



## wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 02:59 PM EDT

PDB ID : 11AA / pdb\_000011aa  
EMDB ID : EMD-75580  
Title : Yeast co-transcriptional pre-60S assembly intermediate Nop12 RNP  
Authors : Piwowarczyk, R.; Klinge, S.  
Deposited on : 2026-02-13  
Resolution : 2.78 Å (reported)  
Based on initial model : 8E5T

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:

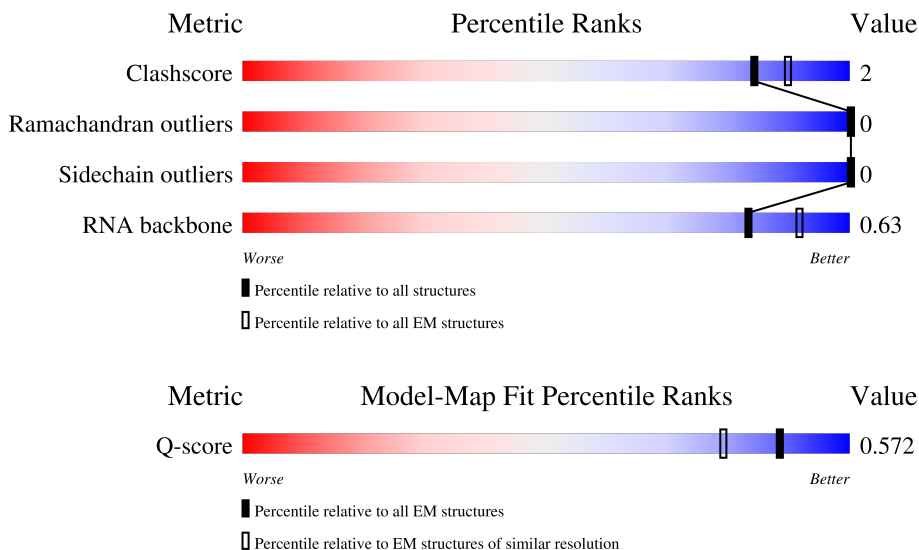
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 2.78 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10754 ( 2.28 - 3.28 )

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	1	3396	 6% . 94%
2	2	159	 6% 29% . . 68%
3	3	232	 28% 7% . 63%

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Mol	Chain	Length	Quality of chain
4	7	231	
5	G	256	
6	H	459	
7	K	376	
8	L	199	
9	N	204	
10	b	291	
11	i	100	
12	m	427	
13	n	605	
14	o	220	
15	p	505	
16	s	807	
17	t	322	

## 2 Entry composition i

There are 18 unique types of molecules in this entry. The entry contains 29525 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	219	4693	2098	857	1519	219	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	51	1082	482	186	363	51	0	0

- Molecule 3 is a RNA chain called Internal transcribed spacer 2 ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	85	1798	805	305	603	85	0	0

- Molecule 4 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	7	52	471	298	89	83	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	178	1385	891	241	251	2	0	0

- Molecule 6 is a protein called Nucleolar protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	186	1534	985	275	269	5	0	0

- Molecule 7 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	K	285	2291	1475	377	435	4	0	0

- Molecule 8 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	L	87	723	455	149	119	0	0

- Molecule 9 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	N	155	1314	823	275	215	1	0	0

- Molecule 10 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	b	219	1801	1156	318	321	6	0	0

- Molecule 11 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	i	81	641	398	131	110	2	0	0

- Molecule 12 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	m	97	810	511	143	153	3	0	0

- Molecule 13 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	n	337	2760	1803	462	486	9	0	0

- Molecule 14 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	133	Total	C	N	O	S	0	0
			1108	716	198	190	4		

- Molecule 15 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	427	Total	C	N	O	S	0	0
			3414	2205	582	615	12		

- Molecule 16 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	212	Total	C	N	O	S	0	0
			1764	1121	304	334	5		

- Molecule 17 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	243	Total	C	N	O	S	0	0
			1931	1235	344	349	3		

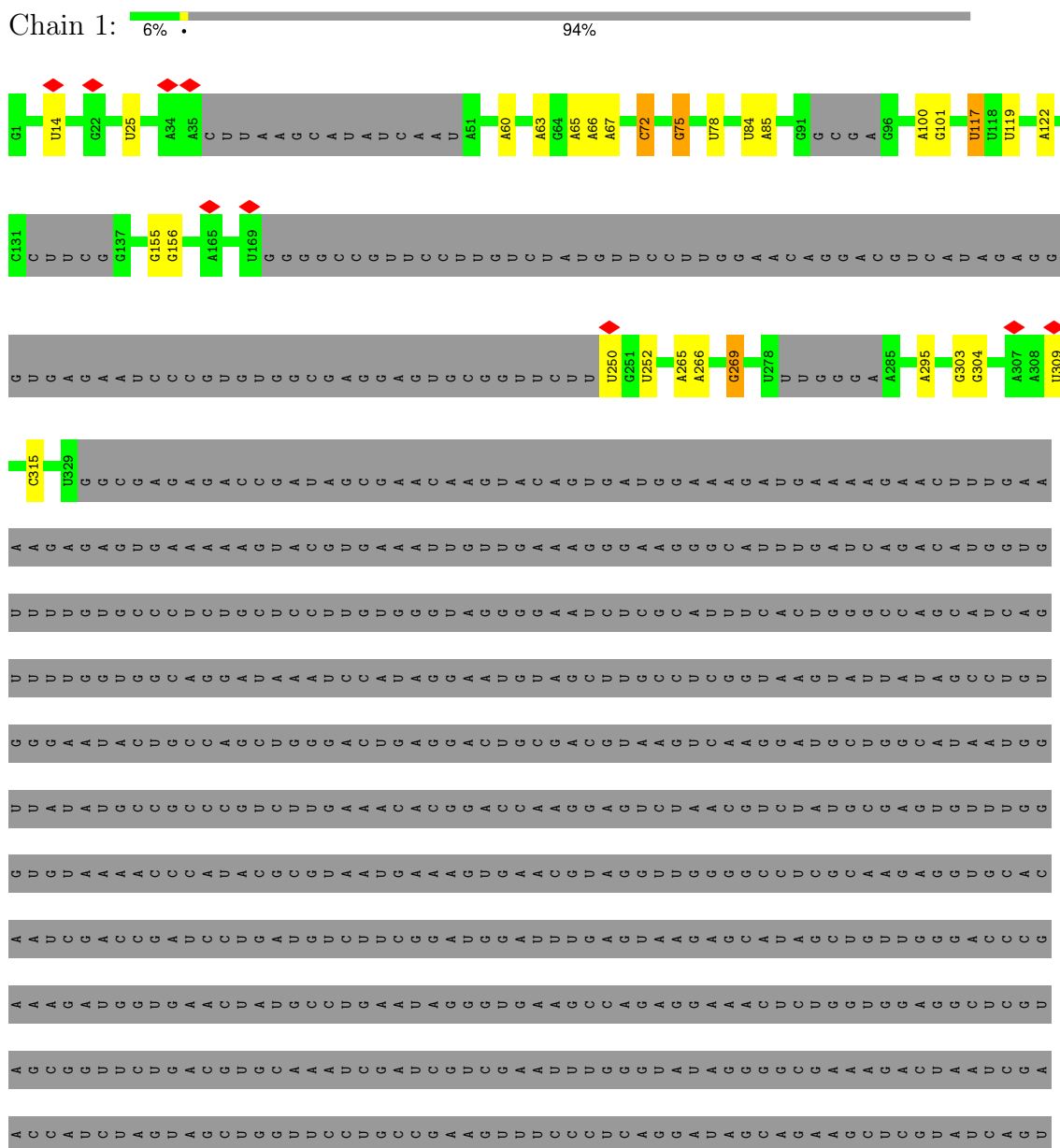
- Molecule 18 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
18	1	5	Total	Mg	0
			5	5	

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

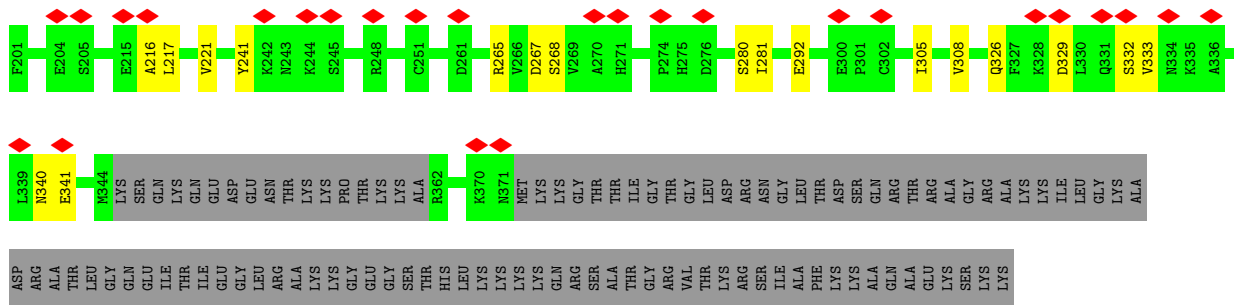
- Molecule 1: 25S ribosomal RNA



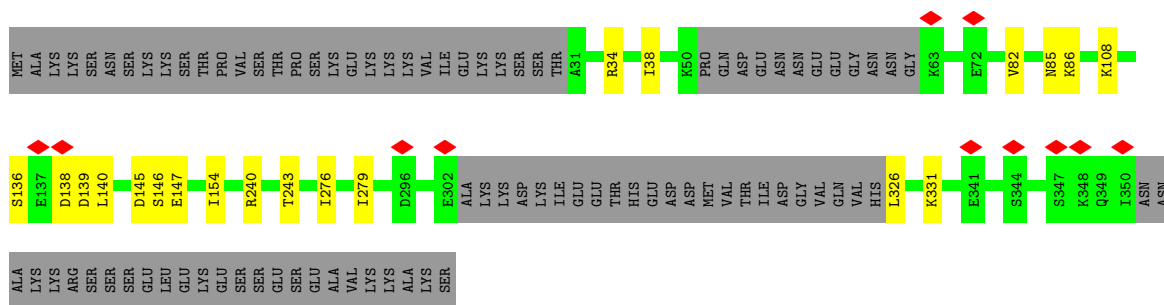




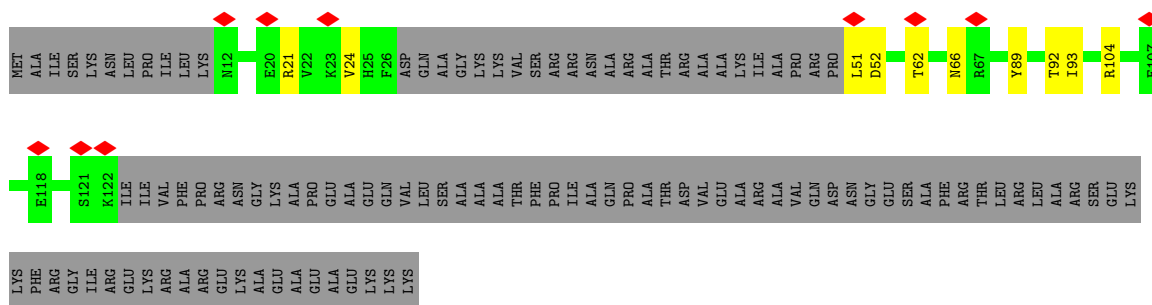
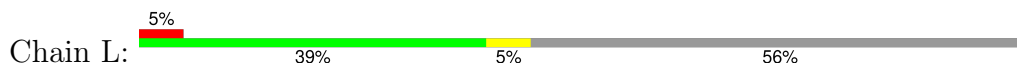




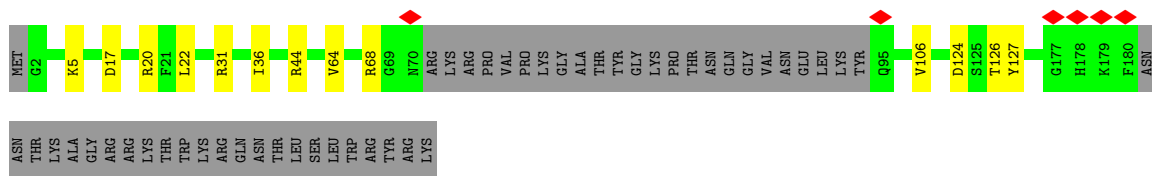
• Molecule 7: Proteasome-interacting protein CIC1



• Molecule 8: 60S ribosomal protein L13-A



• Molecule 9: 60S ribosomal protein L15-A



• Molecule 10: Ribosome biogenesis protein BRX1









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	443499	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	51	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	51.205	Depositor
Minimum map value	-28.454	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.079	Depositor
Recommended contour level	6	Depositor
Map size ( $\text{\AA}$ )	318.84003, 318.84003, 318.84003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.0628, 1.0628, 1.0628	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: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	1	0.09	0/5252	0.24	0/8175
2	2	0.08	0/1204	0.20	0/1869
3	3	0.09	0/2006	0.24	0/3118
4	7	0.10	0/480	0.25	0/633
5	G	0.11	0/1407	0.26	0/1900
6	H	0.14	0/1563	0.36	0/2092
7	K	0.10	0/2326	0.28	0/3134
8	L	0.11	0/736	0.28	0/987
9	N	0.11	0/1340	0.29	0/1793
10	b	0.13	0/1845	0.32	0/2493
11	i	0.15	0/647	0.36	0/859
12	m	0.11	0/826	0.26	0/1108
13	n	0.11	0/2828	0.25	0/3824
14	o	0.14	0/1130	0.34	0/1502
15	p	0.11	0/3479	0.26	0/4693
16	s	0.12	0/1811	0.29	0/2449
17	t	0.11	0/1956	0.27	0/2629
All	All	0.11	0/30836	0.27	0/43258

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	1	4693	0	2361	12	0
2	2	1082	0	551	2	0
3	3	1798	0	907	6	0
4	7	471	0	474	1	0
5	G	1385	0	1459	5	0
6	H	1534	0	1573	13	0
7	K	2291	0	2381	14	0
8	L	723	0	741	6	0
9	N	1314	0	1350	10	0
10	b	1801	0	1813	16	0
11	i	641	0	698	8	0
12	m	810	0	806	7	0
13	n	2760	0	2808	17	0
14	o	1108	0	1159	8	0
15	p	3414	0	3535	17	0
16	s	1764	0	1738	8	0
17	t	1931	0	2050	9	0
18	1	5	0	0	0	0
All	All	29525	0	26404	129	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 2.

The worst 5 of 129 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:p:207:GLU:OE2	15:p:211:ARG:NH1	2.18	0.76
10:b:184:ASP:OD2	10:b:241:GLN:NE2	2.19	0.76
1:1:117:U:O2'	1:1:119:U:OP2	2.01	0.75
9:N:17:ASP:OD1	9:N:20:ARG:NH2	2.23	0.71
15:p:197:GLU:OE1	15:p:200:ARG:NH2	2.25	0.70

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	
4	7	50/231 (22%)	50 (100%)	0	0	100	100
5	G	174/256 (68%)	173 (99%)	1 (1%)	0	100	100
6	H	180/459 (39%)	175 (97%)	5 (3%)	0	100	100
7	K	279/376 (74%)	275 (99%)	4 (1%)	0	100	100
8	L	83/199 (42%)	82 (99%)	1 (1%)	0	100	100
9	N	151/204 (74%)	149 (99%)	2 (1%)	0	100	100
10	b	215/291 (74%)	209 (97%)	6 (3%)	0	100	100
11	i	79/100 (79%)	76 (96%)	3 (4%)	0	100	100
12	m	95/427 (22%)	95 (100%)	0	0	100	100
13	n	329/605 (54%)	326 (99%)	3 (1%)	0	100	100
14	o	131/220 (60%)	127 (97%)	4 (3%)	0	100	100
15	p	421/505 (83%)	414 (98%)	7 (2%)	0	100	100
16	s	206/807 (26%)	204 (99%)	2 (1%)	0	100	100
17	t	237/322 (74%)	233 (98%)	4 (2%)	0	100	100
All	All	2630/5002 (53%)	2588 (98%)	42 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	
4	7	50/205 (24%)	50 (100%)	0	100	100
5	G	144/208 (69%)	144 (100%)	0	100	100
6	H	170/404 (42%)	170 (100%)	0	100	100
7	K	263/346 (76%)	263 (100%)	0	100	100
8	L	73/159 (46%)	73 (100%)	0	100	100
9	N	133/176 (76%)	133 (100%)	0	100	100
10	b	205/263 (78%)	205 (100%)	0	100	100
11	i	67/82 (82%)	67 (100%)	0	100	100
12	m	90/383 (24%)	90 (100%)	0	100	100
13	n	305/548 (56%)	305 (100%)	0	100	100
14	o	118/199 (59%)	118 (100%)	0	100	100
15	p	375/440 (85%)	375 (100%)	0	100	100
16	s	194/723 (27%)	194 (100%)	0	100	100
17	t	216/287 (75%)	216 (100%)	0	100	100
All	All	2403/4423 (54%)	2403 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
9	N	139	HIS
17	t	172	ASN
10	b	148	HIS
17	t	238	GLN
15	p	231	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	213/3396 (6%)	15 (7%)	0
2	2	48/159 (30%)	4 (8%)	0
3	3	83/232 (35%)	13 (15%)	0
All	All	344/3787 (9%)	32 (9%)	0

5 of 32 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	14	U
1	1	25	U
1	1	60	A
1	1	65	A
1	1	66	A

There are no RNA pucker outliers to report.

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

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

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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](#)

There are no chain breaks in this entry.

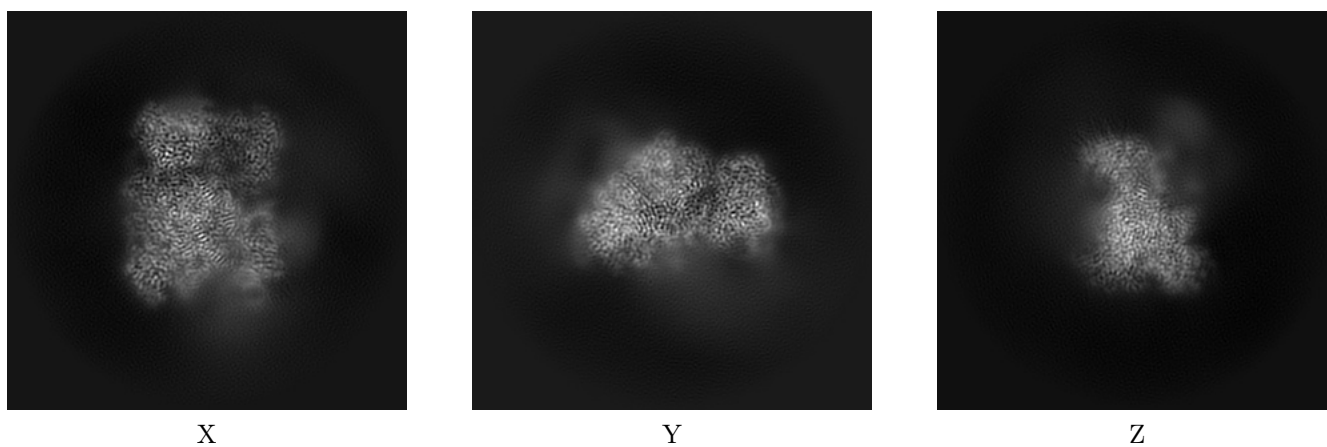
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75580. 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](#)

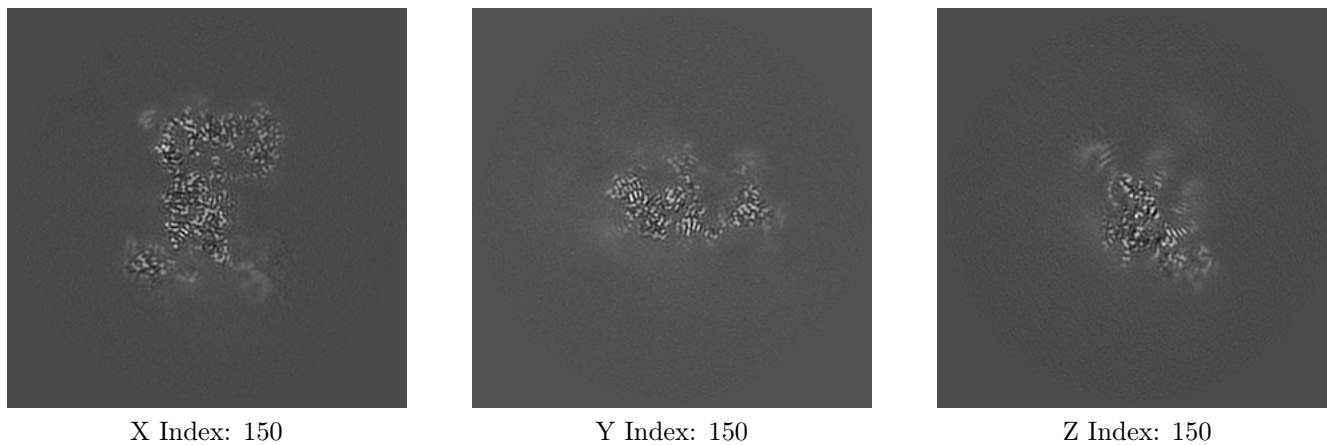
#### 6.1.1 Primary map



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

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

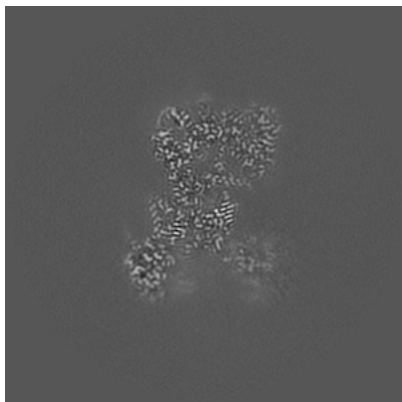
#### 6.2.1 Primary map



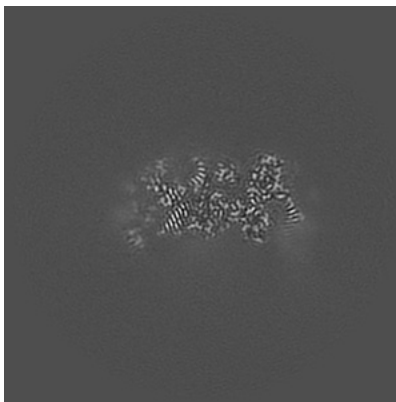
The images above show central slices of the map in three orthogonal directions.

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

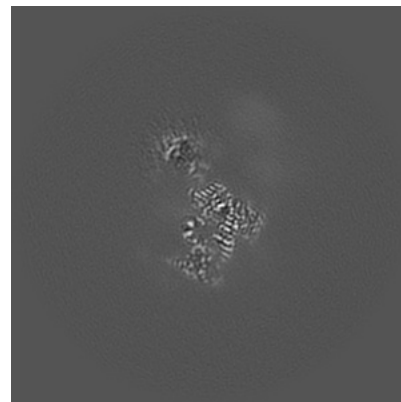
### 6.3.1 Primary map



X Index: 143



Y Index: 127

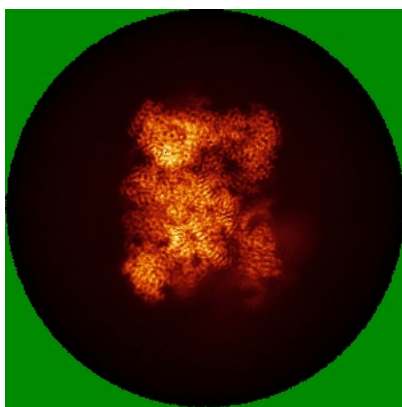


Z Index: 119

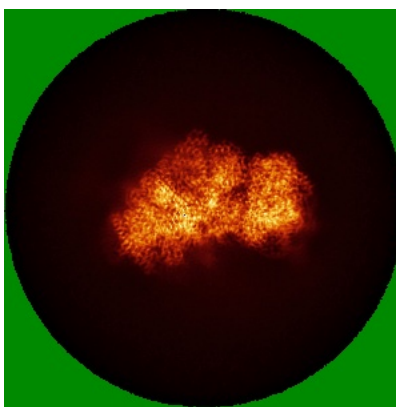
The images above show the largest variance slices of the map in three orthogonal directions.

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

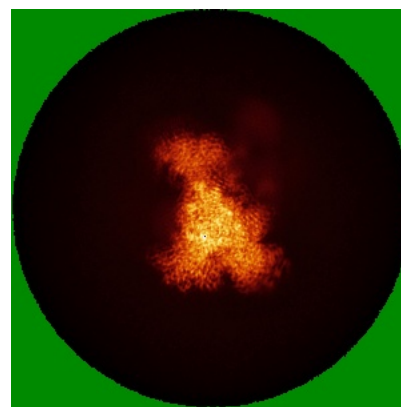
### 6.4.1 Primary map



X



Y

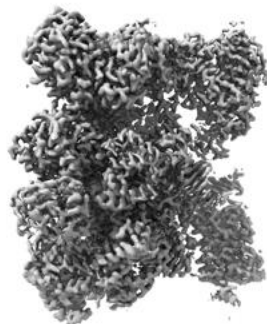


Z

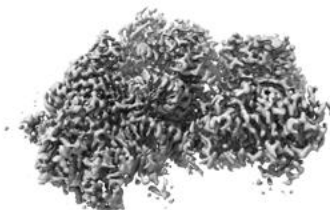
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

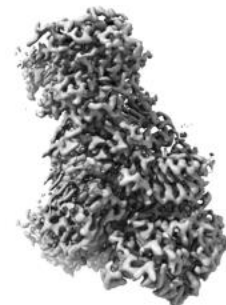
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

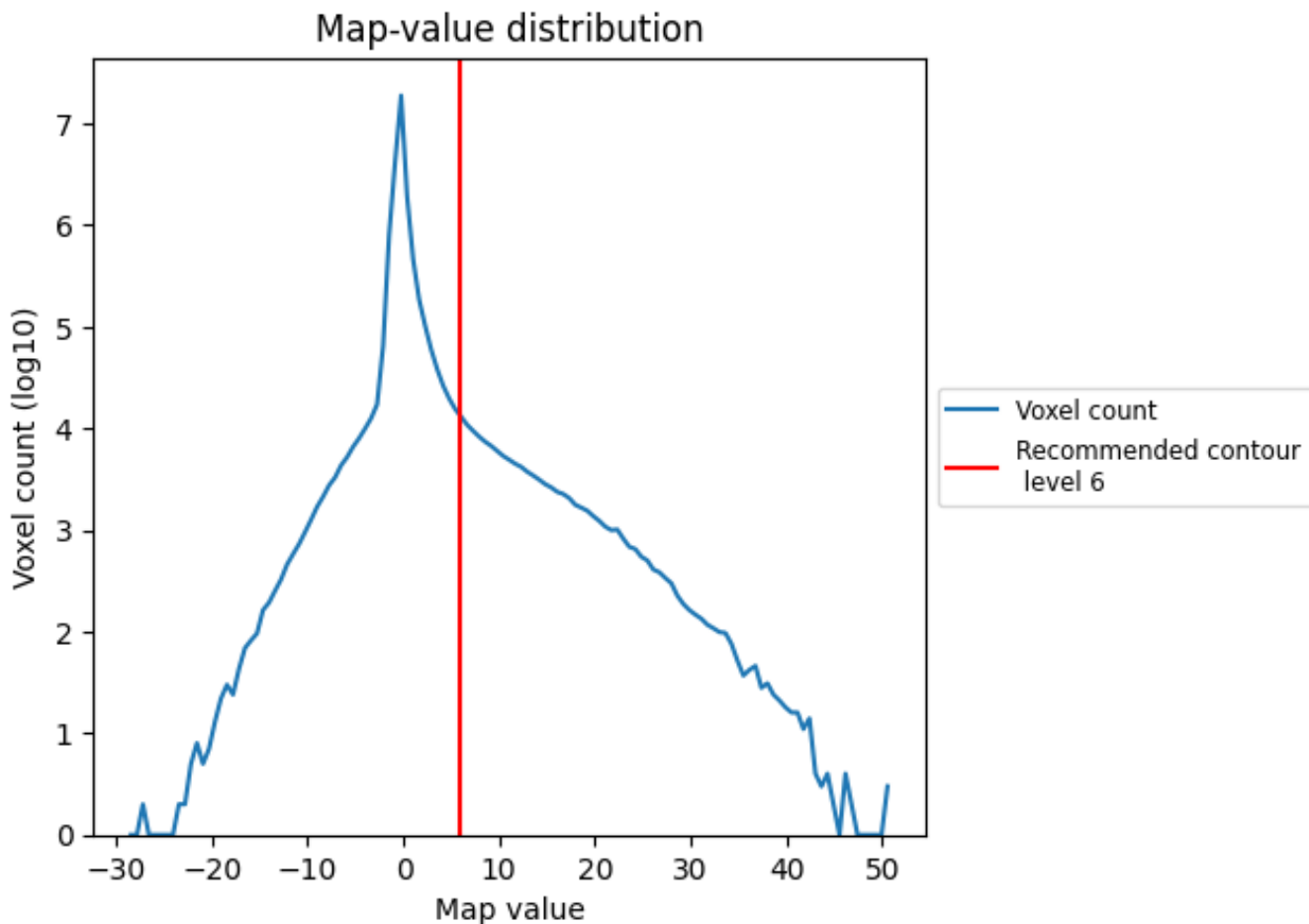
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

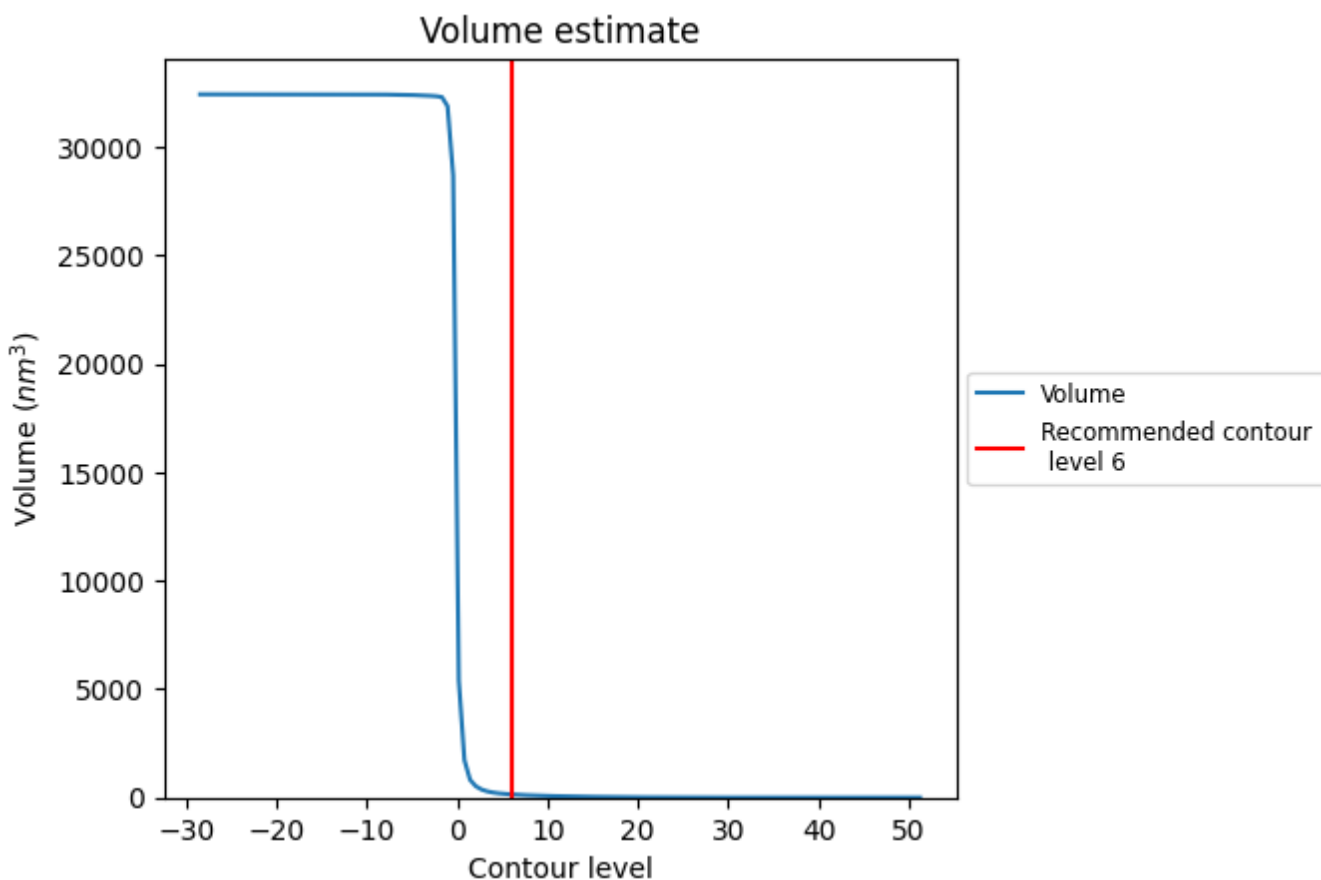
This section contains the results of statistical analysis of the map.

### 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.

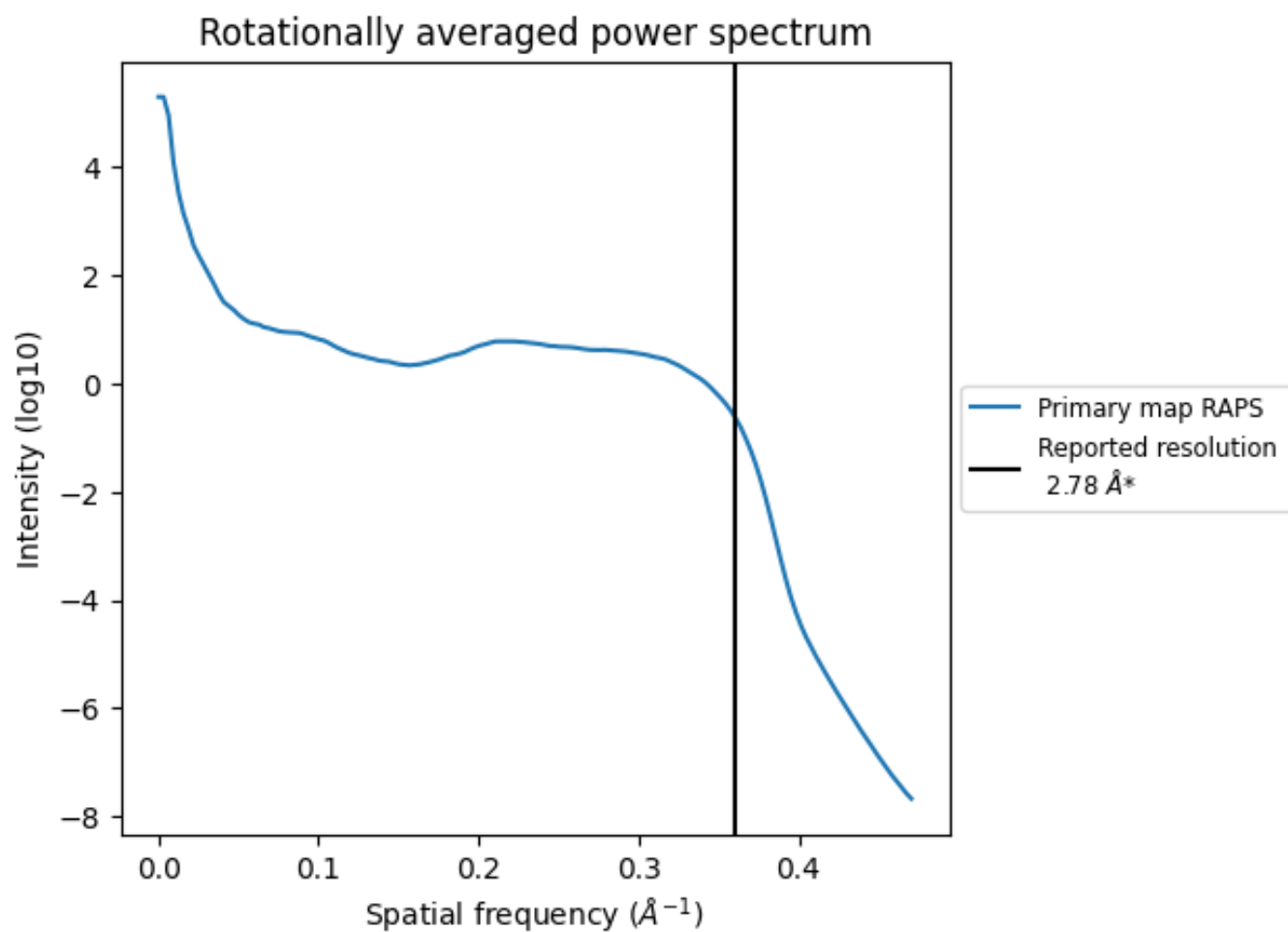
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 146 nm<sup>3</sup>; this corresponds to an approximate mass of 132 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  $0.360 \text{\AA}^{-1}$

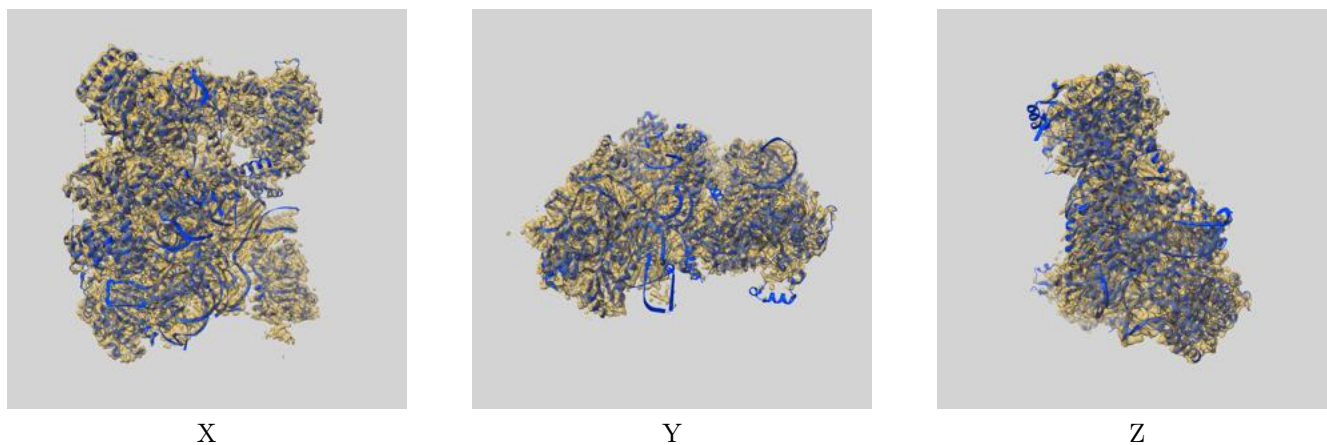
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75580 and PDB model 11AA. Per-residue inclusion information can be found in section 3 on page 7.

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



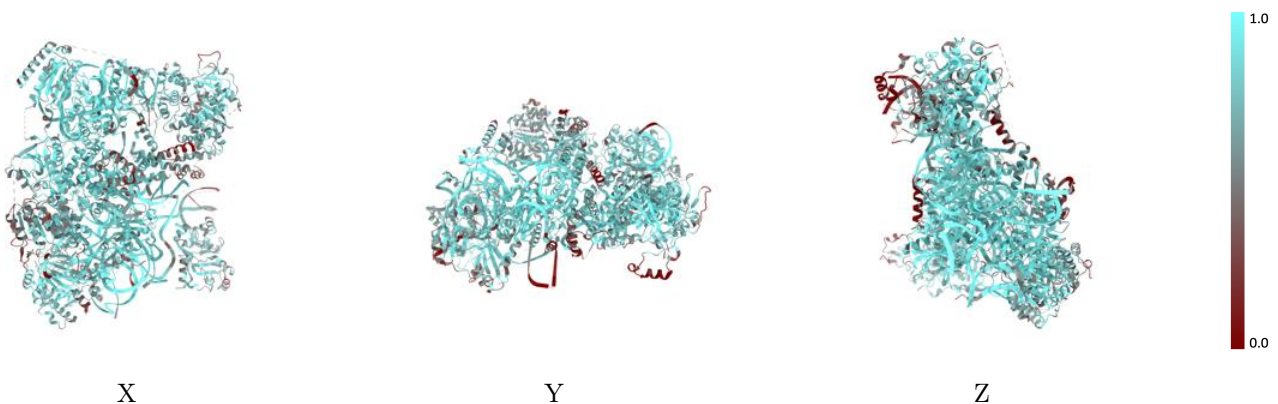
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



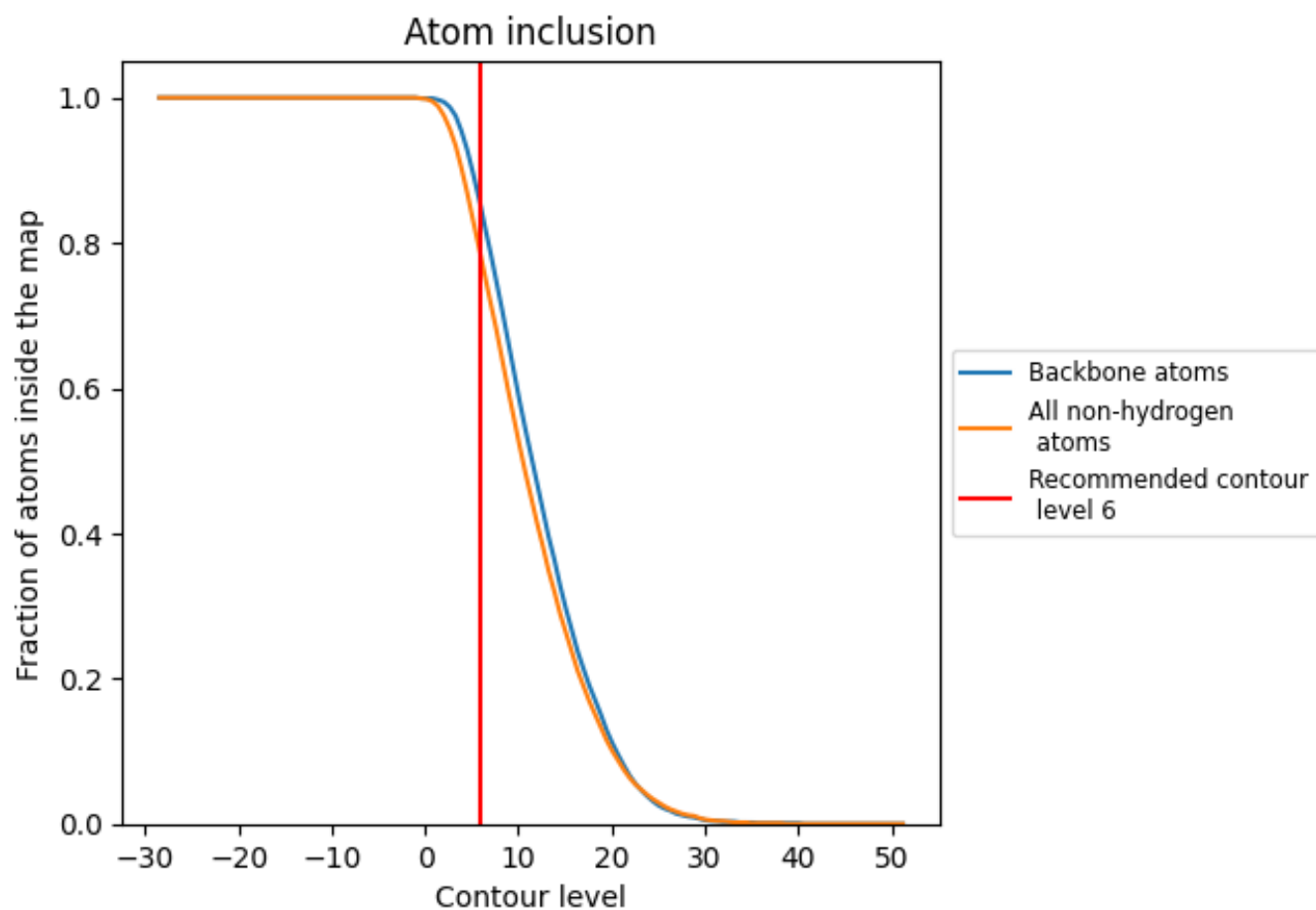
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6).





































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 78% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.5720
1	 0.8770	 0.5940
2	 0.7030	 0.5040
3	 0.9140	 0.6050
7	 0.5070	 0.5600
G	 0.8210	 0.6130
H	 0.6400	 0.4510
K	 0.8470	 0.5990
L	 0.7320	 0.5430
N	 0.8990	 0.6200
b	 0.8290	 0.5650
i	 0.7870	 0.5670
m	 0.7410	 0.5040
n	 0.6960	 0.5740
o	 0.8390	 0.5980
p	 0.7380	 0.5690
s	 0.5390	 0.5260
t	 0.8270	 0.6080

