



wwPDB EM Validation Summary Report ⓘ

Jun 20, 2024 – 03:55 AM JST

PDB ID : 7WTP
EMDB ID : EMD-32794
Title : Cryo-EM structure of a yeast pre-40S ribosomal subunit - State Tsr1-2 (with Rps2)
Authors : Cheng, J.; Lau, B.; Thoms, M.; Ameismeier, M.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2022-02-05
Resolution : 3.80 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

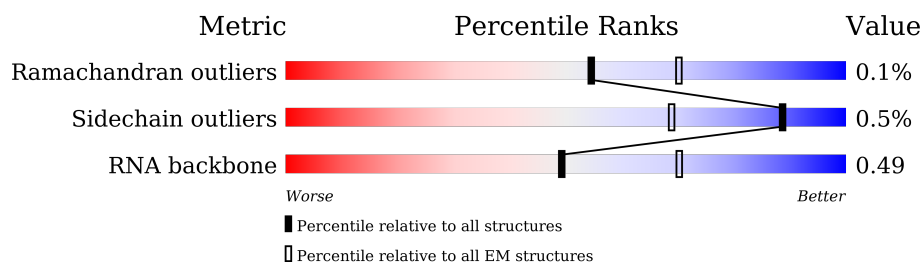
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



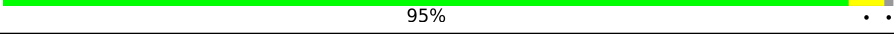
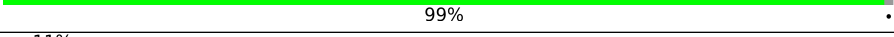

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	C2	1800	
2	SB	255	
3	SC	254	
4	SE	261	
5	SG	236	
6	SH	190	
7	SI	200	
8	SJ	197	

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Mol	Chain	Length	Quality of chain
9	SL	156	 93% 6%
10	SN	151	 99%
11	SO	137	 93% 7%
12	SW	130	 98%
13	SX	145	 97%
14	SY	135	 95%
15	Sb	82	 99%
16	Se	63	 11% 60% 40%
17	CA	274	 66% 34%
18	CB	275	 13% 87%
19	CC	788	 11% 84% 16%

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 52944 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1255	Total	C	N	O	P	0	0
			26763	11971	4765	8772	1255		

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 3 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SG	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SH	185	Total	C	N	O		0	0
			1486	954	266	266			

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SL	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SO	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 12 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 13 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 14 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SY	134	Total	C	N	O		
			1073	676	208	189	0	0

- Molecule 15 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Sb	81	Total	C	N	O	S		
			610	382	110	113	5	0	0

- Molecule 16 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Se	38	Total	C	N	O	S		
			313	198	65	49	1	0	0

- Molecule 17 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CA	181	Total	C	N	O	S		
			1436	917	261	254	4	0	0

- Molecule 18 is a protein called 18S rRNA (guanine(1575)-N(7))-methyltransferase.

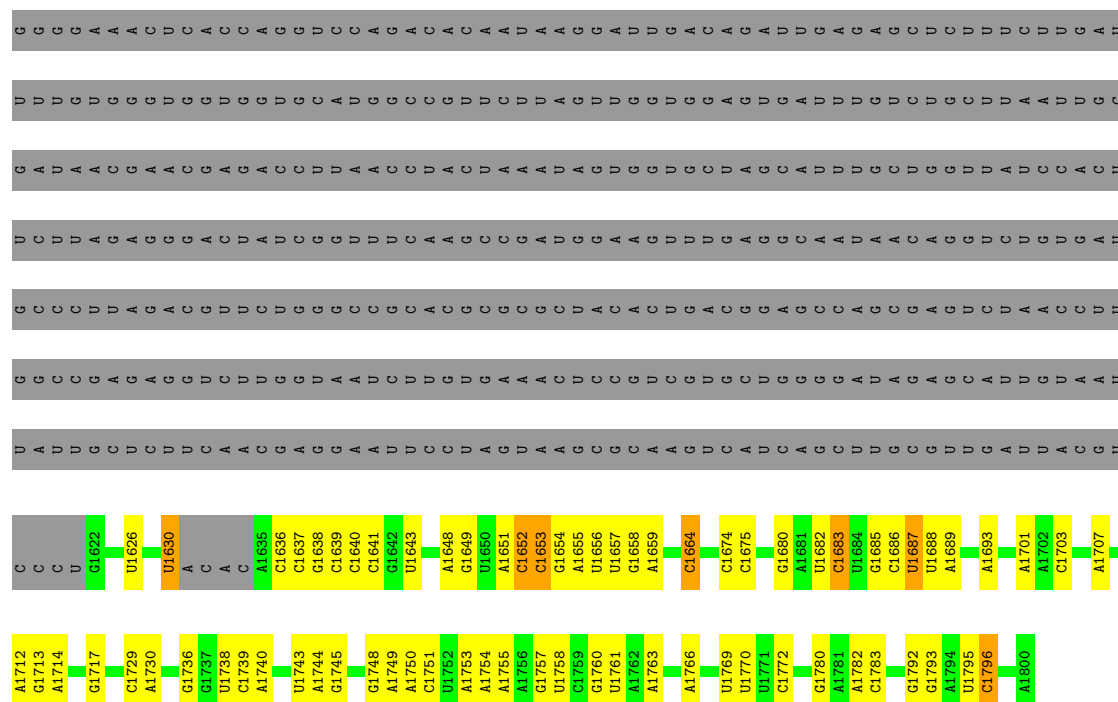
Mol	Chain	Residues	Atoms					AltConf	Trace
18	CB	35	Total	C	N	O	S		
			302	189	69	43	1	0	0

- Molecule 19 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CC	661	Total	C	N	O	S		
			5346	3413	933	986	14	0	0

- Molecule 20 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
20	Sb	1	Total	Zn	
			1	1	0



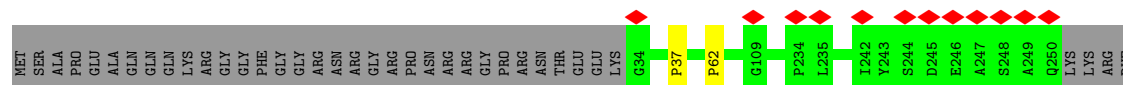
• Molecule 2: 40S ribosomal protein S1-A

Chain SB: 83% 15%



• Molecule 3: 40S ribosomal protein S2

Chain SC: 5% 85% 15%



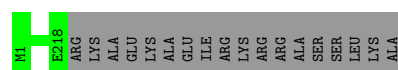
• Molecule 4: 40S ribosomal protein S4-A

Chain SE: 98% 2%



• Molecule 5: 40S ribosomal protein S6-A

Chain SG: 92% 8%



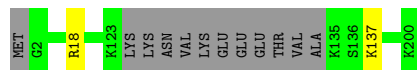
- Molecule 6: 40S ribosomal protein S7-A

Chain SH:  94% ...



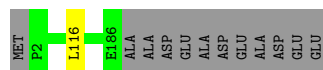
- Molecule 7: 40S ribosomal protein S8-A

Chain SI:  93% • 6%



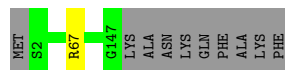
- Molecule 8: 40S ribosomal protein S9-A

Chain SJ:  93% • 6%



- Molecule 9: 40S ribosomal protein S11-A

Chain SL:  93% • 6%



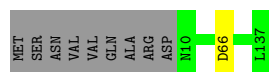
- Molecule 10: 40S ribosomal protein S13

Chain SN:  99% ..



- Molecule 11: 40S ribosomal protein S14-A

Chain SO:  93% • 7%



- Molecule 12: 40S ribosomal protein S22-A

Chain SW:  98% ..



- Molecule 13: 40S ribosomal protein S23-A

Diagram illustrating the structure of the C-terminal domain of the human protein, showing segments labeled MET, G2, Q63, C71, L104, and S145. A red diamond is positioned above the S145 segment.

- Chain SY: 95%

- Chain Sb: 99%

A diagram of a protein structure with three residues: MET, V2, and K82. A red diamond marker is positioned above the V2 residue.

- Chain Se: 

NET	ALA	LYS	VAL	HIS	GLY	SER	LEU	ALA	ARG	ALA	GLY	LYS	VAL	LYS	SER	GLN	THR	PRO	LYS	VAL	GLU	LYS	T24	N51	G52	K53	R54	G59	P60	S61	VAL	GLN
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- Chain CA: 66% 34%

NET	VAL	ALA	ALA	PRO	THR	ALA	ALA	LEU	LYS	LYS	ALA	ALA	ALA	THR	THR	VAL	THR	PRO	VAL	SER	SER	SER	SER	ARG	ARG	ILE	ILE	ILE	GLY	GLY	ILE	ASN	ASN	THR	THR	GLU	SER	ILE	ILE	ASP	ASP	ASP	ASP	ASP	ASP	VAL	VAL	LEU	LEU	ASP	ASP	ASP	SER	SER	ASN	ASN	THR	ALA	LYS	GLU	GLU	GLU	VAL	VAL	GLU	GLY	GLY	GLU	GLU
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GLY	ARG	LYS	THR	HIS	GLU	SER	LYS	THR	VAL	VAL	VAL	ASP	ASP	GLN	GLY	LYS	PRO	ARG	PHE	THR	SER	SER	ALA	ALA	SER	LYS	THR	GLN	GLY	ASN	LYS	ILE	K93	R176	R273	TVR
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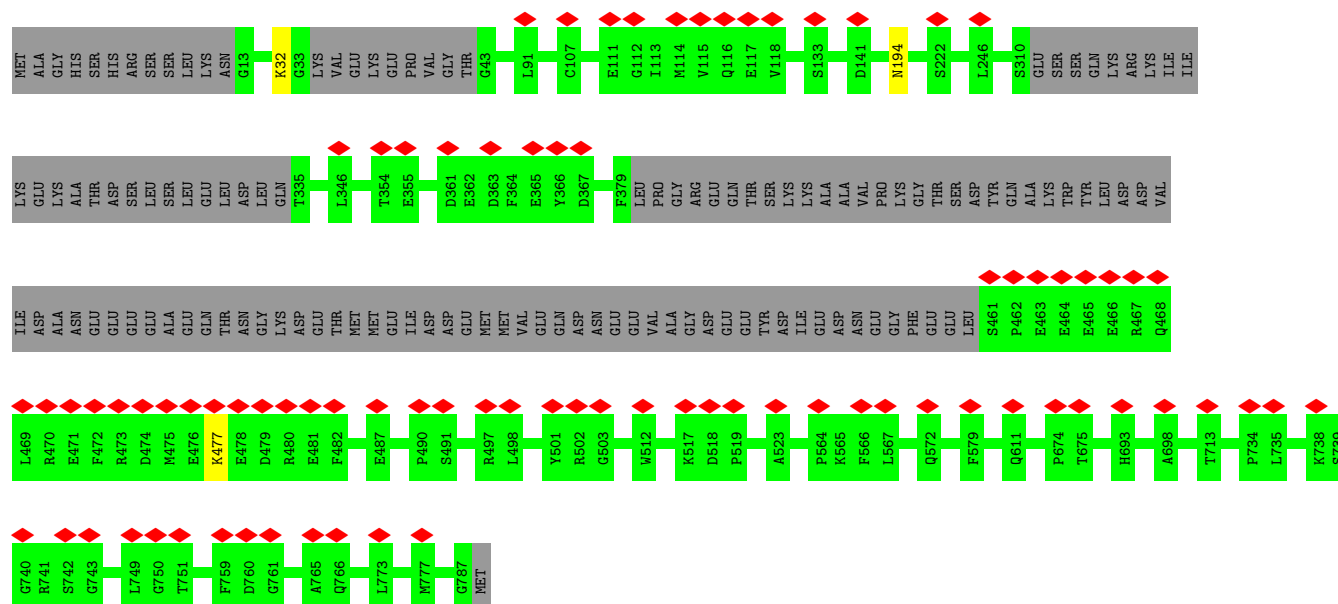
- Chain CB:  13% 87%

MET	SER	ARG	PRO	GLU	GLU	LEU	ALA	ALA	PRO	PRO	GLU	ILE	PHE	TYR	ASN	ASP	SER	GLU	GLU	ALA	HIS	LYS	TYR	THR	GLY	SER	THR	ARG	VAL	GLN	HIS	ILE	ILE	GLN	ALA	LYS	MET	THR	THR	LEU	ARG	ALA	LEU	GLU	LEU	LEU	LEU	ASN	GLN	LEU	PRO	CYS	CYS	SER	PHE	ILE	LEU	ASP	ILE	GLY	GLY	CYS	GLY	SER	GLY	LEU
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SER	GLY	GLY	LEU	THR	GLN	GLU	GLY	ASP	HIS	VAL	TRP	CYS	GLY	LEU	ASP	ILE	SER	PRO	SER	MET	LEU	ALA	THR	GLY	LEU	SER	SER	ARG	GLY	THR	GLY	ILE	PRO	PHE	ARG	ALA	GLY	SER	PHE	ASP	ALA	ALA	ILE	SER	ILE	SER	ILE	ALA
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GLN	TRP	LEU	LEU	CYS	ASN	ALA	ASP	THR	SER	TYR	ASN	ASP	PRO	LYS	GLN	LEU	ARG	LEU	MET	ARG	PHE	PHE	ASN	ASN	THR	LEU	TYR	ALA	ALA	LEU	LYS	LYS	LYS	GLY	GLY	LYS	PHE	VAL	VAL	GLN	GLN	TYR	TYR	ASP	ASP	ASP	ASP	ILE	LEU	GLN	SER	ALA	LYS	LYS	VAL	VAL	ALA	ALA	GLY	PHE	SER	GLY
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GLY	LEU	VAL	VAL	ASP	ASP	PRO	GLU	GLY	SER	LYS	LYS	ASN	LYS	LYS	TYR	TYR	LEU	LEU	VAL	SER	SER	GLY	ALA	PRO	PRO	GLN	GLY	GLU	GLU	GLN	VAL	ASN	ASN	LEU	ASP	GLY	VAL	THR	MET	ASP	GLU	GLU	GLU	ASN	ASN	VAL	LYS	LYS	GLY	GLY	LYS	LYS	GLN	GLN	LEU	ARG	GLN	ARG	LEU	LEU	LYS	ASP	LYS	GLU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27524	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.252	Depositor
Minimum map value	-0.126	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	381.24, 381.24, 381.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.059, 1.059, 1.059	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	C2	0.80	4/29940 (0.0%)	1.10	123/46636 (0.3%)
2	SB	0.37	0/1748	0.70	3/2352 (0.1%)
3	SC	0.51	3/1665 (0.2%)	0.81	6/2263 (0.3%)
4	SE	0.44	0/2109	0.68	1/2839 (0.0%)
5	SG	0.36	0/1779	0.63	0/2379
6	SH	0.33	0/1511	0.70	1/2036 (0.0%)
7	SI	0.42	0/1514	0.65	0/2021
8	SJ	0.38	0/1519	0.66	1/2035 (0.0%)
9	SL	0.52	0/1194	0.65	0/1610
10	SN	0.45	0/1215	0.70	0/1638
11	SO	0.39	0/960	0.76	1/1290 (0.1%)
12	SW	0.47	0/1038	0.72	2/1395 (0.1%)
13	SX	0.46	0/1139	0.72	2/1518 (0.1%)
14	SY	0.41	0/1087	0.74	1/1449 (0.1%)
15	Sb	0.38	0/620	0.67	0/838
16	Se	0.38	0/319	0.79	0/425
17	CA	0.37	0/1462	0.66	0/1969
18	CB	0.26	0/305	0.65	0/394
19	CC	0.27	0/5469	0.56	0/7383
All	All	0.64	7/56593 (0.0%)	0.94	141/82470 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	SH	0	3
10	SN	0	1
13	SX	0	1
14	SY	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	6

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	SC	37	PRO	CG-CD	-11.85	1.11	1.50
3	SC	62	PRO	CG-CD	-9.04	1.20	1.50
1	C2	474	A	N9-C4	-6.09	1.34	1.37
1	C2	118	U	C2-N3	-6.07	1.33	1.37
3	SC	37	PRO	N-CD	5.60	1.55	1.47

The worst 5 of 141 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SC	37	PRO	N-CD-CG	-13.41	83.08	103.20
1	C2	190	C	N3-C2-O2	-12.36	113.25	121.90
3	SC	37	PRO	CA-N-CD	-11.69	95.14	111.50
3	SC	62	PRO	N-CD-CG	-11.05	86.63	103.20
1	C2	645	C	N3-C2-O2	-10.80	114.34	121.90

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	SH	31	SER	Peptide
6	SH	64	VAL	Peptide
6	SH	9	LEU	Peptide
10	SN	21	ASN	Peptide
13	SX	63	GLN	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SB	214/255 (84%)	193 (90%)	21 (10%)	0	100	100
3	SC	215/254 (85%)	194 (90%)	21 (10%)	0	100	100
4	SE	258/261 (99%)	230 (89%)	28 (11%)	0	100	100
5	SG	216/236 (92%)	203 (94%)	13 (6%)	0	100	100
6	SH	183/190 (96%)	164 (90%)	18 (10%)	1 (0%)	29	66
7	SI	184/200 (92%)	173 (94%)	11 (6%)	0	100	100
8	SJ	183/197 (93%)	167 (91%)	16 (9%)	0	100	100
9	SL	144/156 (92%)	126 (88%)	18 (12%)	0	100	100
10	SN	148/151 (98%)	133 (90%)	15 (10%)	0	100	100
11	SO	126/137 (92%)	110 (87%)	16 (13%)	0	100	100
12	SW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
13	SX	142/145 (98%)	123 (87%)	19 (13%)	0	100	100
14	SY	132/135 (98%)	118 (89%)	11 (8%)	3 (2%)	6	38
15	Sb	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
16	Se	36/63 (57%)	28 (78%)	8 (22%)	0	100	100
17	CA	179/274 (65%)	166 (93%)	13 (7%)	0	100	100
18	CB	33/275 (12%)	28 (85%)	5 (15%)	0	100	100
19	CC	653/788 (83%)	624 (96%)	29 (4%)	0	100	100
All	All	3252/3929 (83%)	2964 (91%)	284 (9%)	4 (0%)	54	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	SY	32	ARG
14	SY	52	LYS
6	SH	74	GLN
14	SY	79	VAL

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	SB	192/224 (86%)	191 (100%)	1 (0%)	88	94
3	SC	176/205 (86%)	176 (100%)	0	100	100
4	SE	221/222 (100%)	219 (99%)	2 (1%)	78	88
5	SG	187/201 (93%)	187 (100%)	0	100	100
6	SH	165/170 (97%)	163 (99%)	2 (1%)	71	84
7	SI	150/161 (93%)	148 (99%)	2 (1%)	69	82
8	SJ	158/166 (95%)	158 (100%)	0	100	100
9	SL	129/137 (94%)	128 (99%)	1 (1%)	81	89
10	SN	127/128 (99%)	127 (100%)	0	100	100
11	SO	97/105 (92%)	97 (100%)	0	100	100
12	SW	110/111 (99%)	110 (100%)	0	100	100
13	SX	119/120 (99%)	119 (100%)	0	100	100
14	SY	112/113 (99%)	111 (99%)	1 (1%)	78	88
15	Sb	70/71 (99%)	70 (100%)	0	100	100
16	Se	34/54 (63%)	34 (100%)	0	100	100
17	CA	158/238 (66%)	157 (99%)	1 (1%)	86	92
18	CB	31/233 (13%)	31 (100%)	0	100	100
19	CC	575/703 (82%)	572 (100%)	3 (0%)	88	94
All	All	2811/3362 (84%)	2798 (100%)	13 (0%)	89	94

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	SL	67	ARG
14	SY	8	ARG
19	CC	477	LYS
19	CC	32	LYS
19	CC	194	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
19	CC	194	ASN
16	Se	46	ASN
10	SN	101	HIS
7	SI	32	GLN
13	SX	79	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1247/1800 (69%)	329 (26%)	13 (1%)

5 of 329 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	3	U
1	C2	4	C
1	C2	5	U
1	C2	6	G

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C2	755	A
1	C2	817	A
1	C2	1652	C
1	C2	1051	G
1	C2	1097	U

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 monosaccharides 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](#)

There are no chain breaks in this entry.

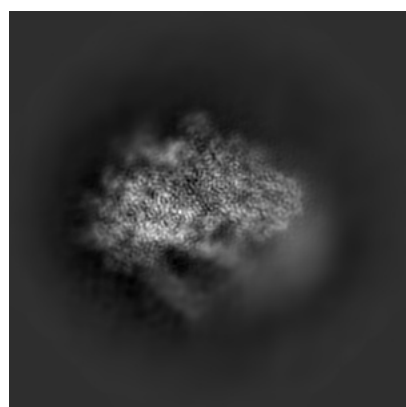
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32794. These allow visual inspection of the internal detail of the map and identification of artifacts.

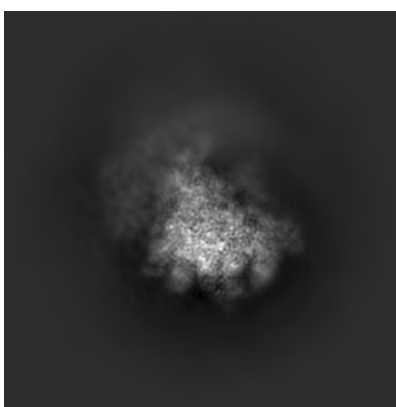
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

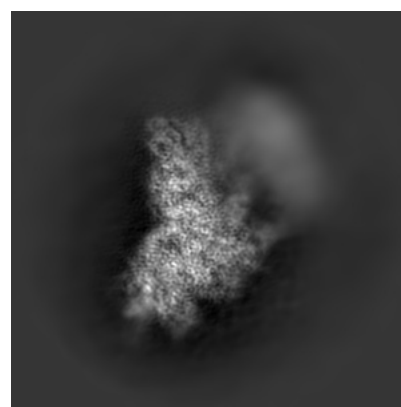
6.1.1 Primary map



X



Y

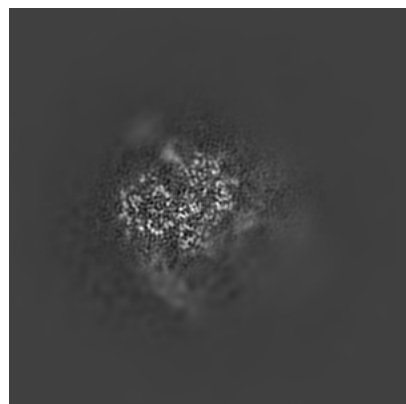


Z

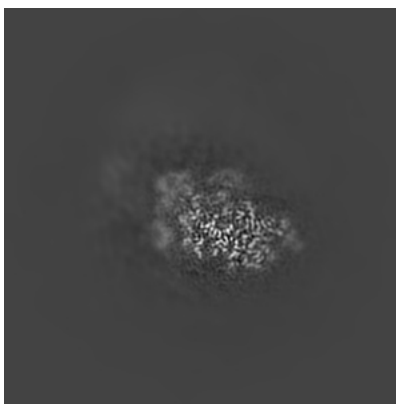
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

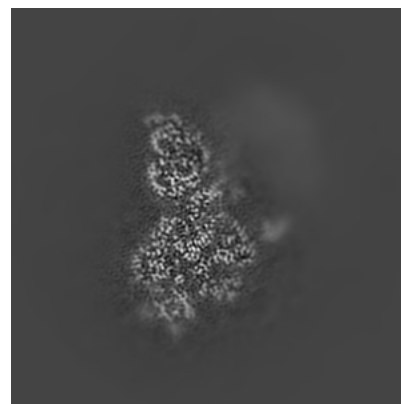
6.2.1 Primary map



X Index: 180



Y Index: 180

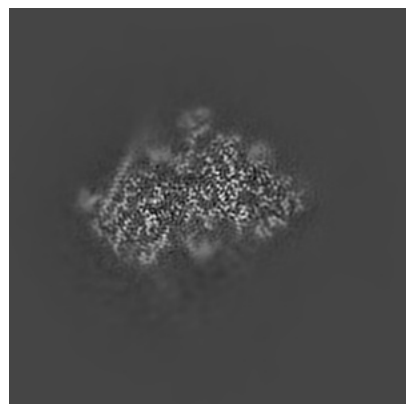


Z Index: 180

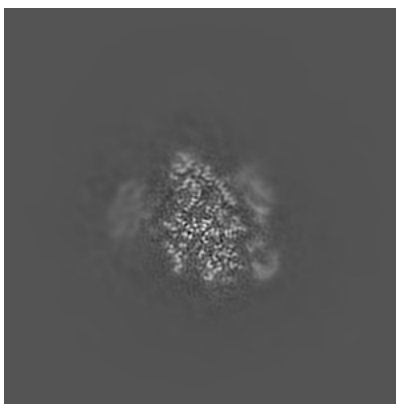
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

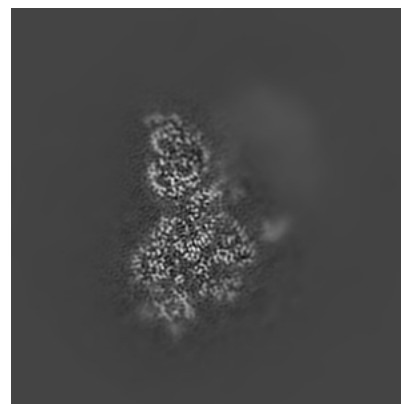
6.3.1 Primary map



X Index: 147



Y Index: 143

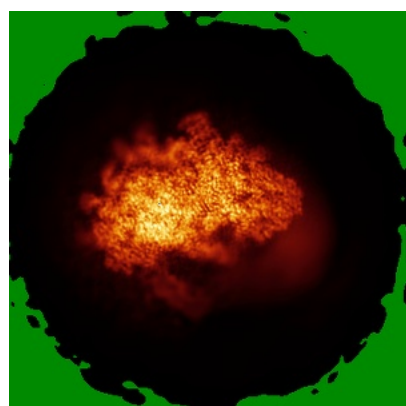


Z Index: 180

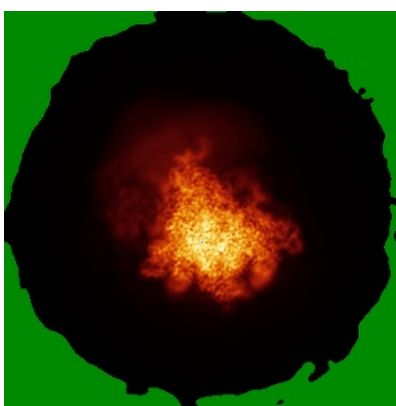
The images above show the largest variance slices of the map in three orthogonal directions.

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

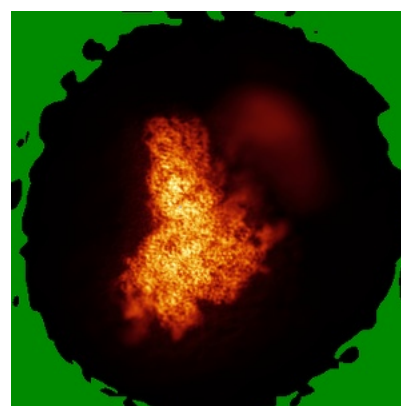
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

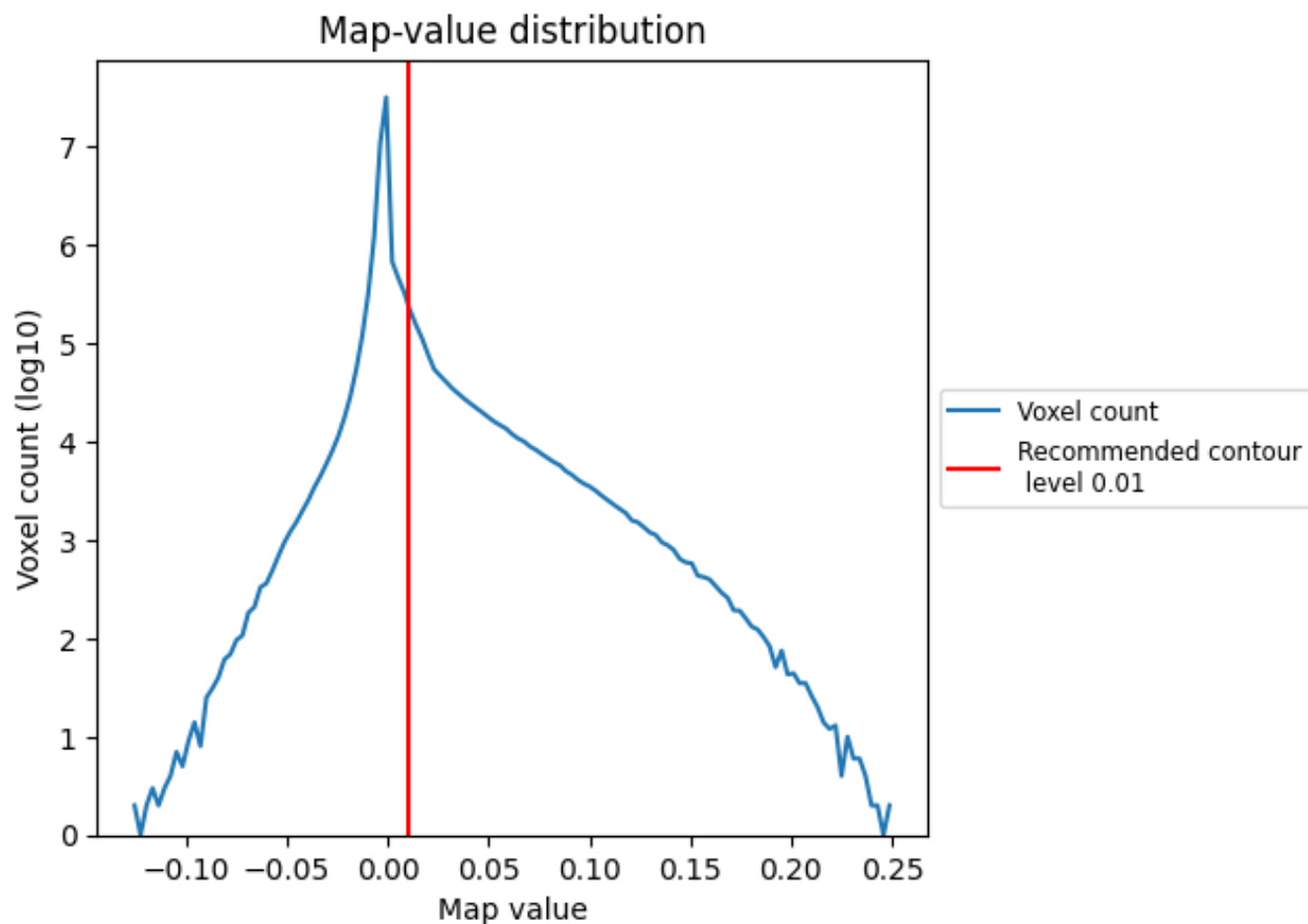
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

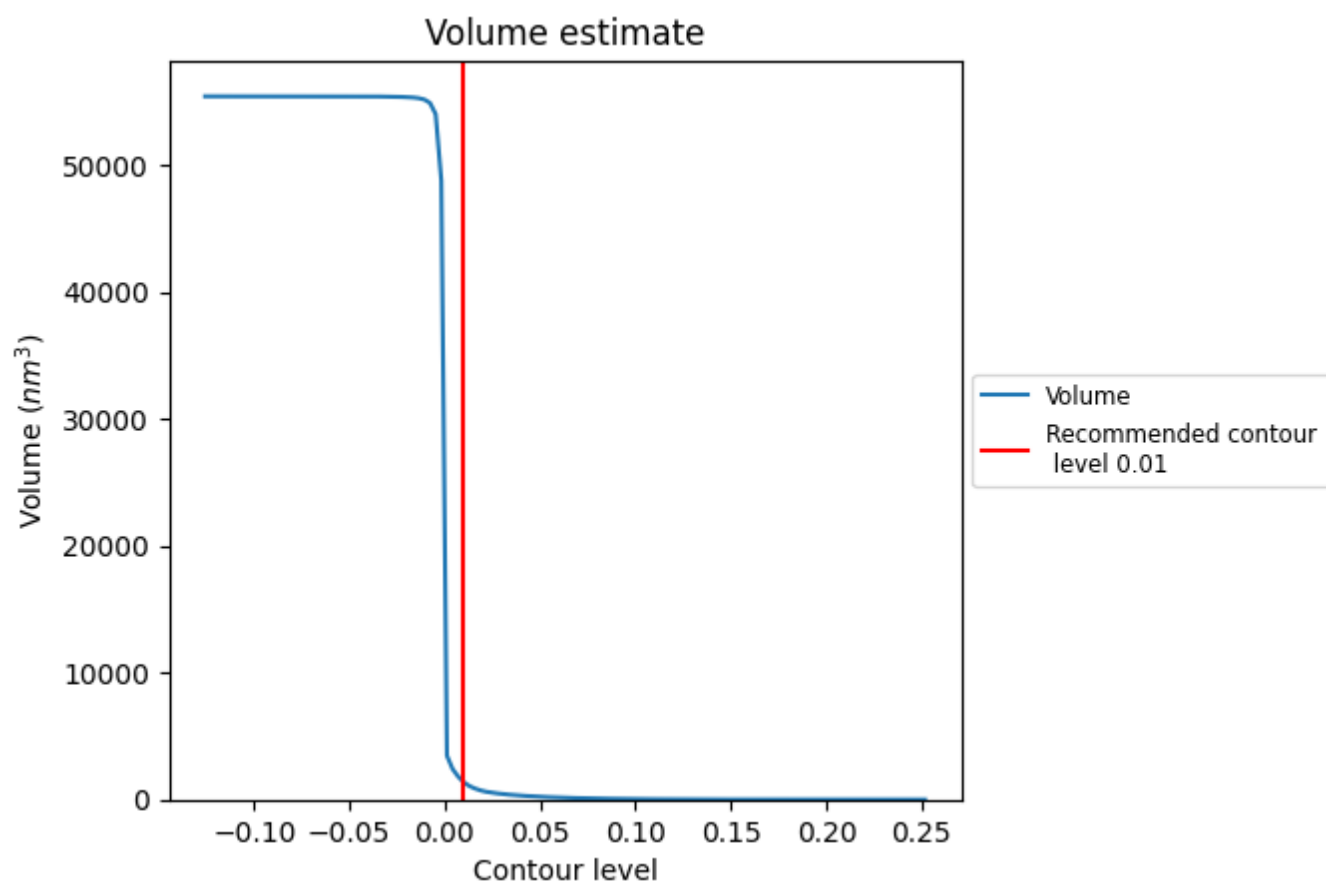
This section contains the results of statistical analysis of the map.

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.

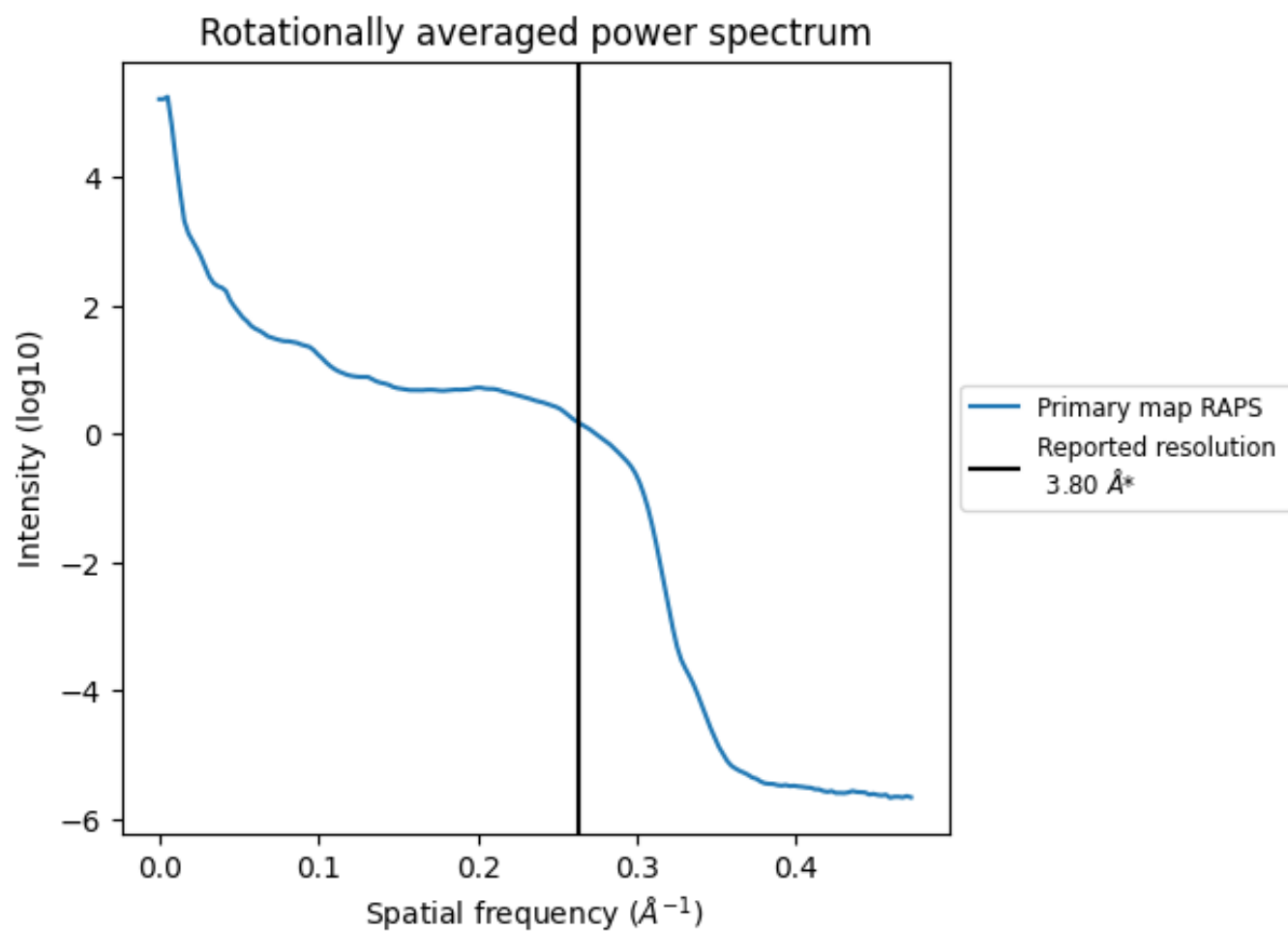
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1359 nm^3 ; this corresponds to an approximate mass of 1228 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 ⓘ

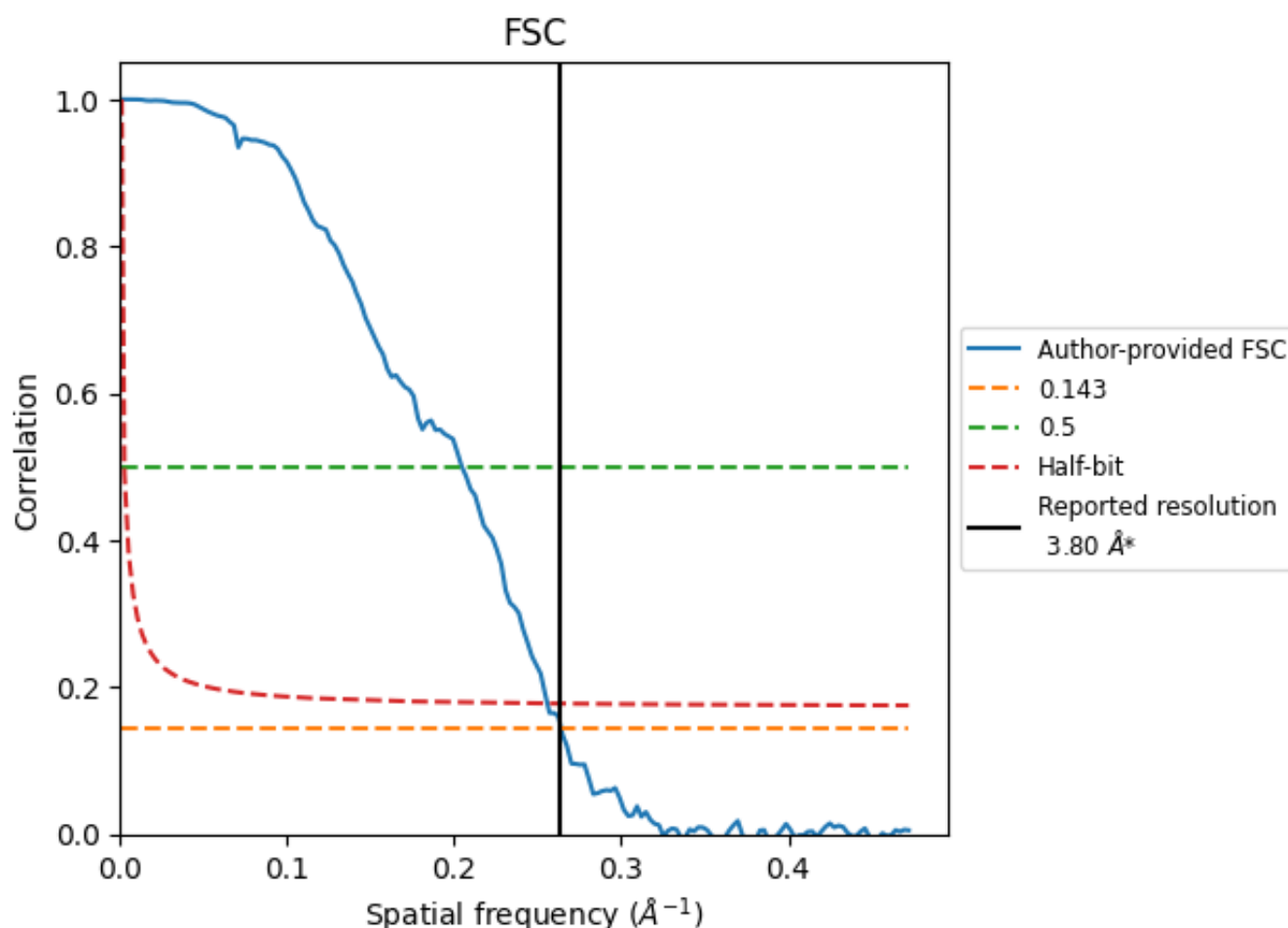


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

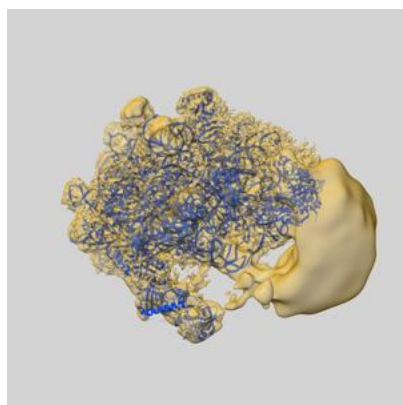
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.79	4.89	3.91
Unmasked-calculated*	-	-	-

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

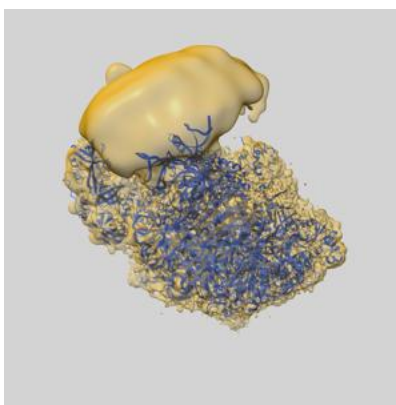
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32794 and PDB model 7WTP. Per-residue inclusion information can be found in section [3](#) on page [7](#).

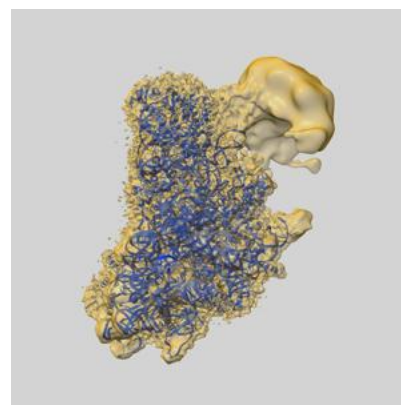
9.1 Map-model overlay [i](#)



X



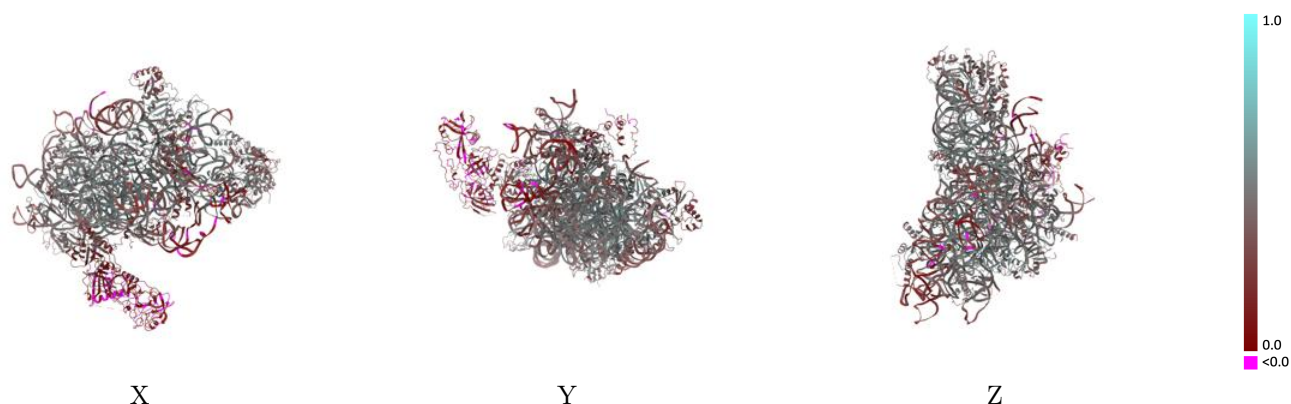
Y



Z

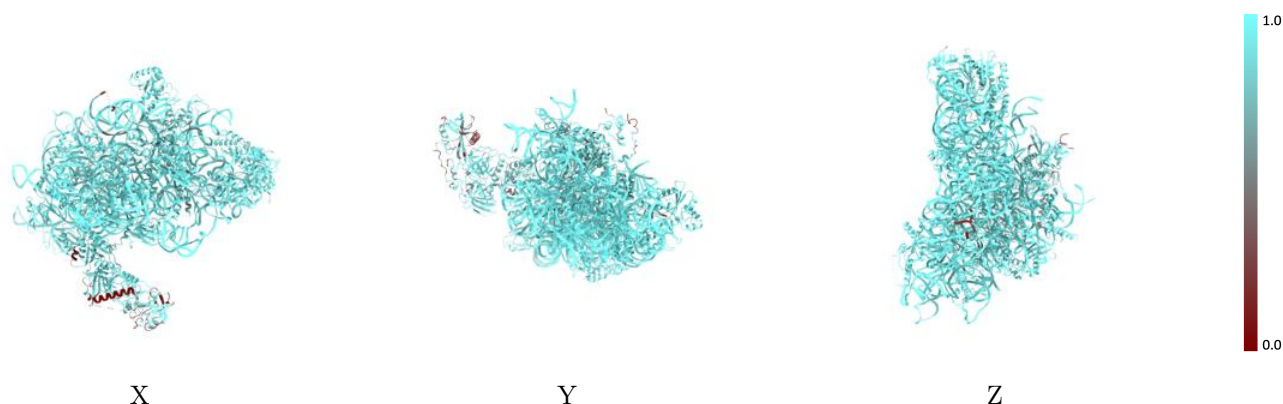
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



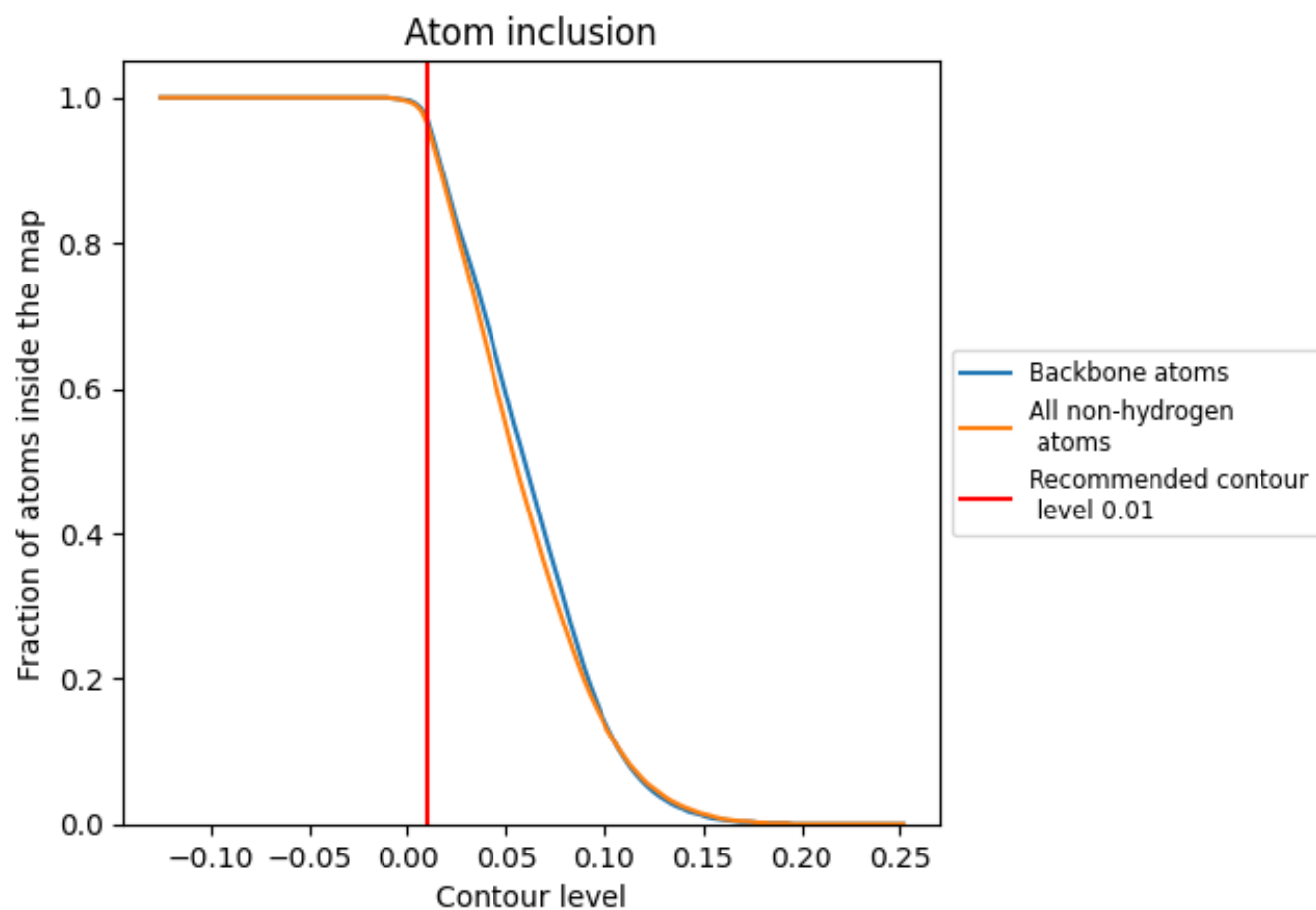
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).









































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9650	 0.3990
C2	 0.9900	 0.4150
CA	 0.9870	 0.4050
CB	 0.9060	 0.3240
CC	 0.7980	 0.1620
SB	 0.9810	 0.4510
SC	 0.8720	 0.3060
SE	 0.9910	 0.4990
SG	 0.9930	 0.4150
SH	 0.9830	 0.3670
SI	 0.9940	 0.4770
SJ	 0.9890	 0.4600
SL	 0.9880	 0.5150
SN	 0.9950	 0.4820
SO	 0.9790	 0.4430
SW	 0.9970	 0.5100
SX	 0.9740	 0.4480
SY	 0.9910	 0.4530
Sb	 0.9900	 0.4600
Se	 0.8360	 0.3640

