



wwPDB EM Validation Summary Report ⓘ

Feb 9, 2025 – 07:09 am GMT

PDB ID : 9GBW
EMDB ID : EMD-51223
Title : Overall structure of the substrate-bound U11 snRNP
Authors : Zhao, J.; Galej, W.P.
Deposited on : 2024-07-31
Resolution : 3.50 Å(reported)
Based on initial models : 4PJO, .

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:

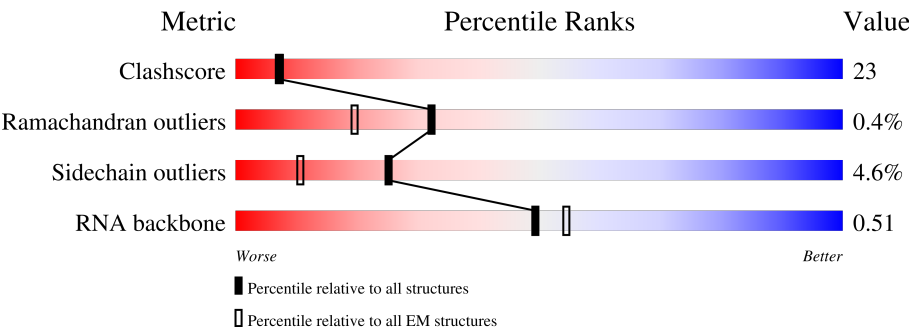
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

1 Overall quality at a glance i

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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	B	132	<div><div>22%</div><div>42%</div><div>53%</div><div>5%</div></div>
2	C	246	<div><div>31%</div><div>29%</div><div>37%</div></div>
3	D	485	<div><div>33%</div><div>26%</div><div>19%</div><div>54%</div></div>
4	E	170	<div><div>7%</div><div>12%</div><div>76%</div></div>
5	G	11	<div><div>18%</div><div>64%</div><div>9%</div><div>9%</div></div>
6	h	119	<div><div>64%</div><div>32%</div></div>
7	j	126	<div><div>63%</div><div>36%</div></div>

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Mol	Chain	Length	Quality of chain
8	k	240	
9	l	92	
10	m	86	
11	n	76	
12	F	339	
13	i	118	
14	R	135	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 13570 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 U11/U12 small nuclear ribonucleoprotein 25 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	132	Total	C	N	O	S	0	0
			1069	676	188	198	7		

- Molecule 2 is a protein called U11/U12 small nuclear ribonucleoprotein 35 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	155	Total	C	N	O	S	0	0
			1261	802	232	226	1		

- Molecule 3 is a protein called Programmed cell death protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	221	Total	C	N	O	S	0	0
			1829	1118	379	328	4		

- Molecule 4 is a protein called Zinc finger matrin-type protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	40	Total	C	N	O	S	0	0
			358	227	69	59	3		

- Molecule 5 is a RNA chain called P120-5'SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	11	Total	C	N	O	P	0	0
			224	101	30	82	11		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	81	Total	C	N	O	S	0	0
			641	408	112	118	3		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	81	Total	C	N	O	S	0	0
			637	400	112	119	6		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	86	Total	C	N	O	S	0	0
			692	435	126	124	7		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	77	Total	C	N	O	S	0	0
			638	405	113	115	5		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	74	Total	C	N	O	S	0	0
			576	373	95	103	5		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	n	73	Total	C	N	O	S	0	0
			568	358	102	102	6		

- Molecule 12 is a protein called U11/U12 small nuclear ribonucleoprotein 48 kDa protein.

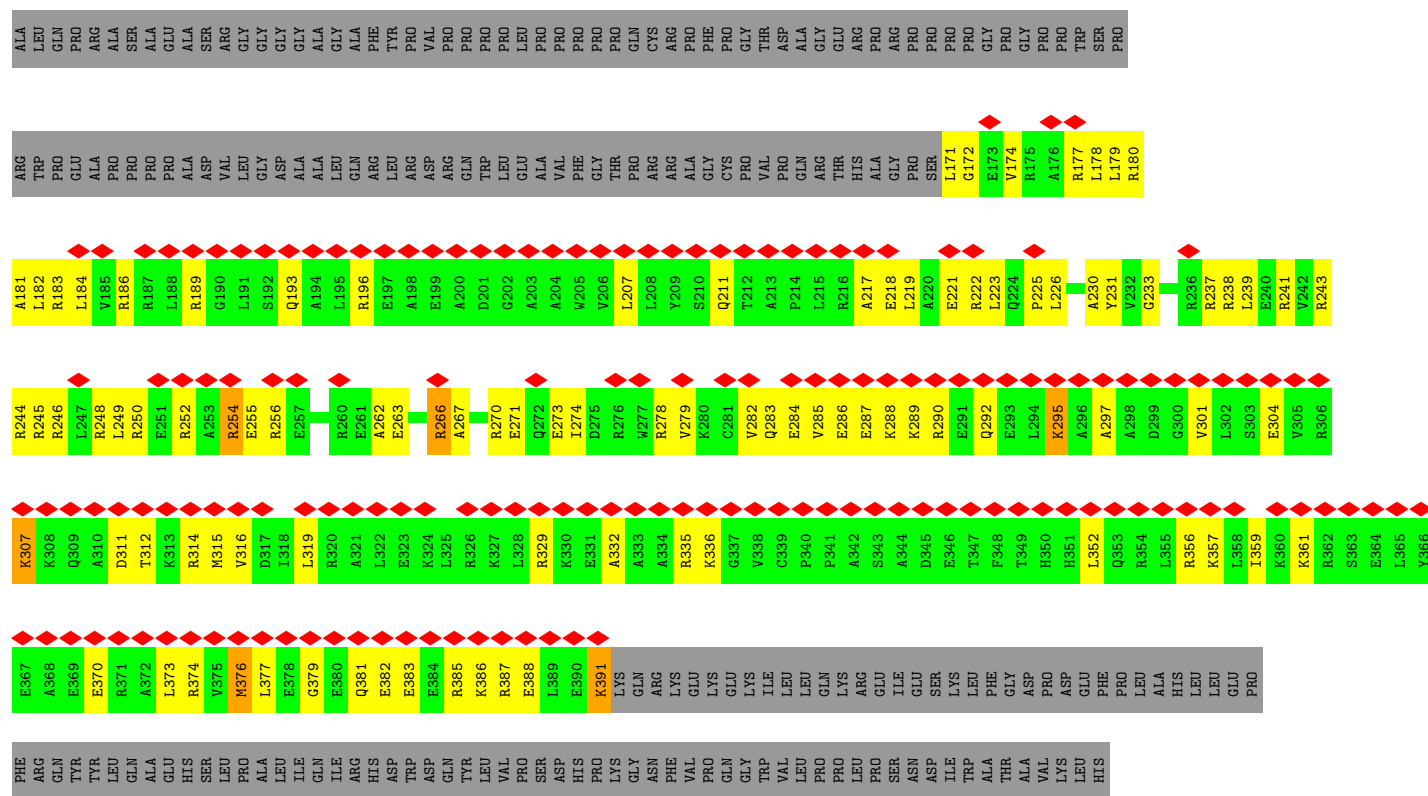
Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	218	Total	C	N	O	S	0	0
			1793	1112	316	354	11		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

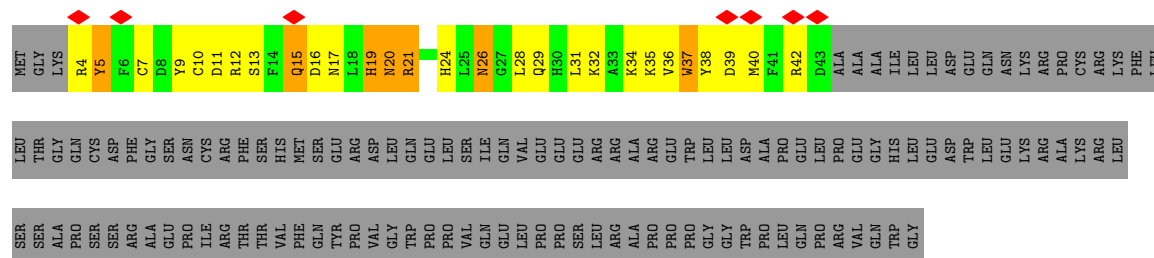
Mol	Chain	Residues	Atoms					AltConf	Trace
13	i	94	Total	C	N	O	S	0	0
			764	478	139	141	6		

- Molecule 14 is a RNA chain called U11 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	R	118	2520	1124	447	831	118	0	0



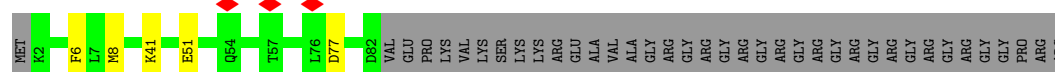
• Molecule 4: Zinc finger matrin-type protein 5



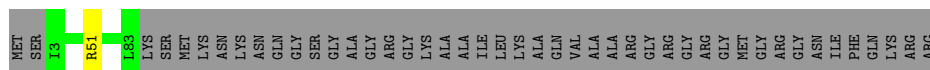
• Molecule 5: P120-5'SS



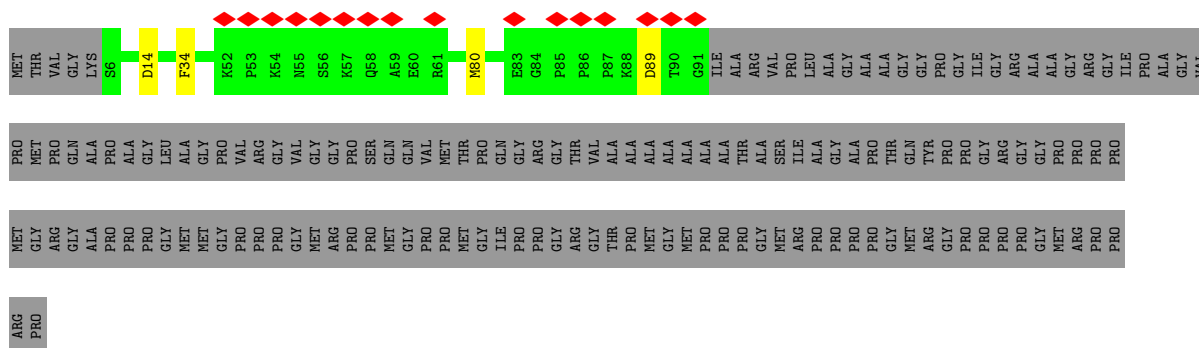
• Molecule 6: Small nuclear ribonucleoprotein Sm D1



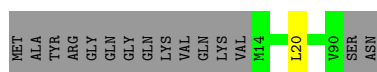
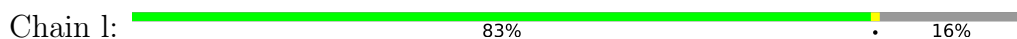
• Molecule 7: Small nuclear ribonucleoprotein Sm D3



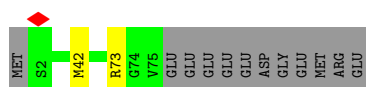
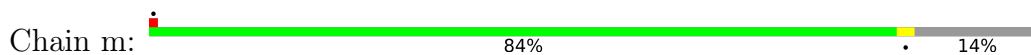
- Molecule 8: Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 9: Small nuclear ribonucleoprotein E



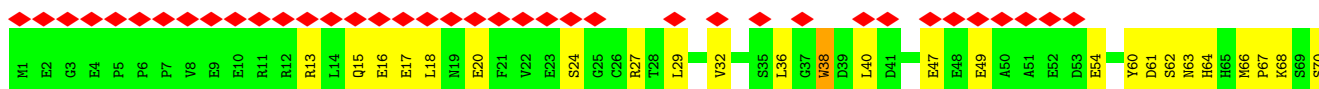
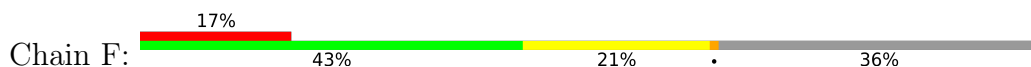
- Molecule 10: Small nuclear ribonucleoprotein F



- Molecule 11: Small nuclear ribonucleoprotein G



- Molecule 12: U11/U12 small nuclear ribonucleoprotein 48 kDa protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52290	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.73	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.125	Depositor
Minimum map value	-0.076	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	321.2, 321.2, 321.2	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.73, 0.73, 0.73	Depositor

5 Model quality

5.1 Standard geometry

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	B	0.31	0/1084	0.61	1/1460 (0.1%)
2	C	0.31	0/1286	0.71	2/1726 (0.1%)
3	D	0.26	0/1842	0.63	0/2454
4	E	0.33	0/368	0.73	1/490 (0.2%)
5	G	0.37	0/247	0.90	1/380 (0.3%)
6	h	0.30	0/649	0.63	0/878
7	j	0.36	0/645	0.57	0/870
8	k	0.31	0/702	0.67	0/936
9	l	0.38	0/646	0.61	0/867
10	m	0.39	0/588	0.55	0/795
11	n	0.36	0/575	0.66	0/768
12	F	0.31	0/1827	0.56	0/2461
13	i	0.38	0/773	0.69	2/1039 (0.2%)
14	R	0.40	0/2815	0.88	4/4382 (0.1%)
All	All	0.34	0/14047	0.70	11/19506 (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
6	h	0	1
11	n	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	i	89	PRO	CA-N-CD	-9.96	97.55	111.50
14	R	101	U	C2-N1-C1'	7.31	126.47	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	86	LEU	CA-CB-CG	7.12	131.68	115.30
2	C	111	ASP	CB-CG-OD2	5.98	123.68	118.30
14	R	101	U	N1-C2-O2	5.97	126.98	122.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	h	41	LYS	Peptide
11	n	43	ASP	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	B	1069	0	1101	69	0
2	C	1261	0	1274	70	0
3	D	1829	0	1924	83	0
4	E	358	0	340	22	0
5	G	224	0	115	16	0
6	h	641	0	681	0	0
7	j	637	0	652	0	0
8	k	692	0	717	0	0
9	l	638	0	657	0	0
10	m	576	0	589	0	0
11	n	568	0	590	0	0
12	F	1793	0	1737	54	0
13	i	764	0	783	0	0
14	R	2520	0	1270	93	0
All	All	13570	0	12430	368	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 23.

The worst 5 of 368 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:B:62:THR:HA	1:B:111:LYS:HA	1.59	0.84
1:B:72:ARG:HA	1:B:75:GLN:HE22	1.45	0.81
1:B:48:MET:SD	1:B:124:SER:OG	2.39	0.79
14:R:128:C:H2'	14:R:129:G:H8	1.47	0.79
2:C:48:ASP:HB3	2:C:51:LEU:HB2	1.67	0.76

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	B	130/132 (98%)	112 (86%)	15 (12%)	3 (2%)	5	31
2	C	153/246 (62%)	131 (86%)	20 (13%)	2 (1%)	10	41
3	D	219/485 (45%)	209 (95%)	10 (5%)	0	100	100
4	E	38/170 (22%)	37 (97%)	1 (3%)	0	100	100
6	h	79/119 (66%)	68 (86%)	11 (14%)	0	100	100
7	j	79/126 (63%)	77 (98%)	2 (2%)	0	100	100
8	k	84/240 (35%)	79 (94%)	5 (6%)	0	100	100
9	l	75/92 (82%)	70 (93%)	5 (7%)	0	100	100
10	m	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
11	n	71/76 (93%)	56 (79%)	15 (21%)	0	100	100
12	F	214/339 (63%)	197 (92%)	17 (8%)	0	100	100
13	i	90/118 (76%)	86 (96%)	4 (4%)	0	100	100
All	All	1304/2229 (58%)	1193 (92%)	106 (8%)	5 (0%)	32	64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	131	GLN
2	C	87	VAL
2	C	103	ARG
1	B	25	THR
1	B	128	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	B	119/119 (100%)	111 (93%)	8 (7%)	13	40
2	C	129/215 (60%)	124 (96%)	5 (4%)	27	56
3	D	183/401 (46%)	175 (96%)	8 (4%)	24	53
4	E	38/151 (25%)	29 (76%)	9 (24%)	0	3
6	h	76/101 (75%)	72 (95%)	4 (5%)	19	46
7	j	71/101 (70%)	70 (99%)	1 (1%)	62	79
8	k	78/177 (44%)	74 (95%)	4 (5%)	20	48
9	l	72/84 (86%)	71 (99%)	1 (1%)	62	79
10	m	63/74 (85%)	61 (97%)	2 (3%)	34	62
11	n	63/66 (96%)	61 (97%)	2 (3%)	34	62
12	F	202/313 (64%)	196 (97%)	6 (3%)	36	63
13	i	89/110 (81%)	84 (94%)	5 (6%)	17	45
All	All	1183/1912 (62%)	1128 (95%)	55 (5%)	25	52

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	E	34	LYS
8	k	14	ASP
13	i	110	LEU
12	F	256	TRP
4	E	37	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
4	E	15	GLN
4	E	17	ASN
9	l	83	ASN
10	m	67	ASN
12	F	158	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	R	115/135 (85%)	28 (24%)	4 (3%)
5	G	10/11 (90%)	3 (30%)	0
All	All	125/146 (85%)	31 (24%)	4 (3%)

5 of 31 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	G	3	A
5	G	4	U
5	G	5	C
14	R	8	G
14	R	10	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	R	78	C
14	R	83	G
14	R	95	G
14	R	106	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

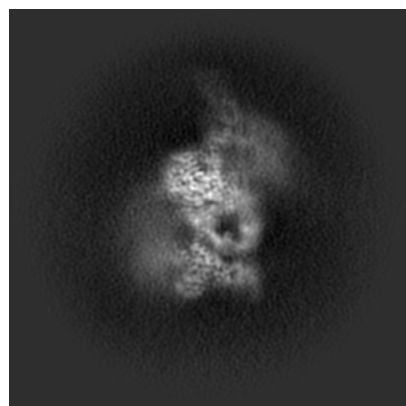
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51223. These allow visual inspection of the internal detail of the map and identification of artifacts.

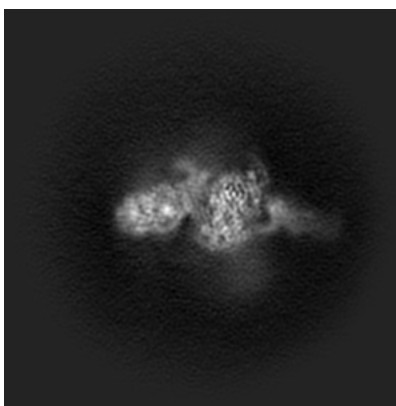
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

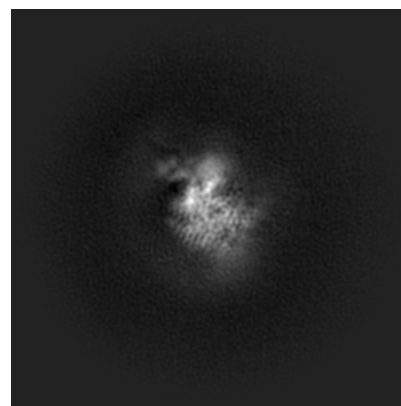
6.1.1 Primary map



X

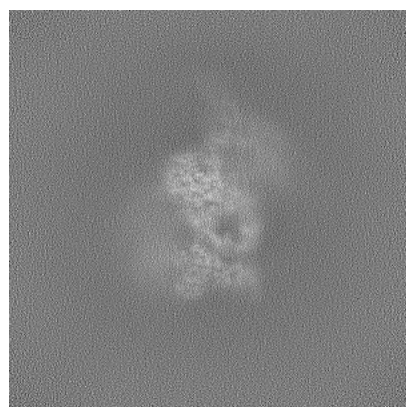


Y

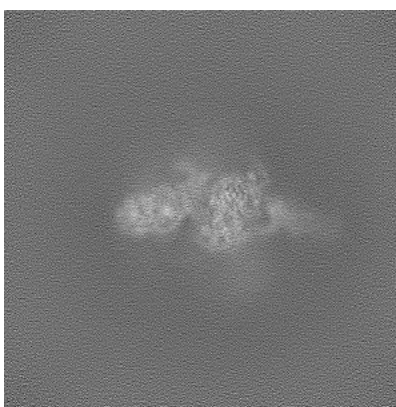


Z

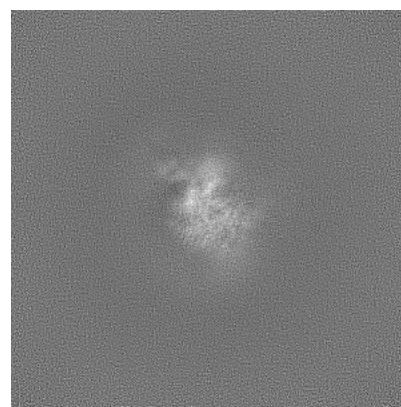
6.1.2 Raw map



X



Y

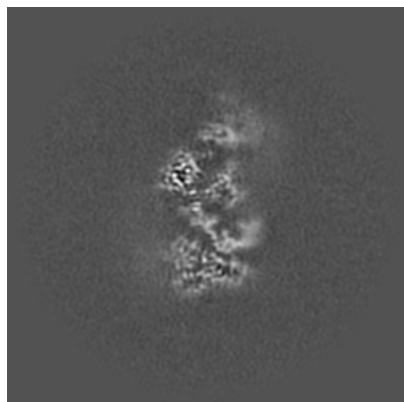


Z

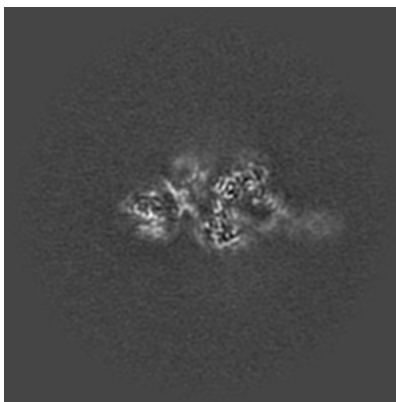
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

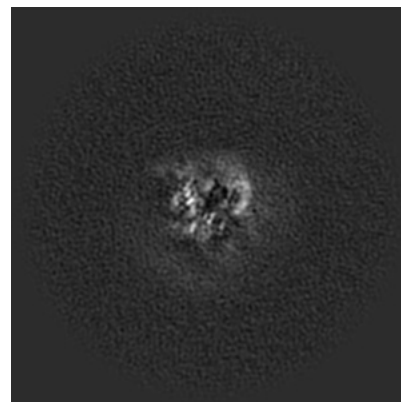
6.2.1 Primary map



X Index: 220

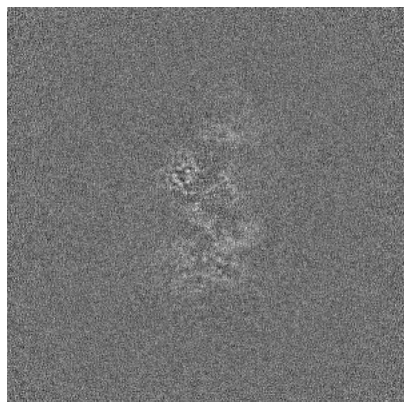


Y Index: 220

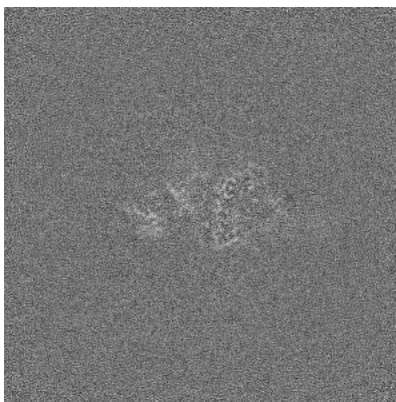


Z Index: 220

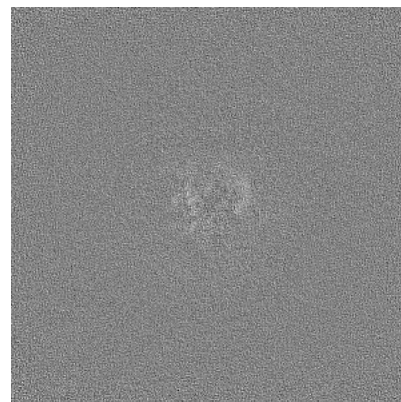
6.2.2 Raw map



X Index: 220



Y Index: 220

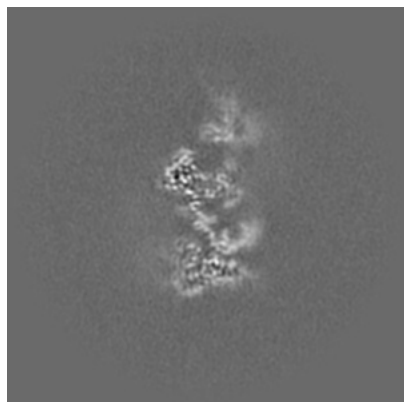


Z Index: 220

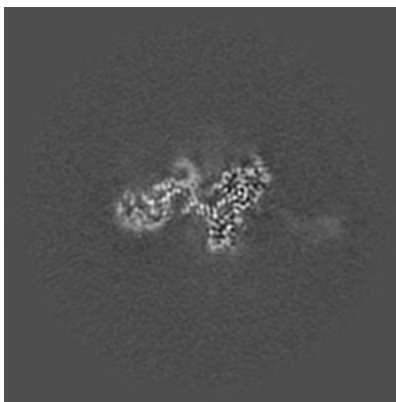
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

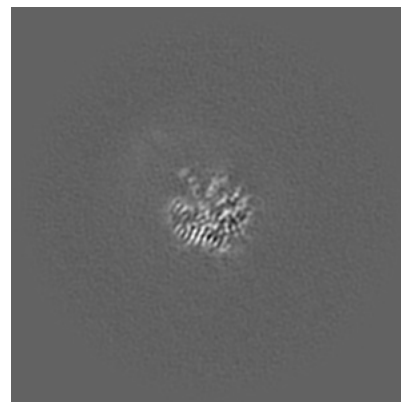
6.3.1 Primary map



X Index: 217

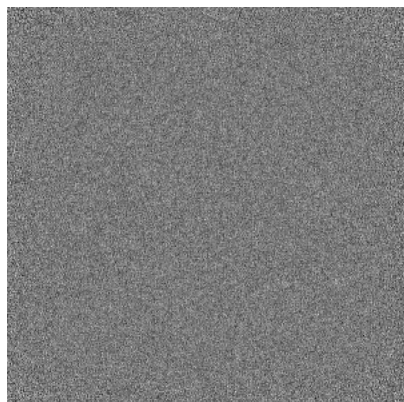


Y Index: 207

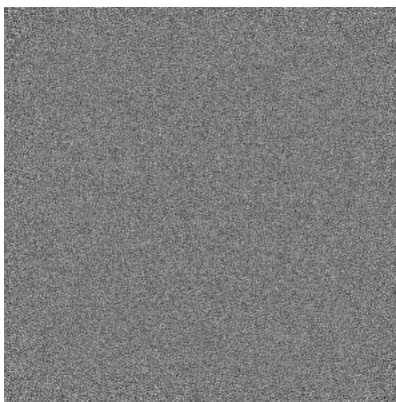


Z Index: 253

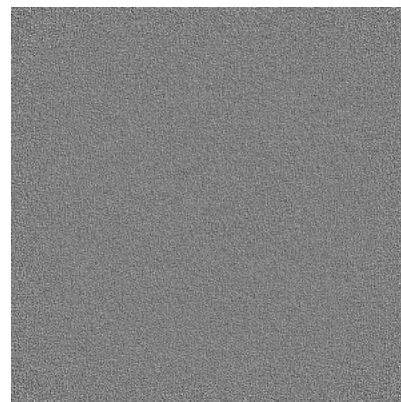
6.3.2 Raw map



X Index: 0



Y Index: 0

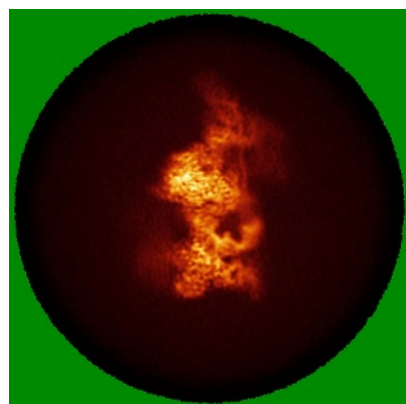


Z Index: 0

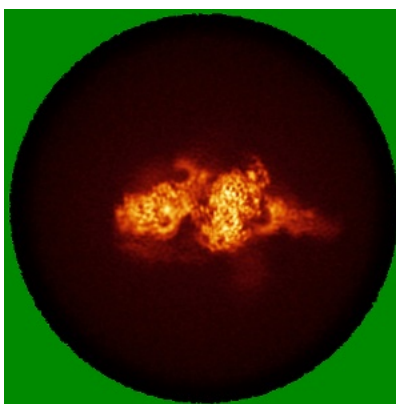
The images above show the largest variance slices of the map in three orthogonal directions.

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

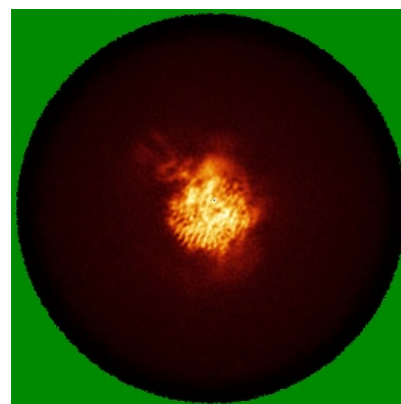
6.4.1 Primary map



X

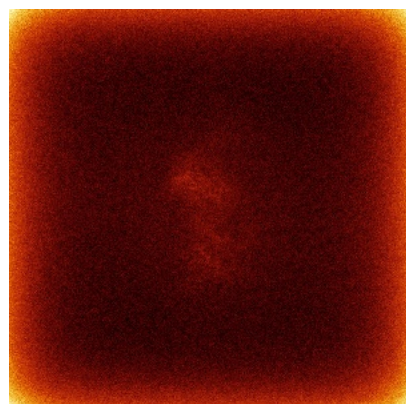


Y

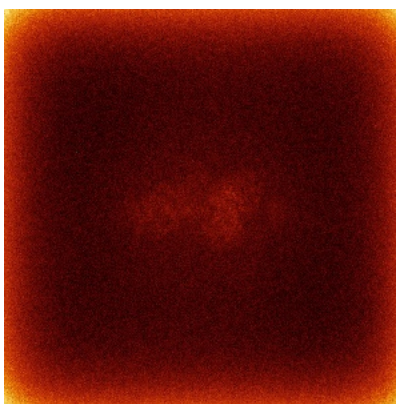


Z

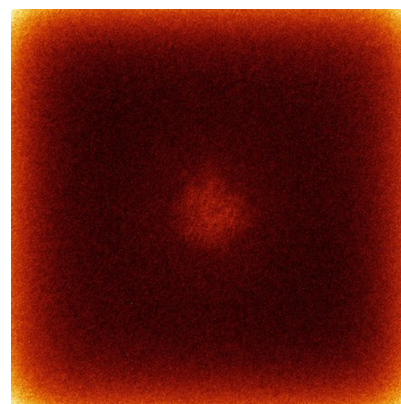
6.4.2 Raw map



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.

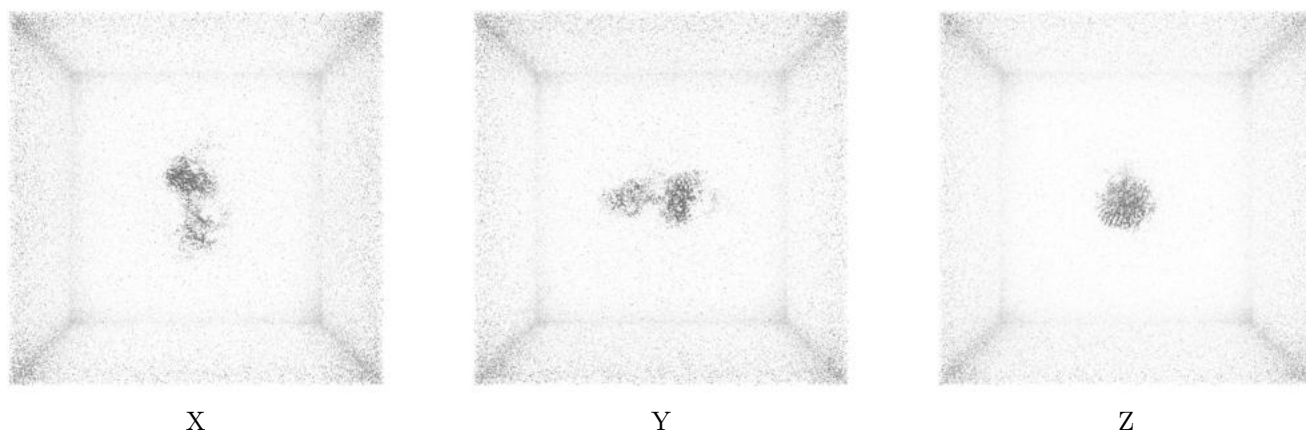
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. 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



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.

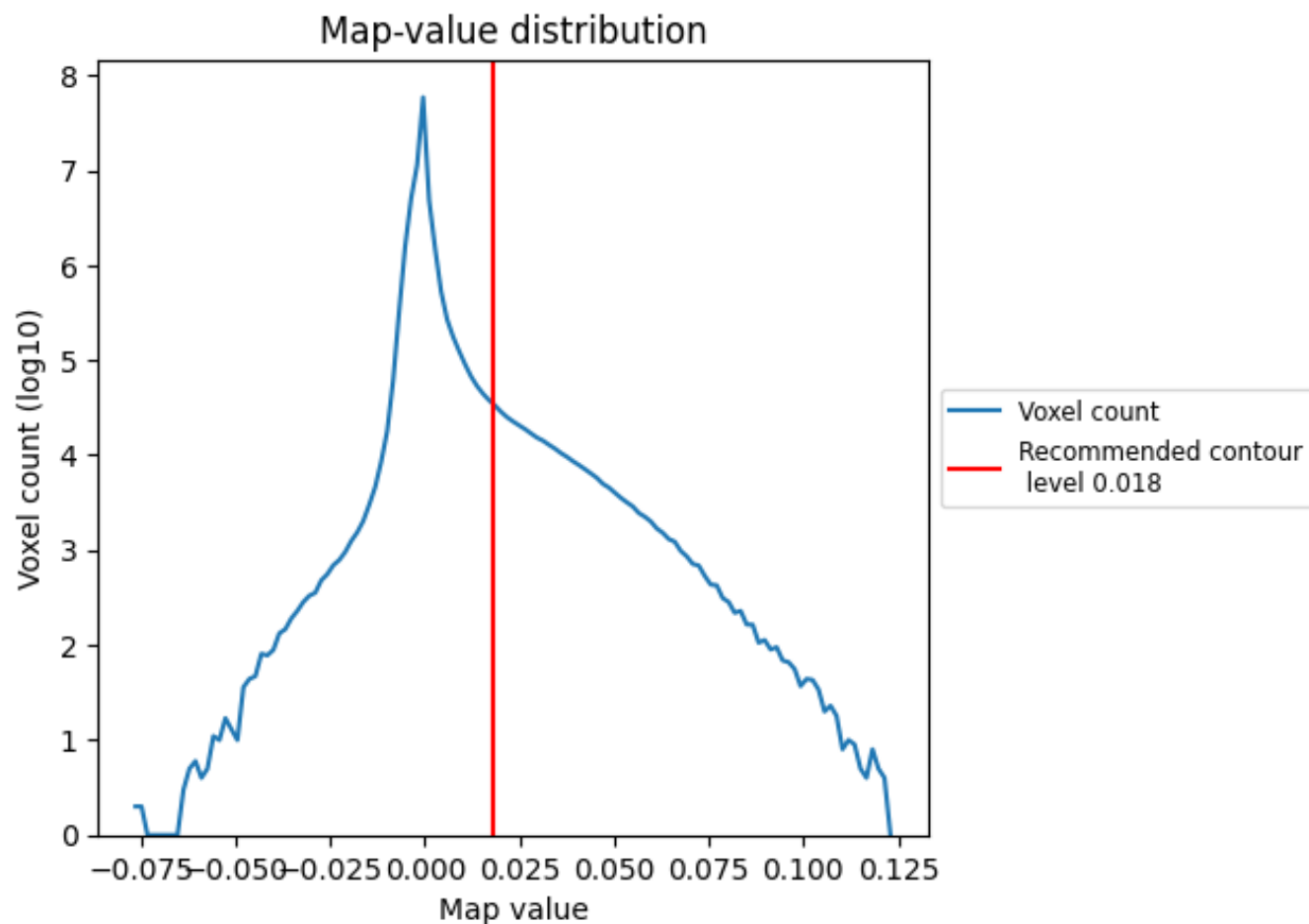
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

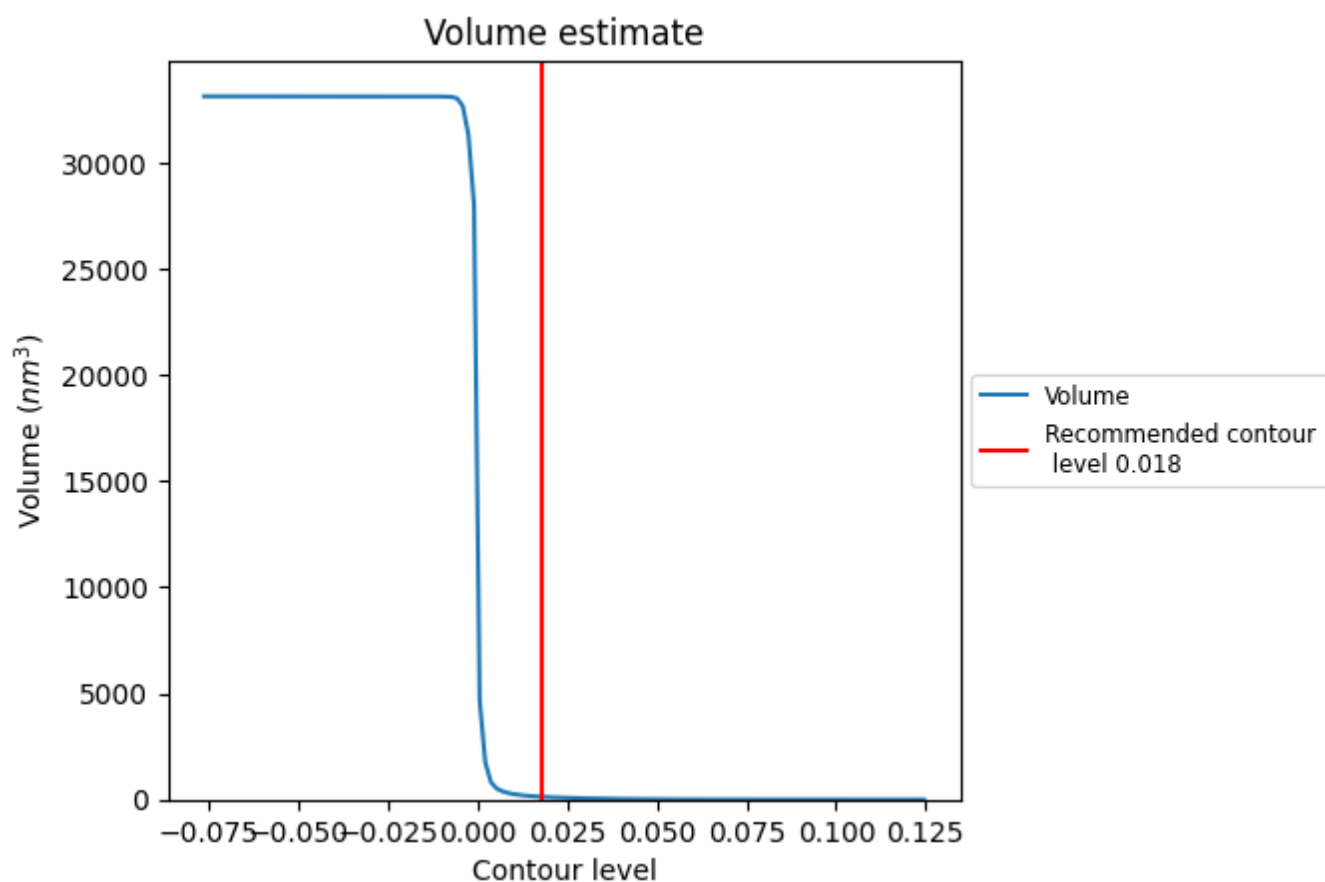
This section contains the results of statistical analysis of the map.

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.

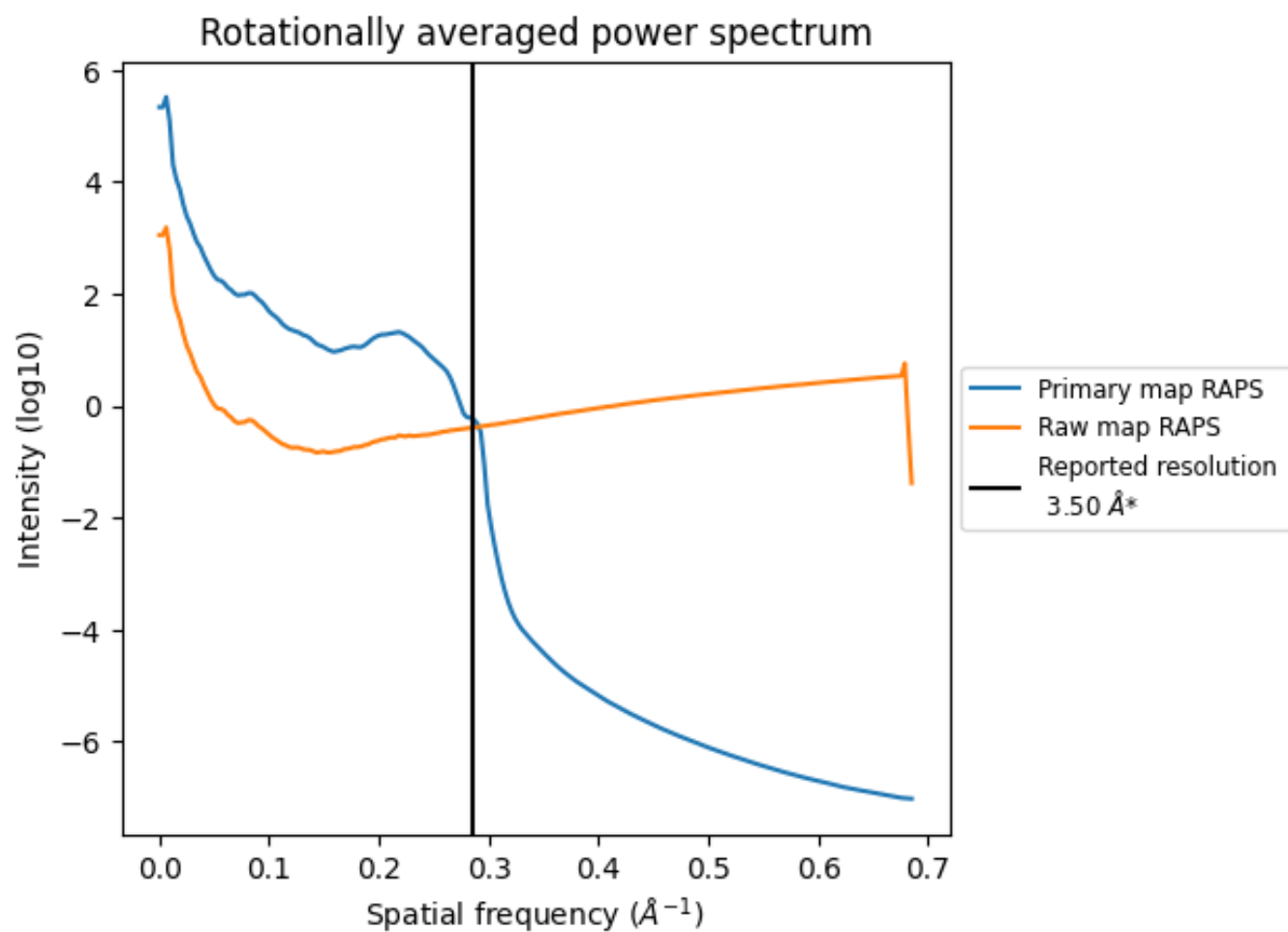
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 129 nm^3 ; this corresponds to an approximate mass of 117 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 ⓘ

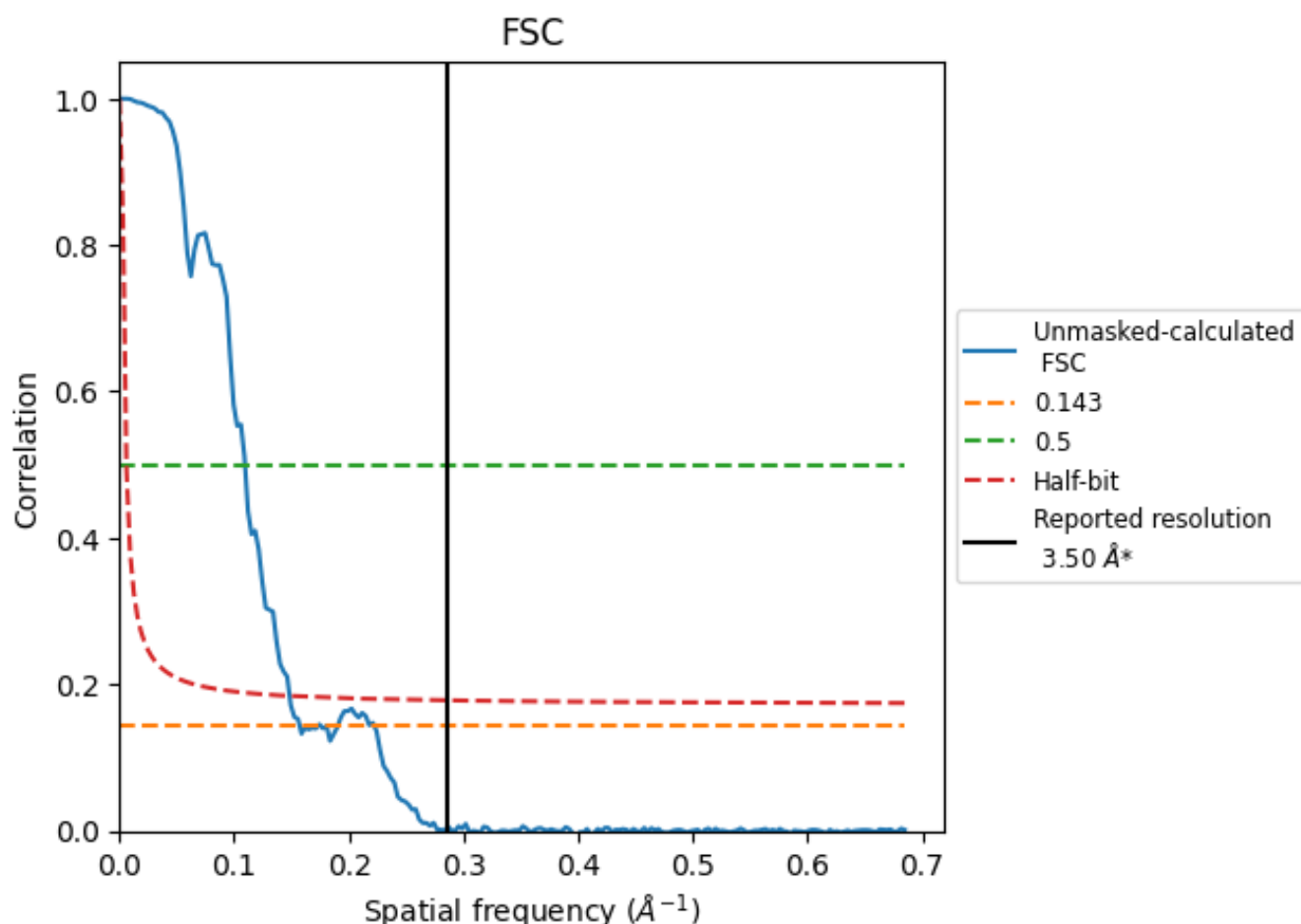


*Reported resolution corresponds to spatial frequency of 0.286 \AA^{-1}

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

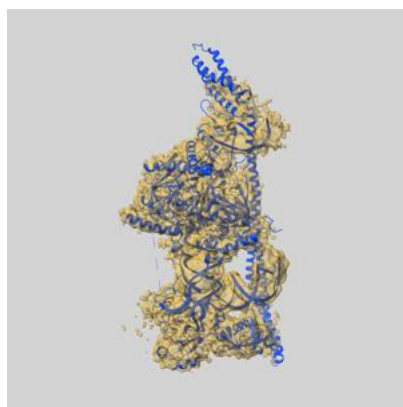
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.36	9.14	6.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.36 differs from the reported value 3.5 by more than 10 %

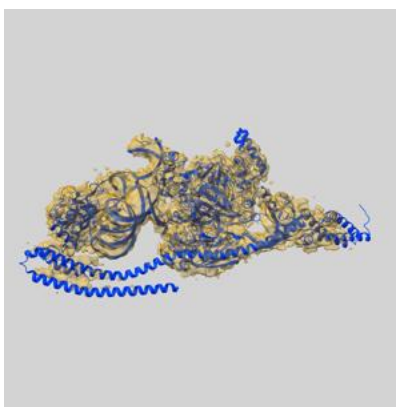
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51223 and PDB model 9GBW. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

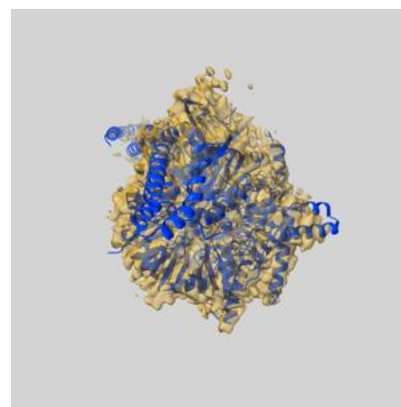
9.1 Map-model overlay [i](#)



X



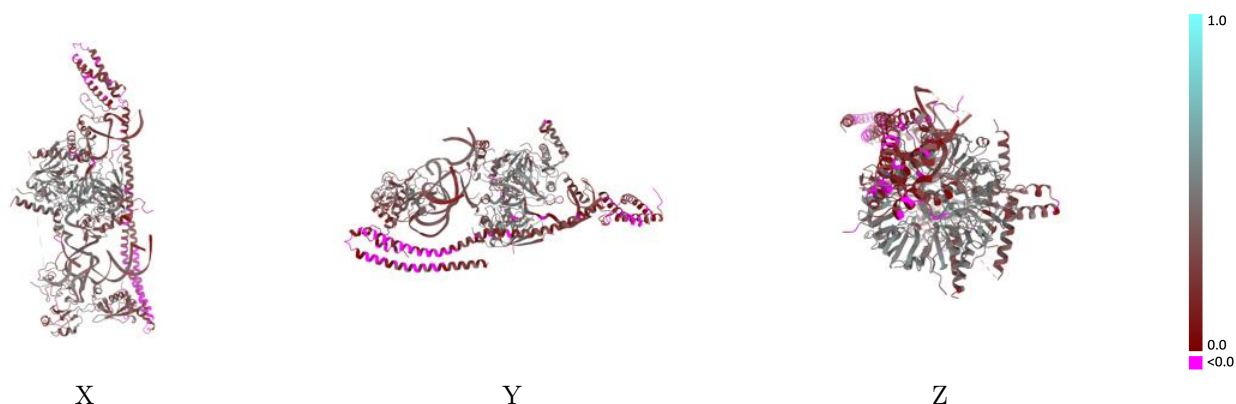
Y



Z

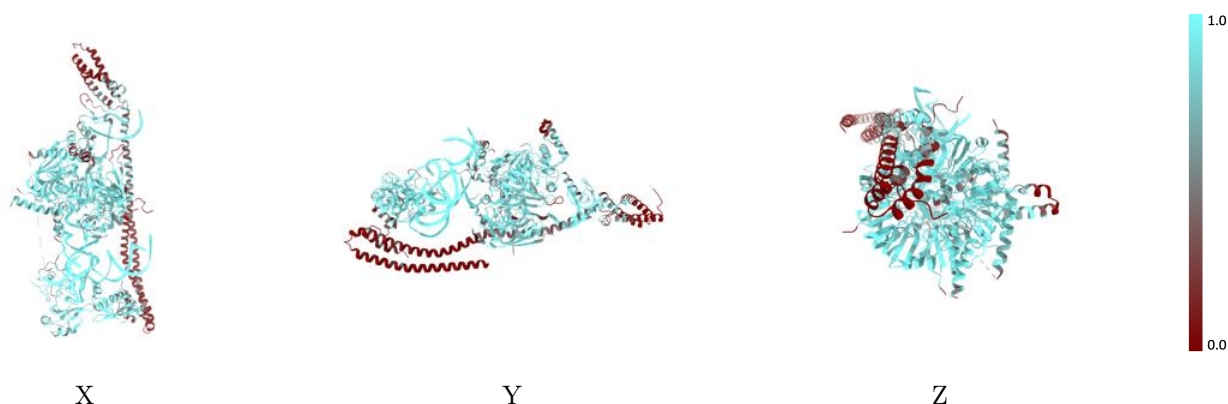
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



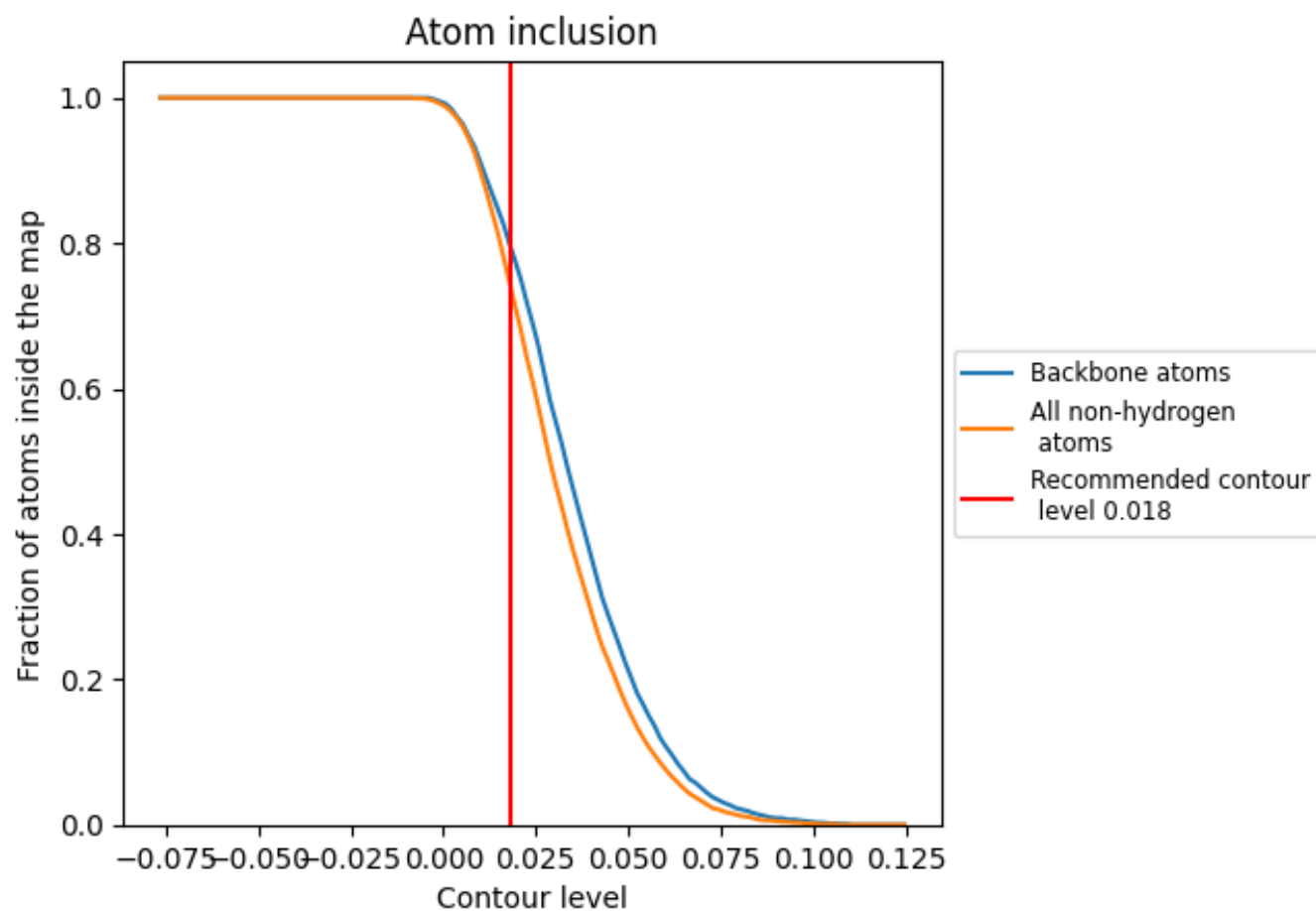
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 74% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7430	<div></div> 0.3200
B	<div></div> 0.7110	<div></div> 0.2930
C	<div></div> 0.8290	<div></div> 0.3090
D	<div></div> 0.2420	<div></div> 0.1120
E	<div></div> 0.6990	<div></div> 0.2970
F	<div></div> 0.6050	<div></div> 0.2840
G	<div></div> 0.9460	<div></div> 0.3850
R	<div></div> 0.9320	<div></div> 0.3280
h	<div></div> 0.8290	<div></div> 0.3670
i	<div></div> 0.8640	<div></div> 0.3890
j	<div></div> 0.9050	<div></div> 0.4540
k	<div></div> 0.7130	<div></div> 0.3630
l	<div></div> 0.9310	<div></div> 0.4620
m	<div></div> 0.9360	<div></div> 0.4860
n	<div></div> 0.9000	<div></div> 0.4540

1.0

0.0

<0.0