



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:33 AM UTC

PDB ID : 7R72 / pdb_00007r72
EMDB ID : EMD-24290
Title : State E1 nucleolar 60S ribosome biogenesis intermediate - Spb4 local model
Authors : Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on : 2021-06-24
Resolution : 3.07 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:

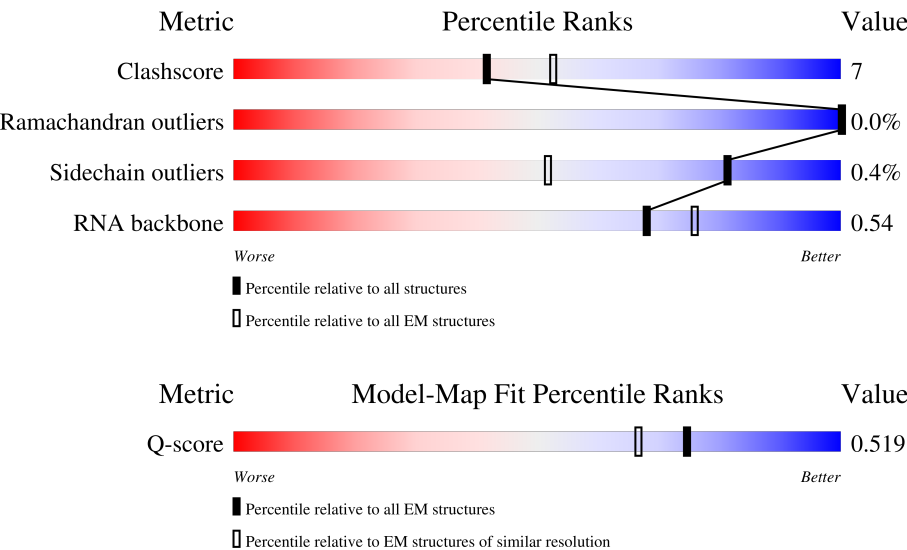
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.07 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.



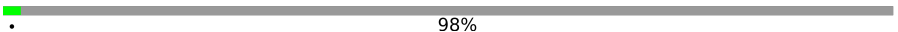
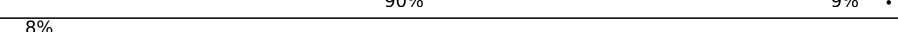
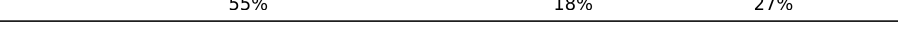
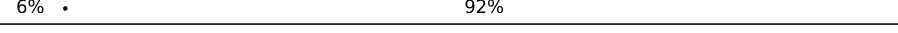
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13977 (2.57 - 3.57)

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	1	641	
2	2	72	
3	8	710	

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Mol	Chain	Length	Quality of chain
4	B	387	 98%
5	G	256	 7% 93%
6	I	663	 43% 8% 50%
7	P	184	 23% 72%
8	R	189	 6% 59% 12% 29%
9	U	121	 73% 11% 16%
10	X	142	 65% 31%
11	Z	136	 87% 12%
12	b	647	 6% 92%
13	c	105	 67% 26% 8%
14	d	113	 5% 40% 24% 36%
15	g	121	 79% 14% 7%
16	j	88	 31% 69%
17	k	78	 88% 10%
18	m	429	 79% 17%
19	n	104	 90% 9%
20	p	460	 8% 55% 18% 27%
21	t	322	 6% 92%
22	u	199	 21% 7% 72%
23	w	841	 5% 18% 5% 78%
24	x	606	 22% 71% 18% 11%

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 39443 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	641	Total	C	N	O	P	0	0
			13716	6122	2470	4483	641		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	59	Total	C	N	O	P	0	0
			1255	560	222	414	59		

- Molecule 3 is a protein called Nucleolar complex protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	8	58	Total	C	N	O	0	0
			480	290	103	87		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	9	Total	C	N	O	S	0	0
			72	48	11	12	1		

- Molecule 5 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	19	Total	C	N	O	0	0
			175	115	34	26		

- Molecule 6 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	334	Total	C	N	O	S	0	0
			2675	1691	467	507	10		

- Molecule 7 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	51	Total	C	N	O	0	0
			433	269	92	72		

- Molecule 8 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	R	134	Total	C	N	O	0	0
			1082	679	220	183		

- Molecule 9 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	102	Total	C	N	O	0	0
			808	524	132	152		

- Molecule 10 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	98	Total	C	N	O	S	0	0
			786	502	138	144	2		

- Molecule 11 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 12 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	b	53	Total	C	N	O	S	0	0
			431	267	86	74	4		

- Molecule 13 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 14 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d	72	Total	C	N	O	S	0	0
			593	384	115	93	1		

- Molecule 15 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 16 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	j	27	Total	C	N	O	S	0	0
			212	127	45	36	4		

- Molecule 17 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	k	77	Total	C	N	O	S	0	0
			612	391	115	106			

- Molecule 18 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	m	412	Total	C	N	O	S	0	0
			3302	2123	583	586	10		

- Molecule 19 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	n	103	Total	C	N	O	S	0	0
			861	544	164	148	5		

- Molecule 20 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	p	337	Total	C	N	O	S	0	0
			2629	1634	470	518	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	454	ALA	GLY	conflict	UNP A6ZPA9

- Molecule 21 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	t	26	Total	C	N	O	0	0
			221	132	49	40		

- Molecule 22 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	u	56	Total	C	N	O	S	0	0
			481	303	98	79	1		

- Molecule 23 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	w	189	Total	C	N	O	S	0	0
			1562	957	287	309	9		

- Molecule 24 is a protein called ATP-dependent rRNA helicase SPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	x	539	Total	C	N	O	S	0	0
			4340	2781	744	795	20		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	405	ALA	THR	conflict	UNP A7A237

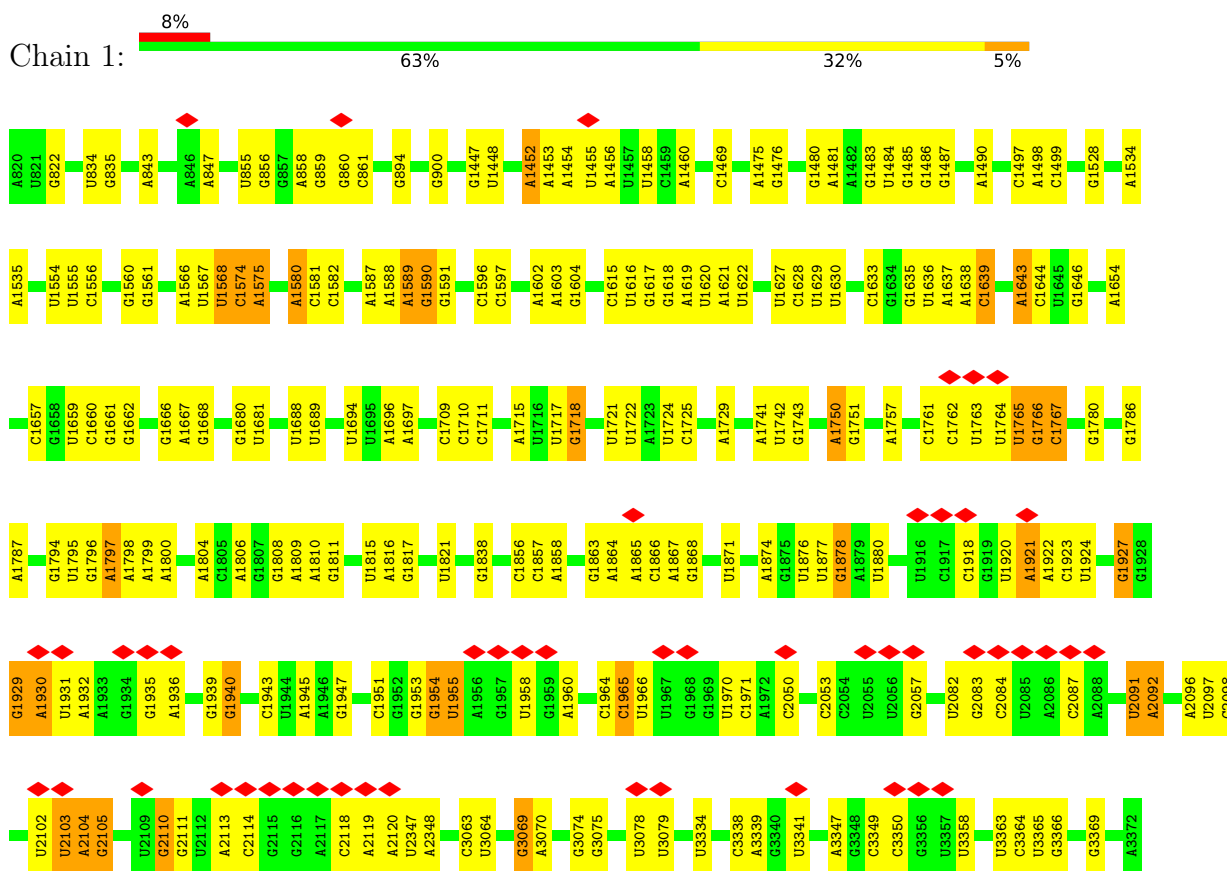
- Molecule 25 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
25	g	1	Total	Zn	0
			1	1	

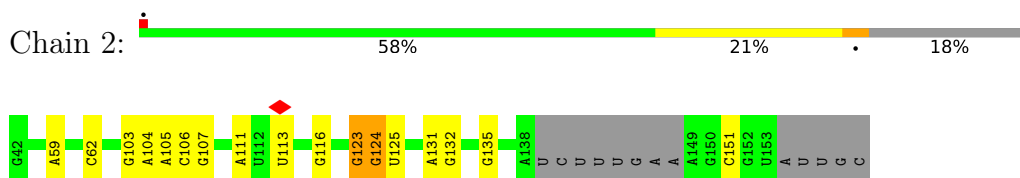
3 Residue-property plots

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: 25S rRNA



• Molecule 2: 5.8S rRNA

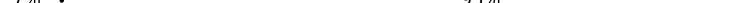


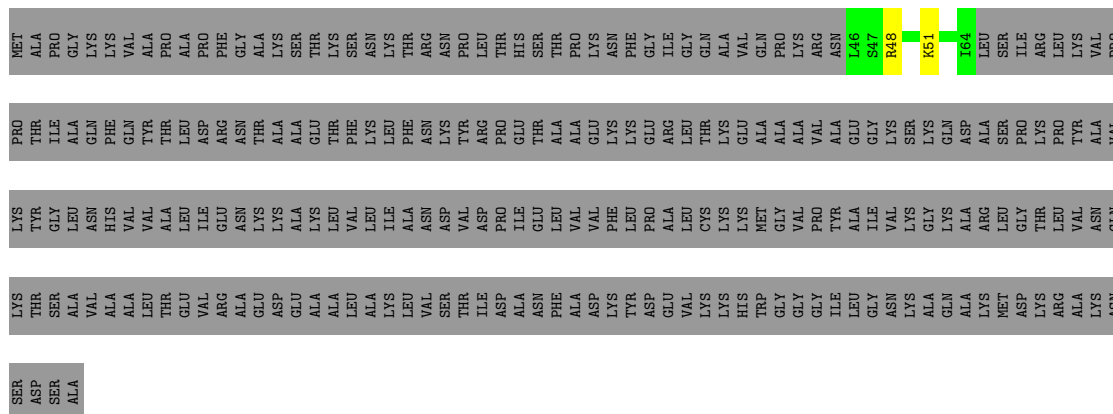
• Molecule 3: Nucleolar complex protein 2





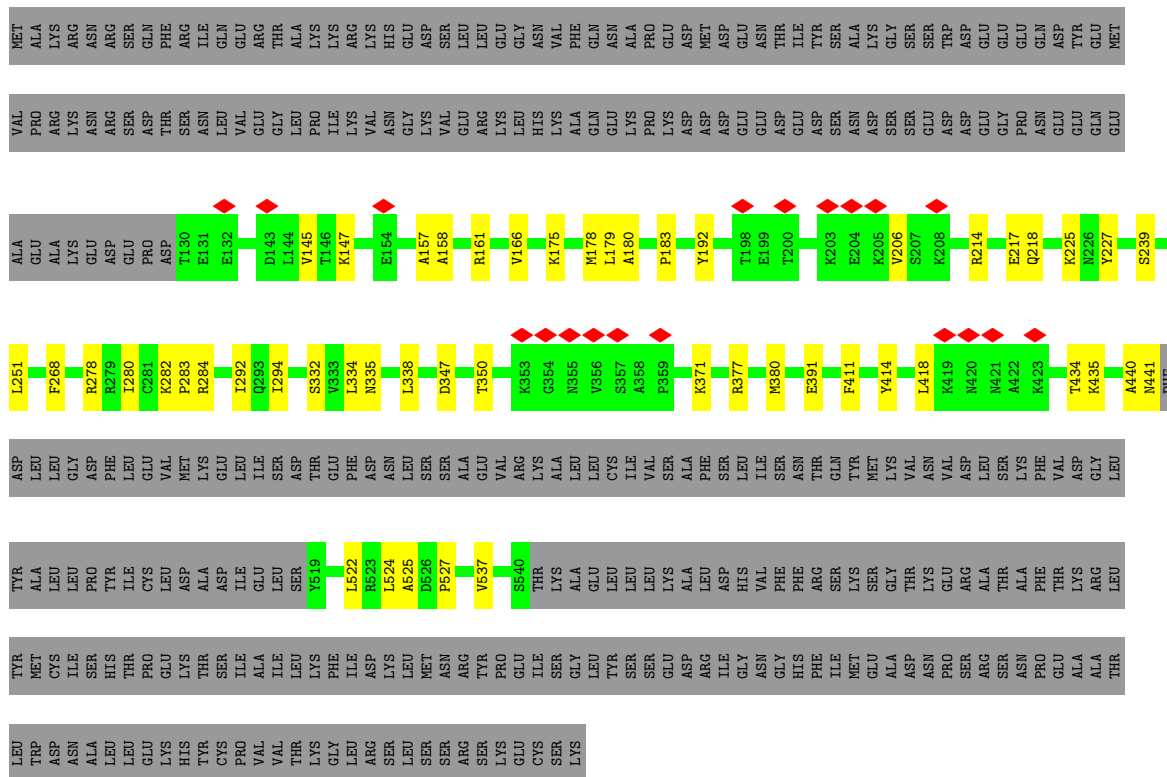
- Molecule 5: 60S ribosomal protein L8-A

Chain G:  7% 93%



- Molecule 6: Nucleolar complex-associated protein 3

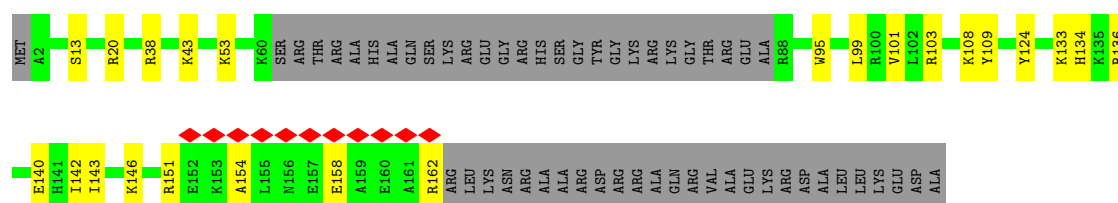
Chain I: 43% 8% 50%



- Molecule 7: 60S ribosomal protein L17-A

Chain P: 23% 72%

- Molecule 8: 60S ribosomal protein L19-A



- Molecule 9: 60S ribosomal protein L22-A



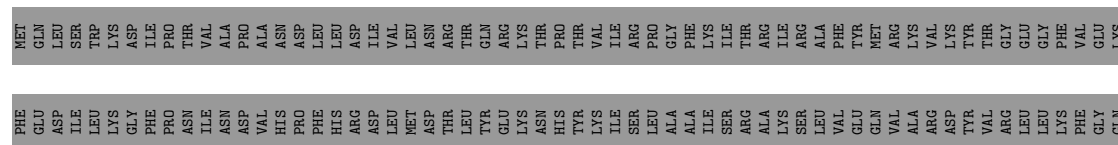
- Molecule 10: 60S ribosomal protein L25



- Molecule 11: 60S ribosomal protein L27-A



- Molecule 12: Nucleolar GTP-binding protein 1



LYS	MET
ALA	GLY
SER	LYS
ALA	GLY
	THR
	PRO
	SER
	PHE
	GLY
	LYS
	ARG
	HIS
	ASN
	K14
	P40
	ALA
	ALA
	LYS
	THR
	ARG
	SER
	TYR
	ASN
	TRP
	GLY
	ALA
	LYS
	ALA
	LYS
	ARG
	ARG
	HIS
	THR
	THR
	GLY
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	GLY
	ARG
	MET
	ARG
	TYR
	LEU
	LYS
	HIS
	VAL
	SER
	ARG
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	LYS
	ASN
	GLY
	PHE
	GLN
	THR
	GLY
	SER
	ALA
	SER

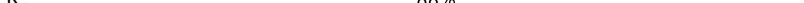
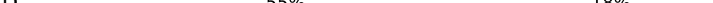
- Chain k:  88% 10%

Diagram illustrating the protein structure of the D19 mutant. The structure shows a yellow bar representing the protein backbone, with green segments indicating specific regions. The regions are labeled: MET, A2, F11, D19, K26, N32, K36, F43, K44, K63, and L78. A red diamond is positioned above the D19 segment, highlighting the site of the mutation.

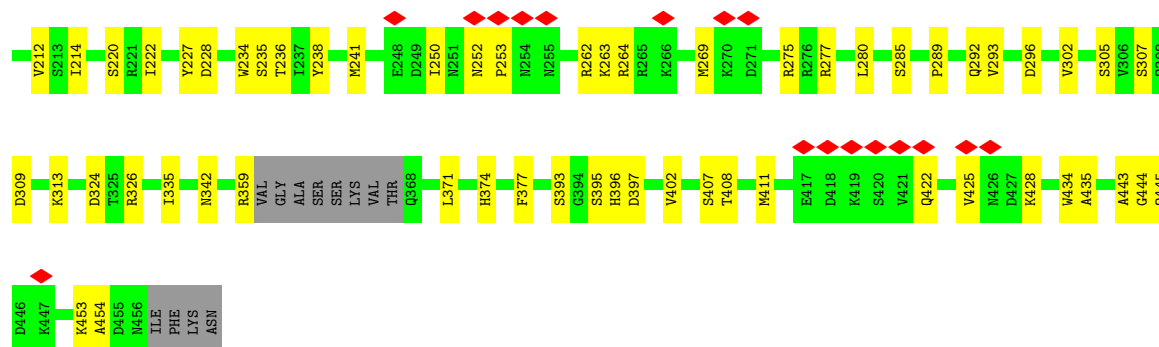
- Chain m: 79% 17%

T746	T747	H751	A752	T753	T764	L767	T771	T785	R789	W792	L793	F794	S795	A796	D799	R800	T801	A802	R803	L804	R805	T806	T807	ILE	K544	S545	A551	ILE	GLU	TRP	ASN	PRO	ASP	ALA	ASN	ASN	GLY	ILE	LEU	ALA	K555	V558	K569	K570	Q571	I589	V597	K598	K599	W602	V612	P613	P614	K628	H629	L630	T631	Q632	H648	P649	L696	A697	S698	S699	F700	R703	L709	D710	R720	W729	D319	L324	P327	K402	F425	R441	T442	L443	D446	P447	S448	L452	D457	D458	G459	V463	V464	E471	V472	V473	T478	D479	PRO	LYS	ASP	V483	H487	T491	E492	N499	V504	L512	G519	E523	K527	T528	K529	F539
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- Chain n: 90% 9%

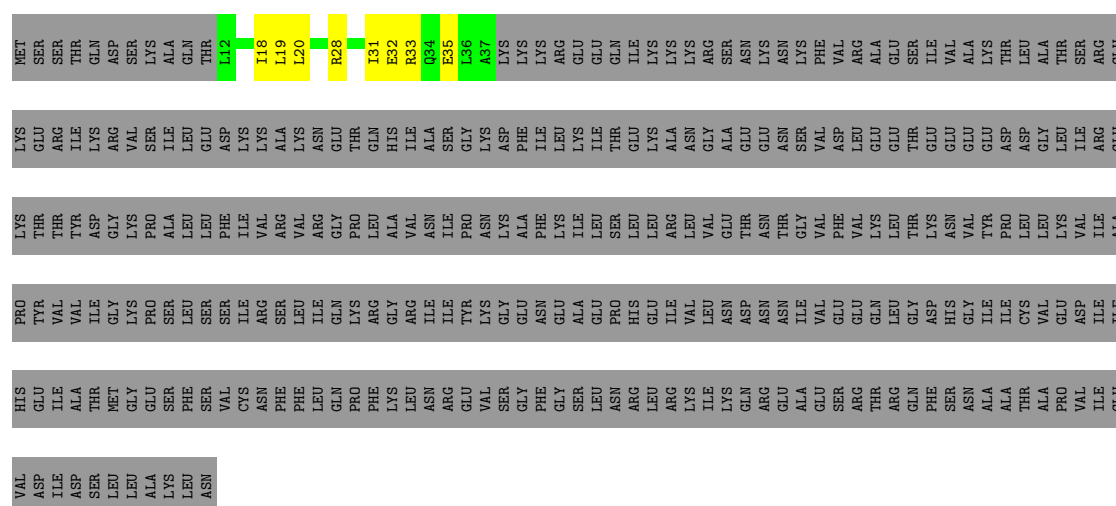
- Chain p: 

[illegible]



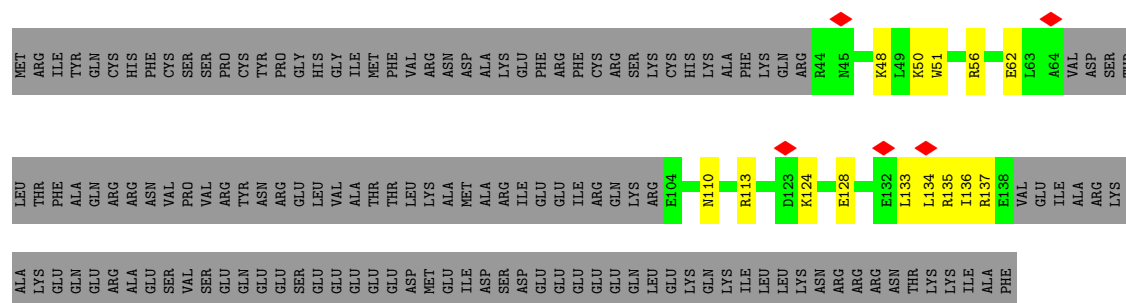
• Molecule 21: Ribosome biogenesis protein RLP7

Chain t: 6% 92%



• Molecule 22: Ribosome biogenesis protein RLP24

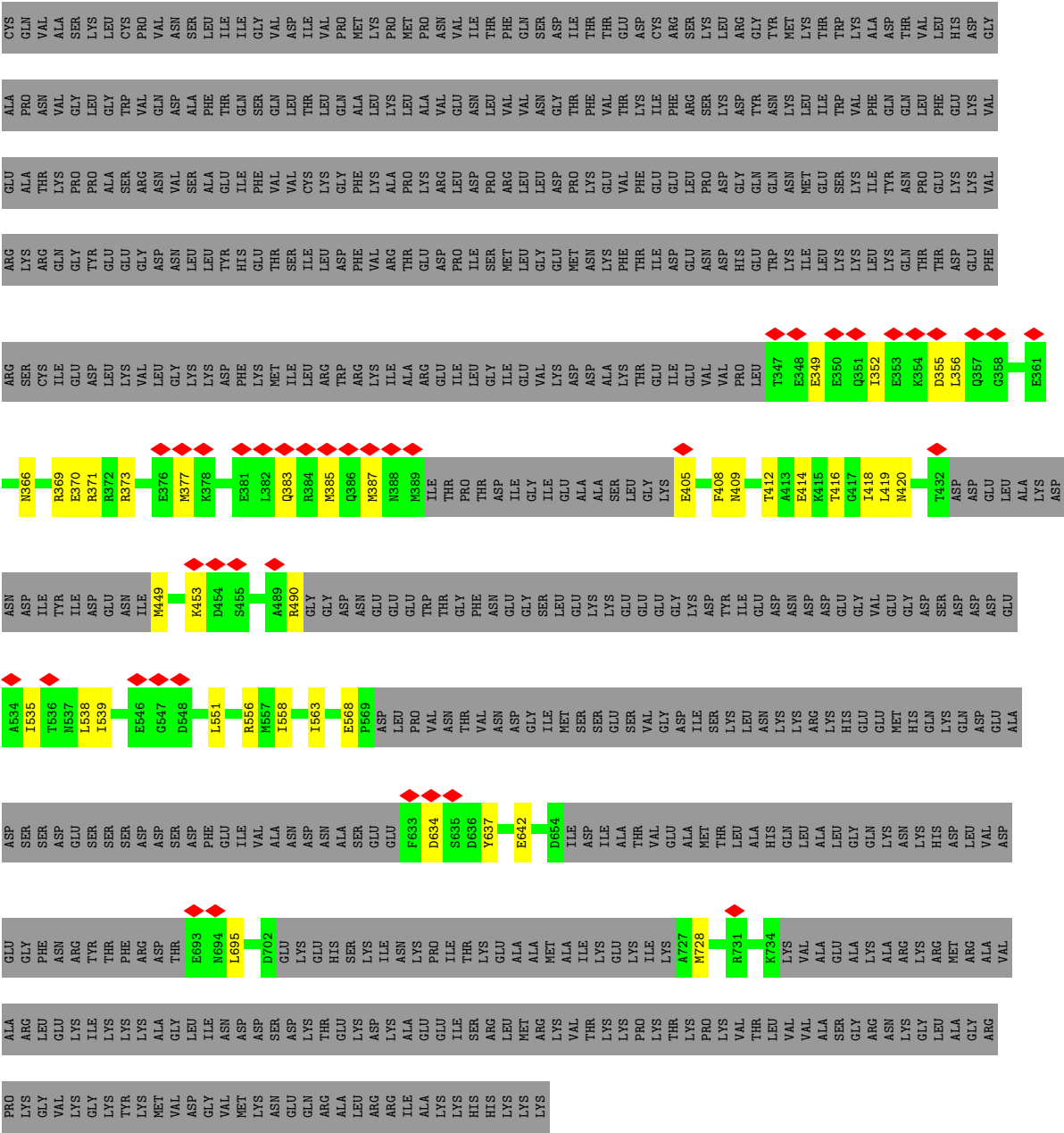
Chain u: 21% 7% 72%



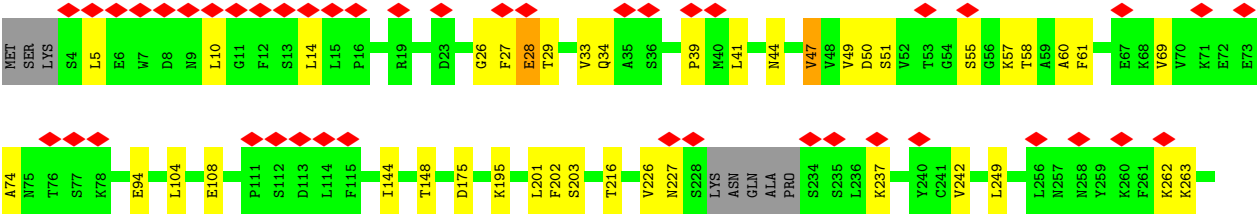
• Molecule 23: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

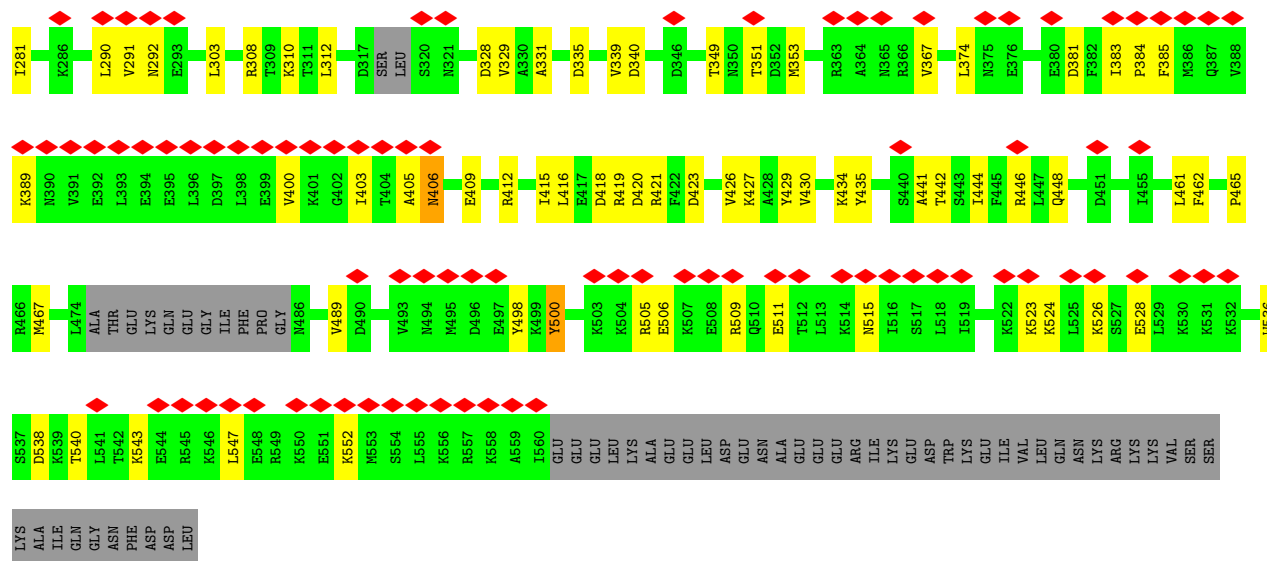
Chain w: 5% 18% 5% 78%





● Molecule 24: ATP-dependent rRNA helicase SPB4





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	211000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.056	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.012	Depositor
Map size ($\text{\AA}$)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.14	0/15338	0.26	0/23887
2	2	0.14	0/1398	0.26	0/2169
3	8	0.10	0/482	0.22	0/630
4	B	0.14	0/72	0.27	0/93
5	G	0.14	0/179	0.29	0/239
6	I	0.13	0/2708	0.31	0/3643
7	P	0.18	0/439	0.55	1/579 (0.2%)
8	R	0.14	0/1095	0.25	0/1465
9	U	0.14	0/825	0.32	0/1120
10	X	0.15	0/794	0.29	0/1066
11	Z	0.14	0/1118	0.29	0/1497
12	b	0.11	0/436	0.30	0/575
13	c	0.12	0/751	0.25	0/1008
14	d	0.13	0/603	0.32	0/804
15	g	0.15	0/891	0.27	0/1191
16	j	0.12	0/216	0.25	0/286
17	k	0.15	0/618	0.30	0/826
18	m	0.16	0/3387	0.37	0/4594
19	n	0.15	0/872	0.31	0/1151
20	p	0.15	0/2675	0.37	0/3625
21	t	0.13	0/221	0.26	0/294
22	u	0.10	0/487	0.34	0/641
23	w	0.12	0/1573	0.29	0/2081
24	x	0.15	0/4419	0.31	0/5958
All	All	0.14	0/41597	0.30	1/59422 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	P	135	ARG	N-CA-C	5.14	117.92	110.42

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	1	13716	0	6905	147	0
2	2	1255	0	640	5	0
3	8	480	0	518	8	0
4	B	72	0	79	0	0
5	G	175	0	188	1	0
6	I	2675	0	2797	39	0
7	P	433	0	434	7	0
8	R	1082	0	1160	22	0
9	U	808	0	822	12	0
10	X	786	0	841	6	0
11	Z	1092	0	1155	14	0
12	b	431	0	460	17	0
13	c	743	0	797	19	0
14	d	593	0	640	20	0
15	g	881	0	945	15	0
16	j	212	0	210	0	0
17	k	612	0	682	5	0
18	m	3302	0	3354	46	0
19	n	861	0	920	5	0
20	p	2629	0	2614	54	0
21	t	221	0	233	9	0
22	u	481	0	511	13	0
23	w	1562	0	1554	42	0
24	x	4340	0	4468	83	0
25	g	1	0	0	0	0
All	All	39443	0	32927	484	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 484 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)
1:1:3350:C:H42	24:x:552:LYS:CE	1.70	1.04
1:1:3350:C:N4	24:x:552:LYS:HE3	1.74	1.02
18:m:519:GLY:HA3	20:p:165:ARG:HH22	1.27	0.99
1:1:3350:C:N4	24:x:552:LYS:CE	2.27	0.98
8:R:151:ARG:HH21	24:x:442:THR:HB	1.28	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	8	56/710 (8%)	56 (100%)	0	0	100	100
4	B	7/387 (2%)	7 (100%)	0	0	100	100
5	G	17/256 (7%)	16 (94%)	1 (6%)	0	100	100
6	I	330/663 (50%)	318 (96%)	12 (4%)	0	100	100
7	P	41/184 (22%)	38 (93%)	3 (7%)	0	100	100
8	R	130/189 (69%)	129 (99%)	1 (1%)	0	100	100
9	U	100/121 (83%)	96 (96%)	4 (4%)	0	100	100
10	X	94/142 (66%)	93 (99%)	1 (1%)	0	100	100
11	Z	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
12	b	51/647 (8%)	49 (96%)	2 (4%)	0	100	100
13	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
14	d	66/113 (58%)	62 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	g	110/121 (91%)	109 (99%)	1 (1%)	0	100	100
16	j	25/88 (28%)	25 (100%)	0	0	100	100
17	k	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
18	m	404/429 (94%)	385 (95%)	19 (5%)	0	100	100
19	n	99/104 (95%)	95 (96%)	4 (4%)	0	100	100
20	p	331/460 (72%)	308 (93%)	23 (7%)	0	100	100
21	t	24/322 (8%)	24 (100%)	0	0	100	100
22	u	52/199 (26%)	52 (100%)	0	0	100	100
23	w	175/841 (21%)	171 (98%)	4 (2%)	0	100	100
24	x	531/606 (88%)	508 (96%)	22 (4%)	1 (0%)	43	71
All	All	2946/6901 (43%)	2837 (96%)	108 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	x	406	ASN

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	
3	8	52/647 (8%)	52 (100%)	0	100	100
4	B	8/323 (2%)	8 (100%)	0	100	100
5	G	19/208 (9%)	19 (100%)	0	100	100
6	I	306/602 (51%)	306 (100%)	0	100	100
7	P	46/146 (32%)	46 (100%)	0	100	100
8	R	112/154 (73%)	112 (100%)	0	100	100
9	U	89/107 (83%)	88 (99%)	1 (1%)	65	76
10	X	87/118 (74%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Z	115/116 (99%)	115 (100%)	0	100	100
12	b	46/573 (8%)	46 (100%)	0	100	100
13	c	81/88 (92%)	81 (100%)	0	100	100
14	d	62/97 (64%)	62 (100%)	0	100	100
15	g	95/103 (92%)	95 (100%)	0	100	100
16	j	25/71 (35%)	25 (100%)	0	100	100
17	k	68/69 (99%)	68 (100%)	0	100	100
18	m	367/381 (96%)	367 (100%)	0	100	100
19	n	92/93 (99%)	92 (100%)	0	100	100
20	p	300/413 (73%)	300 (100%)	0	100	100
21	t	24/287 (8%)	24 (100%)	0	100	100
22	u	49/180 (27%)	49 (100%)	0	100	100
23	w	171/745 (23%)	171 (100%)	0	100	100
24	x	489/548 (89%)	479 (98%)	10 (2%)	48	69
All	All	2703/6069 (44%)	2692 (100%)	11 (0%)	81	84

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	x	403	ILE
24	x	435	TYR
24	x	538	ASP
24	x	500	TYR
24	x	292	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
20	p	342	ASN
23	w	645	GLN
23	w	379	GLN
24	x	98	GLN
18	m	494	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	629/641 (98%)	107 (17%)	2 (0%)
2	2	55/72 (76%)	10 (18%)	1 (1%)
All	All	684/713 (95%)	117 (17%)	3 (0%)

5 of 117 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	822	G
1	1	860	G
1	1	861	C
1	1	1452	A
1	1	1454	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1574	C
1	1	1954	G
2	2	123	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	12
2	2	2
19	n	1
18	m	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	905:U	O3'	1446:A	P	67.43
1	n	70:TYR	C	550:GLU	N	62.35
1	1	2356:A	O3'	3061:G	P	60.76
1	1	1884:A	O3'	1916:U	P	56.47
1	1	2120:A	O3'	2347:U	P	35.66

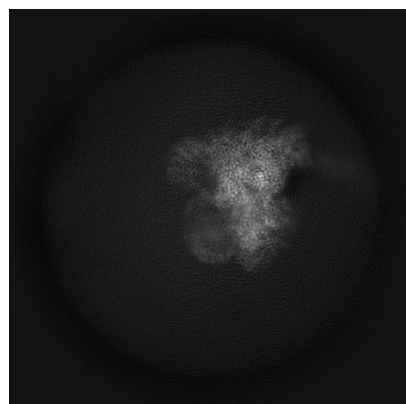
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24290. These allow visual inspection of the internal detail of the map and identification of artifacts.

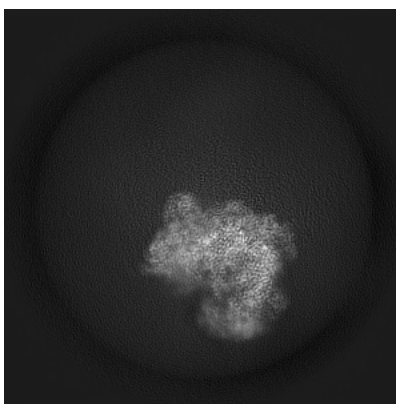
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

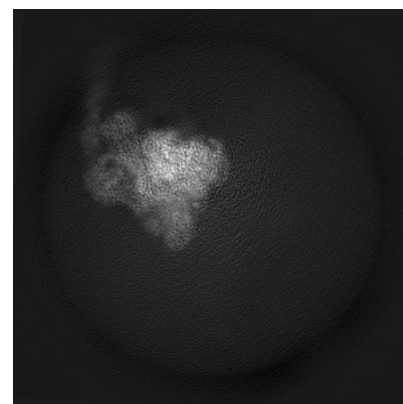
6.1.1 Primary map



X

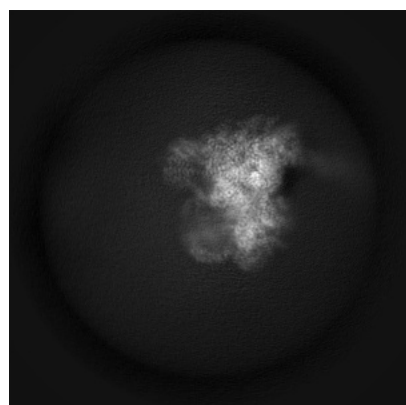


Y

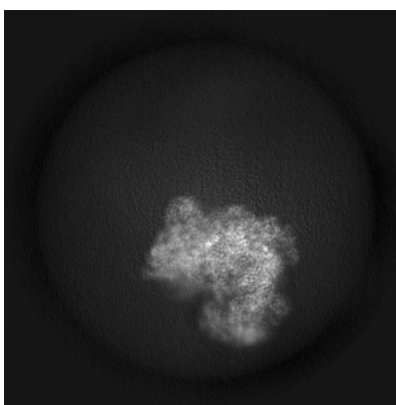


Z

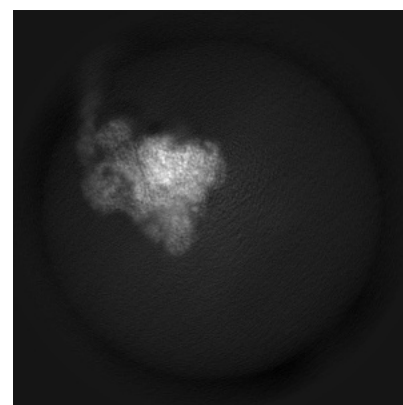
6.1.2 Raw map



X



Y

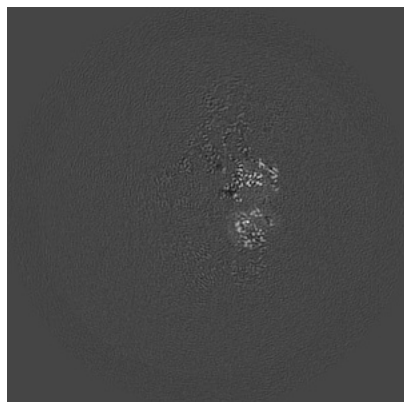


Z

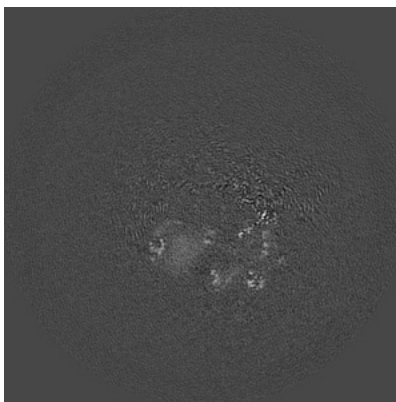
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

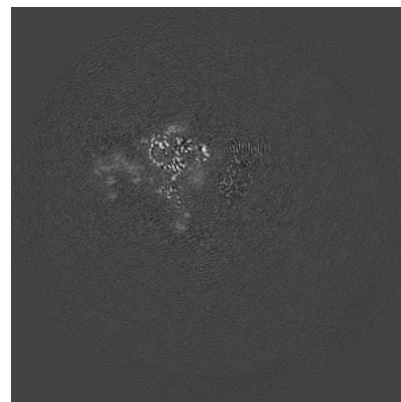
6.2.1 Primary map



X Index: 210

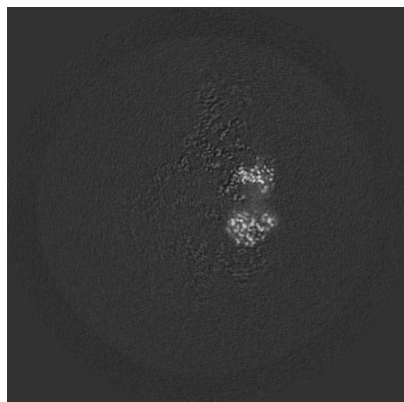


Y Index: 210

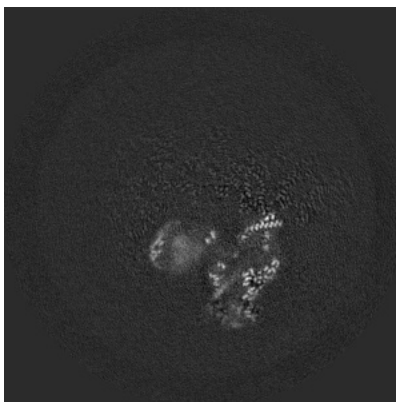


Z Index: 210

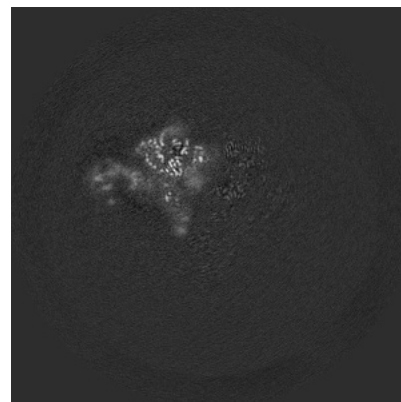
6.2.2 Raw map



X Index: 210



Y Index: 210

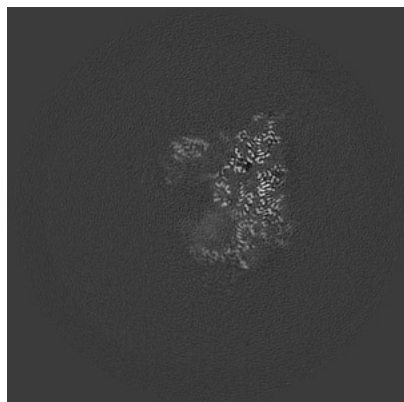


Z Index: 210

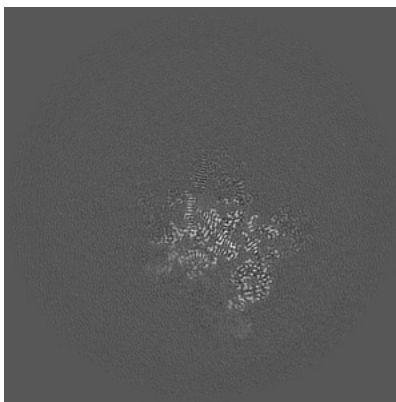
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

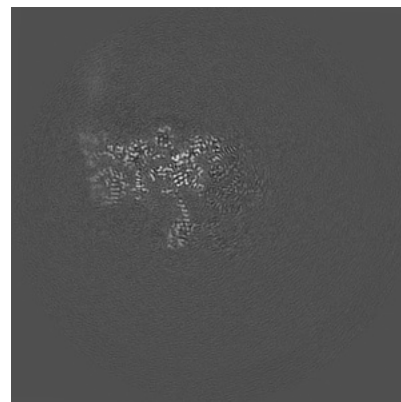
6.3.1 Primary map



X Index: 161

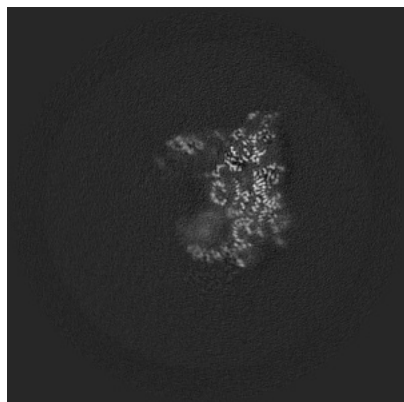


Y Index: 271

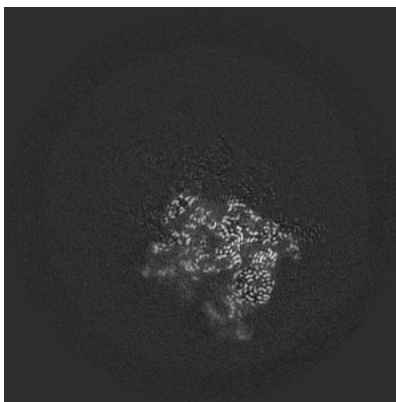


Z Index: 247

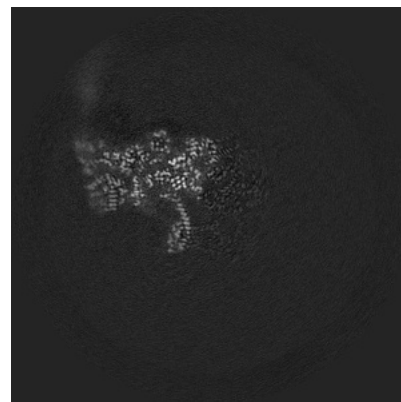
6.3.2 Raw map



X Index: 158



Y Index: 260

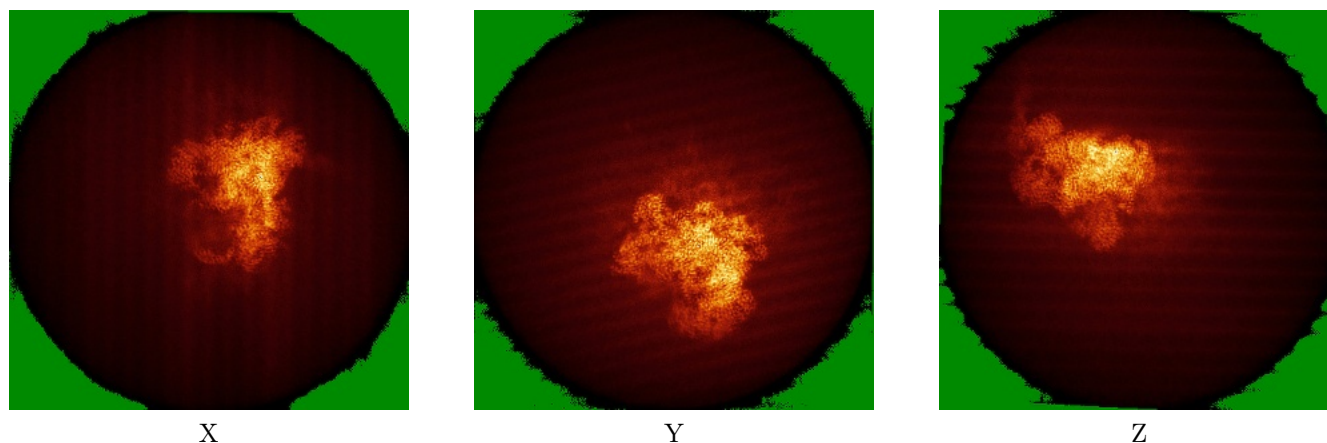


Z Index: 249

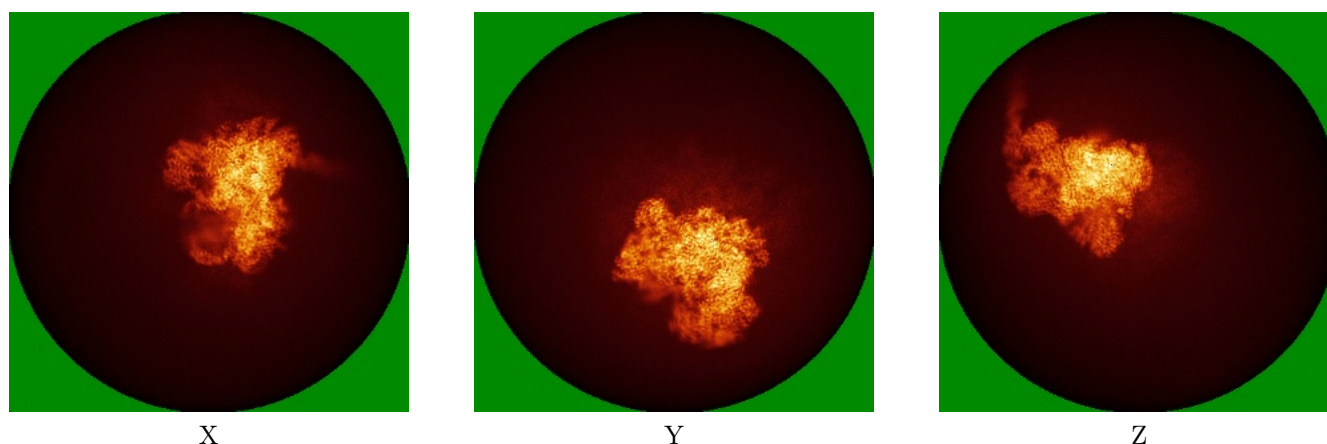
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

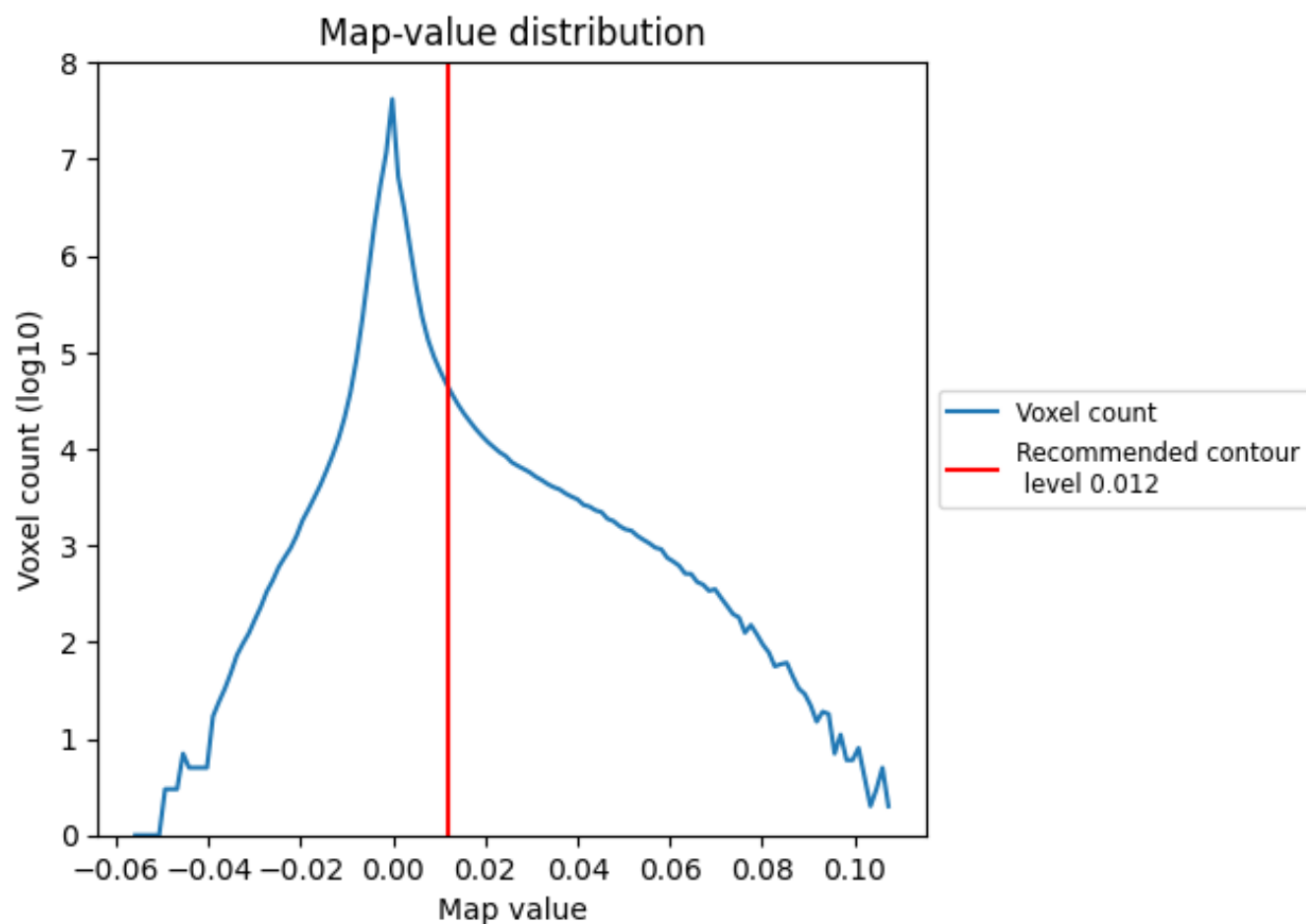
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

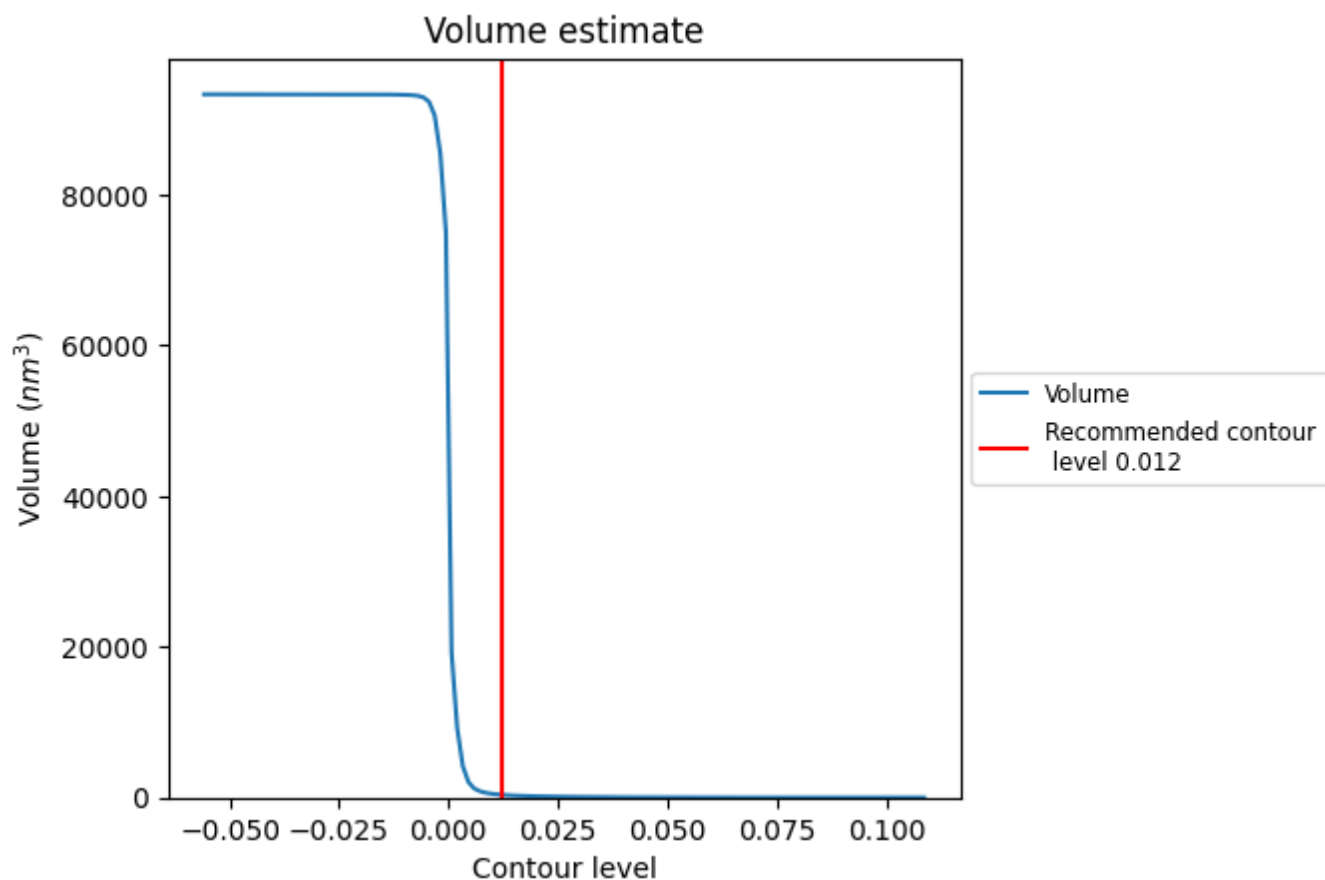
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

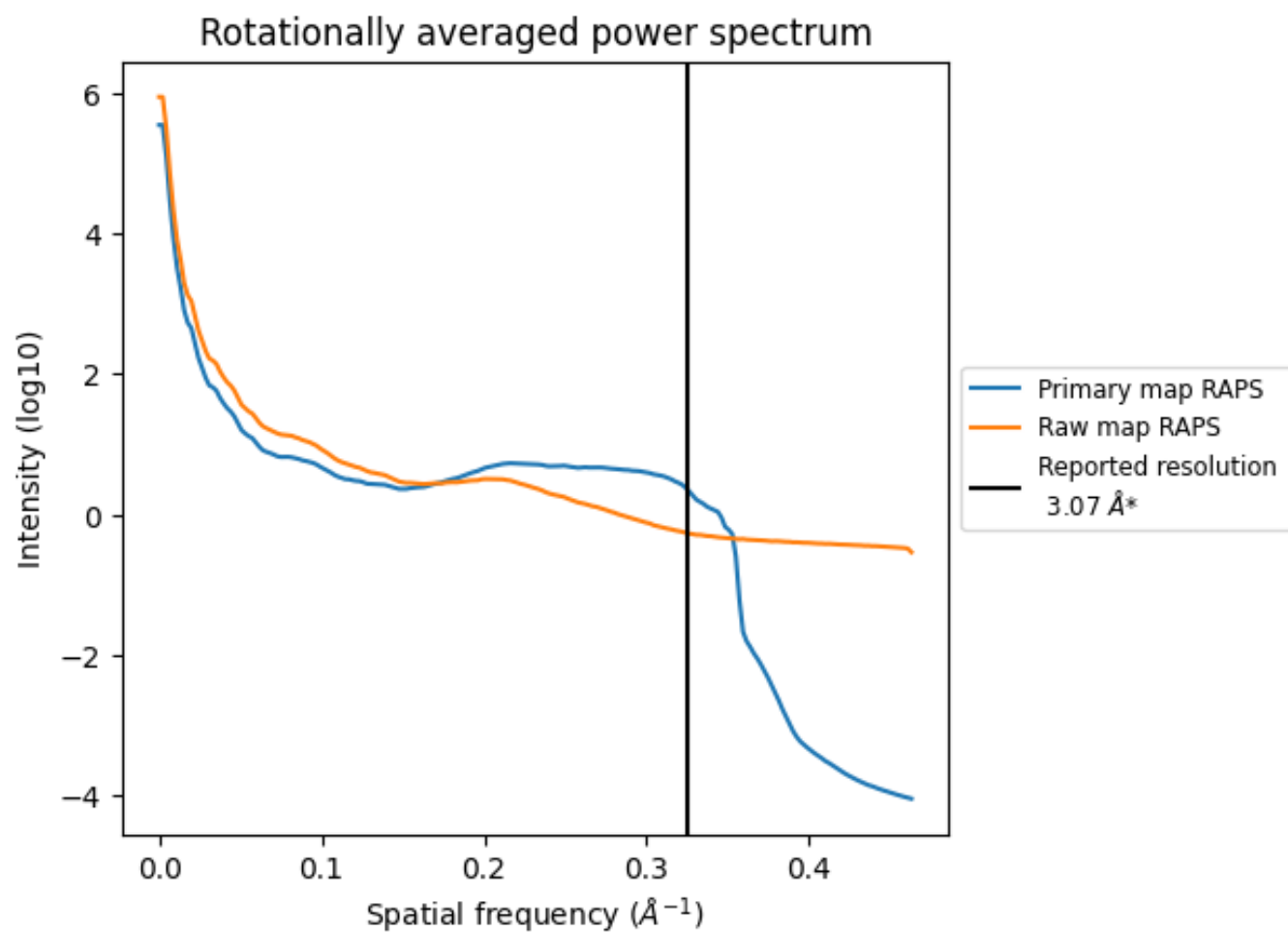
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 369 nm^3 ; this corresponds to an approximate mass of 334 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 ⓘ

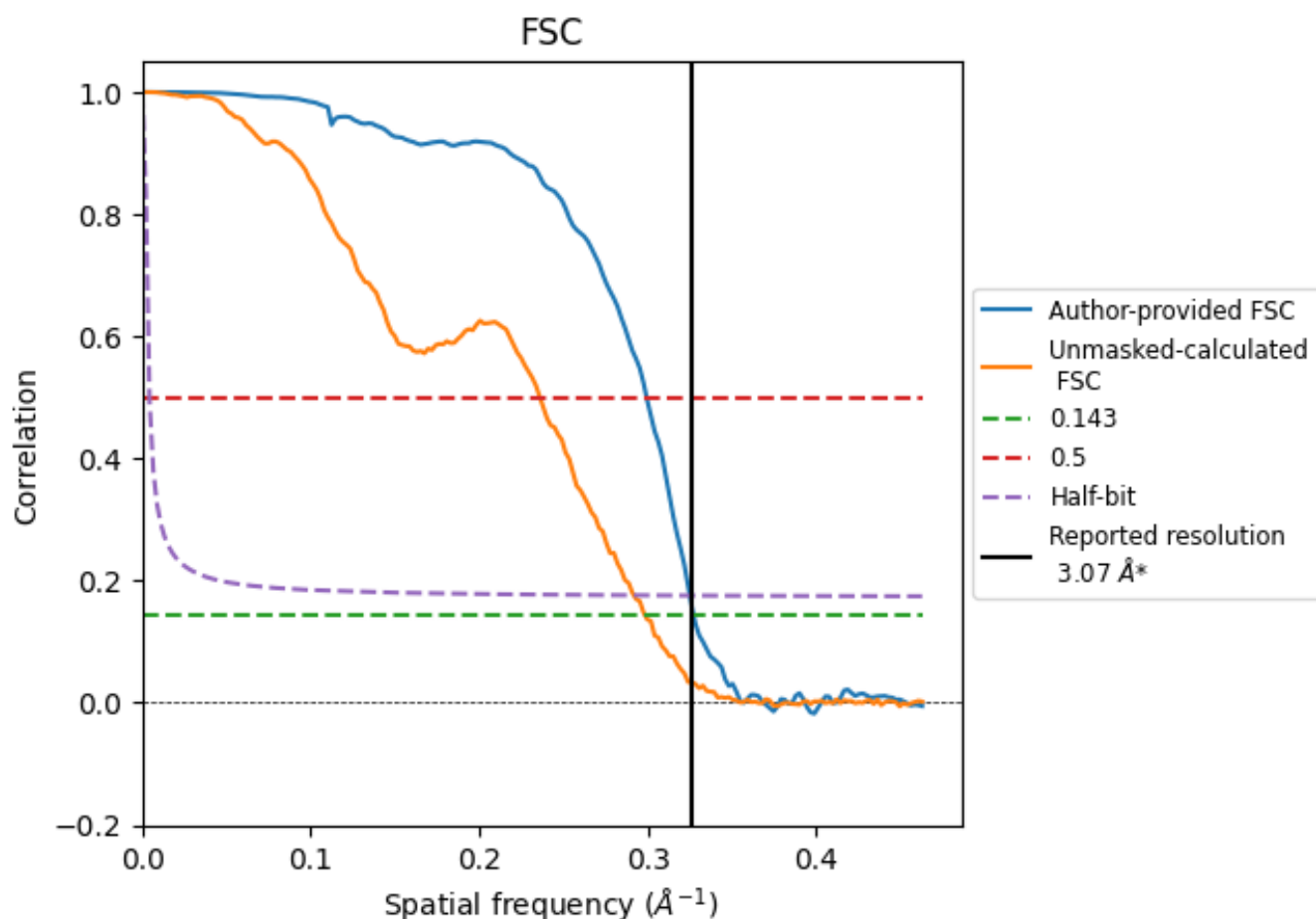


*Reported resolution corresponds to spatial frequency of $0.326 \text{ \AA}^{-1}$

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 0.326 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

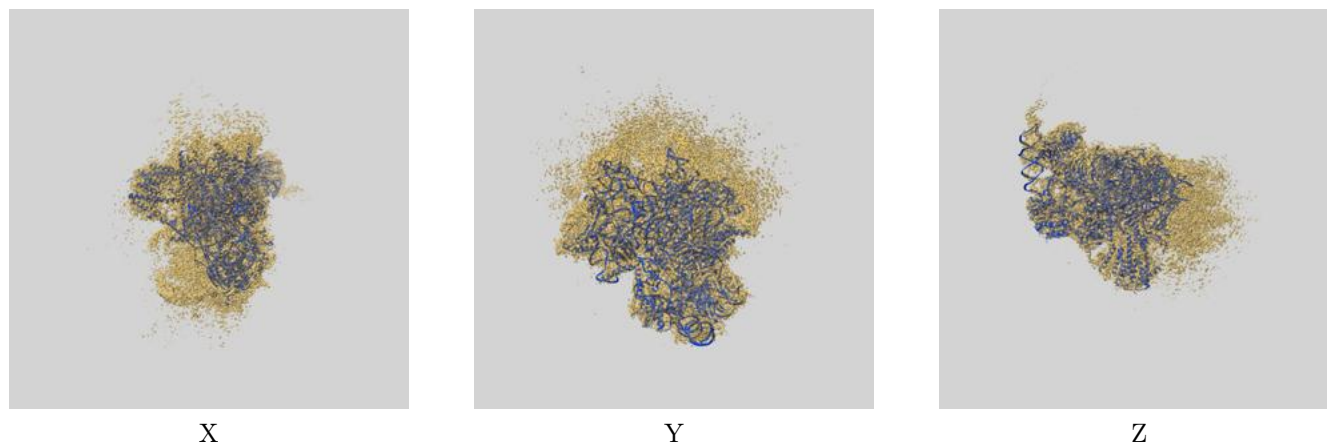
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.07	-	-
Author-provided FSC curve	3.06	3.34	3.08
Unmasked-calculated*	3.35	4.24	3.43

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

9 Map-model fit [i](#)

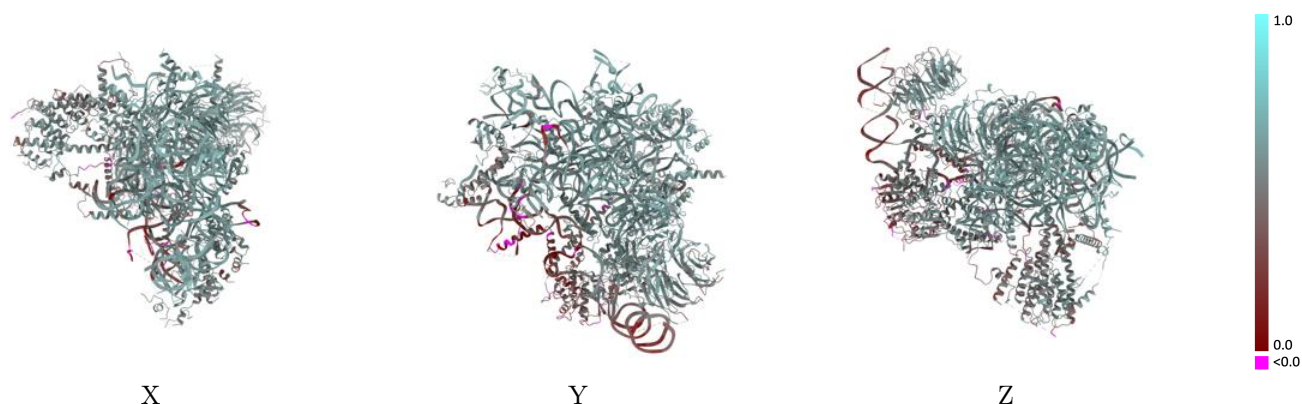
This section contains information regarding the fit between EMDB map EMD-24290 and PDB model 7R72. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



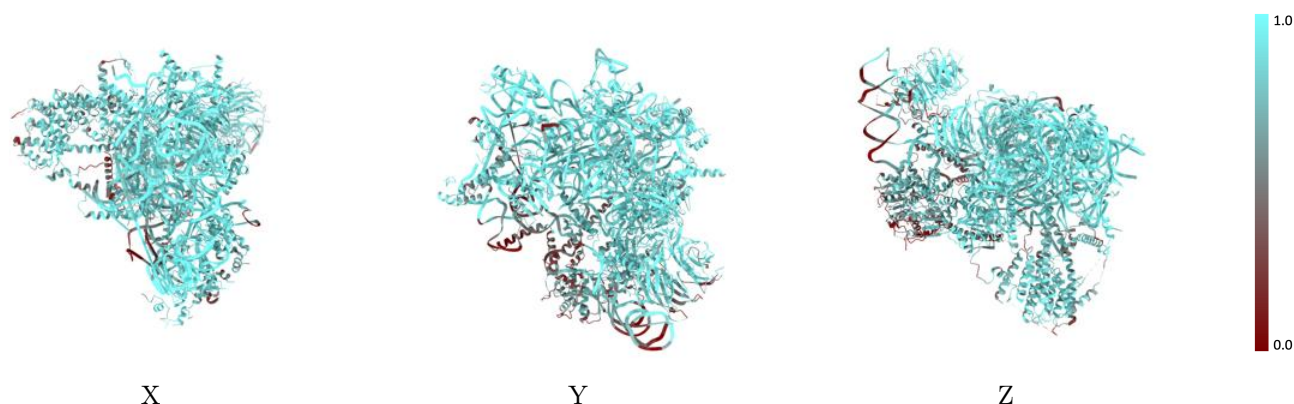
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



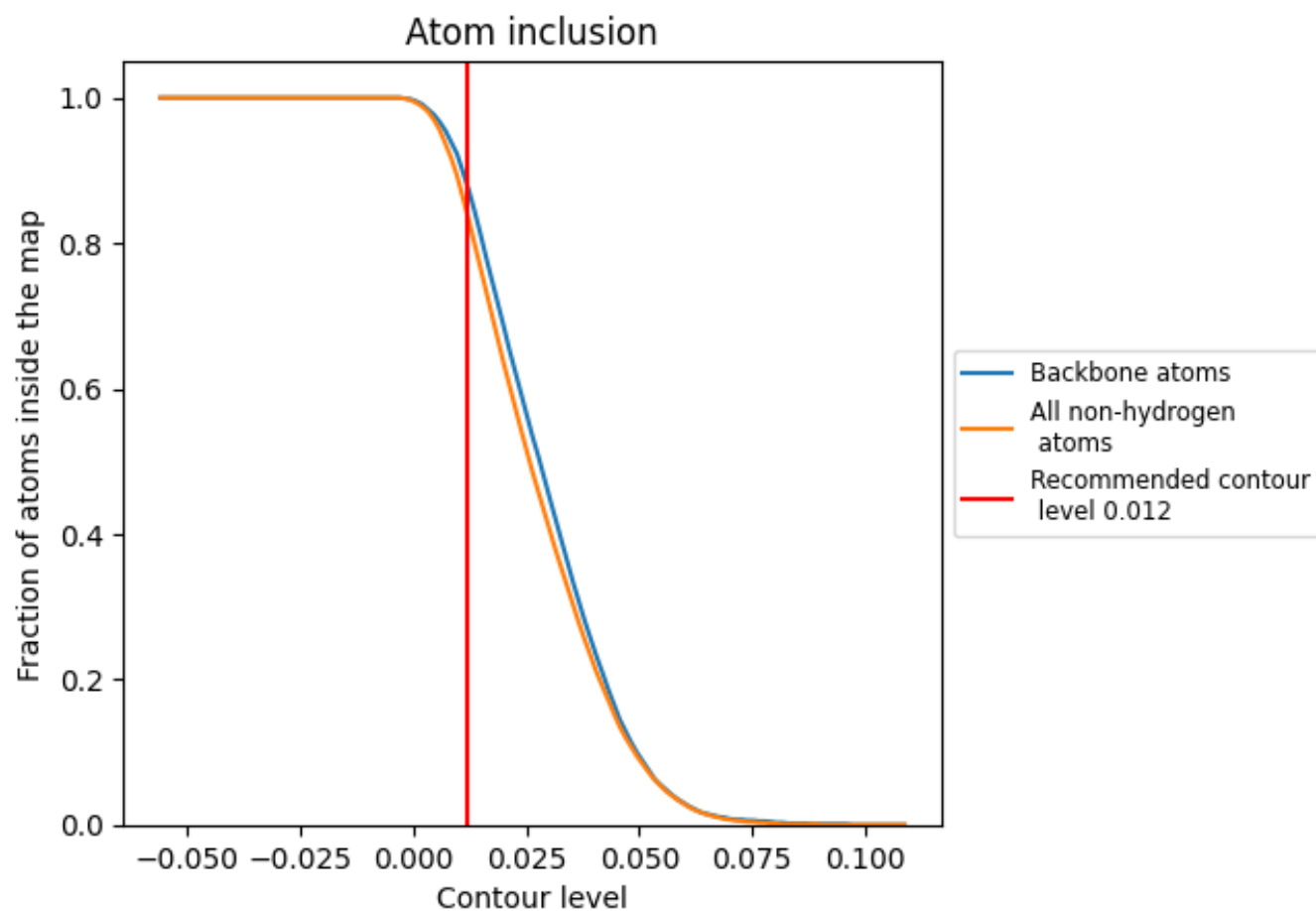
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8400	 0.5190
1	 0.8820	 0.5180
2	 0.9450	 0.5870
8	 0.8310	 0.5190
B	 0.8890	 0.4960
G	 0.9220	 0.5630
I	 0.7920	 0.4860
P	 0.8060	 0.5180
R	 0.8630	 0.5490
U	 0.8750	 0.5370
X	 0.9440	 0.5930
Z	 0.9460	 0.6070
b	 0.7740	 0.4770
c	 0.9370	 0.5790
d	 0.8460	 0.5550
g	 0.9540	 0.6010
j	 0.9120	 0.6040
k	 0.9010	 0.5760
m	 0.9490	 0.5980
n	 0.9470	 0.5950
p	 0.7910	 0.5200
t	 0.9090	 0.5980
u	 0.7830	 0.4630
w	 0.6350	 0.4580
x	 0.6010	 0.3860

