
11:M:183:LEU:HB2	11:M:237:PHE:HB2	1.92	0.52
14:Q:19:DG:H2'	14:Q:20:DT:C7	2.40	0.52
1:A:438:PRO:HD2	1:A:608:GLN:HE22	1.74	0.52
1:A:517:GLN:NE2	1:A:522:PHE:O	2.42	0.52
11:M:630:PHE:CE2	11:M:722:ARG:NH1	2.77	0.52
2:B:747:TYR:O	2:B:770:GLN:NE2	2.40	0.52
1:A:651:GLU:OE2	1:A:762:ARG:NH2	2.42	0.51
3:C:186:VAL:HG12	3:C:270:VAL:HA	1.91	0.51
2:B:757:ALA:O	2:B:761:LEU:HB2	2.10	0.51
11:M:790:GLY:HA3	11:M:852:PRO:HA	1.92	0.51
11:M:783:LYS:NZ	11:M:834:ASP:HB2	2.24	0.51
7:I:76:CYS:SG	7:I:77:SER:N	2.84	0.51
14:Q:19:DG:C2'	14:Q:20:DT:C6	2.95	0.51
2:B:1109:ARG:HB2	2:B:1141:HIS:HB2	1.92	0.50
11:M:644:ILE:HG12	11:M:845:ILE:H	1.75	0.50
14:Q:7:DC:H2''	14:Q:8:DG:C8	2.46	0.50
2:B:95:VAL:HG23	2:B:138:VAL:HG22	1.92	0.50
3:C:176:ASP:OD1	3:C:176:ASP:N	2.45	0.50
1:A:417:GLN:O	2:B:1086:HIS:NE2	2.42	0.50
11:M:15:SER:HB2	11:M:87:ARG:HB2	1.93	0.50
11:M:633:ARG:NH1	11:M:719:SER:O	2.44	0.50
11:M:520:GLN:O	11:M:584:ARG:NH1	2.45	0.50
2:B:903:ARG:NH1	3:C:65:GLU:OE1	2.45	0.50
4:E:17:LEU:HD11	4:E:100:VAL:HG21	1.93	0.50
1:A:83:PRO:HA	1:A:86:LEU:HD23	1.92	0.50
1:A:417:GLN:HA	2:B:1082:CYS:HB3	1.94	0.50
4:E:10:LEU:HD21	4:E:53:LEU:HD11	1.94	0.49
1:A:25:ASN:ND2	1:A:219:GLY:O	2.45	0.49
5:F:129:ASP:OD1	5:F:129:ASP:N	2.45	0.49
11:M:657:LEU:HA	11:M:660:LEU:HB3	1.94	0.49
15:R:17:C:H6	15:R:17:C:O5'	1.94	0.49
1:A:58:THR:CG2	1:A:70:HIS:CE1	2.95	0.49
2:B:906:ARG:NH1	2:B:1043:MET:SD	2.81	0.49
2:B:1080:ARG:HG3	2:B:1092:LEU:HD11	1.94	0.49
3:C:297:ARG:HB2	9:K:91:ILE:HG21	1.94	0.49
11:M:869:LEU:HD13	11:M:872:ILE:HD12	1.93	0.49
11:M:1013:LEU:HA	11:M:1016:TYR:HB3	1.93	0.49
11:M:50:ASN:O	11:M:207:ARG:NH2	2.46	0.49
1:A:413:PRO:HG3	14:Q:19:DG:H22	1.76	0.49
11:M:698:SER:OG	11:M:699:GLU:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Q:17:DA:C2'	14:Q:18:DC:O4'	2.61	0.49
1:A:1128:GLU:O	1:A:1130:CYS:N	2.46	0.49
2:B:591:VAL:HG21	2:B:611:ARG:HB2	1.94	0.49
3:C:62:LEU:HD12	3:C:155:VAL:HG23	1.95	0.49
2:B:1051:ARG:HG3	2:B:1070:PHE:HB3	1.93	0.48
3:C:90:CYS:HG	3:C:93:CYS:HB2	1.77	0.48
1:A:13:GLY:HA2	2:B:1171:LEU:HB3	1.94	0.48
1:A:632:ASP:N	1:A:632:ASP:OD1	2.45	0.48
2:B:634:VAL:HA	2:B:637:LEU:HB2	1.95	0.48
11:M:379:MET:HB2	11:M:401:ALA:HB2	1.94	0.48
1:A:23:SER:O	1:A:28:ARG:NH2	2.47	0.48
7:I:97:MET:O	11:M:859:ARG:NH1	2.45	0.48
1:A:1148:ARG:NH1	1:A:1196:PHE:O	2.46	0.48
2:B:674:TRP:HB3	2:B:693:LEU:HD11	1.94	0.48
2:B:1077:GLU:HG2	2:B:1080:ARG:HH21	1.78	0.48
2:B:1103:SER:OG	2:B:1104:GLN:N	2.46	0.48
2:B:778:VAL:HA	2:B:783:ASN:HD21	1.79	0.48
4:E:76:LYS:HD2	12:N:44:DA:OP1	2.13	0.48
11:M:705:MET:HA	11:M:708:VAL:HG22	1.96	0.48
1:A:416:HIS:HB3	1:A:887:GLU:HB2	1.96	0.48
6:H:91:TYR:HB3	6:H:143:MET:HB2	1.96	0.48
2:B:223:MET:HE3	2:B:240:ARG:HH12	1.79	0.47
4:E:163:THR:O	4:E:167:ARG:NH1	2.47	0.47
11:M:629:CYS:HB3	11:M:730:ILE:HG13	1.95	0.47
2:B:48:LEU:O	2:B:491:ARG:NH1	2.47	0.47
3:C:84:MET:HE3	3:C:101:PHE:O	2.14	0.47
3:C:286:ILE:HG21	9:K:102:LYS:HB2	1.96	0.47
11:M:471:PHE:O	11:M:499:ARG:NH1	2.47	0.47
7:I:7:CYS:SG	7:I:10:CYS:HB3	2.54	0.47
14:Q:17:DA:C8	14:Q:18:DC:C5	3.03	0.47
1:A:1128:GLU:OE2	4:E:9:ARG:NH2	2.48	0.47
2:B:1049:LYS:HG3	2:B:1067:ARG:HG3	1.96	0.47
6:H:43:LEU:HD13	6:H:121:MET:HG3	1.97	0.47
14:Q:17:DA:C1'	14:Q:18:DC:O4'	2.63	0.47
1:A:582:ARG:HD3	1:A:732:GLY:HA3	1.97	0.47
2:B:307:ILE:HG23	2:B:380:LEU:HD22	1.96	0.47
2:B:740:THR:HG23	2:B:741:LEU:N	2.29	0.47
2:B:1051:ARG:NH1	2:B:1071:GLY:O	2.47	0.47
3:C:193:ASP:OD1	3:C:193:ASP:N	2.46	0.47
4:E:166:PRO:HB2	4:E:202:ARG:HD3	1.96	0.47
4:E:168:ILE:HG23	4:E:202:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:121:MET:HE3	6:H:123:LEU:HB2	1.97	0.47
7:I:79:CYS:SG	7:I:108:CYS:HB2	2.54	0.47
6:H:42:HIS:HB2	6:H:122:LEU:HB3	1.96	0.47
11:M:460:GLU:O	11:M:468:ARG:NH2	2.48	0.47
11:M:397:GLU:HG2	11:M:1050:ARG:HD2	1.97	0.47
11:M:41:ALA:HB3	11:M:60:GLN:HB3	1.97	0.46
11:M:832:ASP:OD1	11:M:832:ASP:N	2.48	0.46
1:A:346:ARG:O	2:B:1052:ASN:ND2	2.42	0.46
1:A:769:TRP:O	1:A:777:ARG:NH2	2.48	0.46
2:B:1109:ARG:NH2	2:B:1169:THR:OG1	2.47	0.46
11:M:474:PHE:HB3	11:M:484:VAL:HG23	1.97	0.46
2:B:920:GLN:NE2	2:B:956:THR:OG1	2.46	0.46
11:M:628:PRO:HA	11:M:729:ARG:HA	1.97	0.46
3:C:98:GLN:OE1	3:C:104:VAL:HA	2.15	0.46
1:A:526:PRO:O	1:A:545:GLN:NE2	2.48	0.46
2:B:606:GLU:O	2:B:626:ARG:NH2	2.41	0.46
1:A:413:PRO:HB3	14:Q:20:DT:O2	2.16	0.46
14:Q:17:DA:H1'	14:Q:18:DC:C1'	2.46	0.46
11:M:12:VAL:HG11	11:M:88:LEU:HD13	1.97	0.46
2:B:713:ARG:NH1	13:O:12:U:OP2	2.48	0.46
14:Q:17:DA:C1'	14:Q:18:DC:C6	2.99	0.46
1:A:23:SER:HB3	2:B:1164:THR:HB	1.98	0.45
1:A:25:ASN:OD1	1:A:28:ARG:NH1	2.49	0.45
1:A:28:ARG:HD3	1:A:224:PRO:HD3	1.99	0.45
2:B:718:GLN:HA	2:B:722:HIS:HB2	1.97	0.45
2:B:876:LYS:HD3	2:B:1068:LYS:HB3	1.97	0.45
3:C:56:GLU:HG3	3:C:57:VAL:HG23	1.96	0.45
1:A:734:LYS:HD2	13:O:13:U:H3	1.79	0.45
1:A:445:ARG:NH1	1:A:887:GLU:OE2	2.50	0.45
11:M:22:VAL:HG13	11:M:24:ASP:H	1.82	0.45
2:B:323:GLU:O	2:B:330:ASN:ND2	2.50	0.45
2:B:633:VAL:HG22	2:B:635:GLU:H	1.82	0.45
3:C:20:ASP:OD1	3:C:20:ASP:N	2.49	0.45
11:M:469:PHE:HB3	11:M:486:MET:HB3	1.99	0.45
1:A:712:GLN:HG2	1:A:741:VAL:HG21	1.98	0.45
11:M:1083:TRP:HB3	11:M:1103:PRO:HB3	1.99	0.45
1:A:517:GLN:HG3	1:A:524:LEU:HD13	1.99	0.44
1:A:1122:CYS:HB2	1:A:1149:GLN:HE22	1.82	0.44
11:M:104:LYS:NZ	11:M:138:THR:OG1	2.45	0.44
11:M:434:SER:HB3	11:M:881:ILE:HG21	1.99	0.44
11:M:596:ARG:HA	11:M:596:ARG:HD3	1.87	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:41:DG:C8	12:N:41:DG:O5'	2.70	0.44
1:A:477:LEU:HD13	1:A:593:LEU:HD11	1.99	0.44
11:M:388:PRO:HB3	11:M:450:ILE:HD12	2.00	0.44
1:A:326:VAL:HG23	1:A:434:VAL:HG23	2.00	0.44
11:M:898:ARG:HH22	11:M:940:PRO:HA	1.83	0.44
14:Q:17:DA:C5	14:Q:18:DC:C4	3.05	0.44
11:M:528:THR:HG21	11:M:568:VAL:HG23	1.98	0.44
1:A:56:CYS:O	1:A:59:CYS:O	2.35	0.44
1:A:615:LEU:HG	2:B:778:VAL:HG21	1.99	0.44
8:J:48:MET:HE2	8:J:48:MET:HB2	1.86	0.44
2:B:634:VAL:HG11	2:B:680:LEU:HD11	2.00	0.44
1:A:978:SER:OG	1:A:1049:VAL:O	2.33	0.43
11:M:663:MET:HG2	11:M:706:LEU:HD21	2.00	0.43
11:M:585:TYR:HB3	11:M:618:LEU:HD12	2.00	0.43
1:A:413:PRO:HG3	14:Q:19:DG:H21	1.80	0.43
1:A:575:SER:O	1:A:575:SER:OG	2.34	0.43
2:B:297:LEU:HD22	2:B:370:ARG:HG3	1.99	0.43
7:I:70:ARG:HG2	7:I:85:VAL:HG22	2.00	0.43
11:M:898:ARG:HH21	11:M:951:TYR:HB3	1.83	0.43
11:M:158:VAL:HG22	11:M:189:PRO:HB3	2.01	0.43
13:O:11:C:O2	13:O:11:C:H2'	2.18	0.43
11:M:553:PHE:HB3	11:M:735:MET:HE2	2.01	0.43
12:N:40:DC:C2	12:N:41:DG:C6	3.07	0.43
15:R:18:C:H2'	15:R:19:G:C8	2.53	0.43
1:A:708:TYR:HH	1:A:746:CYS:HG	1.58	0.42
2:B:117:LEU:HD13	2:B:119:TRP:HE1	1.83	0.42
11:M:523:SER:OG	11:M:584:ARG:NH1	2.52	0.42
12:N:40:DC:C4	12:N:41:DG:O6	2.72	0.42
11:M:955:SER:OG	11:M:956:VAL:N	2.52	0.42
2:B:226:LYS:HD3	2:B:577:ASN:HB3	2.01	0.42
3:C:183:ALA:HB2	3:C:281:LEU:HD21	2.00	0.42
14:Q:17:DA:H2''	14:Q:18:DC:C4'	2.49	0.42
2:B:728:GLY:HA3	2:B:768:ASN:HD22	1.85	0.42
8:J:7:CYS:HB3	8:J:11:GLY:H	1.83	0.42
2:B:49:ILE:HG21	2:B:490:LEU:HD13	2.02	0.42
6:H:16:LYS:HB3	6:H:31:GLU:HB2	2.02	0.42
11:M:472:LEU:HD12	11:M:487:PHE:HB2	2.00	0.42
11:M:1013:LEU:HD23	11:M:1017:TYR:HE2	1.85	0.42
1:A:429:PRO:HD2	9:K:67:LEU:HD13	2.02	0.42
2:B:180:VAL:HG12	2:B:181:LYS:HG3	2.02	0.42
11:M:478:GLN:HG2	11:M:483:SER:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:844:ILE:HG13	11:M:846:PRO:HD3	2.02	0.42
1:A:894:ASP:OD1	1:A:894:ASP:N	2.45	0.42
2:B:249:ILE:O	2:B:271:TYR:N	2.52	0.42
3:C:76:LEU:HD23	3:C:132:VAL:HG12	2.02	0.42
11:M:438:LYS:HA	11:M:443:VAL:HA	2.01	0.42
1:A:458:PRO:HB3	2:B:1091:ASN:HD21	1.84	0.42
2:B:516:ARG:NH1	2:B:662:ILE:O	2.53	0.41
10:L:12:CYS:SG	10:L:29:CYS:SG	3.01	0.41
11:M:387:THR:HG1	11:M:390:LYS:H	1.68	0.41
1:A:1106:GLU:OE2	1:A:1141:ARG:NH2	2.51	0.41
3:C:51:ASP:HA	10:L:50:ALA:HB3	2.02	0.41
1:A:742:GLN:HG2	1:A:747:ILE:HA	2.02	0.41
2:B:940:ILE:HD11	8:J:42:ARG:HB3	2.03	0.41
3:C:205:SER:OG	3:C:206:ASP:N	2.54	0.41
2:B:288:VAL:HG13	2:B:293:GLU:HG3	2.02	0.41
3:C:22:ALA:HB2	3:C:278:ALA:HB1	2.01	0.41
3:C:107:ARG:HA	3:C:107:ARG:HD2	1.93	0.41
11:M:291:PHE:HD2	11:M:296:LEU:HB2	1.85	0.41
13:O:17:U:O2'	13:O:19:U:OP2	2.38	0.41
1:A:399:ARG:NH1	1:A:400:SER:O	2.54	0.41
1:A:1258:THR:HB	2:B:1089:SER:HB2	2.02	0.41
11:M:1002:HIS:HA	11:M:1005:MET:HG2	2.03	0.41
1:A:960:VAL:HA	1:A:986:ILE:HG12	2.02	0.41
2:B:399:ARG:HB3	2:B:625:GLY:HA3	2.02	0.41
2:B:797:ARG:NH1	8:J:8:PHE:O	2.53	0.41
11:M:379:MET:HE2	11:M:405:VAL:HG21	2.02	0.41
11:M:1026:LEU:HD23	11:M:1026:LEU:HA	1.92	0.41
1:A:477:LEU:HB3	1:A:593:LEU:HD21	2.03	0.41
2:B:990:THR:HA	2:B:991:PRO:HD3	1.97	0.41
14:Q:22:DC:H2''	14:Q:23:DC:H5'	2.03	0.41
1:A:520:CYS:HA	1:A:521:PRO:HD3	1.95	0.41
2:B:463:HIS:HA	2:B:464:PRO:HD3	1.95	0.41
3:C:99:CYS:HB2	3:C:103:SER:H	1.86	0.41
4:E:99:LEU:HD21	4:E:124:VAL:HG22	2.03	0.41
11:M:16:ASN:OD1	11:M:16:ASN:N	2.53	0.41
15:R:18:C:H2'	15:R:19:G:H8	1.86	0.40
2:B:636:ASN:HB2	2:B:639:LYS:HE3	2.03	0.40
2:B:1158:LEU:HA	2:B:1161:MET:HG2	2.02	0.40
11:M:492:LYS:HG2	11:M:493:VAL:HG13	2.02	0.40
11:M:528:THR:HG22	11:M:529:LEU:H	1.86	0.40
1:A:49:LEU:HB3	1:A:64:ARG:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1063:ILE:HG23	1:A:1067:LEU:HD23	2.03	0.40
1:A:1258:THR:HG23	5:F:72:ARG:HD2	2.04	0.40
11:M:121:LYS:HG3	11:M:262:LEU:HD21	2.02	0.40
11:M:165:GLU:HB3	11:M:184:LYS:HB2	2.04	0.40
1:A:430:THR:OG1	1:A:431:THR:N	2.54	0.40
1:A:1193:THR:HG21	1:A:1207:GLN:HA	2.04	0.40
2:B:291:ASP:HB2	7:I:12:ASN:HA	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	1042/1510 (69%)	1008 (97%)	34 (3%)	0	100	100
2	B	1032/1172 (88%)	1005 (97%)	27 (3%)	0	100	100
3	C	287/319 (90%)	270 (94%)	17 (6%)	0	100	100
4	E	194/205 (95%)	191 (98%)	3 (2%)	0	100	100
5	F	74/144 (51%)	69 (93%)	5 (7%)	0	100	100
6	H	120/146 (82%)	113 (94%)	7 (6%)	0	100	100
7	I	111/114 (97%)	108 (97%)	3 (3%)	0	100	100
8	J	60/71 (84%)	57 (95%)	3 (5%)	0	100	100
9	K	92/116 (79%)	89 (97%)	3 (3%)	0	100	100
10	L	40/51 (78%)	38 (95%)	2 (5%)	0	100	100
11	M	1044/1133 (92%)	999 (96%)	45 (4%)	0	100	100
All	All	4096/4981 (82%)	3947 (96%)	149 (4%)	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	772/1344 (57%)	772 (100%)	0	100	100
2	B	773/1029 (75%)	772 (100%)	1 (0%)	88	89
3	C	220/280 (79%)	219 (100%)	1 (0%)	81	82
4	E	133/191 (70%)	133 (100%)	0	100	100
5	F	50/128 (39%)	50 (100%)	0	100	100
6	H	84/127 (66%)	84 (100%)	0	100	100
7	I	79/104 (76%)	79 (100%)	0	100	100
8	J	47/66 (71%)	47 (100%)	0	100	100
9	K	67/105 (64%)	67 (100%)	0	100	100
10	L	25/45 (56%)	25 (100%)	0	100	100
11	M	822/1005 (82%)	818 (100%)	4 (0%)	81	82
All	All	3072/4424 (69%)	3066 (100%)	6 (0%)	85	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	913	LYS
3	C	227	THR
11	M	627	MET
11	M	722	ARG
11	M	783	LYS
11	M	835	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	ASN
1	A	491	GLN
1	A	501	ASN
1	A	515	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	540	GLN
1	A	608	GLN
1	A	634	GLN
1	A	658	GLN
1	A	742	GLN
1	A	910	ASN
1	A	949	ASN
1	A	950	HIS
1	A	1006	ASN
1	A	1149	GLN
1	A	1166	ASN
1	A	1182	HIS
2	B	124	GLN
2	B	220	GLN
2	B	222	GLN
2	B	417	HIS
2	B	450	ASN
2	B	577	ASN
2	B	600	GLN
2	B	652	HIS
2	B	656	HIS
2	B	711	HIS
2	B	749	GLN
2	B	768	ASN
2	B	779	HIS
2	B	955	GLN
2	B	1042	HIS
2	B	1091	ASN
2	B	1106	HIS
2	B	1166	ASN
3	C	280	GLN
3	C	284	ASN
4	E	126	GLN
7	I	34	HIS
7	I	46	ASN
7	I	105	ASN
8	J	20	GLN
8	J	61	ASN
9	K	29	ASN
9	K	51	HIS
10	L	47	GLN
11	M	19	GLN

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Mol	Chain	Res	Type
11	M	300	ASN
11	M	339	GLN
11	M	656	HIS
11	M	788	HIS
11	M	1002	HIS
11	M	1059	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	O	31/39 (79%)	18 (58%)	2 (6%)
15	R	3/4 (75%)	0	0
All	All	34/43 (79%)	18 (52%)	2 (5%)

All (18) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	O	4	A
13	O	11	C
13	O	12	U
13	O	13	U
13	O	14	U
13	O	15	U
13	O	17	U
13	O	18	U
13	O	19	U
13	O	20	U
13	O	23	U
13	O	24	U
13	O	25	C
13	O	26	U
13	O	27	U
13	O	28	C
13	O	29	U
13	O	31	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	O	17	U
13	O	18	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

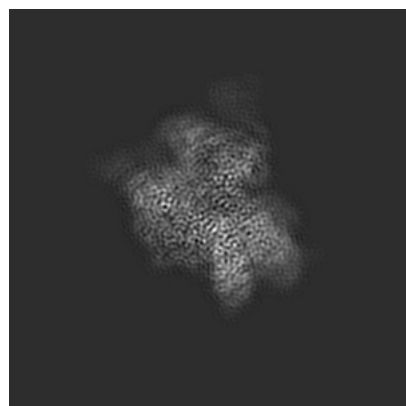
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31305. These allow visual inspection of the internal detail of the map and identification of artifacts.

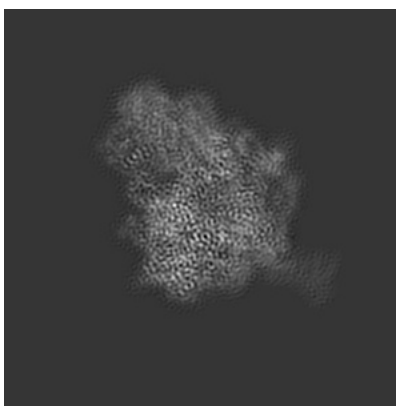
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

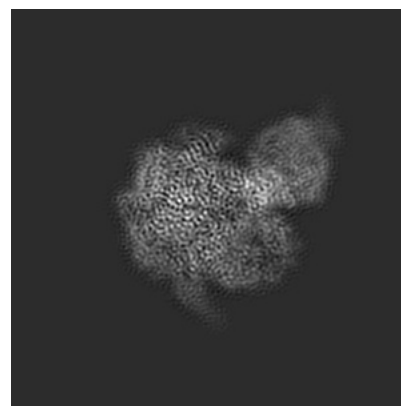
6.1.1 Primary map



X

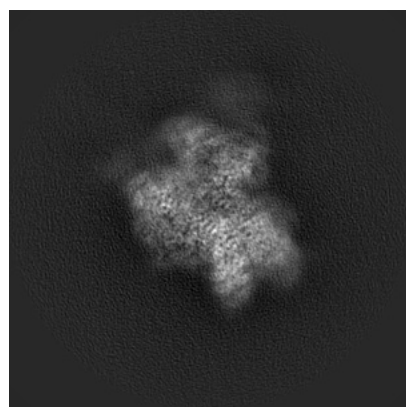


Y

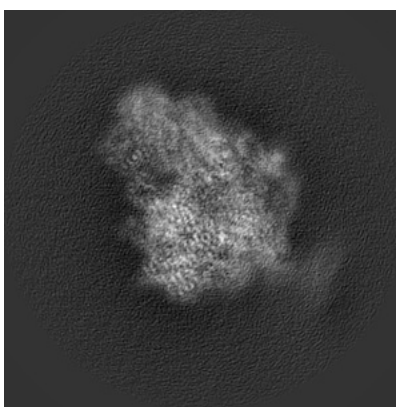


Z

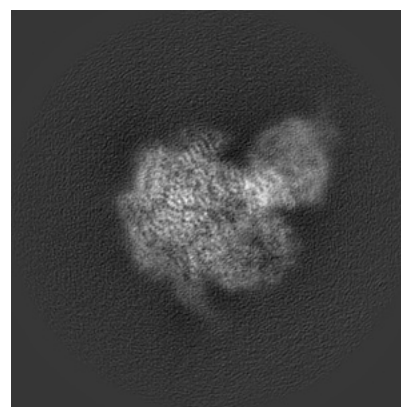
6.1.2 Raw map



X



Y

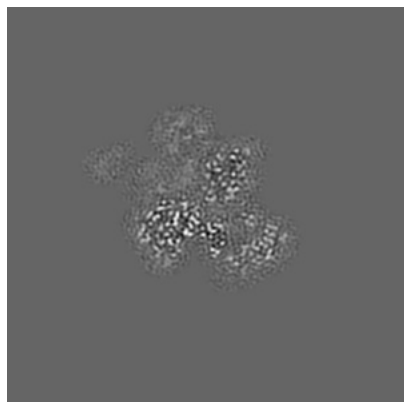


Z

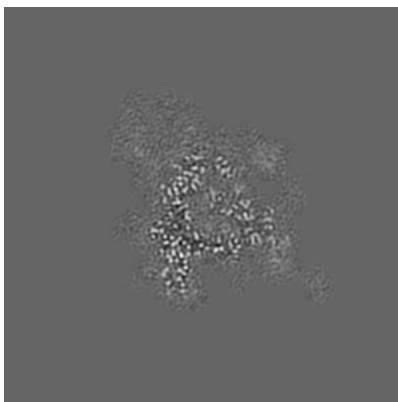
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

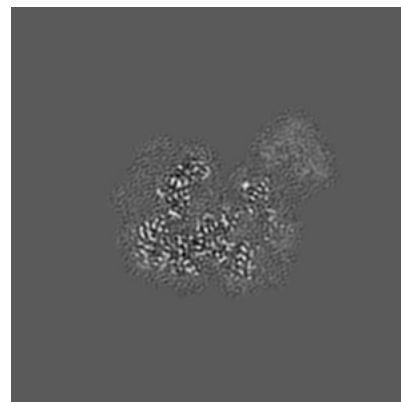
6.2.1 Primary map



X Index: 140

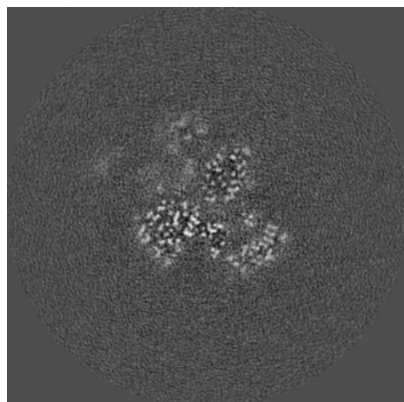


Y Index: 140

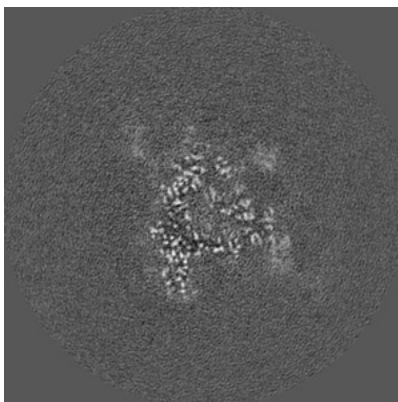


Z Index: 140

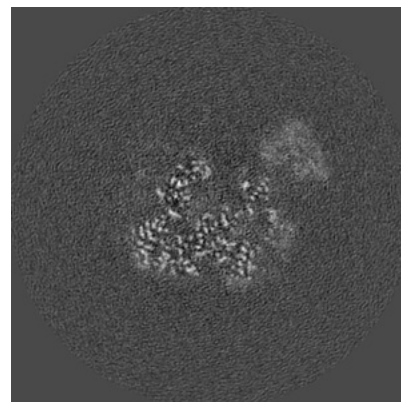
6.2.2 Raw map



X Index: 140



Y Index: 140

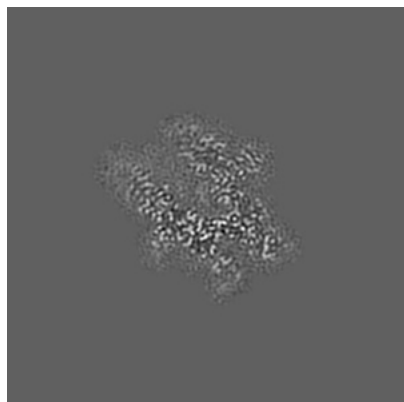


Z Index: 140

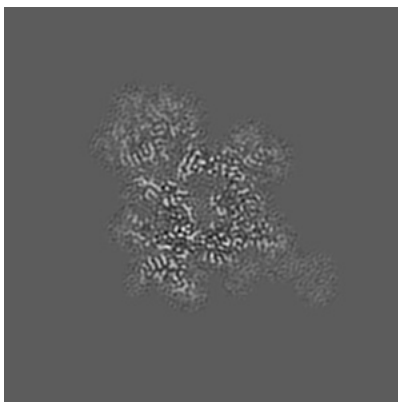
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

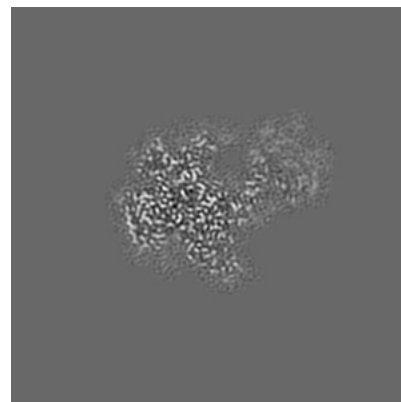
6.3.1 Primary map



X Index: 126

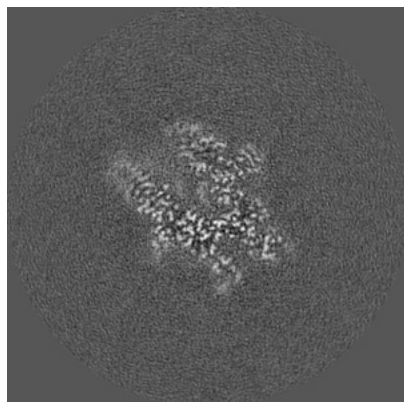


Y Index: 149

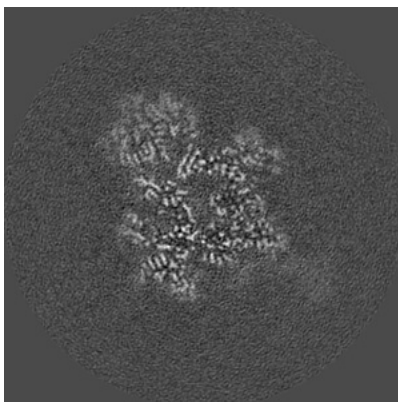


Z Index: 123

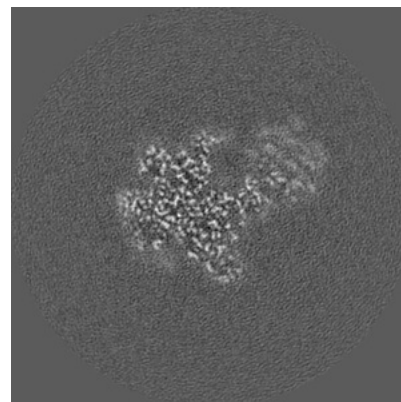
6.3.2 Raw map



X Index: 126



Y Index: 149

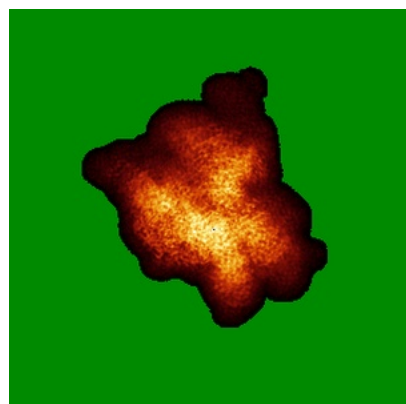


Z Index: 125

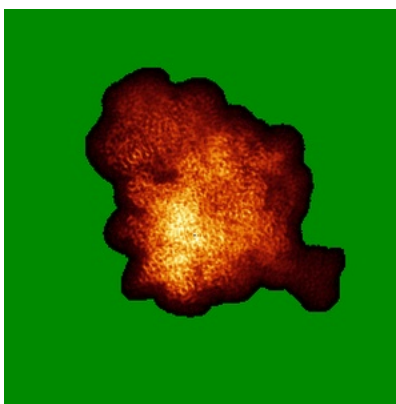
The images above show the largest variance slices of the map in three orthogonal directions.

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

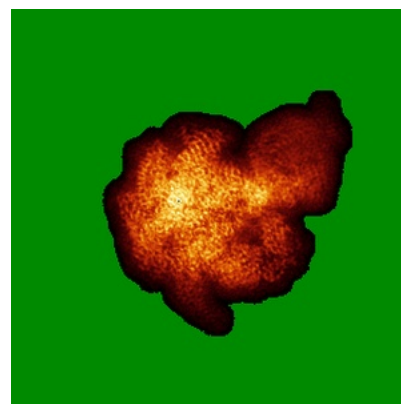
6.4.1 Primary map



X

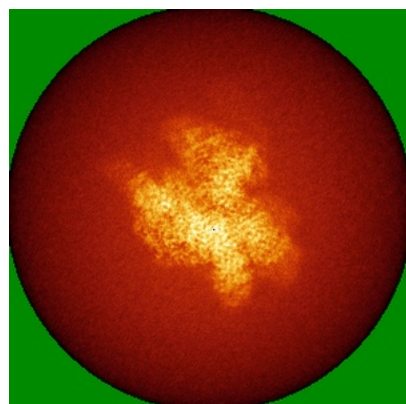


Y

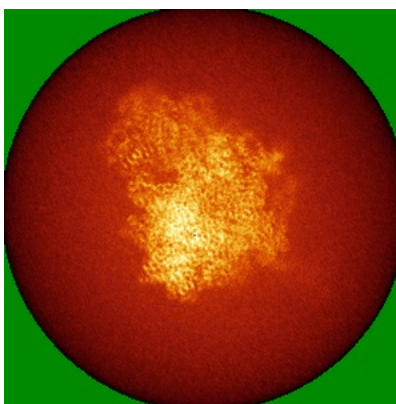


Z

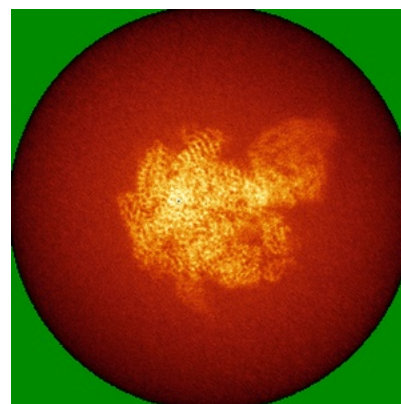
6.4.2 Raw map



X



Y

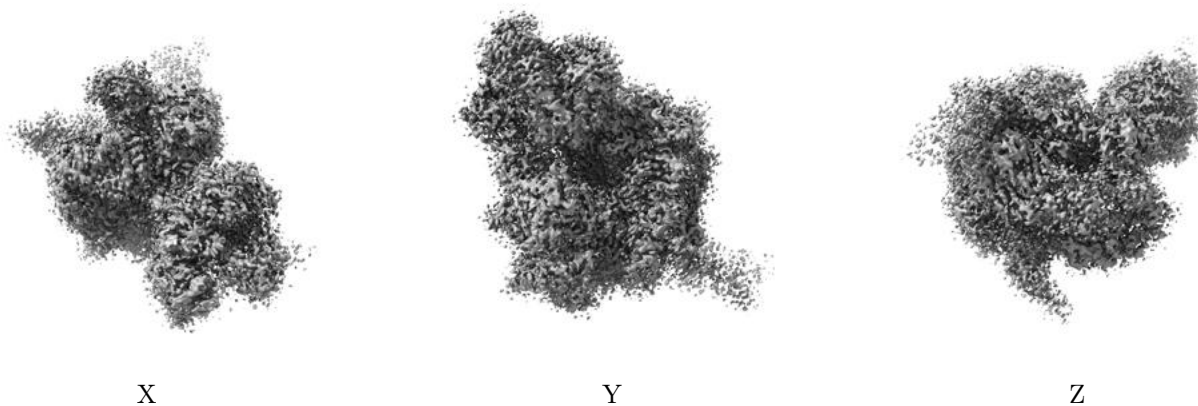


Z

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.

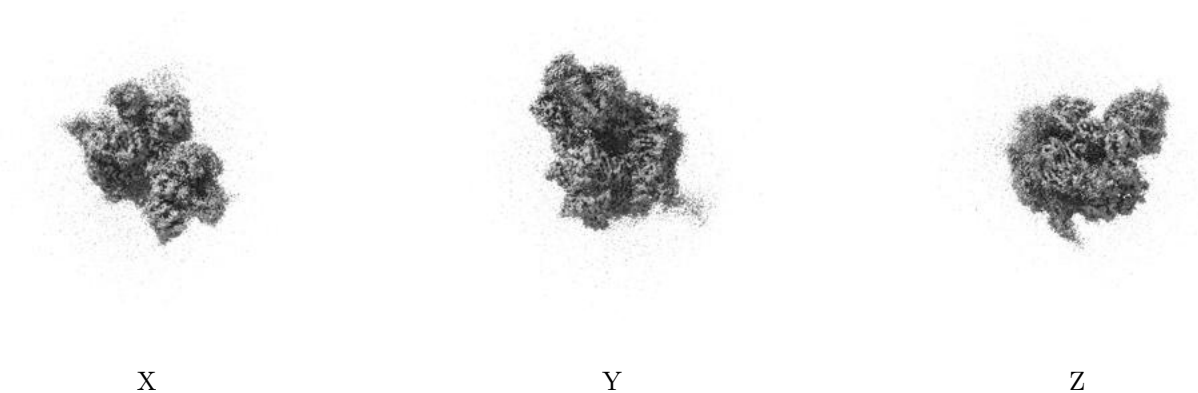
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.019. 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



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.

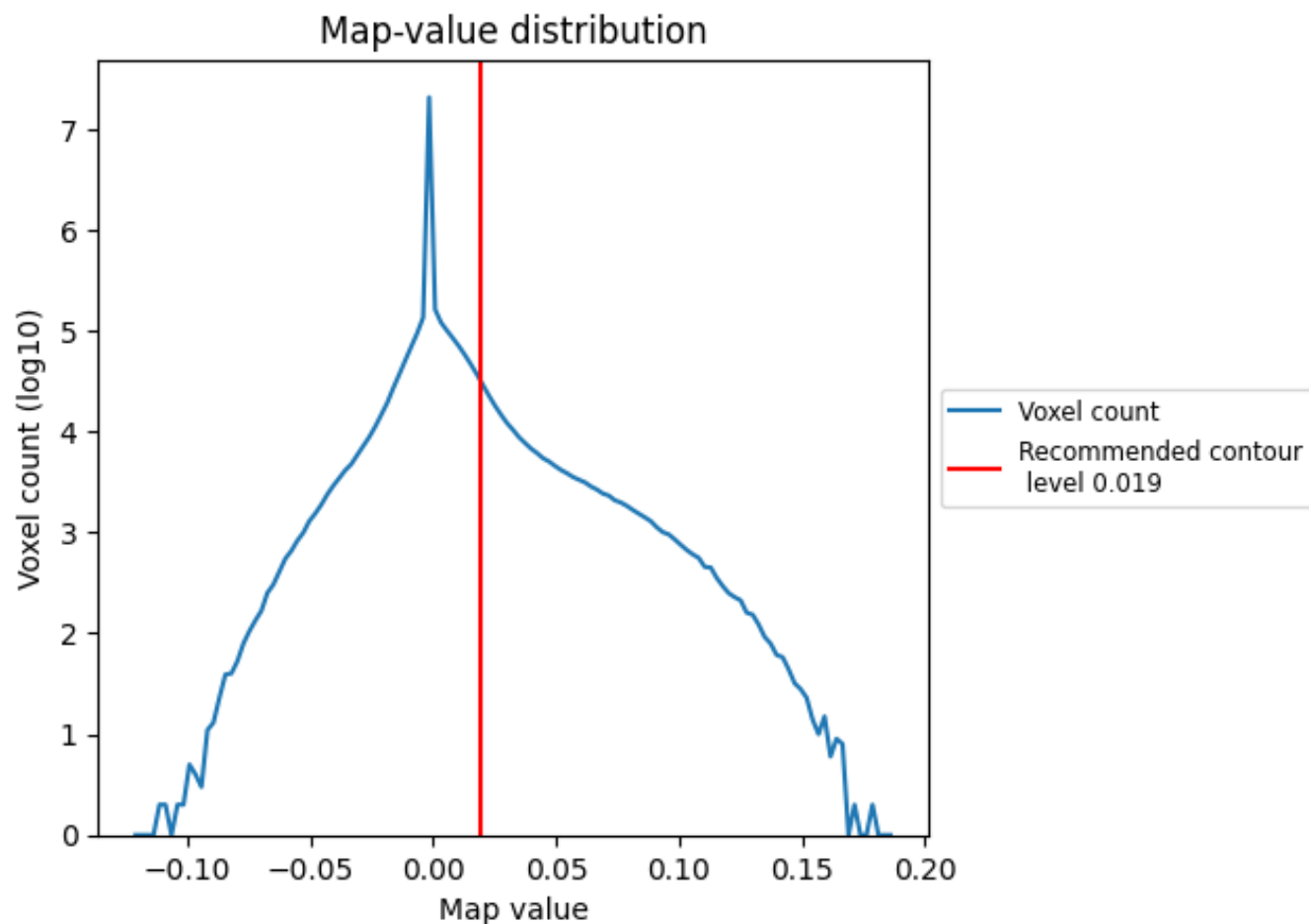
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

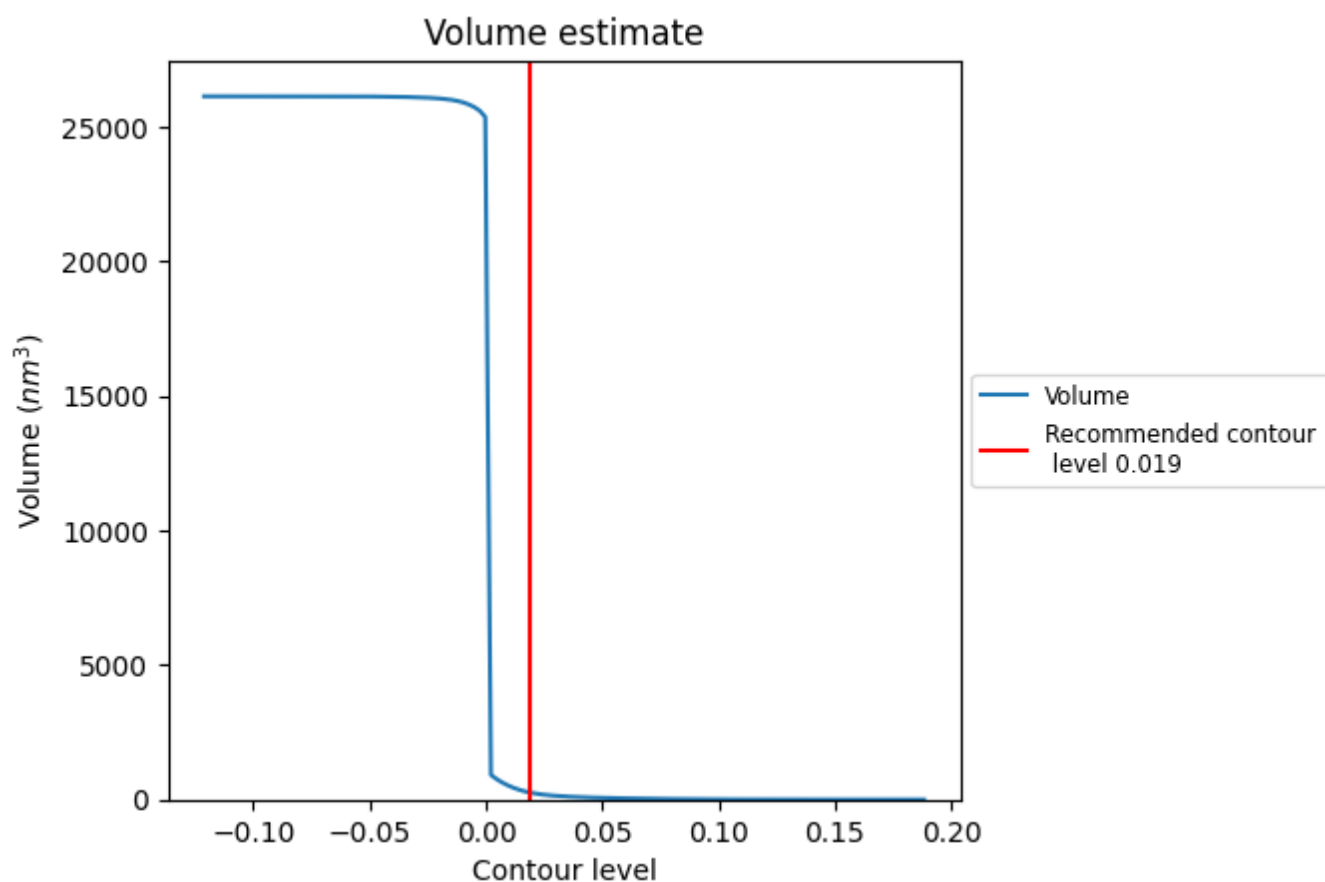
This section contains the results of statistical analysis of the map.

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.

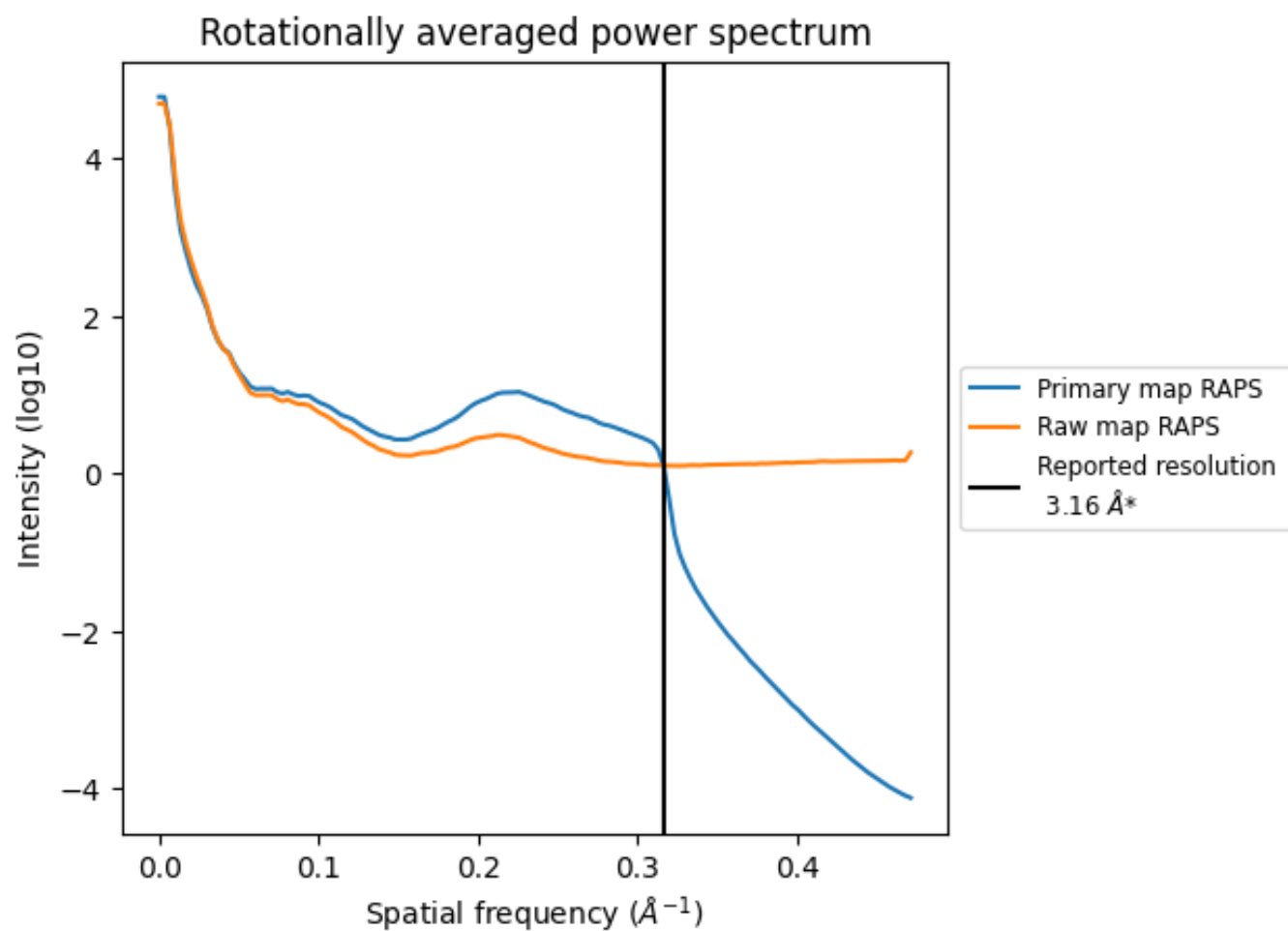
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 260 nm^3 ; this corresponds to an approximate mass of 235 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 ⓘ

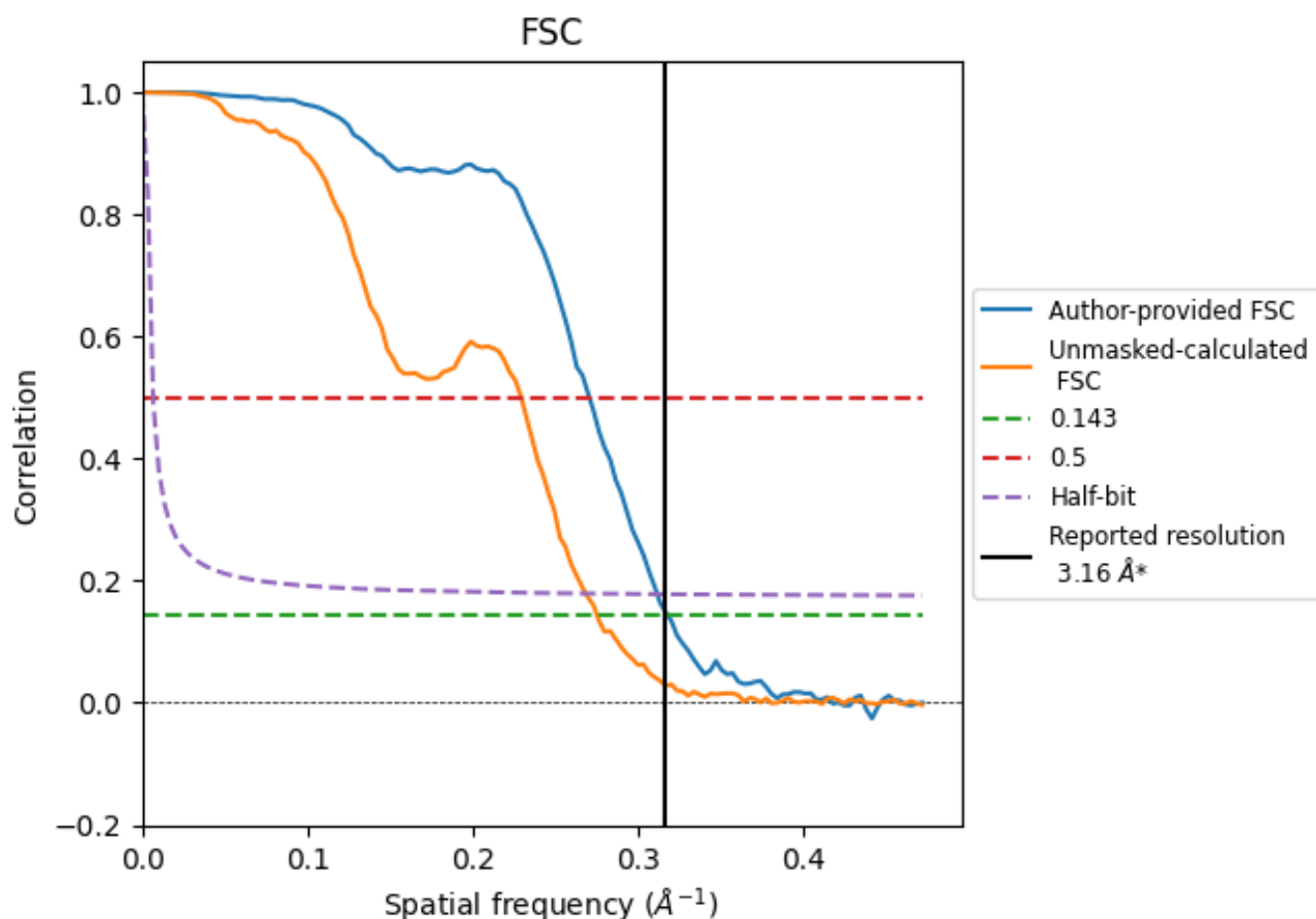


*Reported resolution corresponds to spatial frequency of 0.316 Å⁻¹

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 0.316 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

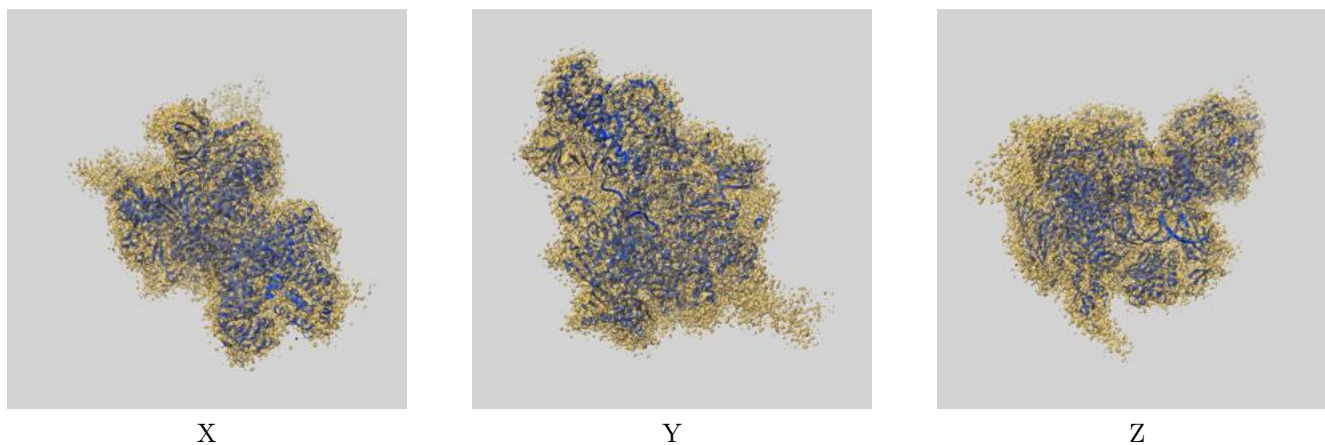
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	3.15	3.70	3.21
Unmasked-calculated*	3.64	4.36	3.73

*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 3.64 differs from the reported value 3.16 by more than 10 %

9 Map-model fit [i](#)

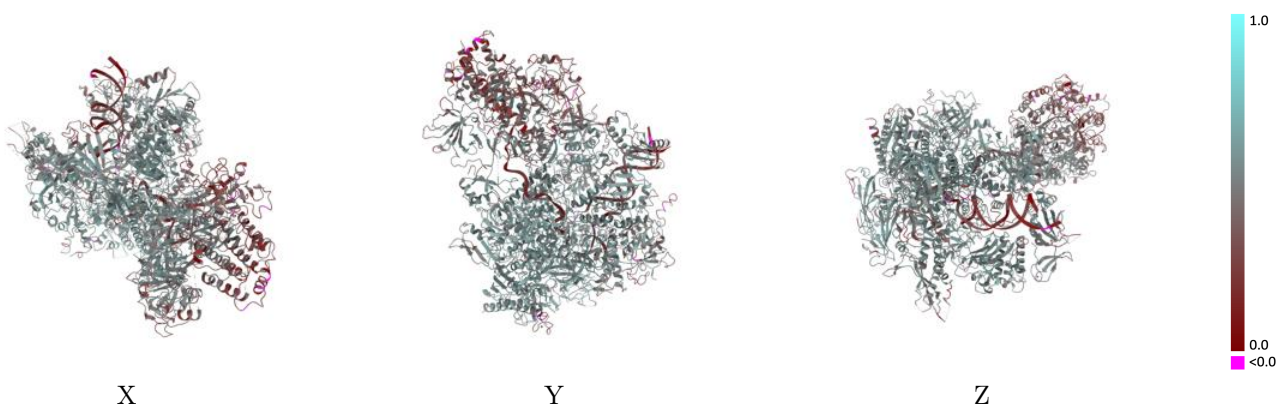
This section contains information regarding the fit between EMDB map EMD-31305 and PDB model 7EU0. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



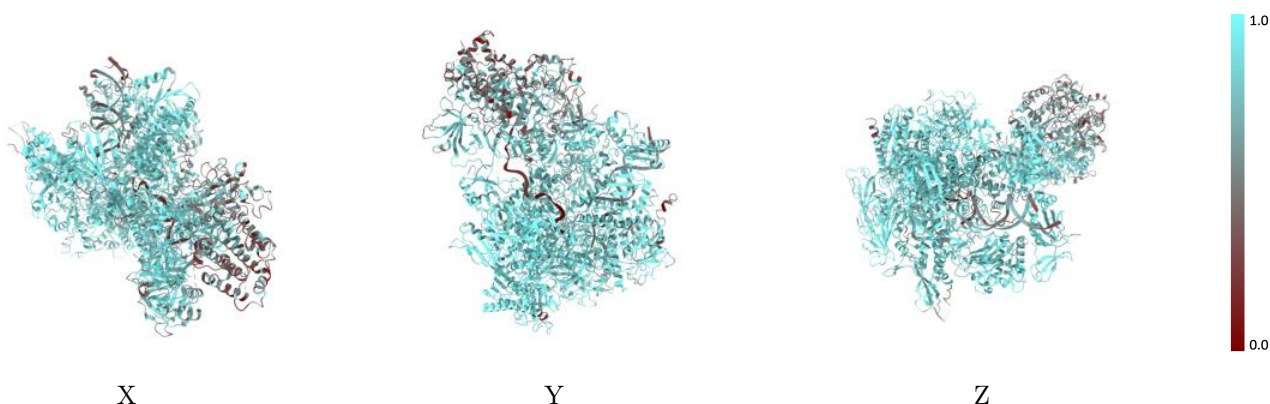
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



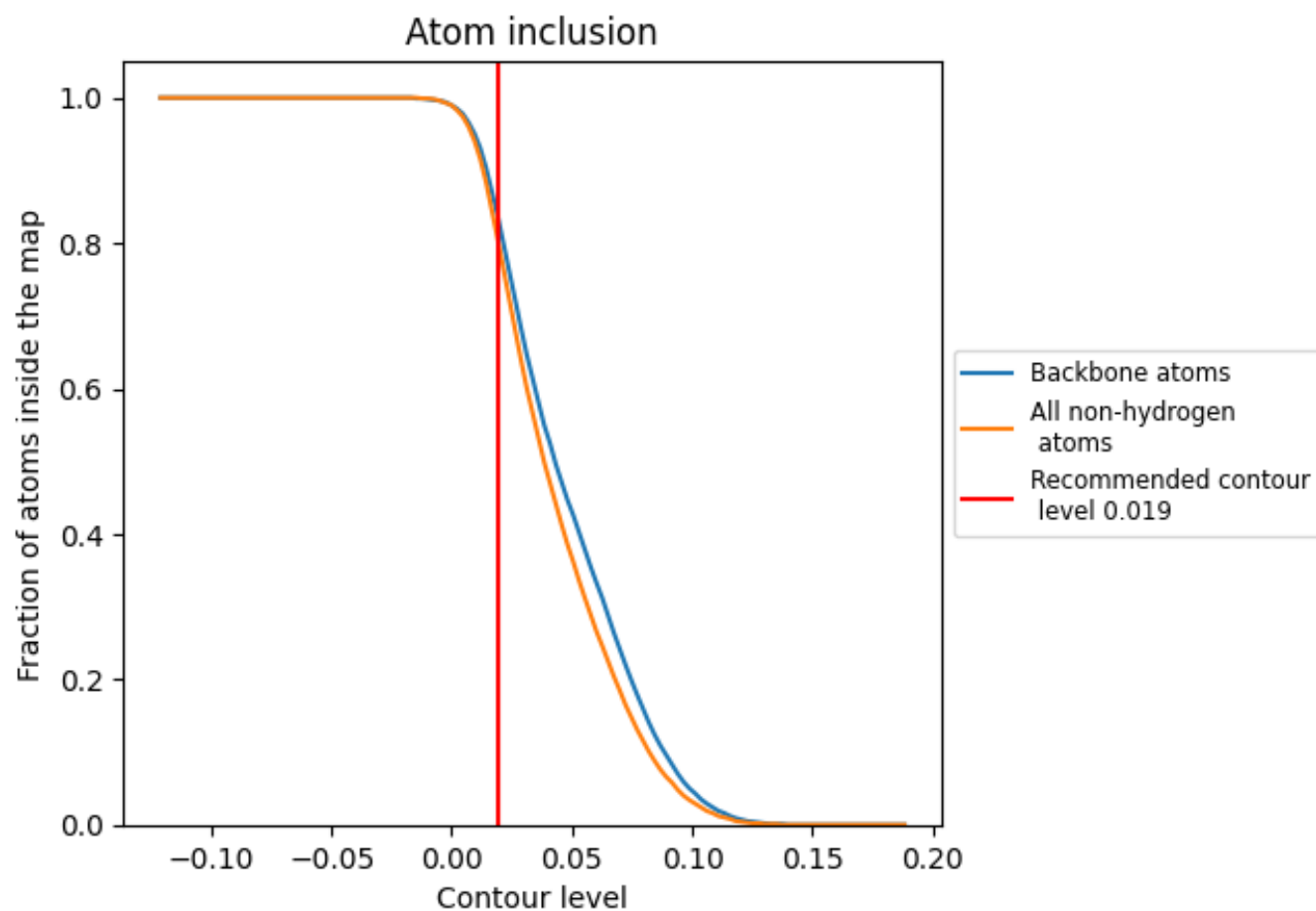
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.019).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8080	 0.4870
A	 0.8540	 0.5240
B	 0.8950	 0.5420
C	 0.8810	 0.5240
E	 0.8710	 0.5010
F	 0.7840	 0.4820
H	 0.8840	 0.5250
I	 0.8300	 0.4990
J	 0.9330	 0.5660
K	 0.9250	 0.5620
L	 0.8960	 0.5160
M	 0.6770	 0.4160
N	 0.5270	 0.1950
O	 0.4320	 0.2660
Q	 0.5790	 0.2560
R	 0.8050	 0.4250

