



wwPDB EM Validation Summary Report ⓘ

Jun 20, 2024 – 05:54 AM JST

PDB ID : 7WTO
EMDB ID : EMD-32793
Title : Cryo-EM structure of a yeast pre-40S ribosomal subunit - State Tsr1-1 (without Rps2)
Authors : Cheng, J.; Lau, B.; Thoms, M.; Ameismeier, M.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2022-02-05
Resolution : 3.50 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

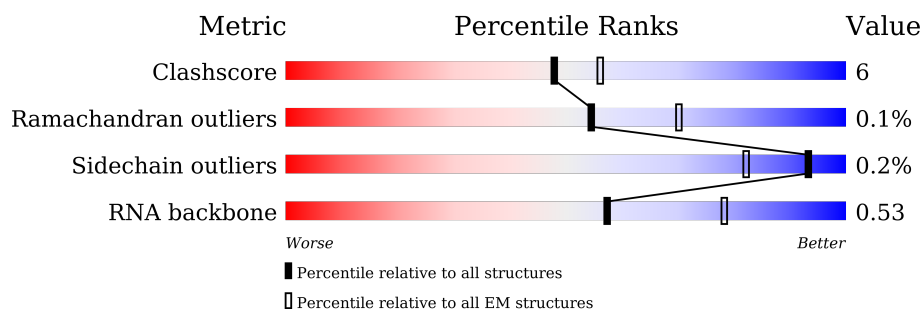
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




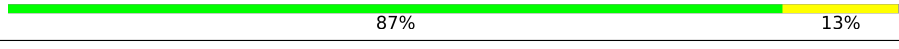
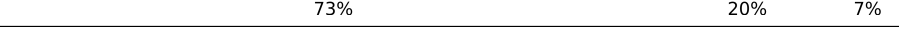
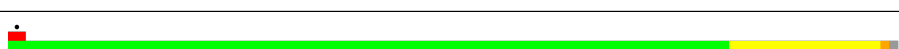

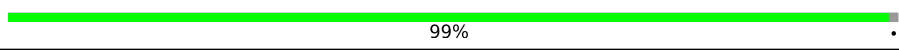

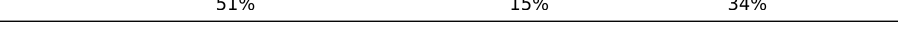

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	SE	261	
4	SG	236	
5	SH	190	
6	SI	200	
7	SJ	197	

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Mol	Chain	Length	Quality of chain
8	SL	156	
9	SN	151	
10	SO	137	
11	SW	130	
12	SX	145	
13	SY	135	
14	Sb	82	
15	Se	63	
16	CA	274	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 44490 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	1200	Total	C	N	O	P	0	0
			25592	11448	4555	8389	1200		

- 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 S4-A.

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

- Molecule 4 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 7 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S13.

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

- Molecule 10 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 16 is a protein called Pre-rRNA-processing protein PNO1.

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

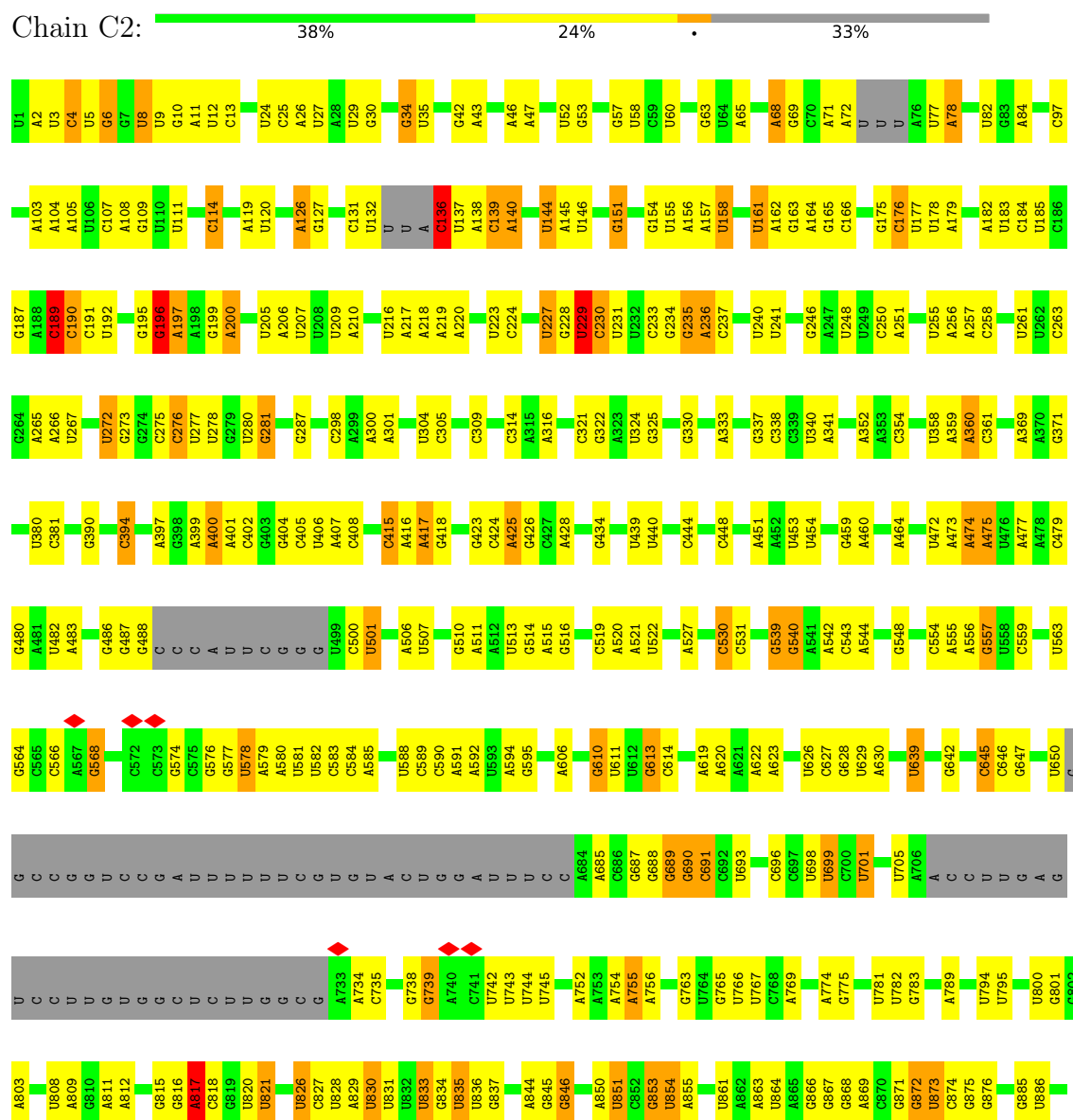
- Molecule 17 is ZINC ION (three-letter code: ZN) (formula: Zn).

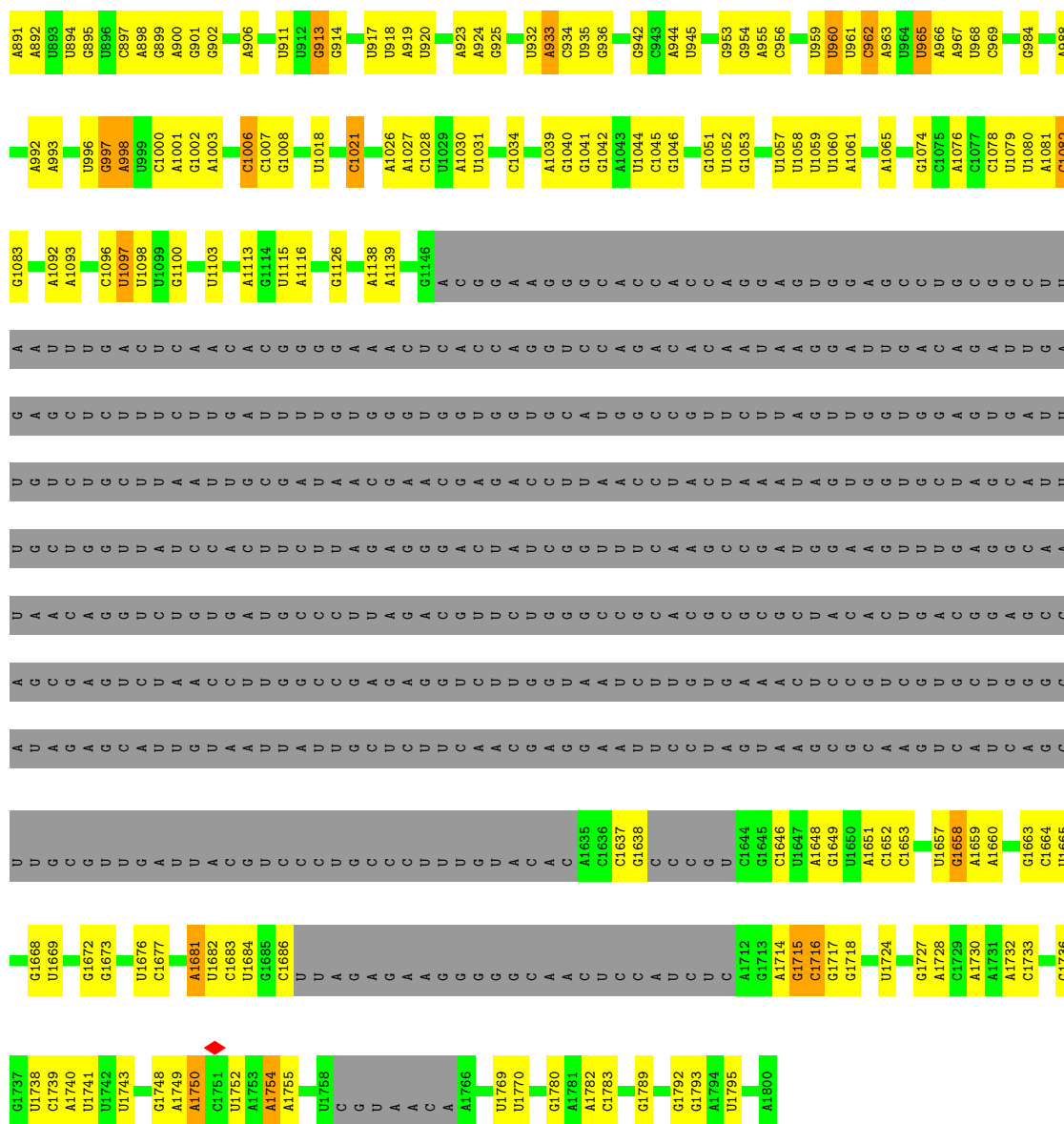
Mol	Chain	Residues	Atoms		AltConf
17	Sb	1	Total	Zn	0
			1	1	

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.

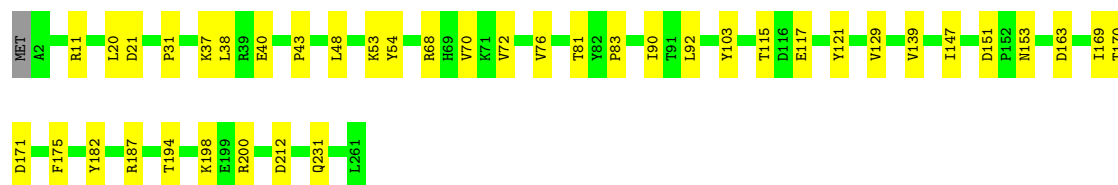
• Molecule 1: 18S rRNA



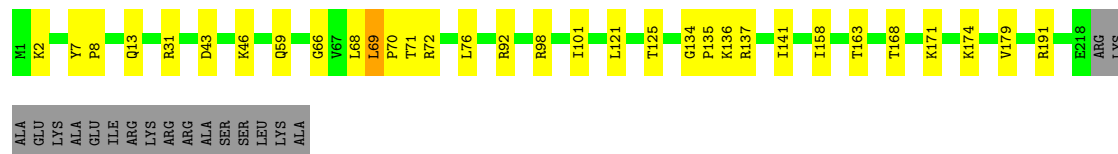
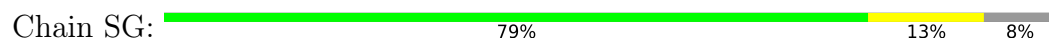


- Molecule 2: 40S ribosomal protein S1-A

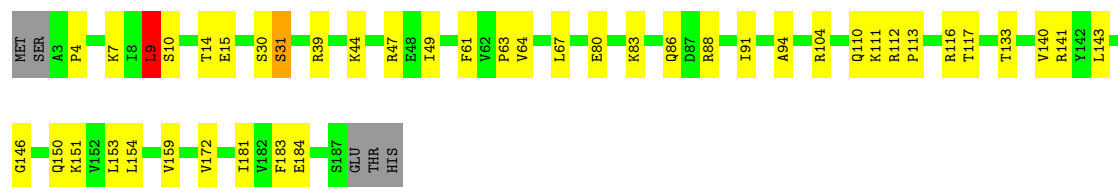
- Molecule 3: 40S ribosomal protein S4-A



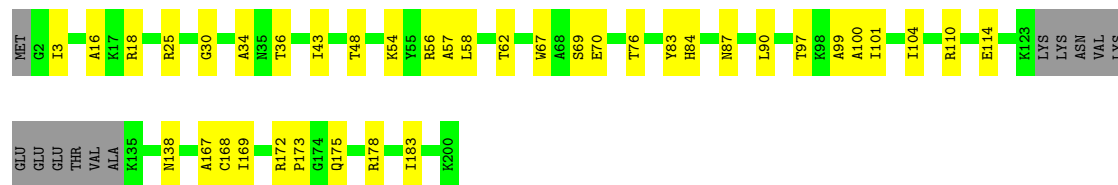
- Molecule 4: 40S ribosomal protein S6-A



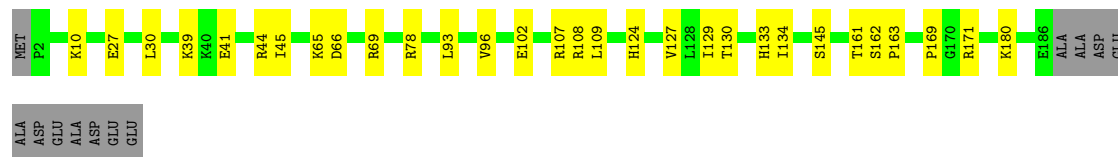
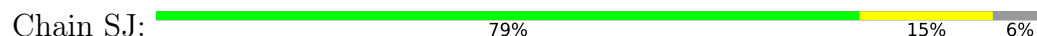
- Molecule 5: 40S ribosomal protein S7-A



- Molecule 6: 40S ribosomal protein S8-A

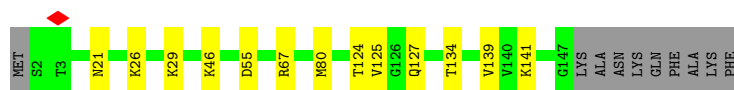


- Molecule 7: 40S ribosomal protein S9-A



- Molecule 8: 40S ribosomal protein S11-A





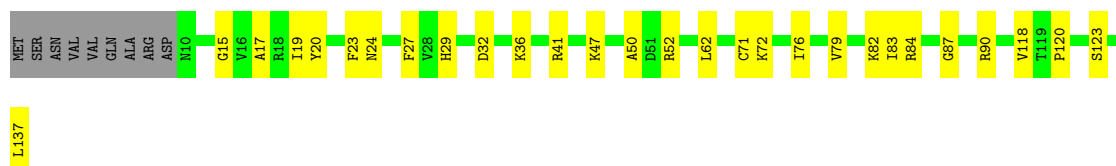
- Molecule 9: 40S ribosomal protein S13

Chain SN: 87% 13%



- Molecule 10: 40S ribosomal protein S14-A

Chain SO: 73% 20% 7%



- Molecule 11: 40S ribosomal protein S22-A

Chain SW: 82% 17%



- Molecule 12: 40S ribosomal protein S23-A

Chain SX: 81% 17%



- Molecule 13: 40S ribosomal protein S24-A

Chain SY: 70% 28%

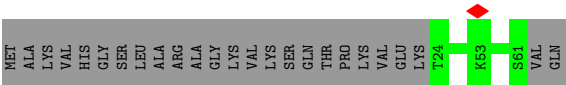


- Molecule 14: 40S ribosomal protein S27-A

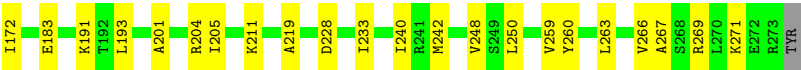
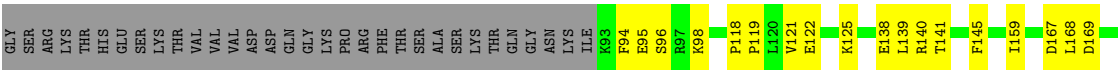
Chain Sb: 99%



- Molecule 15: 40S ribosomal protein S30-A



- Molecule 16: Pre-rRNA-processing protein PNO1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59786	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	0.306	Depositor
Minimum map value	-0.141	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 [i](#)

5.1 Standard geometry [i](#)

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	0.50	1/28630 (0.0%)	0.99	85/44592 (0.2%)
2	SB	0.31	0/1748	0.67	2/2352 (0.1%)
3	SE	0.35	0/2109	0.64	0/2839
4	SG	0.29	0/1779	0.61	1/2379 (0.0%)
5	SH	0.29	0/1511	0.69	1/2036 (0.0%)
6	SI	0.35	0/1514	0.66	0/2021
7	SJ	0.31	0/1519	0.61	0/2035
8	SL	0.37	0/1194	0.62	1/1610 (0.1%)
9	SN	0.33	0/1215	0.61	0/1638
10	SO	0.32	0/960	0.68	0/1290
11	SW	0.35	0/1038	0.65	2/1395 (0.1%)
12	SX	0.35	0/1139	0.66	0/1518
13	SY	0.37	0/1087	0.70	0/1449
14	Sb	0.31	0/620	0.64	0/838
15	Se	0.29	0/319	0.67	0/425
16	CA	0.30	0/1462	0.65	0/1969
All	All	0.44	1/47844 (0.0%)	0.88	92/70386 (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
5	SH	0	4
9	SN	0	1
12	SX	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C2	474	A	N9-C4	-5.05	1.34	1.37

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	190	C	N3-C2-O2	-12.35	113.26	121.90
1	C2	645	C	N3-C2-O2	-11.36	113.95	121.90
1	C2	646	C	N3-C2-O2	-9.09	115.54	121.90
1	C2	190	C	N1-C2-O2	8.75	124.15	118.90
1	C2	646	C	C6-N1-C2	-8.55	116.88	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	SH	110	GLN	Peptide
5	SH	31	SER	Peptide
5	SH	64	VAL	Peptide
5	SH	9	LEU	Peptide
9	SN	21	ASN	Peptide

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	C2	25592	0	12869	246	0
2	SB	1722	0	1793	24	0
3	SE	2068	0	2154	27	0
4	SG	1755	0	1846	23	0
5	SH	1486	0	1576	25	0
6	SI	1489	0	1525	25	0
7	SJ	1494	0	1573	22	0
8	SL	1168	0	1233	8	0
9	SN	1192	0	1255	12	0
10	SO	949	0	985	18	0
11	SW	1021	0	1060	15	0
12	SX	1121	0	1196	18	0
13	SY	1073	0	1132	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	Sb	610	0	633	0	0
15	Se	313	0	343	0	0
16	CA	1436	0	1515	26	0
17	Sb	1	0	0	0	0
All	All	44490	0	32688	454	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 6.

The worst 5 of 454 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:C2:826:U:H3	1:C2:846:G:H1	0.99	0.98
1:C2:486:G:H1	1:C2:501:U:H3	1.12	0.98
1:C2:1646:C:H42	1:C2:1754:A:N6	1.68	0.92
1:C2:1677:C:H42	1:C2:1724:U:H3	0.96	0.90
1:C2:1665:U:H3	1:C2:1736:G:H1	0.90	0.89

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	
2	SB	214/255 (84%)	200 (94%)	14 (6%)	0	100	100
3	SE	258/261 (99%)	239 (93%)	19 (7%)	0	100	100
4	SG	216/236 (92%)	206 (95%)	10 (5%)	0	100	100
5	SH	183/190 (96%)	160 (87%)	22 (12%)	1 (0%)	29	68
6	SI	184/200 (92%)	177 (96%)	7 (4%)	0	100	100
7	SJ	183/197 (93%)	167 (91%)	16 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SL	144/156 (92%)	129 (90%)	15 (10%)	0	100	100
9	SN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
10	SO	126/137 (92%)	113 (90%)	13 (10%)	0	100	100
11	SW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
12	SX	142/145 (98%)	123 (87%)	19 (13%)	0	100	100
13	SY	132/135 (98%)	119 (90%)	12 (9%)	1 (1%)	19	58
14	Sb	79/82 (96%)	68 (86%)	11 (14%)	0	100	100
15	Se	36/63 (57%)	30 (83%)	6 (17%)	0	100	100
16	CA	179/274 (65%)	172 (96%)	7 (4%)	0	100	100
All	All	2351/2612 (90%)	2164 (92%)	185 (8%)	2 (0%)	54	84

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	SY	32	ARG
5	SH	111	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	
2	SB	192/224 (86%)	192 (100%)	0	100	100
3	SE	221/222 (100%)	221 (100%)	0	100	100
4	SG	187/201 (93%)	186 (100%)	1 (0%)	88	94
5	SH	165/170 (97%)	164 (99%)	1 (1%)	86	94
6	SI	150/161 (93%)	150 (100%)	0	100	100
7	SJ	158/166 (95%)	158 (100%)	0	100	100
8	SL	129/137 (94%)	127 (98%)	2 (2%)	62	83
9	SN	127/128 (99%)	127 (100%)	0	100	100
10	SO	97/105 (92%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	SW	110/111 (99%)	110 (100%)	0	100	100
12	SX	119/120 (99%)	118 (99%)	1 (1%)	81	91
13	SY	112/113 (99%)	112 (100%)	0	100	100
14	Sb	70/71 (99%)	70 (100%)	0	100	100
15	Se	34/54 (63%)	34 (100%)	0	100	100
16	CA	158/238 (66%)	158 (100%)	0	100	100
All	All	2029/2221 (91%)	2024 (100%)	5 (0%)	93	98

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	SG	98	ARG
5	SH	7	LYS
8	SL	21	ASN
8	SL	67	ARG
12	SX	70	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	SB	149	GLN
11	SW	24	GLN
13	SY	22	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1191/1800 (66%)	261 (21%)	10 (0%)

5 of 261 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	3	U
1	C2	4	C
1	C2	6	G
1	C2	8	U

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C2	997	G
1	C2	1051	G
1	C2	1097	U
1	C2	417	A
1	C2	555	A

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.

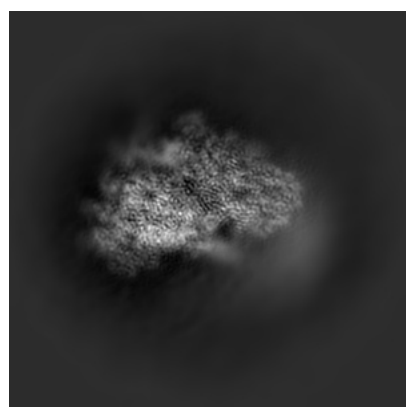
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32793. These allow visual inspection of the internal detail of the map and identification of artifacts.

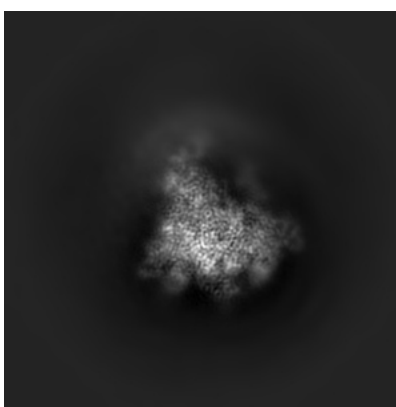
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

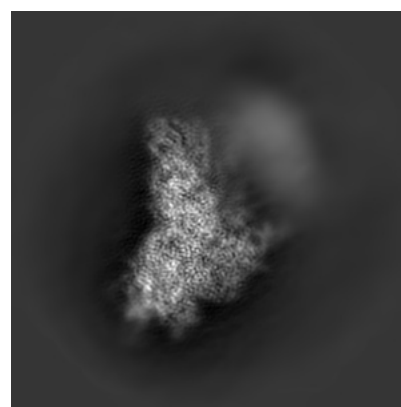
6.1.1 Primary map



X



Y

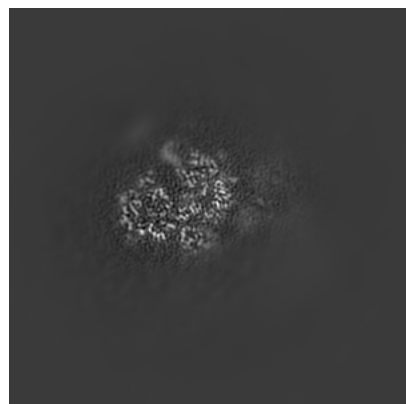


Z

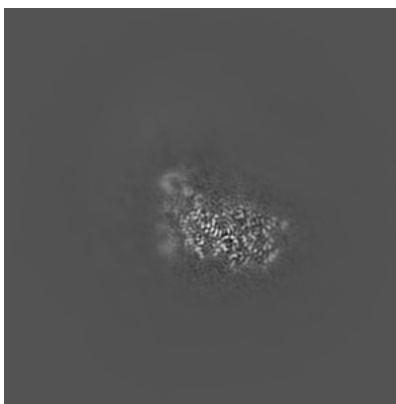
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

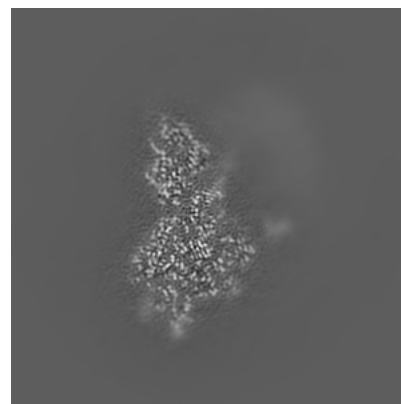
6.2.1 Primary map



X Index: 180



Y Index: 180

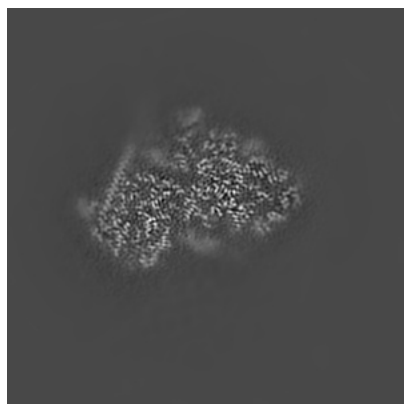


Z Index: 180

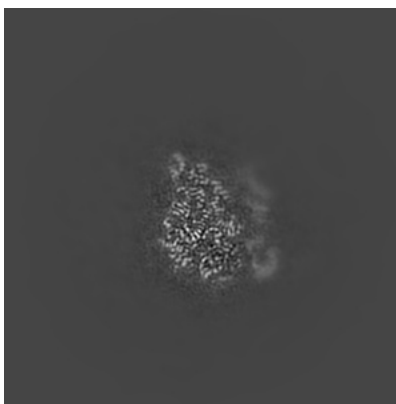
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

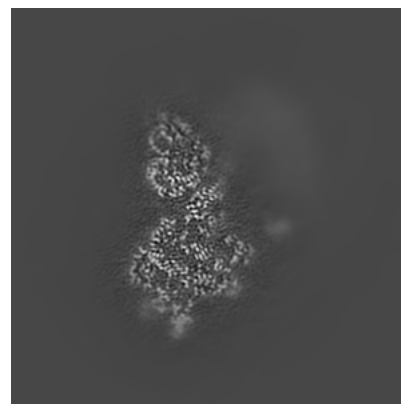
6.3.1 Primary map



X Index: 146



Y Index: 140

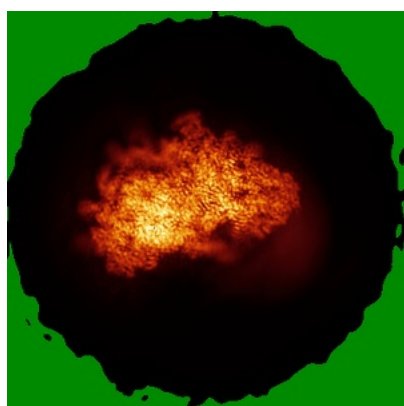


Z Index: 182

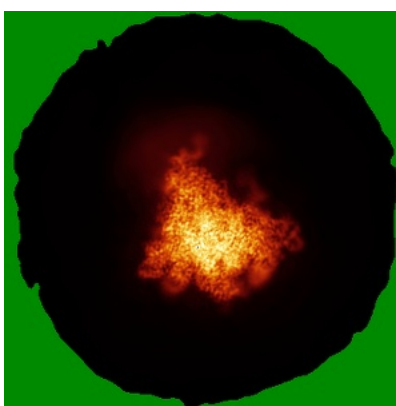
The images above show the largest variance slices of the map in three orthogonal directions.

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

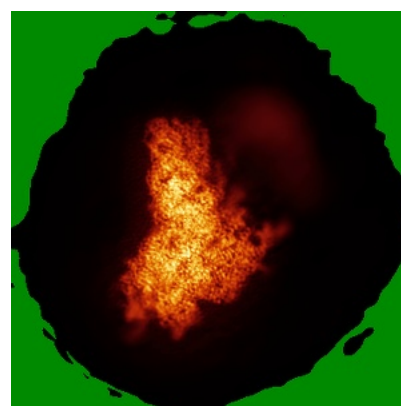
6.4.1 Primary map



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.

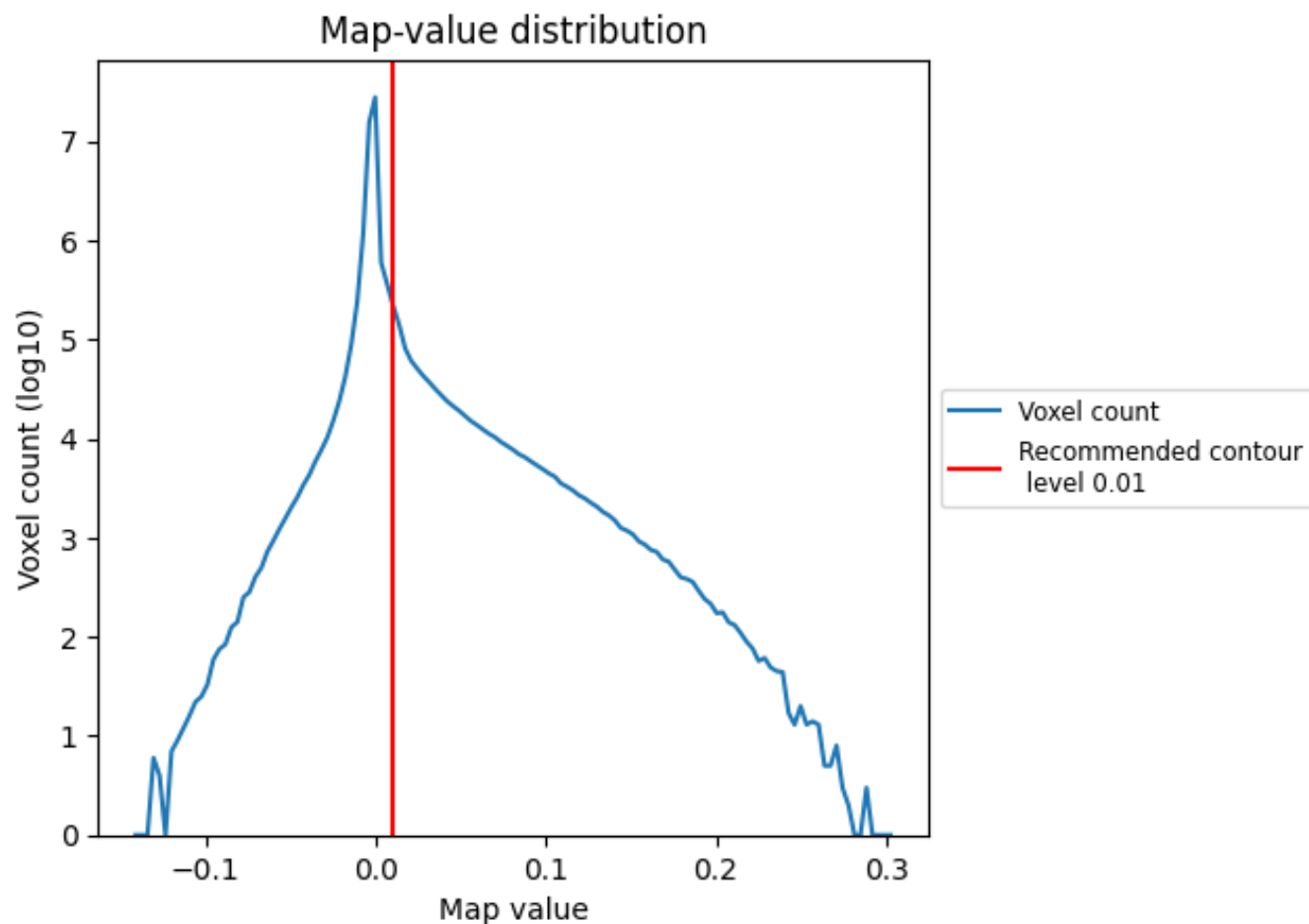
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

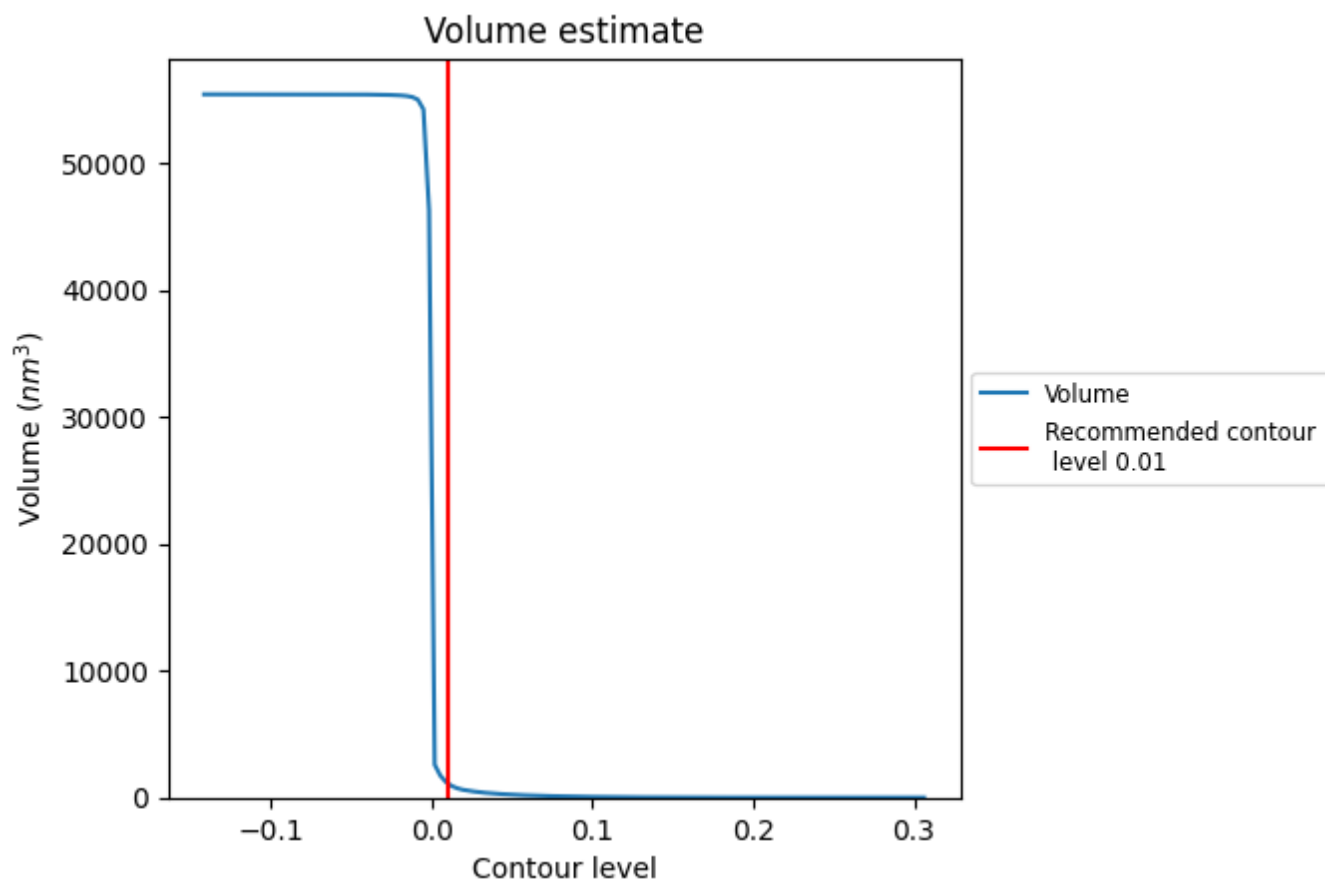
This section contains the results of statistical analysis of the map.

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.

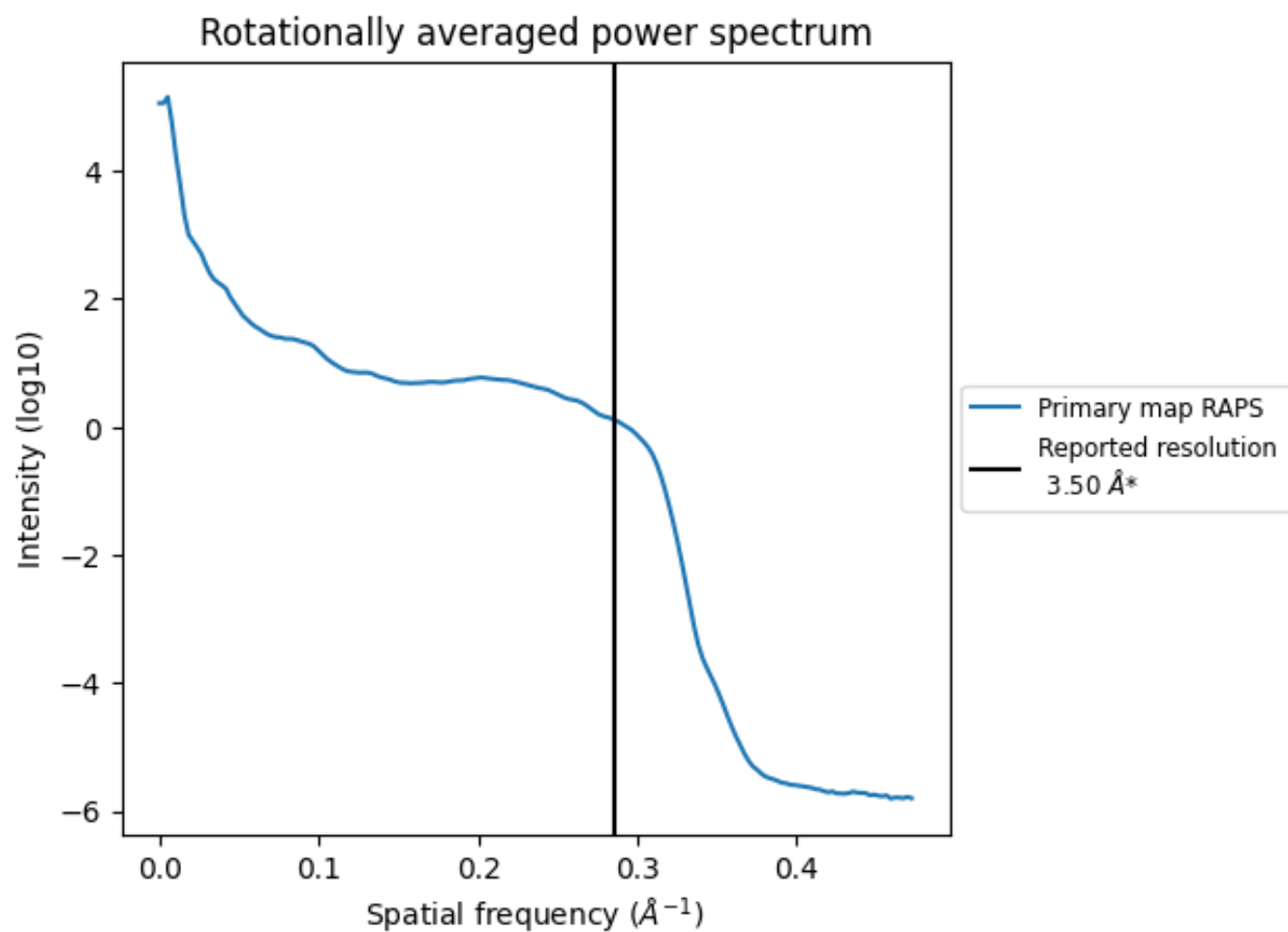
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1147 nm³; this corresponds to an approximate mass of 1036 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 ⓘ

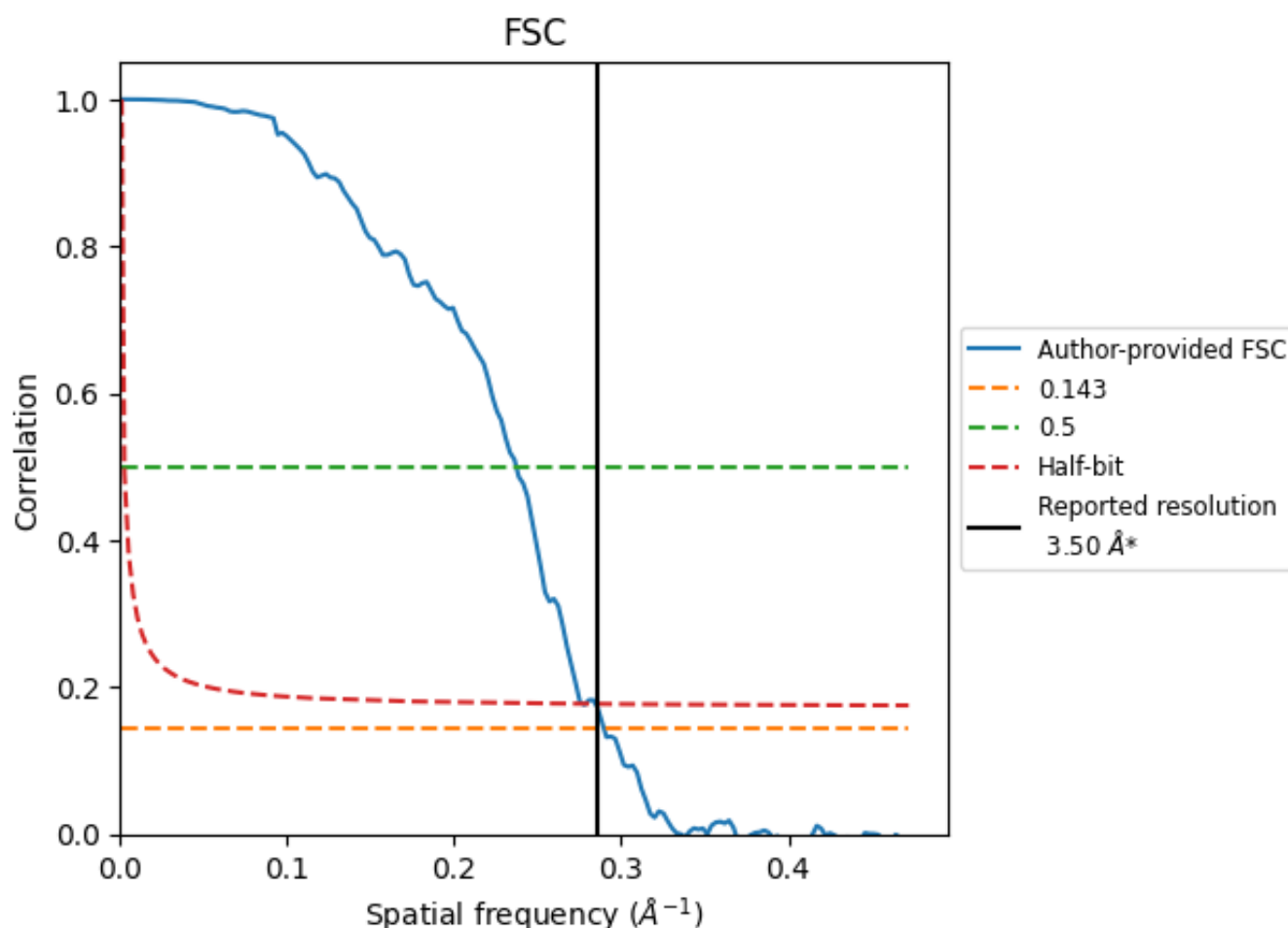


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

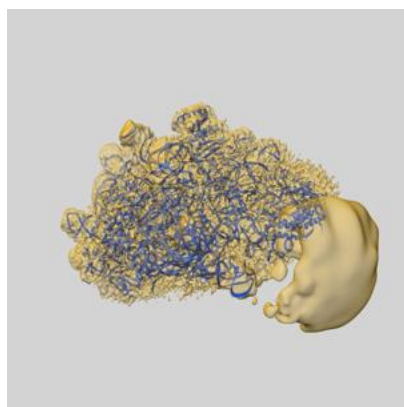
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.45	4.22	3.61
Unmasked-calculated*	-	-	-

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

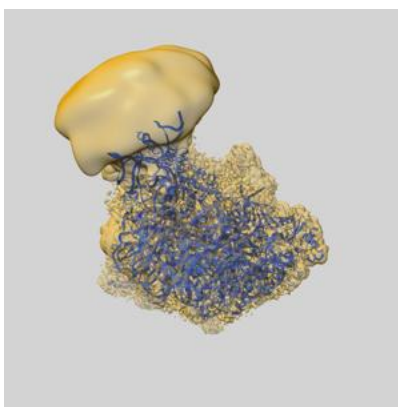
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32793 and PDB model 7WTO. Per-residue inclusion information can be found in section [3](#) on page [7](#).

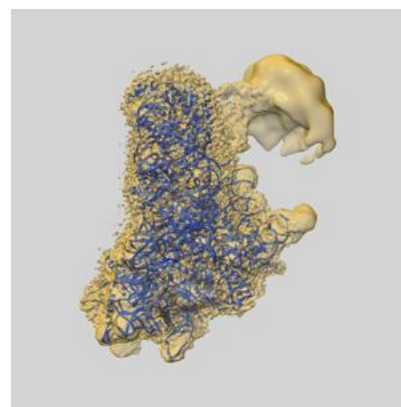
9.1 Map-model overlay [i](#)



X



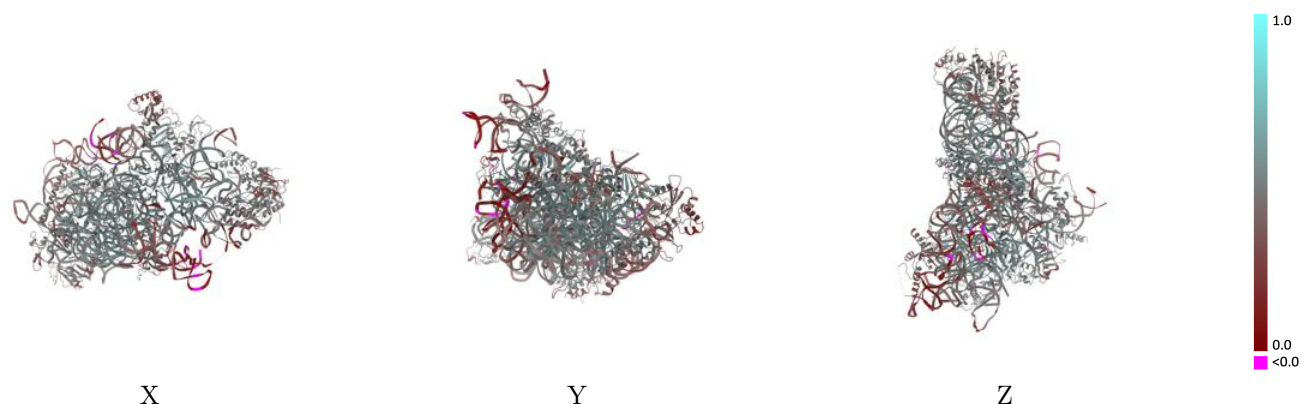
Y



Z

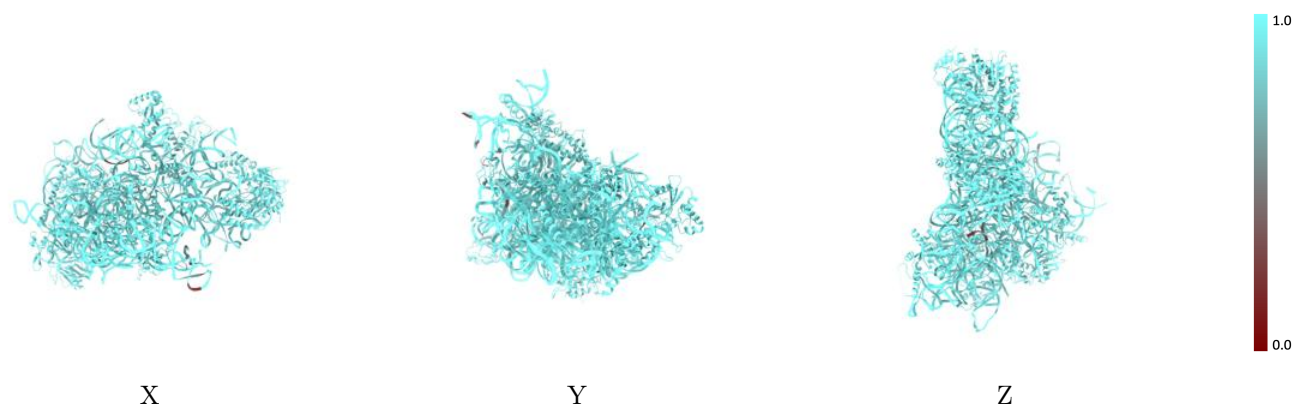
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



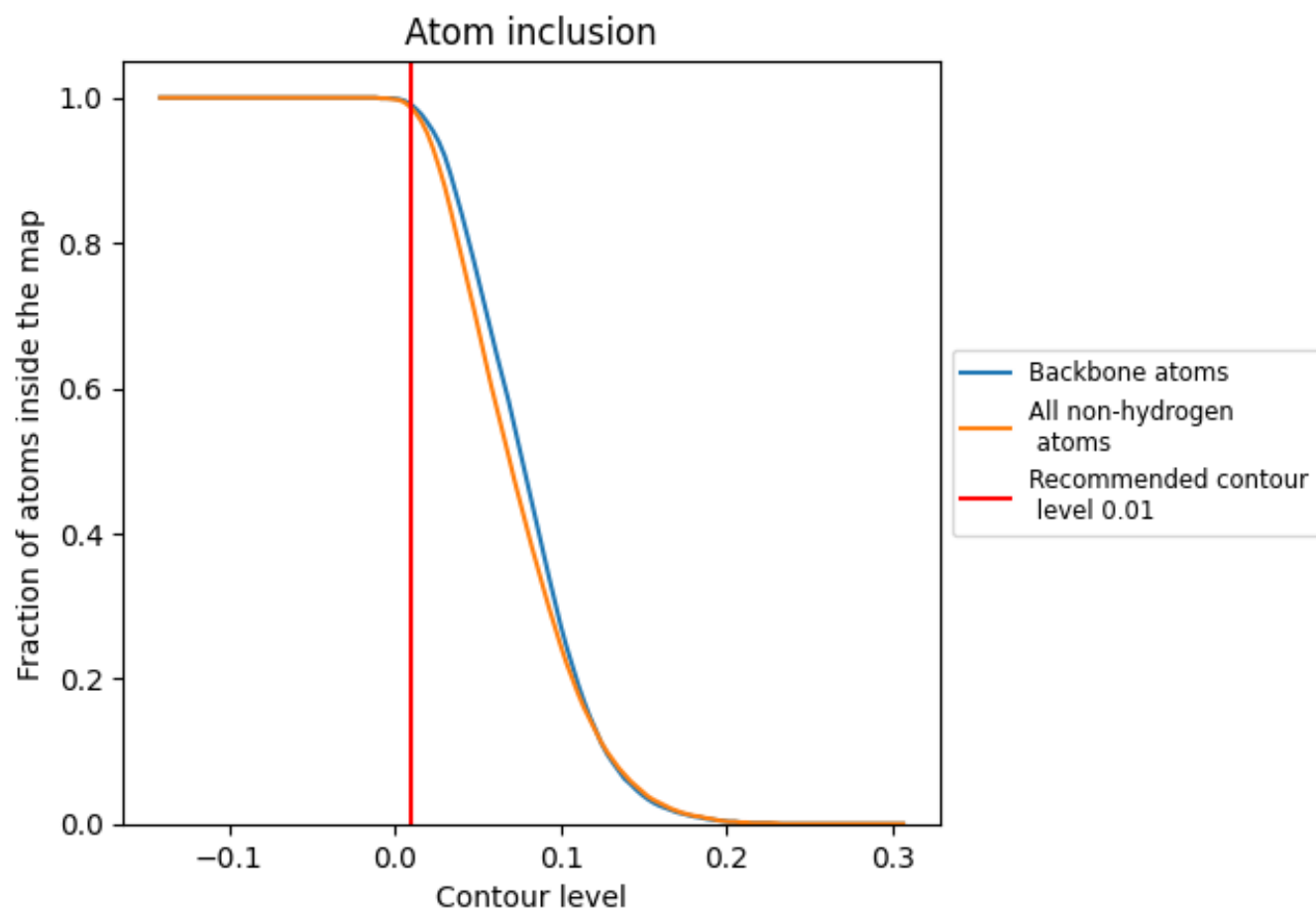
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 99% of all backbone atoms, 99% 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	 0.9860	 0.4570
C2	 0.9850	 0.4450
CA	 0.9860	 0.4280
SB	 0.9860	 0.4730
SE	 0.9910	 0.5190
SG	 0.9960	 0.4500
SH	 0.9880	 0.3900
SI	 0.9940	 0.4920
SJ	 0.9880	 0.4840
SL	 0.9820	 0.5320
SN	 0.9960	 0.5090
SO	 0.9760	 0.4690
SW	 0.9960	 0.5300
SX	 0.9580	 0.4470
SY	 0.9860	 0.4800
Sb	 0.9770	 0.4560
Se	 0.9700	 0.4160

