



## wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 08:07 pm BST

PDB ID : 6FTX  
EMDB ID : EMD-4318  
Title : Structure of the chromatin remodelling enzyme Chd1 bound to a ubiquitiny-  
lated nucleosome  
Authors : Sundaramoorthy, R.; Owen-hughes, T.; Norman, D.G.; Hughes, A.  
Deposited on : 2018-02-25  
Resolution : 4.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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>.

---

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
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) : 2.39

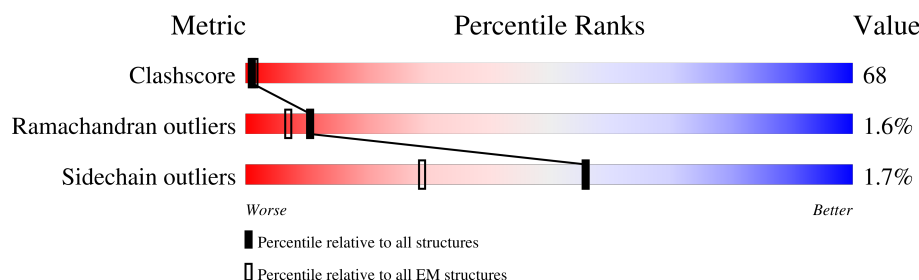
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.50 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

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	97	
2	B	103	
2	F	103	
3	C	130	
3	G	130	
4	D	126	
4	H	126	
5	E	110	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
6	I	159	
7	J	160	
8	N	76	
8	O	76	
9	W	878	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	ADP	W	1302	-	-	X	-

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 21049 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 Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	97	Total	C	N	O	S	0	0
			802	506	155	138	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	83	Total	C	N	O	S	0	0
			662	418	129	114	1		
2	F	92	Total	C	N	O	S	0	0
			686	430	134	121	1		

- Molecule 3 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	103	Total	C	N	O	0	0
			795	501	155	139		
3	G	105	Total	C	N	O	0	0
			809	510	158	141		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	99	ARG	GLY	conflict	UNP P06897
G	99	ARG	GLY	conflict	UNP P06897

- Molecule 4 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	95	Total	C	N	O	S	0	0
			745	469	134	140	2		
4	H	93	Total	C	N	O	S	0	0
			726	457	130	137	2		

- Molecule 5 is a protein called Histone H3.3C.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	110	Total	C	N	O	S	0	0
			866	543	168	152	3		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	26	ALA	-	expression tag	UNP P02302
E	27	ALA	-	expression tag	UNP P02302
E	28	ALA	-	expression tag	UNP P02302
E	30	ALA	PRO	conflict	UNP P02302
E	32	ALA	THR	conflict	UNP P02302
E	33	ALA	GLY	conflict	UNP P02302
E	34	ALA	GLY	conflict	UNP P02302
E	35	ALA	VAL	conflict	UNP P02302
E	36	ALA	LYS	conflict	UNP P02302
E	37	ALA	LYS	conflict	UNP P02302
E	38	ALA	PRO	conflict	UNP P02302
E	86	SER	ARG	conflict	UNP P02302

- Molecule 6 is a DNA chain called DNA (159-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	159	Total	C	N	O	P	0	0
			3238	1537	590	952	159		

- Molecule 7 is a DNA chain called DNA (160-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	160	Total	C	N	O	P	0	0
			3298	1562	616	961	159		

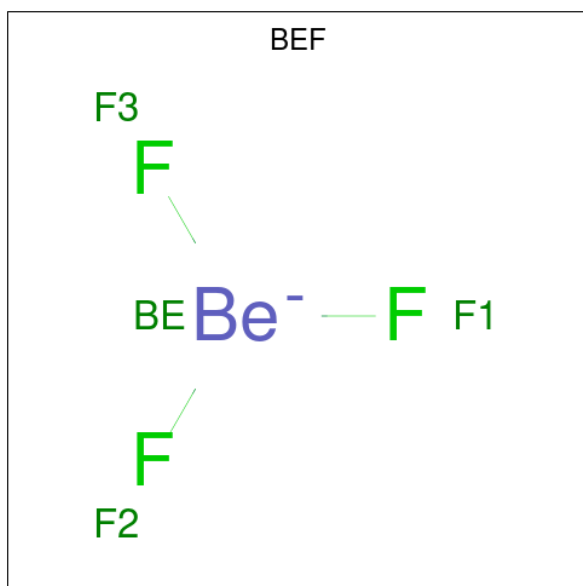
- Molecule 8 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	76	Total	C	N	O	S	0	0
			601	378	105	117	1		
8	O	76	Total	C	N	O	S	0	0
			601	378	105	117	1		

- Molecule 9 is a protein called Chromatin-remodeling ATPase.

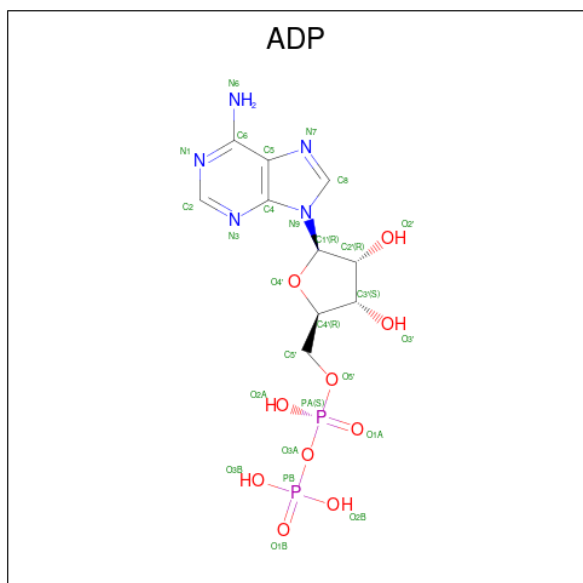
Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	878	Total	C	N	O	S	2	0
			7189	4568	1260	1334	27		

- Molecule 10 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF<sub>3</sub>).



Mol	Chain	Residues	Atoms			AltConf
10	W	1	Total	Be	F	0
			4	1	3	

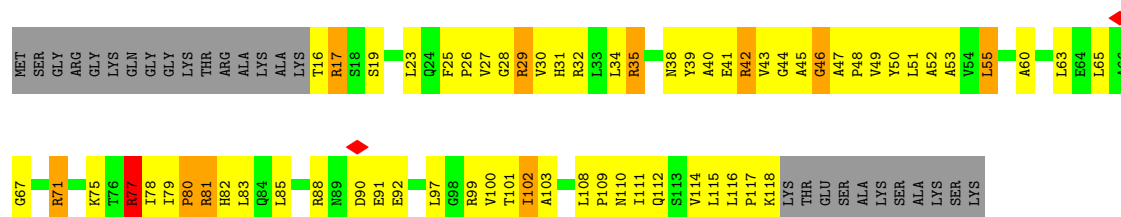
- Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



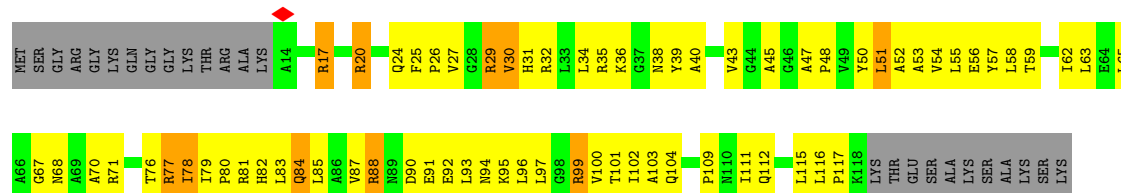
Mol	Chain	Residues	Atoms					AltConf
11	W	1	Total	C	N	O	P	0
			27	10	5	10	2	



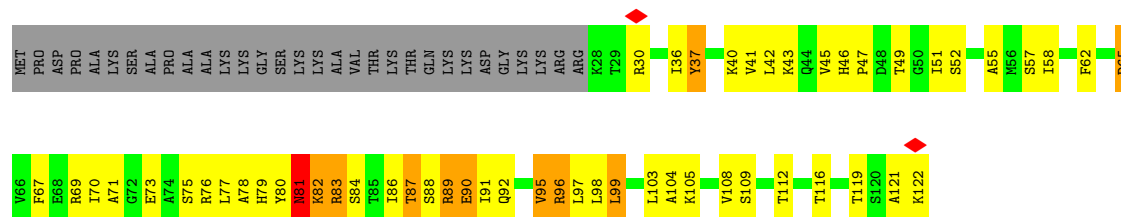




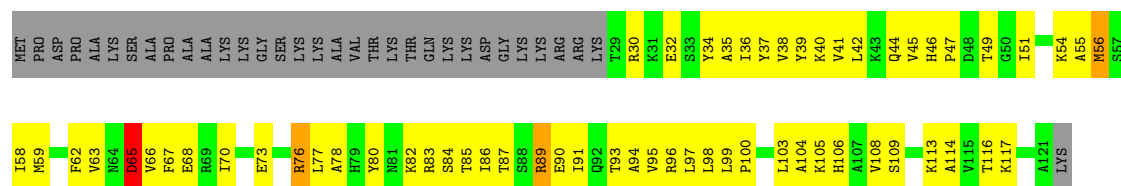
• Molecule 3: Histone H2A type 1



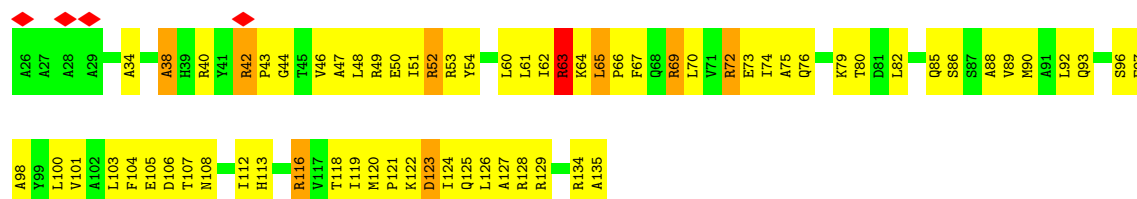
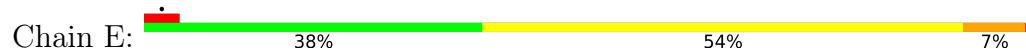
• Molecule 4: Histone H2B



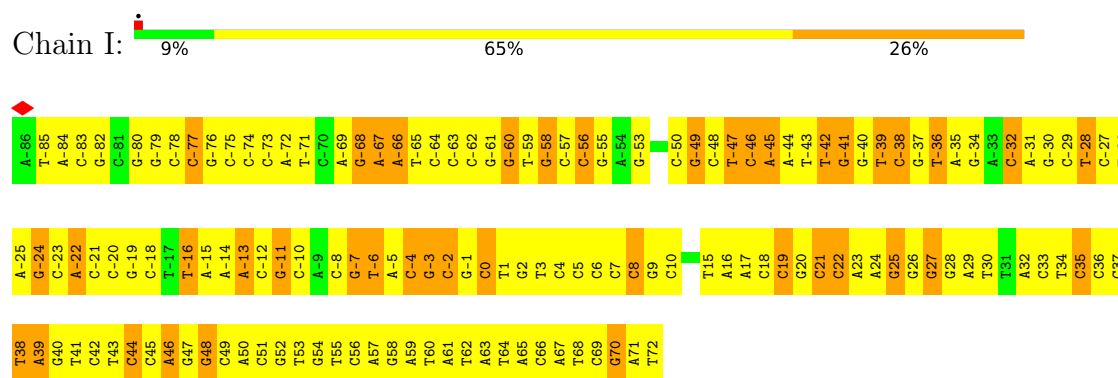
• Molecule 4: Histone H2B



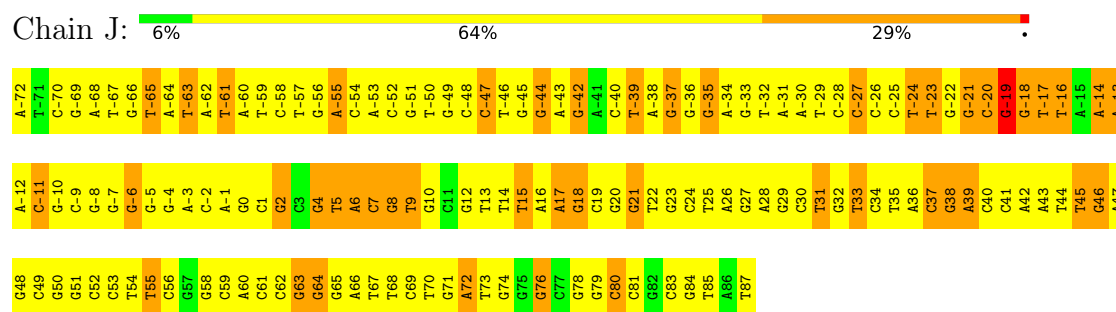
• Molecule 5: Histone H3.3C



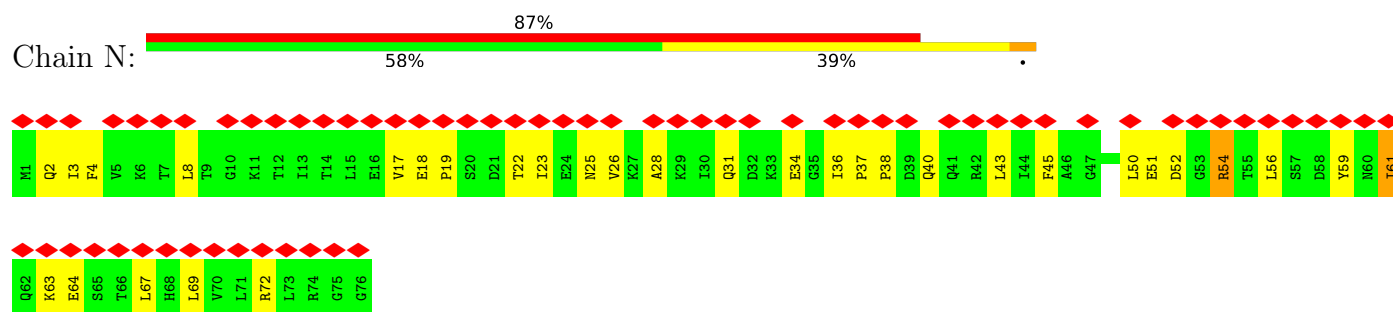
• Molecule 6: DNA (159-MER)



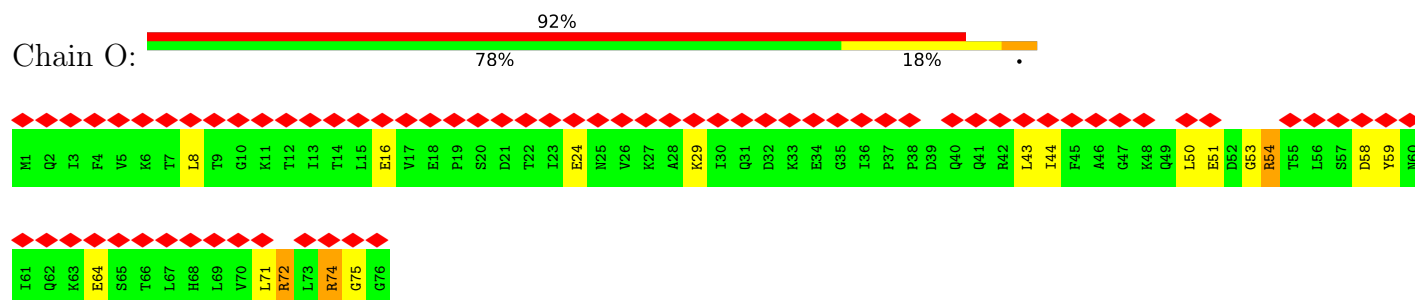
• Molecule 7: DNA (160-MER)



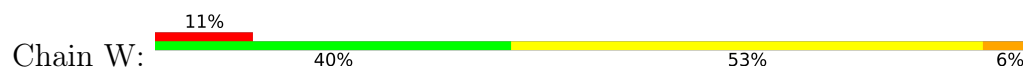
• Molecule 8: Polyubiquitin-B



• Molecule 8: Polyubiquitin-B



• Molecule 9: Chromatin-remodeling ATPase





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	135000	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 ( $e^-/\text{\AA}^2$ )	1.25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	35714	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.118	Depositor
Minimum map value	-0.041	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	336.0, 336.0, 336.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BEF, ADP

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	1.12	6/814 (0.7%)	1.47	10/1092 (0.9%)
2	B	1.14	5/669 (0.7%)	1.69	9/894 (1.0%)
2	F	1.20	5/693 (0.7%)	1.57	11/929 (1.2%)
3	C	1.31	7/805 (0.9%)	1.53	5/1088 (0.5%)
3	G	1.16	3/819 (0.4%)	1.37	5/1106 (0.5%)
4	D	1.20	6/756 (0.8%)	1.37	5/1015 (0.5%)
4	H	1.10	2/737 (0.3%)	1.40	5/993 (0.5%)
5	E	1.01	3/877 (0.3%)	1.33	3/1179 (0.3%)
6	I	1.20	12/3628 (0.3%)	1.35	40/5591 (0.7%)
7	J	1.21	20/3703 (0.5%)	1.35	52/5720 (0.9%)
8	N	0.87	0/607	0.97	1/816 (0.1%)
8	O	0.95	1/607 (0.2%)	0.99	2/816 (0.2%)
9	W	1.03	22/7334 (0.3%)	1.14	20/9875 (0.2%)
All	All	1.12	92/22049 (0.4%)	1.30	168/31114 (0.5%)

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
1	A	0	7
2	B	0	5
2	F	0	7
3	C	0	7
3	G	0	4
4	D	0	3
4	H	0	4
5	E	0	6
6	I	0	1
7	J	0	2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
8	N	0	1
8	O	0	4
9	W	0	17
All	All	0	68

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	I	-2	DC	C4'-O4'	14.73	1.59	1.45
4	D	73	GLU	CD-OE2	10.86	1.37	1.25
9	W	669	GLU	CD-OE2	-10.79	1.13	1.25
6	I	27	DG	O3'-P	-10.78	1.48	1.61
9	W	826	GLU	CD-OE2	-10.39	1.14	1.25

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	0	DC	O5'-P-OP2	-18.68	88.29	110.70
6	I	-3	DG	O5'-P-OP1	-16.02	91.28	105.70
7	J	39	DA	O5'-P-OP2	15.95	129.84	110.70
2	B	40	ARG	NE-CZ-NH1	-15.68	112.46	120.30
6	I	-16	DT	O5'-P-OP2	-15.24	91.98	105.70

There are no chirality outliers.

5 of 68 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	40	ARG	Sidechain
1	A	42	ARG	Sidechain
1	A	49	ARG	Sidechain
1	A	63	ARG	Sidechain
1	A	69	ARG	Sidechain

## 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	A	802	0	841	149	0
2	B	662	0	709	151	0
2	F	686	0	693	144	0
3	C	795	0	846	159	0
3	G	809	0	864	160	0
4	D	745	0	773	114	0
4	H	726	0	747	119	0
5	E	866	0	903	139	0
6	I	3238	0	1783	520	0
7	J	3298	0	1798	559	0
8	N	601	0	629	64	0
8	O	601	0	629	18	0
9	W	7189	0	7208	905	0
10	W	4	0	0	0	0
11	W	27	0	12	12	0
All	All	21049	0	18435	2630	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 68.

The worst 5 of 2630 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)
5:E:63:ARG:NH1	6:I:17:DA:C5'	1.73	1.51
5:E:63:ARG:NH1	6:I:17:DA:H5''	1.26	1.47
5:E:61:LEU:CD1	2:F:37:LEU:HA	1.50	1.41
9:W:345:LYS:HB3	9:W:1036:ALA:CB	1.48	1.40
8:O:54:ARG:HD2	8:O:59:TYR:CE2	1.59	1.38

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	95/97 (98%)	87 (92%)	7 (7%)	1 (1%)	12	46
2	B	81/103 (79%)	69 (85%)	10 (12%)	2 (2%)	4	27
2	F	90/103 (87%)	85 (94%)	5 (6%)	0	100	100
3	C	101/130 (78%)	84 (83%)	13 (13%)	4 (4%)	2	18
3	G	103/130 (79%)	93 (90%)	10 (10%)	0	100	100
4	D	93/126 (74%)	85 (91%)	7 (8%)	1 (1%)	12	46
4	H	91/126 (72%)	81 (89%)	9 (10%)	1 (1%)	12	46
5	E	108/110 (98%)	94 (87%)	9 (8%)	5 (5%)	2	17
8	N	74/76 (97%)	74 (100%)	0	0	100	100
8	O	74/76 (97%)	70 (95%)	3 (4%)	1 (1%)	9	40
9	W	868/878 (99%)	783 (90%)	71 (8%)	14 (2%)	8	37
All	All	1778/1955 (91%)	1605 (90%)	144 (8%)	29 (2%)	10	37

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	82	LYS
5	E	42	ARG
9	W	474	ASN
9	W	600	LYS
9	W	602	VAL

### 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	A	85/85 (100%)	85 (100%)	0	100	100
2	B	68/79 (86%)	68 (100%)	0	100	100
2	F	63/79 (80%)	63 (100%)	0	100	100
3	C	82/101 (81%)	82 (100%)	0	100	100
3	G	83/101 (82%)	82 (99%)	1 (1%)	67	79

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	81/105 (77%)	80 (99%)	1 (1%)	67	79
4	H	79/105 (75%)	78 (99%)	1 (1%)	65	77
5	E	84/84 (100%)	83 (99%)	1 (1%)	67	79
8	N	68/68 (100%)	67 (98%)	1 (2%)	60	75
8	O	68/68 (100%)	68 (100%)	0	100	100
9	W	787/789 (100%)	765 (97%)	22 (3%)	38	59
All	All	1548/1664 (93%)	1521 (98%)	27 (2%)	56	72

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	W	633	ASN
9	W	652	MET
9	W	1132	LEU
9	W	645	HIS
9	W	660	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	G	89	ASN
3	G	112	GLN
9	W	667	ASN
8	N	25	ASN
8	N	40	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 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

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
10	BEF	W	1301	11	0,3,3	-	-	-		
11	ADP	W	1302	10	24,29,29	1.34	3 (12%)	29,45,45	1.97	7 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	ADP	W	1302	10	-	3/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	W	1302	ADP	C5-C4	3.07	1.49	1.40
11	W	1302	ADP	PB-O2B	-2.24	1.46	1.54
11	W	1302	ADP	C2-N3	2.21	1.35	1.32

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	W	1302	ADP	C3'-C2'-C1'	4.98	108.47	100.98
11	W	1302	ADP	O3B-PB-O2B	4.17	123.57	107.64
11	W	1302	ADP	N3-C2-N1	-3.49	123.22	128.68
11	W	1302	ADP	PA-O3A-PB	-3.38	121.23	132.83
11	W	1302	ADP	C4-C5-N7	-3.22	106.05	109.40

There are no chirality outliers.

All (3) torsion outliers are listed below:

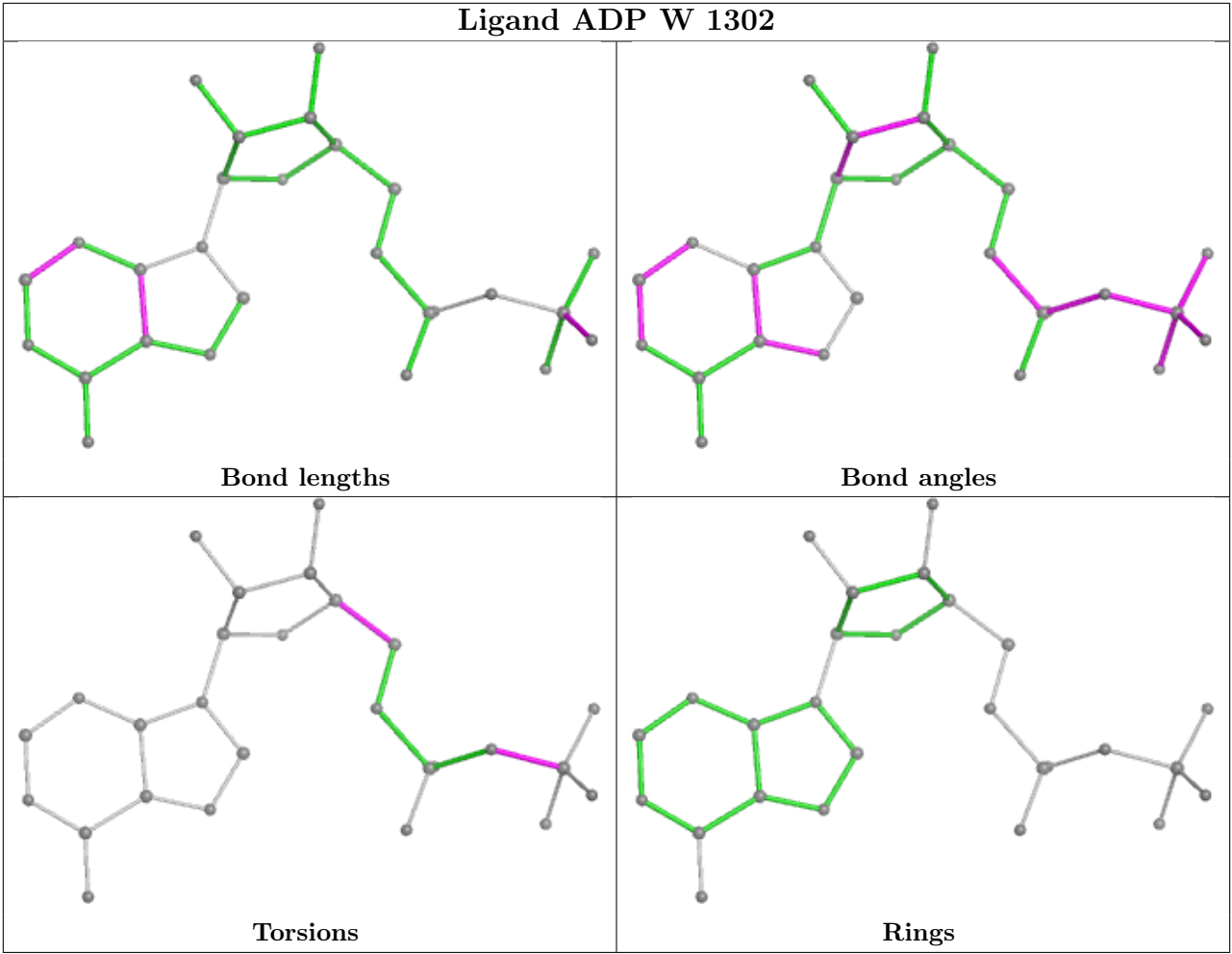
Mol	Chain	Res	Type	Atoms
11	W	1302	ADP	PA-O3A-PB-O2B
11	W	1302	ADP	O4'-C4'-C5'-O5'
11	W	1302	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	W	1302	ADP	12	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	W	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	W	841:TYR	C	1005:ASP	N	49.40
1	W	564:PHE	C	574:ASN	N	14.13
1	W	190:SER	C	199:LYS	N	11.85

Continued on next page...

*Continued from previous page...*

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	W	676:PHE	C	681:MET	N	10.91
1	W	1211:LEU	C	1244:LYS	N	9.17

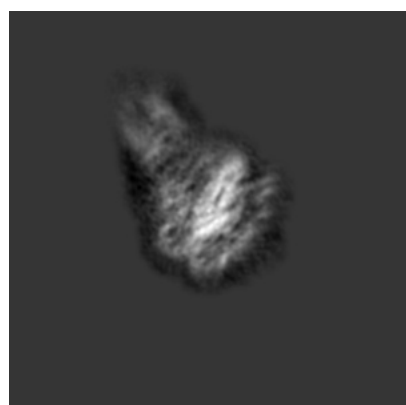
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4318. These allow visual inspection of the internal detail of the map and identification of artifacts.

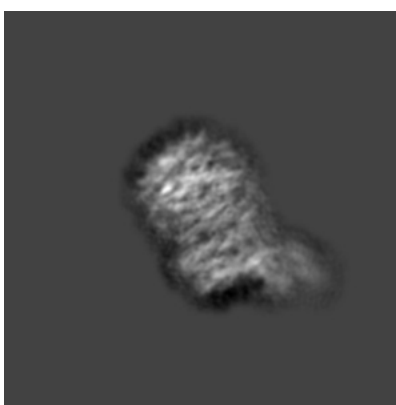
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

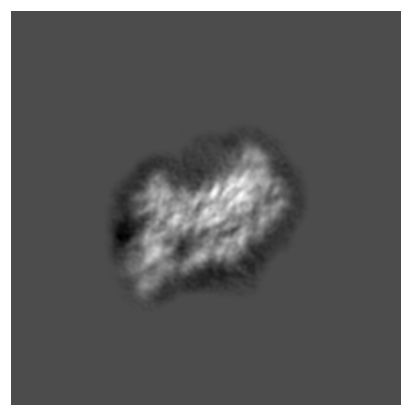
#### 6.1.1 Primary map



X



Y

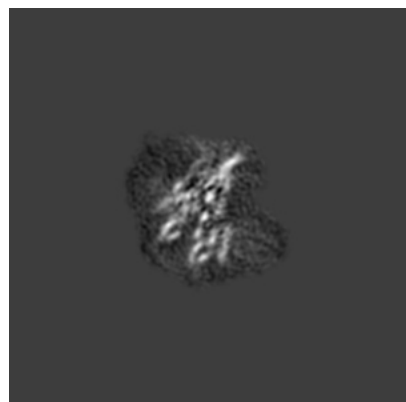


Z

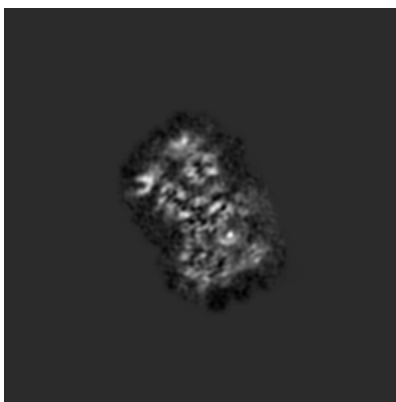
The images above show the map projected in three orthogonal directions.

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

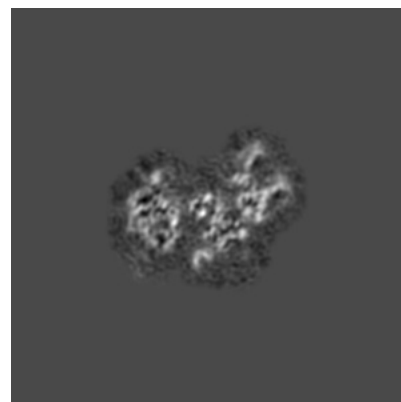
#### 6.2.1 Primary map



X Index: 120



Y Index: 120

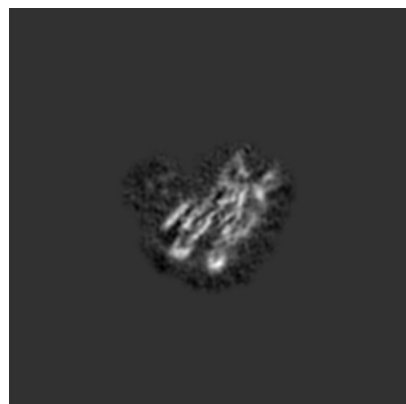


Z Index: 120

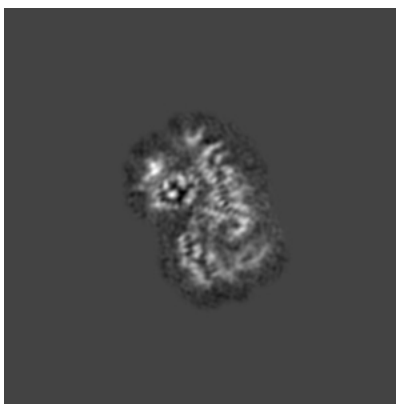
The images above show central slices of the map in three orthogonal directions.

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

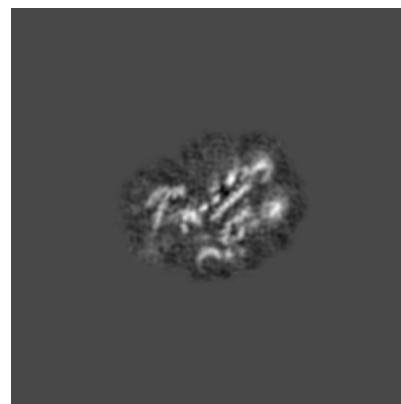
### 6.3.1 Primary map



X Index: 139



Y Index: 128



Z Index: 107

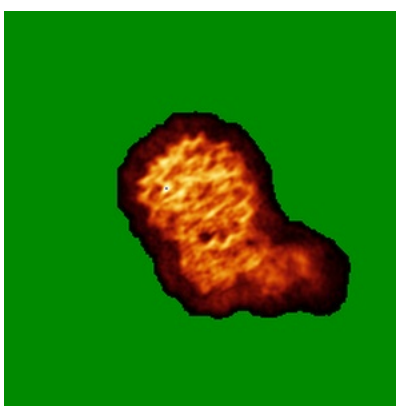
The images above show the largest variance slices of the map in three orthogonal directions.

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

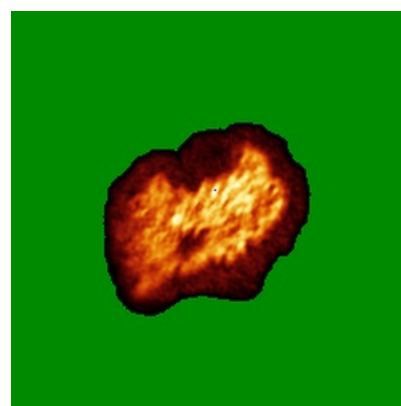
### 6.4.1 Primary map



X



Y

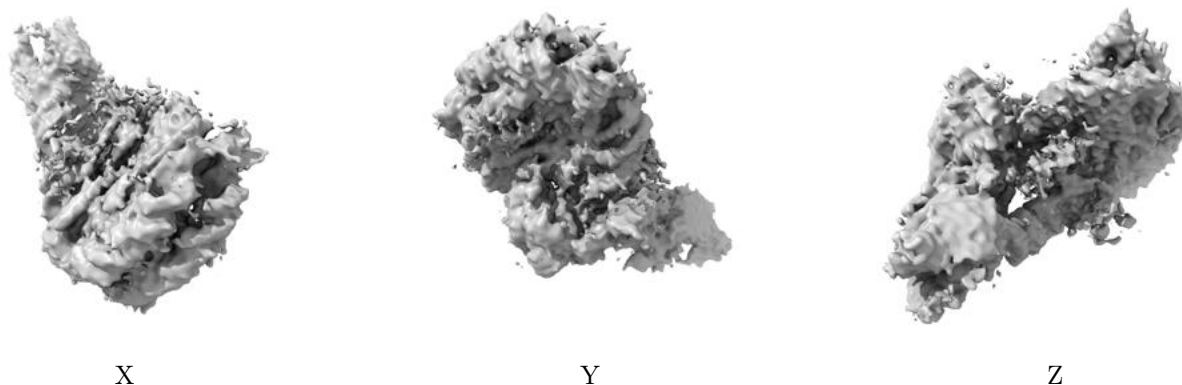


Z

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

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

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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](#)

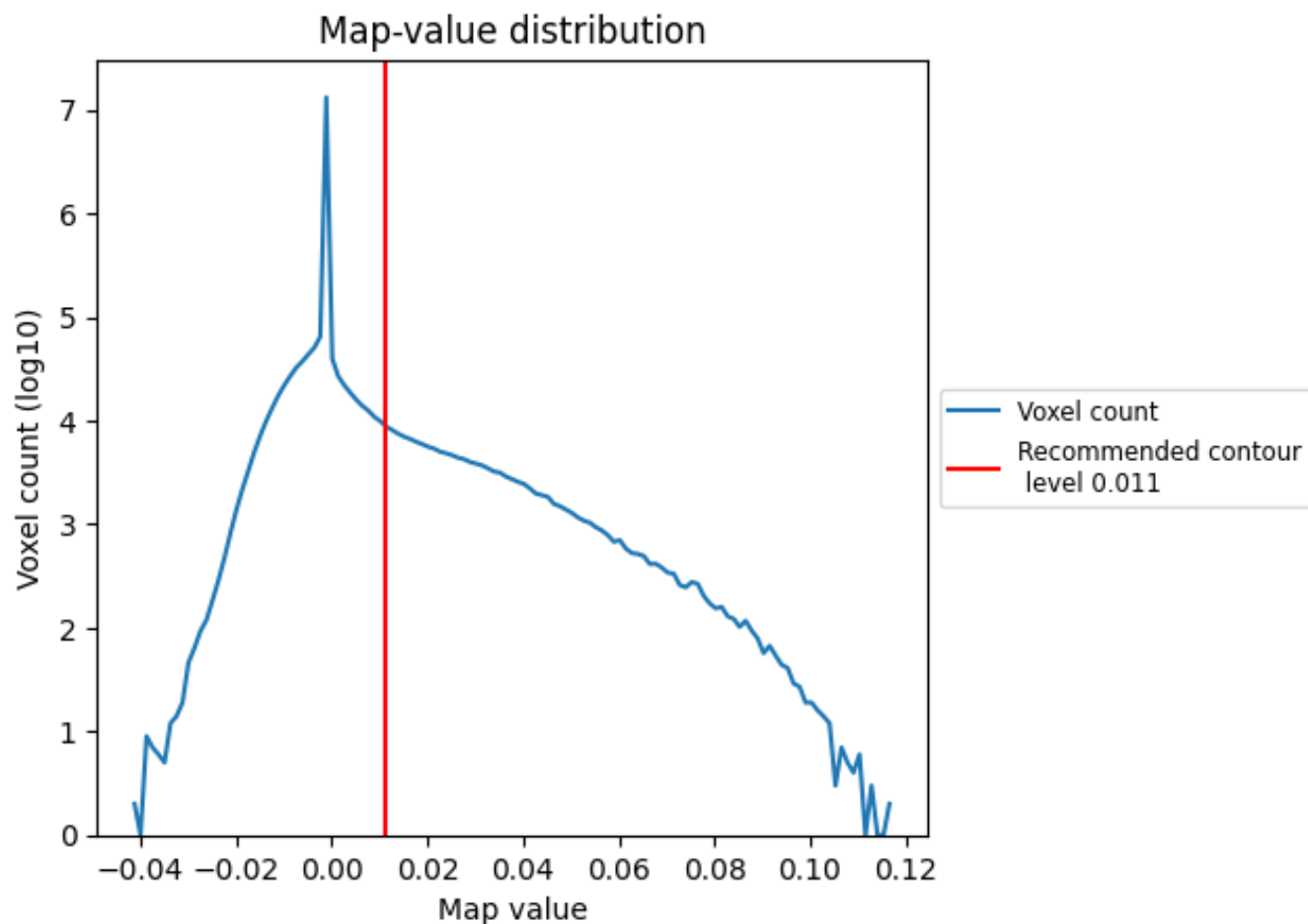
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

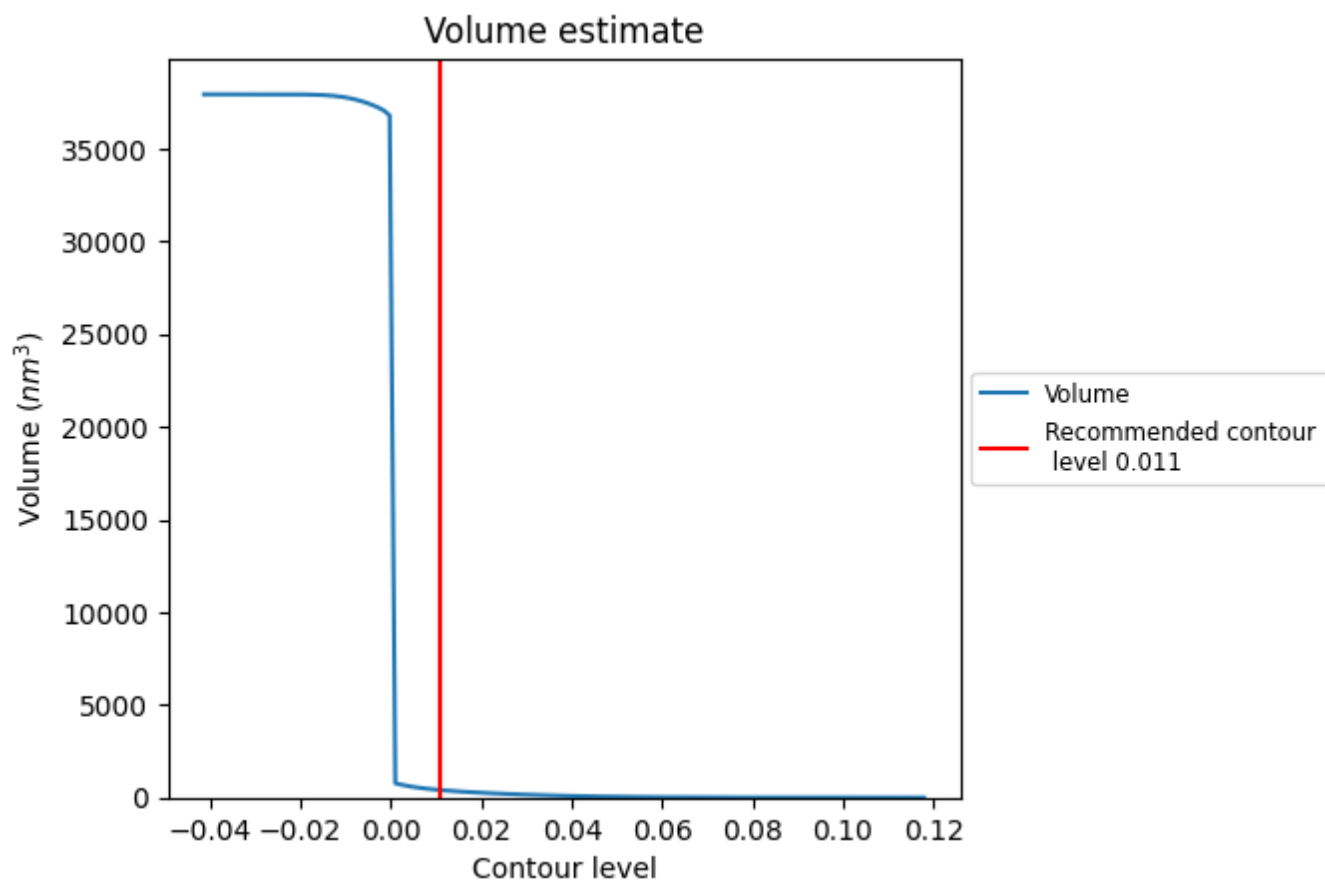
This section contains the results of statistical analysis of the map.

### 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.

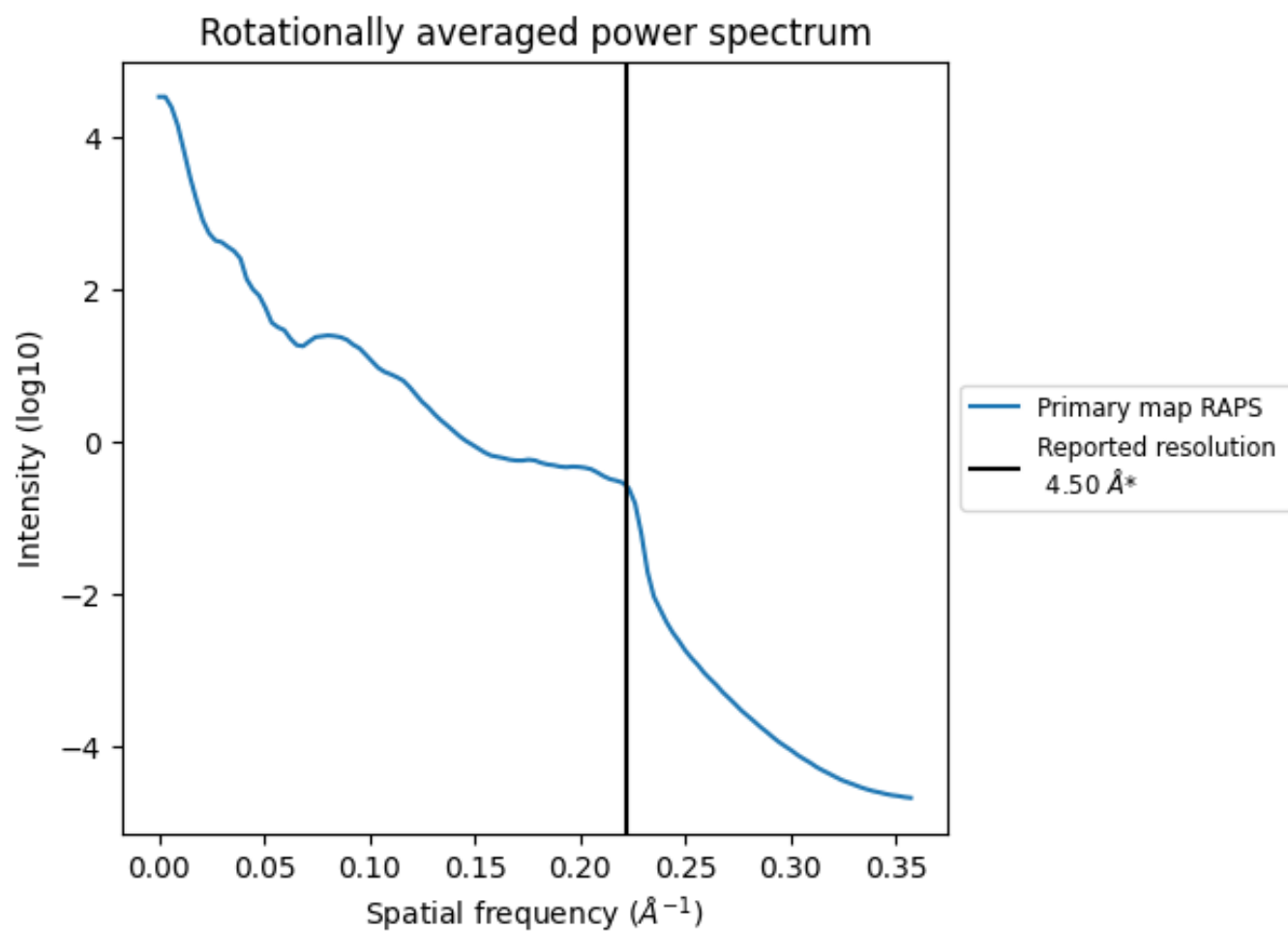
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 403  $\text{nm}^3$ ; this corresponds to an approximate mass of 364 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 ⓘ

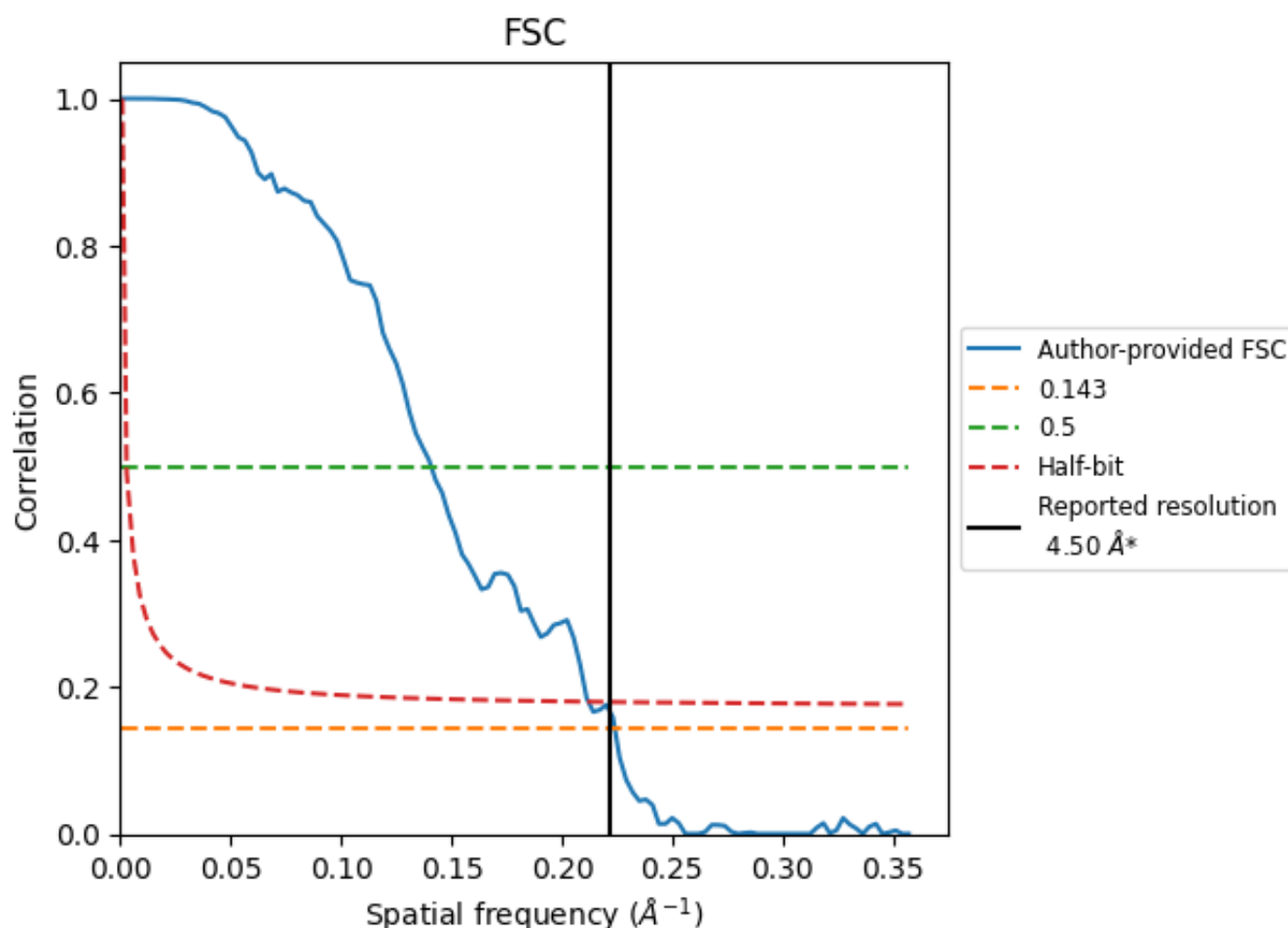


\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

## 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 0.222 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

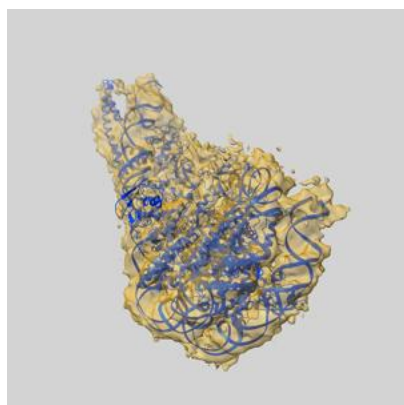
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.46	7.10	4.72
Unmasked-calculated*	-	-	-

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

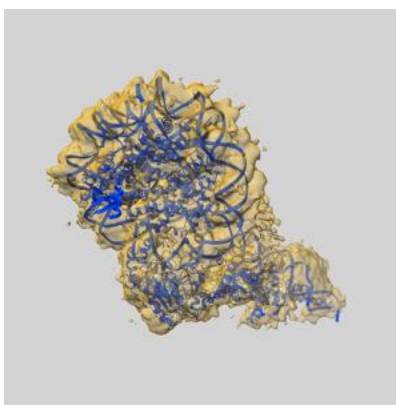
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4318 and PDB model 6FTX. Per-residue inclusion information can be found in section [3](#) on page [8](#).

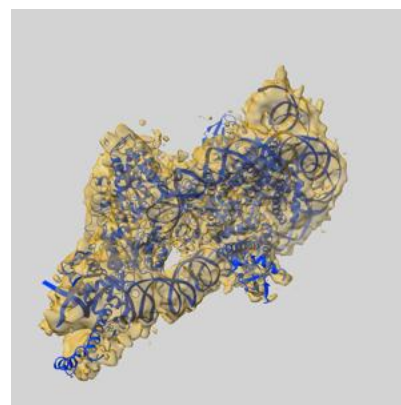
### 9.1 Map-model overlay [i](#)



X



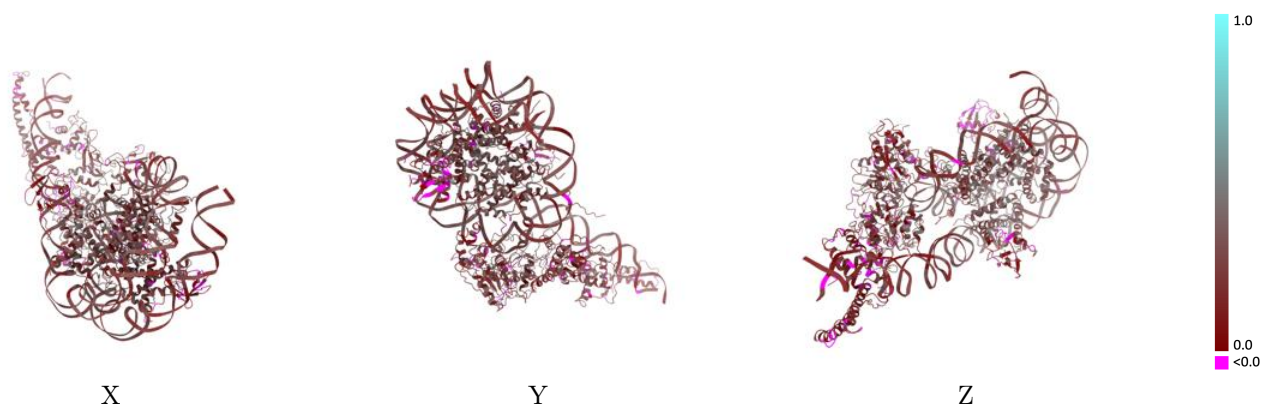
Y



Z

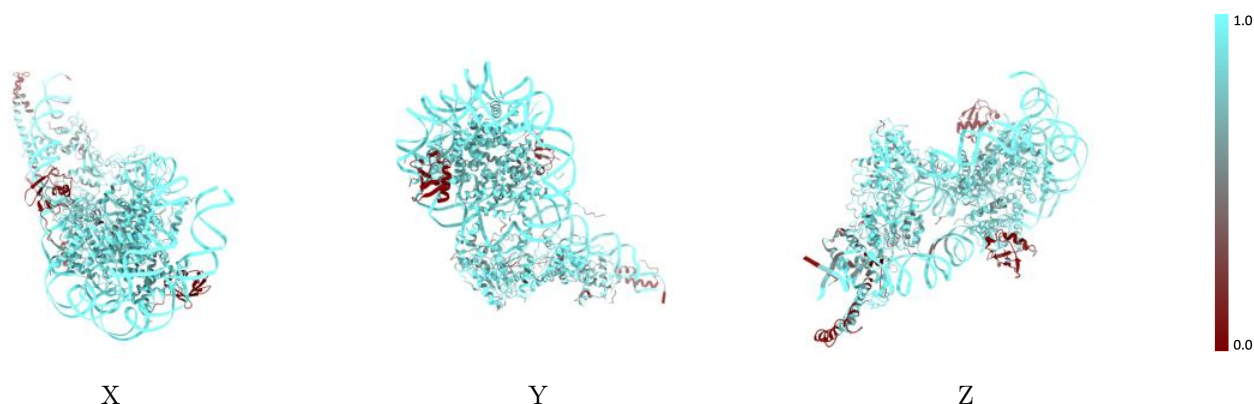
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



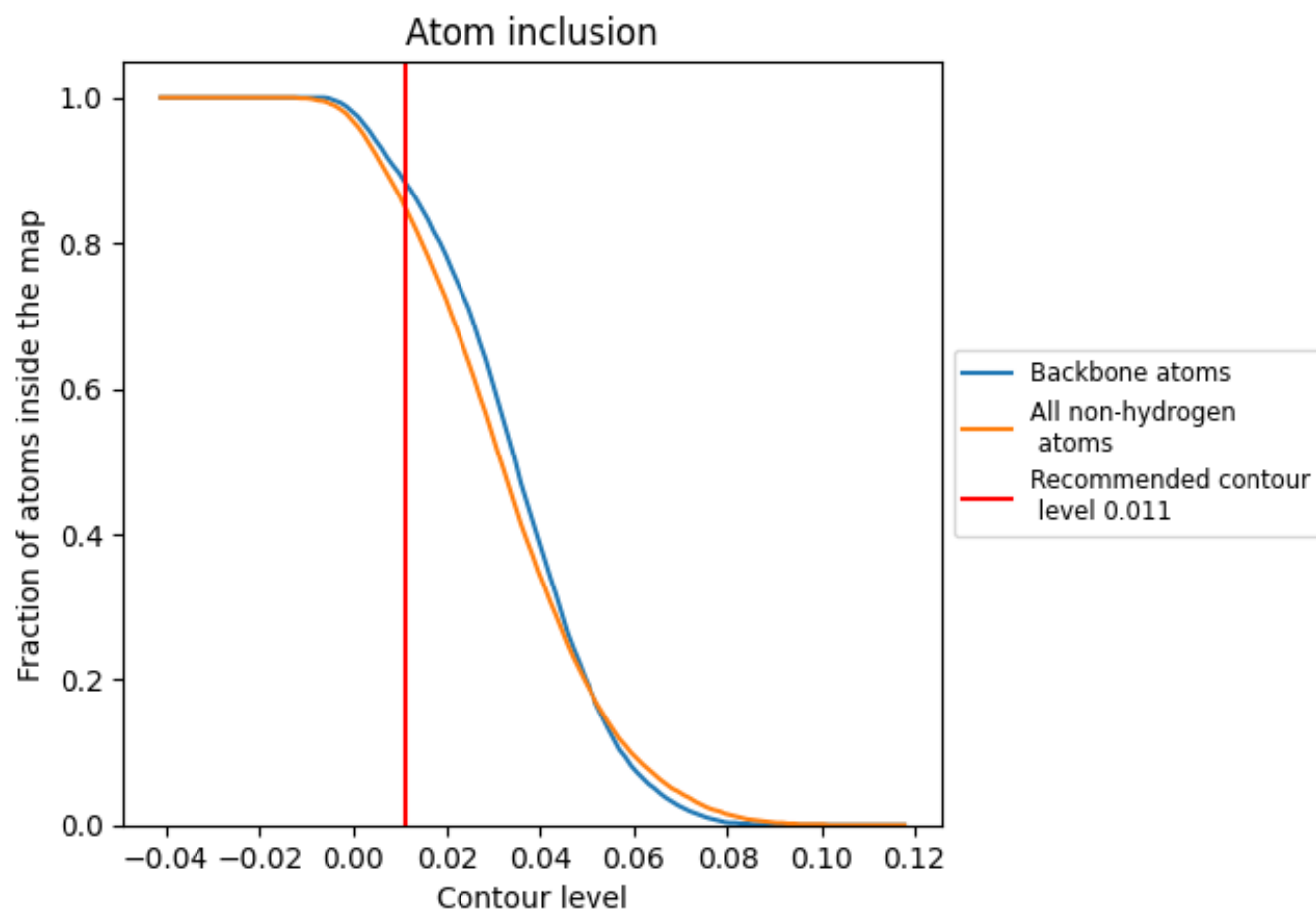
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8500</div>	<div><div></div>0.2300</div>
A	<div><div></div>0.9620</div>	<div><div></div>0.2600</div>
B	<div><div></div>0.9390</div>	<div><div></div>0.2750</div>
C	<div><div></div>0.8930</div>	<div><div></div>0.2760</div>
D	<div><div></div>0.9290</div>	<div><div></div>0.2790</div>
E	<div><div></div>0.8870</div>	<div><div></div>0.2670</div>
F	<div><div></div>0.8930</div>	<div><div></div>0.2510</div>
G	<div><div></div>0.9210</div>	<div><div></div>0.2810</div>
H	<div><div></div>0.9290</div>	<div><div></div>0.2700</div>
I	<div><div></div>0.9670</div>	<div><div></div>0.2470</div>
J	<div><div></div>0.9690</div>	<div><div></div>0.2480</div>
N	<div><div></div>0.1390</div>	<div><div></div>0.1150</div>
O	<div><div></div>0.0810</div>	<div><div></div>0.0360</div>
W	<div><div></div>0.8070</div>	<div><div></div>0.2070</div>

1.0

0.0

<0.0