



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 09:20 am BST

PDB ID : 9TEZ / pdb_00009tez
EMDB ID : EMD-55849
Title : DalDroS bound to the Escherichia coli 50S ribosomal subunit
Authors : Berger, M.J.; Safdari, H.A.; Wilson, D.N.
Deposited on : 2025-11-26
Resolution : 2.88 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 ⓘ 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:

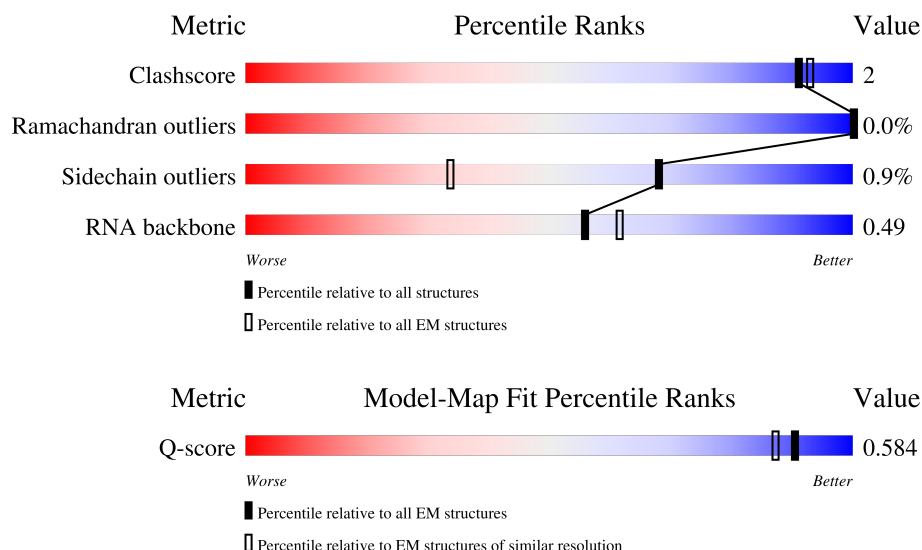
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal 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.





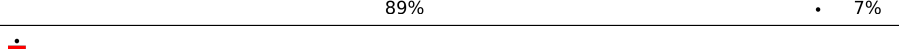
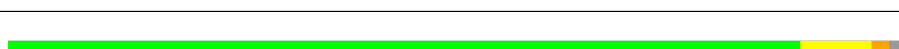


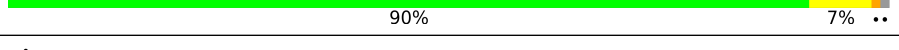
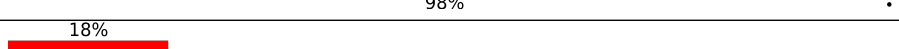


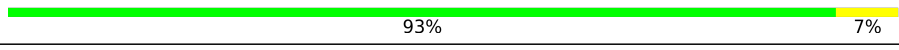
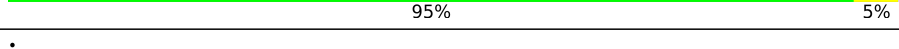
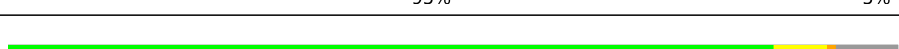
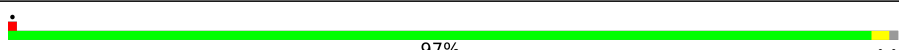
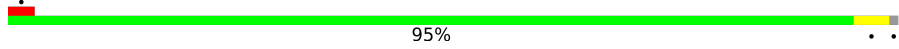
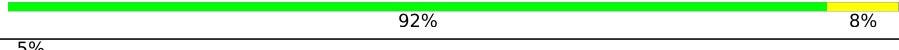
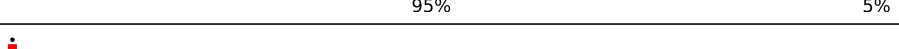

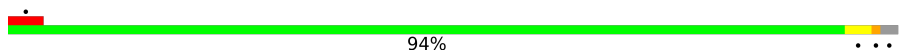
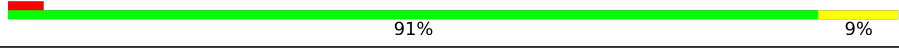




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12111 (2.38 - 3.38)

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	3	38	100%
2	d	209	96%
3	4	70	84%

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Mol	Chain	Length	Quality of chain
4	V	2904	
5	8	20	
6	0	55	
7	1	46	
8	2	65	
9	W	360	
10	b	120	
11	c	273	
12	e	201	
13	f	179	
14	g	177	
15	h	149	
16	i	142	
17	j	123	
18	k	144	
19	m	127	
20	n	117	
21	o	115	
22	p	118	
23	q	103	
24	r	110	
25	s	100	
26	t	104	
27	u	94	
28	v	85	

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Mol	Chain	Length	Quality of chain
29	w	78	 90%9% .
30	x	63	 90%8% .
31	y	59	 97% . .
32	z	57	 86%11% .
33	l	136	 94% . .
34	Z	76	 70%25% . .

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 90140 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 2 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 3 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	59	Total	C	N	O	S	0	0
			472	294	89	84	5		

- Molecule 4 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	V	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 5 is a protein called DalDroS.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	8	15	Total	C	N	O	0	0
			124	79	26	19		

- Molecule 6 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 7 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 8 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 9 is a protein called Peptide chain release factor RF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	254	Total	C	N	O	S	0	0
			1977	1207	376	386	8		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 11 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	270	Total	C	N	O	S	0	0
			2076	1285	422	362	7		

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 14 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 15 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 16 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	i	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 17 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 19 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 20 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 21 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	o	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	p	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 23 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	q	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	r	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	s	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	t	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	u	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	77	Total	C	N	O	S	0	0
			582	360	115	106	1		

- Molecule 29 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 31 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 33 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	134	Total	C	N	O	S	0	0
			1055	675	200	175	5		

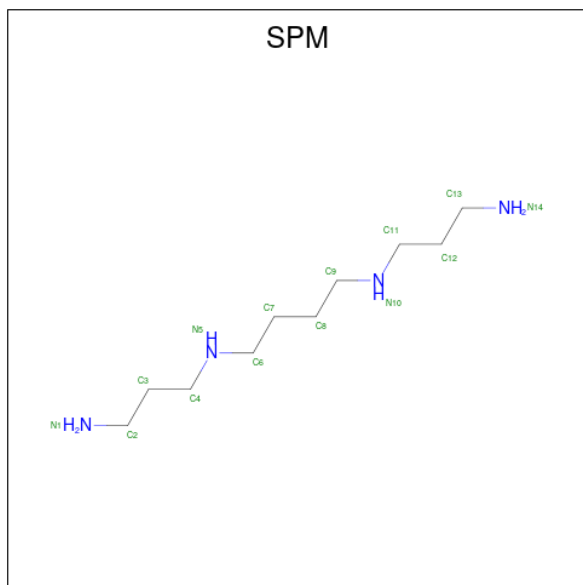
- Molecule 34 is a RNA chain called P-site Phe-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	3	1	Total	Zn	0
			1	1	
35	4	1	Total	Zn	0
			1	1	

- Molecule 36 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf
36	V	1	Total	C	N	0
			14	10	4	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	V	1	Total	Mg	0
			1	1	

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.

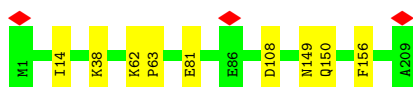
- Molecule 1: Large ribosomal subunit protein bL36A

Chain 3:  100%


There are no outlier residues recorded for this chain.

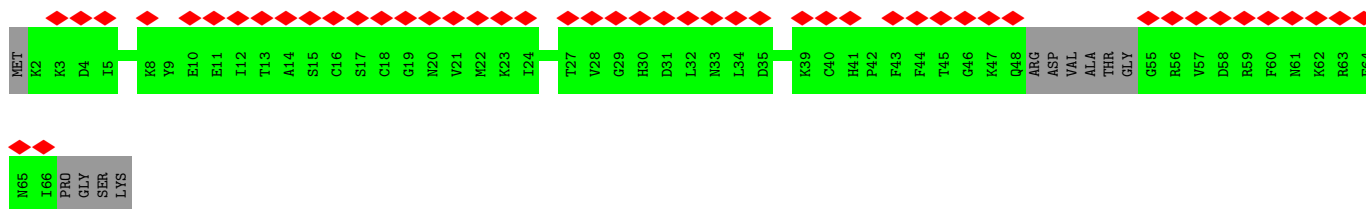
- Molecule 2: Large ribosomal subunit protein uL3

Chain d:  96%



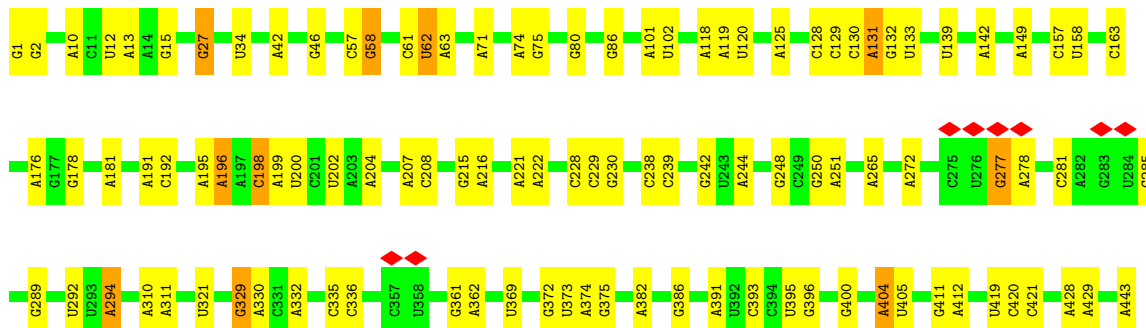
- Molecule 3: Large ribosomal subunit protein bL31A

Chain 4:  70% 84% 16%

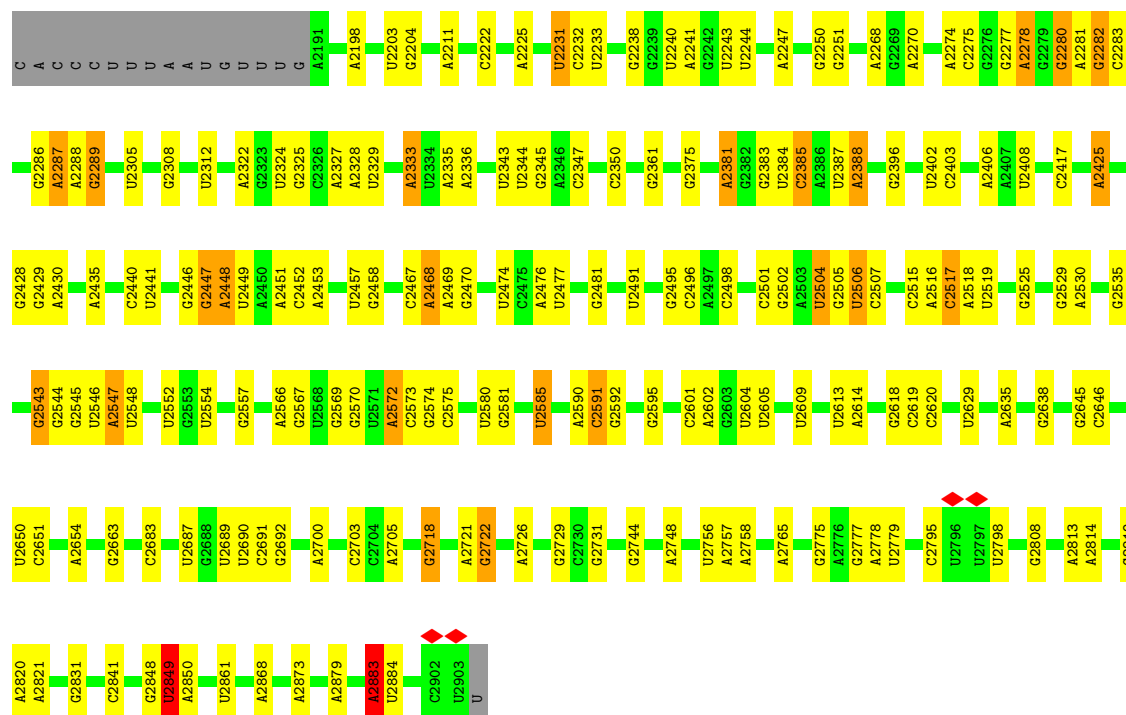


- Molecule 4: 23S rRNA

Chain V:  69% 22% 5%



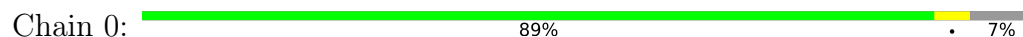




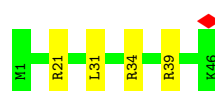
• Molecule 5: DalDroS



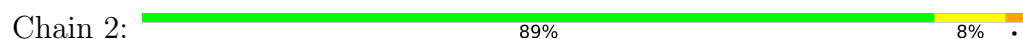
• Molecule 6: Large ribosomal subunit protein bL33



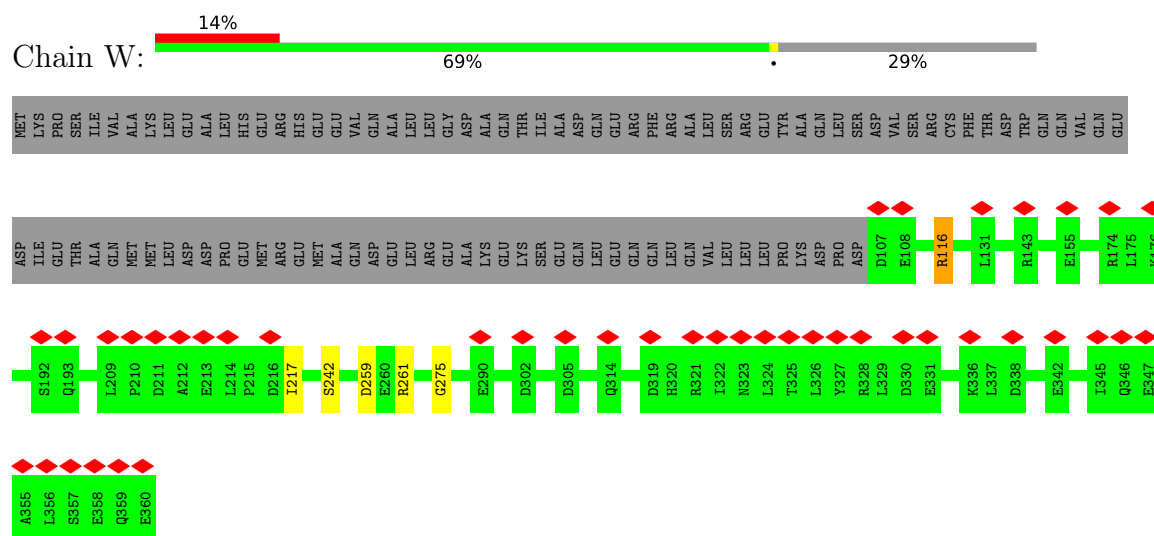
• Molecule 7: Large ribosomal subunit protein bL34



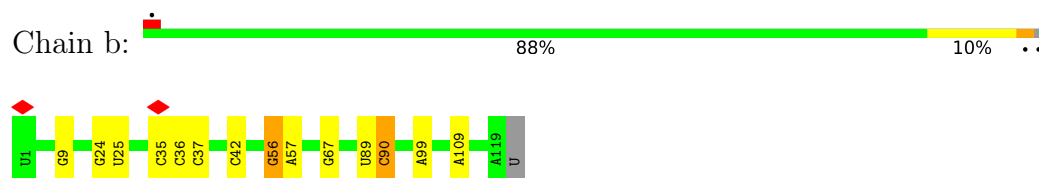
• Molecule 8: Large ribosomal subunit protein bL35



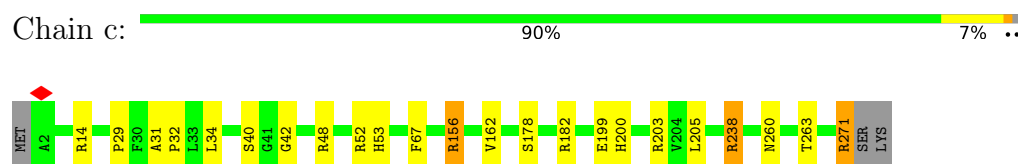
- Molecule 9: Peptide chain release factor RF1



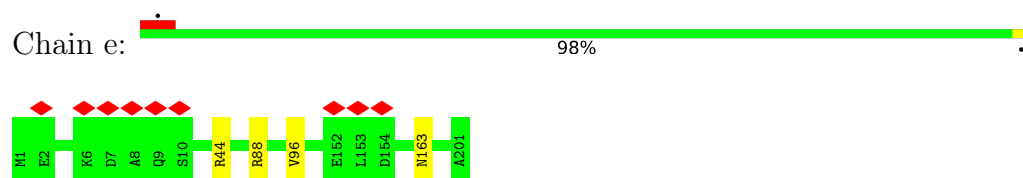
- Molecule 10: 5S rRNA



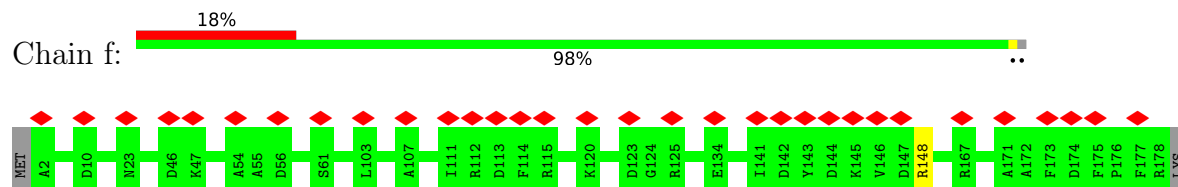
- Molecule 11: Large ribosomal subunit protein uL2



- Molecule 12: Large ribosomal subunit protein uL4

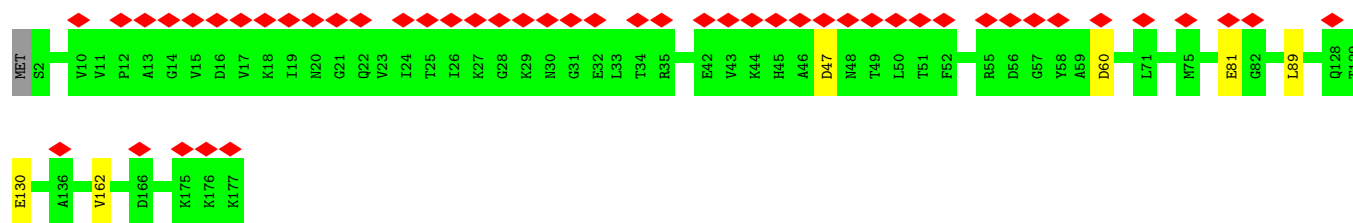


- Molecule 13: Large ribosomal subunit protein uL5

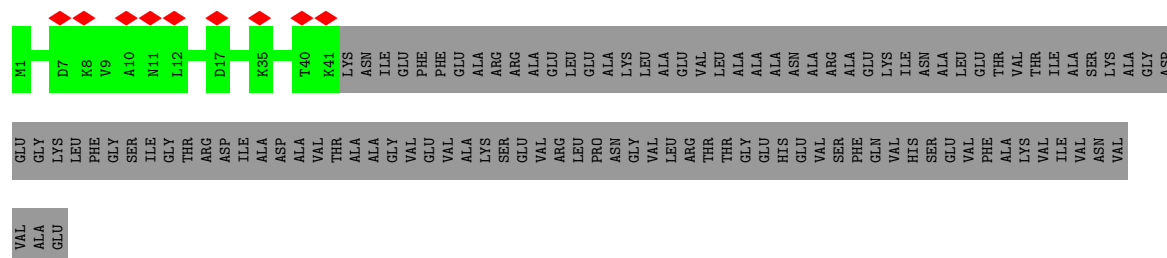


- Molecule 14: Large ribosomal subunit protein uL6





- Molecule 15: Large ribosomal subunit protein bL9



- Molecule 16: Large ribosomal subunit protein uL13



- Molecule 17: Large ribosomal subunit protein uL14



- Molecule 18: 50S ribosomal protein L15



- Molecule 19: Large ribosomal subunit protein bL17



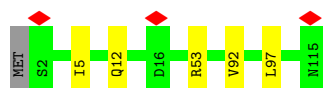
- Molecule 20: Large ribosomal subunit protein uL18

Chain n:  97%




- Molecule 21: Large ribosomal subunit protein bL19

Chain o:  95%

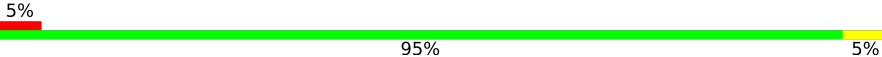


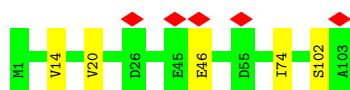
- Molecule 22: Large ribosomal subunit protein bL20

Chain p:  92% 8%



- Molecule 23: Large ribosomal subunit protein bL21

Chain q:  5% 95% 5%



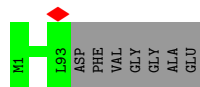
- Molecule 24: Large ribosomal subunit protein uL22

Chain r:  97%



- Molecule 25: Large ribosomal subunit protein uL23

Chain s:  93% 7%



- Molecule 26: Large ribosomal subunit protein uL24

Chain t:  94%




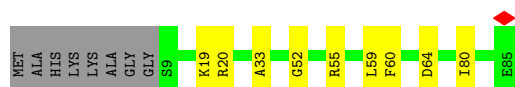
- Molecule 27: 50S ribosomal protein L25

Chain u:  91% 9%



- Molecule 28: Large ribosomal subunit protein bL27

Chain v:  80% 11% 9%



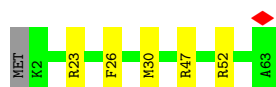
- Molecule 29: Large ribosomal subunit protein bL28

Chain w:  90% 9%



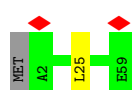
- Molecule 30: Large ribosomal subunit protein uL29

Chain x:  90% 8%




- Molecule 31: Large ribosomal subunit protein uL30

Chain y:  97%

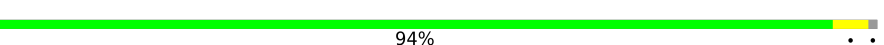


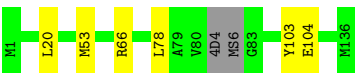
- Molecule 32: Large ribosomal subunit protein bL32

Chain z:  86% 11%

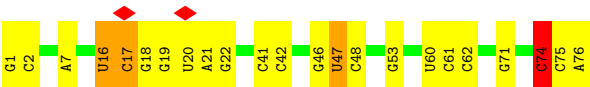


- Molecule 33: Large ribosomal subunit protein uL16

Chain l:  94%



• Molecule 34: P-site Phe-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	202610	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 ($e^-/\text{\AA}^2$)	1.14	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.054	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	345.28, 345.28, 345.28	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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: G7M, ZN, 5MC, 1MG, OMU, PSU, 6MZ, MEQ, 2MG, OMC, 5MU, SPM, MG, OMG, 3TD, H2U, 2MA

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	3	0.61	0/303	0.81	0/397
2	d	0.67	0/1576	0.93	1/2119 (0.0%)
3	4	0.61	0/480	0.87	0/639
4	V	0.63	1/65651 (0.0%)	1.01	171/102413 (0.2%)
5	8	0.76	0/130	0.93	0/178
6	0	0.64	0/424	0.90	0/565
7	1	0.79	0/380	1.04	0/498
8	2	0.74	0/513	0.97	1/676 (0.1%)
9	W	0.57	0/2007	0.85	0/2702
10	b	0.58	0/2850	0.88	1/4444 (0.0%)
11	c	0.70	1/2115 (0.0%)	0.95	0/2844
12	e	0.63	0/1571	0.93	0/2113
13	f	0.56	0/1434	0.93	0/1926
14	g	0.58	0/1343	0.89	0/1816
15	h	0.59	0/306	0.94	0/413
16	i	0.65	0/1152	0.92	0/1551
17	j	0.64	0/955	0.93	0/1279
18	k	0.66	0/1062	0.91	0/1413
19	m	0.72	0/958	0.97	0/1281
20	n	0.62	0/902	0.95	0/1209
21	o	0.66	0/929	0.88	0/1242
22	p	0.69	0/960	0.99	0/1278
23	q	0.59	0/829	0.82	0/1107
24	r	0.64	0/864	0.94	0/1156
25	s	0.60	0/744	0.88	0/994
26	t	0.58	0/787	0.88	0/1051
27	u	0.58	0/766	0.86	0/1025
28	v	0.68	0/589	0.84	0/780
29	w	0.66	0/635	0.92	0/848
30	x	0.52	0/502	0.95	0/667
31	y	0.61	0/453	0.94	0/605

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	z	0.72	0/440	0.94	0/588
33	l	0.65	0/1073	0.94	0/1433
34	Z	0.60	0/1813	0.88	3/2823 (0.1%)
All	All	0.63	2/97496 (0.0%)	0.98	177/146073 (0.1%)

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
4	V	0	9
5	8	0	2
7	1	0	1
8	2	0	3
9	W	0	1
11	c	0	6
12	e	0	1
16	i	0	1
18	k	0	3
19	m	0	2
21	o	0	1
22	p	0	4
29	w	0	2
30	x	0	2
All	All	0	38

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	V	2069	G7M	O3'-P	5.29	1.61	1.56
11	c	53	HIS	CG-CD2	-5.21	1.30	1.35

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	V	2572	A	O3'-P-O5'	-11.51	86.74	104.00
4	V	818	G	O3'-P-O5'	-9.71	89.44	104.00
4	V	2601	C	O3'-P-O5'	-9.55	89.67	104.00
4	V	1818	U	O3'-P-O5'	-9.13	90.30	104.00
4	V	2449	H2U	O3'-P-O5'	-8.93	90.60	104.00

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	V	27	G	Sidechain
4	V	463	G	Sidechain
4	V	512	G	Sidechain
4	V	956	G	Sidechain
4	V	983	A	Sidechain

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	3	302	0	340	0	0
2	d	1566	0	1618	5	0
3	4	472	0	466	0	0
4	V	59130	0	29770	181	0
5	8	124	0	127	0	0
6	0	417	0	451	1	0
7	1	377	0	418	2	0
8	2	504	0	572	3	0
9	W	1977	0	1932	3	0
10	b	2549	0	1291	1	0
11	c	2076	0	2149	11	0
12	e	1552	0	1619	1	0
13	f	1410	0	1444	0	0
14	g	1323	0	1371	1	0
15	h	303	0	327	0	0
16	i	1129	0	1162	6	0
17	j	946	0	1023	2	0
18	k	1053	0	1129	2	0
19	m	945	0	989	5	0
20	n	892	0	923	1	0
21	o	917	0	962	2	0
22	p	947	0	1019	3	0
23	q	816	0	839	2	0
24	r	857	0	922	1	0
25	s	738	0	807	0	0
26	t	779	0	831	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	u	753	0	780	4	0
28	v	582	0	593	5	0
29	w	625	0	652	3	0
30	x	501	0	531	3	0
31	y	449	0	488	1	0
32	z	434	0	445	4	0
33	l	1055	0	1134	3	0
34	Z	1623	0	821	4	0
35	3	1	0	0	0	0
35	4	1	0	0	0	0
36	V	14	0	26	0	0
37	V	1	0	0	0	0
All	All	90140	0	59971	236	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 236 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)
4:V:2030:6MZ:O3'	4:V:2031:A:OP2	1.91	0.87
4:V:2030:6MZ:O3'	4:V:2031:A:P	2.41	0.78
4:V:2327:A:H2'	4:V:2328:A:C8	2.25	0.70
4:V:568:U:H1'	4:V:2030:6MZ:H9C1	1.75	0.68
20:n:27:VAL:HG21	20:n:40:ILE:HD12	1.79	0.65

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	36/38 (95%)	36 (100%)	0	0	100	100
2	d	206/209 (99%)	197 (96%)	9 (4%)	0	100	100
3	4	55/70 (79%)	52 (94%)	3 (6%)	0	100	100
5	8	13/20 (65%)	13 (100%)	0	0	100	100
6	0	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
7	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
8	2	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
9	W	252/360 (70%)	241 (96%)	11 (4%)	0	100	100
11	c	268/273 (98%)	255 (95%)	13 (5%)	0	100	100
12	e	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
13	f	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
14	g	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
15	h	39/149 (26%)	35 (90%)	4 (10%)	0	100	100
16	i	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
17	j	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
18	k	142/144 (99%)	133 (94%)	8 (6%)	1 (1%)	18	44
19	m	116/127 (91%)	109 (94%)	7 (6%)	0	100	100
20	n	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
21	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
22	p	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
23	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
24	r	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
25	s	91/100 (91%)	89 (98%)	2 (2%)	0	100	100
26	t	100/104 (96%)	96 (96%)	4 (4%)	0	100	100
27	u	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
28	v	75/85 (88%)	72 (96%)	3 (4%)	0	100	100
29	w	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
30	x	60/63 (95%)	60 (100%)	0	0	100	100
31	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
32	z	53/57 (93%)	50 (94%)	3 (6%)	0	100	100
33	l	130/136 (96%)	121 (93%)	9 (7%)	0	100	100
All	All	3373/3717 (91%)	3222 (96%)	150 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	k	29	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	34/34 (100%)	34 (100%)	0	100	100
2	d	163/163 (100%)	163 (100%)	0	100	100
3	4	54/62 (87%)	54 (100%)	0	100	100
5	8	15/19 (79%)	15 (100%)	0	100	100
6	0	46/49 (94%)	46 (100%)	0	100	100
7	1	38/38 (100%)	38 (100%)	0	100	100
8	2	51/52 (98%)	51 (100%)	0	100	100
9	W	205/300 (68%)	203 (99%)	2 (1%)	68	87
11	c	215/218 (99%)	214 (100%)	1 (0%)	81	93
12	e	165/165 (100%)	163 (99%)	2 (1%)	63	84
13	f	148/150 (99%)	147 (99%)	1 (1%)	76	90
14	g	137/138 (99%)	133 (97%)	4 (3%)	37	68
15	h	32/114 (28%)	32 (100%)	0	100	100
16	i	116/116 (100%)	116 (100%)	0	100	100
17	j	104/104 (100%)	102 (98%)	2 (2%)	50	77
18	k	103/103 (100%)	102 (99%)	1 (1%)	68	87
19	m	98/103 (95%)	98 (100%)	0	100	100
20	n	86/87 (99%)	86 (100%)	0	100	100
21	o	99/100 (99%)	98 (99%)	1 (1%)	68	87
22	p	89/90 (99%)	88 (99%)	1 (1%)	65	86
23	q	84/84 (100%)	82 (98%)	2 (2%)	43	73
24	r	93/93 (100%)	92 (99%)	1 (1%)	65	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	s	80/84 (95%)	80 (100%)	0	100	100
26	t	83/85 (98%)	80 (96%)	3 (4%)	31	63
27	u	78/78 (100%)	77 (99%)	1 (1%)	61	84
28	v	58/63 (92%)	58 (100%)	0	100	100
29	w	67/68 (98%)	67 (100%)	0	100	100
30	x	54/55 (98%)	54 (100%)	0	100	100
31	y	48/49 (98%)	48 (100%)	0	100	100
32	z	46/48 (96%)	45 (98%)	1 (2%)	45	75
33	l	107/107 (100%)	106 (99%)	1 (1%)	70	88
All	All	2796/3019 (93%)	2772 (99%)	24 (1%)	68	88

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	p	41	LYS
24	r	83	LYS
23	q	102	SER
26	t	52	LEU
14	g	47	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
26	t	53	ASN
33	l	60	GLN
26	t	54	GLN
30	x	27	ASN
12	e	94	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	118/120 (98%)	13 (11%)	0
34	Z	75/76 (98%)	16 (21%)	6 (8%)
4	V	2750/2904 (94%)	371 (13%)	59 (2%)
All	All	2943/3100 (94%)	400 (13%)	65 (2%)

5 of 400 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	V	2	G
4	V	10	A
4	V	34	U
4	V	42	A
4	V	58	G

5 of 65 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	V	2820	A
34	Z	7	A
4	V	1011	G
4	V	984	A
34	Z	16	U

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

25 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	$\# Z > 2$
4	5MC	V	1962	4	18,22,23	0.44	0	26,32,35	0.58	0
4	6MZ	V	2030	4	22,25,26	1.08	2 (9%)	30,36,39	0.86	0
4	1MG	V	745	4	22,26,27	0.82	1 (4%)	33,39,42	0.47	0
4	OMG	V	2251	34,4	23,26,27	0.48	0	33,38,41	0.56	0
4	3TD	V	1915	4	18,22,23	0.96	1 (5%)	22,32,35	0.64	0
4	G7M	V	2069	4	23,26,27	0.65	0	35,39,42	0.72	1 (2%)
2	MEQ	d	150	2	8,9,10	0.68	0	5,10,12	0.65	0
4	5MU	V	1939	4	19,22,23	0.57	0	28,32,35	0.65	0
4	PSU	V	746	4	18,21,22	0.89	1 (5%)	22,30,33	0.75	0
4	2MG	V	2445	4	23,26,27	0.62	0	32,38,41	0.52	0
4	PSU	V	2604	4	18,21,22	0.90	1 (5%)	22,30,33	0.82	0
4	H2U	V	2449	4	18,21,22	0.67	0	21,30,33	1.03	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	6MZ	V	1618	4	22,25,26	0.64	0	30,36,39	0.68	0
4	PSU	V	1911	4	18,21,22	1.00	1 (5%)	22,30,33	0.63	0
4	PSU	V	955	4	18,21,22	0.88	1 (5%)	22,30,33	0.77	1 (4%)
4	PSU	V	2457	4	18,21,22	0.86	1 (5%)	22,30,33	0.66	0
4	OMU	V	2552	4	19,22,23	0.45	0	26,31,34	0.40	0
4	PSU	V	2504	4	18,21,22	0.99	1 (5%)	22,30,33	0.80	1 (4%)
4	PSU	V	2580	4	18,21,22	0.97	1 (5%)	22,30,33	0.81	1 (4%)
4	PSU	V	2605	4	18,21,22	1.28	2 (11%)	22,30,33	0.91	0
4	5MU	V	747	4	19,22,23	0.37	0	28,32,35	0.56	0
4	OMC	V	2498	4	19,22,23	0.58	0	26,31,34	0.48	0
4	PSU	V	1917	4	18,21,22	0.94	1 (5%)	22,30,33	0.54	0
4	2MA	V	2503	4	22,25,26	0.56	0	33,37,40	0.72	0
4	2MG	V	1835	4	23,26,27	0.43	0	32,38,41	0.47	0

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
4	5MC	V	1962	4	-	2/7/25/26	0/2/2/2
4	6MZ	V	2030	4	-	2/9/27/28	0/3/3/3
4	1MG	V	745	4	-	0/7/25/26	0/3/3/3
4	OMG	V	2251	34,4	-	0/9/27/28	0/3/3/3
4	3TD	V	1915	4	-	0/7/25/26	0/2/2/2
4	G7M	V	2069	4	-	1/7/25/26	0/3/3/3
2	MEQ	d	150	2	-	2/8/9/11	-
4	5MU	V	1939	4	-	0/7/25/26	0/2/2/2
4	PSU	V	746	4	-	4/7/25/26	0/2/2/2
4	2MG	V	2445	4	-	0/9/27/28	0/3/3/3
4	PSU	V	2604	4	-	0/7/25/26	0/2/2/2
4	H2U	V	2449	4	-	0/7/38/39	0/2/2/2
4	6MZ	V	1618	4	-	0/9/27/28	0/3/3/3
4	PSU	V	1911	4	-	0/7/25/26	0/2/2/2
4	PSU	V	955	4	-	0/7/25/26	0/2/2/2
4	PSU	V	2457	4	-	0/7/25/26	0/2/2/2
4	OMU	V	2552	4	-	2/9/27/28	0/2/2/2
4	PSU	V	2504	4	-	0/7/25/26	0/2/2/2
4	PSU	V	2580	4	-	1/7/25/26	0/2/2/2
4	PSU	V	2605	4	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	5MU	V	747	4	-	1/7/25/26	0/2/2/2
4	OMC	V	2498	4	-	0/9/27/28	0/2/2/2
4	PSU	V	1917	4	-	0/7/25/26	0/2/2/2
4	2MA	V	2503	4	-	2/7/25/26	0/3/3/3
4	2MG	V	1835	4	-	1/9/27/28	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	V	1911	PSU	C6-C5	3.97	1.39	1.35
4	V	1917	PSU	C6-C5	3.67	1.39	1.35
4	V	1915	3TD	C6-C5	3.54	1.39	1.35
4	V	2504	PSU	C6-C5	3.45	1.39	1.35
4	V	2604	PSU	C6-C5	3.39	1.39	1.35

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	V	2580	PSU	C3'-C2'-C1'	2.95	105.08	101.64
4	V	2449	H2U	N3-C2-N1	2.72	119.53	116.65
4	V	2449	H2U	O2-C2-N1	-2.43	120.06	123.11
4	V	2504	PSU	C2'-C3'-C4'	-2.35	98.08	102.64
4	V	955	PSU	C2'-C3'-C4'	-2.11	98.54	102.64

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	V	746	PSU	C2'-C1'-C5-C4
4	V	746	PSU	C2'-C1'-C5-C6
4	V	1835	2MG	N3-C2-N2-CM2
4	V	2030	6MZ	O4'-C4'-C5'-O5'
4	V	2030	6MZ	C3'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	V	2030	6MZ	4	0
4	V	2251	OMG	1	0
2	d	150	MEQ	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	V	1835	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\# Z > 2$
36	SPM	V	3001	-	13,13,13	0.23	0	12,12,12	0.28	0

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
36	SPM	V	3001	-	-	2/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	V	3001	SPM	C7-C8-C9-N10
36	V	3001	SPM	C8-C9-N10-C11

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	V	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	2030:6MZ	O3'	2031:A	P	2.41

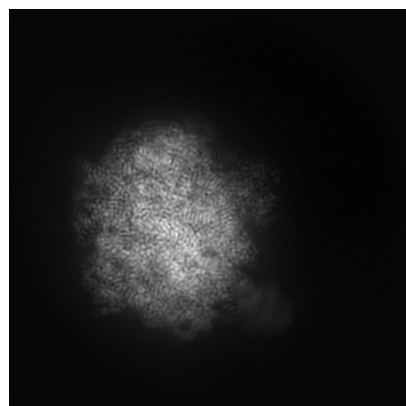
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55849. These allow visual inspection of the internal detail of the map and identification of artifacts.

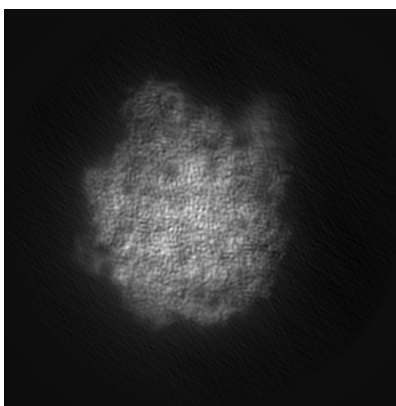
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

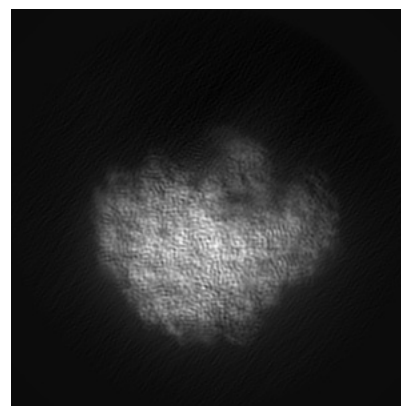
6.1.1 Primary map



X

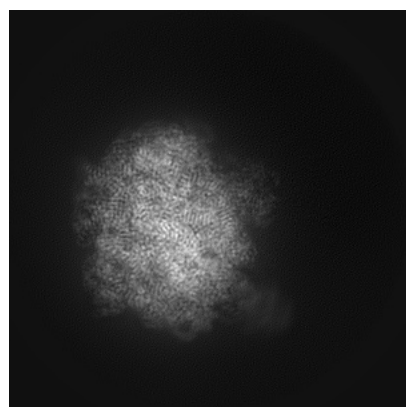


Y

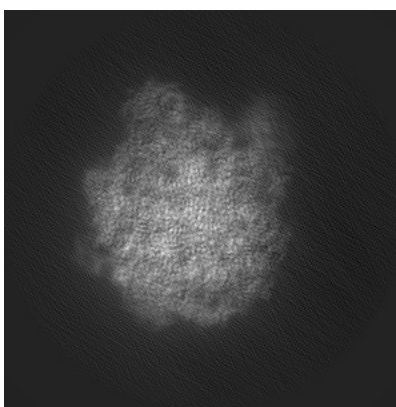


Z

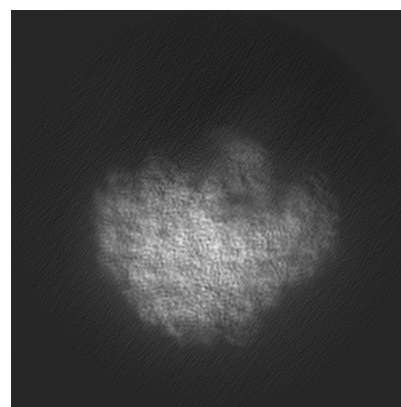
6.1.2 Raw map



X



Y

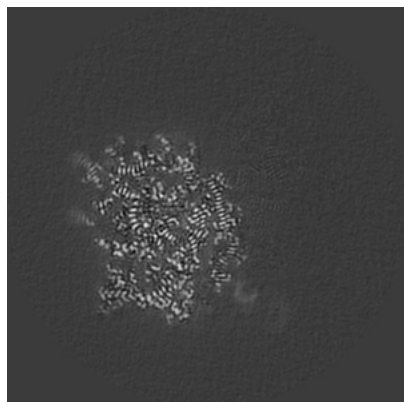


Z

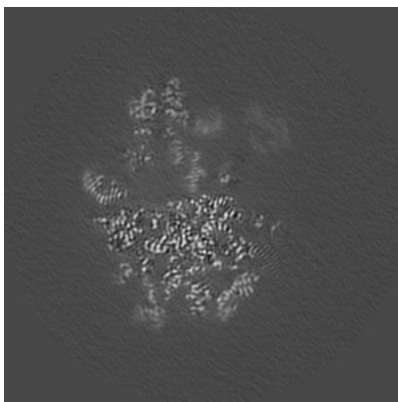
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

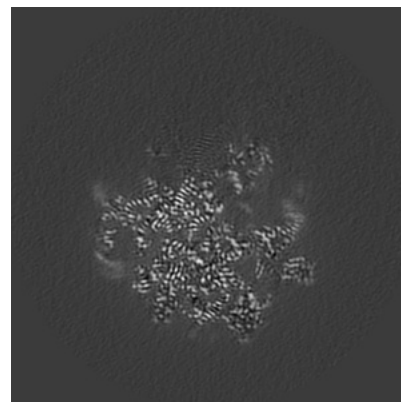
6.2.1 Primary map



X Index: 208

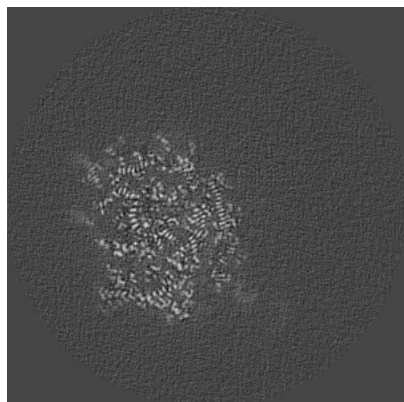


Y Index: 208

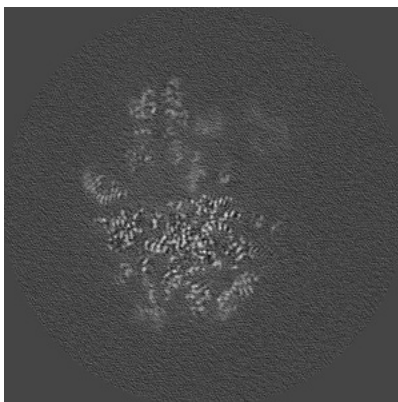


Z Index: 208

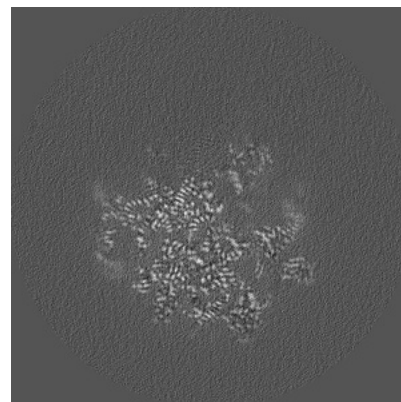
6.2.2 Raw map



X Index: 208



Y Index: 208

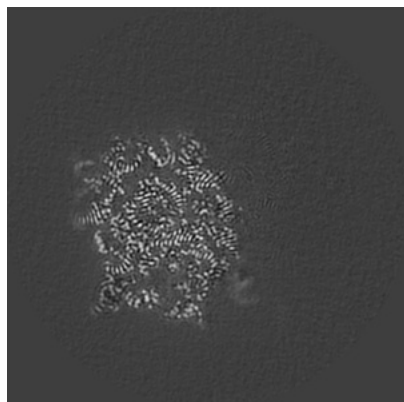


Z Index: 208

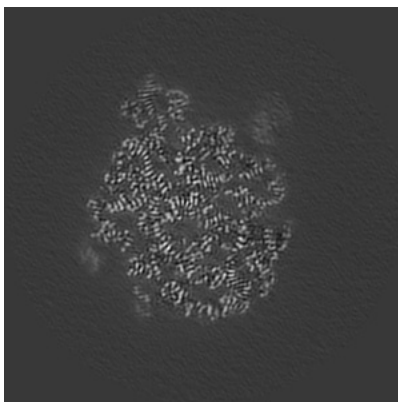
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

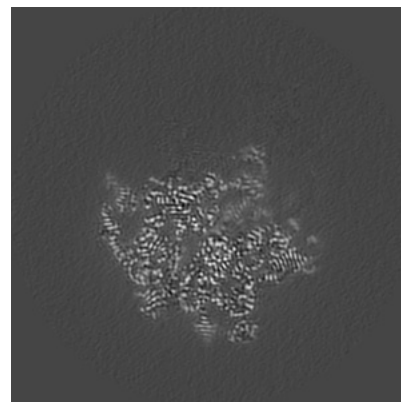
6.3.1 Primary map



X Index: 200

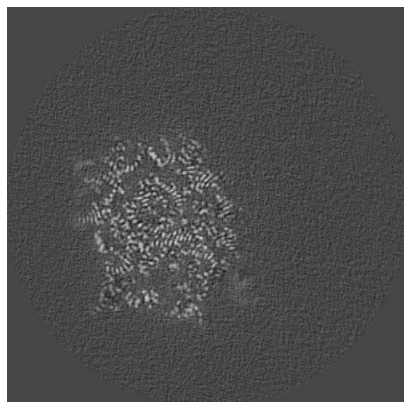


Y Index: 169

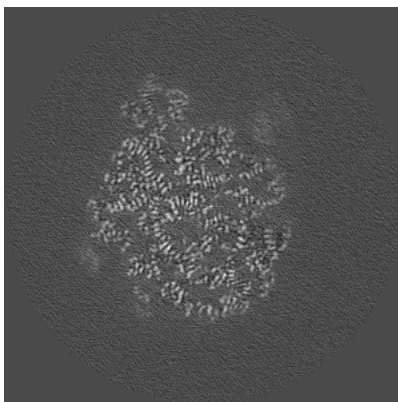


Z Index: 194

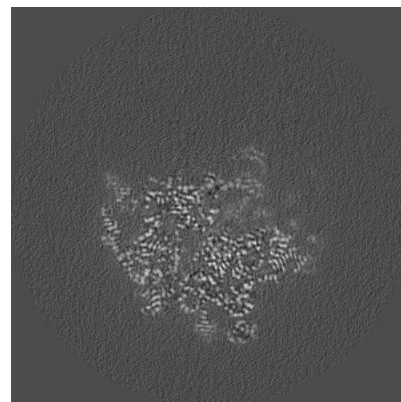
6.3.2 Raw map



X Index: 200



Y Index: 169

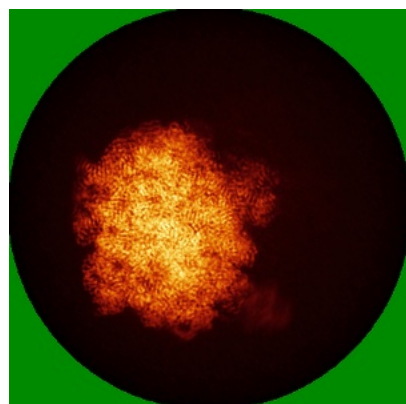


Z Index: 193

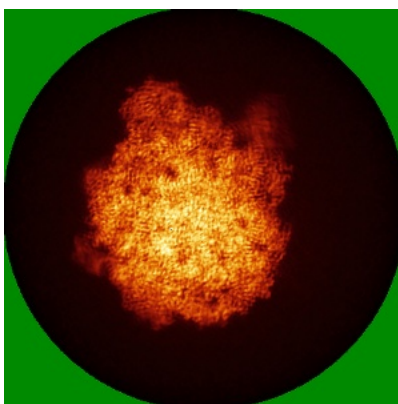
The images above show the largest variance slices of the map in three orthogonal directions.

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

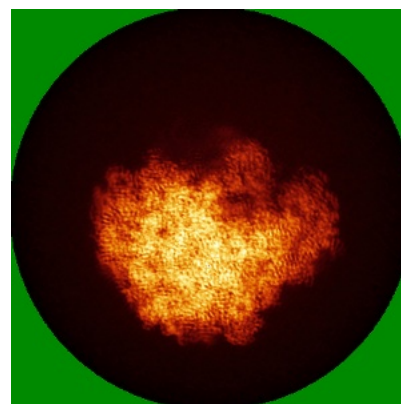
6.4.1 Primary map



X

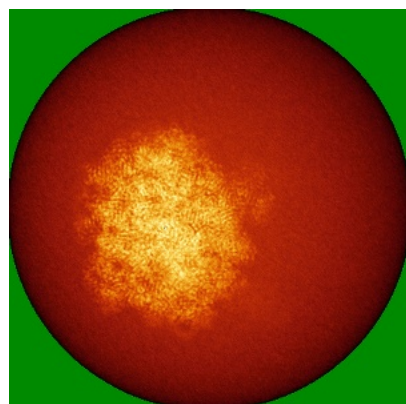


Y

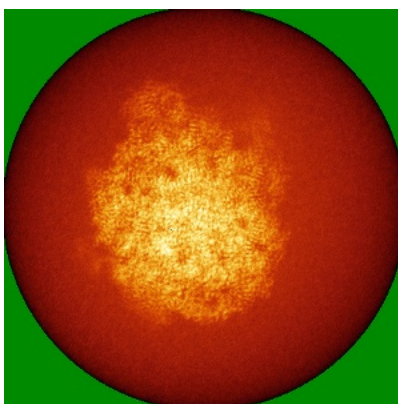


Z

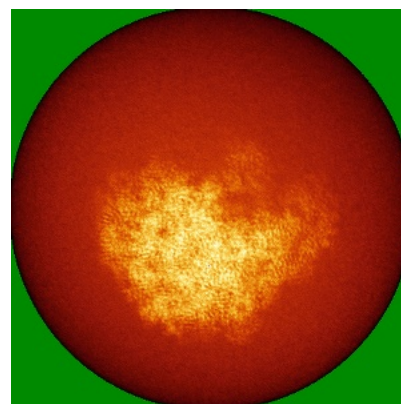
6.4.2 Raw map



X



Y

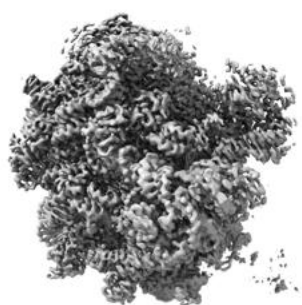


Z

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](#)

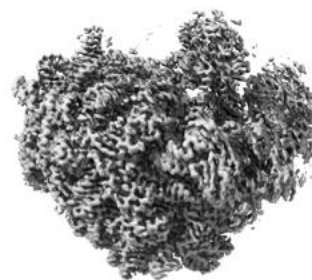
6.5.1 Primary map



X



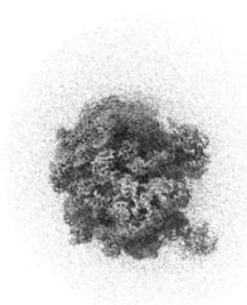
Y



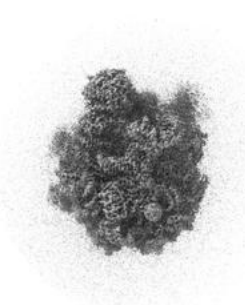
Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

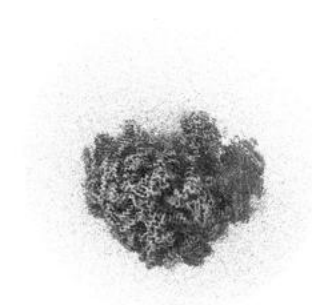
6.5.2 Raw map



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.

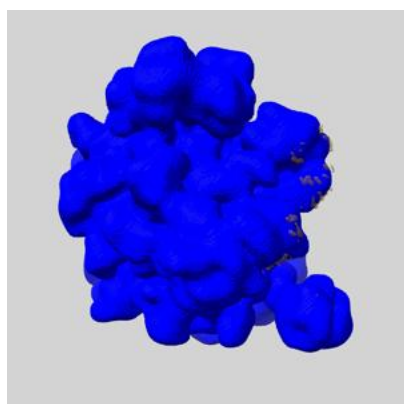
6.6 Mask visualisation [i](#)

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

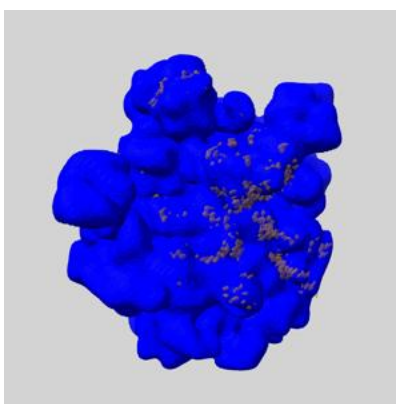
A mask typically either:

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

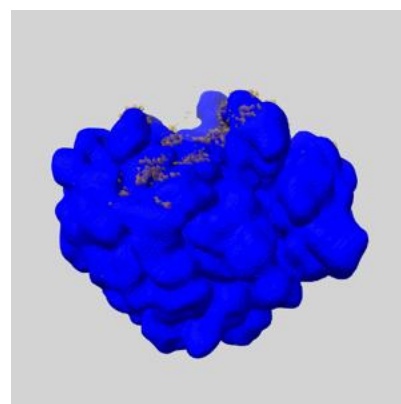
6.6.1 emd_55849_msk_1.map [i](#)



X



Y

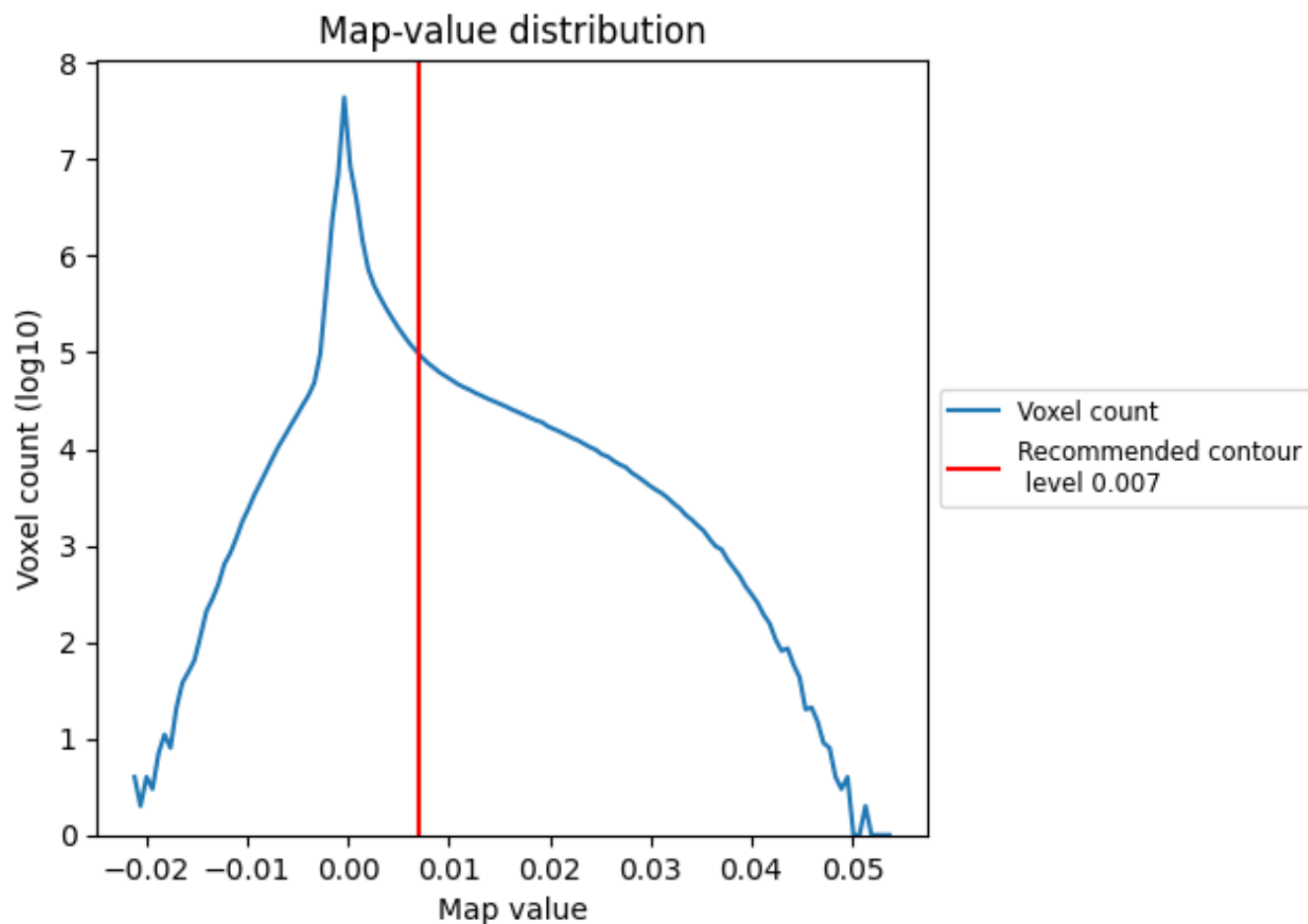


Z

7 Map analysis [i](#)

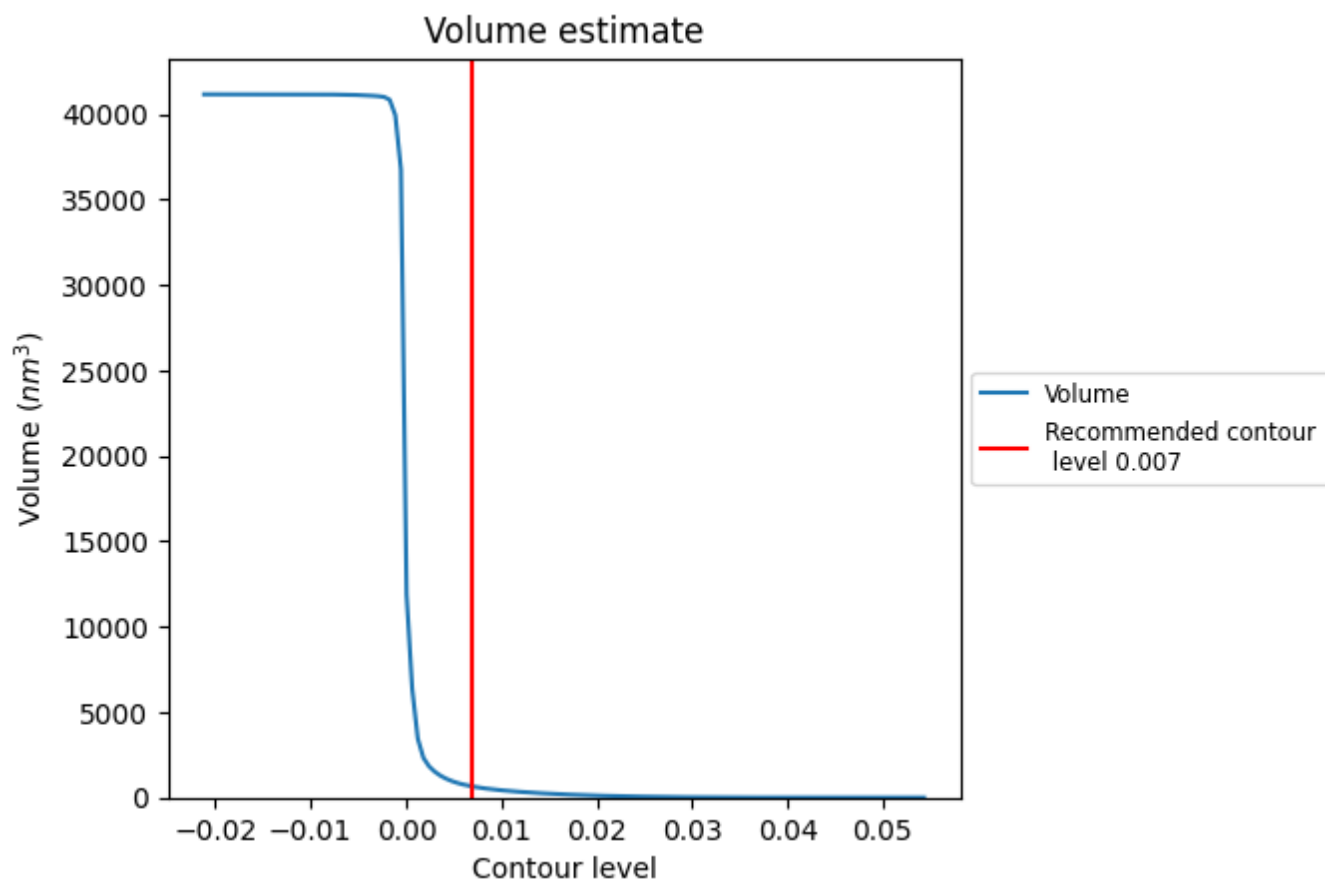
This section contains the results of statistical analysis of the map.

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.

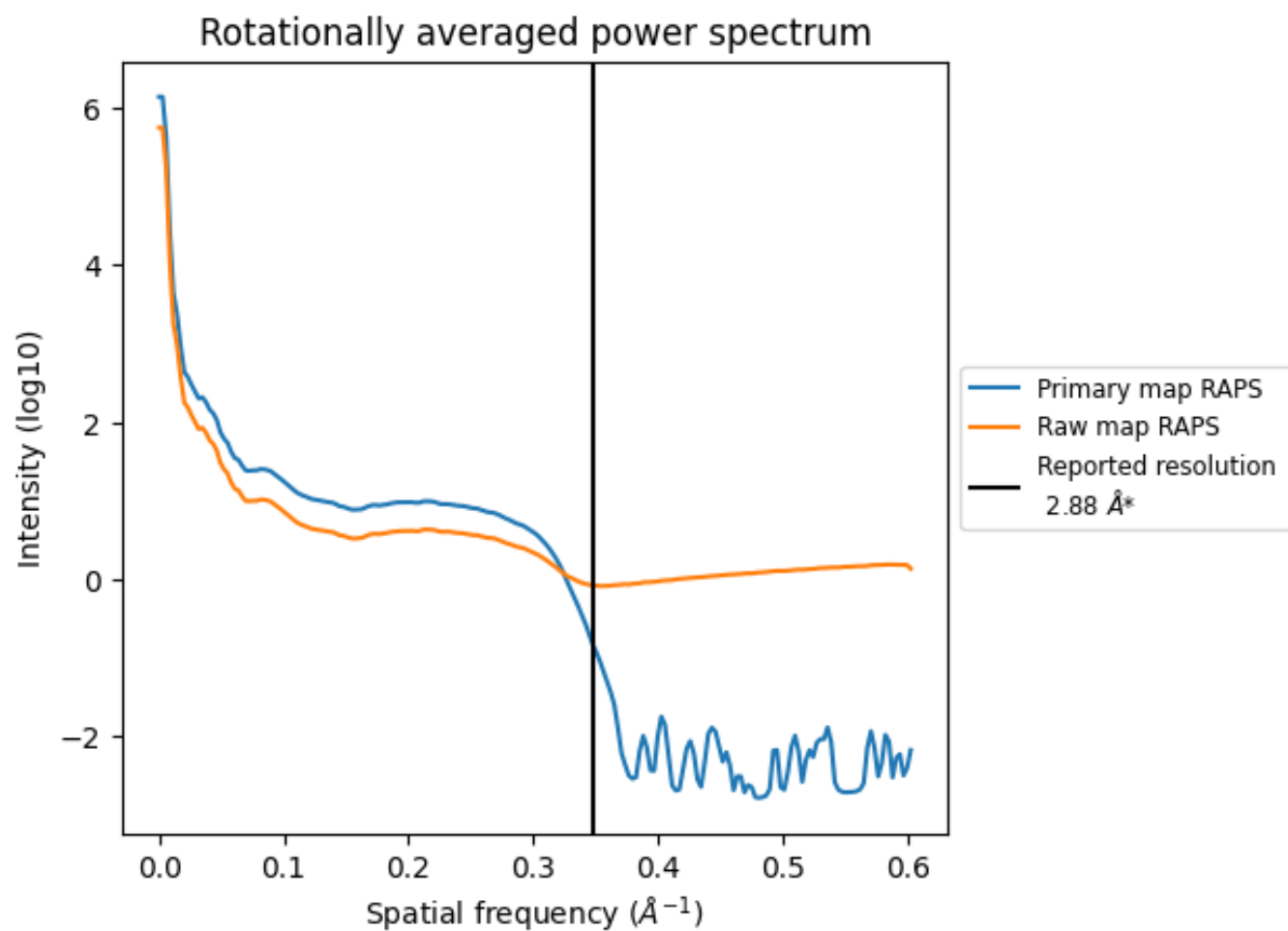
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 647 nm^3 ; this corresponds to an approximate mass of 584 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 ⓘ

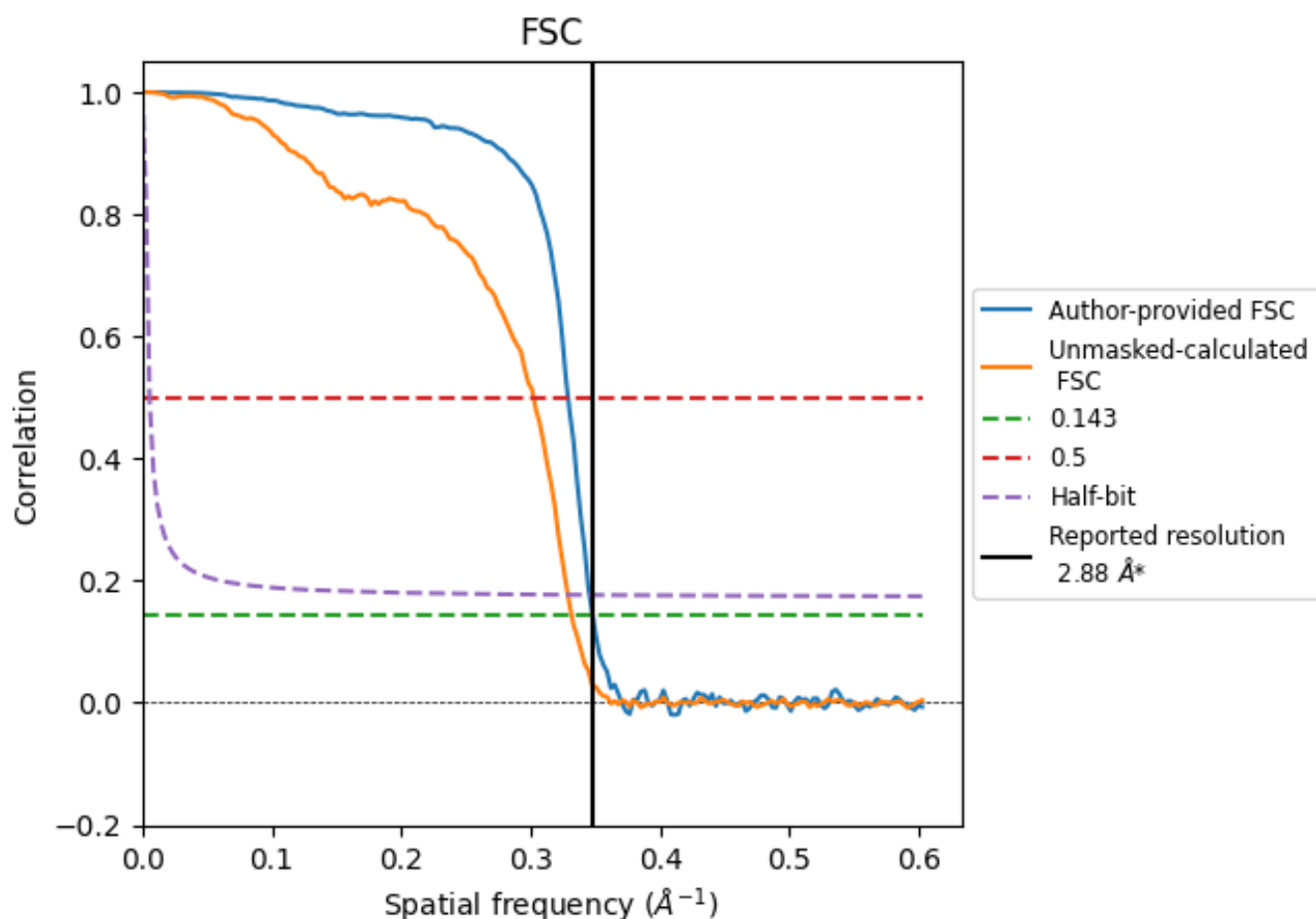


*Reported resolution corresponds to spatial frequency of 0.347 Å⁻¹

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 0.347 \AA^{-1}

8.2 Resolution estimates [i](#)

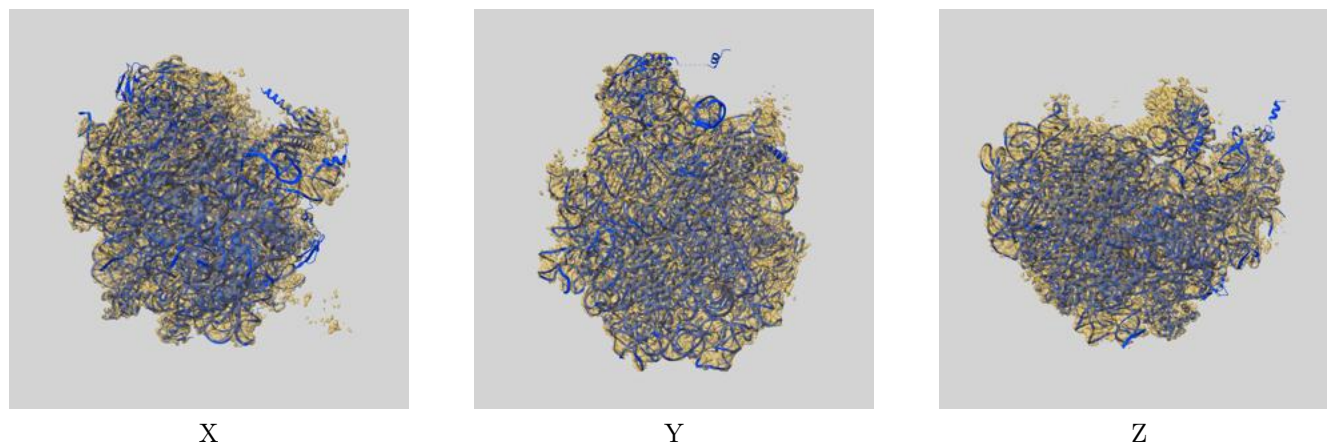
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	2.87	3.04	2.89
Unmasked-calculated*	3.02	3.31	3.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

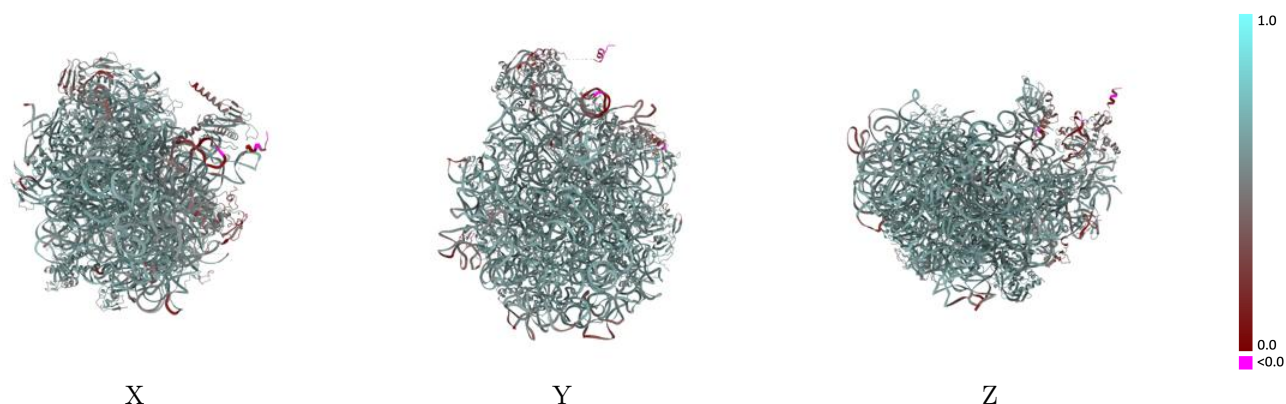
This section contains information regarding the fit between EMDB map EMD-55849 and PDB model 9TEZ. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



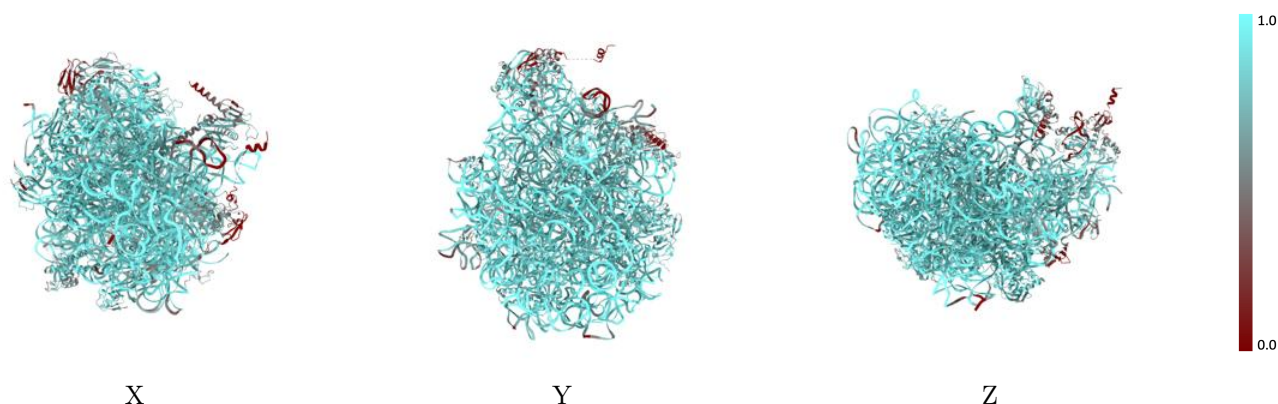
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



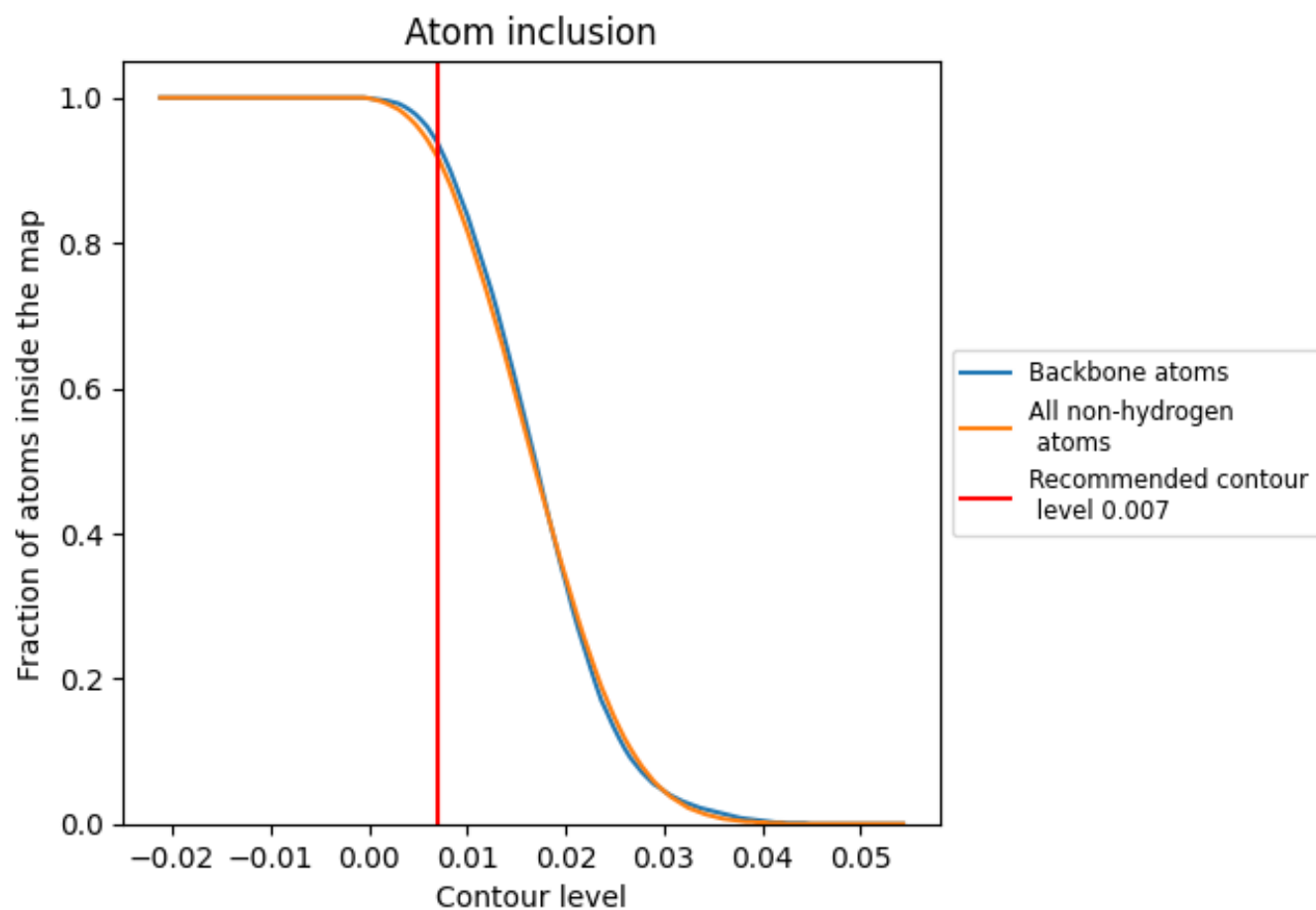
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.5840
0	 0.8630	 0.5610
1	 0.9520	 0.6160
2	 0.9610	 0.6230
3	 0.9040	 0.5830
4	 0.1400	 0.2720
8	 0.9660	 0.5940
V	 0.9620	 0.5950
W	 0.6290	 0.4940
Z	 0.8740	 0.5330
b	 0.9310	 0.5740
c	 0.9230	 0.6060
d	 0.9120	 0.6020
e	 0.8330	 0.5840
f	 0.6130	 0.4680
g	 0.5480	 0.4720
h	 0.6370	 0.4780
i	 0.9160	 0.5990
j	 0.8780	 0.5880
k	 0.8970	 0.5960
l	 0.9090	 0.5920
m	 0.9560	 0.6140
n	 0.7980	 0.5470
o	 0.8410	 0.5850
p	 0.9530	 0.6170
q	 0.8620	 0.5930
r	 0.9080	 0.5950
s	 0.8630	 0.5780
t	 0.8270	 0.5570
u	 0.7910	 0.5540
v	 0.9080	 0.5950
w	 0.9200	 0.5990
x	 0.8160	 0.5550
y	 0.8670	 0.5790
z	 0.9020	 0.6000

