



## wwPDB EM Validation Summary Report ⓘ

Sep 15, 2025 – 02:02 PM EDT

PDB ID : 9PZG / pdb\_00009pzg  
EMDB ID : EMD-72071  
Title : Bacterial ribosomal 2'-O-methyltransferase RsmI in complex with the small ribosomal subunit  
Authors : Barmada, M.I.; Conn, G.L.  
Deposited on : 2025-08-11  
Resolution : 2.42 Å (reported)  
Based on initial models : 5wh4, 7oe1

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

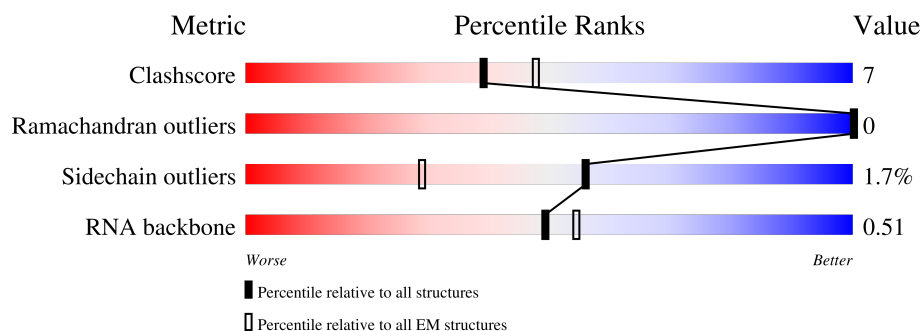
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.42 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	<div> <div>9%</div> <div>58%</div> <div>33%</div> <div>8%</div> <div>.</div> </div>
2	B	241	<div> <div>62%</div> <div>77%</div> <div>14%</div> <div>10%</div> </div>
3	C	233	<div> <div>10%</div> <div>76%</div> <div>12%</div> <div>12%</div> </div>
4	D	206	<div> <div>.</div> <div>86%</div> <div>12%</div> <div>.</div> </div>
5	E	167	<div> <div>75%</div> <div>15%</div> <div>10%</div> </div>
6	F	135	<div> <div>5%</div> <div>57%</div> <div>17%</div> <div>26%</div> </div>
7	G	179	<div> <div>81%</div> <div>75%</div> <div>9%</div> <div>16%</div> </div>

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Mol	Chain	Length	Quality of chain
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	V	303	
22	W	303	

## 2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 55661 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1532	Total	C	N	O	P	0	0
			32880	14667	6033	10648	1532		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	18	Total	C	N	O	0	0
			148	94	28	26		

- Molecule 22 is a protein called Ribosomal RNA small subunit methyltransferase I.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	271	Total	C	N	O	S	0	0
			2087	1326	369	388	4		
22	W	276	Total	C	N	O	S	0	0
			2130	1349	378	399	4		

There are 34 discrepancies between the modelled and reference sequences:

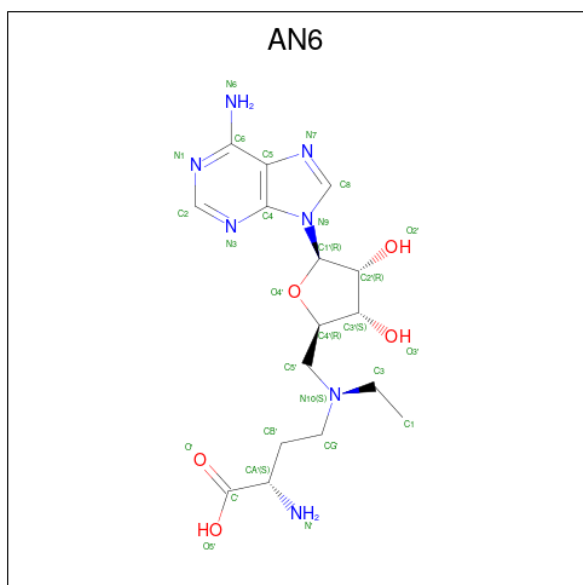
Chain	Residue	Modelled	Actual	Comment	Reference
V	-16	MET	-	initiating methionine	UNP P67088
V	-15	HIS	-	expression tag	UNP P67088
V	-14	HIS	-	expression tag	UNP P67088
V	-13	HIS	-	expression tag	UNP P67088
V	-12	HIS	-	expression tag	UNP P67088
V	-11	HIS	-	expression tag	UNP P67088
V	-10	HIS	-	expression tag	UNP P67088
V	-9	ALA	-	expression tag	UNP P67088
V	-8	SER	-	expression tag	UNP P67088
V	-7	GLY	-	expression tag	UNP P67088
V	-6	LEU	-	expression tag	UNP P67088
V	-5	VAL	-	expression tag	UNP P67088
V	-4	PRO	-	expression tag	UNP P67088
V	-3	ARG	-	expression tag	UNP P67088
V	-2	GLY	-	expression tag	UNP P67088
V	-1	SER	-	expression tag	UNP P67088
V	0	HIS	-	expression tag	UNP P67088
W	-16	MET	-	initiating methionine	UNP P67088
W	-15	HIS	-	expression tag	UNP P67088
W	-14	HIS	-	expression tag	UNP P67088
W	-13	HIS	-	expression tag	UNP P67088
W	-12	HIS	-	expression tag	UNP P67088
W	-11	HIS	-	expression tag	UNP P67088
W	-10	HIS	-	expression tag	UNP P67088
W	-9	ALA	-	expression tag	UNP P67088
W	-8	SER	-	expression tag	UNP P67088
W	-7	GLY	-	expression tag	UNP P67088
W	-6	LEU	-	expression tag	UNP P67088
W	-5	VAL	-	expression tag	UNP P67088

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Chain	Residue	Modelled	Actual	Comment	Reference
W	-4	PRO	-	expression tag	UNP P67088
W	-3	ARG	-	expression tag	UNP P67088
W	-2	GLY	-	expression tag	UNP P67088
W	-1	SER	-	expression tag	UNP P67088
W	0	HIS	-	expression tag	UNP P67088

- Molecule 23 is 5'-{[(3S)-3-amino-3-carboxypropyl](ethyl)amino}-5'-deoxyadenosine (CCD ID: AN6) (formula: C<sub>16</sub>H<sub>25</sub>N<sub>7</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				AltConf
23	A	1	Total	C	N	O	0
			28	16	7	5	
23	V	1	Total	C	N	O	0
			28	16	7	5	

- Molecule 24 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
24	A	78	Total	Mg	0
			78	78	
24	W	1	Total	Mg	0
			1	1	

- Molecule 25 is water.

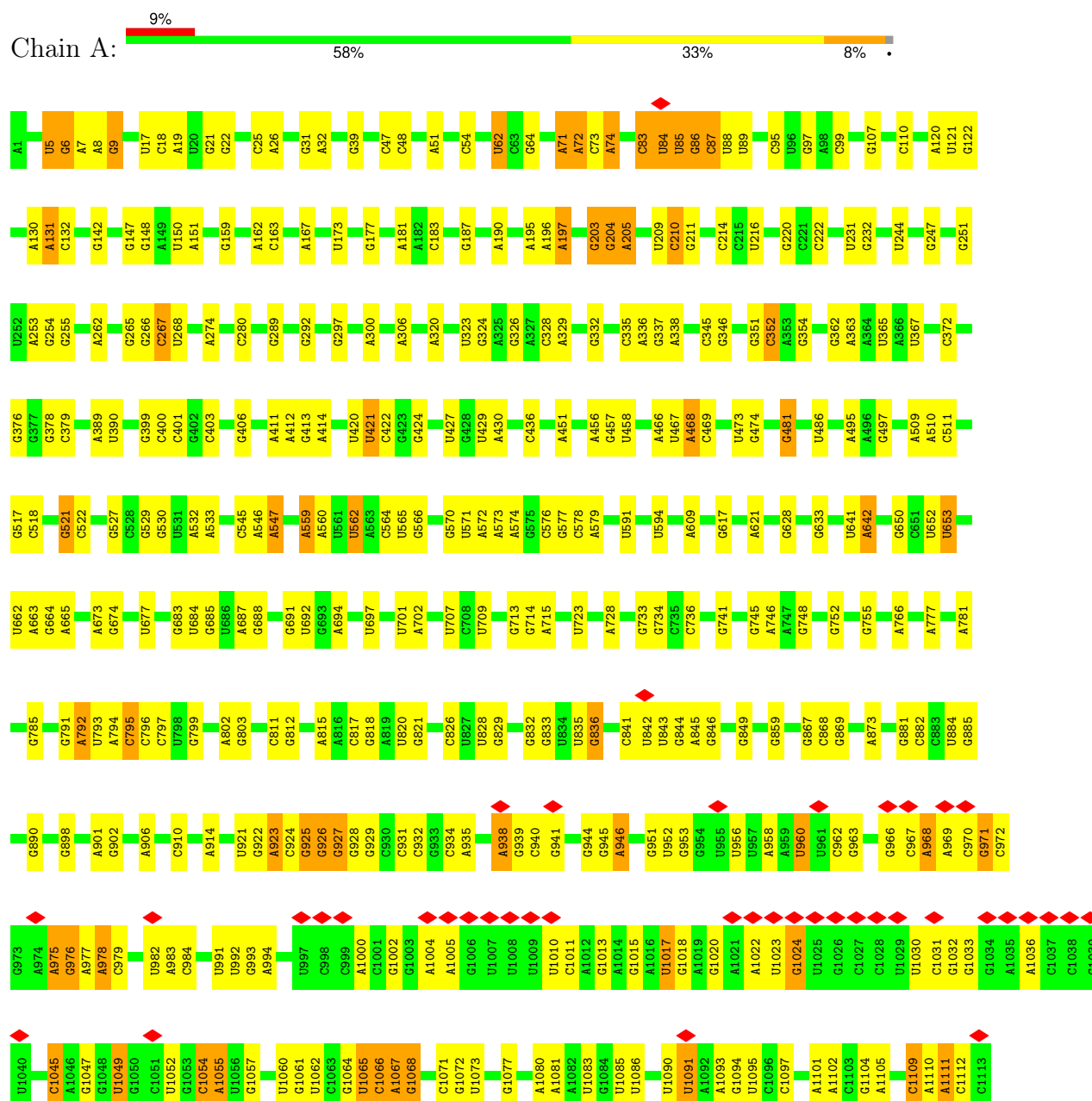


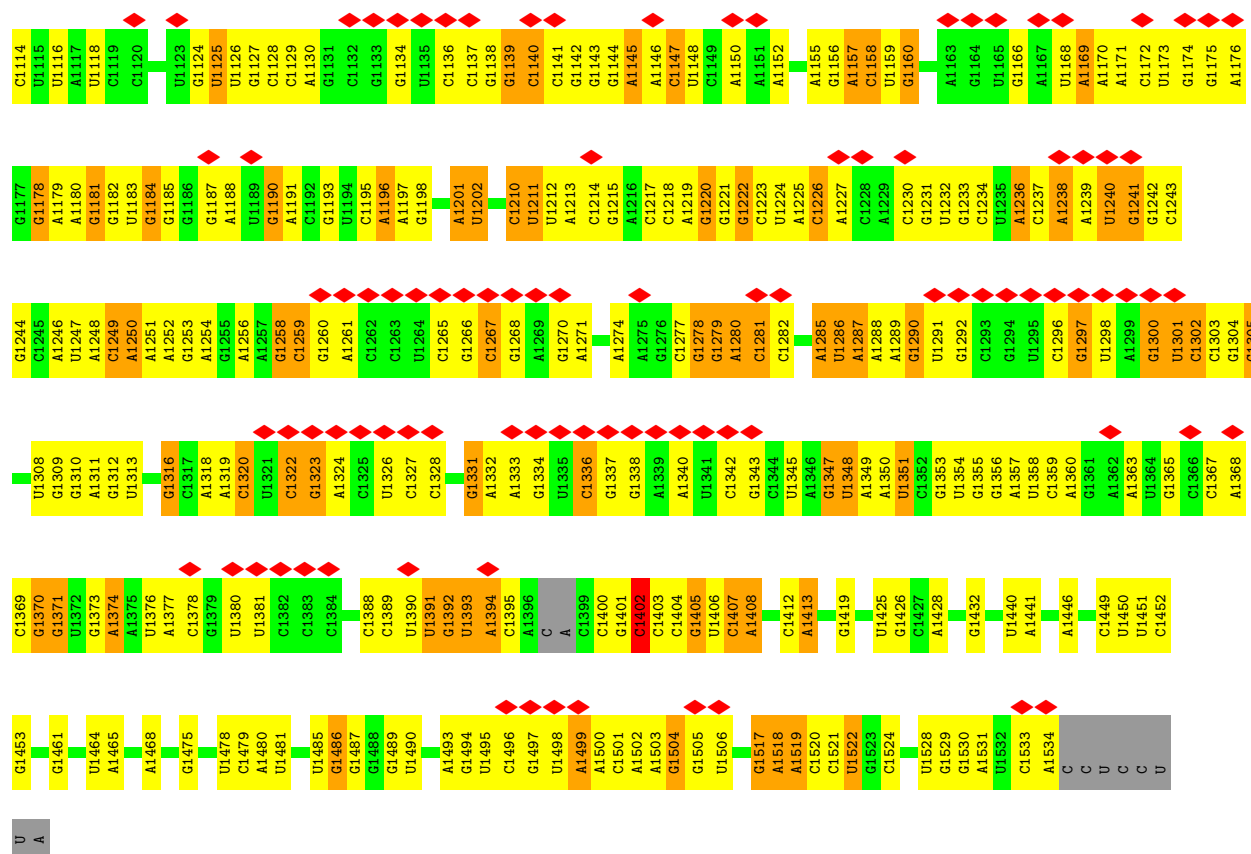
Mol	Chain	Residues	Atoms		AltConf
25	A	107	Total 107	O 107	0
25	B	4	Total 4	O 4	0
25	D	7	Total 7	O 7	0
25	E	2	Total 2	O 2	0
25	F	2	Total 2	O 2	0
25	H	11	Total 11	O 11	0
25	K	5	Total 5	O 5	0
25	L	5	Total 5	O 5	0
25	O	4	Total 4	O 4	0
25	Q	2	Total 2	O 2	0
25	R	3	Total 3	O 3	0
25	T	2	Total 2	O 2	0
25	V	4	Total 4	O 4	0
25	W	12	Total 12	O 12	0

### 3 Residue-property plots

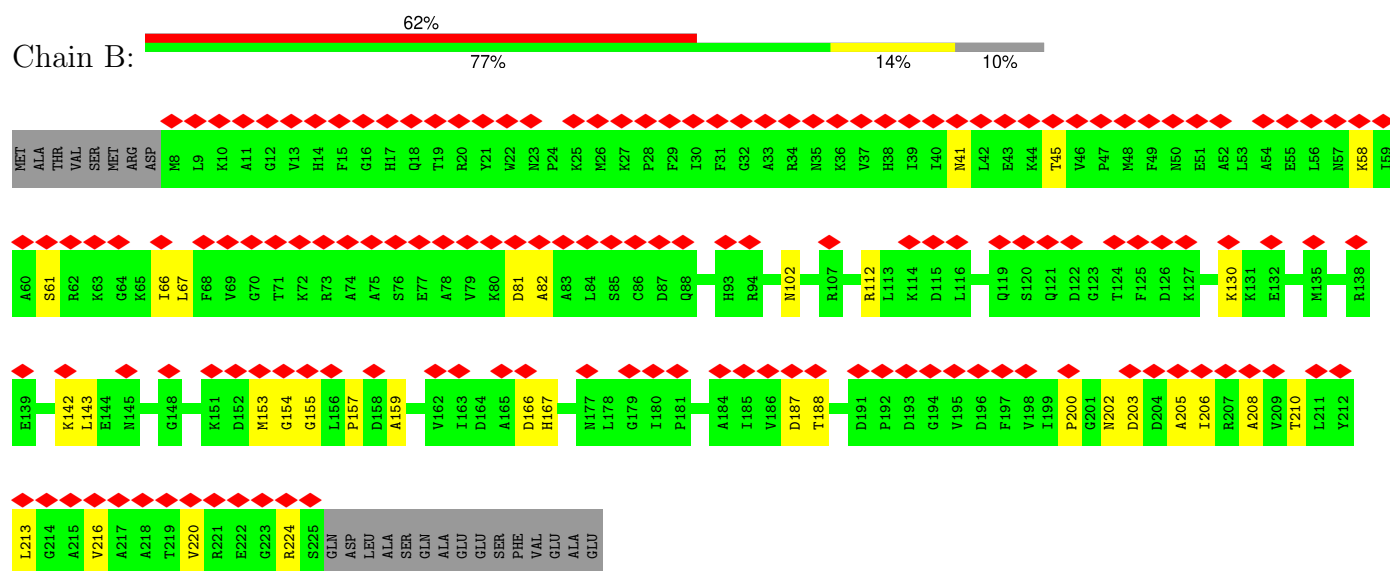
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

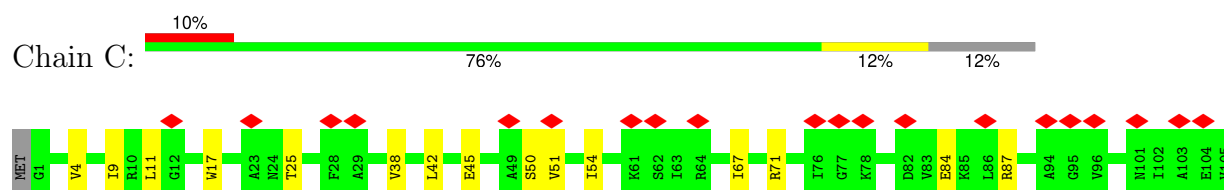




• Molecule 2: Small ribosomal subunit protein uS2



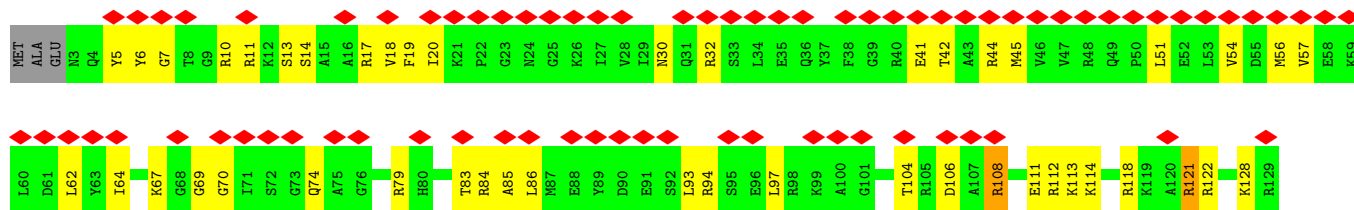
• Molecule 3: Small ribosomal subunit protein uS3



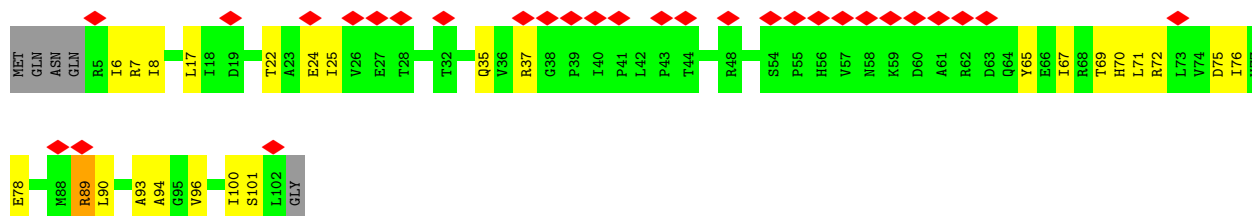




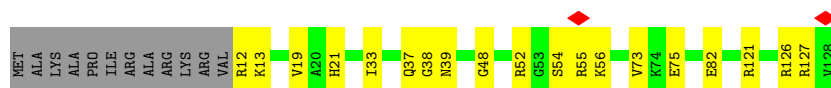
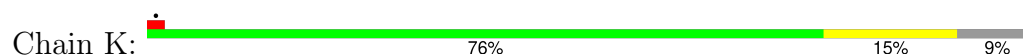
- Molecule 9: Small ribosomal subunit protein uS9



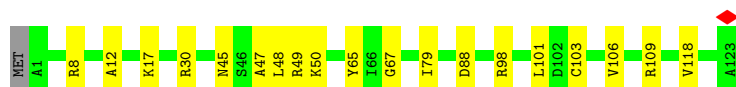
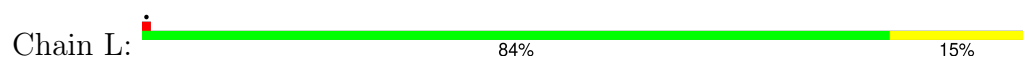
- Molecule 10: Small ribosomal subunit protein uS10



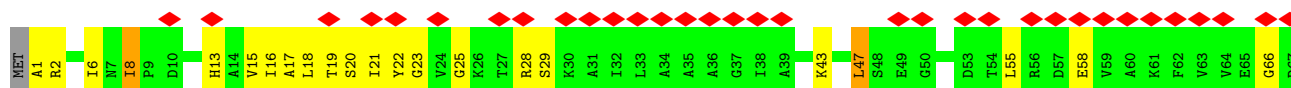
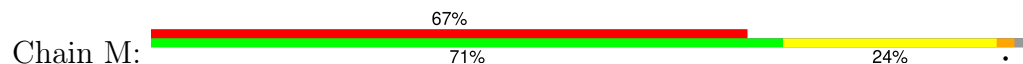
- Molecule 11: Small ribosomal subunit protein uS11



- Molecule 12: Small ribosomal subunit protein uS12

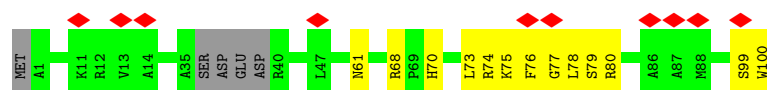
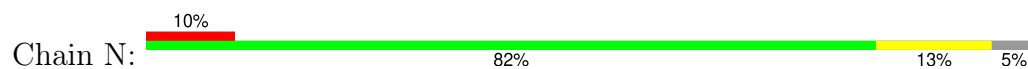


- Molecule 13: Small ribosomal subunit protein uS13

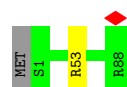




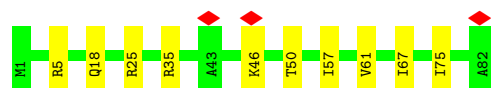
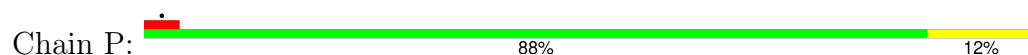
- Molecule 14: Small ribosomal subunit protein uS14



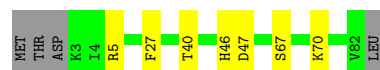
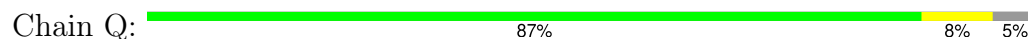
- Molecule 15: Small ribosomal subunit protein uS15



- Molecule 16: Small ribosomal subunit protein bS16



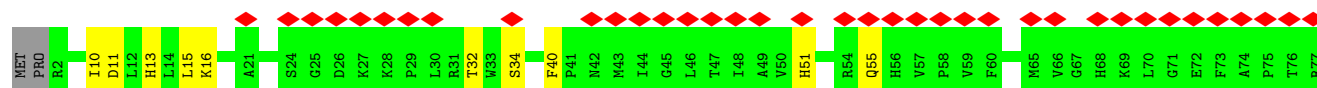
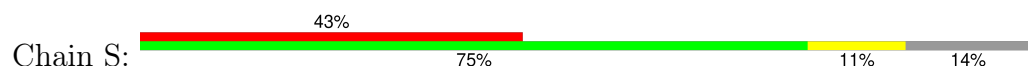
- Molecule 17: Small ribosomal subunit protein uS17



- Molecule 18: Small ribosomal subunit protein bS18



- Molecule 19: Small ribosomal subunit protein uS19





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	74553	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	49.27	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.400	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: B8T, AN6, MA6, 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	0.18	0/36737	0.27	0/57304
2	B	0.12	0/1735	0.31	0/2338
3	C	0.10	0/1651	0.28	0/2225
4	D	0.12	0/1665	0.35	0/2227
5	E	0.16	0/1118	0.35	0/1504
6	F	0.14	0/835	0.38	0/1128
7	G	0.10	0/1187	0.28	0/1591
8	H	0.12	0/989	0.31	0/1326
9	I	0.14	0/1034	0.40	0/1375
10	J	0.12	0/796	0.32	0/1077
11	K	0.18	0/893	0.34	0/1205
12	L	0.15	0/969	0.39	0/1300
13	M	0.11	0/892	0.30	0/1193
14	N	0.11	0/785	0.35	0/1043
15	O	0.12	0/722	0.29	0/964
16	P	0.12	0/659	0.34	0/884
17	Q	0.12	0/657	0.30	0/881
18	R	0.12	0/462	0.31	0/621
19	S	0.10	0/652	0.27	0/877
20	T	0.14	0/671	0.33	0/888
21	U	0.14	0/150	0.41	0/198
22	V	0.22	0/2122	0.36	0/2878
22	W	0.27	0/2167	0.42	0/2940
All	All	0.17	0/59548	0.29	0/87967

There are no bond length outliers.

There are no bond angle outliers.

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	32880	0	16540	361	0
2	B	1704	0	1732	22	0
3	C	1624	0	1699	14	0
4	D	1643	0	1710	24	0
5	E	1105	0	1148	19	0
6	F	817	0	808	14	0
7	G	1174	0	1230	13	0
8	H	979	0	1034	8	0
9	I	1022	0	1070	36	0
10	J	786	0	828	15	0
11	K	877	0	887	21	0
12	L	955	0	1019	16	0
13	M	883	0	944	25	0
14	N	774	0	827	12	0
15	O	714	0	737	1	0
16	P	649	0	666	6	0
17	Q	648	0	691	5	0
18	R	455	0	478	6	0
19	S	637	0	665	7	0
20	T	665	0	714	3	0
21	U	148	0	157	2	0
22	V	2087	0	2140	37	0
22	W	2130	0	2168	30	0
23	A	28	0	22	4	0
23	V	28	0	24	2	0
24	A	78	0	0	0	0
24	W	1	0	0	0	0
25	A	107	0	0	2	0
25	B	4	0	0	0	0
25	D	7	0	0	0	0
25	E	2	0	0	0	0
25	F	2	0	0	0	0
25	H	11	0	0	1	0
25	K	5	0	0	1	0
25	L	5	0	0	0	0
25	O	4	0	0	0	0
25	Q	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	R	3	0	0	0	0
25	T	2	0	0	0	0
25	V	4	0	0	0	0
25	W	12	0	0	1	0
All	All	55661	0	39938	582	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 7.

The worst 5 of 582 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:1402:B8T:O4'	1:A:1402:B8T:C4'	1.65	1.26
23:A:1601:AN6:C4'	23:A:1601:AN6:O4'	1.68	1.18
13:M:1:ALA:O	13:M:2:ARG:NH1	2.06	0.89
1:A:1528:U:O4	21:U:39:LYS:NZ	2.11	0.82
1:A:802:A:H3'	1:A:803:G:H8	1.45	0.82

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	216/241 (90%)	202 (94%)	14 (6%)	0	100	100
3	C	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
4	D	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
5	E	148/167 (89%)	143 (97%)	5 (3%)	0	100	100
6	F	98/135 (73%)	91 (93%)	7 (7%)	0	100	100
7	G	148/179 (83%)	138 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
9	I	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
10	J	96/103 (93%)	89 (93%)	7 (7%)	0	100	100
11	K	115/129 (89%)	114 (99%)	1 (1%)	0	100	100
12	L	121/124 (98%)	112 (93%)	9 (7%)	0	100	100
13	M	112/118 (95%)	105 (94%)	7 (6%)	0	100	100
14	N	92/101 (91%)	86 (94%)	6 (6%)	0	100	100
15	O	86/89 (97%)	86 (100%)	0	0	100	100
16	P	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
17	Q	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
18	R	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
19	S	77/92 (84%)	70 (91%)	7 (9%)	0	100	100
20	T	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
21	U	16/71 (22%)	13 (81%)	3 (19%)	0	100	100
22	V	267/303 (88%)	265 (99%)	2 (1%)	0	100	100
22	W	274/303 (90%)	267 (97%)	7 (3%)	0	100	100
All	All	2819/3182 (89%)	2679 (95%)	140 (5%)	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	B	180/199 (90%)	180 (100%)	0	100	100
3	C	170/190 (90%)	165 (97%)	5 (3%)	37	56
4	D	172/173 (99%)	169 (98%)	3 (2%)	56	73
5	E	113/126 (90%)	113 (100%)	0	100	100
6	F	87/116 (75%)	85 (98%)	2 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	123/147 (84%)	122 (99%)	1 (1%)	79	89
8	H	104/105 (99%)	103 (99%)	1 (1%)	73	85
9	I	105/107 (98%)	100 (95%)	5 (5%)	21	35
10	J	86/90 (96%)	83 (96%)	3 (4%)	31	49
11	K	90/99 (91%)	90 (100%)	0	100	100
12	L	103/104 (99%)	101 (98%)	2 (2%)	52	70
13	M	92/96 (96%)	90 (98%)	2 (2%)	47	65
14	N	79/84 (94%)	78 (99%)	1 (1%)	65	80
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	64 (98%)	1 (2%)	60	77
17	Q	74/78 (95%)	72 (97%)	2 (3%)	40	58
18	R	48/65 (74%)	47 (98%)	1 (2%)	48	67
19	S	70/79 (89%)	69 (99%)	1 (1%)	62	79
20	T	65/66 (98%)	64 (98%)	1 (2%)	60	77
21	U	15/61 (25%)	13 (87%)	2 (13%)	3	3
22	V	215/243 (88%)	212 (99%)	3 (1%)	62	79
22	W	220/243 (90%)	217 (99%)	3 (1%)	62	79
All	All	2352/2613 (90%)	2313 (98%)	39 (2%)	56	73

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	R	46	THR
22	V	285	GLN
19	S	55	GLN
21	U	37	TYR
22	W	213	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
19	S	51	HIS
20	T	77	ASN
20	T	69	ASN
22	V	275	ASN

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Mol	Chain	Res	Type
9	I	3	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1530/1542 (99%)	334 (21%)	10 (0%)

5 of 334 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	6	G
1	A	9	G
1	A	31	G
1	A	32	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1391	U
1	A	1392	G
1	A	1497	G
1	A	1067	A
1	A	1201	A

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

3 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	B8T	A	1402	24,1,23	19,22,23	4.80	13 (68%)	25,31,34	1.25	3 (12%)
1	MA6	A	1519	1	19,26,27	0.98	2 (10%)	18,38,41	0.72	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MA6	A	1518	1	19,26,27	0.95	2 (10%)	18,38,41	0.66	1 (5%)

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	B8T	A	1402	24,1,23	-	6/7/27/28	0/2/2/2
1	MA6	A	1519	1	-	1/7/29/30	0/3/3/3
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1402	B8T	O4'-C4'	9.25	1.65	1.45
1	A	1402	B8T	C3'-C4'	-9.23	1.29	1.53
1	A	1402	B8T	C4-N3	8.03	1.46	1.32
1	A	1402	B8T	C2-N3	6.38	1.49	1.36
1	A	1402	B8T	C6-C5	6.25	1.49	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1402	B8T	C41-N4-C4	-2.26	118.03	122.45
1	A	1402	B8T	C6-C5-C4	2.14	119.58	117.00
1	A	1519	MA6	C2-N1-C6	2.08	118.88	116.84
1	A	1402	B8T	C2'-C3'-C4'	2.04	106.56	102.61
1	A	1518	MA6	C2-N1-C6	2.03	118.83	116.84

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1402	B8T	C2'-C1'-N1-C6
1	A	1519	MA6	C5-C6-N6-C9
1	A	1402	B8T	O4'-C4'-C5'-O5'
1	A	1402	B8T	C4'-C5'-O5'-P
1	A	1402	B8T	C3'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1402	B8T	2	0
1	A	1519	MA6	2	0
1	A	1518	MA6	3	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 81 ligands modelled in this entry, 79 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z  > 2$
23	AN6	V	801	-	25,30,30	1.01	2 (8%)	24,43,43	0.80	0
23	AN6	A	1601	1	25,30,30	3.72	7 (28%)	24,43,43	1.44	2 (8%)

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
23	AN6	V	801	-	-	8/15/35/35	0/3/3/3
23	AN6	A	1601	1	-	11/15/35/35	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	1601	AN6	O4'-C4'	10.42	1.68	1.45
23	A	1601	AN6	C3'-C4'	-10.31	1.26	1.53
23	A	1601	AN6	O4'-C1'	-7.91	1.30	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	1601	AN6	C5'-N10	4.52	1.56	1.47
23	A	1601	AN6	O2'-C2'	-3.63	1.34	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1601	AN6	N3-C2-N1	-5.12	121.72	128.67
23	A	1601	AN6	C4'-O4'-C1'	-2.17	107.94	109.92

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

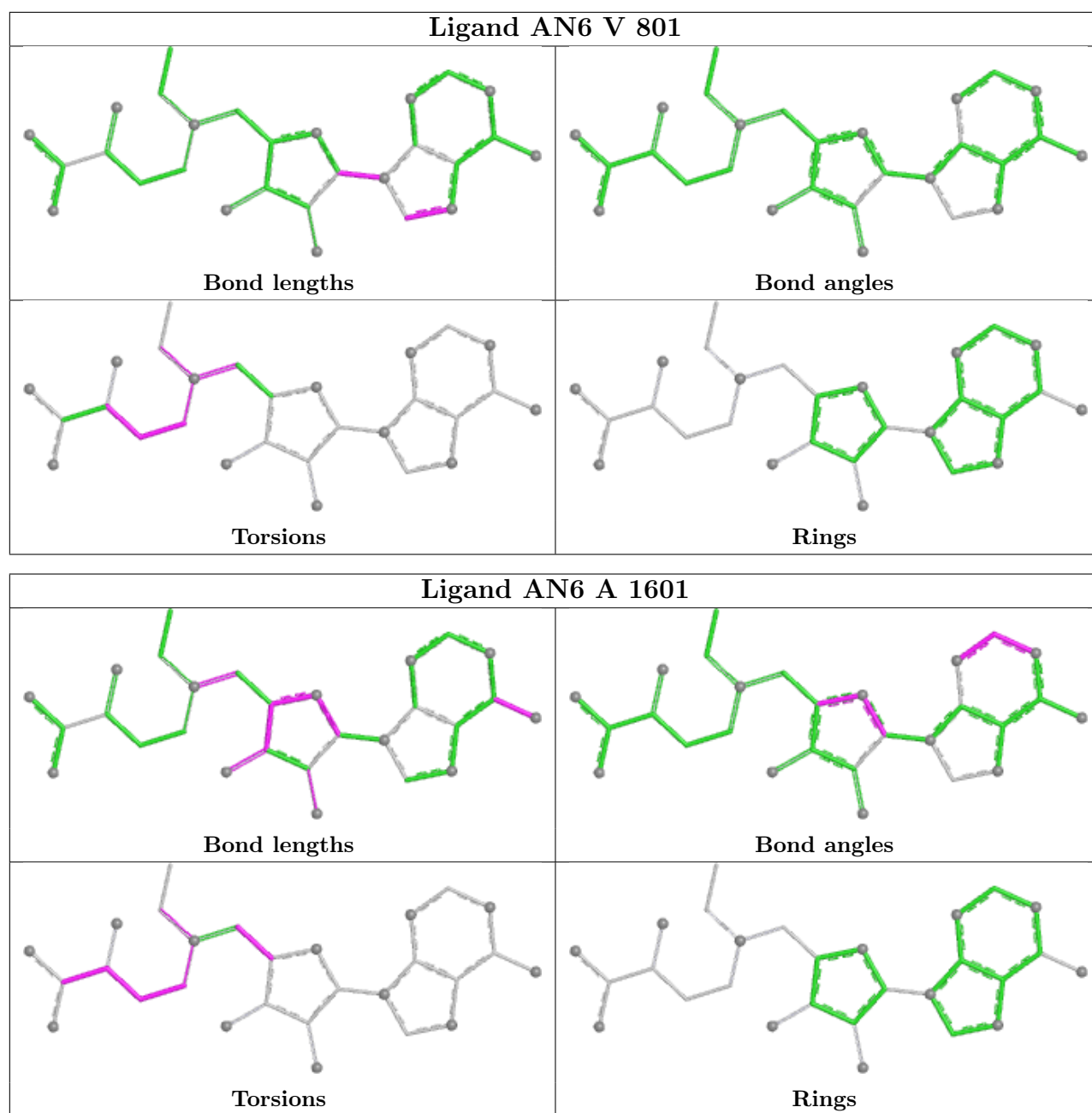
Mol	Chain	Res	Type	Atoms
23	A	1601	AN6	C3'-C4'-C5'-N10
23	A	1601	AN6	O4'-C4'-C5'-N10
23	A	1601	AN6	N'-CA'-CB'-CG'
23	V	801	AN6	CA'-CB'-CG'-N10
23	A	1601	AN6	CB'-CG'-N10-C5'

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	V	801	AN6	2	0
23	A	1601	AN6	4	0

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 than 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.



## 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.

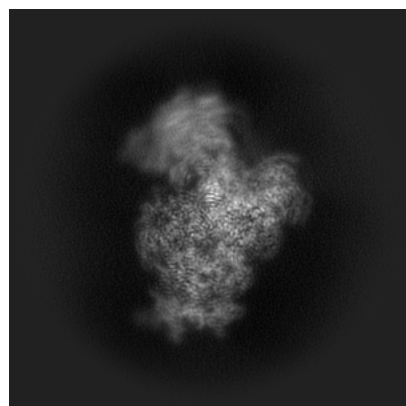
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72071. These allow visual inspection of the internal detail of the map and identification of artifacts.

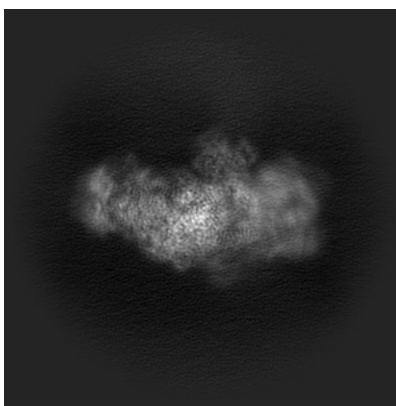
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

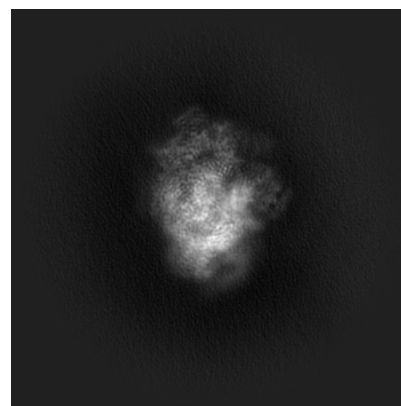
#### 6.1.1 Primary map



X

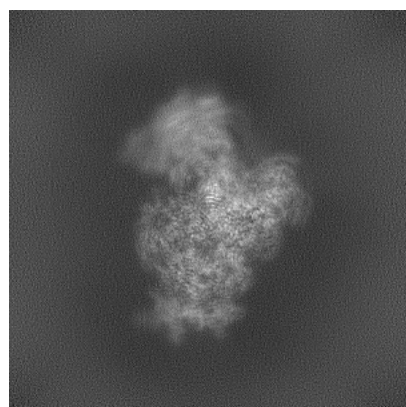


Y

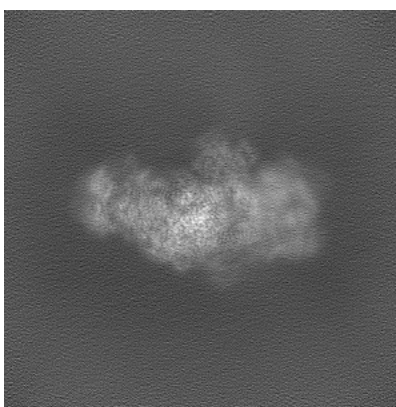


Z

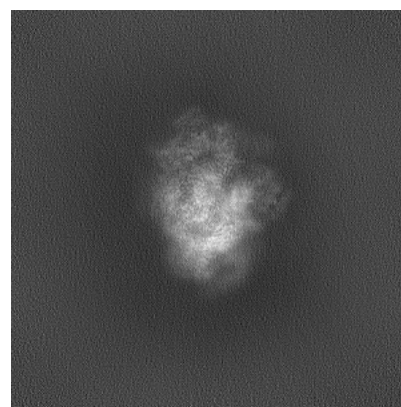
#### 6.1.2 Raw map



X



Y

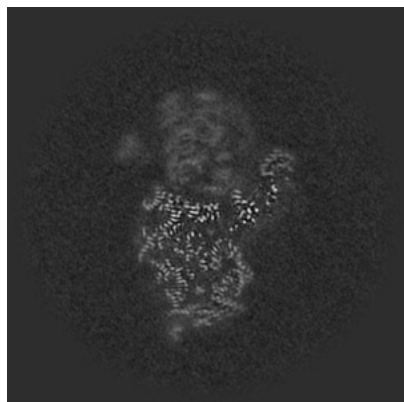


Z

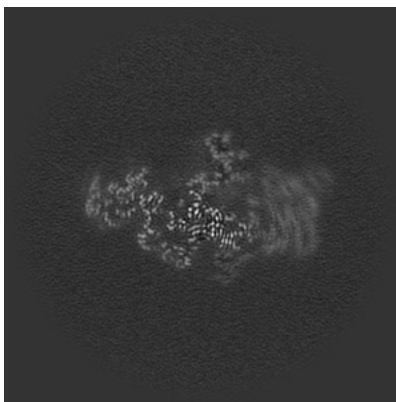
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

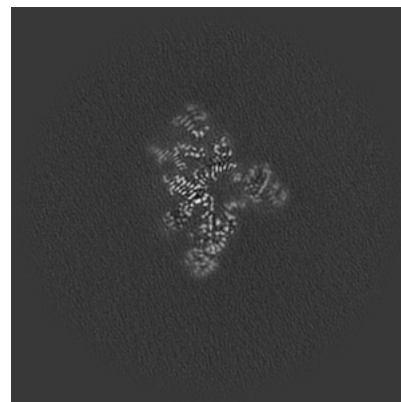
### 6.2.1 Primary map



X Index: 224

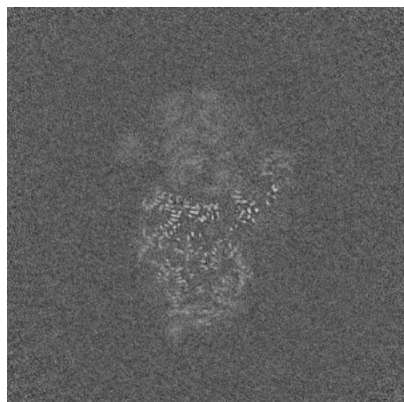


Y Index: 224

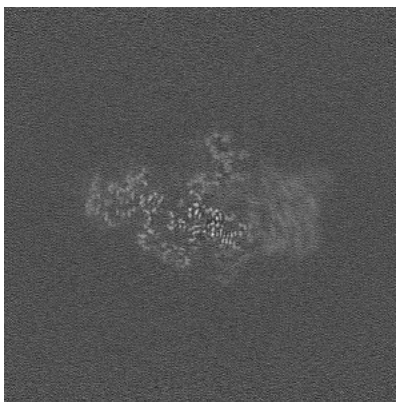


Z Index: 224

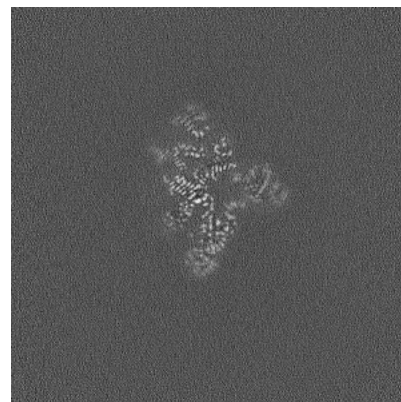
### 6.2.2 Raw map



X Index: 224



Y Index: 224



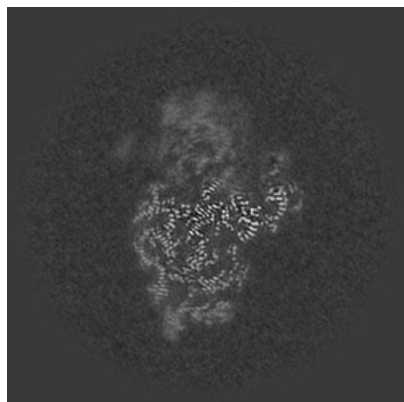
Z Index: 224

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

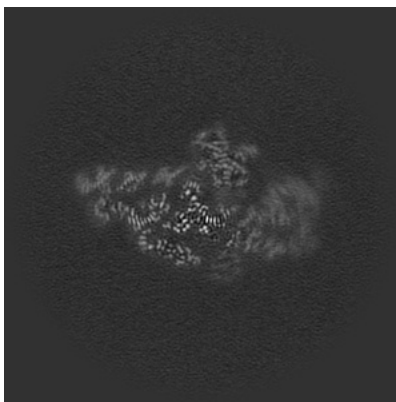


## 6.3 Largest variance slices [i](#)

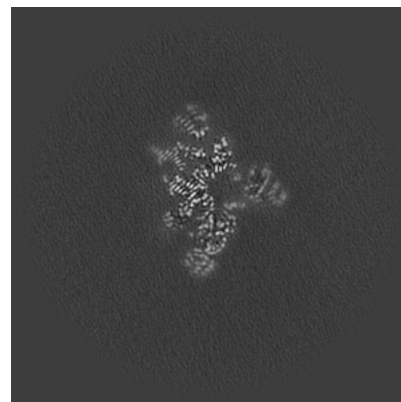
### 6.3.1 Primary map



X Index: 216

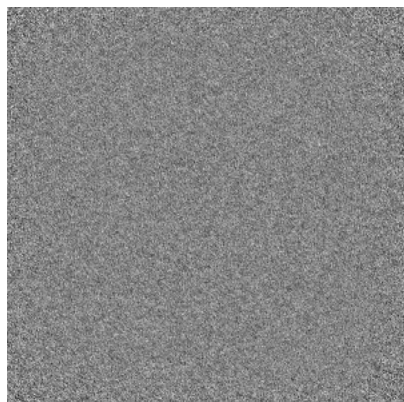


Y Index: 234

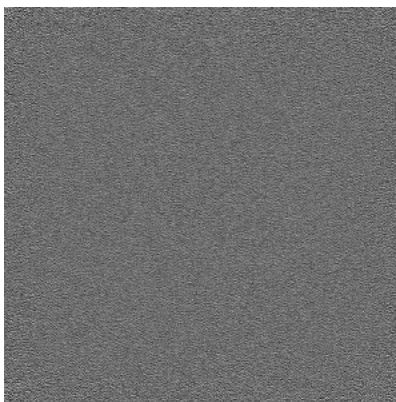


Z Index: 223

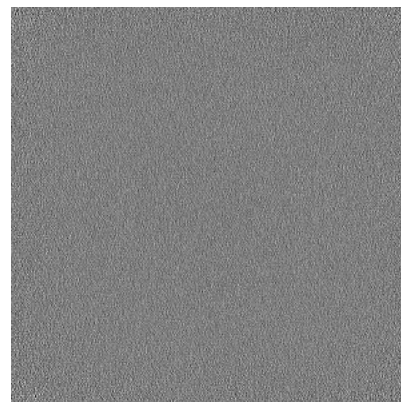
### 6.3.2 Raw map



X Index: 0



Y Index: 0

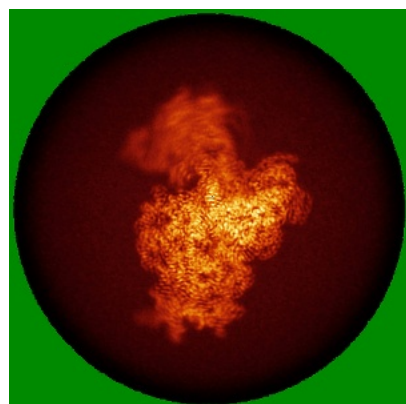


Z Index: 447

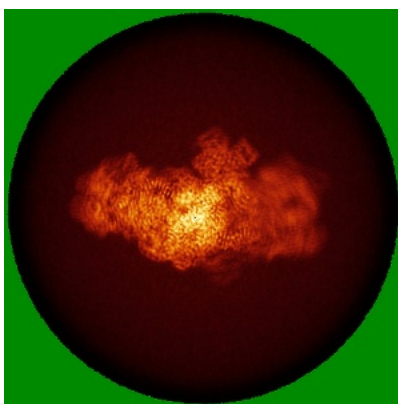
The images above show the largest variance slices of the map in three orthogonal directions.

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

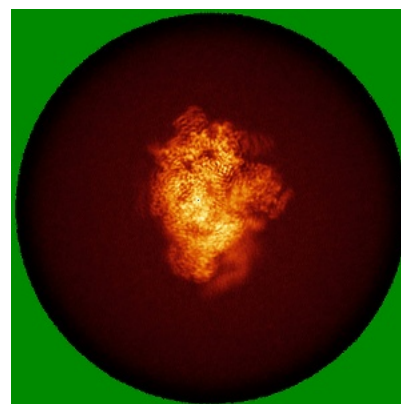
### 6.4.1 Primary map



X

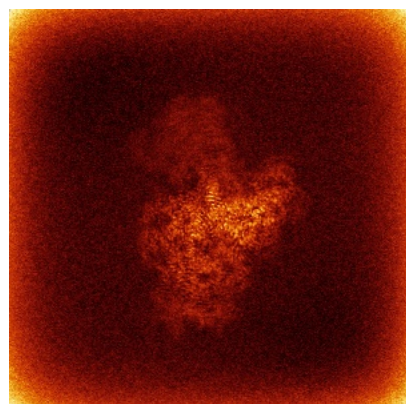


Y

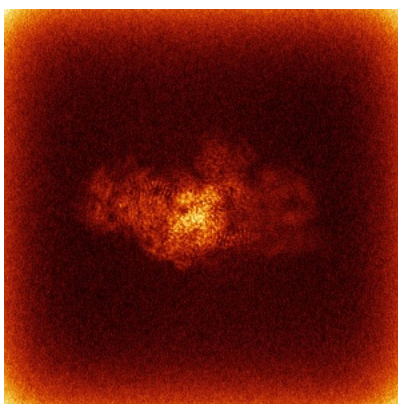


Z

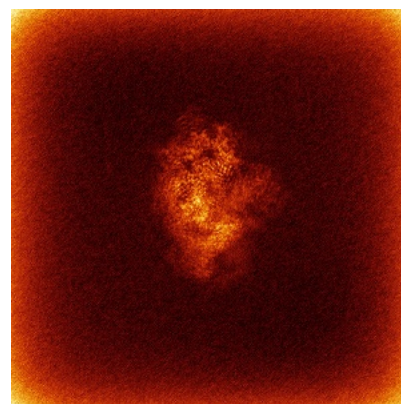
### 6.4.2 Raw map



X



Y



Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



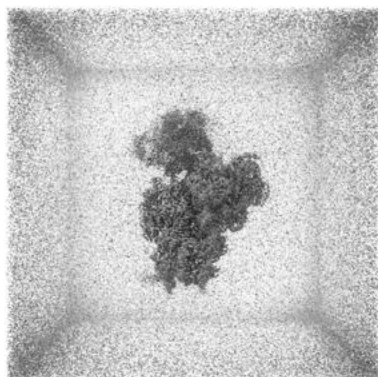
Y



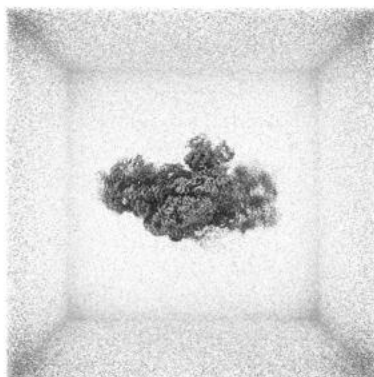
Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

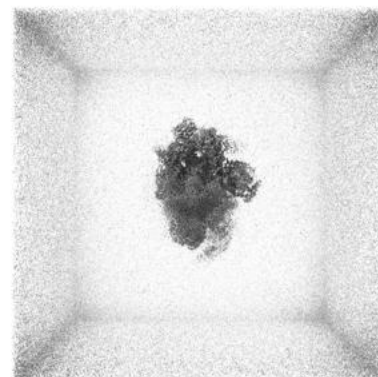
### 6.5.2 Raw map



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.

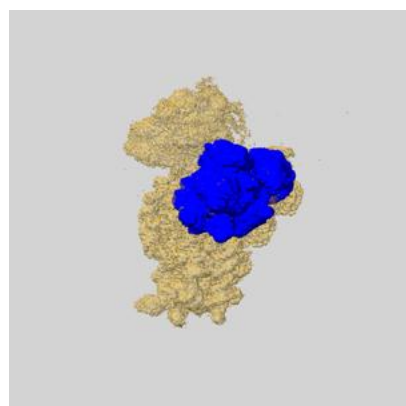
## 6.6 Mask visualisation [i](#)

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

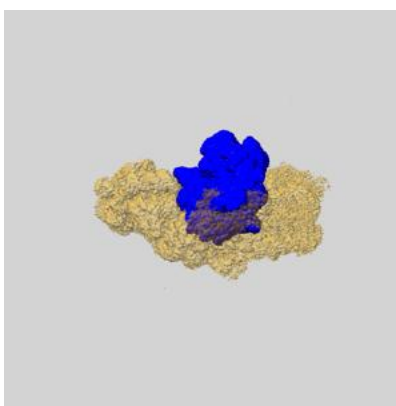
A mask typically either:

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

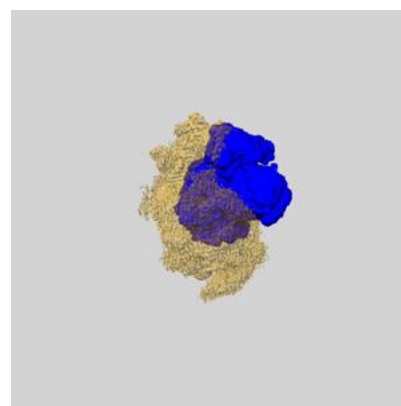
### 6.6.1 emd\_72071\_msk\_1.map [i](#)



X



Y



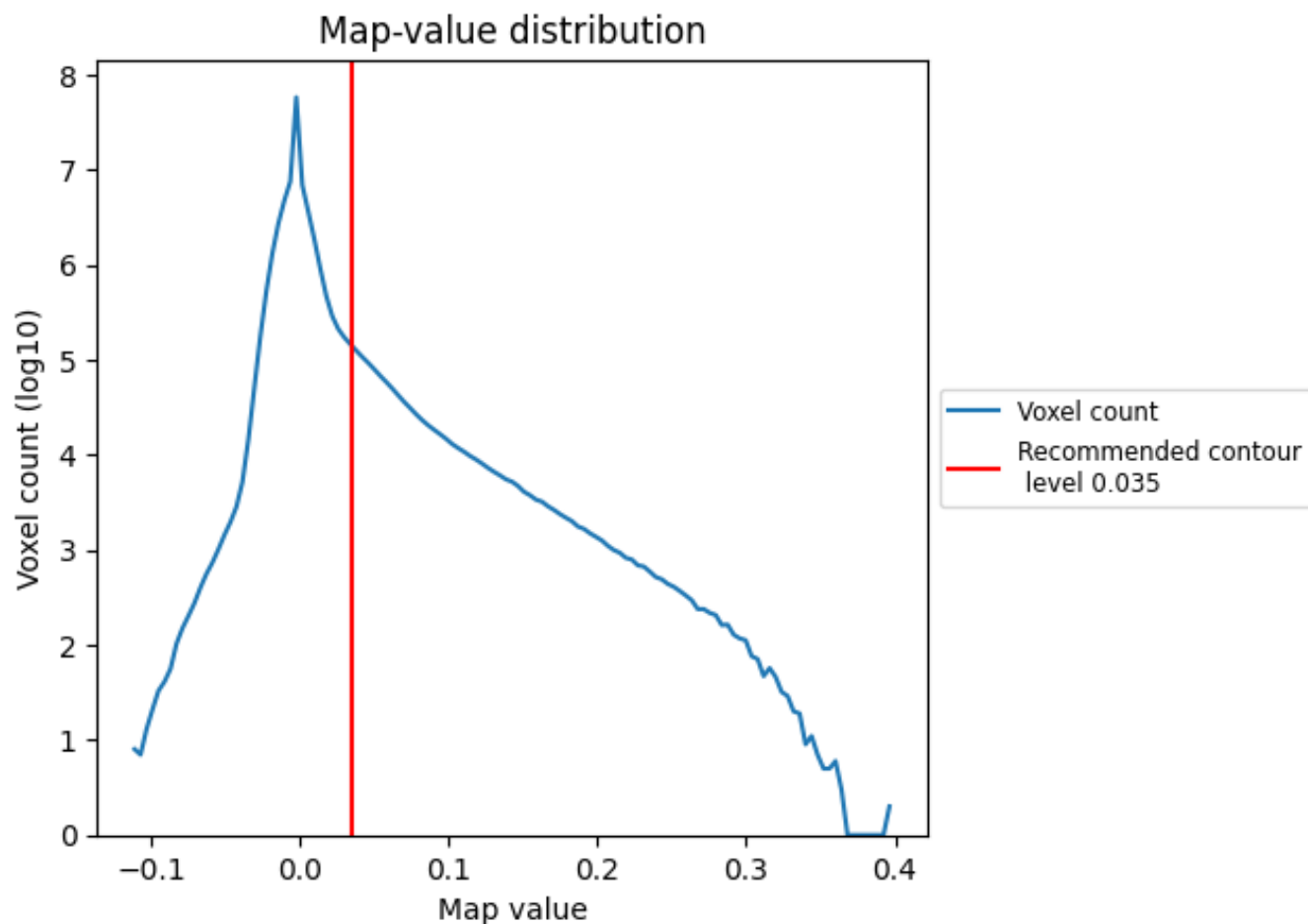
Z



## 7 Map analysis [i](#)

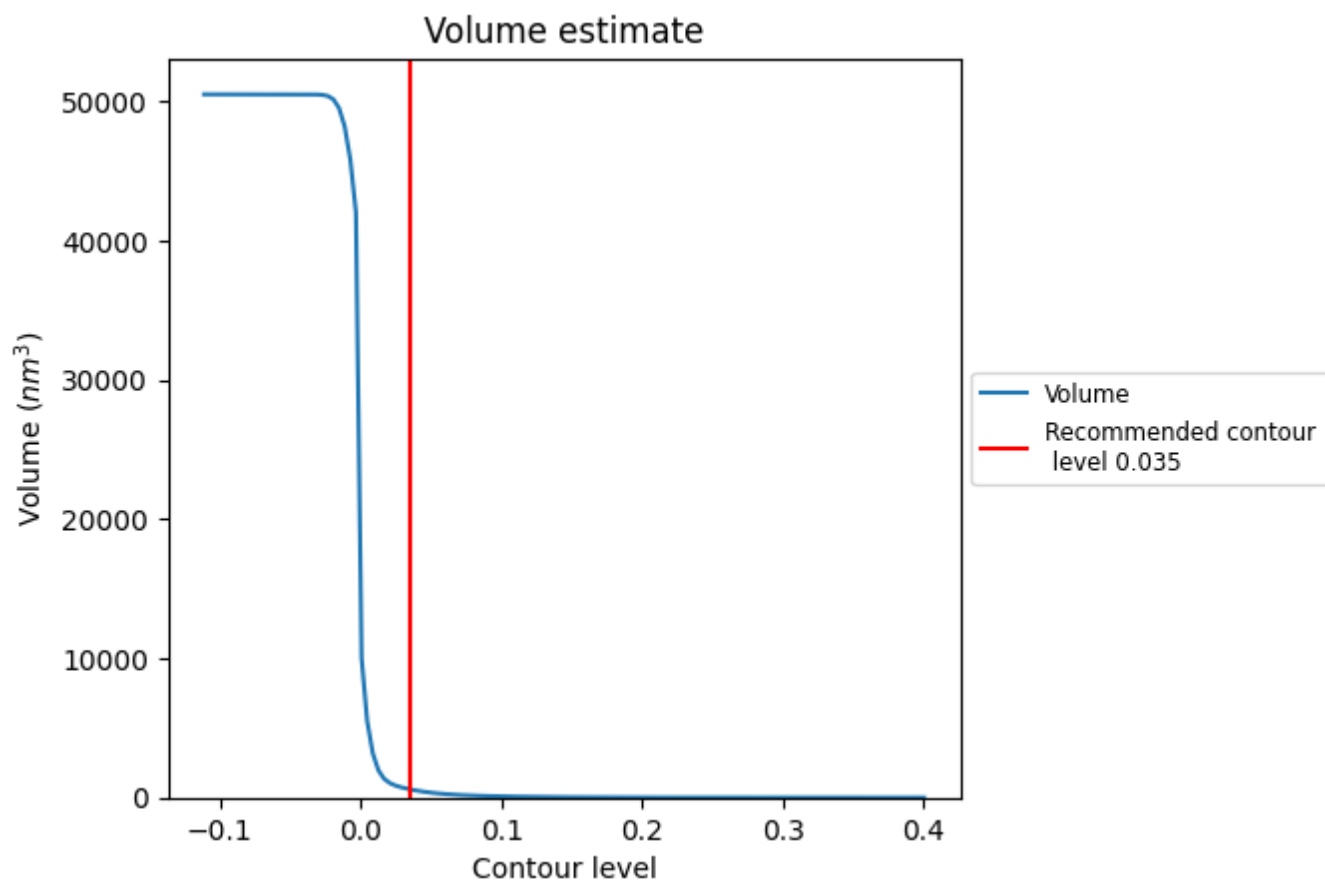
This section contains the results of statistical analysis of the map.

### 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.

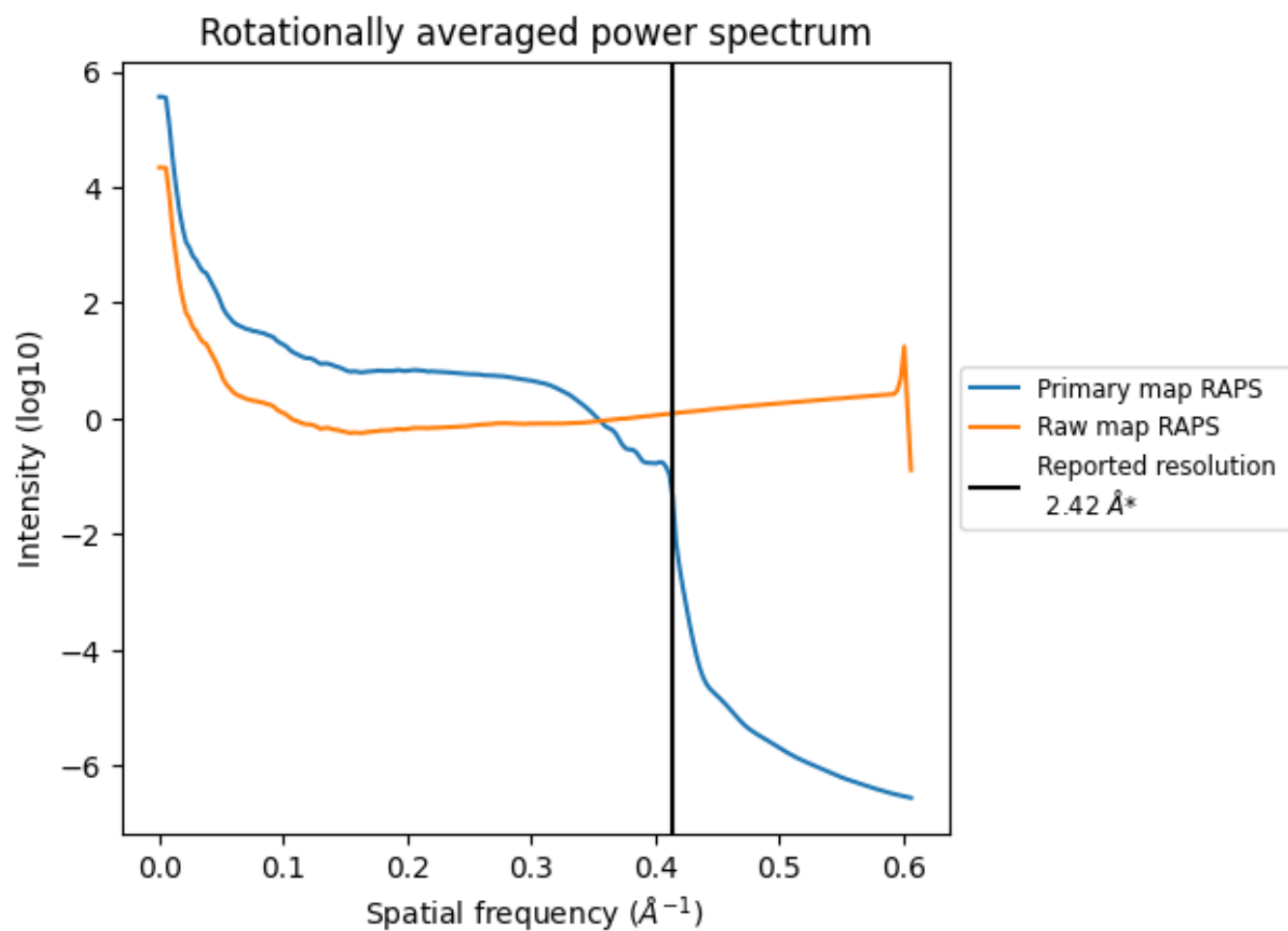
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 594 nm<sup>3</sup>; this corresponds to an approximate mass of 536 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 ⓘ

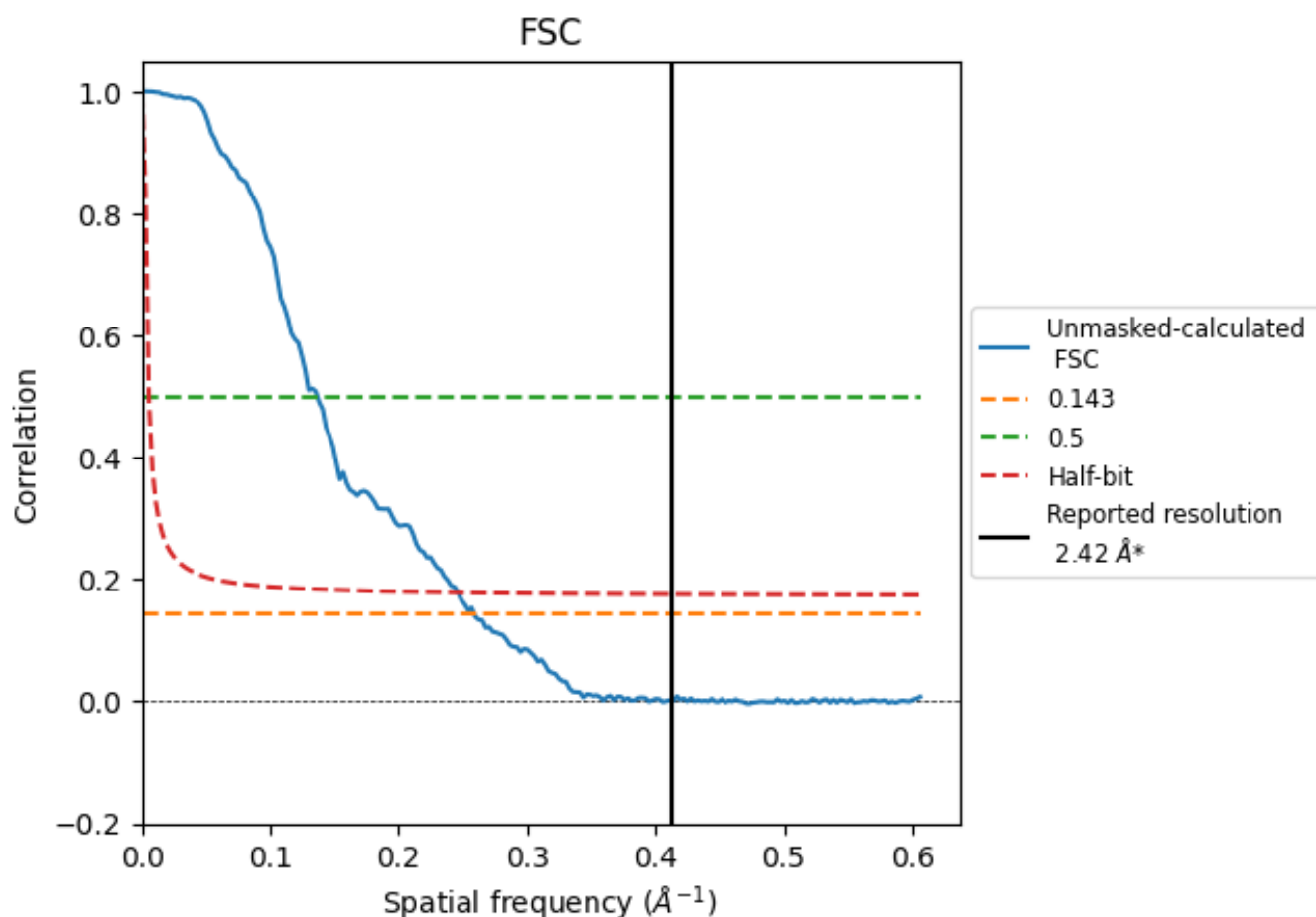


\*Reported resolution corresponds to spatial frequency of 0.413  $\text{\AA}^{-1}$

## 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 0.413 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

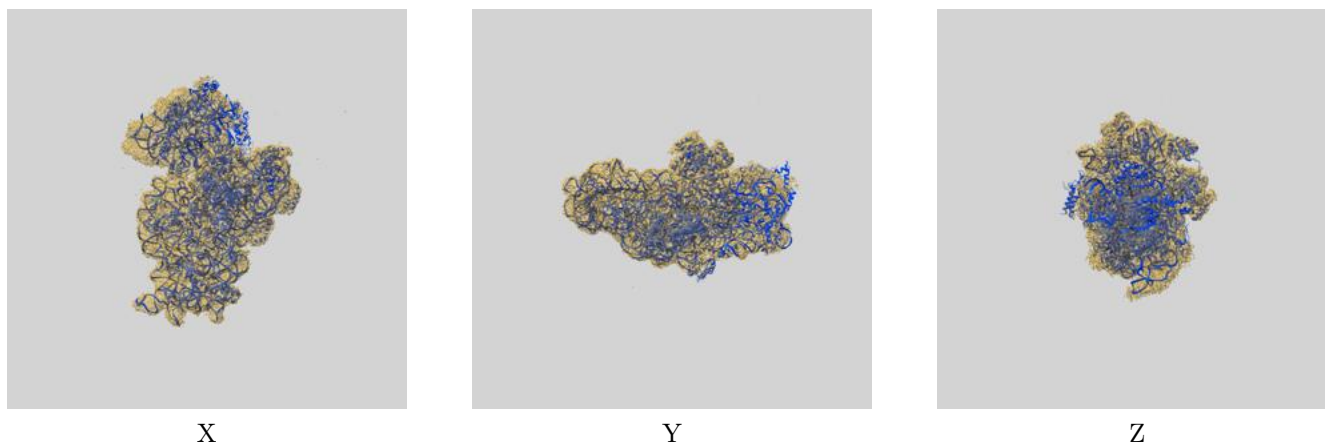
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.42	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.86	7.33	4.06

\*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 3.86 differs from the reported value 2.42 by more than 10 %

## 9 Map-model fit [i](#)

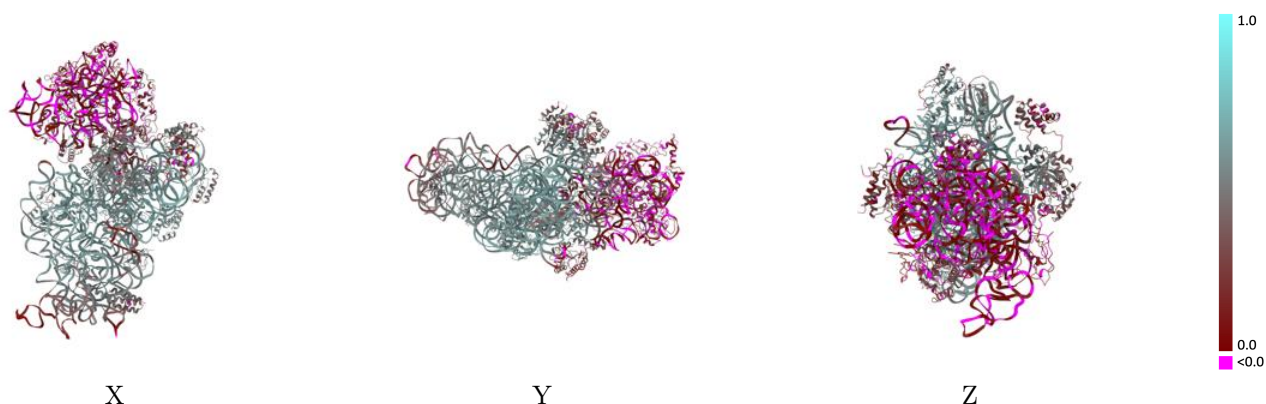
This section contains information regarding the fit between EMDB map EMD-72071 and PDB model 9PZG. Per-residue inclusion information can be found in section [3](#) on page [10](#).

### 9.1 Map-model overlay [i](#)



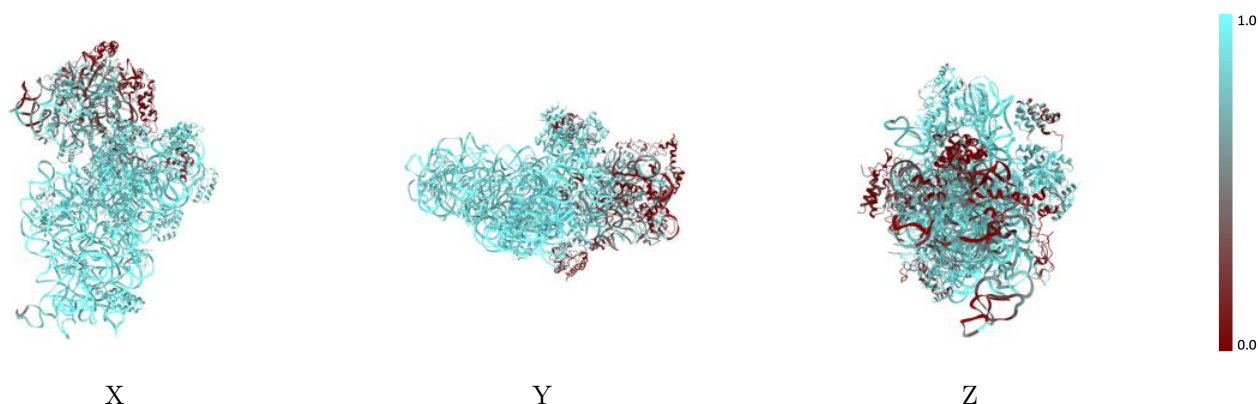
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



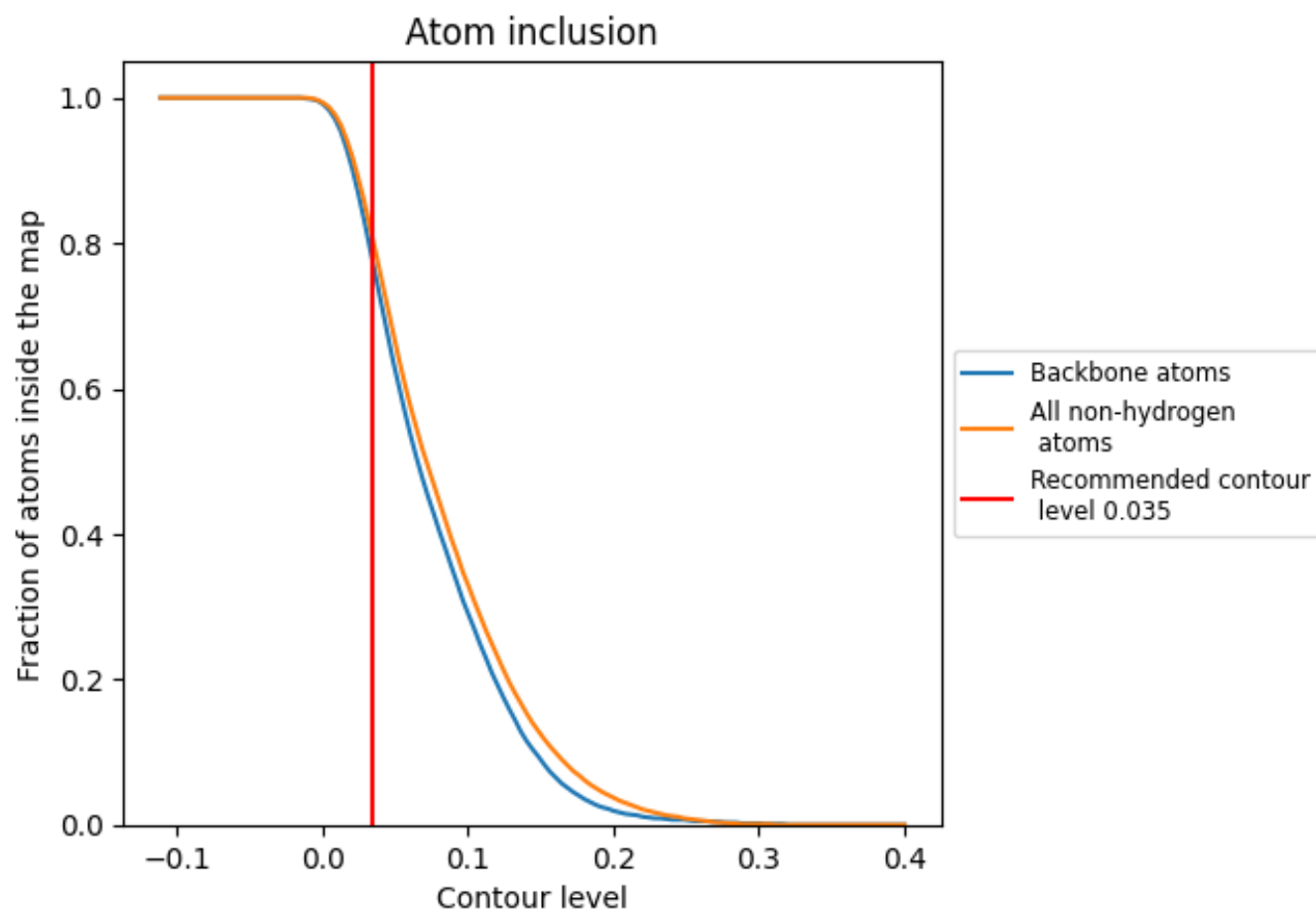
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

## 9.4 Atom inclusion [i](#)



















































At the recommended contour level, 77% of all backbone atoms, 80% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8040	 0.3860
A	 0.8640	 0.3990
B	 0.3010	 0.2930
C	 0.7150	 0.2770
D	 0.9060	 0.4870
E	 0.9590	 0.5710
F	 0.8330	 0.4510
G	 0.0650	 0.1370
H	 0.9540	 0.5820
I	 0.3780	 0.0540
J	 0.6120	 0.1110
K	 0.9170	 0.4800
L	 0.9560	 0.5720
M	 0.2940	 0.0620
N	 0.7810	 0.1200
O	 0.9460	 0.5530
P	 0.9140	 0.5150
Q	 0.9350	 0.5350
R	 0.9470	 0.5560
S	 0.4250	 0.1020
T	 0.9340	 0.4640
U	 0.3220	 0.1750
V	 0.8400	 0.4140
W	 0.8100	 0.4440

