



## wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 08:51 PM EDT

PDB ID : 5U0P  
EMDB ID : EMD-8479  
Title : Cryo-EM structure of the transcriptional Mediator  
Authors : Tsai, K.-L.; Yu, X.; Gopalan, S.; Chao, T.-C.; Zhang, Y.; Florens, L.; Washburn, M.P.; Murakami, K.; Conaway, R.C.; Conaway, J.W.; Asturias, F.  
Deposited on : 2016-11-26  
Resolution : 4.40 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) : 2.31.2

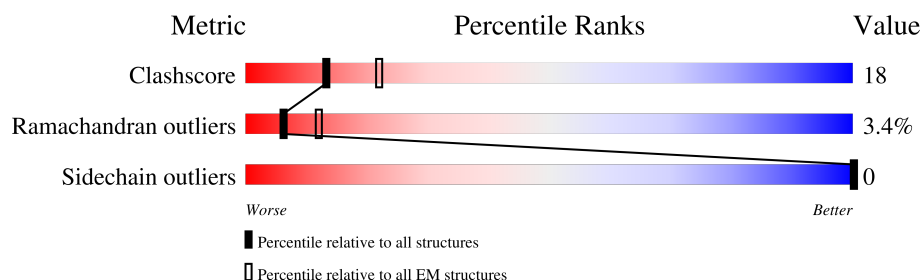
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.40 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.










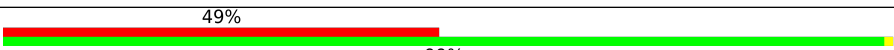
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	N	931	
2	F	216	
3	H	200	
4	Q	545	
5	R	207	
6	T	193	
7	K	116	
8	V	136	

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Mol	Chain	Length	Quality of chain
9	D	239	
10	G	376	
11	U	138	
12	3	139	
13	I	121	
14	2	273	
15	S	139	
16	J	132	

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 20268 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 Mediator complex subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	520	Total	C	N	O	S	0	0
			3887	2498	683	698	8		

- Molecule 2 is a protein called Mediator complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	195	Total	C	N	O	S	0	0
			1590	1014	266	301	9		

- Molecule 3 is a protein called Mediator complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	182	Total	C	N	O	S	0	0
			1493	941	257	292	3		

- Molecule 4 is a protein called Mediator complex subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Q	508	Total	C	N	O	S	0	0
			3831	2419	659	734	19		

- Molecule 5 is a protein called Mediator complex subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	207	Total	C	N	O	S	0	0
			1694	1082	288	316	8		

- Molecule 6 is a protein called Mediator complex subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	179	Total	C	N	O	S	0	0
			1455	950	237	263	5		

- Molecule 7 is a protein called Mediator complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	98	Total	C	N	O	S	0	0
			769	486	128	154	1		

- Molecule 8 is a protein called Mediator complex subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	118	Total	C	N	O	S	0	0
			949	599	161	187	2		

- Molecule 9 is a protein called Mediator complex subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	D	96	Total	C	N	O	0	0
			480	288	96	96		

- Molecule 10 is a protein called Mediator complex subunit 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	G	194	Total	C	N	O	0	0
			965	577	194	194		

- Molecule 11 is a protein called Mediator complex subunit 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	U	122	Total	C	N	O	0	0
			608	364	122	122		

- Molecule 12 is a protein called Mediator complex subunit 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	3	103	Total	C	N	O	0	0
			515	309	103	103		

- Molecule 13 is a protein called Mediator complex subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	I	75	Total	C	N	O	0	0
			374	224	75	75		

- Molecule 14 is a protein called Mediator complex subunit 27.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	2	78	Total	C	N	O	0	0
			388	232	78	78		

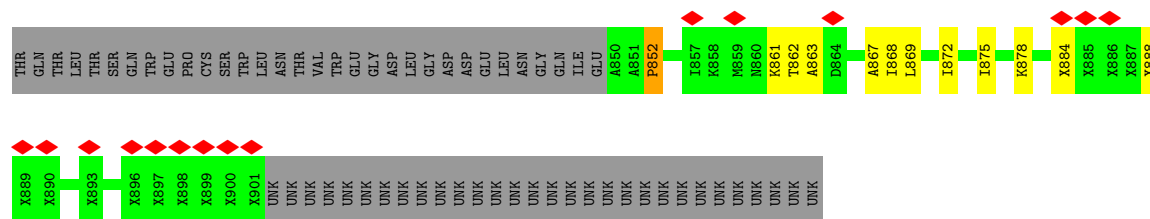
- Molecule 15 is a protein called Mediator complex subunit 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	S	122	Total	C	N	O	0	0
			610	366	122	122		

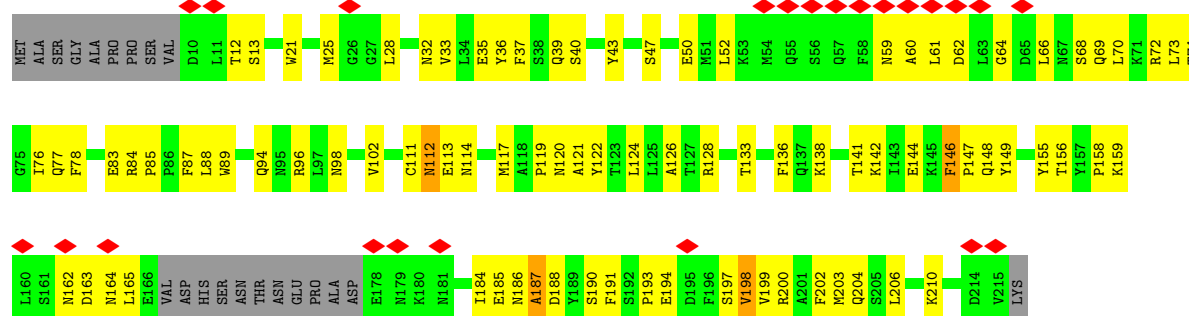
- Molecule 16 is a protein called Mediator complex subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	J	132	Total	C	N	O	0	0
			660	396	132	132		

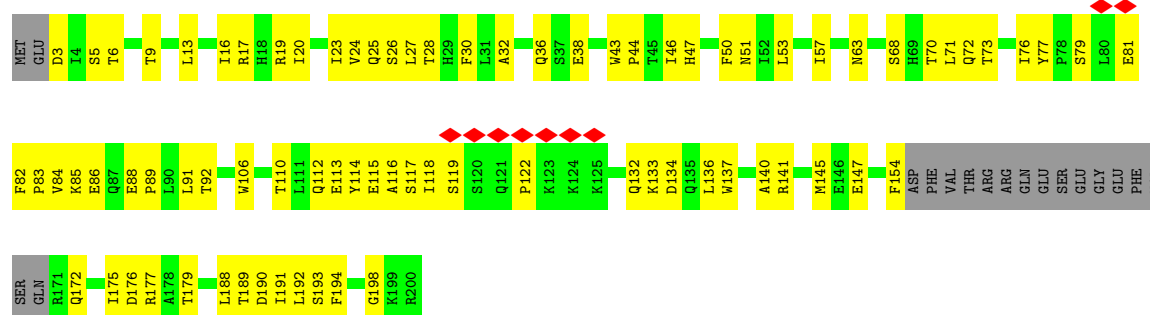




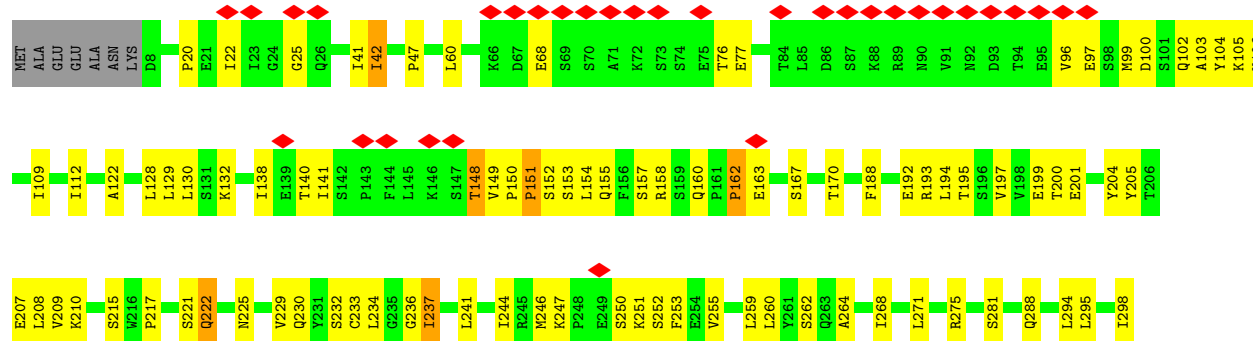
• Molecule 2: Mediator complex subunit 6



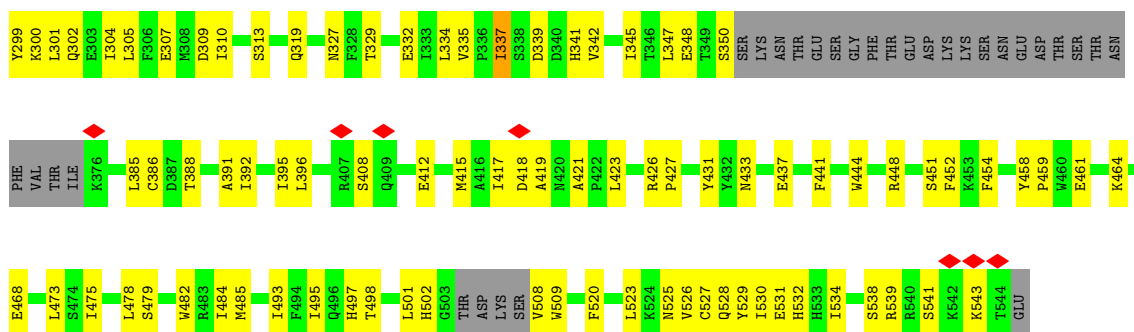
• Molecule 3: Mediator complex subunit 8



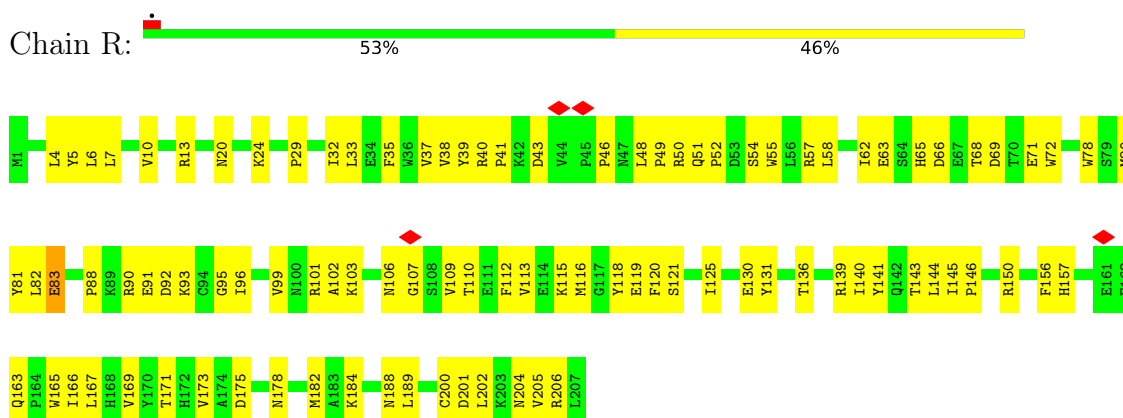
• Molecule 4: Mediator complex subunit 17



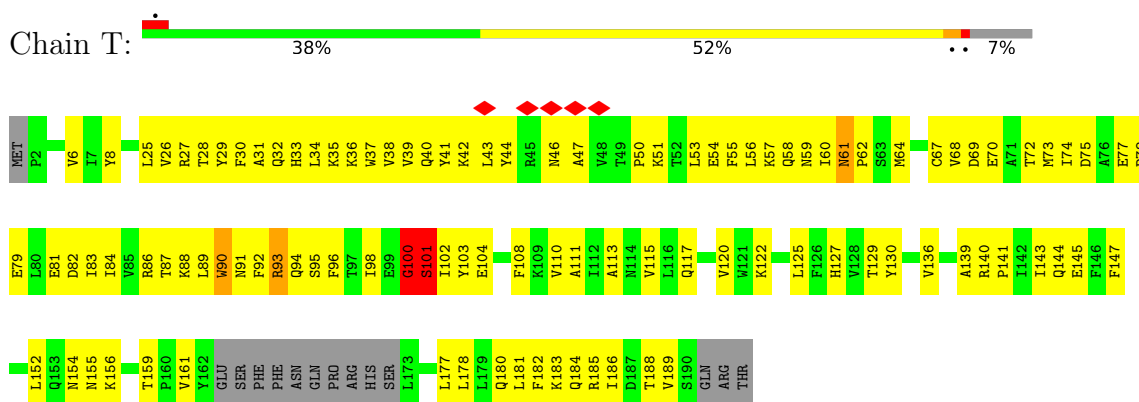




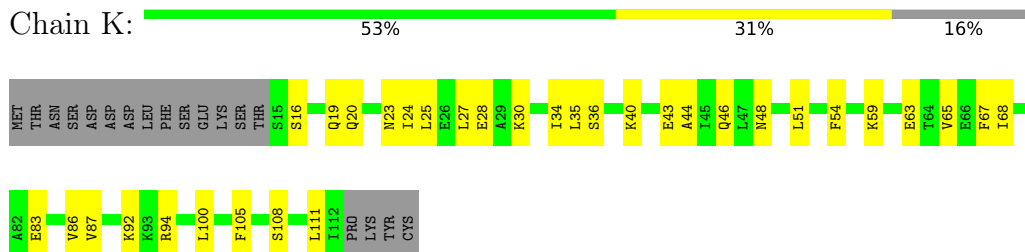
• Molecule 5: Mediator complex subunit 18



• Molecule 6: Mediator complex subunit 20



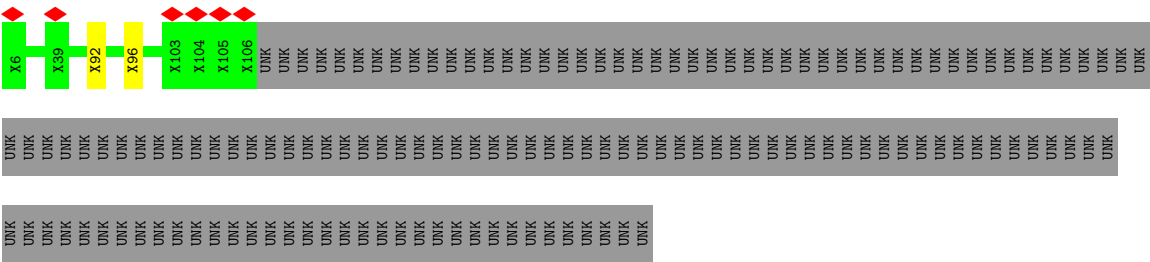
• Molecule 7: Mediator complex subunit 11



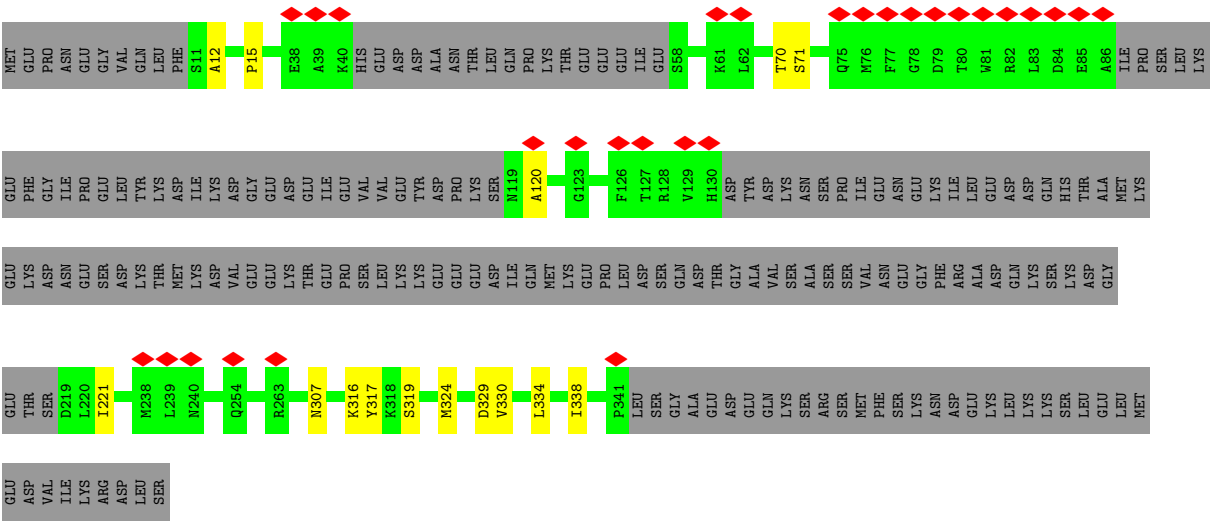
• Molecule 8: Mediator complex subunit 22



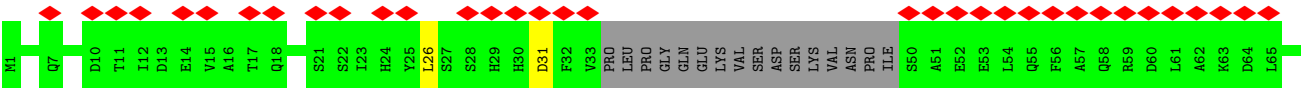
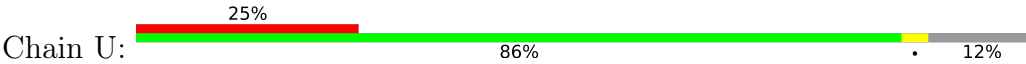
• Molecule 9: Mediator complex subunit 4



• Molecule 10: Mediator complex subunit 7



• Molecule 11: Mediator complex subunit 21





The diagram illustrates a sequence of 40 numbered boxes (X1 to X40) arranged in two rows. The top row contains boxes X1 through X40, and the bottom row contains boxes X192 through X342. Each box is green with a red diamond on top. The boxes are connected by lines, indicating a sequence or flow. The top row has a continuous sequence of boxes, while the bottom row has a sequence of boxes with gaps between them.

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42484	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 ( $e^-/\text{\AA}^2$ )	9.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.017	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	461.12, 461.12, 461.12	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	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	N	0.33	0/3865	0.57	5/5275 (0.1%)
2	F	0.27	0/1629	0.47	0/2209
3	H	0.28	0/1523	0.44	0/2063
4	Q	0.32	0/3901	0.46	2/5286 (0.0%)
5	R	0.30	0/1739	0.48	0/2362
6	T	0.67	2/1489 (0.1%)	0.71	4/2020 (0.2%)
7	K	0.31	0/778	0.49	0/1049
8	V	0.30	0/963	0.46	0/1309
10	G	0.26	0/961	0.42	0/1336
11	U	0.23	0/606	0.42	0/844
12	3	0.27	0/514	0.47	1/718 (0.1%)
13	I	0.24	0/373	0.44	0/520
14	2	0.25	0/382	0.36	0/524
All	All	0.34	2/18723 (0.0%)	0.50	12/25515 (0.0%)

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	T	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	T	100	GLY	C-O	19.55	1.54	1.23
6	T	100	GLY	C-N	10.44	1.58	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	T	100	GLY	O-C-N	-12.32	102.99	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	T	100	GLY	CA-C-N	12.21	144.07	117.20
6	T	101	SER	N-CA-CB	-9.02	96.97	110.50
1	N	194	PRO	CA-N-CD	-8.72	99.28	111.50
6	T	100	GLY	CA-C-O	-7.87	106.43	120.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	T	100	GLY	Peptide,Mainchain

## 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	N	3887	0	3543	216	0
2	F	1590	0	1527	73	0
3	H	1493	0	1467	71	0
4	Q	3831	0	3571	120	0
5	R	1694	0	1670	83	0
6	T	1455	0	1476	91	0
7	K	769	0	783	31	0
8	V	949	0	961	29	0
9	D	480	0	100	1	0
10	G	965	0	402	7	0
11	U	608	0	265	4	0
12	3	515	0	209	10	0
13	I	374	0	163	2	0
14	2	388	0	155	2	0
15	S	610	0	138	0	0
16	J	660	0	141	1	0
All	All	20268	0	16571	670	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 18.

The worst 5 of 670 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:N:191:PHE:CB	1:N:194:PRO:HG2	1.56	1.35
6:T:30:PHE:O	6:T:100:GLY:O	1.54	1.24
6:T:6:VAL:O	6:T:159:THR:HG22	1.39	1.20
1:N:191:PHE:HB3	1:N:194:PRO:CG	1.75	1.16
1:N:191:PHE:HB3	1:N:194:PRO:HG2	1.15	1.12

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	N	489/931 (52%)	391 (80%)	67 (14%)	31 (6%)	1	19
2	F	191/216 (88%)	166 (87%)	18 (9%)	7 (4%)	3	28
3	H	178/200 (89%)	171 (96%)	6 (3%)	1 (1%)	25	65
4	Q	502/545 (92%)	447 (89%)	39 (8%)	16 (3%)	4	30
5	R	205/207 (99%)	191 (93%)	11 (5%)	3 (2%)	10	46
6	T	175/193 (91%)	153 (87%)	14 (8%)	8 (5%)	2	24
7	K	96/116 (83%)	90 (94%)	6 (6%)	0	100	100
8	V	116/136 (85%)	108 (93%)	8 (7%)	0	100	100
10	G	186/376 (50%)	165 (89%)	15 (8%)	6 (3%)	4	30
11	U	118/138 (86%)	112 (95%)	5 (4%)	1 (1%)	19	60
12	3	101/139 (73%)	80 (79%)	12 (12%)	9 (9%)	1	12
13	I	73/121 (60%)	64 (88%)	7 (10%)	2 (3%)	5	34
14	2	66/273 (24%)	63 (96%)	1 (2%)	2 (3%)	4	31
All	All	2496/3591 (70%)	2201 (88%)	209 (8%)	86 (3%)	6	29

5 of 86 Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	N	215	PHE
1	N	257	PRO
1	N	431	VAL
1	N	544	VAL
1	N	852	PRO

### 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	N	369/799 (46%)	369 (100%)	0	100	100
2	F	177/198 (89%)	177 (100%)	0	100	100
3	H	168/185 (91%)	168 (100%)	0	100	100
4	Q	391/509 (77%)	391 (100%)	0	100	100
5	R	191/191 (100%)	191 (100%)	0	100	100
6	T	164/178 (92%)	164 (100%)	0	100	100
7	K	88/108 (82%)	88 (100%)	0	100	100
8	V	112/129 (87%)	112 (100%)	0	100	100
All	All	1660/2297 (72%)	1660 (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 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	63	ASN
6	T	59	ASN
4	Q	319	GLN
7	K	75	GLN
5	R	148	GLN

### 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](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	S	6
16	J	3
9	D	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	56:UNK	C	160:UNK	N	37.47
1	J	204:UNK	C	310:UNK	N	31.08
1	S	265:UNK	C	271:UNK	N	28.46
1	S	366:UNK	C	381:UNK	N	26.50
1	S	287:UNK	C	301:UNK	N	18.90

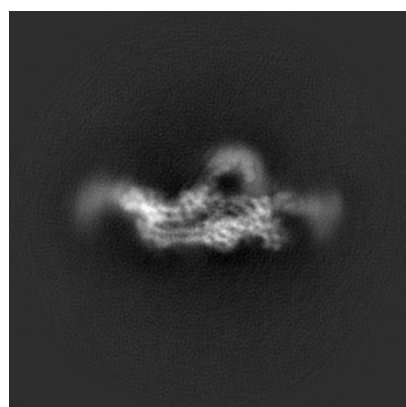
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8479. These allow visual inspection of the internal detail of the map and identification of artifacts.

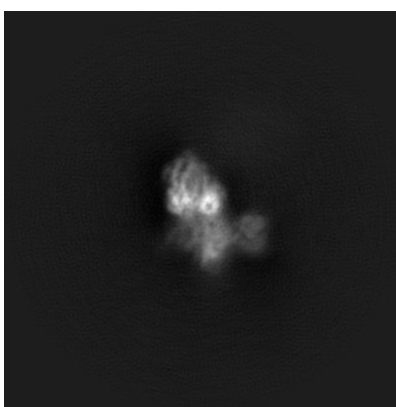
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

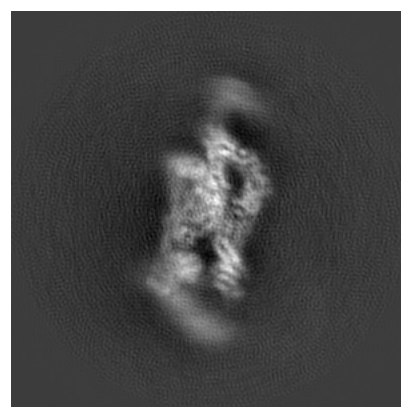
#### 6.1.1 Primary map



X



Y

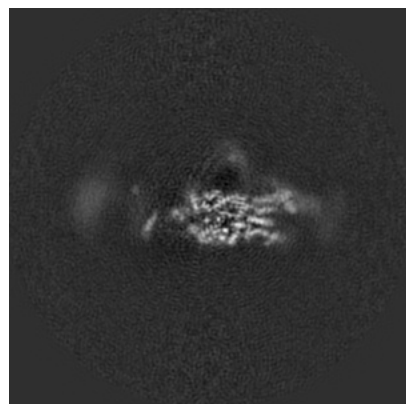


Z

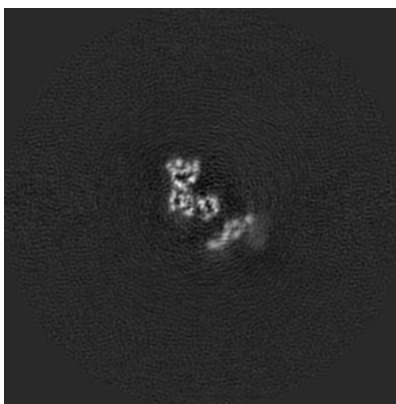
The images above show the map projected in three orthogonal directions.

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

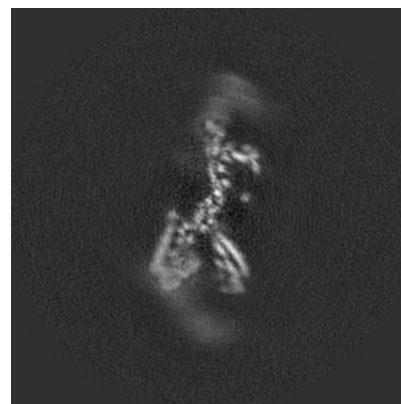
#### 6.2.1 Primary map



X Index: 176



Y Index: 176

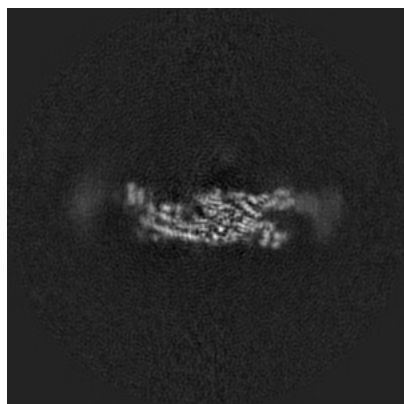


Z Index: 176

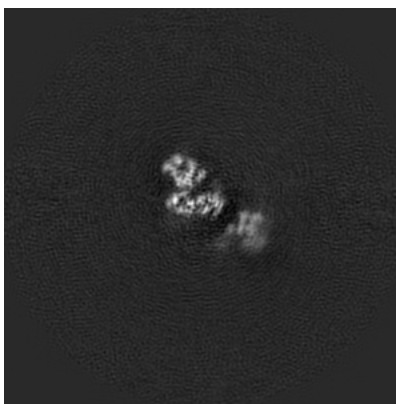
The images above show central slices of the map in three orthogonal directions.

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

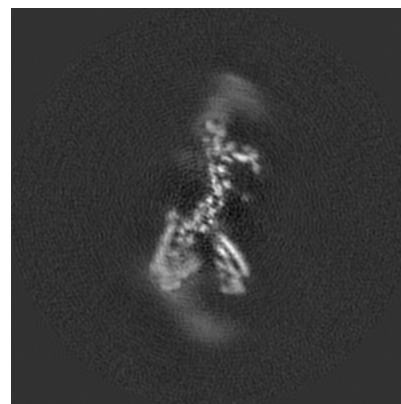
### 6.3.1 Primary map



X Index: 183



Y Index: 183



Z Index: 177

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 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

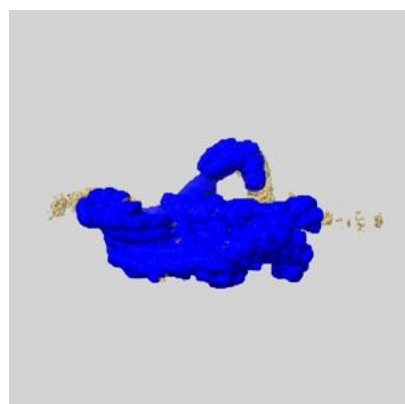
## 6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

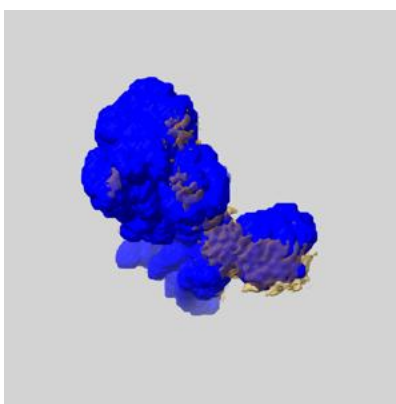
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

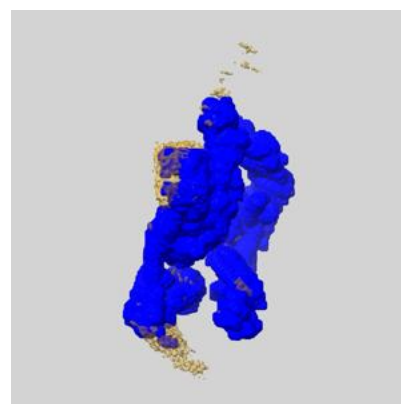
### 6.5.1 emd\_8479\_msk\_1.map [i](#)



X



Y

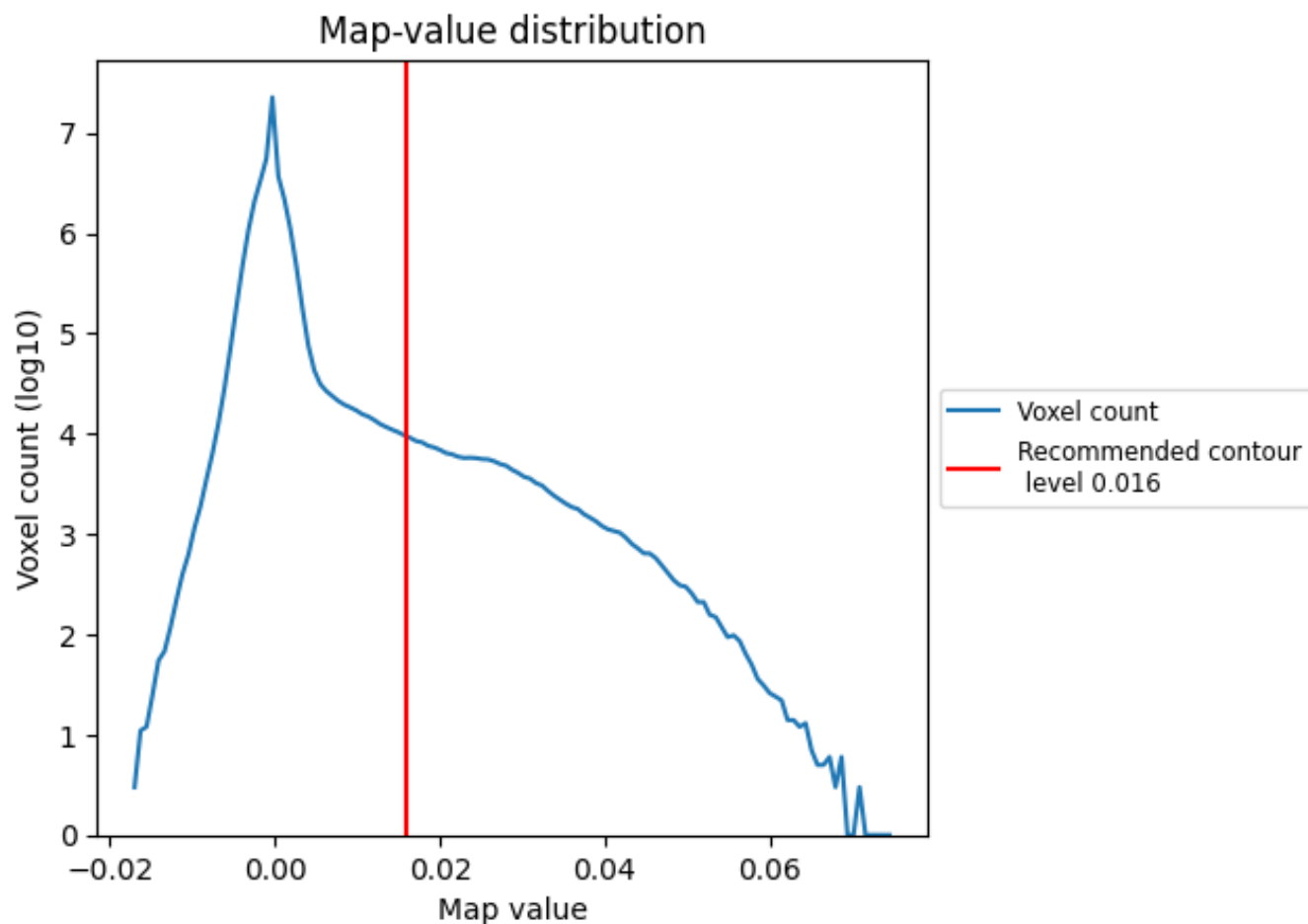


Z

## 7 Map analysis [i](#)

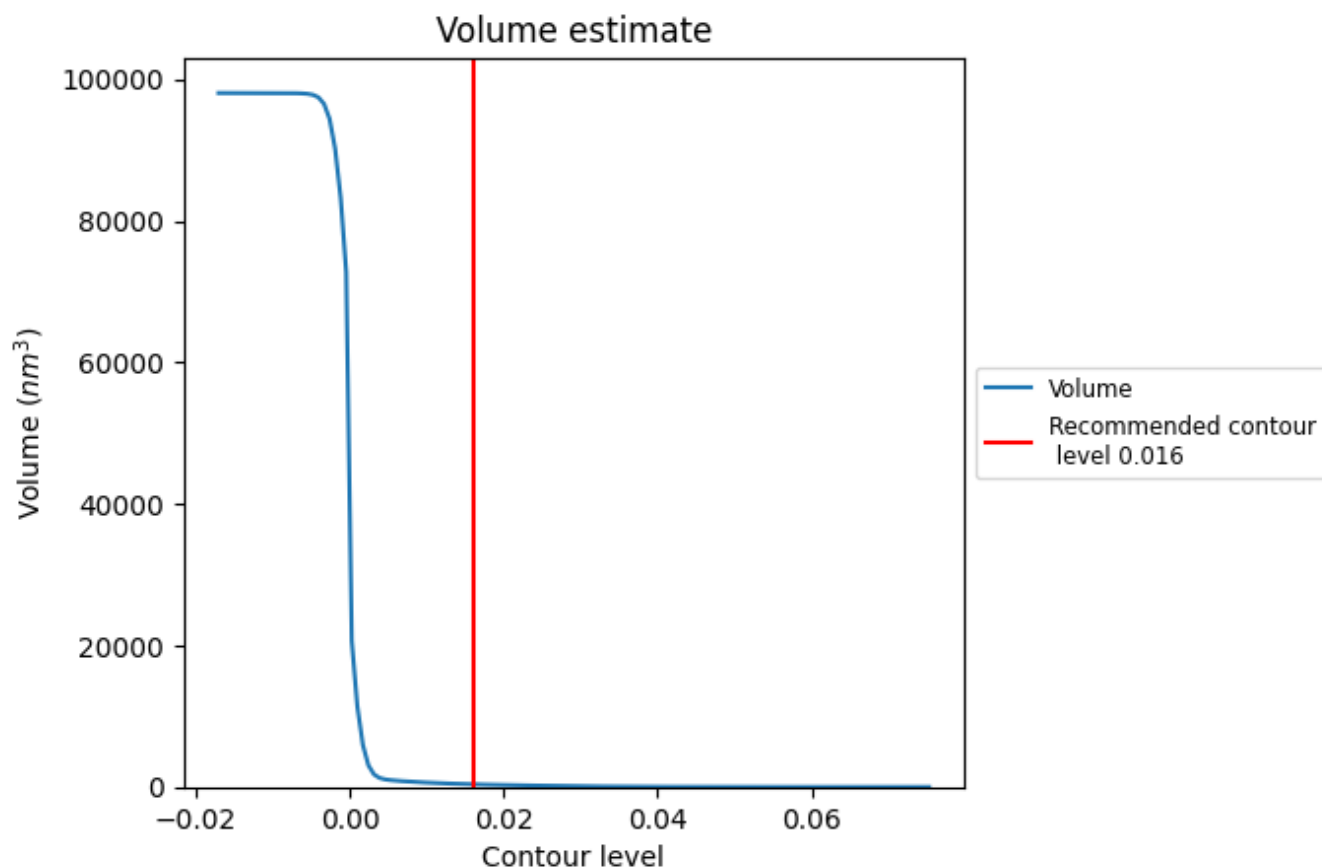
This section contains the results of statistical analysis of the map.

### 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.

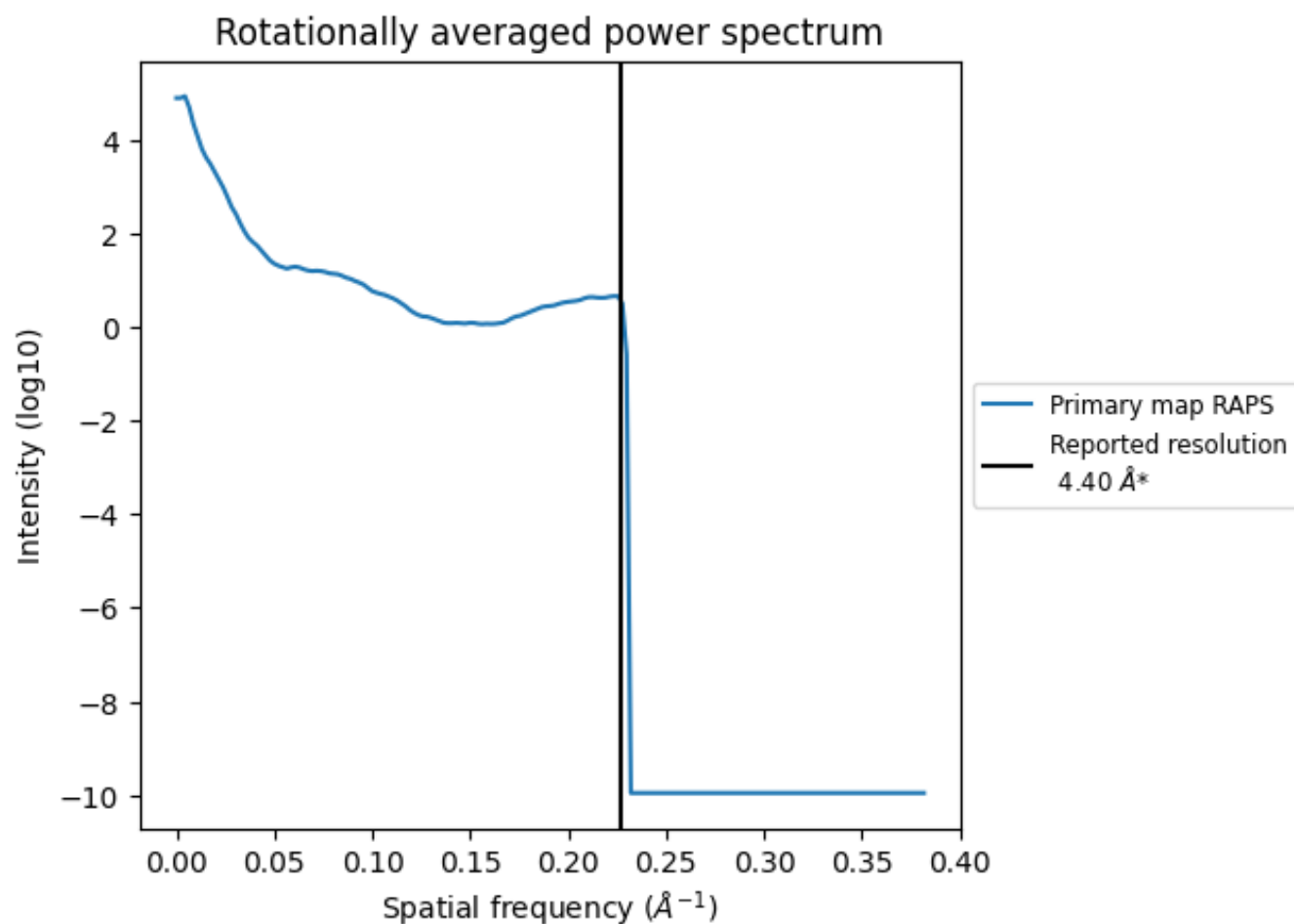
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 375 nm<sup>3</sup>; this corresponds to an approximate mass of 339 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 ⓘ



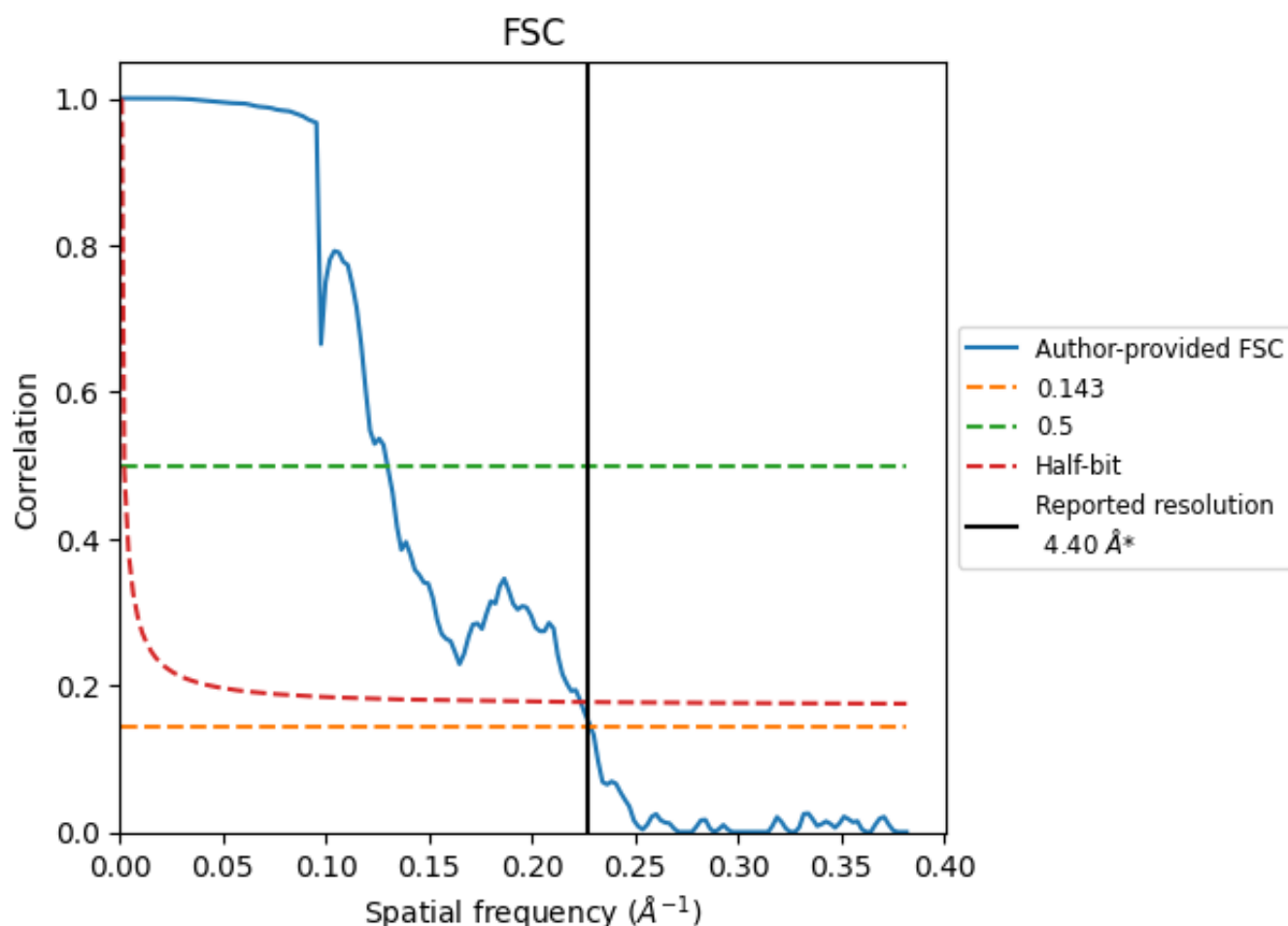
\*Reported resolution corresponds to spatial frequency of 0.227 Å<sup>-1</sup>



## 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 0.227 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

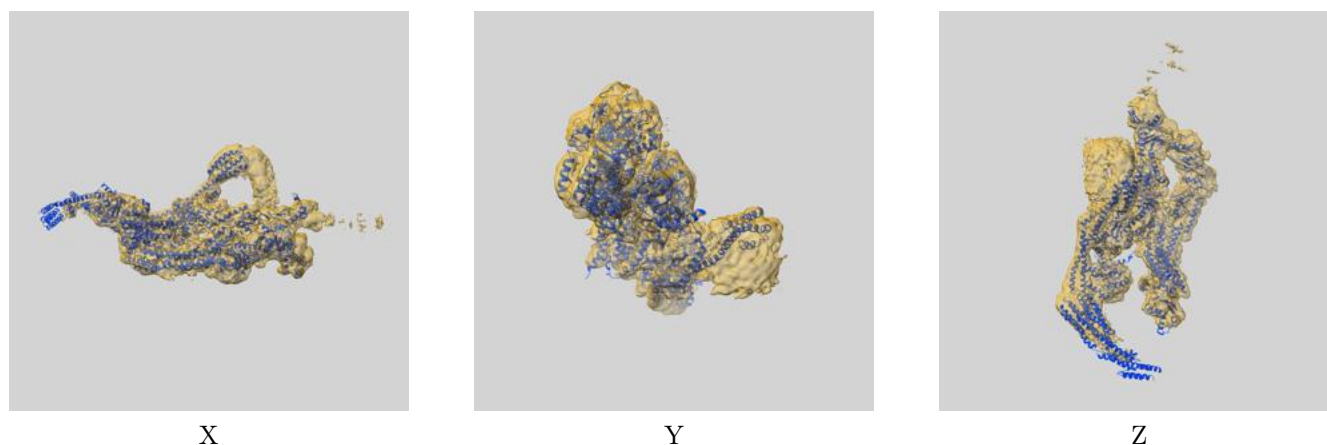
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.38	7.70	4.47
Unmasked-calculated*	-	-	-

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

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

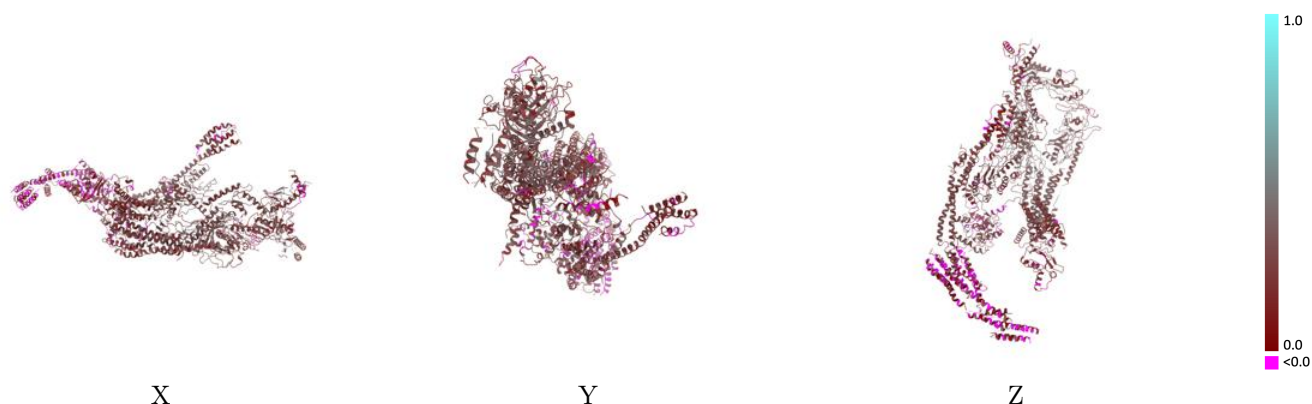
This section contains information regarding the fit between EMDB map EMD-8479 and PDB model 5U0P. Per-residue inclusion information can be found in section [3](#) on page [7](#).

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



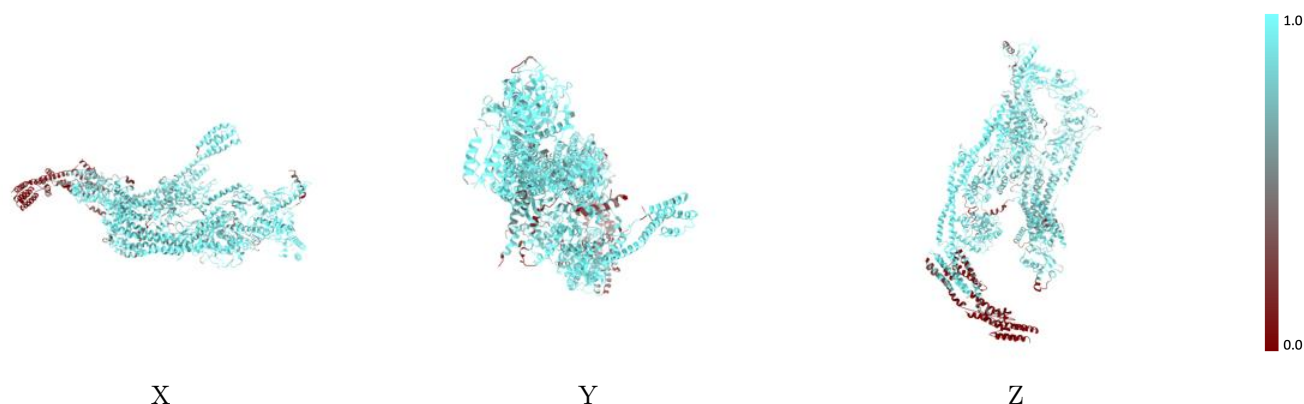
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



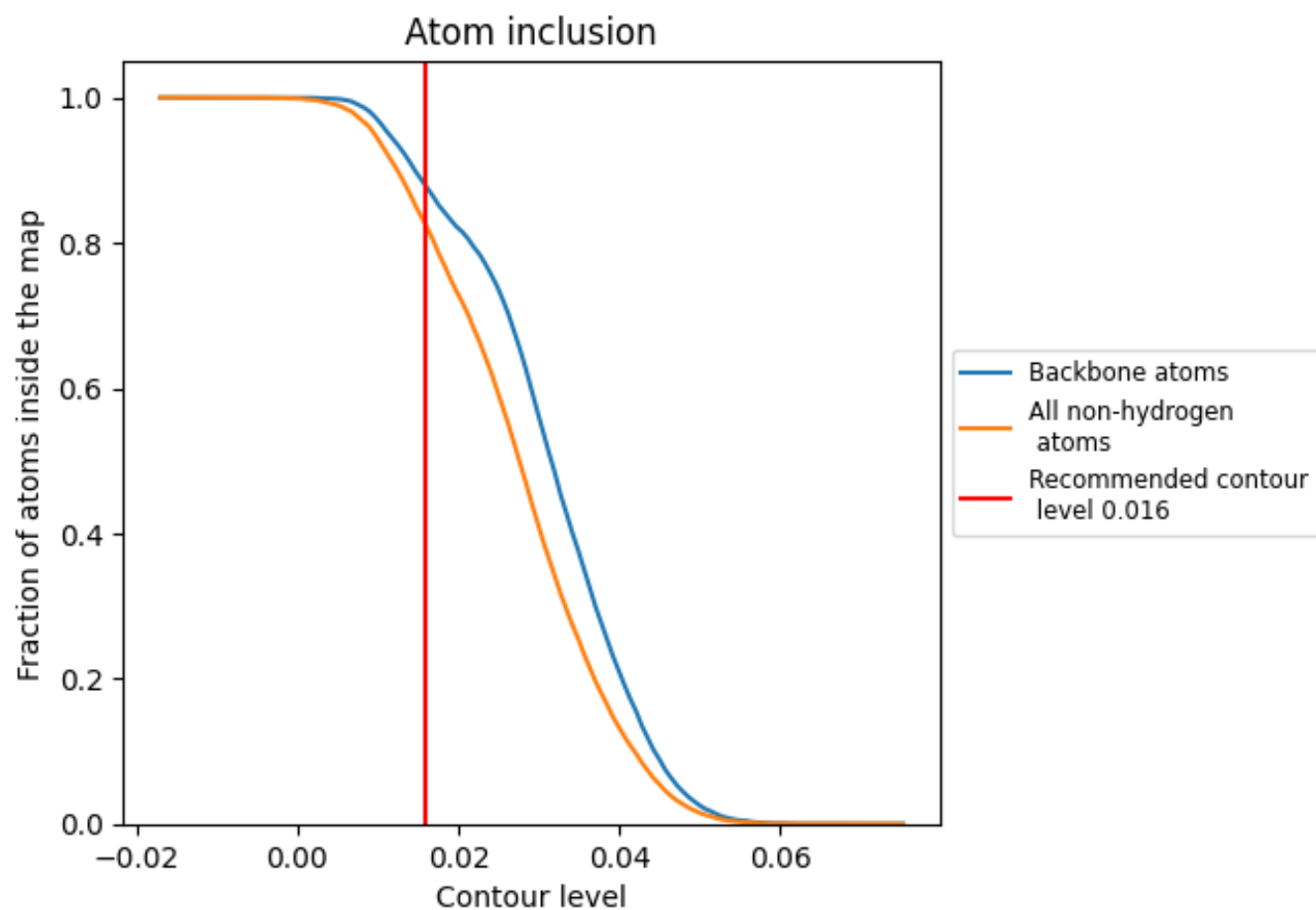
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).



































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 82% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8242	 0.2360
2	 0.9845	 0.3370
3	 0.9437	 0.1970
D	 0.9167	 0.2030
F	 0.7729	 0.2050
G	 0.8528	 0.1470
H	 0.8496	 0.2330
I	 0.9465	 0.2020
J	 0.5015	 0.0640
K	 0.9012	 0.2780
N	 0.8710	 0.2620
Q	 0.8372	 0.2720
R	 0.8903	 0.2900
S	 0.0393	 0.0540
T	 0.9029	 0.2510
U	 0.7039	 0.1750
V	 0.8852	 0.2750

