



wwPDB EM Validation Summary Report ⓘ

Aug 31, 2026 – 10:16 AM EDT

PDB ID : 9Z07 / pdb_00009z07
EMDB ID : EMD-73698
Title : Cryo-EM structure of DNMT1 in complex with unmethylated nucleosome core particle
Authors : Fang, J.; Song, J.
Deposited on : 2025-10-31
Resolution : 3.19 Å (reported)
Based on initial models : 4WXX, 3PTA, 7JZV

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

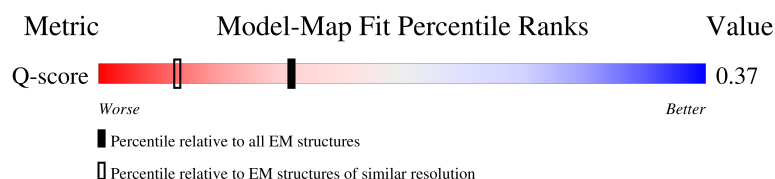
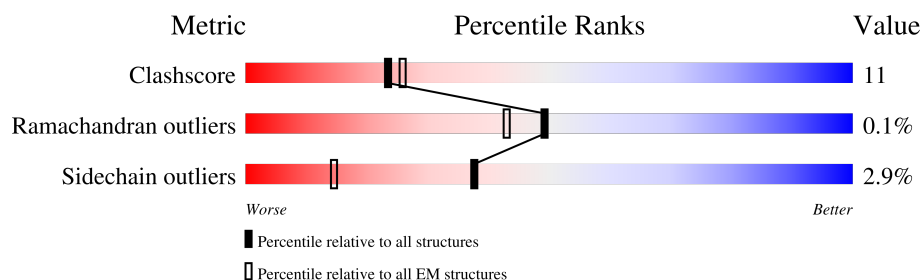
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.19 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.



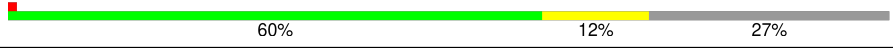
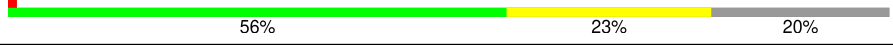
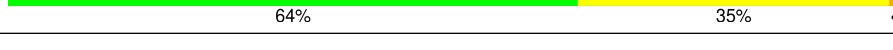
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14455 (2.69 - 3.69)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1250	14% 49% 19% 32%
2	N	130	70% 14% 15%
2	n	130	71% 14% 15%
3	O	123	63% 11% 24%

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Mol	Chain	Length	Quality of chain
3	o	123	
4	P	136	
4	p	136	
5	Q	103	
5	q	103	
6	X	149	
7	Y	149	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17917 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 (cytosine-5)-methyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	854	Total	C	N	O	S	0	0
			5705	3631	1003	1028	43		

- Molecule 2 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	N	111	Total	C	N	O	0	0
			849	533	167	149		
2	n	110	Total	C	N	O	0	0
			836	526	163	147		

- Molecule 3 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	O	94	Total	C	N	O	S	0	0
			735	463	132	138	2		
3	o	98	Total	C	N	O	S	0	0
			766	481	140	143	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	0	MET	-	initiating methionine	UNP P02281
O	29	THR	SER	engineered mutation	UNP P02281
o	0	MET	-	initiating methionine	UNP P02281
o	29	THR	SER	engineered mutation	UNP P02281

- Molecule 4 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	100	Total	C	N	O	S	0	0
			808	509	154	143	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	p	99	Total	C	N	O	S	0	0
			820	518	159	141	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	18	CYS	LYS	conflict	UNP A0A310TTQ1
P	23	CYS	LYS	conflict	UNP A0A310TTQ1
P	110	SER	CYS	conflict	UNP A0A310TTQ1
p	18	CYS	LYS	conflict	UNP A0A310TTQ1
p	23	CYS	LYS	conflict	UNP A0A310TTQ1
p	110	SER	CYS	conflict	UNP A0A310TTQ1

- Molecule 5 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	82	Total	C	N	O	S	0	0
			647	409	124	113	1		
5	q	80	Total	C	N	O	S	0	0
			638	401	125	111	1		

- Molecule 6 is a DNA chain called Chain x DNA (149-MER).

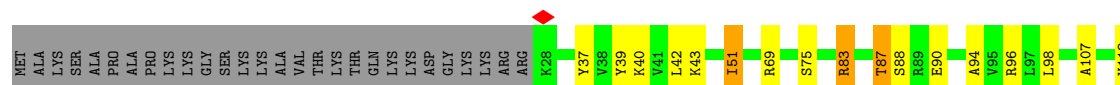
Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	149	Total	C	N	O	P	0	0
			3073	1454	580	890	149		

- Molecule 7 is a DNA chain called Chain Y DNA (149-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	149	Total	C	N	O	P	0	0
			3036	1443	546	898	149		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

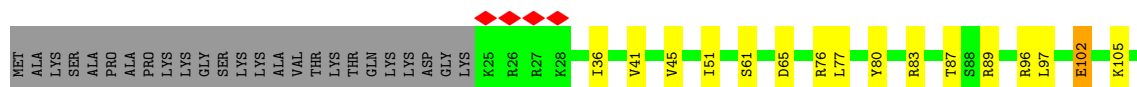
Mol	Chain	Residues	Atoms		AltConf
8	A	4	Total	Zn	0
			4	4	





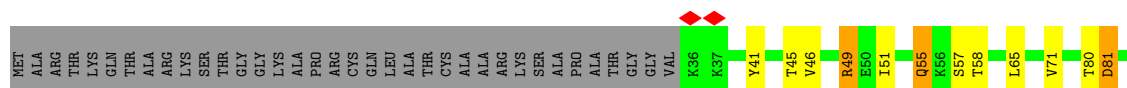
- Molecule 3: Histone H2B 1.1

Chain o: 63% 15% 20%



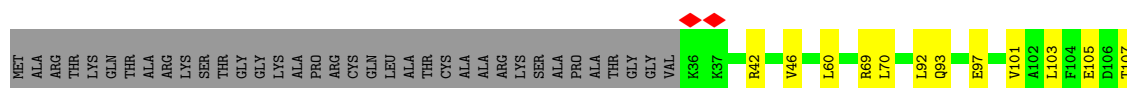
- Molecule 4: Histone H3

Chain P: 60% 11% 26%



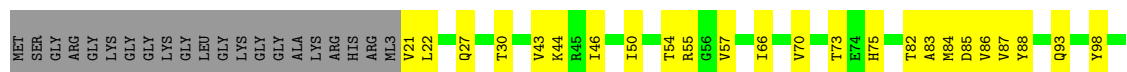
- Molecule 4: Histone H3

Chain p: 60% 12% 27%



- Molecule 5: Histone H4

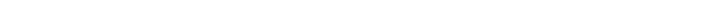
Chain Q: 56% 23% 20%

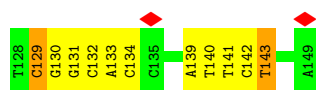


- Molecule 5: Histone H4

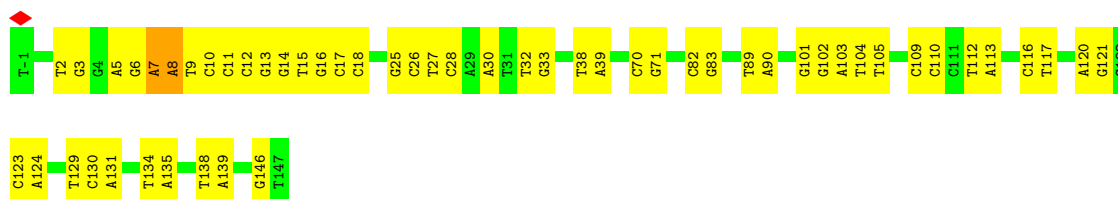
Chain q: 56% 17% 22%



- Chain X:  63% 36%



- Chain Y: 64% 35%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	212957	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	45.687	Depositor
Minimum map value	-11.619	Depositor
Average map value	-0.025	Depositor
Map value standard deviation	0.725	Depositor
Recommended contour level	2.8	Depositor
Map size (Å)	342.40002, 342.40002, 342.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0/5834	0.41	0/8007
2	N	0.29	0/859	0.44	0/1161
2	n	0.26	0/846	0.41	0/1144
3	O	0.32	0/746	0.50	0/1004
3	o	0.30	0/777	0.49	1/1043 (0.1%)
4	P	0.36	0/820	0.52	0/1103
4	p	0.30	0/832	0.47	0/1115
5	Q	0.42	0/654	0.56	0/876
5	q	0.35	0/645	0.70	1/862 (0.1%)
6	X	0.41	3/3452 (0.1%)	0.55	3/5330 (0.1%)
7	Y	0.38	1/3400 (0.0%)	0.55	5/5241 (0.1%)
All	All	0.32	4/18865 (0.0%)	0.50	10/26886 (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
1	A	0	3
3	O	0	3
3	o	0	1
4	P	0	2
4	p	0	2
5	q	0	1
All	All	0	12

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	X	134	DC	O3'-P	7.28	1.72	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	X	143	DT	O3'-P	6.48	1.70	1.61
6	X	2	DC	O3'-P	6.43	1.70	1.61
7	Y	8	DA	O3'-P	-5.80	1.52	1.61

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	Y	8	DA	O3'-P-O5'	-16.48	79.28	104.00
5	q	88	TYR	CB-CA-C	-13.74	87.48	110.85
7	Y	8	DA	P-O3'-C3'	9.27	134.10	120.20
6	X	127	DC	P-O3'-C3'	8.59	133.09	120.20
3	o	80	TYR	CB-CA-C	-6.60	98.00	110.67

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1023	ARG	Sidechain
1	A	1516	ARG	Sidechain
1	A	652	ARG	Sidechain
3	O	69	ARG	Sidechain
3	O	83	ARG	Sidechain

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	5705	0	4828	181	0
2	N	849	0	900	20	0
2	n	836	0	882	16	0
3	O	735	0	760	12	0
3	o	766	0	790	17	0
4	P	808	0	827	14	0
4	p	820	0	866	10	0
5	Q	647	0	685	19	0
5	q	638	0	676	17	0
6	X	3073	0	1671	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Y	3036	0	1675	45	0
8	A	4	0	0	0	0
All	All	17917	0	14560	353	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 11.

The worst 5 of 353 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:A:1457:TYR:HA	1:A:1475:VAL:HA	1.46	0.92
1:A:1478:CYS:HB3	1:A:1485:CYS:SG	2.08	0.92
1:A:1324:LEU:HD12	1:A:1324:LEU:O	1.70	0.92
1:A:751:CYS:HB3	1:A:782:LEU:HD21	1.50	0.90
1:A:923:TYR:N	1:A:999:ILE:O	2.05	0.88

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	840/1250 (67%)	810 (96%)	30 (4%)	0	100	100
2	N	109/130 (84%)	106 (97%)	2 (2%)	1 (1%)	14	47
2	n	108/130 (83%)	103 (95%)	5 (5%)	0	100	100
3	O	92/123 (75%)	91 (99%)	1 (1%)	0	100	100
3	o	96/123 (78%)	94 (98%)	2 (2%)	0	100	100
4	P	98/136 (72%)	92 (94%)	6 (6%)	0	100	100
4	p	97/136 (71%)	95 (98%)	2 (2%)	0	100	100
5	Q	80/103 (78%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	q	78/103 (76%)	77 (99%)	1 (1%)	0	100	100
All	All	1598/2234 (72%)	1545 (97%)	52 (3%)	1 (0%)	49	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	N	11	ARG

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	457/1084 (42%)	448 (98%)	9 (2%)	48	72
2	N	86/102 (84%)	84 (98%)	2 (2%)	44	70
2	n	84/102 (82%)	82 (98%)	2 (2%)	43	70
3	O	80/103 (78%)	76 (95%)	4 (5%)	22	55
3	o	82/103 (80%)	81 (99%)	1 (1%)	63	79
4	P	83/111 (75%)	80 (96%)	3 (4%)	31	63
4	p	87/111 (78%)	85 (98%)	2 (2%)	44	70
5	Q	66/78 (85%)	62 (94%)	4 (6%)	17	49
5	q	65/78 (83%)	60 (92%)	5 (8%)	12	41
All	All	1090/1872 (58%)	1058 (97%)	32 (3%)	38	67

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	q	74	GLU
5	q	84	MET
3	O	51	ILE
3	O	42	LEU
5	q	86	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
4	P	113	HIS
3	o	81	ASN
1	A	1505	ASN
1	A	1573	HIS
4	P	55	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 ⓘ

There are no chain breaks in this entry.

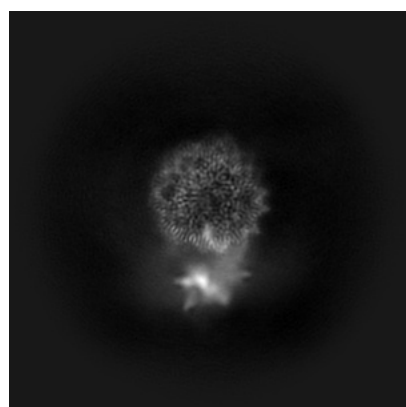
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73698. These allow visual inspection of the internal detail of the map and identification of artifacts.

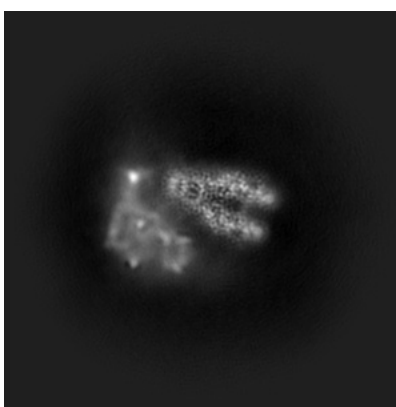
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

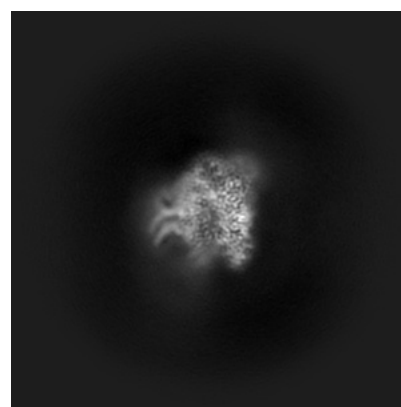
6.1.1 Primary map



X



Y

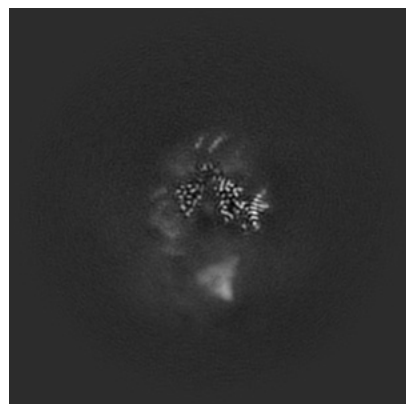


Z

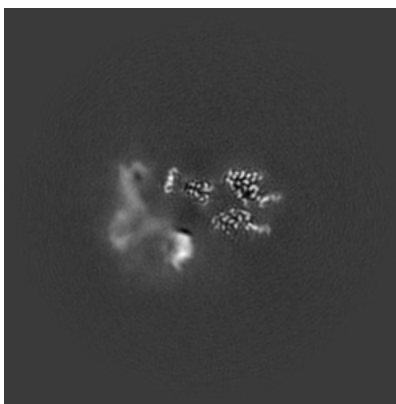
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

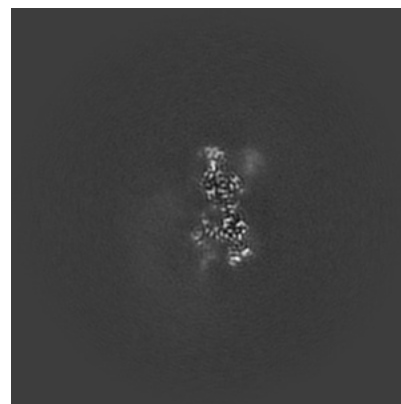
6.2.1 Primary map



X Index: 160



Y Index: 160

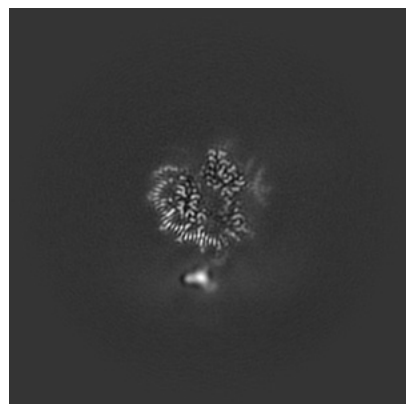


Z Index: 160

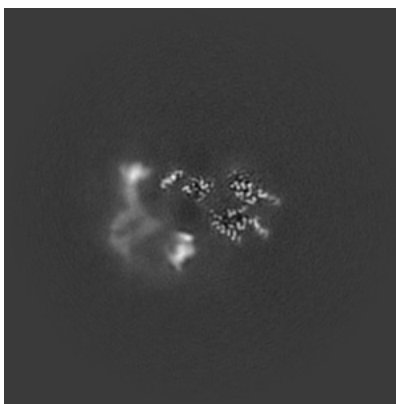
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

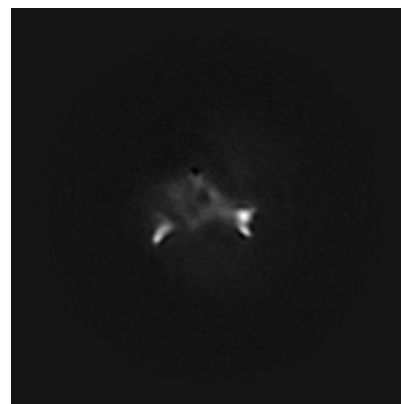
6.3.1 Primary map



X Index: 183



Y Index: 157

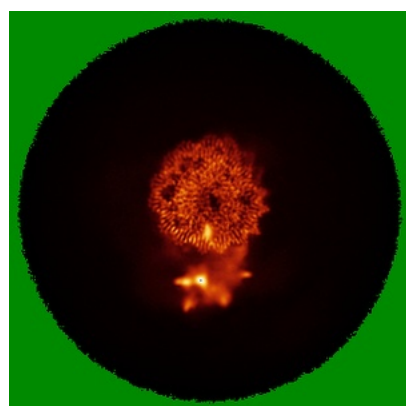


Z Index: 103

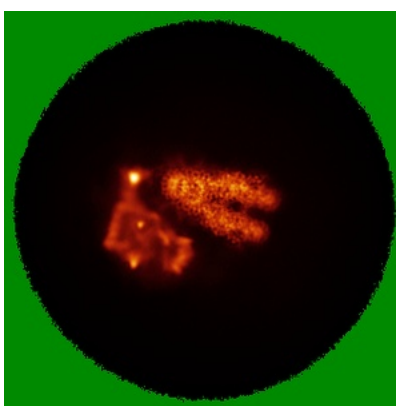
The images above show the largest variance slices of the map in three orthogonal directions.

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

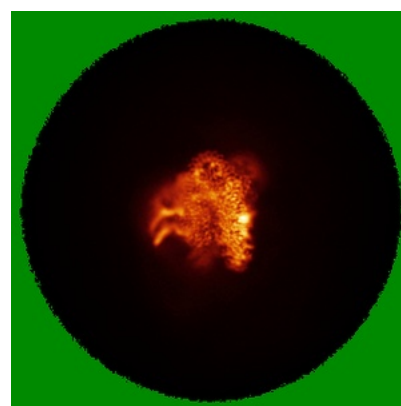
6.4.1 Primary map



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

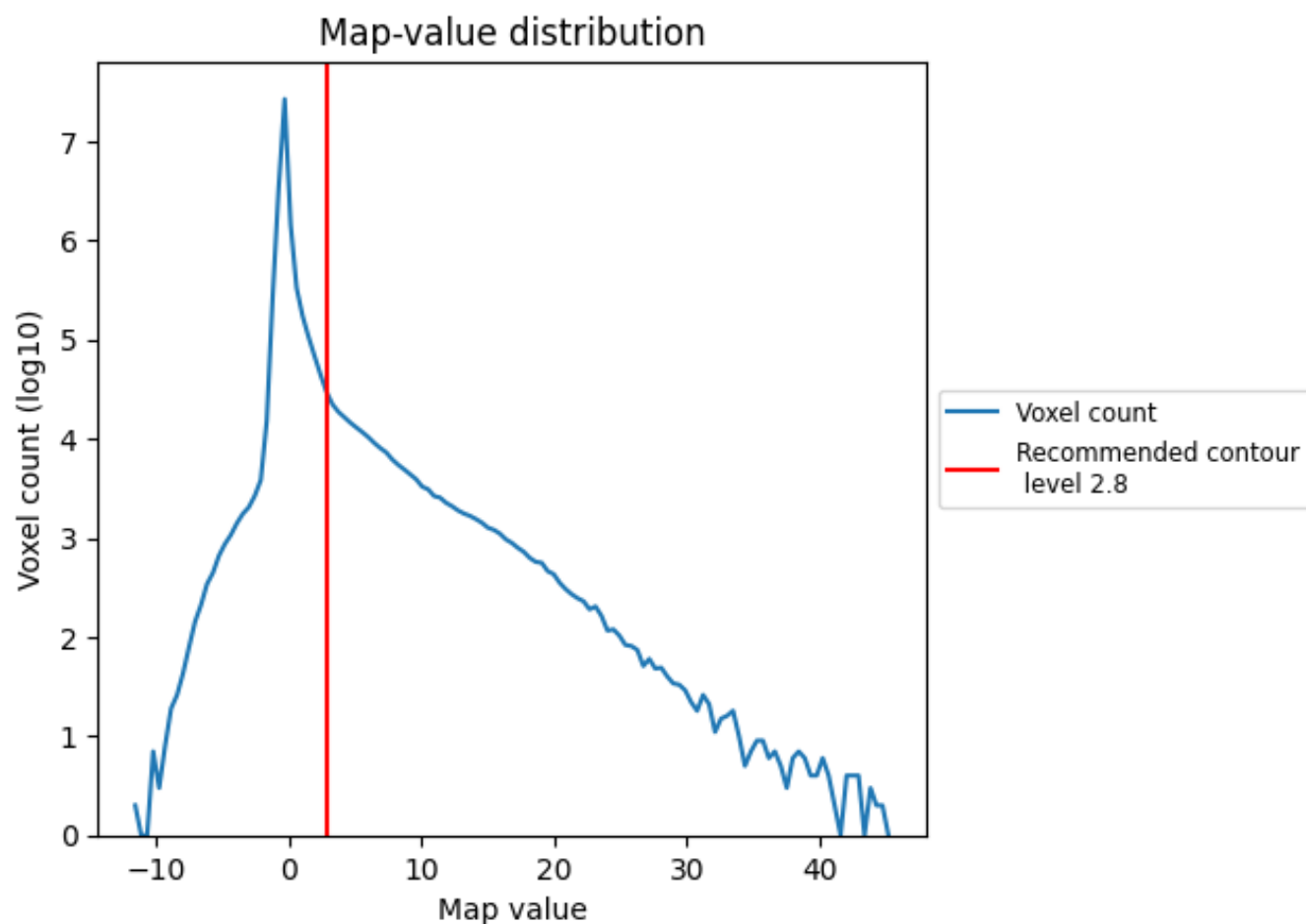
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

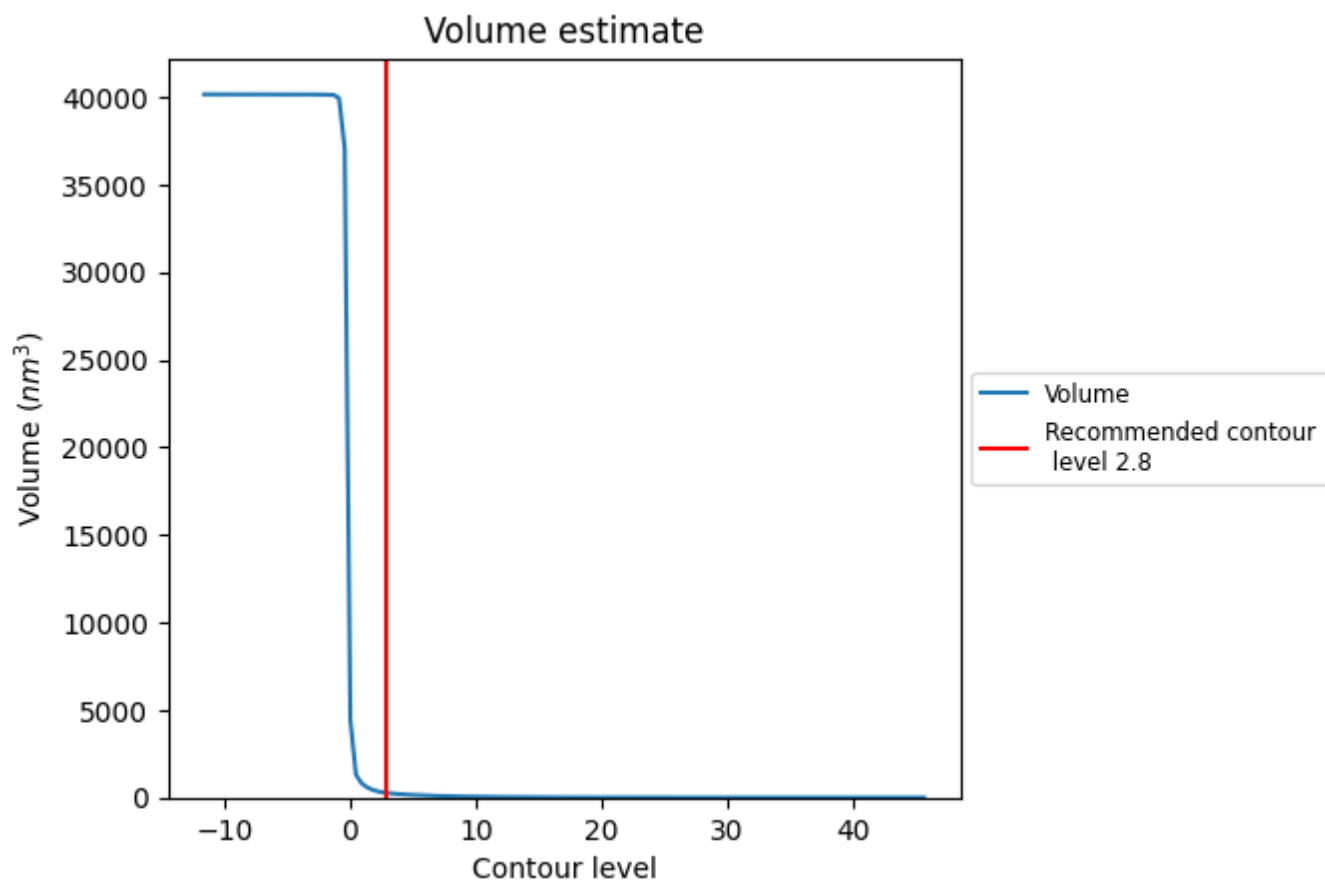
This section contains the results of statistical analysis of the map.

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.

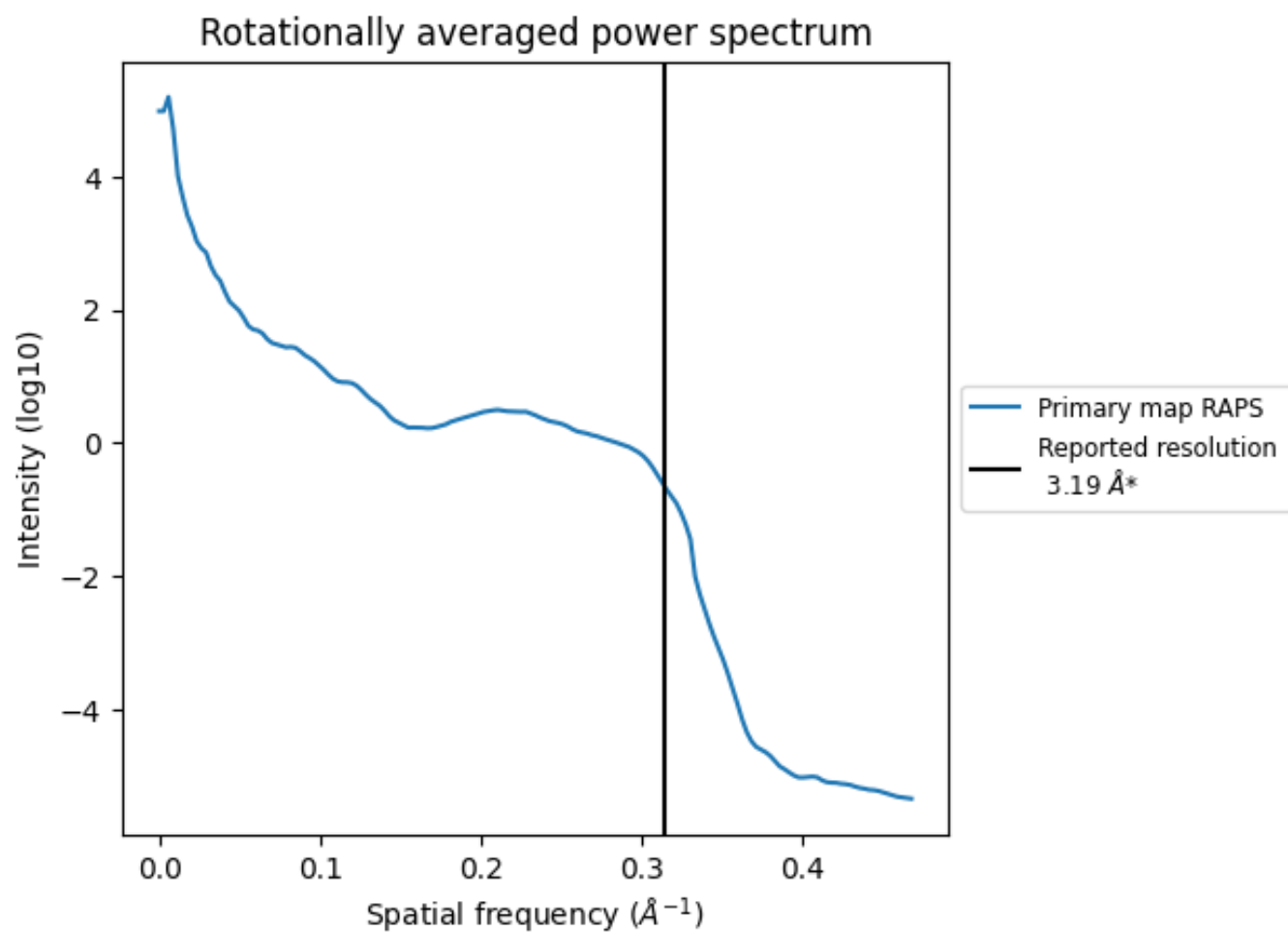
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 275 nm³; this corresponds to an approximate mass of 249 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 0.313 $\text{\AA}^{-1}$

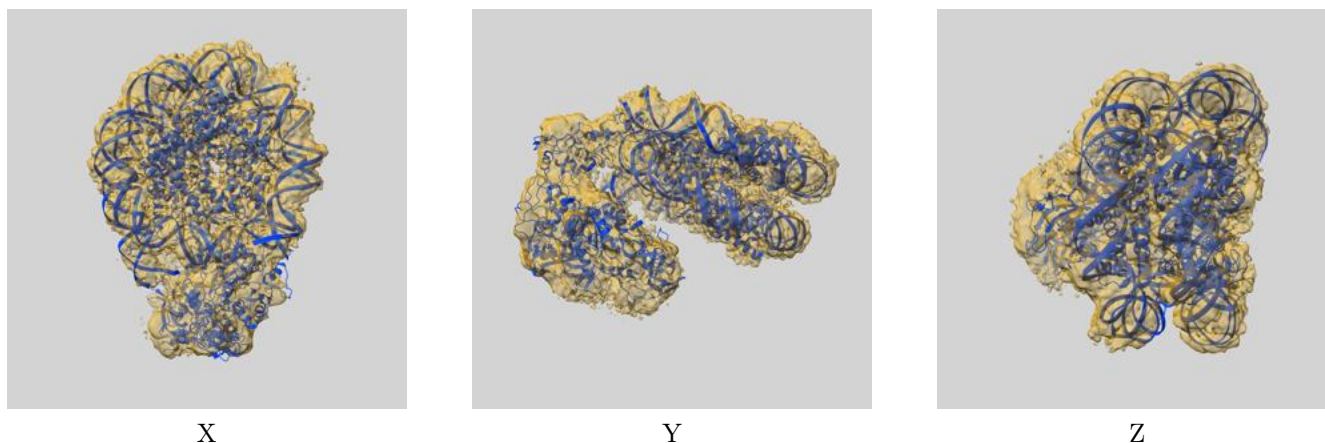
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

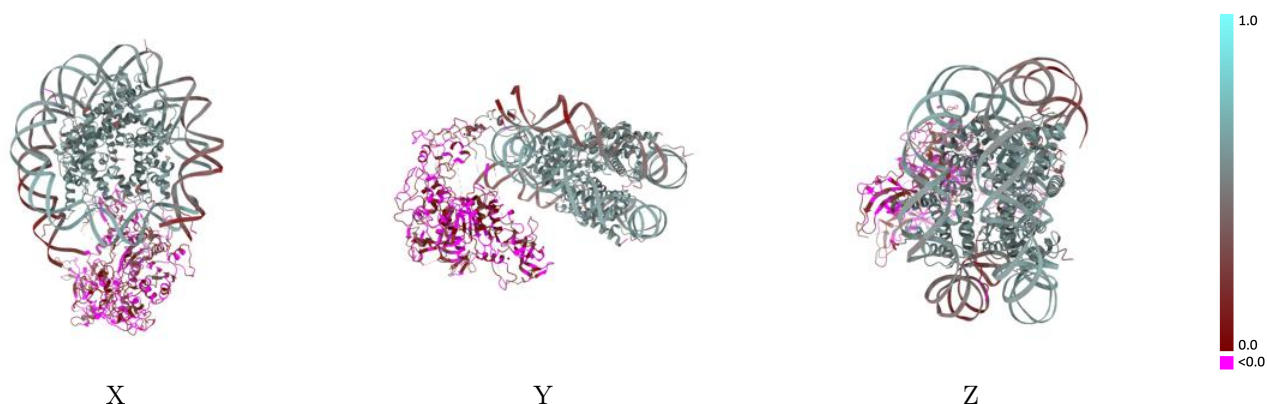
This section contains information regarding the fit between EMDB map EMD-73698 and PDB model 9Z07. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



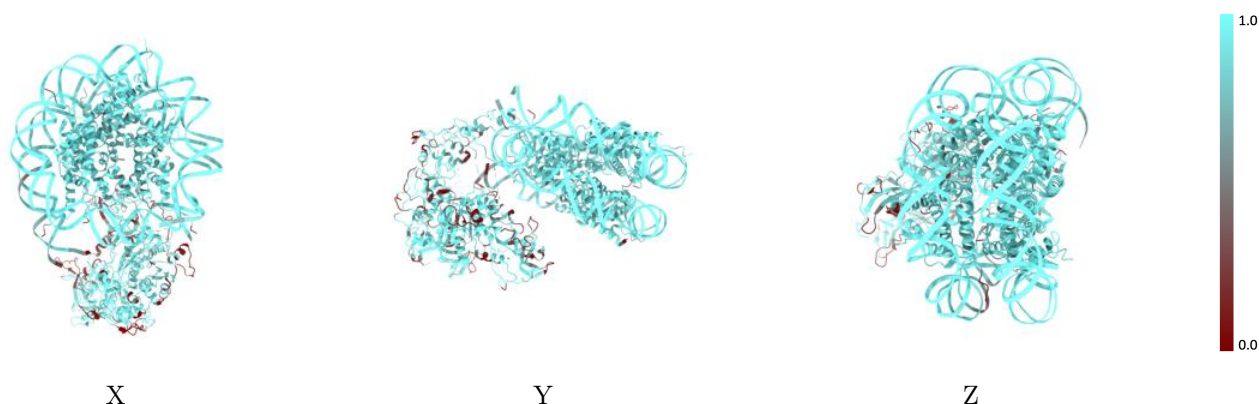
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



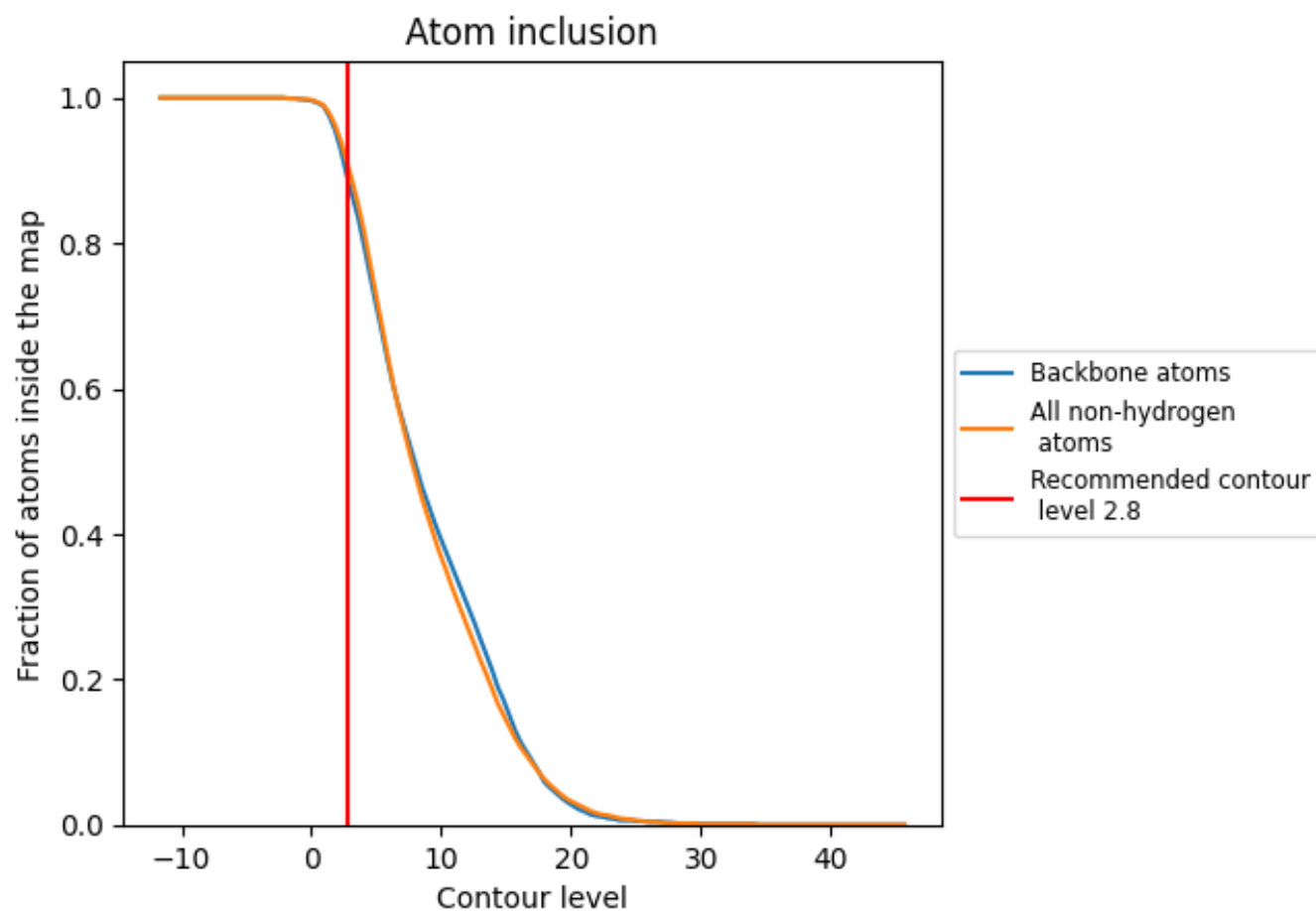
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 91% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9070	0.3700
A	0.8040	0.0600
N	0.9540	0.5480
O	0.9750	0.5410
P	0.9530	0.5540
Q	0.9820	0.5650
X	0.9560	0.4850
Y	0.9610	0.4860
n	0.9400	0.5460
o	0.9200	0.5170
p	0.9380	0.5350
q	0.9620	0.5640

1.0

0.0

<0.0