wwPDB EM Validation Summary Report (i)

Sep 17, 2026 – 03:09 AM EDT

PDB ID	:	8E3O / pdb_00008e3o
EMDB ID	:	EMD-27869
Title	:	E. coli 50S ribosome bound to solithromycin and VM1
Authors	:	Pellegrino, J.; Lee, D.J.; Fraser, J.S.; Seiple, I.B.
Deposited on	:	2022-08-17
Resolution	:	1.99 Å(reported)

This is a wwPDB EM Validation Summary 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 (i) 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 (1)) were used in the production of this report:

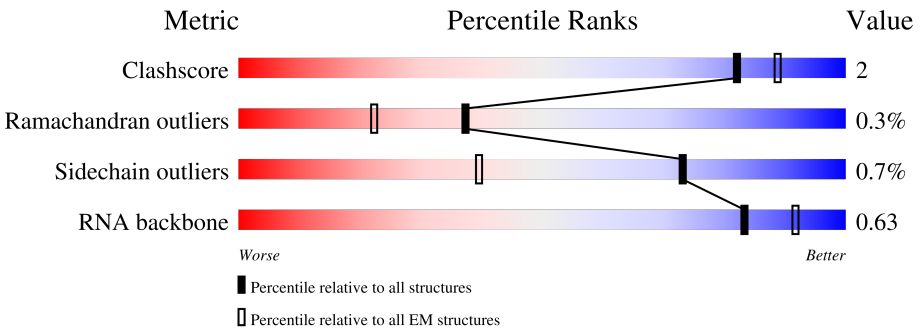
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.50

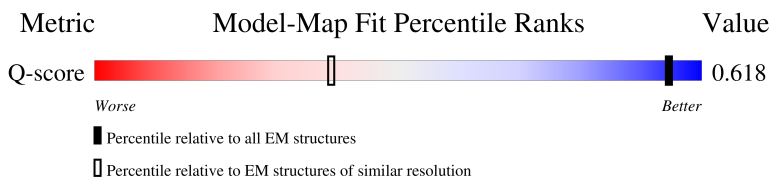
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.99 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	1416 (1.50 - 2.49)

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 <=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	I	2904	8% 79% 19% •
2	J	118	• 86% 14%
3	K	271	86% 14%

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Mol	Chain	Length	Quality of chain
4	L	144	89% 11%
5	M	201	6% 97%
6	N	209	93% 5%
7	O	142	88% 11%
8	P	110	5% 91% 8%
9	Q	56	11% 75% 25%
10	R	46	96%

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 116035 atoms, of which 42142 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	I	2897	93497	27757	31291	11443	20109	2897	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	J	118	3810	1126	1281	464	821	118	0	0

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	K	271	4237	1288	2154	423	365	7	0	0

- Molecule 4 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	L	144	2182	654	1129	207	190	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	M	201	3170	974	1618	283	290	5	0	0

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	N	209	3182	979	1617	288	294	4	0	0

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	O	142	2291	714	1162	212	199	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	P	110	1775	532	918	166	156	3	0	0

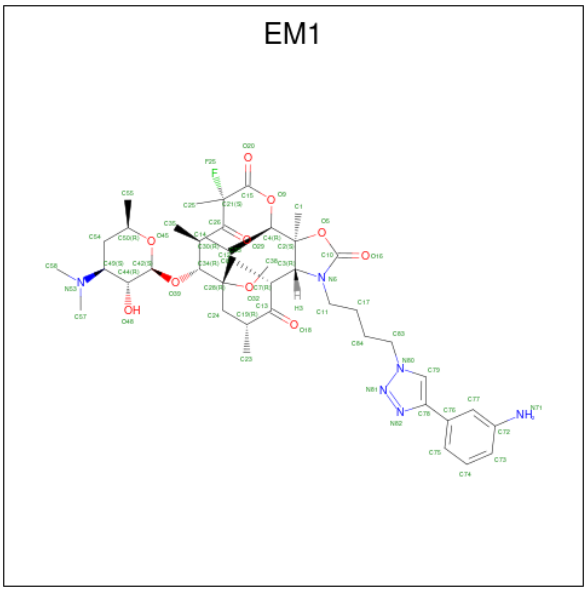
- Molecule 9 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	Q	56	898	269	454	94	80	1	0	0

- Molecule 10 is a protein called 50S ribosomal protein L34.

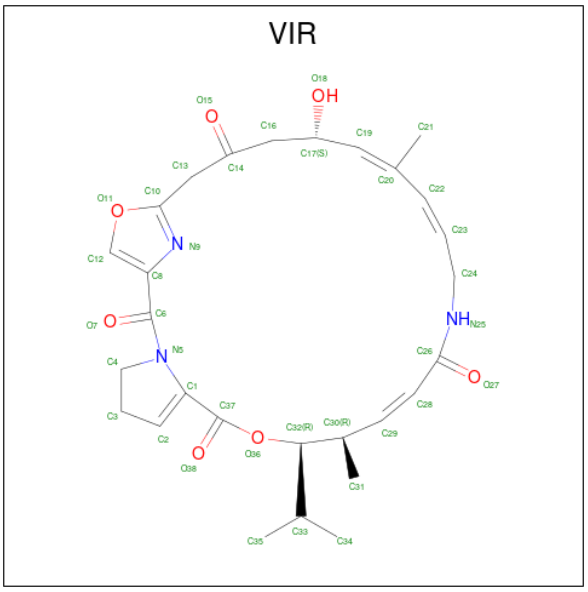
Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	R	46	794	228	417	90	57	2	0	0

- Molecule 11 is (3aS,4R,7S,9R,10R,11R,13R,15R,15aR)-1-{4-[4-(3-aminophenyl)-1H-1,2,3-triazol-1-yl]butyl}-4-ethyl-7-fluoro-11-methoxy-3a ,7,9,11,13,15-hexamethyl-2,6,8,14-tetraoxotetradecahydro-2H-oxacyclotetradecino[4,3-d][1,3]oxazol-10-yl 3,4,6-trideoxy-3-(dimethylamino)-beta-D-xylo-hexopyranoside (CCD ID: EM1) (formula: $C_{43}H_{65}FN_6O_{10}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	H	N	O	
11	I	1	126	43	1	66	6	10	0

- Molecule 12 is VIRGINIAMYCIN M1 (CCD ID: VIR) (formula: $C_{28}H_{35}N_3O_7$) (labeled as "Ligand of Interest" by depositor).



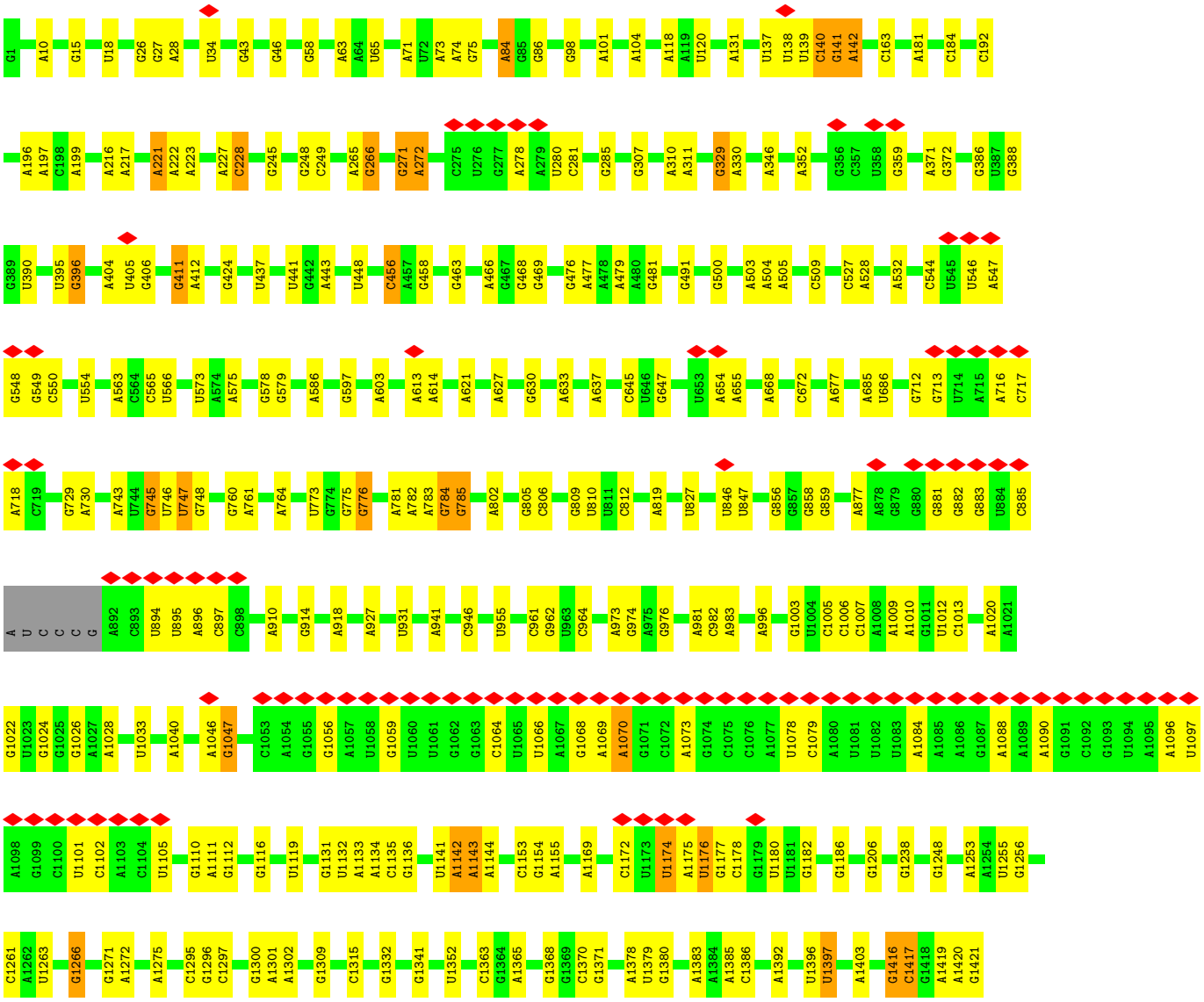
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O		
12	I	1	73	28	35	3	7		0

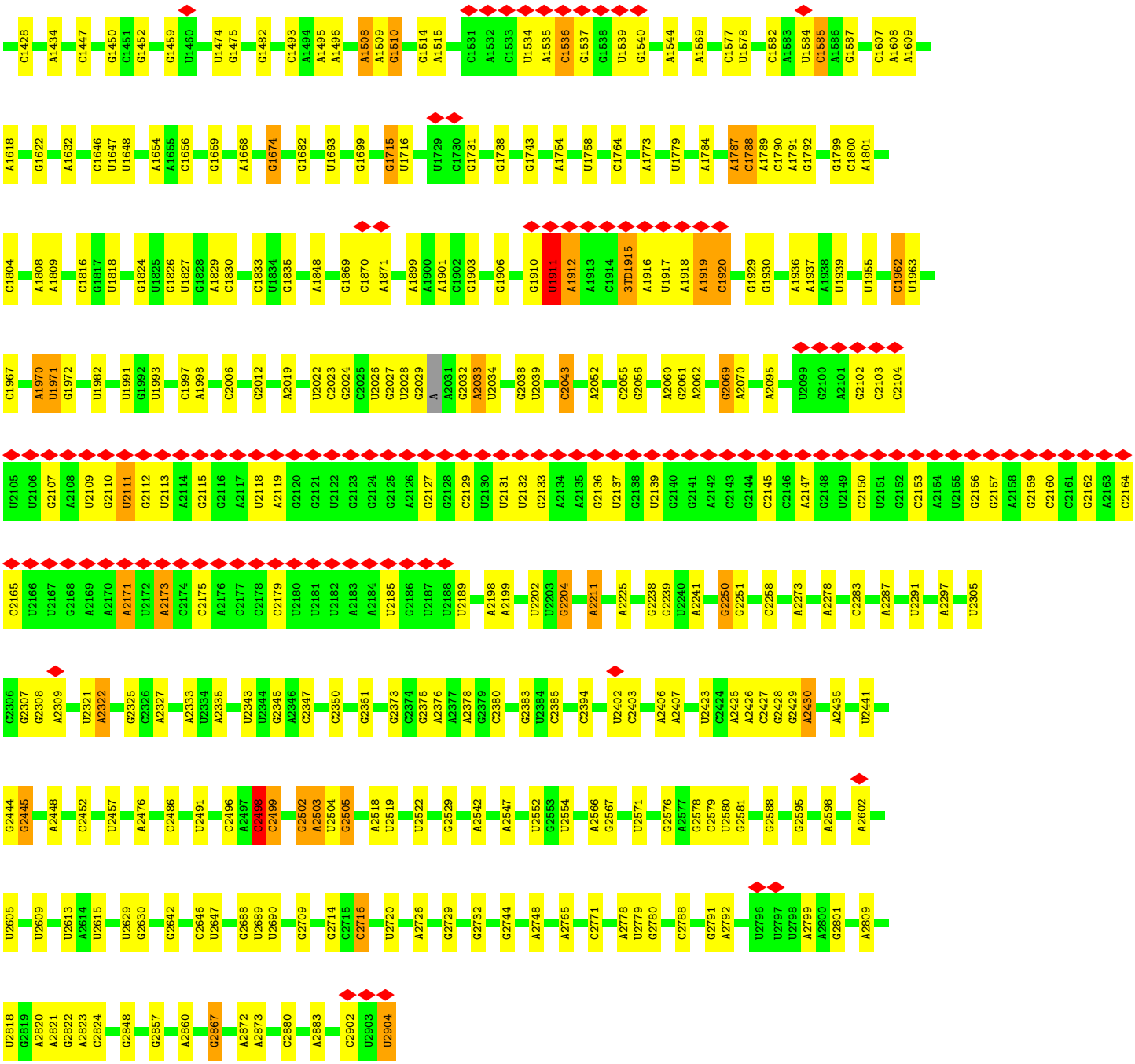
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 23S ribosomal RNA

Chain I:



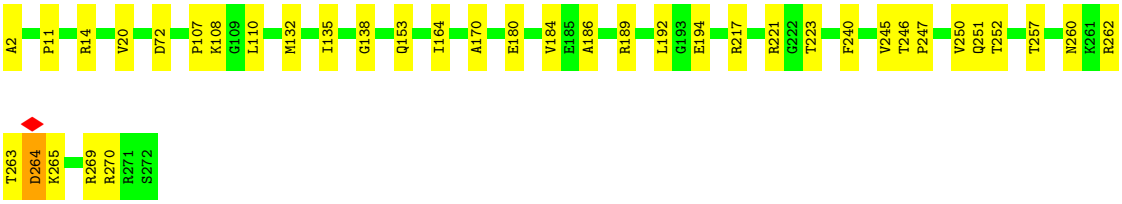


- Molecule 2: 5S ribosomal RNA

Chain J:

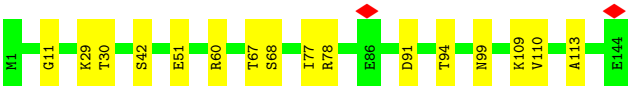
- Molecule 3: 50S ribosomal protein L2

Chain K:



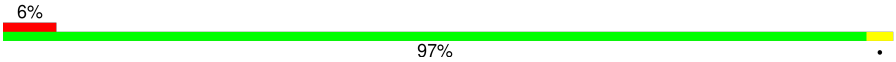
- Molecule 4: 50S ribosomal protein L15

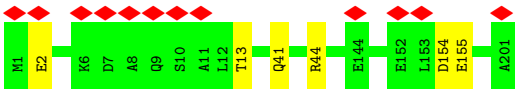
Chain L:



- Molecule 5: 50S ribosomal protein L4

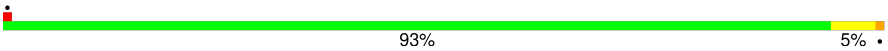
Chain M:





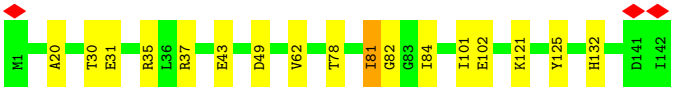
- Molecule 6: 50S ribosomal protein L3

Chain N:



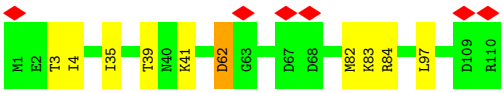
- Molecule 7: 50S ribosomal protein L13

Chain O:



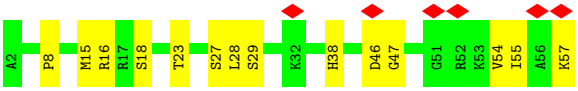
- Molecule 8: 50S ribosomal protein L22

Chain P:



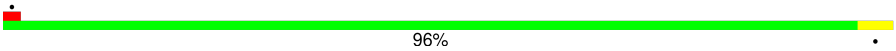
- Molecule 9: 50S ribosomal protein L32

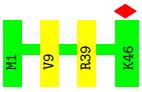
Chain Q:



- Molecule 10: 50S ribosomal protein L34

Chain R:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	401340	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 ($e^-/Å^2$)	35.7	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	21.221	Depositor
Minimum map value	-6.576	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.665	Depositor
Recommended contour level	2	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.648, 0.648, 0.648	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: 3TD, PSU, 5MU, OMC, EM1, 2MA, OMG, VIR, 5MC, 1MG, OMU, 6MZ, 2MG, 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	I	0.12	0/69165	0.18	0/107896
2	J	0.08	0/2828	0.14	0/4410
3	K	0.16	0/2122	0.34	0/2852
4	L	0.15	0/1062	0.33	0/1413
5	M	0.13	0/1571	0.26	0/2113
6	N	0.15	0/1586	0.29	0/2134
7	O	0.15	0/1152	0.26	0/1551
8	P	0.15	0/864	0.30	0/1156
9	Q	0.15	0/450	0.39	0/599
10	R	0.17	0/380	0.39	0/498
All	All	0.12	0/81180	0.20	0/124622

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	N	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	N	151	THR	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	62206	31291	31305	197	0
2	J	2529	1281	1281	5	0
3	K	2083	2154	2154	29	0
4	L	1053	1129	1129	12	0
5	M	1552	1618	1618	5	0
6	N	1565	1617	1616	17	0
7	O	1129	1162	1162	14	0
8	P	857	918	922	5	0
9	Q	444	454	458	7	0
10	R	377	417	418	2	0
11	I	60	66	65	0	0
12	I	38	35	35	0	0
All	All	73893	42142	42163	255	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 2.

The worst 5 of 255 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:N:151:THR:O	6:N:153:GLY:N	2.00	0.93
1:I:2032:G:O2'	6:N:150:GLN:NE2	2.05	0.88
1:I:1779:U:OP2	1:I:1784:A:N6	2.08	0.87
1:I:1826:G:O2'	1:I:1971:U:OP2	1.96	0.84
1:I:1090:A:N6	1:I:1101:U:O2	2.12	0.82

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	
3	K	269/271 (99%)	245 (91%)	23 (9%)	1 (0%)	30	27
4	L	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
5	M	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
6	N	207/209 (99%)	199 (96%)	5 (2%)	3 (1%)	9	4
7	O	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
8	P	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
9	Q	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
10	R	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
All	All	1163/1179 (99%)	1106 (95%)	53 (5%)	4 (0%)	37	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	N	150	GLN
6	N	152	PRO
3	K	264	ASP
6	N	151	THR

5.3.2 Protein sidechains (i)

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	
3	K	216/216 (100%)	216 (100%)	0	100	100
4	L	103/103 (100%)	102 (99%)	1 (1%)	68	75
5	M	165/165 (100%)	165 (100%)	0	100	100
6	N	164/164 (100%)	164 (100%)	0	100	100
7	O	116/116 (100%)	115 (99%)	1 (1%)	70	78
8	P	93/93 (100%)	90 (97%)	3 (3%)	34	35
9	Q	47/47 (100%)	45 (96%)	2 (4%)	26	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	R	38/38 (100%)	38 (100%)	0	100	100
All	All	942/942 (100%)	935 (99%)	7 (1%)	73	82

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	P	62	ASP
8	P	97	LEU
9	Q	57	LYS
9	Q	23	THR
8	P	41	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
6	N	150	GLN
8	P	9	HIS
10	R	26	ASN
8	P	40	ASN
9	Q	6	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	I	2894/2904 (99%)	347 (11%)	7 (0%)
2	J	117/118 (99%)	8 (6%)	0
All	All	3011/3022 (99%)	355 (11%)	7 (0%)

5 of 355 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	I	10	A
1	I	15	G
1	I	34	U
1	I	43	G
1	I	46	G

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	I	1787	A
1	I	1911	PSU
1	I	2425	A
1	I	1919	A
1	I	784	G

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

21 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	PSU	I	955	1	18,21,22	0.94	1 (5%)	21,30,33	1.94	4 (19%)
1	2MA	I	2503	1	22,25,26	1.34	3 (13%)	32,37,40	2.00	7 (21%)
1	OMG	I	2251	1	23,26,27	0.75	1 (4%)	32,38,41	1.93	9 (28%)
1	PSU	I	746	1	18,21,22	0.98	1 (5%)	21,30,33	1.86	4 (19%)
1	OMC	I	2498	1	19,22,23	0.88	1 (5%)	25,31,34	1.01	2 (8%)
1	6MZ	I	1618	1	22,25,26	1.08	1 (4%)	29,36,39	2.14	9 (31%)
1	PSU	I	2504	1	18,21,22	0.94	1 (5%)	21,30,33	1.93	4 (19%)
1	2MG	I	2445	1	23,26,27	0.80	1 (4%)	33,38,41	2.11	9 (27%)
1	PSU	I	1911	1	18,21,22	0.85	0	21,30,33	2.04	4 (19%)
1	PSU	I	1917	1	18,21,22	0.86	0	21,30,33	1.95	4 (19%)
1	5MU	I	747	1	19,22,23	1.04	3 (15%)	27,32,35	2.12	6 (22%)
1	3TD	I	1915	1	19,22,23	1.05	2 (10%)	23,32,35	1.83	3 (13%)
1	PSU	I	2580	1	18,21,22	0.98	0	21,30,33	1.95	5 (23%)
1	5MC	I	1962	1	19,22,23	1.24	2 (10%)	26,32,35	1.13	3 (11%)
1	PSU	I	2605	1	18,21,22	0.93	1 (5%)	21,30,33	1.95	4 (19%)
1	5MU	I	1939	1	19,22,23	1.06	3 (15%)	27,32,35	2.07	6 (22%)
1	OMU	I	2552	1	19,22,23	0.97	2 (10%)	25,31,34	1.92	6 (24%)
1	PSU	I	2457	1	18,21,22	0.95	0	21,30,33	1.96	4 (19%)
1	G7M	I	2069	1	23,26,27	0.53	0	34,39,42	0.93	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	2MG	I	1835	1	23,26,27	0.77	0	33,38,41	2.12	8 (24%)
1	1MG	I	745	1	23,26,27	0.93	1 (4%)	33,39,42	1.72	6 (18%)

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	PSU	I	955	1	-	0/7/25/26	0/2/2/2
1	2MA	I	2503	1	-	2/7/25/26	0/3/3/3
1	OMG	I	2251	1	-	0/9/27/28	0/3/3/3
1	PSU	I	746	1	-	0/7/25/26	0/2/2/2
1	OMC	I	2498	1	-	2/9/27/28	0/2/2/2
1	6MZ	I	1618	1	-	2/9/27/28	0/3/3/3
1	PSU	I	2504	1	-	2/7/25/26	0/2/2/2
1	2MG	I	2445	1	-	2/9/27/28	0/3/3/3
1	PSU	I	1911	1	-	2/7/25/26	0/2/2/2
1	PSU	I	1917	1	-	0/7/25/26	0/2/2/2
1	5MU	I	747	1	-	1/7/25/26	0/2/2/2
1	3TD	I	1915	1	-	4/7/25/26	0/2/2/2
1	PSU	I	2580	1	-	0/7/25/26	0/2/2/2
1	5MC	I	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	I	2605	1	-	0/7/25/26	0/2/2/2
1	5MU	I	1939	1	-	0/7/25/26	0/2/2/2
1	OMU	I	2552	1	-	0/9/27/28	0/2/2/2
1	PSU	I	2457	1	-	0/7/25/26	0/2/2/2
1	G7M	I	2069	1	-	0/7/25/26	0/3/3/3
1	2MG	I	1835	1	-	0/9/27/28	0/3/3/3
1	1MG	I	745	1	-	0/7/25/26	0/3/3/3

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	1962	5MC	C5-C4	-3.99	1.41	1.44
1	I	2503	2MA	C6-N1	3.85	1.40	1.35
1	I	1618	6MZ	C6-N6	3.75	1.38	1.34
1	I	2503	2MA	C5-N7	-3.03	1.33	1.39
1	I	2498	OMC	C2-N1	-2.52	1.34	1.40

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	2445	2MG	C2-N3-C4	7.10	120.89	112.00
1	I	1835	2MG	C2-N3-C4	7.08	120.86	112.00
1	I	1915	3TD	N1-C2-N3	6.48	120.84	116.13
1	I	2503	2MA	C5-C4-N3	-5.97	120.89	127.18
1	I	1911	PSU	N1-C2-N3	5.63	121.10	115.17

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	I	1618	6MZ	C5-C6-N6-C9
1	I	1618	6MZ	N1-C6-N6-C9
1	I	1915	3TD	C2'-C1'-C5-C4
1	I	1915	3TD	O4'-C1'-C5-C4
1	I	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	I	2503	2MA	2	0
1	I	2498	OMC	1	0
1	I	1911	PSU	5	0
1	I	1915	3TD	1	0
1	I	1962	5MC	1	0
1	I	745	1MG	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	$\#\|Z\| > 2$
11	EM1	I	3001	-	60,64,64	0.66	2 (3%)	78,97,97	1.24	6 (7%)
12	VIR	I	3002	-	38,40,40	1.29	3 (7%)	42,55,55	1.14	2 (4%)

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
11	EM1	I	3001	-	-	18/75/112/112	0/4/5/5
12	VIR	I	3002	-	-	18/48/58/58	0/2/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	I	3002	VIR	C28-C26	-5.32	1.37	1.48
12	I	3002	VIR	C12-C8	2.98	1.37	1.34
12	I	3002	VIR	C8-C6	-2.69	1.45	1.49
11	I	3001	EM1	C24-C19	2.43	1.57	1.54
11	I	3001	EM1	C21-C15	-2.05	1.52	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	I	3001	EM1	C28-C24-C19	4.96	124.18	116.10
11	I	3001	EM1	C24-C19-C13	4.38	120.67	113.32
12	I	3002	VIR	O11-C10-C13	4.30	121.67	117.70
11	I	3001	EM1	C24-C28-C34	3.77	114.73	110.18
12	I	3002	VIR	C12-C8-N9	-3.12	106.83	109.15

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	I	3001	EM1	C13-C19-C24-C28
11	I	3001	EM1	C23-C19-C24-C28
11	I	3001	EM1	C24-C28-C34-C30
11	I	3001	EM1	O32-C28-C34-O39

Continued on next page...

Continued from previous page...

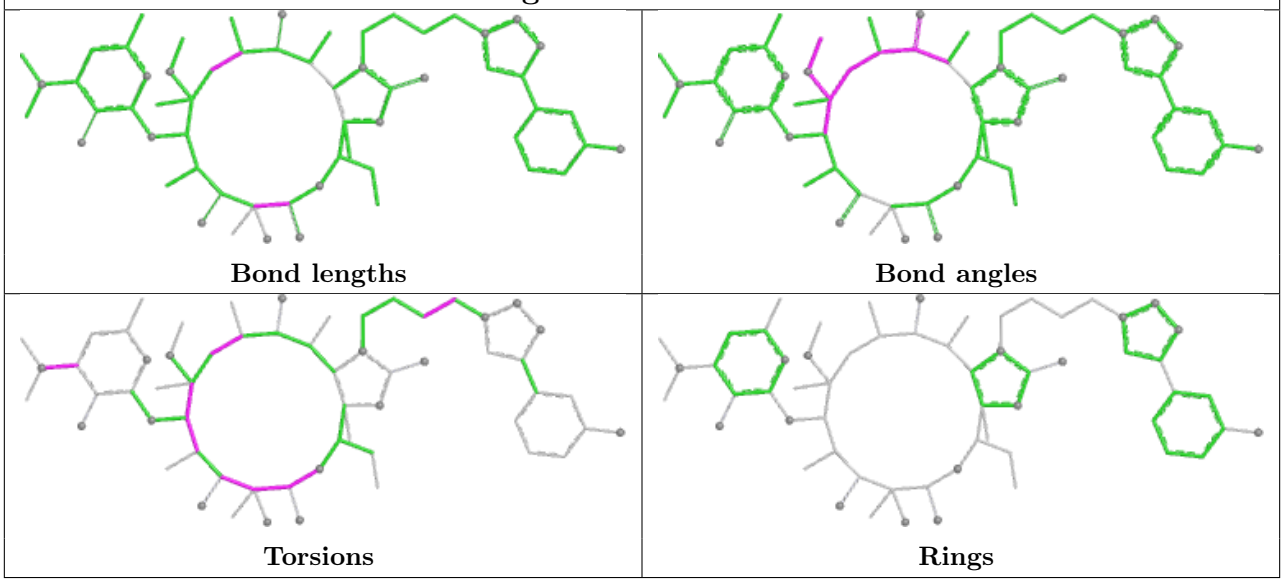
Mol	Chain	Res	Type	Atoms
11	I	3001	EM1	C33-C28-C34-C30

There are no ring outliers.

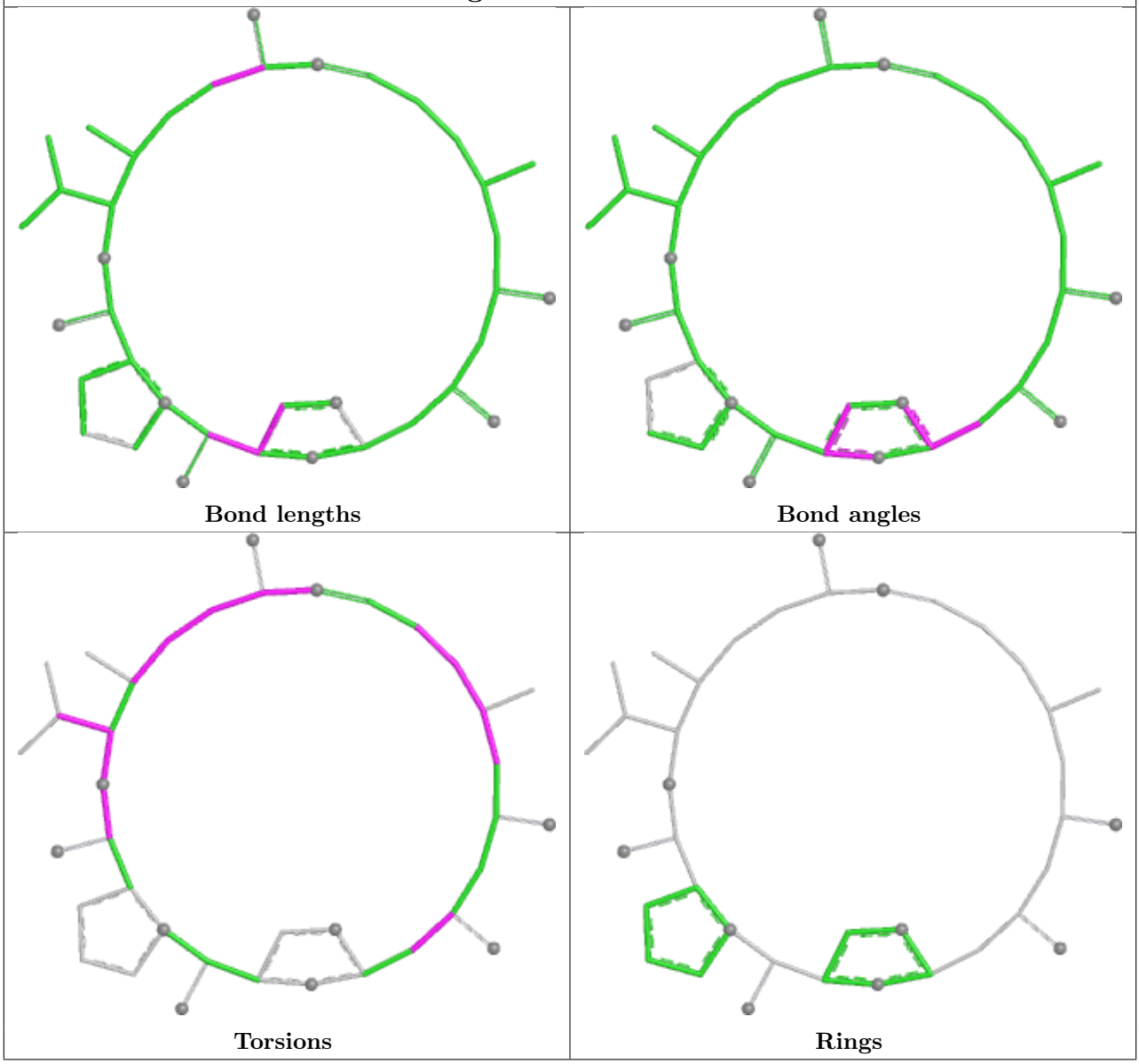
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand EM1 I 3001



Ligand VIR I 3002



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.

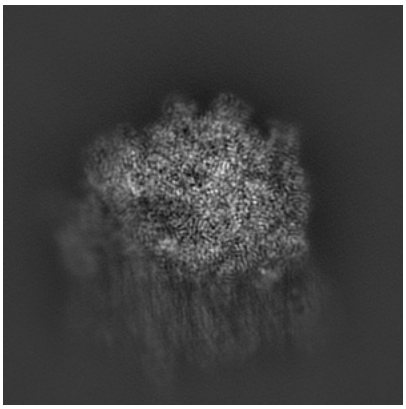
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-27869. These allow visual inspection of the internal detail of the map and identification of artifacts.

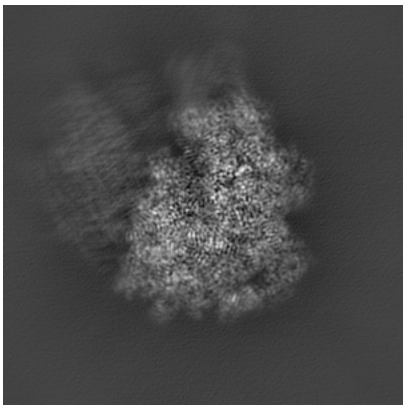
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

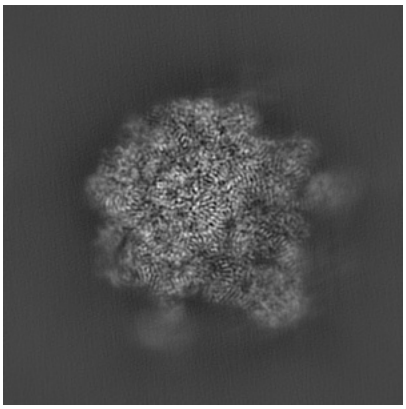
6.1.1 Primary map



X

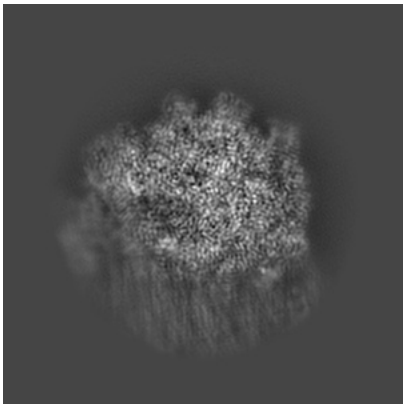


Y

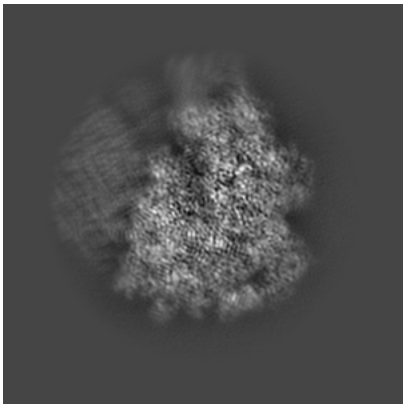


Z

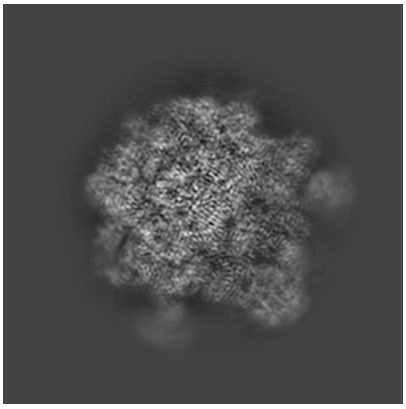
6.1.2 Raw map



X



Y

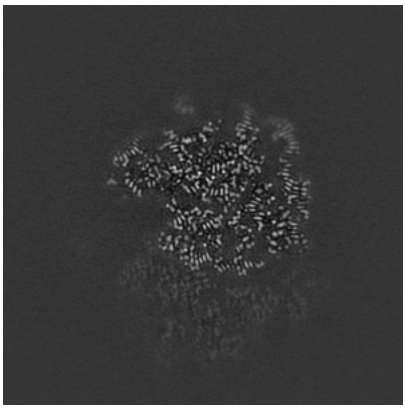


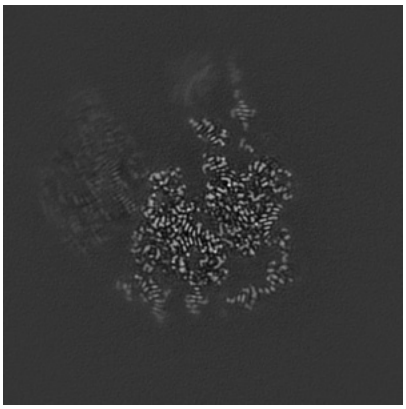
Z

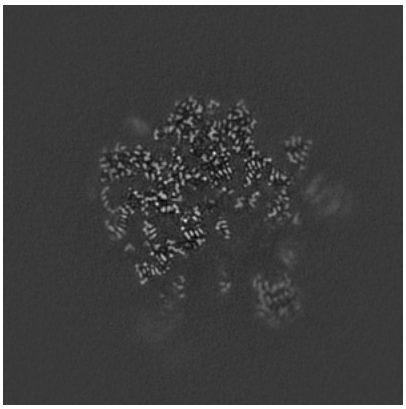
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

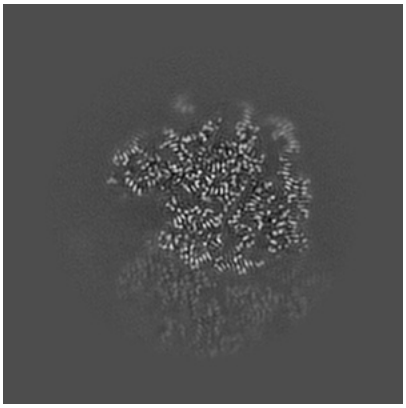
6.2.1 Primary map

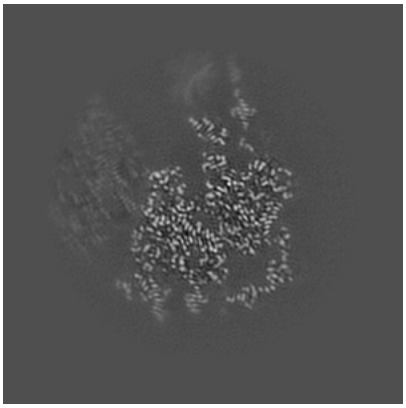

X Index: 250

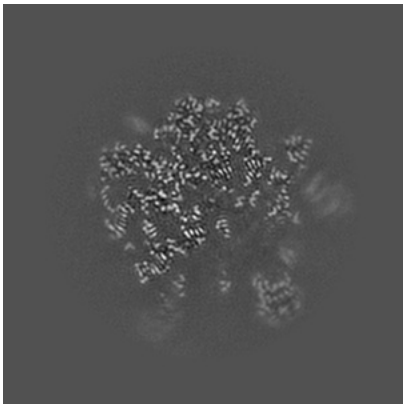

Y Index: 250


Z Index: 250

6.2.2 Raw map


X Index: 250

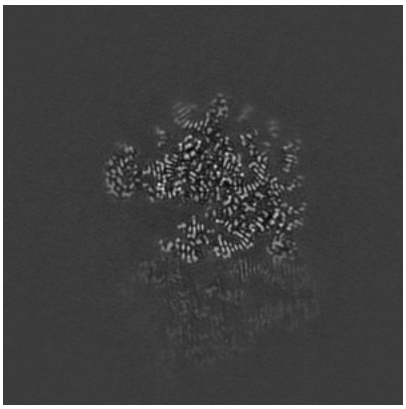

Y Index: 250


Z Index: 250

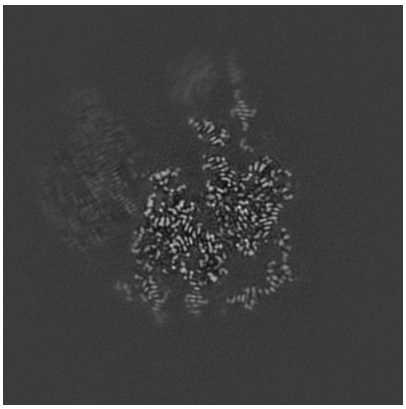
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

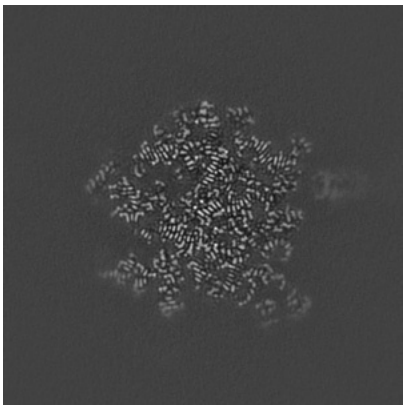
6.3.1 Primary map



X Index: 265

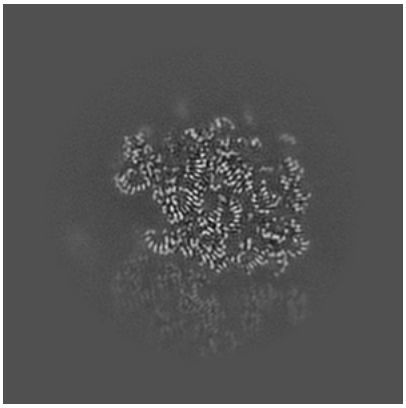


Y Index: 251

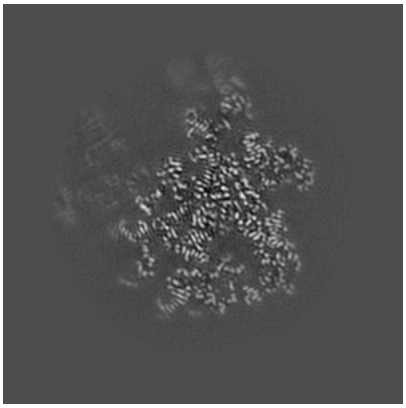


Z Index: 270

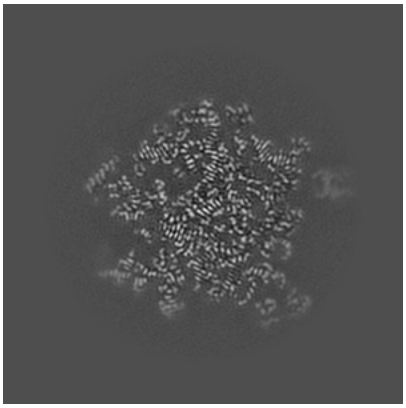
6.3.2 Raw map



X Index: 241



Y Index: 287

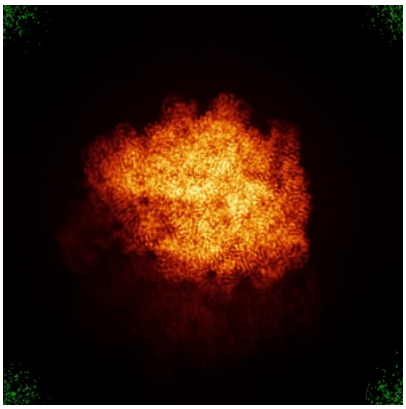


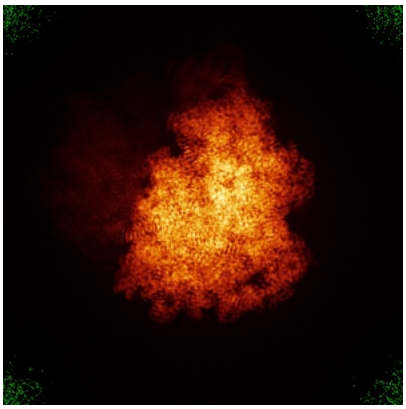
Z Index: 271

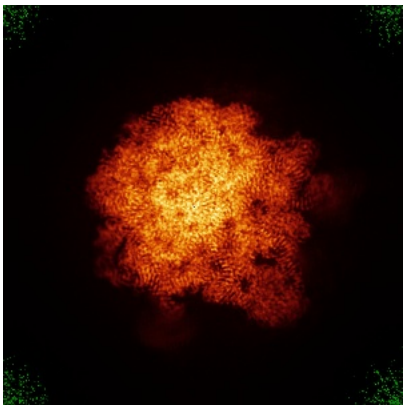
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

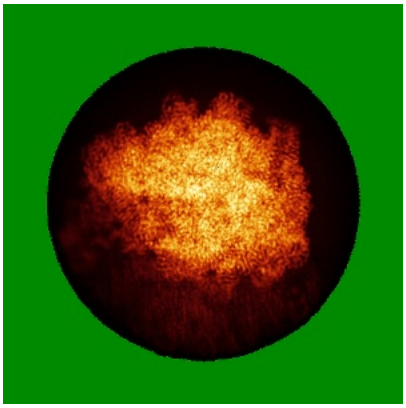
6.4.1 Primary map

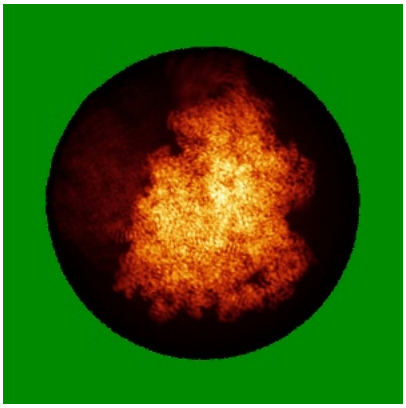

X

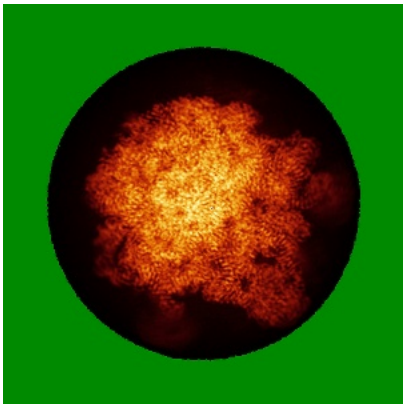

Y


Z

6.4.2 Raw map


X


Y


Z

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

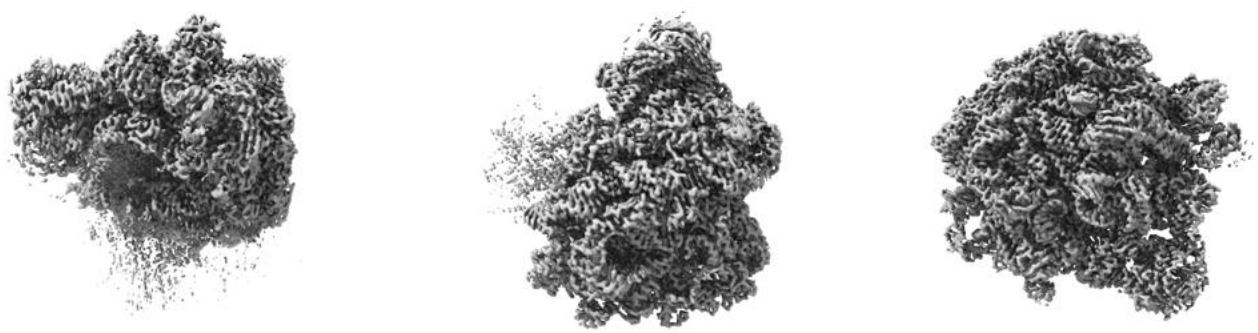
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

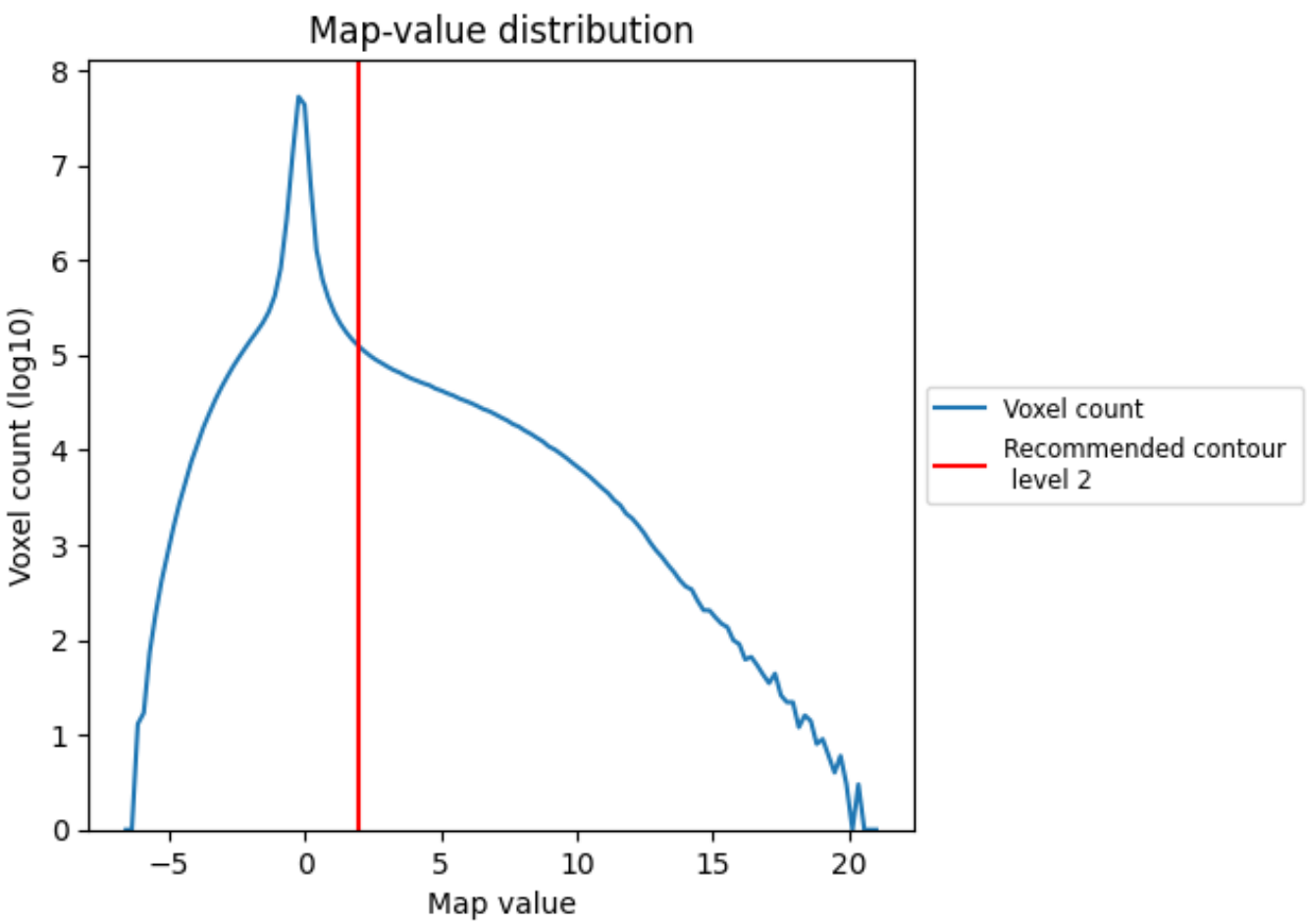
6.6 Mask visualisation (i)

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

7 Map analysis (i)

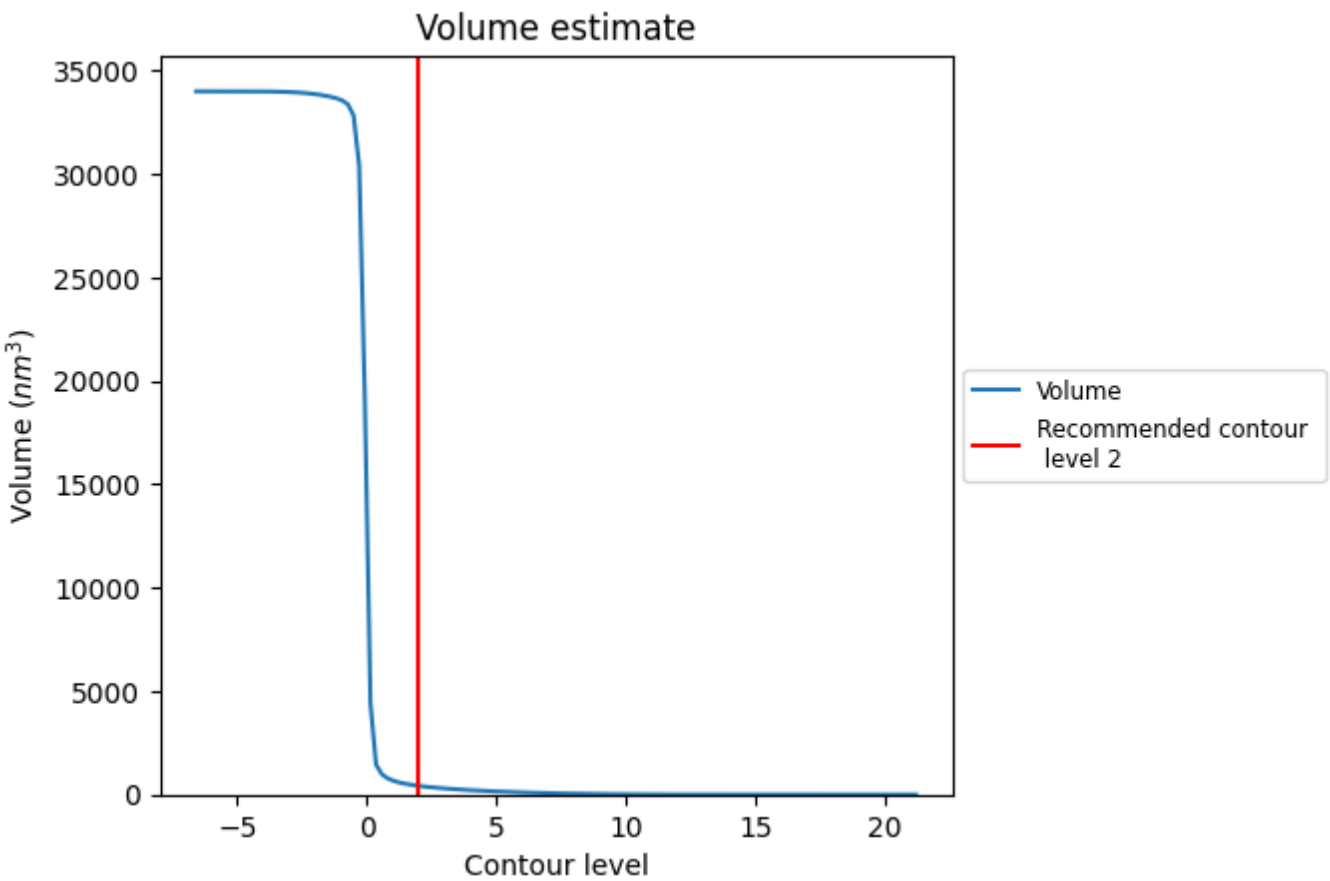
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

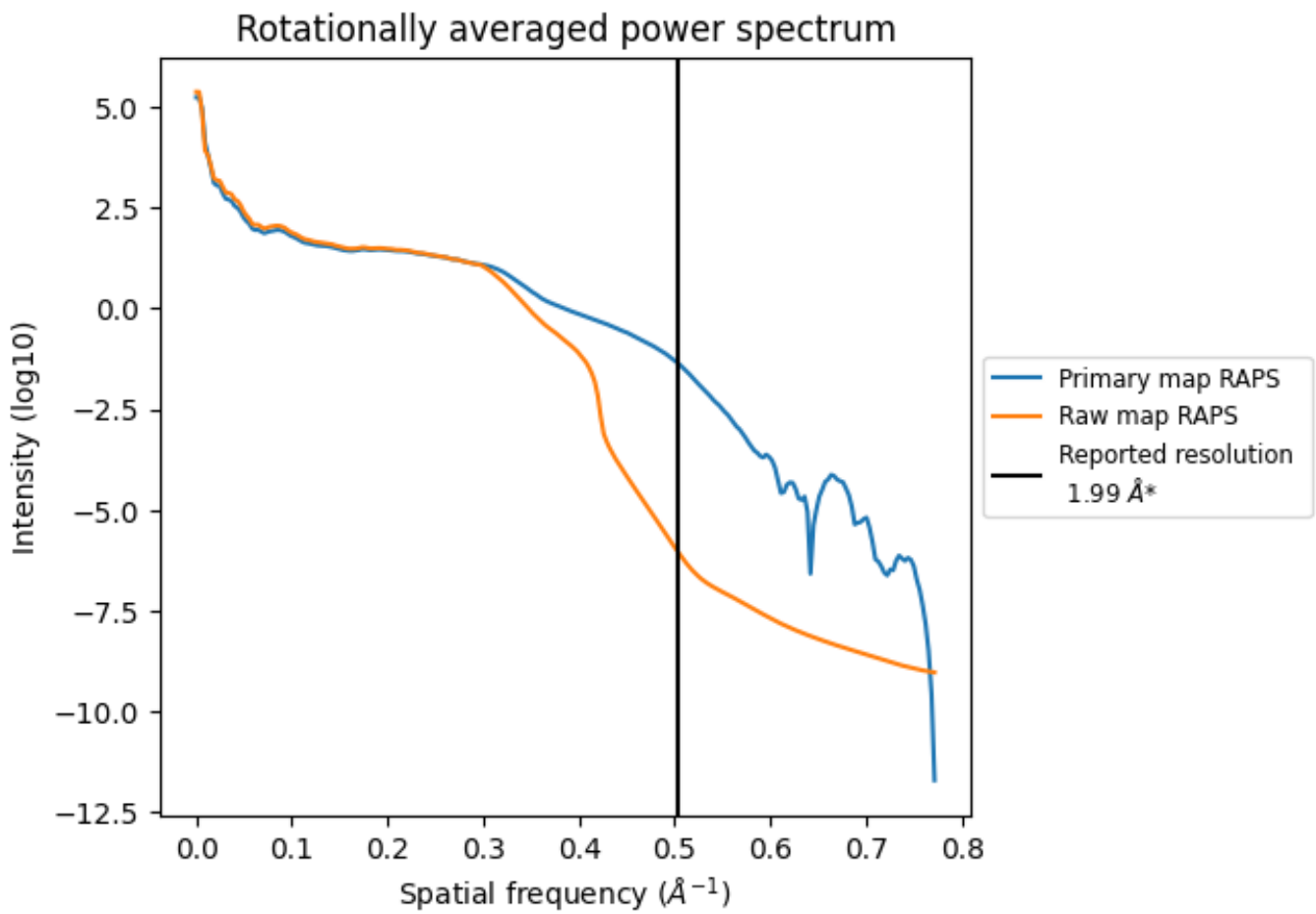
7.2 Volume estimate (i)



The volume at the recommended contour level is 423 nm^3; this corresponds to an approximate mass of 382 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 (i)

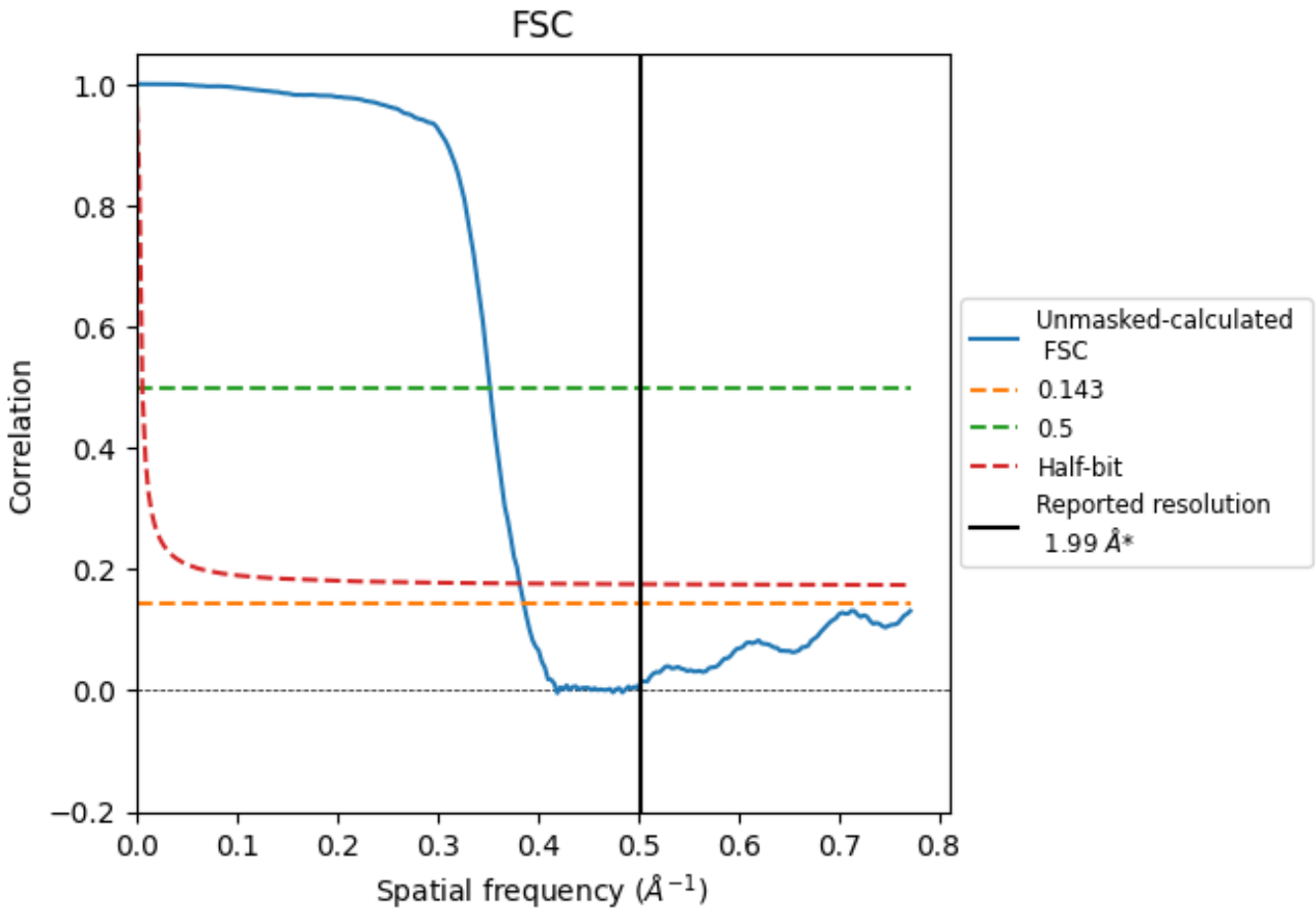


*Reported resolution corresponds to spatial frequency of 0.503 Å^{-1}

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 0.503 Å^{-1}

8.2 Resolution estimates (i)

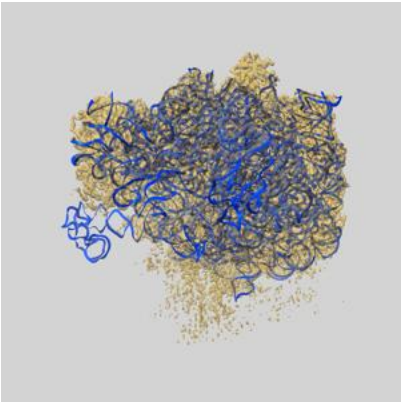
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.99	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.59	2.84	2.62

*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 2.59 differs from the reported value 1.99 by more than 10 %

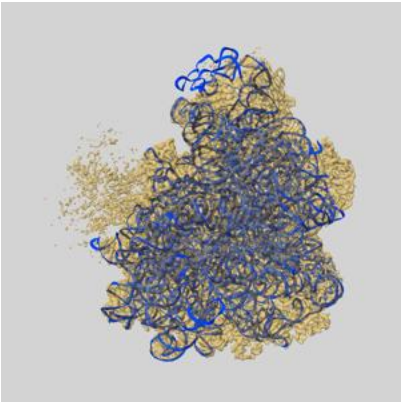
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-27869 and PDB model 8E3O. Per-residue inclusion information can be found in section 3 on page 7.

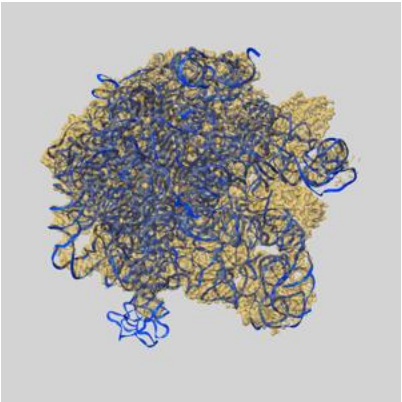
9.1 Map-model overlay (i)



X



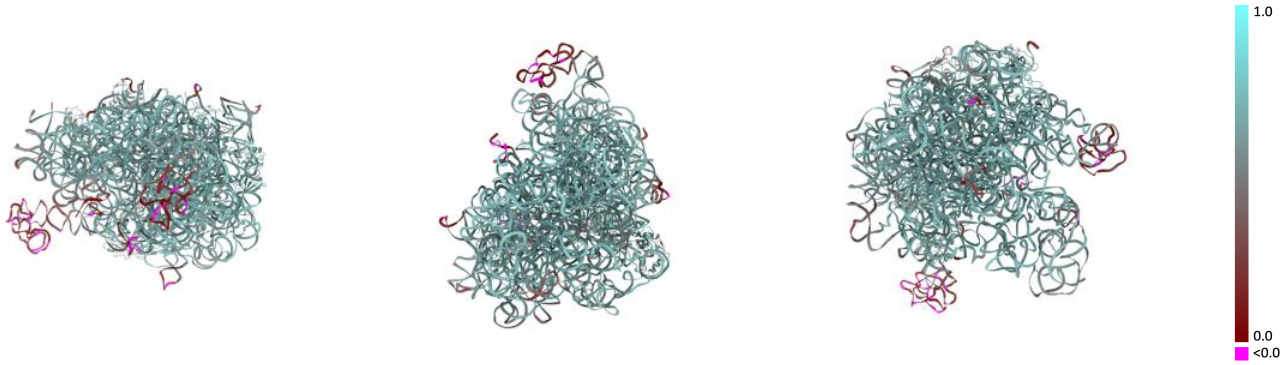
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.0 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.

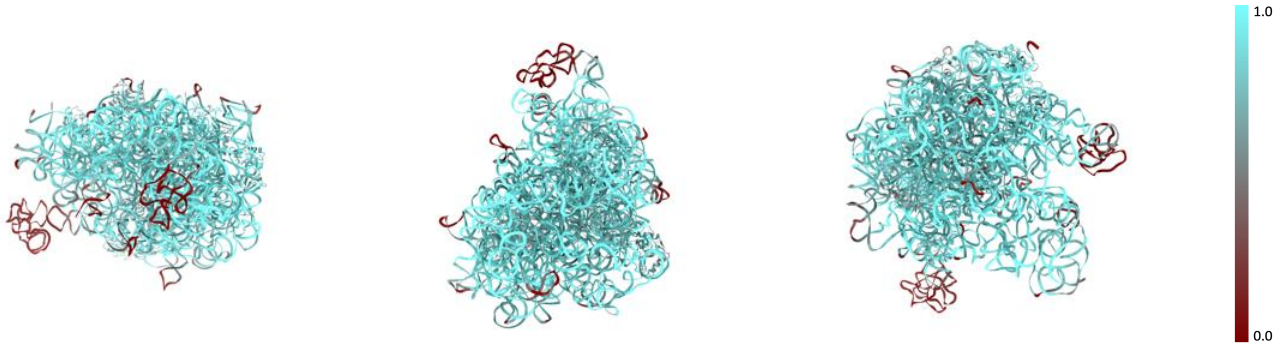
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

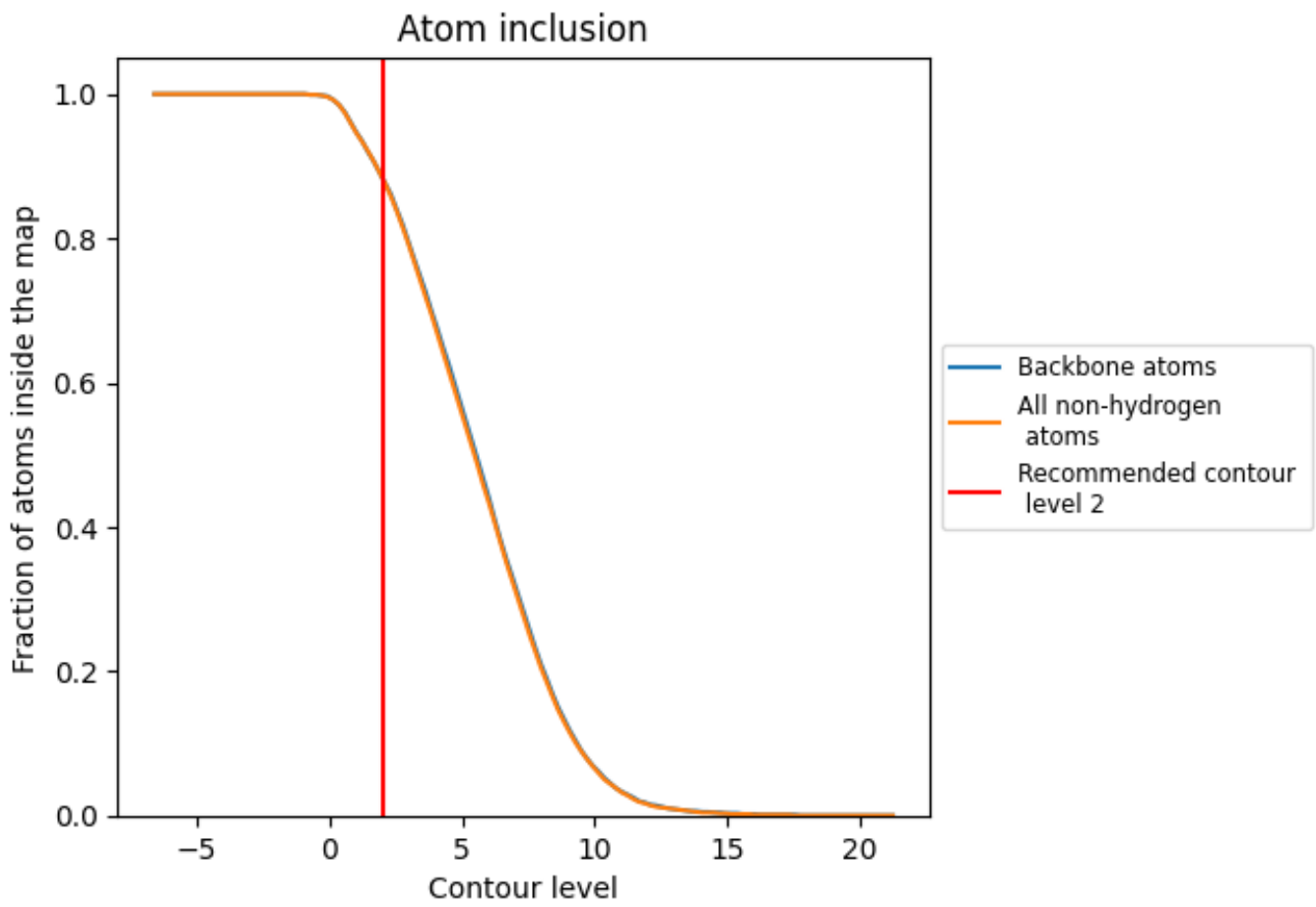
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (2).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8840	0.6180
I	0.8900	0.6170
J	0.8380	0.5910
K	0.9010	0.6480
L	0.8500	0.6370
M	0.7870	0.6270
N	0.8780	0.6550
O	0.8900	0.6540
P	0.8220	0.6090
Q	0.7360	0.5150
R	0.9240	0.6870