



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:07 AM UTC

PDB ID : 7BOD / pdb_00007bod
EMDB ID : EMD-12239
Title : Bacterial 30S ribosomal subunit assembly complex state M (body domain)
Authors : Schedlbauer, A.; Iturrioz, I.; Ochoa-Lizarralde, B.; Diercks, T.; Lopez-Alonso, J.; Kaminishi, T.; Capuni, R.; Astigarraga, E.; Gil-Carton, D.; Fucini, P.; Connell, S.R.
Deposited on : 2021-01-25
Resolution : 2.88 Å (reported)
Based on initial model : 4YBB

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
Mogul : 2022.3.0, CSD as543be (2022)
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

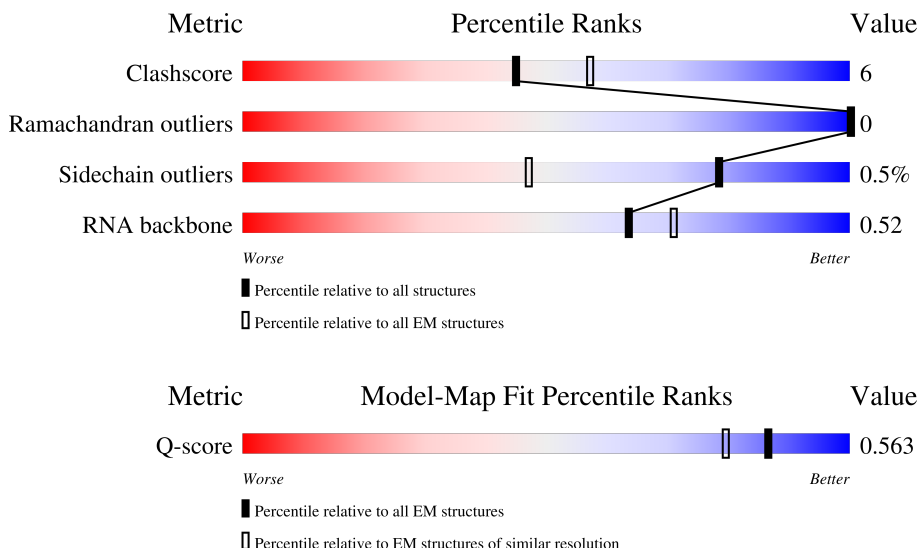
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.88 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	12111 (2.38 - 3.38)

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	1542	
2	D	206	
3	E	167	

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Mol	Chain	Length	Quality of chain
4	F	135	
5	H	130	
6	K	129	
7	L	124	
8	O	89	
9	P	82	
10	Q	84	
11	R	75	
12	T	87	
13	U	71	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 33389 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 RNA chain called 16S rRNA (body domain of 30S subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1078	Total	C	N	O	P	0	0
			23172	10337	4269	7488	1078		

- Molecule 2 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 4 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 6 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 7 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 8 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 9 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 10 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 11 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 12 is a protein called 30S ribosomal protein S20.

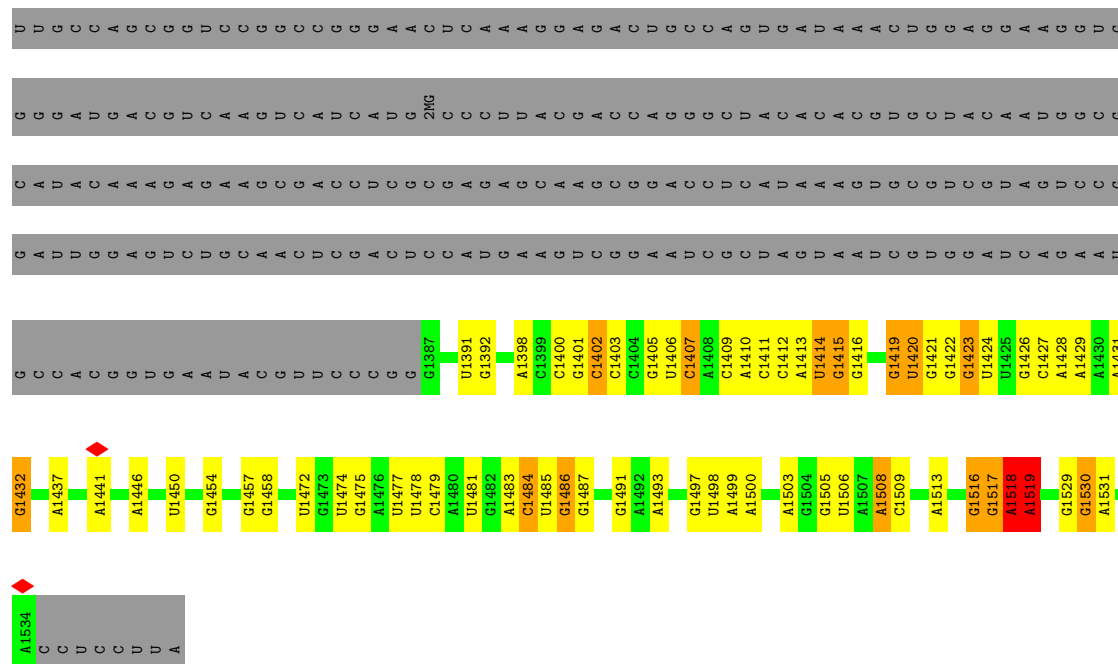
Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 13 is a protein called 30S ribosomal protein S21.

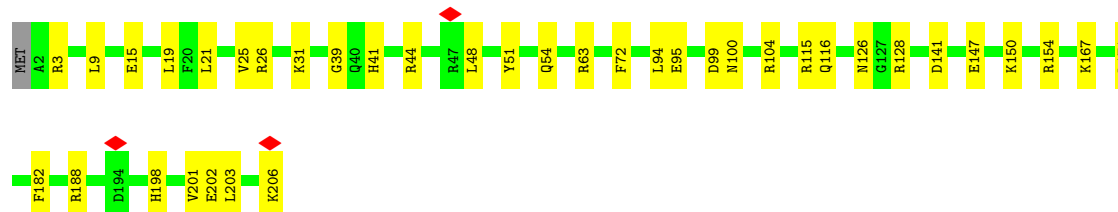
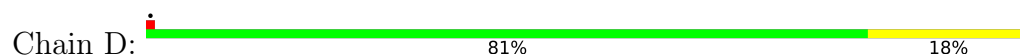
Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	52	Total	C	N	O	S	0	0
			430	269	89	71	1		

- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

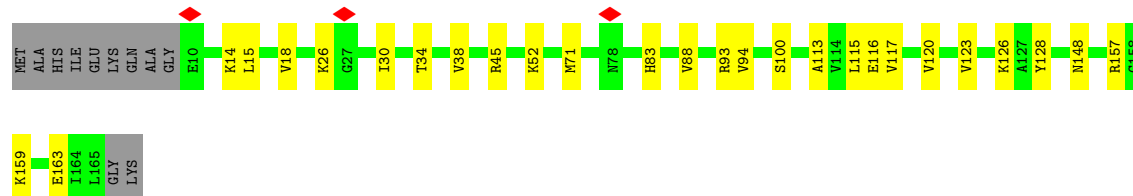
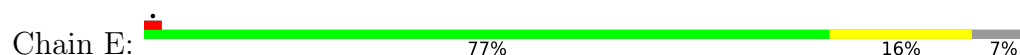
Mol	Chain	Residues	Atoms		AltConf
14	A	101	Total	Mg	0
			101	101	



- Molecule 2: 30S ribosomal protein S4



- Molecule 3: 30S ribosomal protein S5



- Molecule 4: 30S ribosomal protein S6



THR
ALA
ASP
ASP
GLU
ALA
ALA
GLY
ASP
SER
GLU
GLU
GLU
GLU

- Molecule 5: 30S ribosomal protein S8

Chain H:  76% 23%

MET S2 A8 D9 M10 L11 T12 R13 S14 T14 ARG R15 Q18 M27 P28 S29 E47 P57 L61 K64 Q67 G68 K69 V72 I75 Q76 R77 V78 S79 L99 V103 V104 S105 G109 V110 M111 A116 T125 T126 V129 A130

- Molecule 6: 30S ribosomal protein S11

Chain K:  8% 62% 29% 9%

MET ALA LYS PRO ILE ARG ALA ARG LYS VAL R13 K14 Q15 V16 S17 D18 G19 V20 A21 H22 I31 V32 T33 I34 T35 D36 G39 N40 A41 A45 T46 R56 T59 P60 F61 A62 V65 A66 A67 C70 A71 D72 I79 L82 E83 V84 M85 V86 K87 E94 S95 T96 I97 L100 R101 A102 A103 G104 F105 R106 I107 T108 R109 T110 T111 D112 V113 T114 P115 R128 V129

- Molecule 7: 30S ribosomal protein S12

Chain L:  6% 85% 14%

MET A2 R14 K15 V16 E25 P42 K43 M46 C53 N59 T67 V79 G85 R86 V87 K88 D2T89 L90 R94 Y95 H96 L102 D103 V107 K108 D109 Y117 K120 A124

- Molecule 8: 30S ribosomal protein S15

Chain O:  76% 22%

MET S2 R17 S24 T25 E26 V27 Q28 V29 L32 H38 E45 H46 K47 L56 M59 R63 Y69 L70 K71 R72 K73 D74 R77 L81 R89

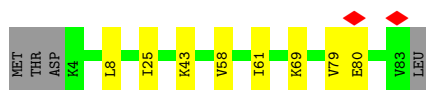
- Molecule 9: 30S ribosomal protein S16

Chain P:  87% 12%

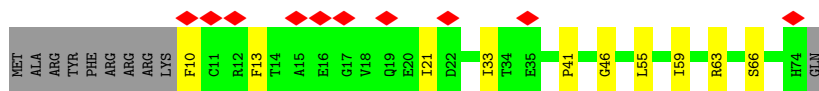
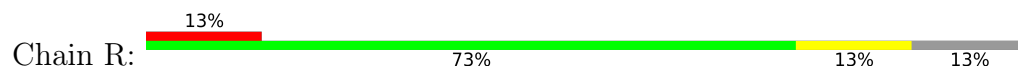
K1 R5 R8 P15 R31 S44 E45 K46 R56 T66 I67 R70 L74 A81 A82

- Molecule 10: 30S ribosomal protein S17

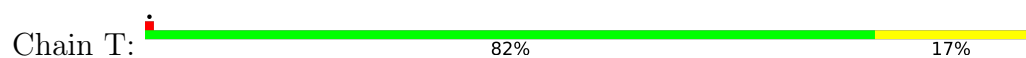
Chain Q:  86% 10% 5%



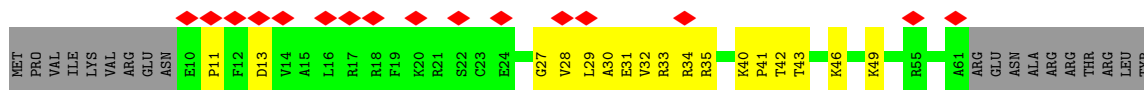
- Molecule 11: 30S ribosomal protein S18



- Molecule 12: 30S ribosomal protein S20



- Molecule 13: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25682	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, UR3, 4OC, MA6, 2MG, 5MC, PSU, D2T, G7M

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	0.26	0/25749	0.27	0/40169
2	D	0.47	0/1665	0.63	1/2227 (0.0%)
3	E	0.61	0/1165	0.75	0/1568
4	F	0.84	0/881	1.06	0/1189
5	H	0.62	0/989	0.79	1/1326 (0.1%)
6	K	0.75	0/893	0.93	0/1205
7	L	0.64	0/960	0.81	0/1286
8	O	0.43	0/722	0.60	0/964
9	P	0.77	0/659	0.97	1/884 (0.1%)
10	Q	0.69	0/657	0.80	0/881
11	R	0.53	0/544	0.66	0/731
12	T	0.24	0/676	0.39	0/895
13	U	0.17	0/436	0.40	0/577
All	All	0.39	0/35996	0.45	3/53902 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	109	GLY	CA-C-O	-5.86	118.23	122.45
2	D	39	GLY	CA-C-O	-5.36	118.29	122.52
9	P	46	LYS	N-CA-C	-5.16	106.66	113.17

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	23172	0	11665	181	0
2	D	1643	0	1707	28	0
3	E	1152	0	1196	17	0
4	F	862	0	864	9	0
5	H	979	0	1031	21	0
6	K	877	0	887	24	0
7	L	957	0	1017	15	0
8	O	714	0	734	14	0
9	P	649	0	666	8	0
10	Q	648	0	691	6	0
11	R	535	0	552	8	0
12	T	670	0	719	11	0
13	U	430	0	458	12	0
14	A	101	0	0	0	0
All	All	33389	0	22187	320	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 6.

All (320) 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)
6:K:35:THR:HG22	6:K:41:ALA:HA	1.39	1.01
1:A:523:A:N6	7:L:89:D2T:OD1	1.96	0.97
1:A:1413:A:H61	1:A:1487:G:H1	1.20	0.89
5:H:14:ILE:HD11	5:H:61:LEU:HD12	1.59	0.85
1:A:1426:G:H1	1:A:1474:U:H3	1.23	0.84
5:H:29:SER:HB3	5:H:57:PRO:HB2	1.60	0.83
3:E:83:HIS:HE1	3:E:148:ASN:H	1.21	0.83
8:O:29:VAL:HG11	8:O:81:LEU:HD21	1.61	0.81
1:A:677:U:H3	1:A:713:G:H22	1.28	0.81
5:H:12:THR:HG22	5:H:15:ARG:HH21	1.46	0.81
8:O:73:LYS:O	8:O:74:ASP:OD1	1.98	0.80
1:A:923:A:H5'	3:E:26:LYS:HD3	1.69	0.76
1:A:376:G:H5''	9:P:5:ARG:HB2	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1406:U:O2	1:A:1517:G:N2	2.22	0.72
6:K:87:LYS:HG3	6:K:114:THR:HA	1.72	0.71
1:A:8:A:N6	2:D:202:GLU:O	2.22	0.71
1:A:683:G:N2	6:K:39:GLY:O	2.25	0.70
11:R:10:PHE:HB2	11:R:46:GLY:HA3	1.74	0.69
1:A:86:G:N3	1:A:87:C:N4	2.41	0.69
1:A:1500:A:H5''	1:A:1508:A:H5'	1.75	0.69
6:K:16:VAL:HG11	6:K:36:ASP:HB3	1.75	0.69
1:A:523:A:C6	7:L:89:D2T:OD1	2.46	0.68
1:A:523:A:N1	7:L:89:D2T:OD1	2.27	0.68
1:A:664:G:H22	1:A:741:G:H1	1.40	0.68
1:A:156:C:H42	1:A:165:G:H1	1.40	0.67
1:A:1409:C:H2'	1:A:1410:A:H8	1.60	0.67
3:E:14:LYS:NZ	3:E:116:GLU:OE1	2.27	0.66
1:A:406:G:H21	2:D:116:GLN:HE22	1.43	0.66
3:E:34:THR:HG22	3:E:52:LYS:HG2	1.78	0.66
1:A:310:G:H5''	9:P:31:ARG:HB2	1.79	0.65
12:T:2:ALA:HB3	12:T:8:LYS:HG2	1.78	0.65
1:A:1457:G:OP1	12:T:34:LYS:NZ	2.26	0.65
1:A:278:G:OP2	10:Q:43:LYS:NZ	2.29	0.65
1:A:1530:G:O6	13:U:46:LYS:NZ	2.28	0.64
1:A:1413:A:N6	1:A:1487:G:H1	1.92	0.64
5:H:15:ARG:NH1	5:H:75:ILE:O	2.31	0.64
6:K:22:HIS:HD2	6:K:85:MET:HB2	1.63	0.64
8:O:69:TYR:HA	8:O:72:ARG:HE	1.63	0.64
1:A:78:A:C6	1:A:79:G:H1'	2.34	0.63
1:A:1409:C:H2'	1:A:1410:A:C8	2.33	0.63
5:H:13:ARG:HD2	5:H:27:MET:HG3	1.81	0.63
13:U:31:GLU:HG3	13:U:34:ARG:HH22	1.64	0.63
1:A:843:U:H2'	1:A:844:G:C8	2.35	0.62
2:D:95:GLU:HA	2:D:100:ASN:ND2	2.15	0.61
2:D:126:ASN:O	2:D:128:ARG:NH1	2.31	0.61
6:K:128:ARG:O	6:K:129:VAL:HG13	2.01	0.61
1:A:36:C:OP1	7:L:120:LYS:NZ	2.33	0.61
7:L:46:ASN:ND2	7:L:89:D2T:SB	2.74	0.61
1:A:401:C:O2'	1:A:621:A:N3	2.33	0.61
1:A:1437:A:H5''	12:T:29:ARG:HH12	1.66	0.61
5:H:67:GLN:OE1	5:H:69:LYS:HE2	2.01	0.60
1:A:1413:A:N1	1:A:1487:G:N2	2.44	0.60
1:A:911:U:OP2	7:L:94:ARG:NH2	2.34	0.60
1:A:823:C:HO2'	5:H:2:SER:N	1.99	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1391:U:H2'	1:A:1392:G:C8	2.37	0.60
3:E:83:HIS:CE1	3:E:148:ASN:H	2.11	0.59
3:E:115:LEU:HD13	3:E:123:VAL:HG11	1.84	0.59
2:D:41:HIS:HB3	2:D:44:ARG:HH21	1.68	0.59
6:K:94:GLU:HA	6:K:97:ILE:HD12	1.84	0.59
1:A:1474:U:H2'	1:A:1475:G:H8	1.68	0.58
1:A:1428:A:H2'	1:A:1429:A:C8	2.39	0.58
2:D:15:GLU:OE2	2:D:63:ARG:NH1	2.36	0.58
6:K:33:THR:HG22	6:K:35:THR:HG23	1.85	0.58
1:A:31:G:O2'	1:A:48:C:N4	2.38	0.57
1:A:559:A:OP2	3:E:126:LYS:NZ	2.38	0.57
2:D:147:GLU:HA	2:D:150:LYS:HG3	1.87	0.57
1:A:77:A:H2'	1:A:78:A:C8	2.40	0.57
8:O:26:GLU:OE2	8:O:77:ARG:NE	2.28	0.57
1:A:212:G:O2'	1:A:213:G:OP1	2.21	0.57
1:A:713:G:H2'	1:A:714:G:C8	2.40	0.56
8:O:56:LEU:HA	8:O:59:MET:HE2	1.88	0.56
1:A:1426:G:H2'	1:A:1427:C:C6	2.41	0.56
6:K:59:THR:HG23	6:K:62:ALA:H	1.70	0.56
13:U:28:VAL:O	13:U:32:VAL:HG23	2.05	0.56
1:A:451:A:H61	1:A:481:G:H5'	1.70	0.56
1:A:1405:G:HO2'	1:A:1518:MA6:HO2'	1.54	0.56
1:A:77:A:H2'	1:A:78:A:H8	1.71	0.55
2:D:95:GLU:HA	2:D:100:ASN:HD22	1.71	0.55
13:U:31:GLU:HG3	13:U:34:ARG:NH2	2.21	0.55
2:D:25:VAL:HG13	2:D:26:ARG:HG3	1.89	0.55
1:A:161:A:N1	1:A:347:G:O2'	2.31	0.55
1:A:696:A:N3	1:A:786:G:O2'	2.36	0.54
1:A:523:A:C2	7:L:88:LYS:HB3	2.42	0.54
1:A:769:G:H4'	1:A:1513:A:H4'	1.89	0.54
10:Q:25:ILE:HD11	10:Q:61:ILE:HD11	1.88	0.54
1:A:67:C:H2'	1:A:68:G:C8	2.43	0.54
8:O:45:GLU:O	8:O:47:LYS:NZ	2.40	0.54
1:A:1477:U:H2'	1:A:1478:U:H6	1.74	0.53
1:A:1423:G:H2'	1:A:1424:U:O4'	2.08	0.53
1:A:126:G:OP1	1:A:605:U:O2'	2.22	0.53
1:A:486:U:H2'	1:A:487:A:H8	1.73	0.53
1:A:1428:A:H2'	1:A:1429:A:H8	1.73	0.53
7:L:42:PRO:HA	7:L:90:LEU:HD23	1.89	0.53
1:A:477:C:H2'	1:A:478:A:C8	2.43	0.53
4:F:49:TYR:OH	11:R:63:ARG:O	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Q:79:VAL:HG12	10:Q:80:GLU:HG2	1.91	0.53
1:A:52:C:H2'	1:A:53:A:C8	2.43	0.53
1:A:427:U:OP2	1:A:428:G:O2'	2.23	0.53
7:L:25:GLU:OE1	7:L:59:ASN:ND2	2.38	0.53
2:D:116:GLN:HE21	2:D:154:ARG:HH12	1.57	0.52
5:H:18:GLN:HE21	5:H:72:VAL:HB	1.73	0.52
4:F:10:VAL:HG11	4:F:18:VAL:HG21	1.90	0.52
1:A:720:C:H5''	11:R:41:PRO:HA	1.91	0.52
1:A:1474:U:H2'	1:A:1475:G:C8	2.45	0.52
4:F:49:TYR:CE1	11:R:66:SER:HA	2.43	0.52
1:A:1410:A:H2'	1:A:1411:C:C6	2.44	0.52
1:A:494:G:O2'	1:A:496:A:H1'	2.10	0.52
10:Q:58:VAL:HB	10:Q:80:GLU:HB2	1.92	0.52
8:O:26:GLU:HG3	8:O:81:LEU:HD22	1.91	0.52
1:A:1530:G:H2'	1:A:1531:A:C8	2.45	0.51
9:P:8:ARG:HH22	9:P:15:PRO:HG3	1.74	0.51
12:T:24:ARG:HH21	12:T:27:MET:HE1	1.75	0.51
1:A:269:C:H2'	1:A:270:A:C8	2.46	0.51
5:H:12:THR:HG22	5:H:15:ARG:NH2	2.22	0.51
5:H:47:GLU:HG2	5:H:64:LYS:HB2	1.92	0.51
5:H:111:MET:HG3	5:H:116:ALA:HB2	1.92	0.51
1:A:298:A:O2'	1:A:299:G:OP1	2.28	0.51
7:L:85:GLY:HA3	7:L:96:HIS:HD2	1.75	0.51
13:U:40:LYS:HG2	13:U:42:THR:HG22	1.93	0.51
8:O:29:VAL:HG23	8:O:63:ARG:HG3	1.91	0.51
9:P:66:THR:HG22	9:P:67:ILE:N	2.26	0.51
1:A:356:A:N3	1:A:368:U:O2'	2.38	0.51
12:T:44:LYS:HE2	12:T:86:LEU:HB2	1.92	0.51
1:A:86:G:H1'	1:A:87:C:H5	1.76	0.51
5:H:11:LEU:HD22	5:H:75:ILE:HD11	1.94	0.50
2:D:198:HIS:HA	2:D:201:VAL:HG22	1.93	0.50
6:K:45:ALA:HB3	6:K:70:CYS:HB2	1.93	0.50
1:A:1415:G:H3'	1:A:1416:G:H8	1.76	0.50
1:A:1518:MA6:N6	1:A:1519:MA6:H103	2.27	0.50
1:A:352:C:O2'	1:A:354:G:OP1	2.19	0.50
1:A:475:C:H2'	1:A:476:U:C6	2.47	0.50
9:P:44:SER:C	9:P:46:LYS:H	2.19	0.50
2:D:116:GLN:NE2	2:D:154:ARG:HH12	2.08	0.50
1:A:1420:U:H2'	1:A:1421:G:C8	2.46	0.50
5:H:10:MET:HB2	5:H:27:MET:HE3	1.94	0.50
6:K:67:ALA:HB2	6:K:96:THR:HG23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1516:2MG:N2	1:A:1519:MA6:OP2	2.36	0.50
1:A:171:A:H2'	1:A:172:A:C8	2.47	0.49
4:F:4:TYR:CE2	4:F:71:ILE:HG13	2.47	0.49
1:A:1485:U:O2'	1:A:1486:G:H5''	2.12	0.49
1:A:390:U:H2'	1:A:391:G:C8	2.48	0.49
1:A:410:G:OP2	2:D:31:LYS:NZ	2.44	0.49
6:K:106:ARG:HH21	6:K:108:THR:HG22	1.77	0.49
1:A:252:U:O4	1:A:253:A:N6	2.45	0.49
1:A:475:C:H2'	1:A:476:U:H6	1.78	0.49
1:A:685:G:O2'	1:A:686:U:O5'	2.27	0.49
1:A:1402:4OC:HM22	1:A:1403:C:H5'	1.95	0.49
1:A:652:U:O4	1:A:752:G:O2'	2.29	0.48
1:A:471:U:O2'	1:A:472:U:OP1	2.30	0.48
1:A:1414:U:O2	1:A:1486:G:O6	2.32	0.48
7:L:79:VAL:HG12	7:L:102:LEU:HD23	1.95	0.48
5:H:105:SER:HB3	5:H:126:ILE:HD11	1.96	0.48
1:A:685:G:H4'	1:A:686:U:OP1	2.13	0.48
1:A:1410:A:H2'	1:A:1411:C:H6	1.77	0.48
6:K:21:ALA:HB2	6:K:82:LEU:HD12	1.95	0.48
1:A:855:U:OP2	1:A:871:U:N3	2.41	0.47
11:R:33:ILE:HD11	11:R:59:ILE:HG21	1.96	0.47
1:A:501:C:H2'	1:A:502:A:C8	2.48	0.47
1:A:1518:MA6:H8	1:A:1518:MA6:OP2	2.13	0.47
6:K:35:THR:HG22	6:K:41:ALA:CA	2.27	0.47
1:A:684:U:O2'	6:K:40:ASN:HB3	2.15	0.47
1:A:80:A:H3'	1:A:81:A:O4'	2.15	0.47
2:D:54:GLN:HG3	2:D:203:LEU:HD13	1.97	0.47
1:A:131:A:O2'	1:A:262:A:N3	2.46	0.47
4:F:38:ARG:HB3	4:F:63:ASN:HB2	1.96	0.46
1:A:96:U:H2'	1:A:97:G:H8	1.80	0.46
1:A:108:G:H5'	1:A:109:A:H5'	1.97	0.46
1:A:1420:U:H2'	1:A:1421:G:H8	1.80	0.46
2:D:171:LEU:HD23	2:D:182:PHE:HA	1.97	0.46
1:A:1412:C:H2'	1:A:1413:A:C8	2.50	0.46
1:A:908:A:H2'	1:A:909:A:C8	2.50	0.46
9:P:8:ARG:NH1	9:P:15:PRO:HB3	2.30	0.46
1:A:212:G:H2'	1:A:213:G:H8	1.81	0.46
1:A:460:A:H61	1:A:472:U:H3	1.63	0.46
4:F:11:HIS:N	4:F:83:ALA:O	2.40	0.46
1:A:718:A:O2'	13:U:35:ARG:NH2	2.48	0.46
1:A:362:G:N1	1:A:365:U:OP2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:U:O2'	1:A:466:A:N7	2.36	0.46
1:A:815:A:N7	1:A:1509:C:O2'	2.46	0.46
1:A:259:G:OP1	12:T:36:TYR:OH	2.32	0.46
1:A:628:G:H2'	1:A:629:A:C8	2.51	0.46
1:A:789:U:N3	1:A:792:A:OP2	2.39	0.46
4:F:43:GLY:HA2	4:F:58:HIS:CE1	2.51	0.46
5:H:79:SER:HB2	5:H:125:ILE:O	2.16	0.46
6:K:85:MET:SD	6:K:111:THR:HB	2.56	0.46
1:A:147:G:H2'	1:A:148:G:C8	2.51	0.46
1:A:202:G:O2'	1:A:468:A:H8	1.99	0.46
13:U:40:LYS:O	13:U:43:THR:OG1	2.29	0.46
1:A:797:C:H2'	1:A:798:U:H6	1.81	0.46
2:D:72:PHE:CE2	2:D:94:LEU:HD11	2.51	0.46
5:H:103:VAL:HG12	5:H:126:ILE:HD12	1.98	0.45
1:A:134:G:H1'	1:A:325:A:C5	2.51	0.45
4:F:2:ARG:HD3	4:F:91:ARG:HD2	1.99	0.45
8:O:47:LYS:HE2	8:O:47:LYS:HB2	1.78	0.45
1:A:20:U:H2'	1:A:21:G:O4'	2.16	0.45
1:A:677:U:O2	1:A:777:A:O2'	2.32	0.45
1:A:429:U:H5'	2:D:9:LEU:HD12	1.98	0.45
2:D:188:ARG:HA	2:D:188:ARG:HD2	1.85	0.45
3:E:45:ARG:HD2	3:E:71:MET:HB2	1.98	0.45
6:K:61:PHE:O	6:K:65:VAL:HG23	2.17	0.45
13:U:27:GLY:O	13:U:30:ALA:N	2.47	0.45
1:A:73:C:O2'	1:A:74:A:O4'	2.34	0.45
1:A:80:A:C2	1:A:81:A:H1'	2.52	0.45
1:A:266:G:H3'	10:Q:69:LYS:HB2	1.97	0.45
2:D:3:ARG:HH11	2:D:115:ARG:HD3	1.82	0.45
2:D:167:LYS:HD2	2:D:167:LYS:N	2.31	0.45
3:E:14:LYS:HG2	3:E:113:ALA:HB1	1.99	0.45
6:K:14:LYS:HA	6:K:14:LYS:HD2	1.73	0.45
1:A:86:G:H21	1:A:87:C:H42	1.64	0.45
1:A:131:A:H2'	1:A:132:C:C6	2.52	0.44
1:A:324:G:N2	1:A:327:A:OP2	2.49	0.44
2:D:51:TYR:HA	2:D:54:GLN:HE21	1.82	0.44
1:A:212:G:H2'	1:A:213:G:C8	2.52	0.44
1:A:371:A:H2'	1:A:372:C:O4'	2.16	0.44
1:A:685:G:HO2'	1:A:686:U:C5'	2.27	0.44
1:A:410:G:H2'	1:A:429:U:C4	2.53	0.44
5:H:77:ARG:NH2	5:H:79:SER:O	2.50	0.44
1:A:797:C:H2'	1:A:798:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1427:C:H2'	1:A:1428:A:H8	1.82	0.44
4:F:16:GLU:O	4:F:19:PRO:HD2	2.17	0.44
5:H:10:MET:O	5:H:14:ILE:HG12	2.18	0.44
6:K:87:LYS:HD3	6:K:113:VAL:HG23	1.99	0.44
7:L:89:D2T:H7	7:L:89:D2T:H4	1.87	0.44
12:T:54:MET:HE3	12:T:54:MET:HB3	1.91	0.44
1:A:745:G:H2'	1:A:746:A:C8	2.52	0.44
1:A:486:U:H2'	1:A:487:A:C8	2.53	0.43
1:A:719:C:OP2	1:A:720:C:N4	2.42	0.43
1:A:890:G:O2'	1:A:906:A:N6	2.51	0.43
11:R:59:ILE:O	11:R:63:ARG:HG3	2.18	0.43
1:A:864:A:H2'	1:A:865:A:C8	2.54	0.43
2:D:126:ASN:HD21	2:D:141:ASP:HA	1.82	0.43
8:O:28:GLN:O	8:O:32:LEU:HD23	2.18	0.43
1:A:212:G:HO2'	1:A:213:G:P	2.39	0.43
13:U:29:LEU:O	13:U:33:ARG:HG2	2.17	0.43
1:A:17:U:H2'	1:A:18:C:C6	2.53	0.43
1:A:1484:C:N4	1:A:1485:U:O4	2.52	0.43
6:K:100:LEU:C	6:K:102:ALA:N	2.77	0.43
1:A:180:U:H2'	1:A:181:A:H5'	2.01	0.43
1:A:720:C:H2'	1:A:721:G:C8	2.53	0.43
3:E:115:LEU:HB3	3:E:120:VAL:CG2	2.49	0.43
5:H:8:ALA:O	5:H:12:THR:HG23	2.18	0.43
5:H:75:ILE:CD1	5:H:129:VAL:HG22	2.48	0.43
7:L:107:VAL:HG23	7:L:117:TYR:HB3	2.00	0.43
3:E:157:ARG:NH1	5:H:99:LEU:O	2.49	0.43
9:P:56:ARG:HD2	9:P:56:ARG:HA	1.63	0.43
13:U:40:LYS:HG3	13:U:41:PRO:HD2	2.01	0.43
13:U:49:LYS:HD2	13:U:49:LYS:HA	1.89	0.43
1:A:96:U:H2'	1:A:97:G:C8	2.53	0.43
1:A:196:A:HO2'	1:A:221:C:HO2'	1.63	0.43
1:A:436:C:H2'	1:A:437:U:C6	2.54	0.43
2:D:99:ASP:OD1	2:D:100:ASN:N	2.51	0.43
1:A:324:G:N1	1:A:327:A:OP2	2.47	0.43
1:A:6:G:O6	3:E:100:SER:N	2.44	0.43
1:A:555:U:H2'	1:A:556:C:C6	2.54	0.43
1:A:1402:4OC:H6	1:A:1402:4OC:O5'	2.19	0.43
1:A:1431:A:C6	1:A:1432:G:C6	3.07	0.43
12:T:8:LYS:O	12:T:12:ILE:HG12	2.18	0.43
1:A:560:A:H4'	1:A:561:U:H5''	2.00	0.42
1:A:921:U:H2'	1:A:922:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1406:U:H2'	1:A:1407:5MC:O4'	2.19	0.42
1:A:82:G:N3	1:A:82:G:H2'	2.34	0.42
1:A:197:A:N1	1:A:220:G:O2'	2.44	0.42
1:A:517:G:N1	1:A:533:A:OP1	2.40	0.42
1:A:757:U:OP1	1:A:822:U:O2'	2.33	0.42
1:A:205:A:H2'	1:A:206:C:O4'	2.19	0.42
2:D:206:LYS:HE3	2:D:206:LYS:HB2	1.74	0.42
1:A:8:A:C6	2:D:206:LYS:HB3	2.55	0.42
9:P:70:ARG:O	9:P:74:LEU:HG	2.19	0.42
3:E:159:LYS:HD3	3:E:163:GLU:OE2	2.19	0.42
6:K:84:VAL:HB	6:K:110:ILE:HD12	2.02	0.42
12:T:35:VAL:O	12:T:39:ILE:HG13	2.20	0.42
3:E:38:VAL:HG12	3:E:117:VAL:HG21	2.02	0.42
1:A:62:U:O2'	1:A:379:C:O2	2.37	0.42
1:A:600:A:H2'	1:A:601:G:C8	2.55	0.42
1:A:740:U:OP1	8:O:38:HIS:HE1	2.03	0.42
1:A:751:U:H4'	8:O:24:SER:HA	2.02	0.42
2:D:100:ASN:O	2:D:104:ARG:HG2	2.20	0.42
3:E:15:LEU:HD21	3:E:18:VAL:HG13	2.01	0.42
8:O:25:THR:HB	8:O:70:LEU:HD22	2.00	0.42
1:A:411:A:H4'	1:A:412:A:H5'	2.02	0.42
1:A:464:U:H2'	1:A:466:A:OP2	2.20	0.42
1:A:559:A:H4'	1:A:560:A:H3'	2.02	0.42
1:A:696:A:H2'	1:A:697:U:C6	2.54	0.42
11:R:21:ILE:HG21	11:R:55:LEU:HD23	2.01	0.42
7:L:102:LEU:HB3	7:L:103:ASP:H	1.64	0.42
10:Q:58:VAL:HG12	10:Q:79:VAL:HB	2.01	0.42
1:A:59:A:H5''	1:A:387:U:H5''	2.02	0.41
1:A:163:C:H2'	1:A:164:G:O4'	2.20	0.41
1:A:524:G:H2'	1:A:525:C:C6	2.55	0.41
1:A:779:C:H2'	1:A:780:A:O4'	2.20	0.41
3:E:83:HIS:HE1	3:E:148:ASN:N	2.03	0.41
1:A:95:C:H2'	1:A:96:U:C6	2.56	0.41
1:A:413:G:H1'	1:A:428:G:H21	1.85	0.41
2:D:19:LEU:HB2	2:D:21:LEU:HG	2.03	0.41
11:R:13:PHE:CZ	11:R:55:LEU:HD21	2.55	0.41
3:E:93:ARG:HB2	3:E:128:TYR:HB2	2.03	0.41
1:A:258:G:H5''	12:T:82:GLN:HE21	1.85	0.41
1:A:767:A:H2'	1:A:768:A:O4'	2.21	0.41
1:A:859:G:H2'	1:A:860:A:C8	2.55	0.41
1:A:74:A:H2'	1:A:75:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:U:H5''	1:A:311:C:O2'	2.20	0.41
1:A:384:G:H2'	1:A:385:C:C6	2.56	0.41
1:A:539:A:H2'	1:A:540:G:C8	2.56	0.41
1:A:649:A:H2'	1:A:650:G:O4'	2.21	0.41
1:A:1419:G:O2'	1:A:1420:U:H5'	2.21	0.41
13:U:11:PRO:HB2	13:U:13:ASP:OD1	2.21	0.41
1:A:730:G:C5	1:A:731:G:H1'	2.56	0.41
1:A:1486:G:H2'	1:A:1487:G:O4'	2.21	0.41
2:D:48:LEU:HD12	2:D:48:LEU:HA	1.94	0.41
6:K:84:VAL:HB	6:K:110:ILE:CD1	2.50	0.41
8:O:17:ARG:H	8:O:17:ARG:HG2	1.74	0.41
1:A:1458:G:H5''	12:T:26:SER:HB2	2.03	0.40
7:L:53:CYS:HB2	7:L:67:ILE:HD11	2.04	0.40
1:A:89:U:O2'	1:A:90:C:O5'	2.40	0.40
1:A:841:C:H42	1:A:845:A:H62	1.68	0.40
6:K:31:ILE:HG23	6:K:46:THR:HG22	2.04	0.40
1:A:208:U:O2'	1:A:211:G:O6	2.30	0.40
1:A:56:U:H2'	1:A:57:G:C8	2.56	0.40
1:A:841:C:N4	1:A:845:A:H62	2.19	0.40
6:K:114:THR:HA	6:K:115:PRO:HD3	1.94	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	
2	D	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
3	E	154/167 (92%)	151 (98%)	3 (2%)	0	100	100
4	F	104/135 (77%)	104 (100%)	0	0	100	100
5	H	127/130 (98%)	125 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	K	115/129 (89%)	112 (97%)	3 (3%)	0	100	100
7	L	120/124 (97%)	116 (97%)	4 (3%)	0	100	100
8	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
9	P	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
10	Q	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
11	R	63/75 (84%)	63 (100%)	0	0	100	100
12	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
13	U	50/71 (70%)	47 (94%)	3 (6%)	0	100	100
All	All	1264/1379 (92%)	1238 (98%)	26 (2%)	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	
2	D	172/173 (99%)	172 (100%)	0	100	100
3	E	119/126 (94%)	116 (98%)	3 (2%)	42	72
4	F	92/116 (79%)	91 (99%)	1 (1%)	65	86
5	H	104/105 (99%)	104 (100%)	0	100	100
6	K	90/99 (91%)	90 (100%)	0	100	100
7	L	102/103 (99%)	102 (100%)	0	100	100
8	O	76/77 (99%)	76 (100%)	0	100	100
9	P	65/65 (100%)	65 (100%)	0	100	100
10	Q	74/78 (95%)	73 (99%)	1 (1%)	59	83
11	R	56/65 (86%)	56 (100%)	0	100	100
12	T	65/66 (98%)	65 (100%)	0	100	100
13	U	43/61 (70%)	43 (100%)	0	100	100
All	All	1058/1134 (93%)	1053 (100%)	5 (0%)	78	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	30	ILE
3	E	88	VAL
3	E	94	VAL
4	F	64	VAL
10	Q	8	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	40	GLN
2	D	116	GLN
2	D	126	ASN
2	D	152	GLN
2	D	164	GLN
3	E	78	ASN
3	E	83	HIS
3	E	89	HIS
3	E	97	GLN
3	E	135	ASN
3	E	146	ASN
3	E	148	ASN
4	F	58	HIS
5	H	18	GLN
6	K	22	HIS
6	K	29	ASN
7	L	6	GLN
7	L	73	ASN
7	L	96	HIS
8	O	35	GLN
8	O	38	HIS
8	O	40	GLN
9	P	9	HIS
9	P	26	ASN
9	P	29	ASN
9	P	59	HIS
10	Q	50	ASN
11	R	74	HIS
12	T	3	ASN
12	T	61	GLN
12	T	78	ASN
12	T	82	GLN

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Mol	Chain	Res	Type
12	T	84	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1076/1542 (69%)	193 (17%)	5 (0%)

All (193) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	9	G
1	A	22	G
1	A	39	G
1	A	44	A
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	54	C
1	A	70	U
1	A	71	A
1	A	73	C
1	A	74	A
1	A	75	G
1	A	79	G
1	A	80	A
1	A	81	A
1	A	82	G
1	A	84	U
1	A	85	U
1	A	86	G
1	A	87	C
1	A	89	U
1	A	90	C
1	A	91	U
1	A	92	U
1	A	93	U
1	A	94	G

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Mol	Chain	Res	Type
1	A	95	C
1	A	109	A
1	A	110	C
1	A	116	A
1	A	120	A
1	A	121	U
1	A	128	G
1	A	129	A
1	A	130	A
1	A	131	A
1	A	143	A
1	A	149	A
1	A	151	A
1	A	156	C
1	A	173	U
1	A	177	G
1	A	181	A
1	A	191	G
1	A	197	A
1	A	204	G
1	A	207	C
1	A	208	U
1	A	209	U
1	A	210	C
1	A	211	G
1	A	212	G
1	A	213	G
1	A	220	G
1	A	240	G
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	271	C
1	A	280	C
1	A	289	G
1	A	299	G
1	A	321	A
1	A	327	A
1	A	328	C
1	A	332	G
1	A	344	A

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Mol	Chain	Res	Type
1	A	345	C
1	A	346	G
1	A	348	G
1	A	352	C
1	A	354	G
1	A	356	A
1	A	367	U
1	A	372	C
1	A	392	C
1	A	398	U
1	A	406	G
1	A	411	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	446	G
1	A	456	A
1	A	467	U
1	A	468	A
1	A	472	U
1	A	474	G
1	A	481	G
1	A	482	A
1	A	484	G
1	A	486	U
1	A	495	A
1	A	509	A
1	A	511	C
1	A	512	U
1	A	518	C
1	A	522	C
1	A	527	G7M
1	A	530	G
1	A	547	A
1	A	559	A
1	A	562	U
1	A	564	C
1	A	572	A
1	A	573	A

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Mol	Chain	Res	Type
1	A	576	C
1	A	577	G
1	A	579	A
1	A	619	U
1	A	633	G
1	A	650	G
1	A	653	U
1	A	665	A
1	A	682	G
1	A	686	U
1	A	687	A
1	A	703	G
1	A	718	A
1	A	720	C
1	A	721	G
1	A	723	U
1	A	724	G
1	A	734	G
1	A	755	G
1	A	777	A
1	A	785	G
1	A	792	A
1	A	793	U
1	A	794	A
1	A	815	A
1	A	817	C
1	A	828	U
1	A	832	G
1	A	836	G
1	A	841	C
1	A	842	U
1	A	845	A
1	A	849	G
1	A	864	A
1	A	872	A
1	A	884	U
1	A	885	G
1	A	889	A
1	A	899	C
1	A	901	A
1	A	902	G
1	A	914	A

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Mol	Chain	Res	Type
1	A	923	A
1	A	926	G
1	A	930	C
1	A	1398	A
1	A	1400	C
1	A	1401	G
1	A	1414	U
1	A	1415	G
1	A	1419	G
1	A	1420	U
1	A	1422	G
1	A	1423	G
1	A	1432	G
1	A	1441	A
1	A	1446	A
1	A	1450	U
1	A	1454	G
1	A	1472	U
1	A	1479	C
1	A	1481	U
1	A	1483	A
1	A	1484	C
1	A	1486	G
1	A	1491	G
1	A	1493	A
1	A	1497	G
1	A	1499	A
1	A	1503	A
1	A	1505	G
1	A	1506	U
1	A	1508	A
1	A	1517	G
1	A	1518	MA6
1	A	1519	MA6
1	A	1529	G
1	A	1530	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	212	G
1	A	298	A

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Mol	Chain	Res	Type
1	A	428	G
1	A	471	U
1	A	685	G

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

9 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	G7M	A	527	1	23,26,27	2.61	8 (34%)	34,39,42	1.97	8 (23%)
1	5MC	A	1407	1	19,22,23	1.65	3 (15%)	26,32,35	1.18	3 (11%)
1	UR3	A	1498	1	19,22,23	0.97	0	26,32,35	1.79	2 (7%)
1	2MG	A	1516	1	23,26,27	1.26	4 (17%)	33,38,41	2.15	9 (27%)
1	4OC	A	1402	1	20,23,24	0.76	0	25,32,35	0.94	1 (4%)
1	MA6	A	1519	1	23,26,27	1.53	5 (21%)	33,38,41	2.32	11 (33%)
1	MA6	A	1518	1	23,26,27	1.50	5 (21%)	33,38,41	2.36	14 (42%)
7	D2T	L	89	7	8,9,10	1.03	1 (12%)	6,11,13	1.50	1 (16%)
1	PSU	A	516	1	18,21,22	1.40	3 (16%)	21,30,33	2.09	5 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
1	4OC	A	1402	1	-	1/9/29/30	0/2/2/2
1	MA6	A	1519	1	-	2/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	A	1518	1	-	3/11/29/30	0/3/3/3
7	D2T	L	89	7	-	2/7/12/14	-
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	G7M	C4-N3	6.38	1.48	1.34
1	A	1407	5MC	C5-C4	6.04	1.48	1.44
1	A	527	G7M	C2-N3	5.23	1.45	1.33
1	A	527	G7M	C5-N7	-5.06	1.33	1.39
1	A	527	G7M	C2-N2	4.72	1.45	1.34
1	A	1519	MA6	C5-C4	4.69	1.47	1.39
1	A	1518	MA6	C5-C4	4.54	1.47	1.39
1	A	527	G7M	C5-C6	3.83	1.54	1.43
1	A	516	PSU	C4-N3	-3.01	1.33	1.38
1	A	1516	2MG	C5-C4	3.00	1.47	1.38
1	A	1518	MA6	C5-C6	2.93	1.48	1.41
1	A	516	PSU	C6-C5	2.88	1.38	1.35
1	A	1519	MA6	C5-C6	2.85	1.48	1.41
7	L	89	D2T	O-C	2.82	1.30	1.20
1	A	527	G7M	O6-C6	-2.66	1.18	1.23
1	A	1516	2MG	C6-N1	-2.60	1.34	1.38
1	A	527	G7M	C2-N1	2.56	1.43	1.37
1	A	1407	5MC	C6-C5	2.55	1.38	1.34
1	A	1407	5MC	C6-N1	-2.38	1.34	1.38
1	A	1518	MA6	C8-N7	2.29	1.36	1.31
1	A	1519	MA6	C5-N7	-2.28	1.34	1.39
1	A	1518	MA6	C5-N7	-2.21	1.35	1.39
1	A	527	G7M	C6-N1	2.21	1.43	1.38
1	A	1519	MA6	C4-N9	-2.20	1.33	1.37
1	A	1516	2MG	C5-N7	-2.19	1.34	1.39
1	A	516	PSU	C2-N3	-2.12	1.34	1.37
1	A	1519	MA6	C8-N7	2.11	1.35	1.31
1	A	1518	MA6	C4-N9	-2.04	1.33	1.37
1	A	1516	2MG	C4-N9	-2.01	1.32	1.38

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	UR3	C4-N3-C2	-7.20	118.79	124.58
1	A	1516	2MG	C2-N3-C4	6.89	120.62	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	516	PSU	N1-C2-N3	6.53	122.06	115.17
1	A	1516	2MG	C5-C4-N3	-5.82	119.13	128.39
1	A	1519	MA6	C5-C4-N3	-5.63	118.96	126.72
1	A	1518	MA6	C5-C4-N3	-5.63	118.96	126.72
1	A	527	G7M	C2-N3-C4	4.80	120.56	112.30
1	A	1518	MA6	C9-N6-C6	-4.60	108.81	120.52
1	A	1519	MA6	N3-C4-N9	4.33	134.53	127.17
1	A	1519	MA6	C9-N6-C6	-4.30	109.57	120.52
1	A	1516	2MG	N9-C4-N3	4.26	134.48	125.95
1	A	516	PSU	C4-N3-C2	-4.25	120.52	126.37
1	A	527	G7M	C5-C4-N3	-4.23	120.15	128.15
1	A	1519	MA6	C2-N1-C6	4.21	122.12	111.83
1	A	1518	MA6	C2-N1-C6	4.16	122.00	111.83
1	A	527	G7M	C5-C6-N1	4.16	120.44	111.84
1	A	1518	MA6	N3-C4-N9	4.16	134.24	127.17
1	A	1518	MA6	C4-C5-N7	-4.05	105.95	110.58
1	A	1519	MA6	C4-C5-N7	-3.88	106.15	110.58
1	A	1518	MA6	C2-N3-C4	3.69	120.85	111.83
1	A	1519	MA6	C2-N3-C4	3.64	120.71	111.83
1	A	527	G7M	CN7-N7-C5	3.63	131.32	126.80
1	A	1518	MA6	C10-N6-C6	-3.62	111.31	120.52
1	A	516	PSU	O2-C2-N1	-3.62	119.06	122.79
1	A	1407	5MC	C5-C6-N1	-3.50	119.51	123.31
1	A	1498	UR3	C5-C4-N3	3.49	119.63	115.04
1	A	527	G7M	O6-C6-C5	-3.32	120.61	128.01
1	A	1516	2MG	C6-C5-N7	3.28	136.27	130.29
1	A	1518	MA6	N1-C2-N3	-3.22	123.72	128.58
1	A	527	G7M	C2-N1-C6	-3.21	119.28	125.11
1	A	1519	MA6	N1-C2-N3	-3.19	123.75	128.58
1	A	1519	MA6	C10-N6-C6	-3.11	112.62	120.52
7	L	89	D2T	O-C-CA	-3.02	117.01	124.77
1	A	527	G7M	CN7-N7-C8	-2.89	120.41	124.79
1	A	1518	MA6	C5-N7-C8	2.84	107.92	103.45
1	A	527	G7M	N9-C4-N3	2.79	131.52	125.95
1	A	1519	MA6	C4-N9-C8	2.75	108.62	105.74
1	A	1518	MA6	C4-N9-C8	2.67	108.54	105.74
1	A	1519	MA6	C5-N7-C8	2.65	107.61	103.45
1	A	1519	MA6	N1-C6-N6	2.63	120.06	116.86
1	A	1407	5MC	C5-C4-N3	-2.56	119.13	121.75
1	A	1516	2MG	C4-C5-N7	-2.45	106.79	110.67
1	A	1516	2MG	N1-C2-N2	2.44	119.05	116.56
1	A	1518	MA6	C10-N6-C9	-2.37	108.56	116.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1518	MA6	C6-C5-N7	2.30	137.10	133.43
1	A	1518	MA6	N9-C8-N7	-2.22	110.79	113.94
1	A	1407	5MC	O2-C2-N3	-2.15	118.94	122.33
1	A	1518	MA6	N1-C6-N6	2.14	119.47	116.86
1	A	516	PSU	C5-C6-N1	-2.12	119.19	122.14
1	A	1516	2MG	O6-C6-C5	-2.11	120.96	126.53
1	A	1516	2MG	CM2-N2-C2	-2.10	119.14	123.65
1	A	1516	2MG	N2-C2-N3	-2.08	117.86	120.51
1	A	1402	4OC	C6-C5-C4	2.06	119.49	117.00
1	A	516	PSU	O4'-C1'-C2'	2.00	107.92	105.15

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	527	G7M	O4'-C4'-C5'-O5'
1	A	1518	MA6	O4'-C4'-C5'-O5'
1	A	1518	MA6	C3'-C4'-C5'-O5'
1	A	527	G7M	C3'-C4'-C5'-O5'
1	A	1519	MA6	C5-C6-N6-C10
7	L	89	D2T	CG-CB-SB-CB1
1	A	1402	4OC	C3'-C2'-O2'-CM2
1	A	1518	MA6	C5-C6-N6-C10
1	A	1519	MA6	C4'-C5'-O5'-P
7	L	89	D2T	SB-CB-CG-OD2

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1407	5MC	1	0
1	A	1516	2MG	1	0
1	A	1402	4OC	2	0
1	A	1519	MA6	2	0
1	A	1518	MA6	3	0
7	L	89	D2T	5	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 101 ligands modelled in this entry, 101 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

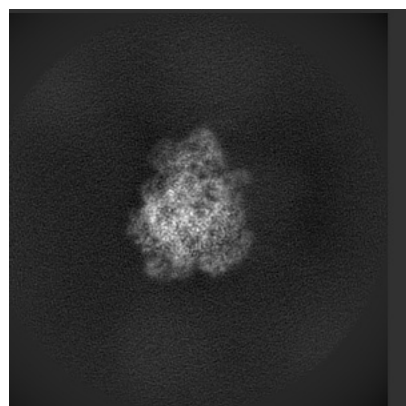
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12239. These allow visual inspection of the internal detail of the map and identification of artifacts.

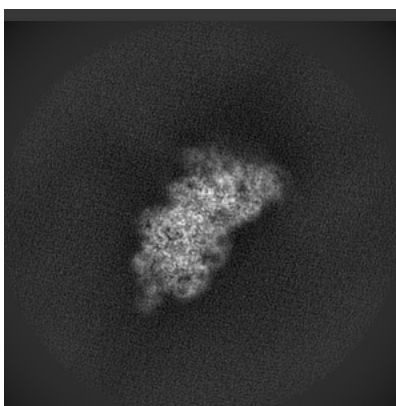
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

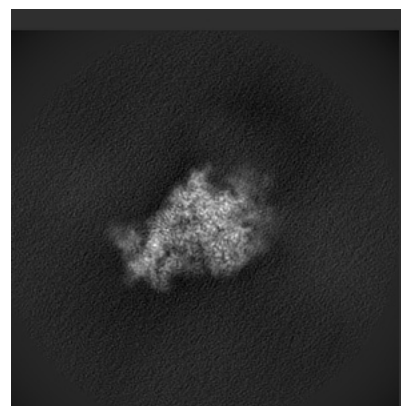
6.1.1 Primary map



X

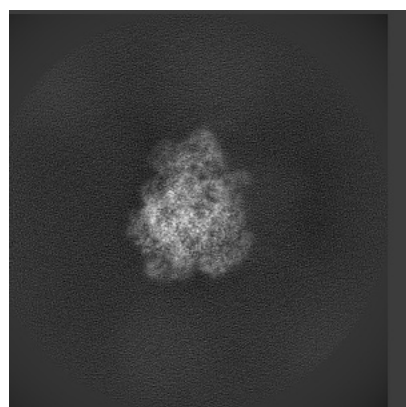


Y

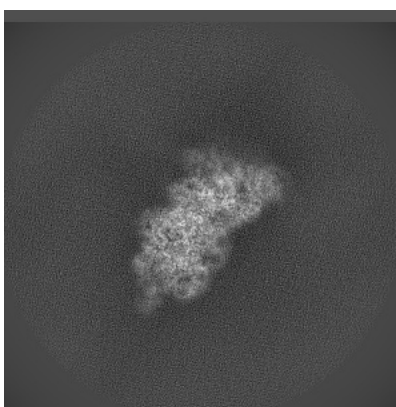


Z

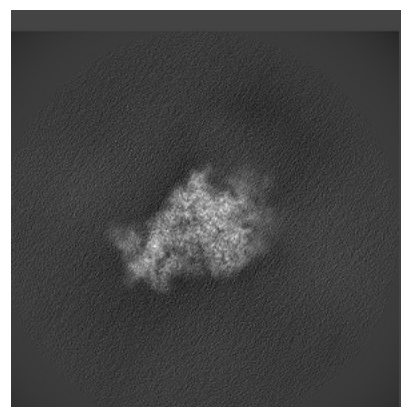
6.1.2 Raw map



X



Y

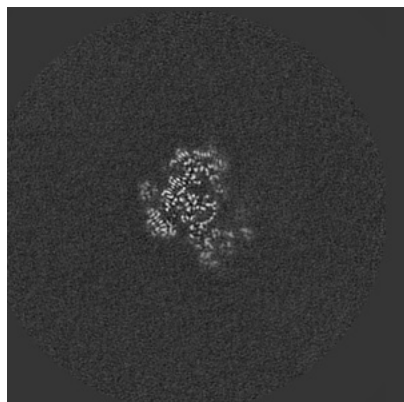


Z

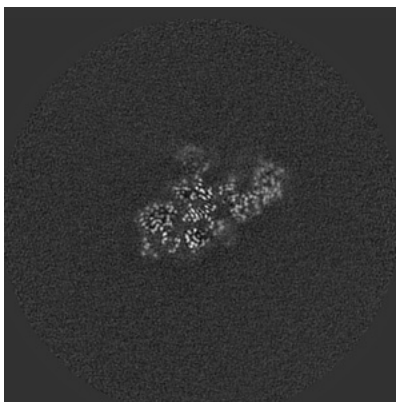
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

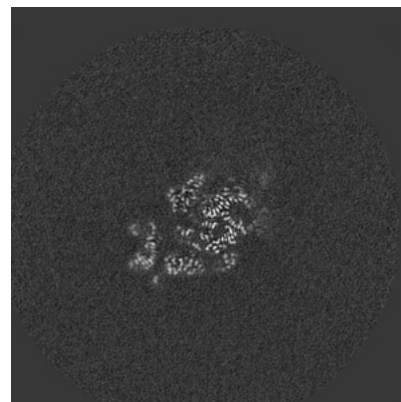
6.2.1 Primary map



X Index: 200

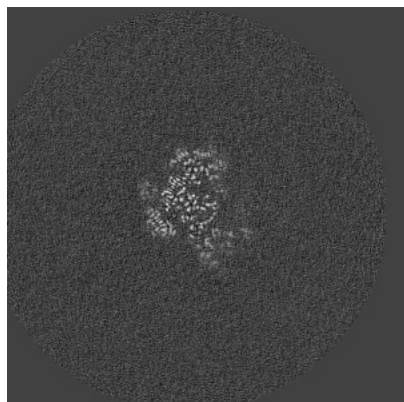


Y Index: 200

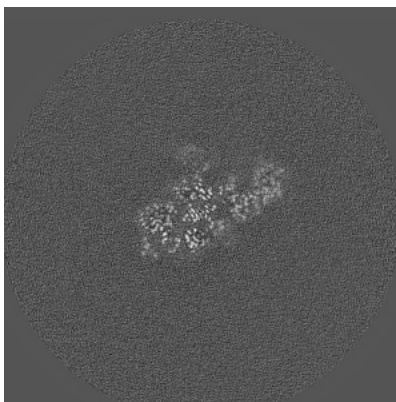


Z Index: 200

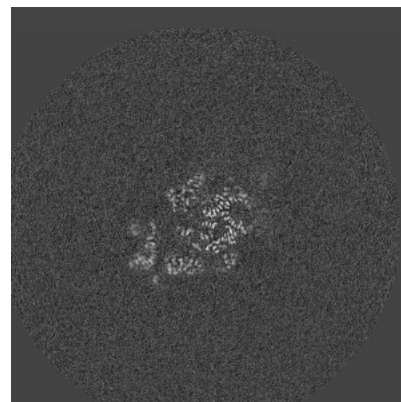
6.2.2 Raw map



X Index: 200



Y Index: 200

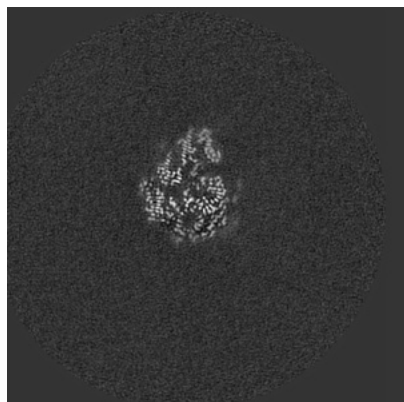


Z Index: 200

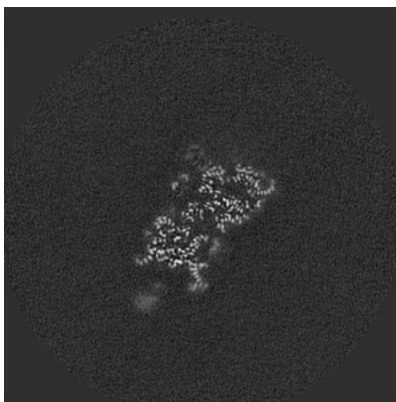
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

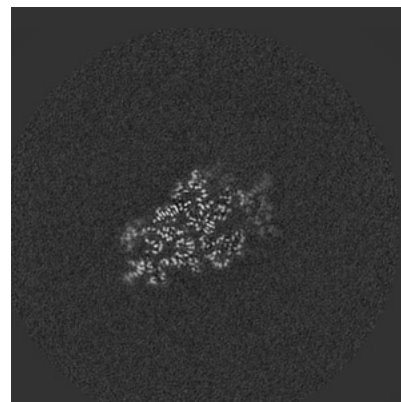
6.3.1 Primary map



X Index: 215

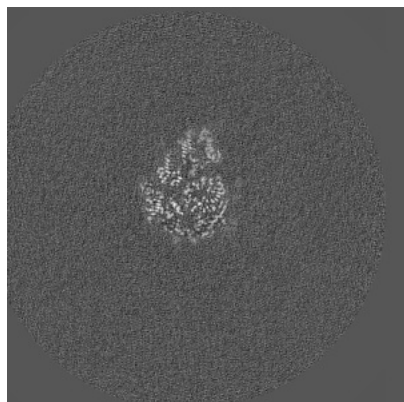


Y Index: 178

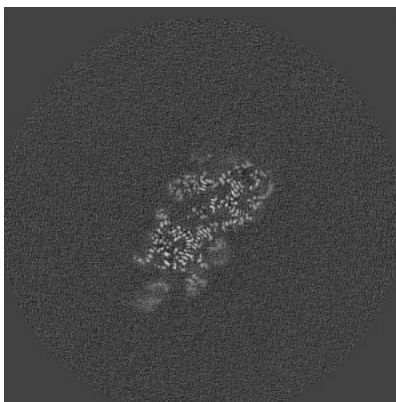


Z Index: 188

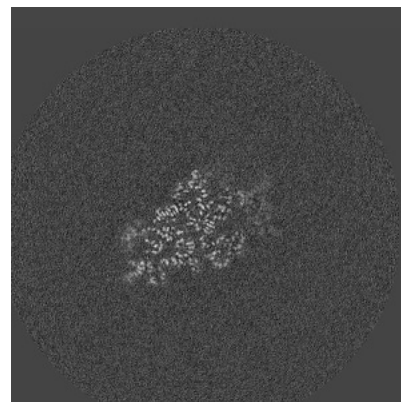
6.3.2 Raw map



X Index: 214



Y Index: 173

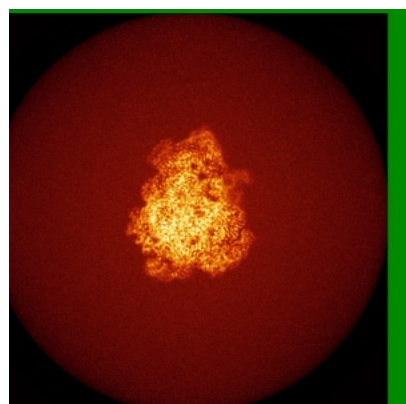


Z Index: 188

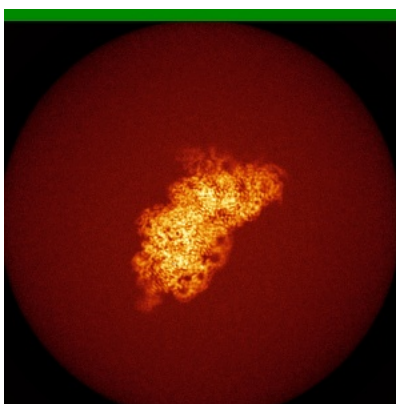
The images above show the largest variance slices of the map in three orthogonal directions.

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

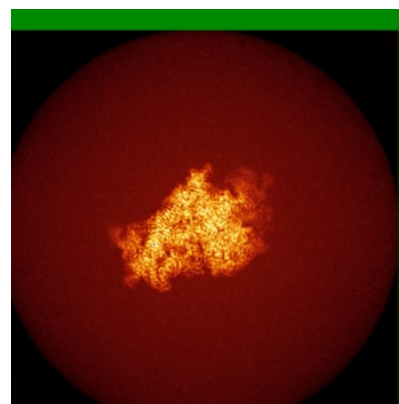
6.4.1 Primary map



X

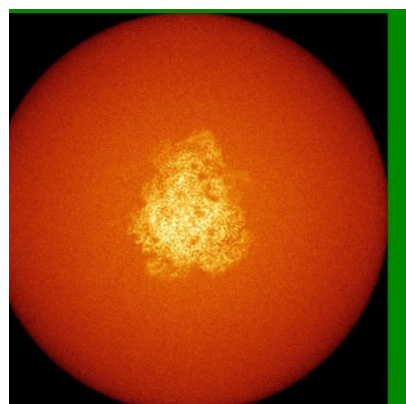


Y

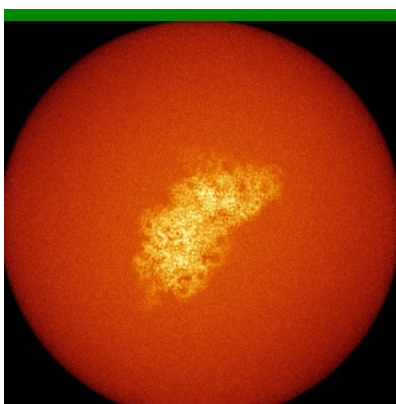


Z

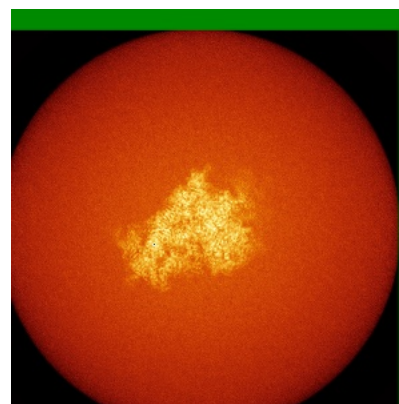
6.4.2 Raw map



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.

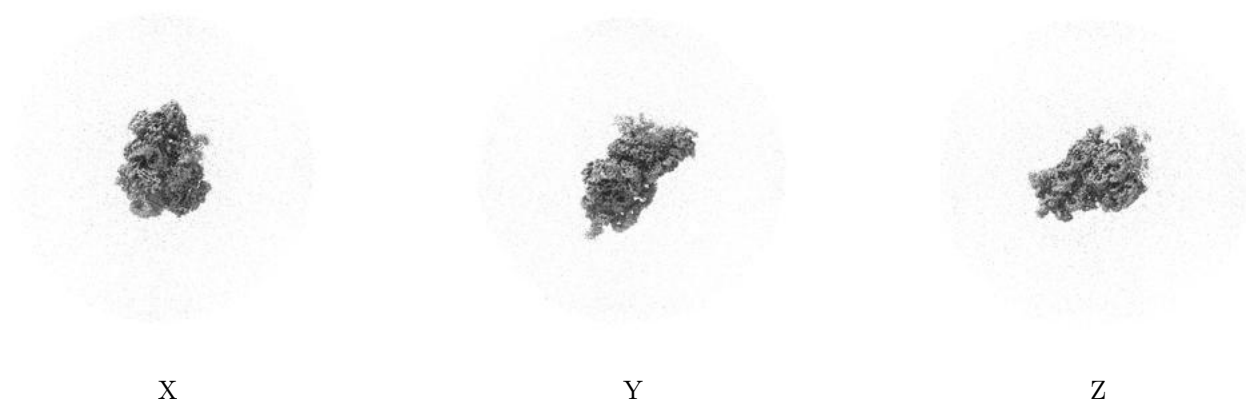
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. 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.

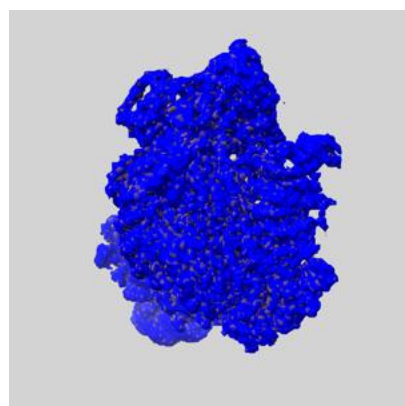
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

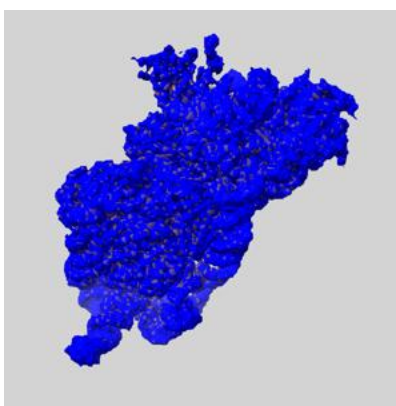
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

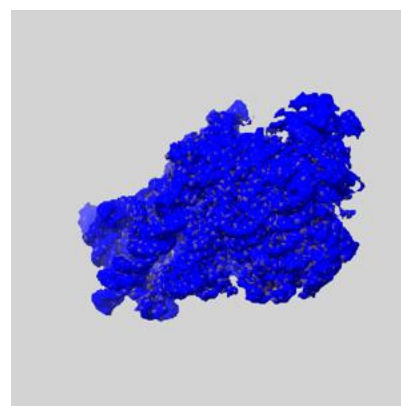
6.6.1 emd_12239_msk_1.map [i](#)



X



Y

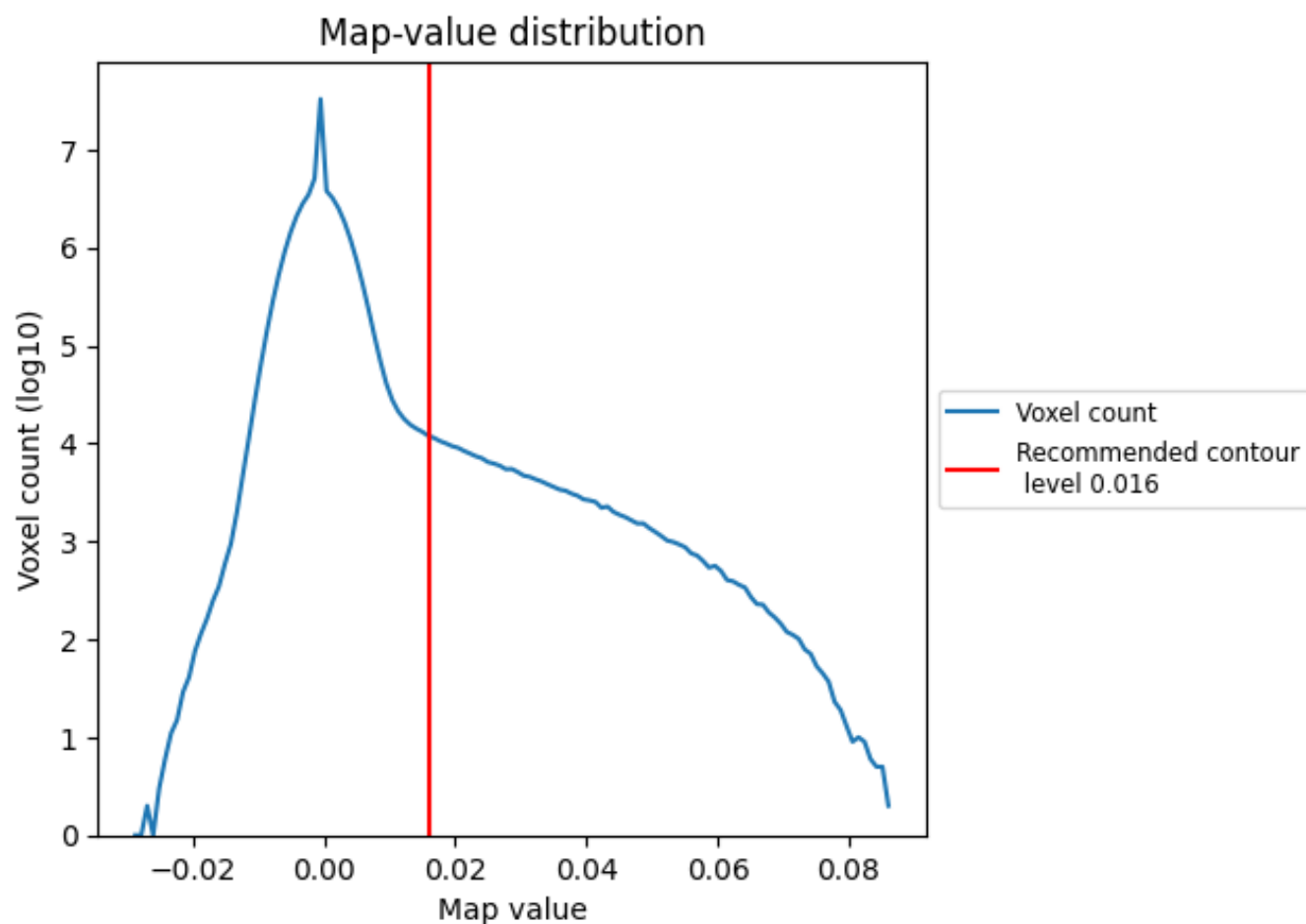


Z

7 Map analysis [i](#)

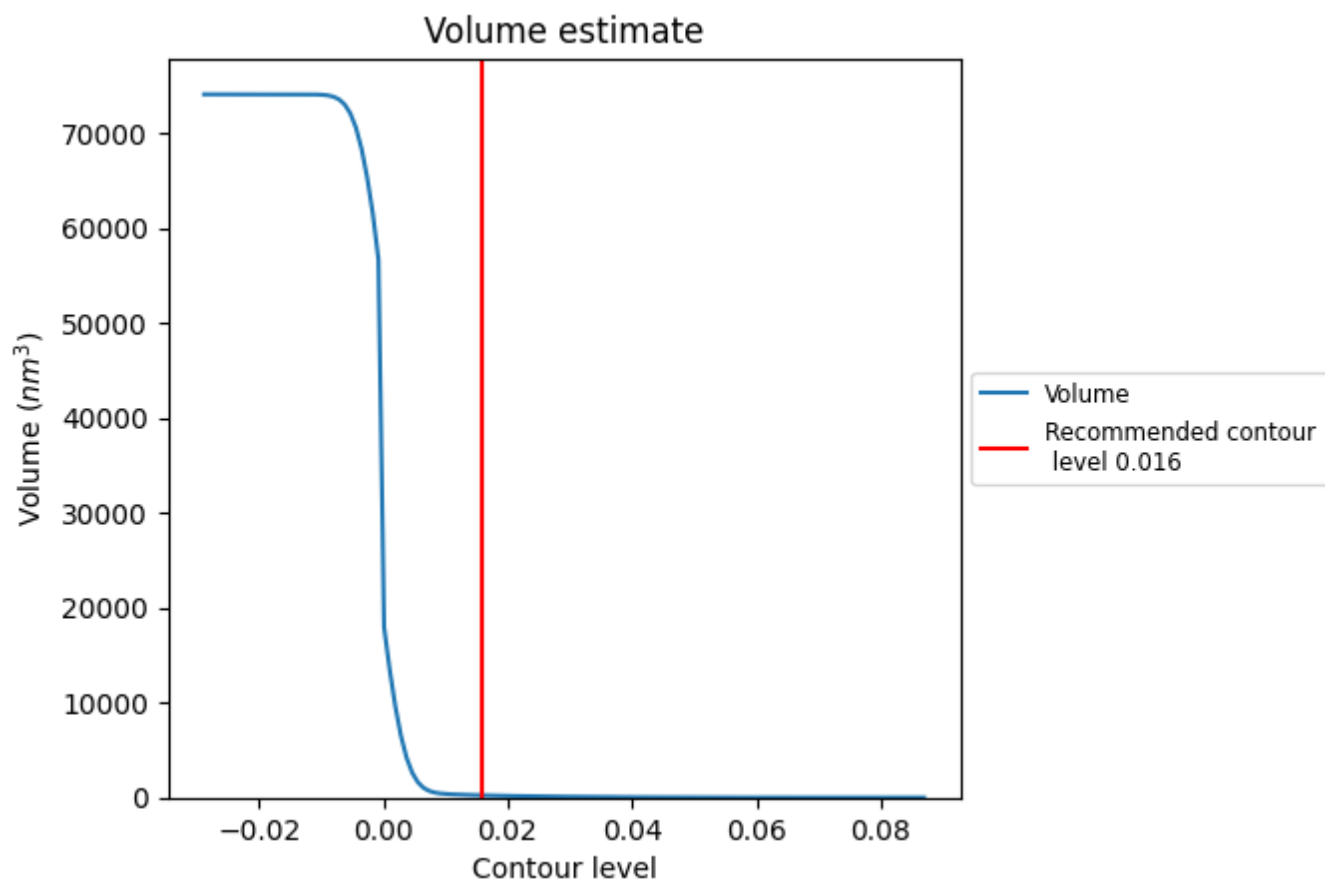
This section contains the results of statistical analysis of the map.

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.

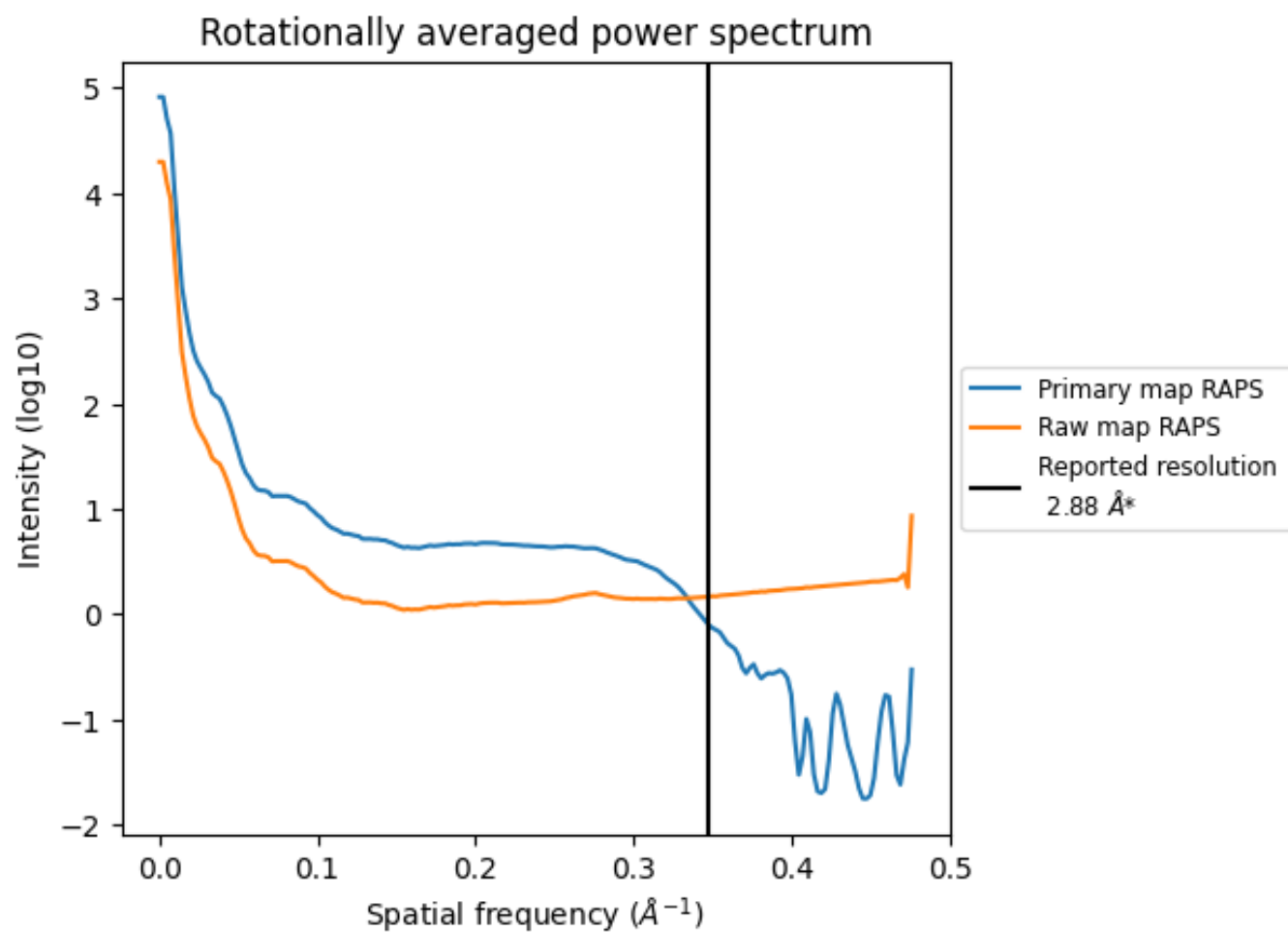
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 232 nm³; this corresponds to an approximate mass of 210 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 ⓘ

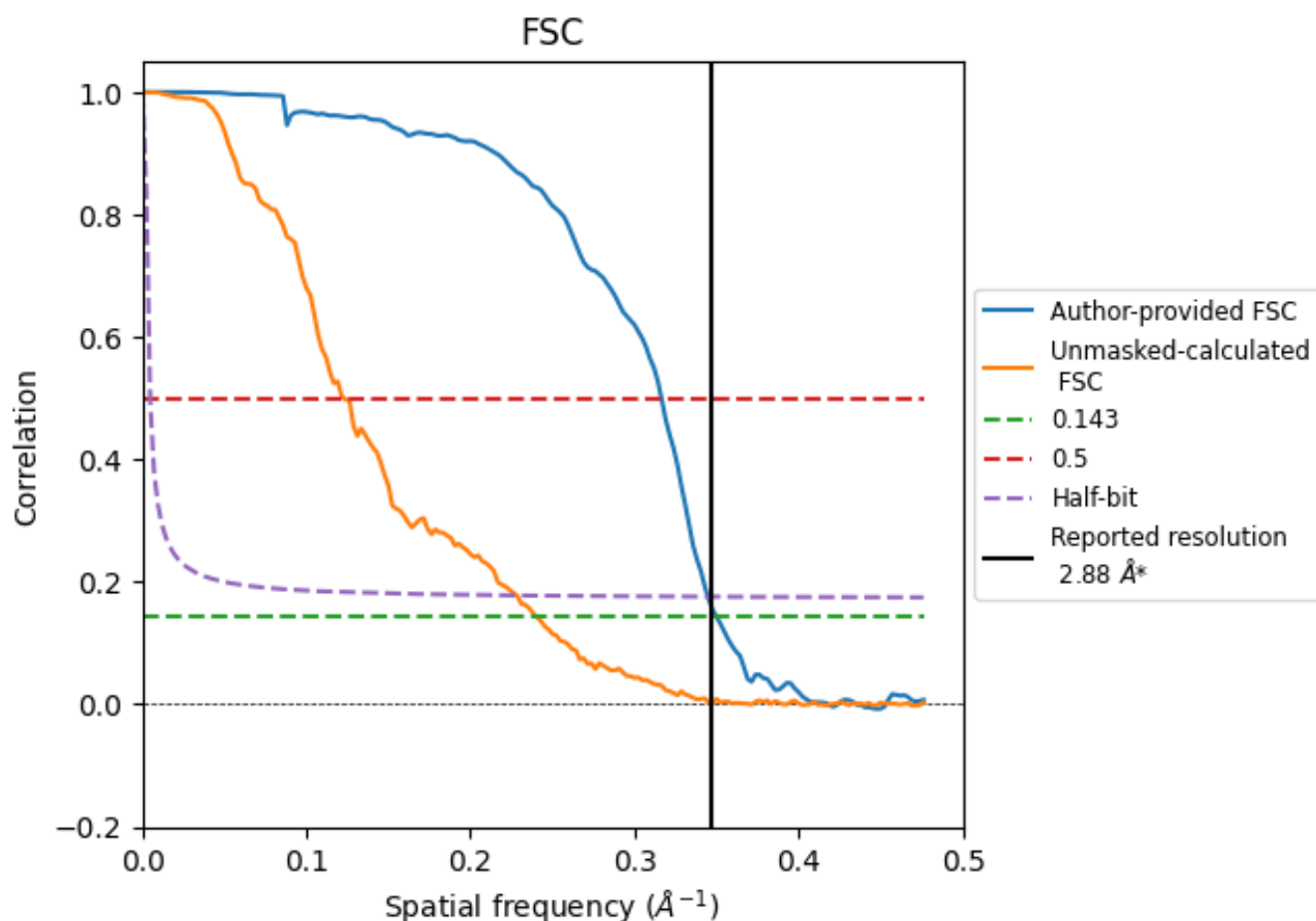


*Reported resolution corresponds to spatial frequency of 0.347 $\text{\AA}^{-1}$

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 0.347 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

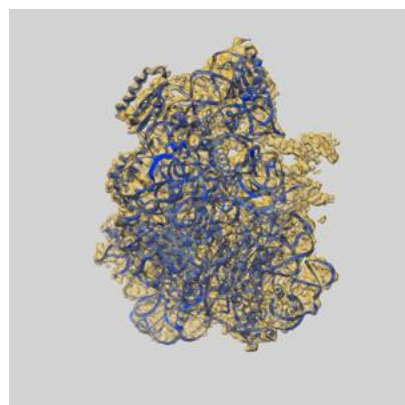
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	2.86	3.16	2.90
Unmasked-calculated*	4.16	8.14	4.38

*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 4.16 differs from the reported value 2.88 by more than 10 %

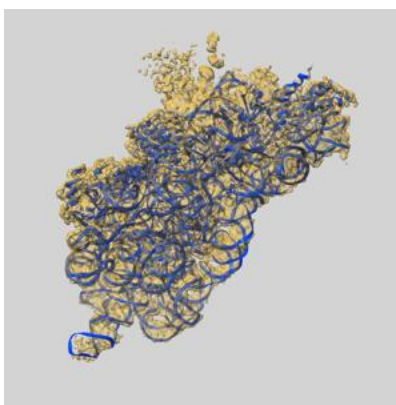
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12239 and PDB model 7BOD. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

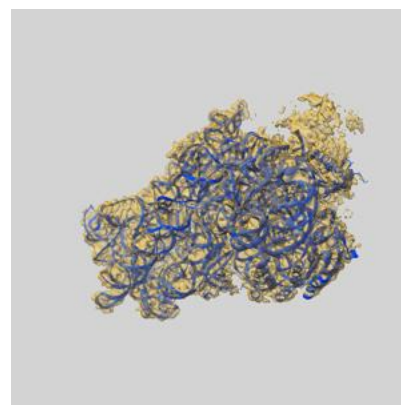
9.1 Map-model overlay [i](#)



X



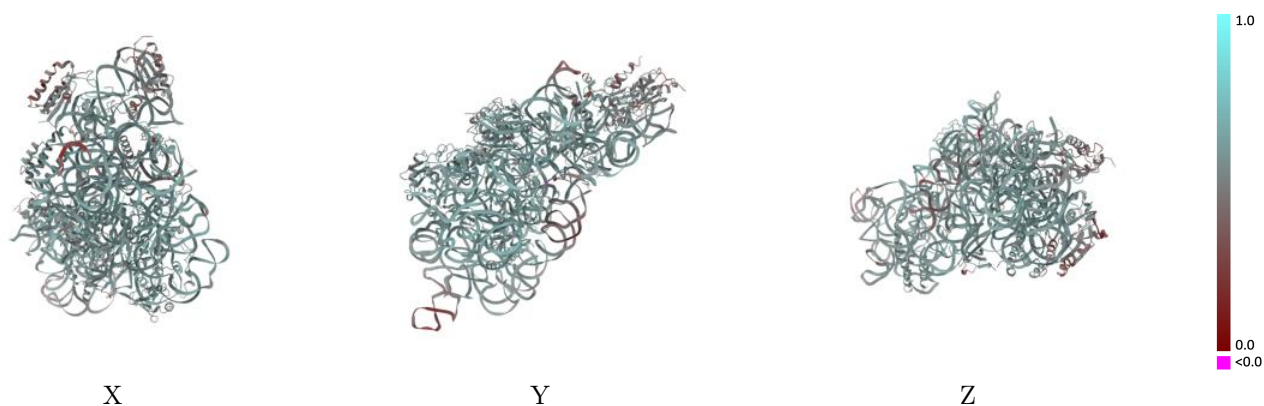
Y



Z

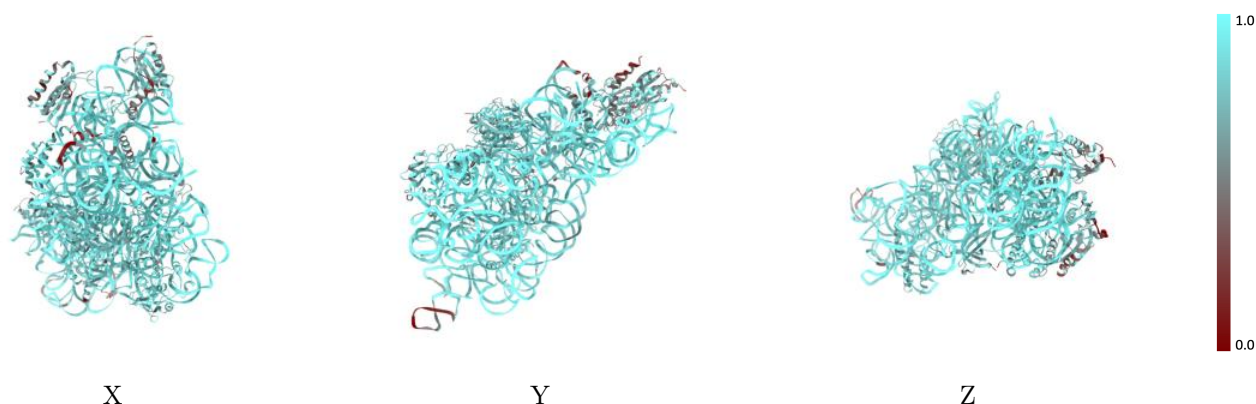
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



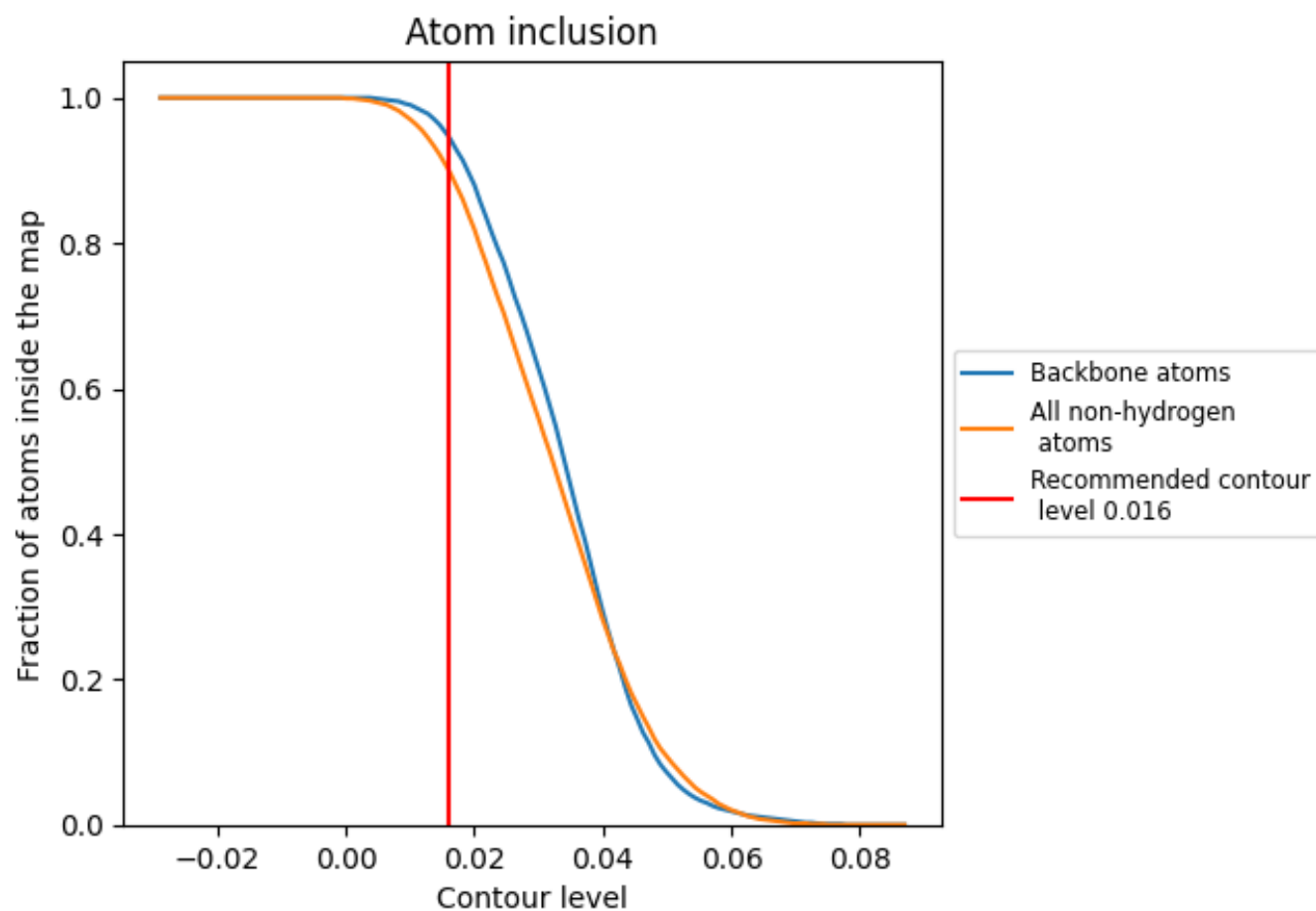
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 90% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.5630
A	 0.9510	 0.5740
D	 0.8370	 0.5690
E	 0.8150	 0.5570
F	 0.6400	 0.4510
H	 0.8190	 0.5580
K	 0.6860	 0.4570
L	 0.8410	 0.5720
O	 0.8260	 0.5430
P	 0.8660	 0.5690
Q	 0.8130	 0.5580
R	 0.7240	 0.5290
T	 0.8580	 0.5640
U	 0.4910	 0.4760

