



## wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 09:11 am GMT

PDB ID : 5FJ9  
EMDB ID : EMD-3179  
Title : Cryo-EM structure of yeast apo RNA polymerase III at 4.6 Å  
Authors : Hoffmann, N.A.; Jakobi, A.J.; Moreno-Morcillo, M.; Glatt, S.; Kosinski, J.; Hagen, W.J.; Sachse, C.; Muller, C.W.  
Deposited on : 2015-10-06  
Resolution : 4.60 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

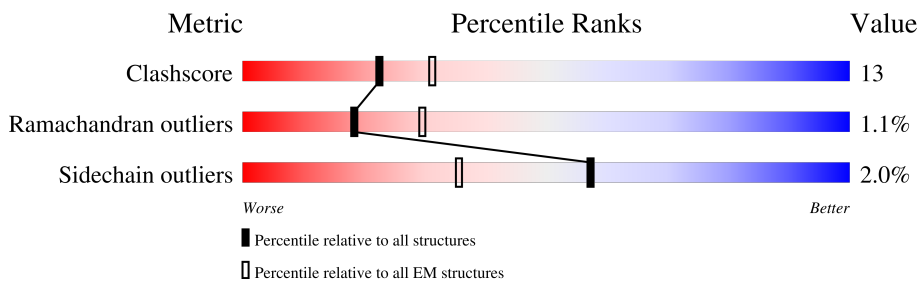
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.60 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

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  $\geq 3$ , 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	A	1460	
2	B	1149	
3	C	335	
4	D	161	
5	E	215	
6	F	155	
7	G	212	
8	H	146	

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Mol	Chain	Length	Quality of chain
9	I	110	
10	J	70	
11	K	142	
12	L	70	
13	M	282	
14	N	422	
15	O	654	
16	P	317	
17	Q	104	

## 2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 38680 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 DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1412	11071	6979	1954	2079	59	0	0

- Molecule 2 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1114	8788	5558	1516	1654	60	0	0

- Molecule 3 is a protein called DNA-DIRECTED RNA POLYMERASES I AND III SUBUNIT RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	335	2655	1681	454	511	9	0	0

- Molecule 4 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	119	977	628	156	187	6	0	0

- Molecule 5 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	215	1759	1116	310	321	12	0	0

- Molecule 6 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	83	671	429	114	125	3	0	0

- Molecule 7 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	191	1544	1007	250	281	6	0	0

- Molecule 8 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	140	1120	703	188	224	5	0	0

- Molecule 9 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	92	728	455	117	145	11	0	0

- Molecule 10 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	67	549	350	95	98	6	0	0

- Molecule 11 is a protein called DNA-DIRECTED RNA POLYMERASES I AND III SUBUNIT RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	101	792	496	130	161	5	0	0

- Molecule 12 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	45	358	221	71	62	4	0	0

- Molecule 13 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	165	1347	862	229	255	1	0	0

- Molecule 14 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	105	802	508	144	147	3	0	0

- Molecule 15 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	528	4247	2705	725	798	19	0	0

- Molecule 16 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	98	820	533	126	157	4	0	0

- Molecule 17 is a protein called DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	Q	70	446	282	80	84	0	0

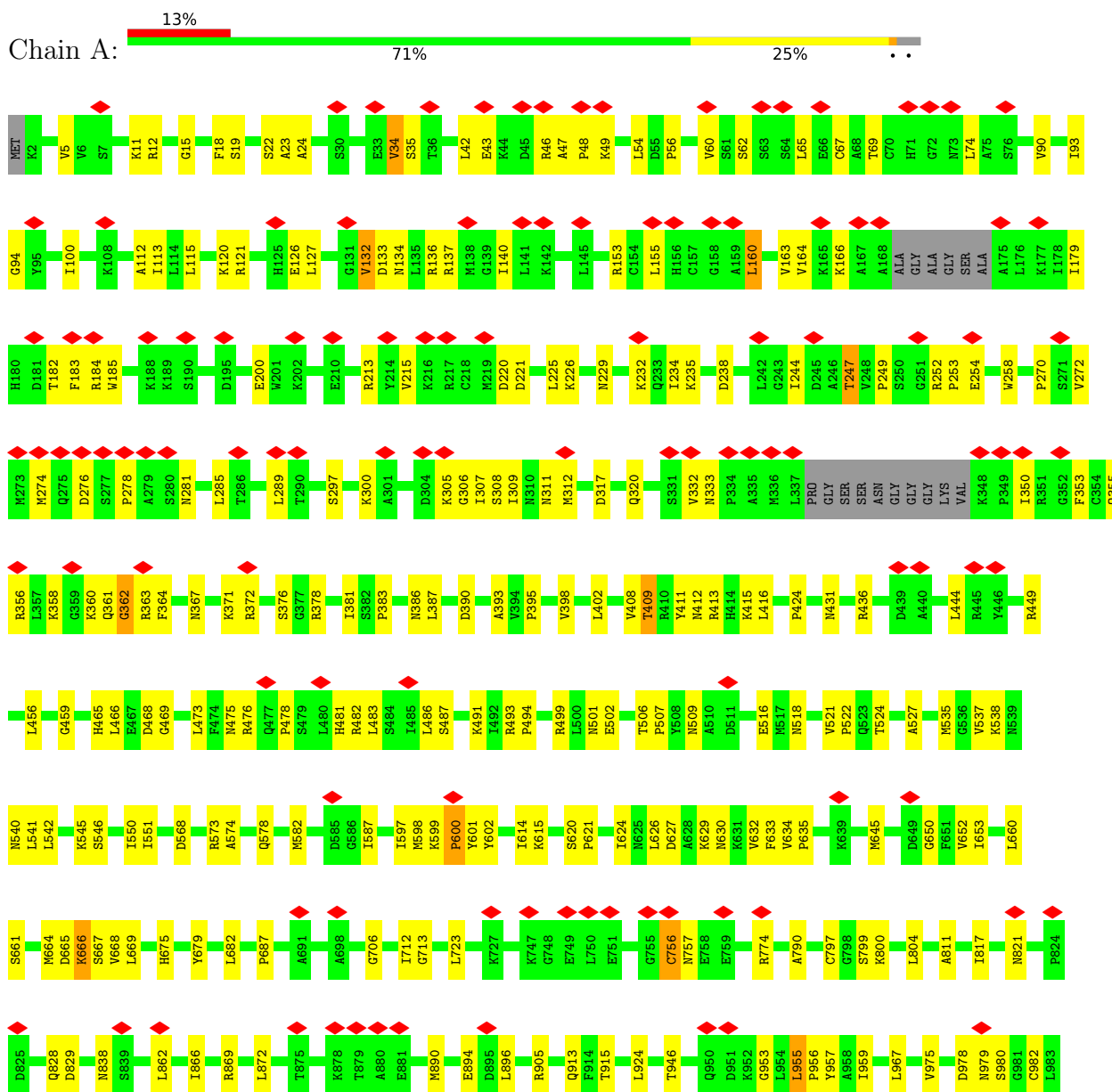
- Molecule 18 is ZINC ION (three-letter code: ZN) (formula: Zn).

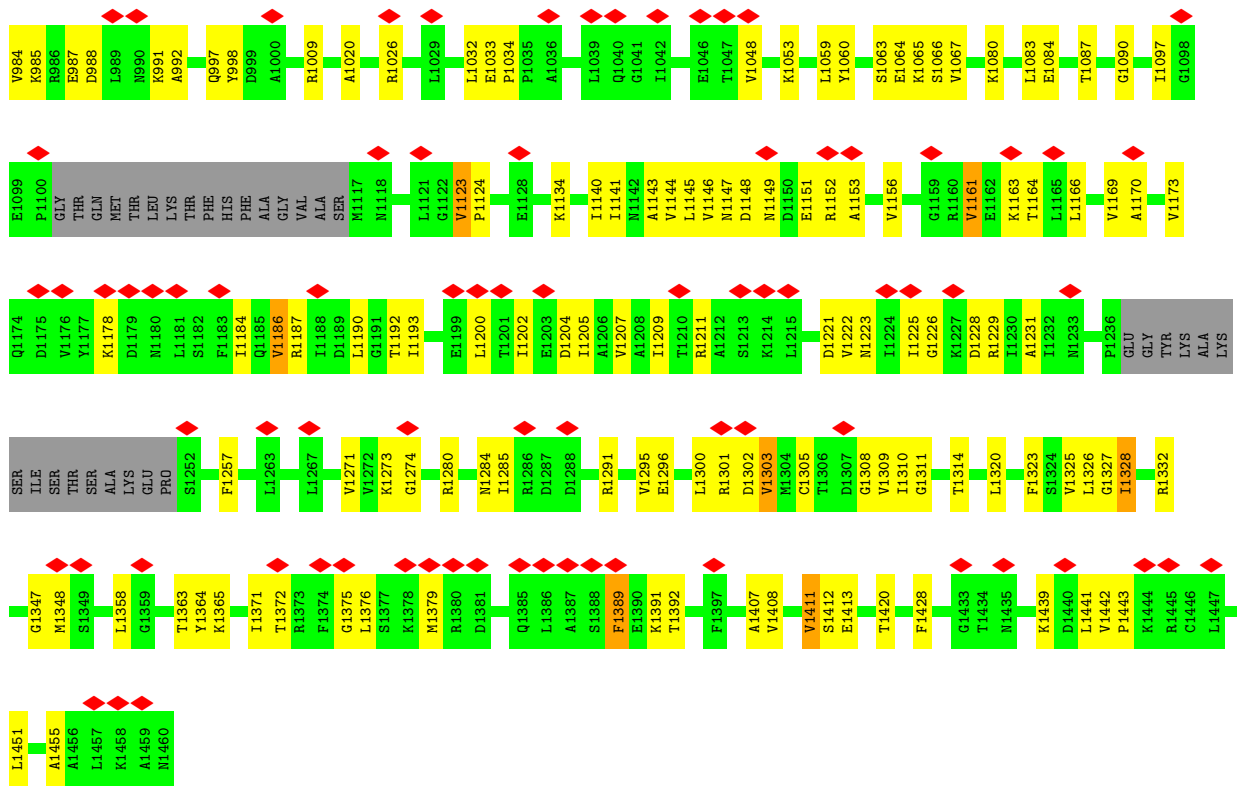
Mol	Chain	Residues	Atoms		AltConf
18	A	2	Total	Zn	0
			2	2	
18	B	1	Total	Zn	0
			1	1	
18	I	1	Total	Zn	0
			1	1	
18	J	1	Total	Zn	0
			1	1	
18	L	1	Total	Zn	0
			1	1	

### 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: DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC1

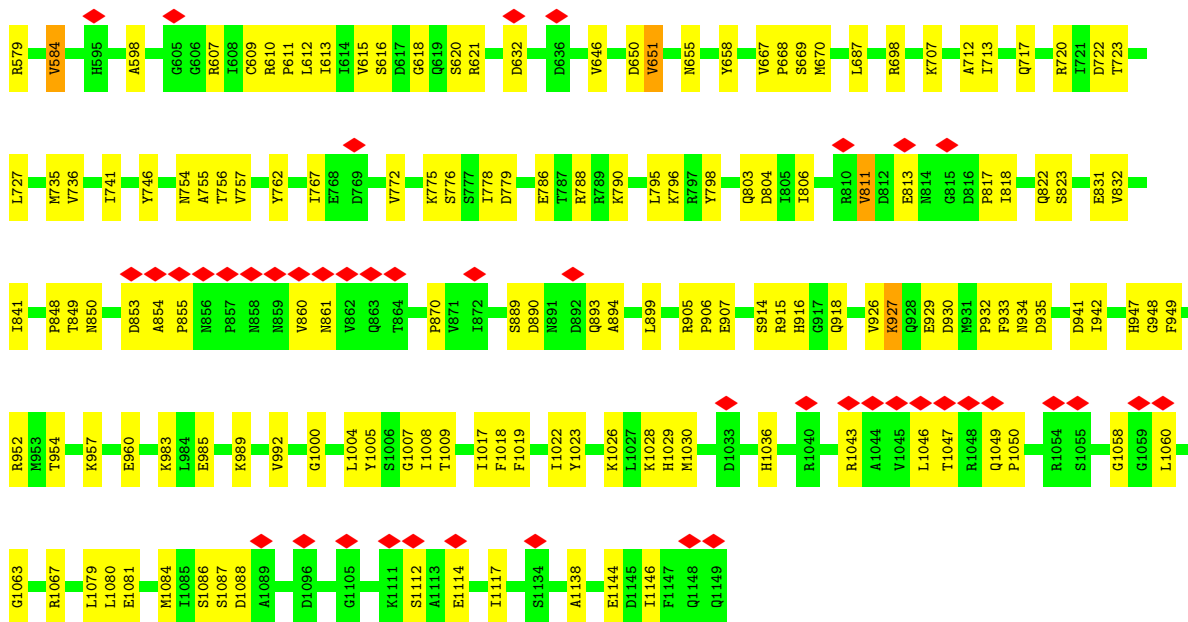




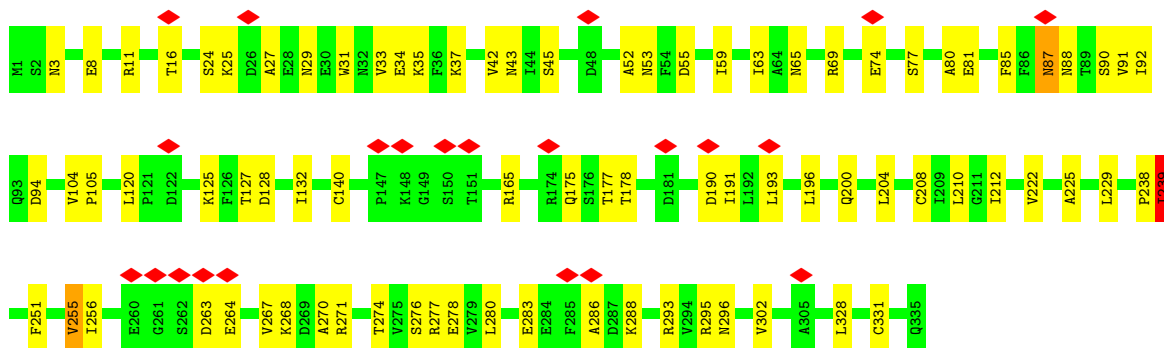
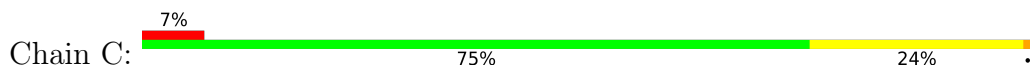
• Molecule 2: DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC2



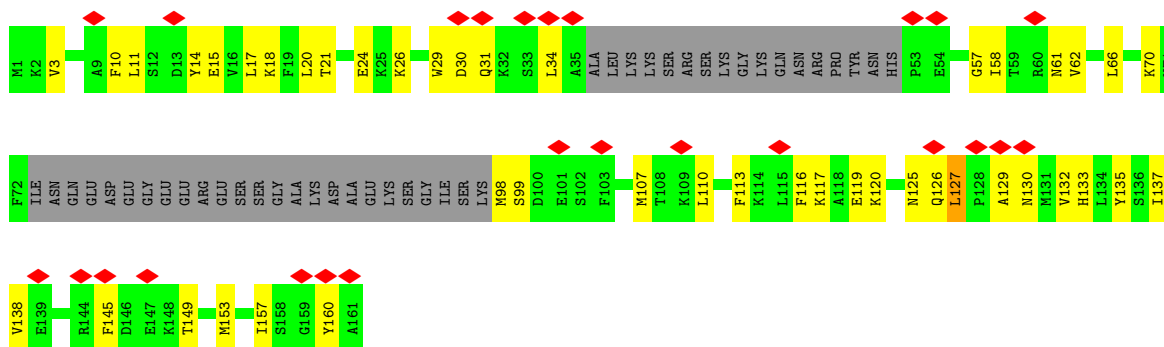




• Molecule 3: DNA-DIRECTED RNA POLYMERASES I AND III SUBUNIT RPAC1



• Molecule 4: DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC9



• Molecule 5: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68818	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	42	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	4200	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.322	Depositor
Minimum map value	-0.126	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.055	Depositor
Map size ( $\text{\AA}$ )	320.86398, 320.86398, 320.86398	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.084, 1.084, 1.084	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	A	0.22	0/11267	0.46	0/15220
2	B	0.22	0/8943	0.45	0/12068
3	C	0.23	0/2711	0.45	0/3676
4	D	0.23	0/991	0.52	0/1328
5	E	0.22	0/1795	0.44	0/2416
6	F	0.21	0/683	0.42	0/923
7	G	0.23	0/1583	0.50	0/2146
8	H	0.21	0/1138	0.44	0/1540
9	I	0.22	0/745	0.42	0/1007
10	J	0.21	0/558	0.44	0/750
11	K	0.22	0/803	0.45	0/1083
12	L	0.22	0/360	0.48	0/478
13	M	0.23	0/1378	0.46	0/1863
14	N	0.23	0/810	0.52	0/1088
15	O	0.23	0/4310	0.50	0/5813
16	P	0.29	0/837	0.55	0/1134
17	Q	0.24	0/278	0.49	0/377
All	All	0.22	0/39190	0.47	0/52910

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	A	11071	0	11200	272	0
2	B	8788	0	8902	221	0
3	C	2655	0	2628	55	0
4	D	977	0	983	33	0
5	E	1759	0	1788	48	0
6	F	671	0	692	9	0
7	G	1544	0	1540	62	0
8	H	1120	0	1089	28	0
9	I	728	0	672	18	0
10	J	549	0	560	8	0
11	K	792	0	790	23	0
12	L	358	0	381	18	0
13	M	1347	0	1315	39	0
14	N	802	0	851	40	0
15	O	4247	0	4413	157	0
16	P	820	0	795	51	0
17	Q	446	0	324	10	0
18	A	2	0	0	0	0
18	B	1	0	0	0	0
18	I	1	0	0	0	0
18	J	1	0	0	0	0
18	L	1	0	0	0	0
All	All	38680	0	38923	975	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 13.

The worst 5 of 975 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)
15:O:516:LEU:CD2	15:O:567:ARG:HE	1.08	1.58
15:O:516:LEU:HD23	15:O:567:ARG:NE	1.20	1.41
15:O:516:LEU:HD23	15:O:567:ARG:CD	1.60	1.30
15:O:516:LEU:CD2	15:O:567:ARG:NE	1.84	1.23
1:A:597:ILE:HB	1:A:600:PRO:HG3	1.15	1.15

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	A	1402/1460 (96%)	1157 (82%)	233 (17%)	12 (1%)	17	56
2	B	1112/1149 (97%)	948 (85%)	155 (14%)	9 (1%)	19	60
3	C	333/335 (99%)	282 (85%)	47 (14%)	4 (1%)	13	50
4	D	113/161 (70%)	80 (71%)	33 (29%)	0	100	100
5	E	213/215 (99%)	172 (81%)	38 (18%)	3 (1%)	11	47
6	F	81/155 (52%)	73 (90%)	8 (10%)	0	100	100
7	G	185/212 (87%)	154 (83%)	25 (14%)	6 (3%)	4	30
8	H	136/146 (93%)	116 (85%)	20 (15%)	0	100	100
9	I	88/110 (80%)	77 (88%)	10 (11%)	1 (1%)	14	52
10	J	65/70 (93%)	53 (82%)	11 (17%)	1 (2%)	10	46
11	K	99/142 (70%)	83 (84%)	15 (15%)	1 (1%)	15	54
12	L	43/70 (61%)	33 (77%)	10 (23%)	0	100	100
13	M	161/282 (57%)	135 (84%)	22 (14%)	4 (2%)	5	35
14	N	101/422 (24%)	78 (77%)	22 (22%)	1 (1%)	15	54
15	O	522/654 (80%)	428 (82%)	88 (17%)	6 (1%)	14	52
16	P	92/317 (29%)	60 (65%)	26 (28%)	6 (6%)	1	18
17	Q	33/104 (32%)	29 (88%)	4 (12%)	0	100	100
All	All	4779/6004 (80%)	3958 (83%)	767 (16%)	54 (1%)	18	52

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	587	ILE
1	A	632	VAL
1	A	1371	ILE
9	I	35	ILE
11	K	47	ILE

### 5.3.2 Protein sidechains [i](#)

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	A	1225/1257 (98%)	1208 (99%)	17 (1%)	67	81
2	B	975/1006 (97%)	958 (98%)	17 (2%)	60	78
3	C	296/296 (100%)	293 (99%)	3 (1%)	76	86
4	D	110/145 (76%)	108 (98%)	2 (2%)	59	77
5	E	197/197 (100%)	192 (98%)	5 (2%)	47	68
6	F	73/137 (53%)	70 (96%)	3 (4%)	30	56
7	G	170/190 (90%)	167 (98%)	3 (2%)	59	77
8	H	123/128 (96%)	123 (100%)	0	100	100
9	I	83/98 (85%)	83 (100%)	0	100	100
10	J	62/65 (95%)	60 (97%)	2 (3%)	39	62
11	K	91/130 (70%)	88 (97%)	3 (3%)	38	61
12	L	40/57 (70%)	39 (98%)	1 (2%)	47	68
13	M	143/249 (57%)	140 (98%)	3 (2%)	53	72
14	N	88/360 (24%)	87 (99%)	1 (1%)	73	85
15	O	486/593 (82%)	468 (96%)	18 (4%)	34	59
16	P	94/285 (33%)	89 (95%)	5 (5%)	22	49
17	Q	31/56 (55%)	30 (97%)	1 (3%)	39	62
All	All	4287/5249 (82%)	4203 (98%)	84 (2%)	57	73

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	97	VAL
15	O	336	LEU
14	N	412	VAL
15	O	195	CYS
15	O	567	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18

such sidechains are listed below:

Mol	Chain	Res	Type
15	O	580	ASN
16	P	307	HIS
16	P	219	GLN
4	D	122	GLN
15	O	544	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 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 6 ligands modelled in this entry, 6 are 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
17	Q	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Q	1088:UNK	C	1090:UNK	N	15.14
1	Q	69:PRO	C	1070:UNK	N	8.39

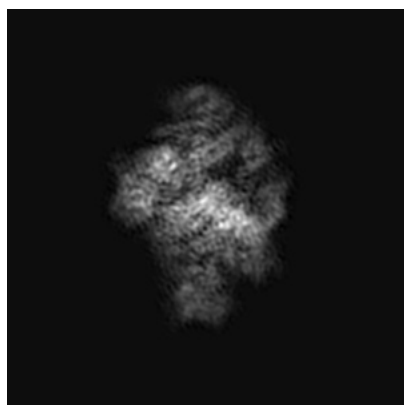
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3179. These allow visual inspection of the internal detail of the map and identification of artifacts.

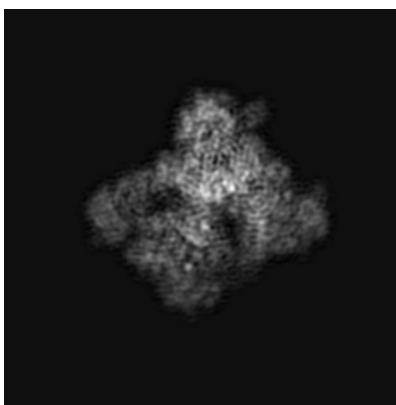
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

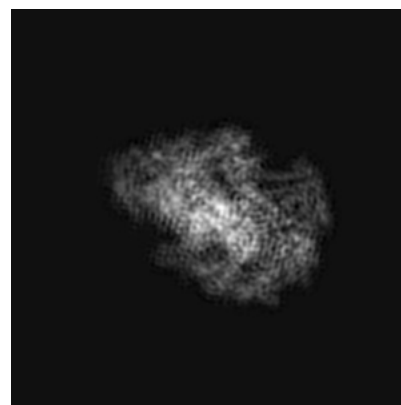
#### 6.1.1 Primary map



X



Y

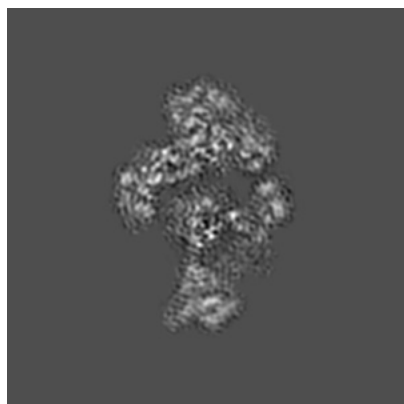


Z

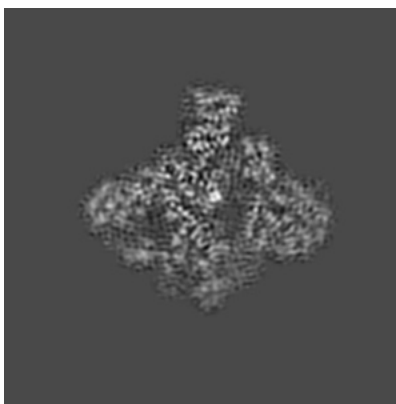
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

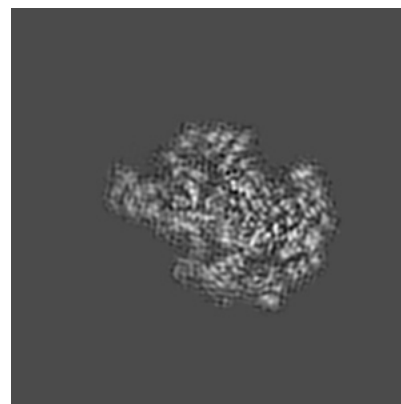
#### 6.2.1 Primary map



X Index: 148



Y Index: 148

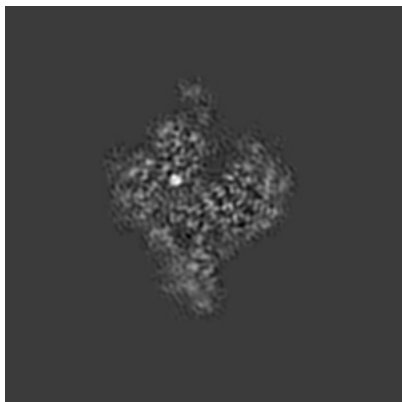


Z Index: 148

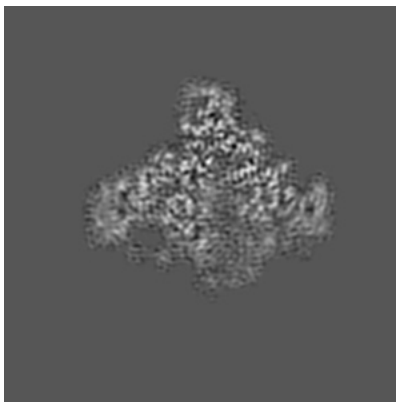
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

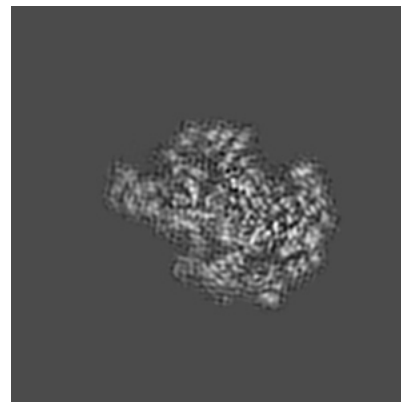
### 6.3.1 Primary map



X Index: 164



Y Index: 139



Z Index: 148

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

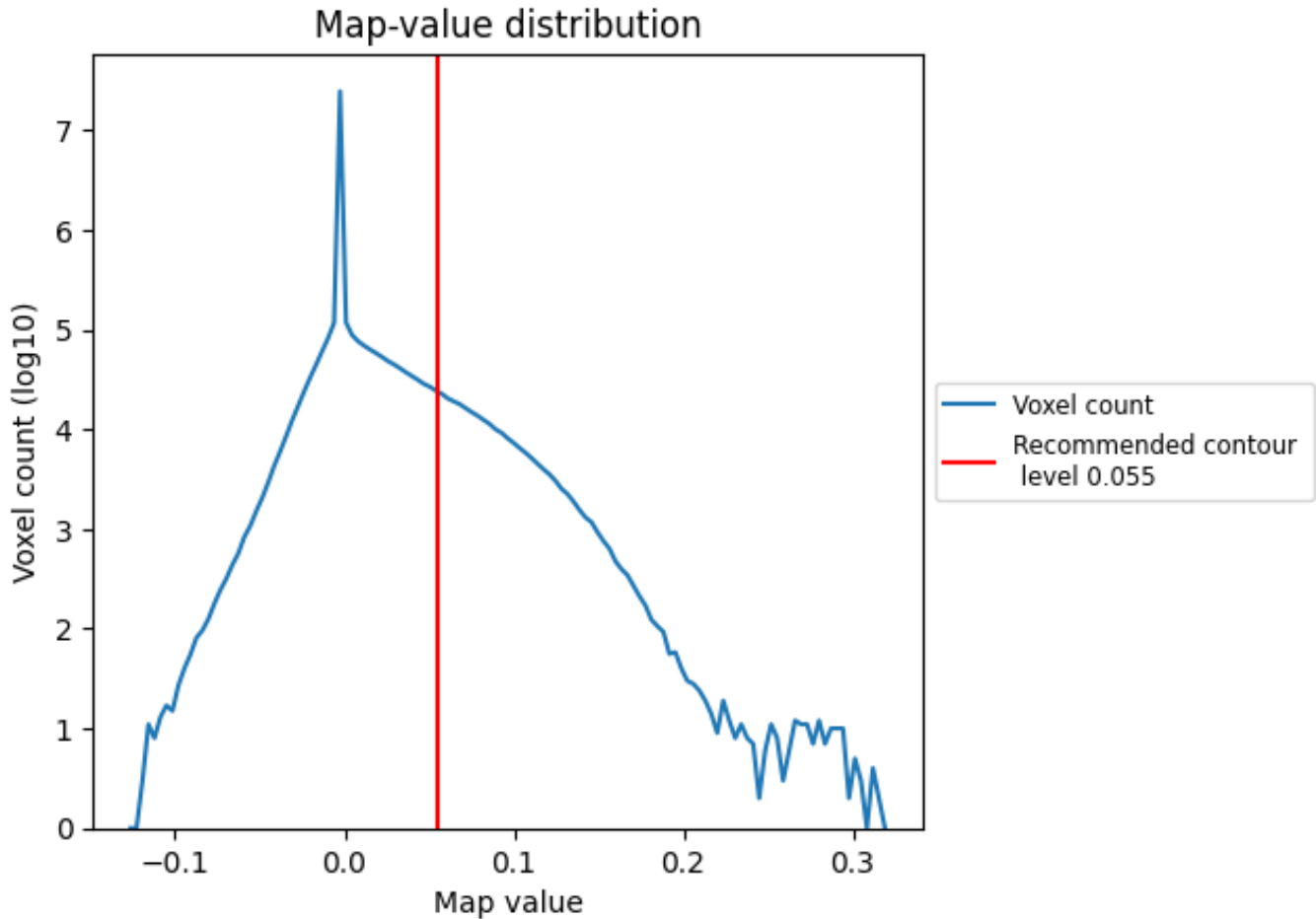
## 6.5 Mask visualisation

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.

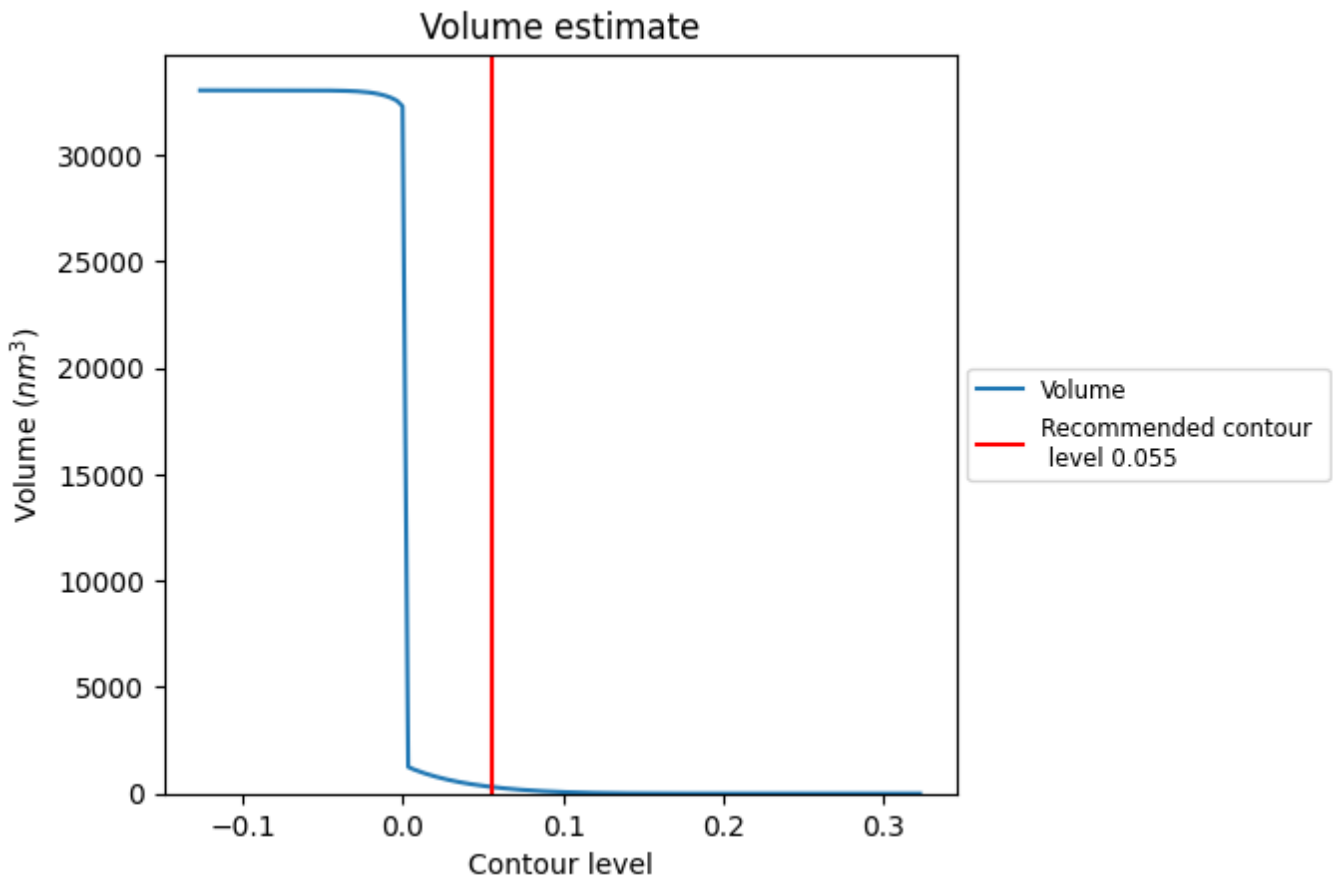
### 7.1 Map-value distribution [i](#)



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.



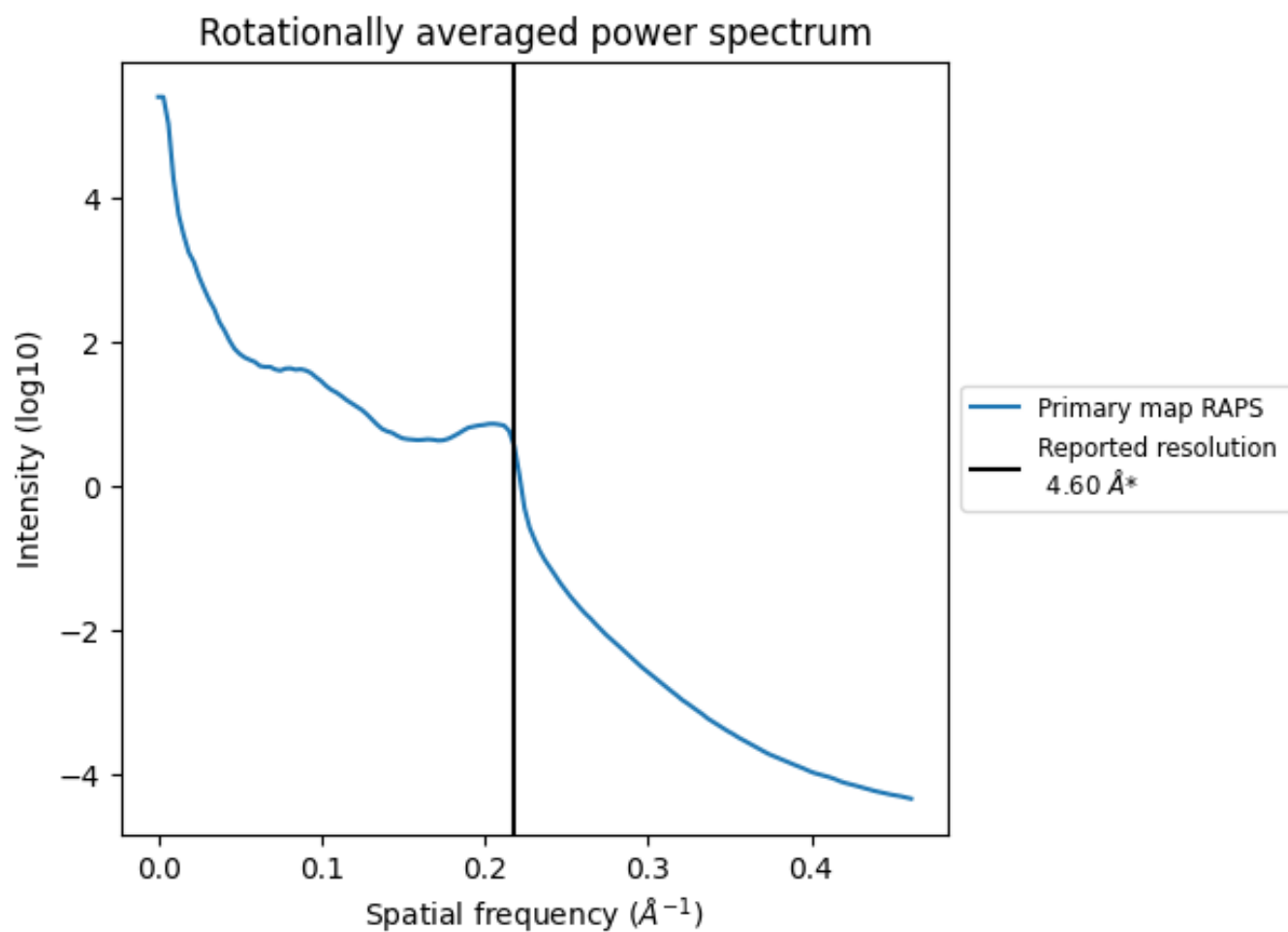
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 315 nm<sup>3</sup>; this corresponds to an approximate mass of 285 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 [i](#)

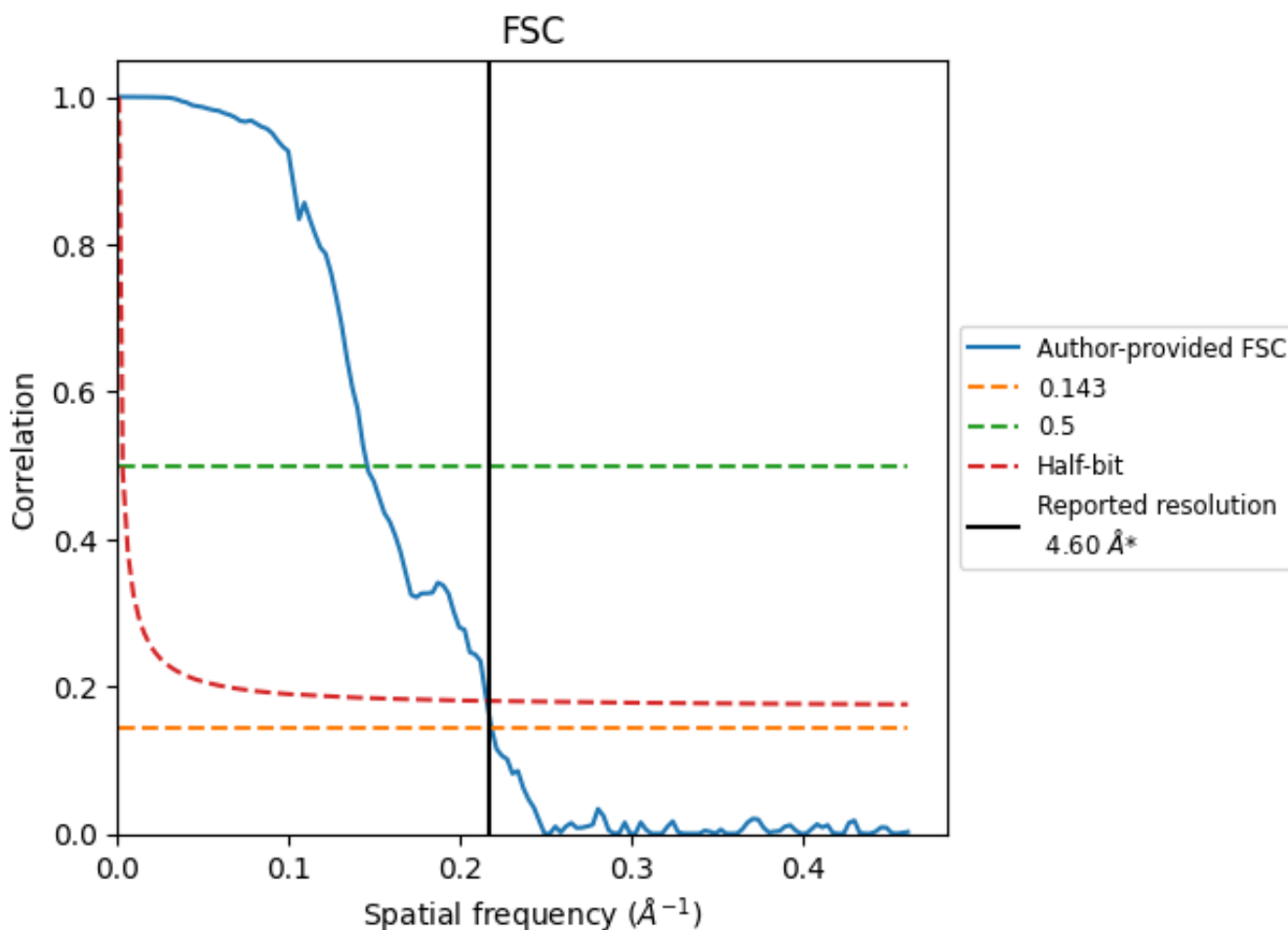


\*Reported resolution corresponds to spatial frequency of  $0.217 \text{\AA}^{-1}$

## 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 0.217 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

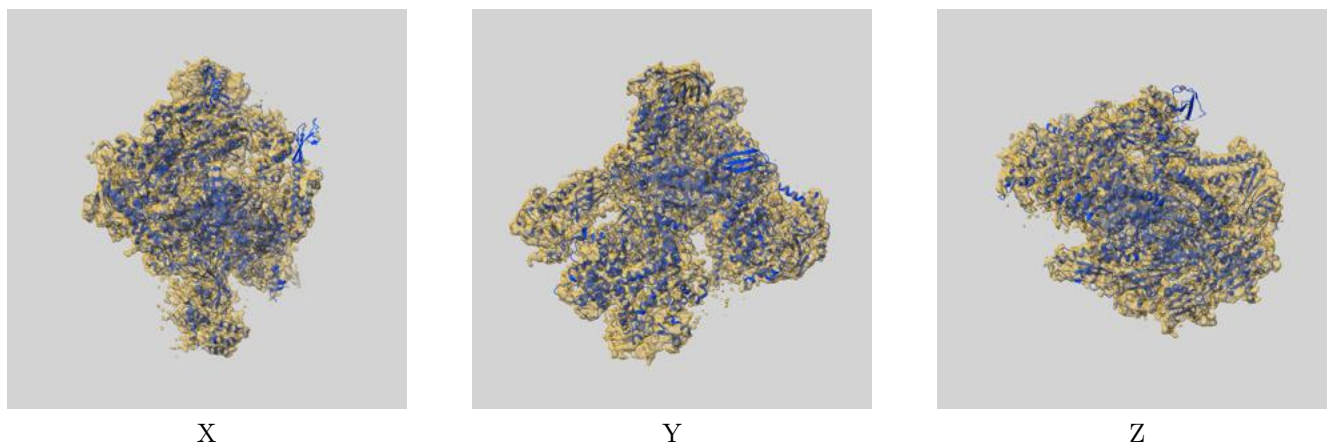
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	4.58	6.86	4.64
Unmasked-calculated*	-	-	-

\*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-3179 and PDB model 5FJ9. Per-residue inclusion information can be found in section 3 on page 7.

### 9.1 Map-model overlay [i](#)



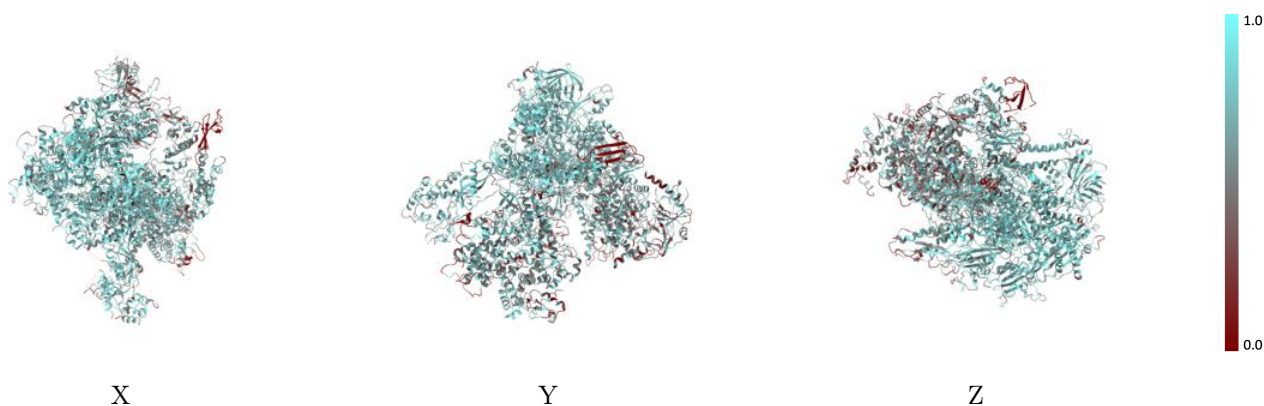
The images above show the 3D surface view of the map at the recommended contour level 0.055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



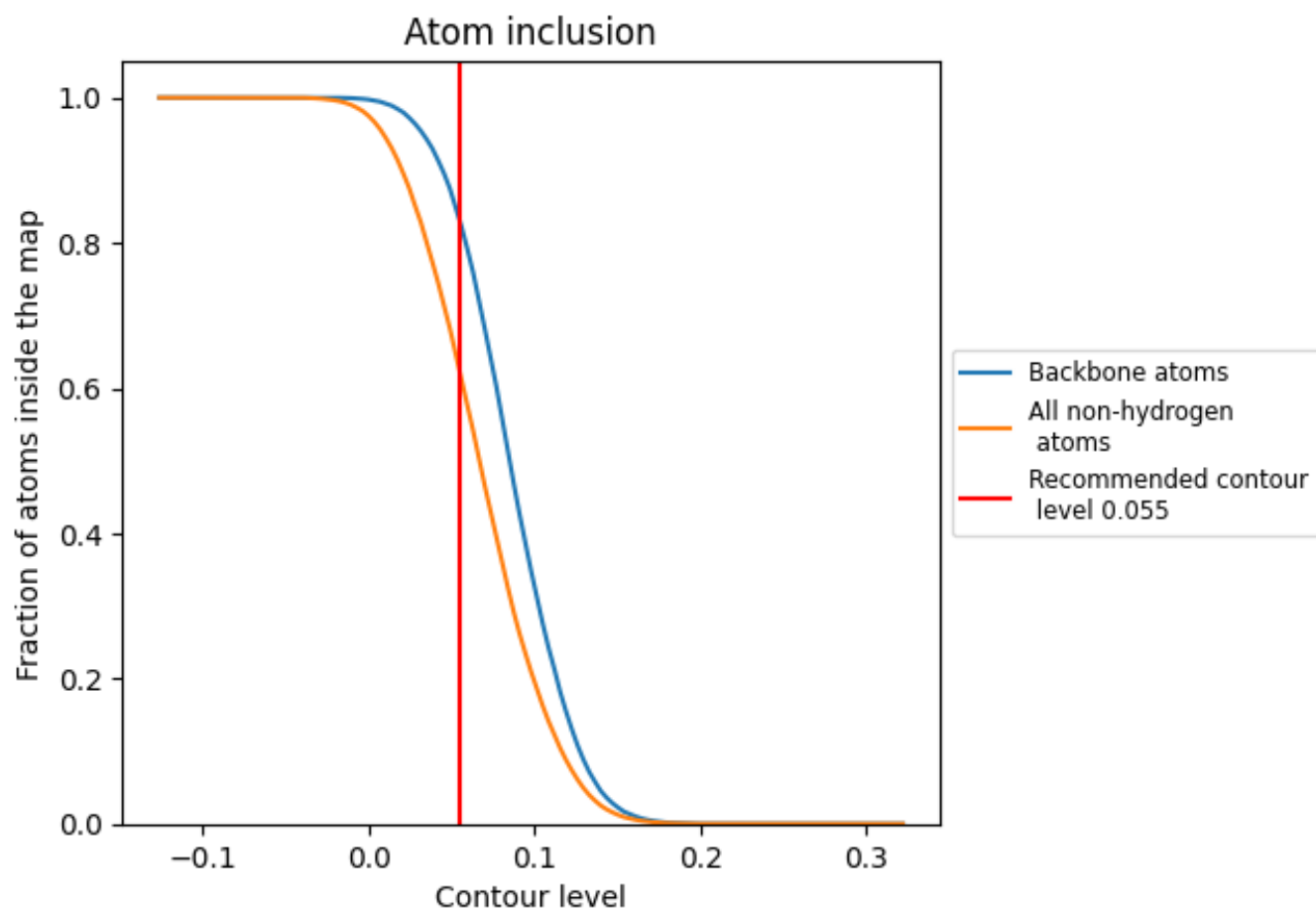
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.055).





































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 62% 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 (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6227	 0.2480
A	 0.6463	 0.2650
B	 0.6529	 0.2820
C	 0.7074	 0.2880
D	 0.6108	 0.1860
E	 0.6498	 0.2410
F	 0.7274	 0.3350
G	 0.6223	 0.2270
H	 0.6877	 0.2780
I	 0.2137	 0.1050
J	 0.7303	 0.2940
K	 0.6897	 0.2940
L	 0.6503	 0.2430
M	 0.4766	 0.1820
N	 0.4722	 0.1830
O	 0.5565	 0.1840
P	 0.4796	 0.1130
Q	 0.5440	 0.2160

