



wwPDB EM Validation Summary Report ⓘ

Feb 23, 2025 – 01:22 AM JST

PDB ID : 9J1K
EMDB ID : EMD-61074
Title : Tip region of monocin
Authors : Wang, J.W.; Gu, Z.W.
Deposited on : 2024-08-05
Resolution : 2.88 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

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.dev117
MolProbity : 4.02b-467
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) : 2.41.2

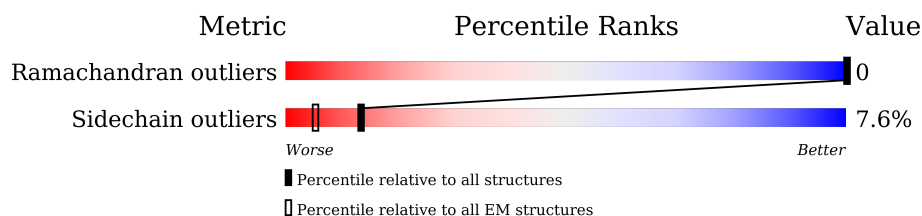
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





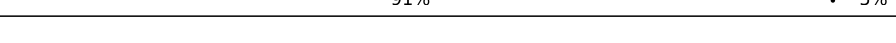




The reported resolution of this entry is 2.88 Å.

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.













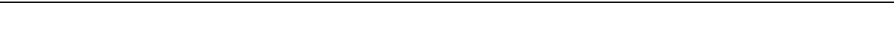

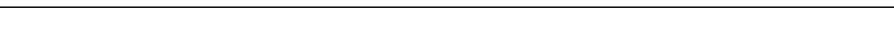
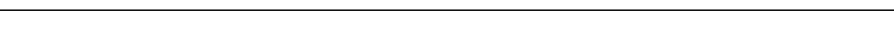











Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 ≥ 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	170	
1	B	170	
1	C	170	
1	D	170	
1	E	170	
1	F	170	
1	G	170	
1	H	170	
1	I	170	

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Mol	Chain	Length	Quality of chain
1	N	170	 85% 9% 6%
1	S	170	 89% 6% 5%
1	T	170	 86% 8% 5%
1	U	170	 89% 6% 5%
1	V	170	 86% 8% 6%
1	W	170	 91% 6% 6%
1	Y	170	 89% 6% 5%
1	Z	170	 89% 6% 5%
1	a	170	 91% 5% 5%
1	b	170	 87% 8% 5%
1	c	170	 88% 7% 5%
1	d	170	 85% 9% 6%
1	e	170	 88% 7% 5%
1	f	170	 88% 6% 5%
1	g	170	 89% 5% 6%
1	h	170	 86% 8% 6%
1	n	170	 90% 5% 5%
1	o	170	 87% 8% 5%
1	p	170	 89% 6% 5%
1	q	170	 88% 6% 6%
1	r	170	 90% 6% 6%
2	J	622	 7% 92%
2	O	622	 7% 92%
2	i	622	 8% 92%
3	K	272	 93% 7%

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Mol	Chain	Length	Quality of chain
3	P	272	 94% 6%
3	X	272	 94% 5%
3	j	272	 93% 7%
3	k	272	 96% .
3	s	272	 94% 6%
4	L	378	 96% .
4	Q	378	 97% .
4	l	378	 96% .
5	M	99	 25% . 73%
5	R	99	 24% . 73%
5	m	99	 25% . 73%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 60066 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 AA protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	E	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	F	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	G	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	H	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	a	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	b	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	c	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	d	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	g	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	A	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	B	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	C	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	I	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	N	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	S	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	T	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	V	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	W	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	Y	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	Z	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	e	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	f	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	h	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	n	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	o	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	p	161	Total	C	N	O	S	0	0
			1198	759	191	242	6		
1	q	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		
1	r	160	Total	C	N	O	S	0	0
			1194	757	190	241	6		

- Molecule 2 is a protein called FtbJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	50	Total	C	N	O	S	0	0
			396	247	70	77	2		
2	O	50	Total	C	N	O	S	0	0
			396	247	70	77	2		
2	i	50	Total	C	N	O	S	0	0
			396	247	70	77	2		

- Molecule 3 is a protein called FtbK.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	272	Total	C	N	O	S	0	0
			2210	1411	370	419	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	k	272	Total	C	N	O	S	0	0
			2210	1411	370	419	10		
3	P	272	Total	C	N	O	S	0	0
			2210	1411	370	419	10		
3	X	272	Total	C	N	O	S	0	0
			2210	1411	370	419	10		
3	j	272	Total	C	N	O	S	0	0
			2210	1411	370	419	10		
3	s	272	Total	C	N	O	S	0	0
			2210	1411	370	419	10		

- Molecule 4 is a protein called FtbL.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	378	Total	C	N	O	S	0	0
			3040	1930	499	600	11		
4	Q	378	Total	C	N	O	S	0	0
			3040	1930	499	600	11		
4	l	378	Total	C	N	O	S	0	0
			3040	1930	499	600	11		


- Molecule 5 is a protein called CCA-adding enzyme.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	27	Total	C	N	O	0	0
			198	124	33	41		
5	R	27	Total	C	N	O	0	0
			198	124	33	41		
5	m	27	Total	C	N	O	0	0
			198	124	33	41		

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: AA protein

Chain D: 




- Molecule 1: AA protein

Chain E: 




- Molecule 1: AA protein

Chain F: 




- Molecule 1: AA protein

Chain G: 




- Molecule 1: AA protein

Chain H: 




- Molecule 1: AA protein

Chain a:  91% 5%




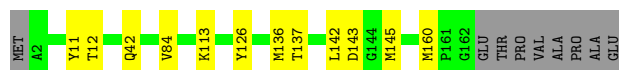
- Molecule 1: AA protein

Chain b:  87% 8% 5%




- Molecule 1: AA protein

Chain c:  88% 7% 5%




- Molecule 1: AA protein

Chain d:  85% 9% 6%




- Molecule 1: AA protein

Chain g:  89% 5% 6%



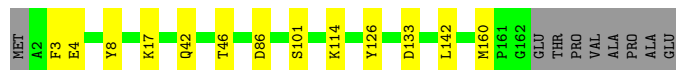
- Molecule 1: AA protein

Chain A:  89% 6% 5%




- Molecule 1: AA protein

Chain B:  87% 8% 5%




- Molecule 1: AA protein

Chain C:  89% 6% 5%




• Molecule 1: AA protein

Chain I:  88% 6% 5%




• Molecule 1: AA protein

Chain N:  85% 9% 6%




• Molecule 1: AA protein

Chain S:  89% 6% 5%




• Molecule 1: AA protein

Chain T:  86% 8% 5%




• Molecule 1: AA protein

Chain U:  89% 6% 5%



• Molecule 1: AA protein

Chain V:  86% 8% 6%




• Molecule 1: AA protein

Chain W:  91% 6%




• Molecule 1: AA protein

Chain Y:  89% 6% 5%




• Molecule 1: AA protein

Chain Z:  89% 6% 5%




• Molecule 1: AA protein

Chain e:  88% 7% 5%




• Molecule 1: AA protein

Chain f:  88% 6% 5%




• Molecule 1: AA protein

Chain h:  86% 8% 6%



• Molecule 1: AA protein

Chain n:  90% 5% 5%

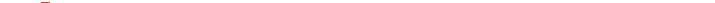


• Molecule 1: AA protein

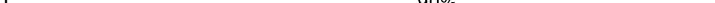
MET
A2
N6
L7
Y8
C9
D10
Y11
L26
L36
D52
D86
V103
K114
Y126
L142
M160
P161
G162
GIU
THR
PRO
VAL
ALA
PRO
PRO
ALA
GIU

- Chain p: 89% 6% 5%



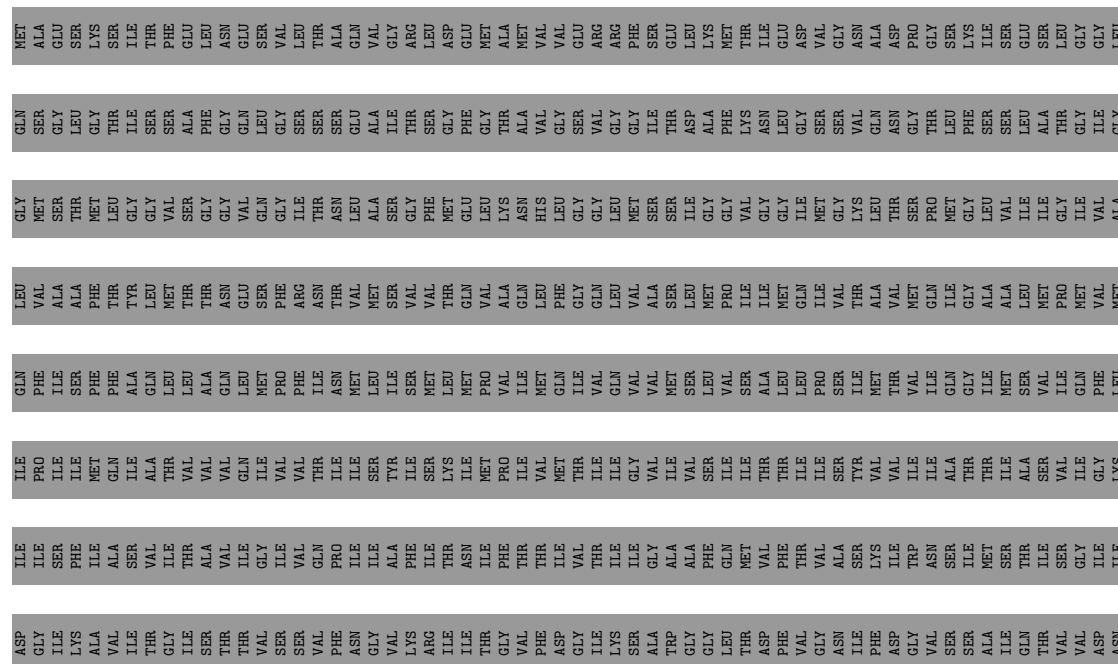
- Chain q:  88% 6% 6%



- Chain r:  90% . 6%



- Chain J:  7% 92%



- Molecule 2: FtbJ

Chain 0: 7% 92%

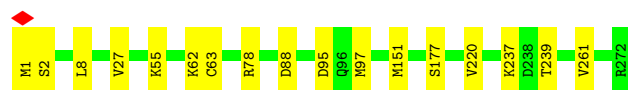
- Molecule 2: Ftb.J

Chain i:  8% 92%

[illegible]

- Molecule 3: FtbK

Chain s:  94% 6%



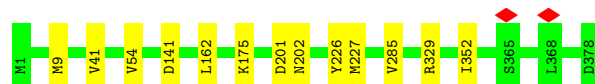
- Molecule 4: FtbL

Chain L:  96%



- Molecule 4: FtbL

Chain Q:  97%



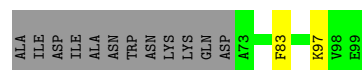
- Molecule 4: FtbL

Chain I:  96%



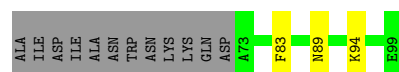
- Molecule 5: CCA-adding enzyme

Chain M:  25% 73%



- Molecule 5: CCA-adding enzyme

Chain R:  24% 73%



- Molecule 5: CCA-adding enzyme



MET	ALA	THR	GLU	ILE	ARG	VAL	LEU	LYS	ASN	VAL	ASP	ASP	THR	VAL	PHE	TYR	PRO	LYS	THR	HIS	VAL	THR	ALA	VAL	GLU	GLY	LEU	ASP	SER	ALA	THR	THR	THR	SER	GLY	LEU	MET	PRO	ALA	SER	ASP	LYS	THR	LYS	LEU	ASN	GLY	ILE	GLU	ALA	ASN	ALA	GLU	LYS	ASN	ASN	VAL	THR
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ALA	ILE	ASP	ILE	ALA	ASN	TRP	ASN	LYS	LYS	GLN	ASP	A73			N79			K97	V98	E99
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44283	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.763	Depositor
Minimum map value	-0.503	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.060	Depositor
Recommended contour level	0.23	Depositor
Map size (\AA)	549.9904, 549.9904, 549.9904	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.25	0/1218	0.45	0/1644
1	B	0.25	0/1218	0.45	0/1644
1	C	0.26	0/1218	0.48	0/1644
1	D	0.26	0/1218	0.47	0/1644
1	E	0.25	0/1218	0.48	0/1644
1	F	0.27	0/1218	0.49	0/1644
1	G	0.25	0/1218	0.44	0/1644
1	H	0.25	0/1214	0.52	0/1639
1	I	0.25	0/1218	0.44	0/1644
1	N	0.26	0/1214	0.54	0/1639
1	S	0.26	0/1218	0.48	0/1644
1	T	0.25	0/1218	0.46	0/1644
1	U	0.26	0/1218	0.47	0/1644
1	V	0.25	0/1214	0.49	0/1639
1	W	0.25	0/1214	0.45	0/1639
1	Y	0.25	0/1218	0.45	0/1644
1	Z	0.26	0/1218	0.49	0/1644
1	a	0.26	0/1218	0.51	0/1644
1	b	0.25	0/1218	0.47	0/1644
1	c	0.25	0/1218	0.45	0/1644
1	d	0.25	0/1214	0.49	0/1639
1	e	0.26	0/1218	0.49	0/1644
1	f	0.25	0/1218	0.44	0/1644
1	g	0.25	0/1214	0.45	0/1639
1	h	0.26	0/1214	0.55	0/1639
1	n	0.26	0/1218	0.50	0/1644
1	o	0.25	0/1218	0.48	0/1644
1	p	0.26	0/1218	0.47	0/1644
1	q	0.25	0/1214	0.49	0/1639
1	r	0.25	0/1214	0.46	0/1639
2	J	0.31	0/400	0.69	0/539
2	O	0.32	0/400	0.68	0/539
2	i	0.30	0/400	0.67	1/539 (0.2%)
3	K	0.26	0/2264	0.51	0/3069

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	P	0.26	0/2264	0.51	0/3069
3	X	0.26	0/2264	0.51	1/3069 (0.0%)
3	j	0.26	0/2264	0.50	0/3069
3	k	0.26	0/2264	0.53	1/3069 (0.0%)
3	s	0.25	0/2264	0.50	0/3069
4	L	0.25	0/3094	0.45	0/4176
4	Q	0.25	0/3094	0.45	0/4176
4	l	0.25	0/3094	0.45	0/4176
5	M	0.28	0/198	0.64	0/266
5	R	0.25	0/198	0.47	0/266
5	m	0.31	0/198	0.66	0/266
All	All	0.26	0/61164	0.49	3/82632 (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	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	k	151	MET	CA-CB-CG	6.09	123.65	113.30
2	i	579	LEU	CA-CB-CG	5.10	127.03	115.30
3	X	151	MET	CA-CB-CG	5.01	121.81	113.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	PHE	Peptide
1	D	3	PHE	Peptide

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

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	159/170 (94%)	151 (95%)	8 (5%)	0	100	100
1	B	159/170 (94%)	153 (96%)	6 (4%)	0	100	100
1	C	159/170 (94%)	152 (96%)	7 (4%)	0	100	100
1	D	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	E	159/170 (94%)	152 (96%)	7 (4%)	0	100	100
1	F	159/170 (94%)	152 (96%)	7 (4%)	0	100	100
1	G	159/170 (94%)	146 (92%)	13 (8%)	0	100	100
1	H	158/170 (93%)	151 (96%)	7 (4%)	0	100	100
1	I	159/170 (94%)	148 (93%)	11 (7%)	0	100	100
1	N	158/170 (93%)	151 (96%)	7 (4%)	0	100	100
1	S	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	T	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	U	159/170 (94%)	149 (94%)	10 (6%)	0	100	100
1	V	158/170 (93%)	153 (97%)	5 (3%)	0	100	100
1	W	158/170 (93%)	152 (96%)	6 (4%)	0	100	100
1	Y	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	Z	159/170 (94%)	151 (95%)	8 (5%)	0	100	100
1	a	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	b	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	c	159/170 (94%)	149 (94%)	10 (6%)	0	100	100
1	d	158/170 (93%)	153 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	e	159/170 (94%)	153 (96%)	6 (4%)	0	100	100
1	f	159/170 (94%)	148 (93%)	11 (7%)	0	100	100
1	g	158/170 (93%)	152 (96%)	6 (4%)	0	100	100
1	h	158/170 (93%)	149 (94%)	9 (6%)	0	100	100
1	n	159/170 (94%)	149 (94%)	10 (6%)	0	100	100
1	o	159/170 (94%)	150 (94%)	9 (6%)	0	100	100
1	p	159/170 (94%)	149 (94%)	10 (6%)	0	100	100
1	q	158/170 (93%)	153 (97%)	5 (3%)	0	100	100
1	r	158/170 (93%)	152 (96%)	6 (4%)	0	100	100
2	J	48/622 (8%)	46 (96%)	2 (4%)	0	100	100
2	O	48/622 (8%)	46 (96%)	2 (4%)	0	100	100
2	i	48/622 (8%)	46 (96%)	2 (4%)	0	100	100
3	K	270/272 (99%)	265 (98%)	5 (2%)	0	100	100
3	P	270/272 (99%)	265 (98%)	5 (2%)	0	100	100
3	X	270/272 (99%)	263 (97%)	7 (3%)	0	100	100
3	j	270/272 (99%)	264 (98%)	6 (2%)	0	100	100
3	k	270/272 (99%)	261 (97%)	9 (3%)	0	100	100
3	s	270/272 (99%)	261 (97%)	9 (3%)	0	100	100
4	L	376/378 (100%)	363 (96%)	13 (4%)	0	100	100
4	Q	376/378 (100%)	363 (96%)	13 (4%)	0	100	100
4	l	376/378 (100%)	364 (97%)	12 (3%)	0	100	100
5	M	25/99 (25%)	20 (80%)	5 (20%)	0	100	100
5	R	25/99 (25%)	20 (80%)	5 (20%)	0	100	100
5	m	25/99 (25%)	21 (84%)	4 (16%)	0	100	100
All	All	7728/10029 (77%)	7386 (96%)	342 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	124/131 (95%)	115 (93%)	9 (7%)	11	32
1	B	124/131 (95%)	111 (90%)	13 (10%)	5	16
1	C	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	D	124/131 (95%)	115 (93%)	9 (7%)	11	32
1	E	124/131 (95%)	117 (94%)	7 (6%)	17	44
1	F	124/131 (95%)	110 (89%)	14 (11%)	4	14
1	G	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	H	124/131 (95%)	109 (88%)	15 (12%)	4	11
1	I	124/131 (95%)	113 (91%)	11 (9%)	8	23
1	N	124/131 (95%)	109 (88%)	15 (12%)	4	11
1	S	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	T	124/131 (95%)	110 (89%)	14 (11%)	4	14
1	U	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	V	124/131 (95%)	110 (89%)	14 (11%)	4	14
1	W	124/131 (95%)	118 (95%)	6 (5%)	21	51
1	Y	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	Z	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	a	124/131 (95%)	117 (94%)	7 (6%)	17	44
1	b	124/131 (95%)	111 (90%)	13 (10%)	5	16
1	c	124/131 (95%)	112 (90%)	12 (10%)	6	19
1	d	124/131 (95%)	109 (88%)	15 (12%)	4	11
1	e	124/131 (95%)	112 (90%)	12 (10%)	6	19
1	f	124/131 (95%)	113 (91%)	11 (9%)	8	23
1	g	124/131 (95%)	116 (94%)	8 (6%)	14	37
1	h	124/131 (95%)	110 (89%)	14 (11%)	4	14
1	n	124/131 (95%)	116 (94%)	8 (6%)	14	37
1	o	124/131 (95%)	111 (90%)	13 (10%)	5	16
1	p	124/131 (95%)	114 (92%)	10 (8%)	9	27
1	q	124/131 (95%)	113 (91%)	11 (9%)	8	23
1	r	124/131 (95%)	117 (94%)	7 (6%)	17	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	43/510 (8%)	39 (91%)	4 (9%)	7	21
2	O	43/510 (8%)	38 (88%)	5 (12%)	4	12
2	i	43/510 (8%)	41 (95%)	2 (5%)	22	52
3	K	245/245 (100%)	225 (92%)	20 (8%)	9	26
3	P	245/245 (100%)	229 (94%)	16 (6%)	14	37
3	X	245/245 (100%)	230 (94%)	15 (6%)	15	40
3	j	245/245 (100%)	225 (92%)	20 (8%)	9	26
3	k	245/245 (100%)	234 (96%)	11 (4%)	23	53
3	s	245/245 (100%)	228 (93%)	17 (7%)	13	34
4	L	339/339 (100%)	325 (96%)	14 (4%)	26	57
4	Q	339/339 (100%)	326 (96%)	13 (4%)	28	60
4	l	339/339 (100%)	325 (96%)	14 (4%)	26	57
5	M	22/83 (26%)	20 (91%)	2 (9%)	7	22
5	R	22/83 (26%)	19 (86%)	3 (14%)	3	8
5	m	22/83 (26%)	20 (91%)	2 (9%)	7	22
All	All	6402/8196 (78%)	5916 (92%)	486 (8%)	13	30

5 of 486 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	P	103	GLU
1	p	12	THR
1	U	126	TYR
1	o	126	TYR
3	s	55	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	h	110	GLN
4	l	88	GLN
4	l	335	GLN
1	d	79	ASN
1	N	110	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](#)

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](#)

There are no chain breaks in this entry.

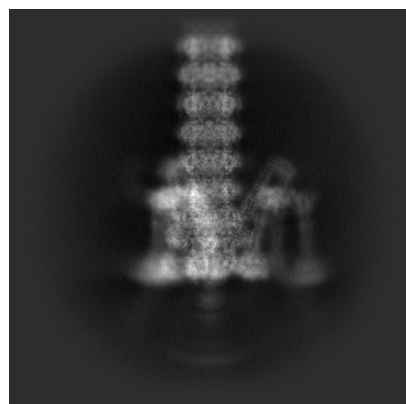
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61074. These allow visual inspection of the internal detail of the map and identification of artifacts.

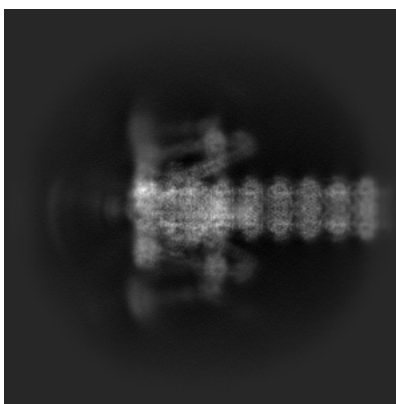
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

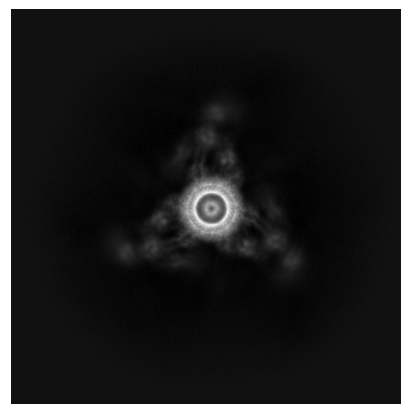
6.1.1 Primary map



X

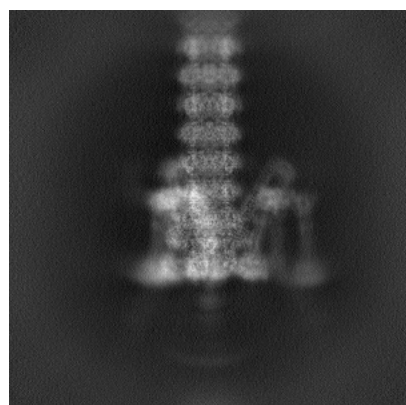


Y

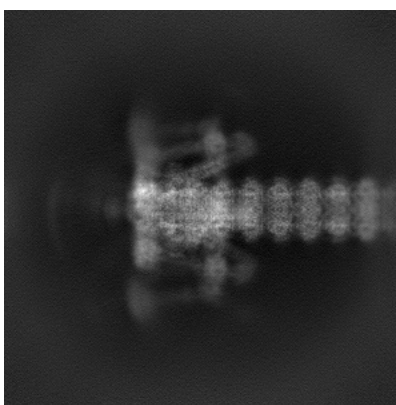


Z

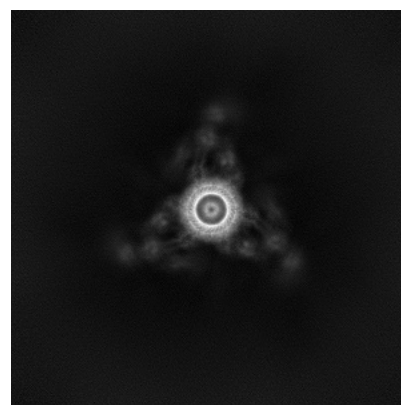
6.1.2 Raw map



X



Y

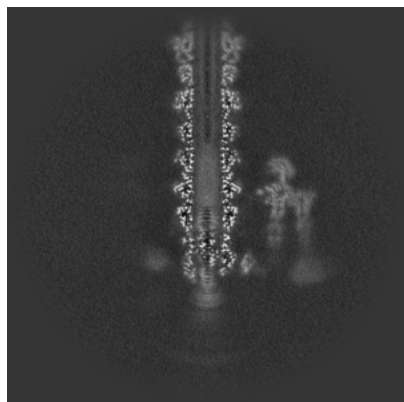


Z

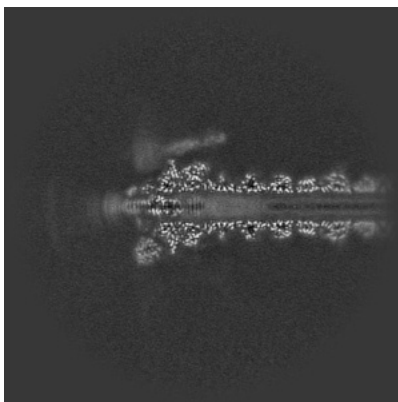
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

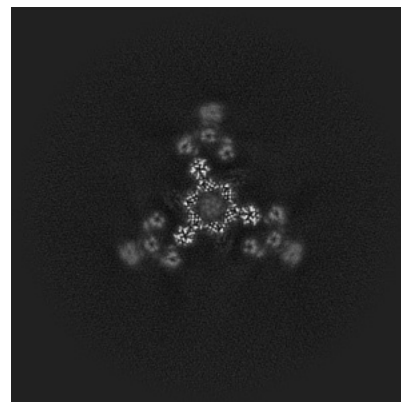
6.2.1 Primary map



X Index: 256

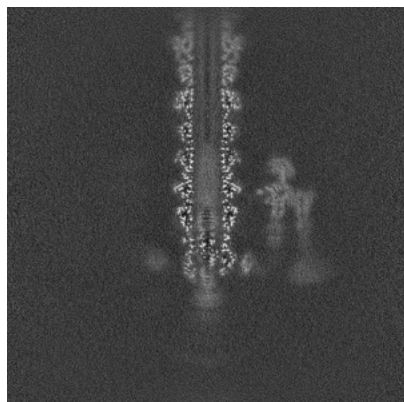


Y Index: 256

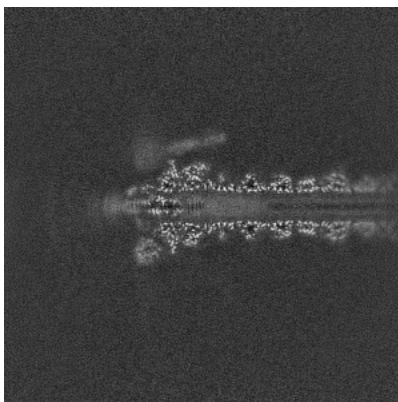


Z Index: 256

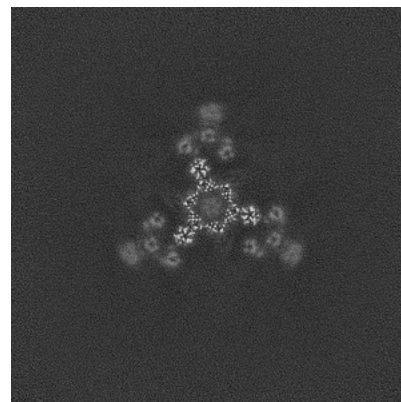
6.2.2 Raw map



X Index: 256



Y Index: 256

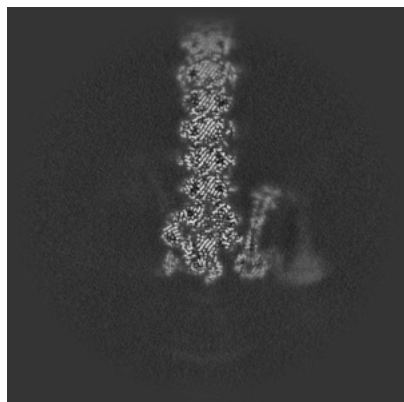


Z Index: 256

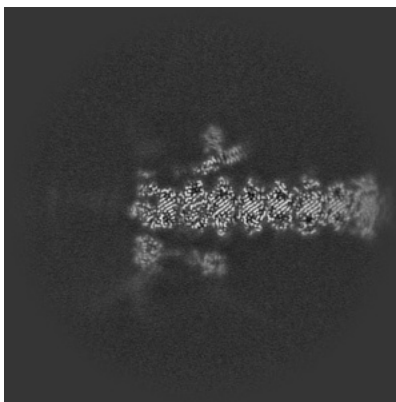
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

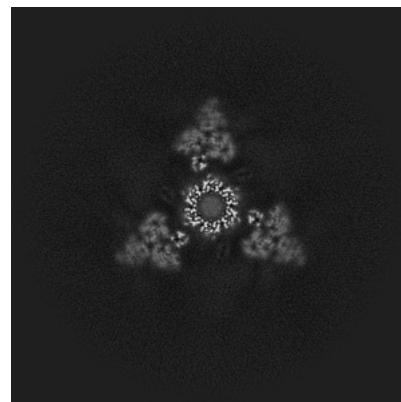
6.3.1 Primary map



X Index: 276

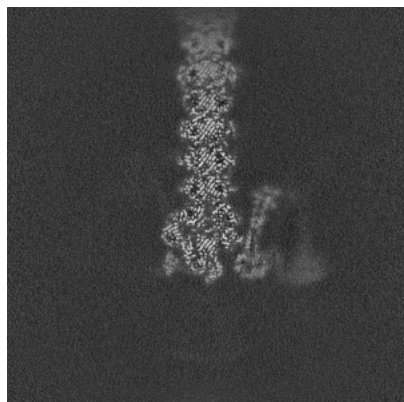


Y Index: 235

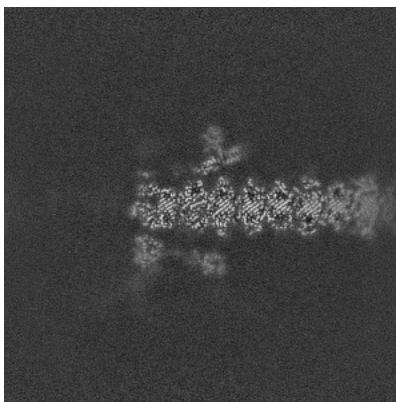


Z Index: 273

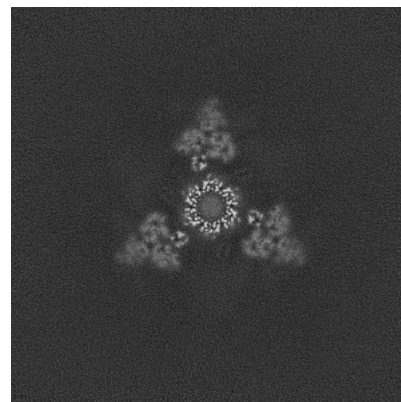
6.3.2 Raw map



X Index: 276



Y Index: 235

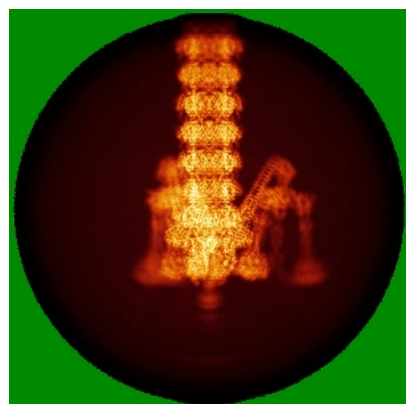


Z Index: 273

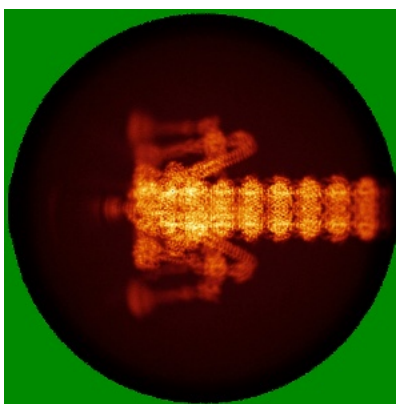
The images above show the largest variance slices of the map in three orthogonal directions.

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

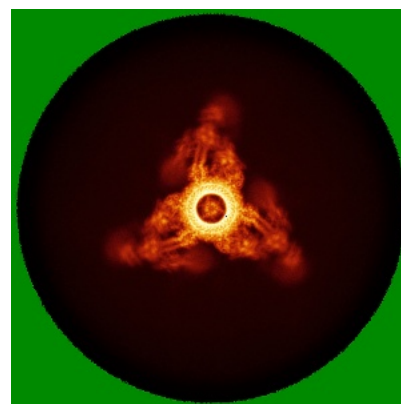
6.4.1 Primary map



X

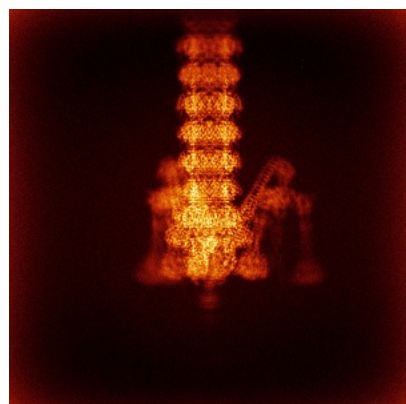


Y

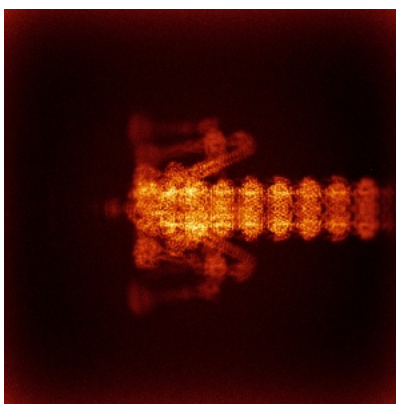


Z

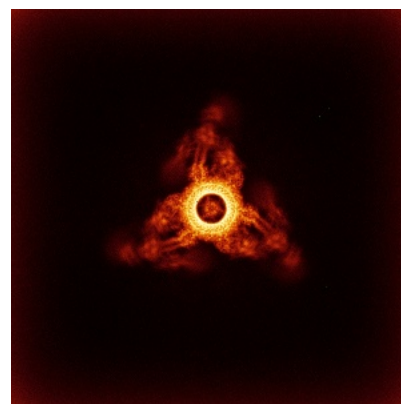
6.4.2 Raw map



X



Y

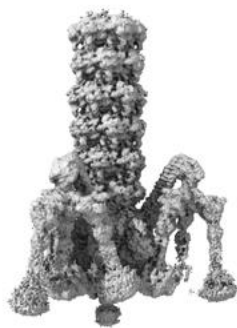


Z

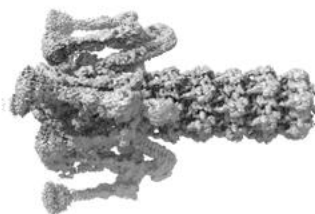
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



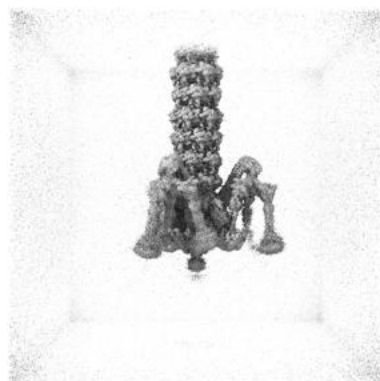
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.23. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

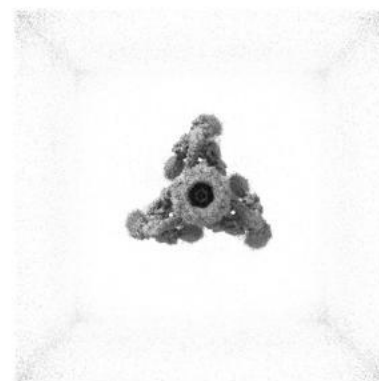
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

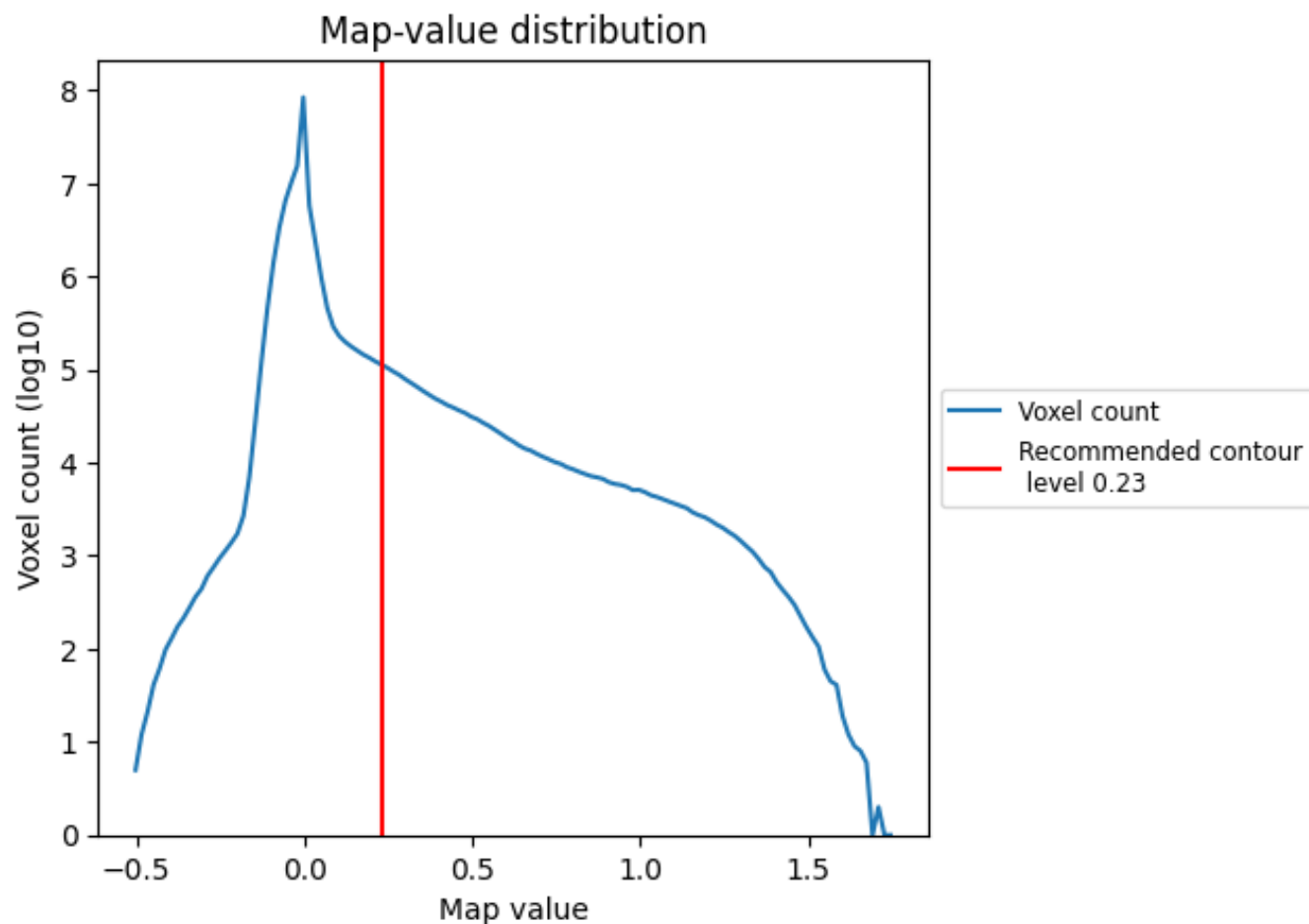
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

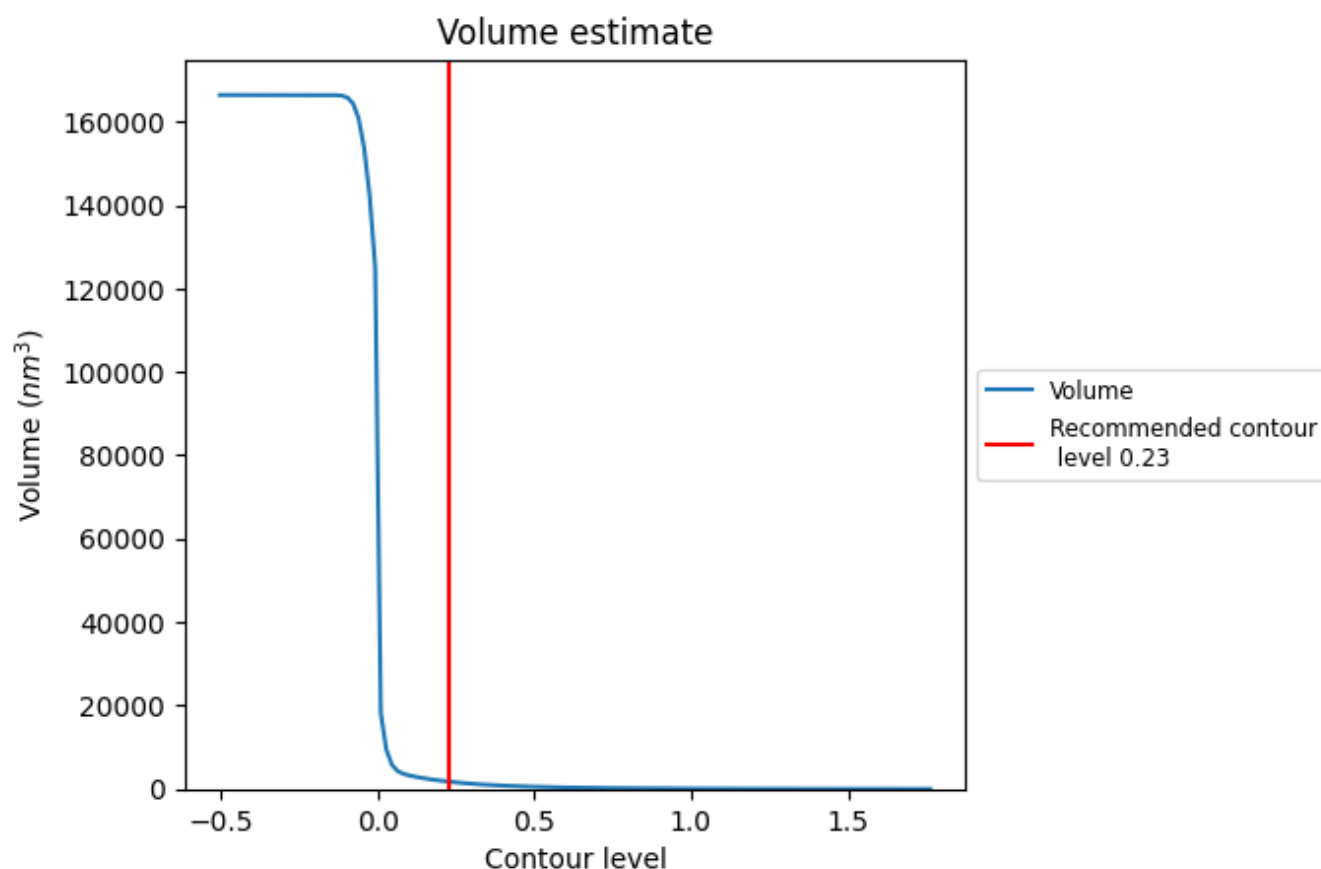
This section contains the results of statistical analysis of the map.

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.

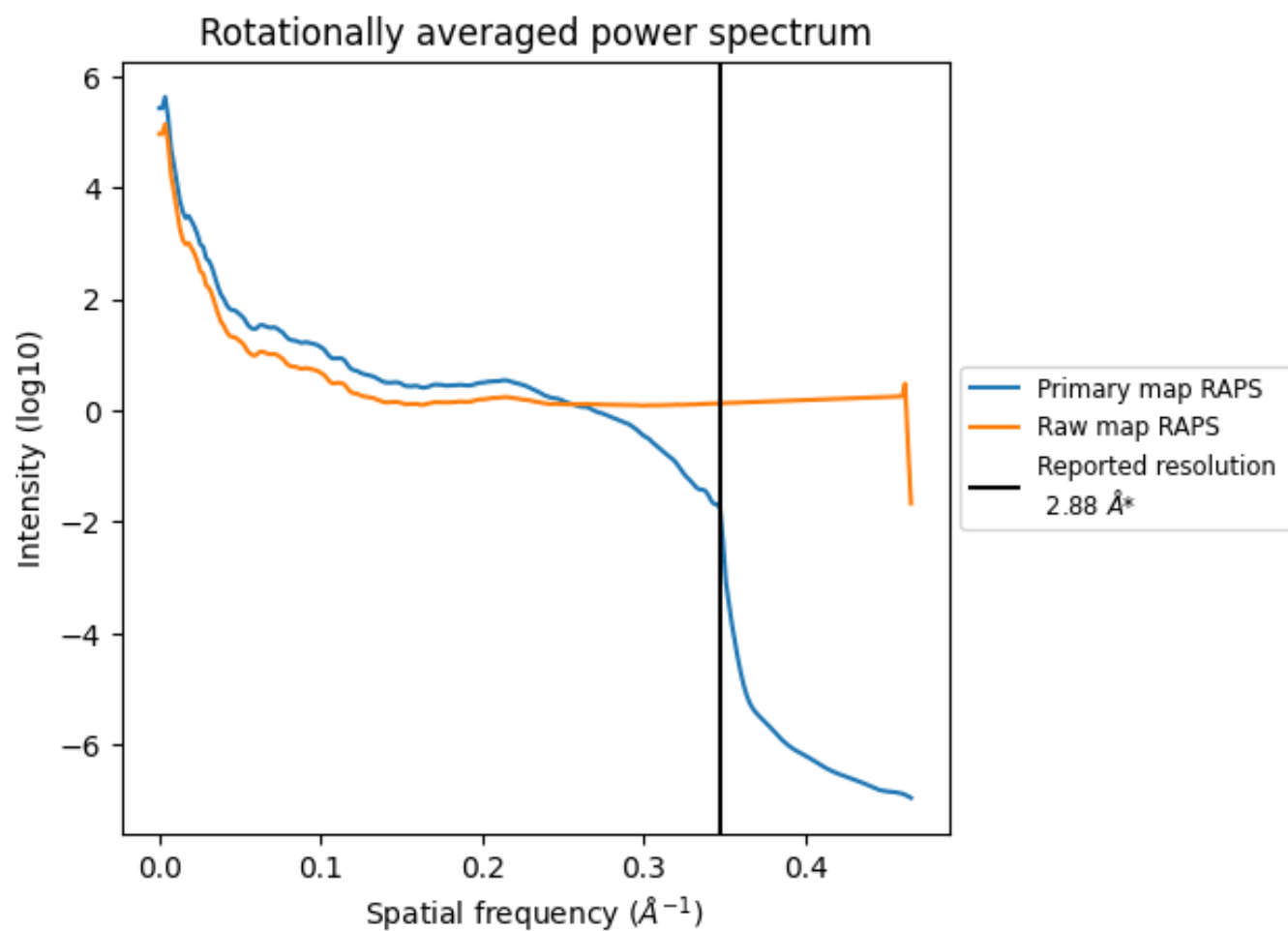
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1737 nm³; this corresponds to an approximate mass of 1569 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 ⓘ

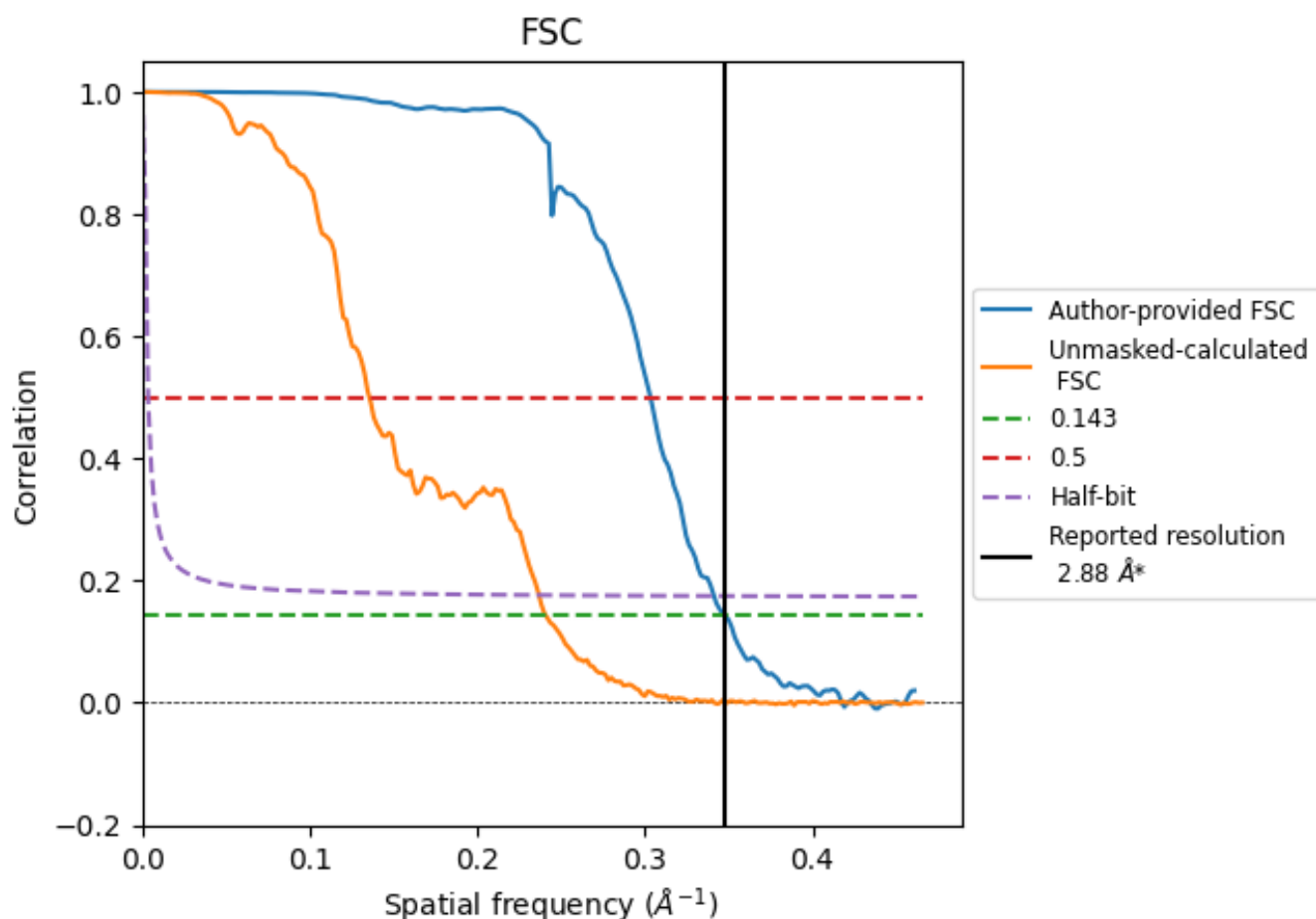


*Reported resolution corresponds to spatial frequency of 0.347 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.347 \AA^{-1}

8.2 Resolution estimates [i](#)

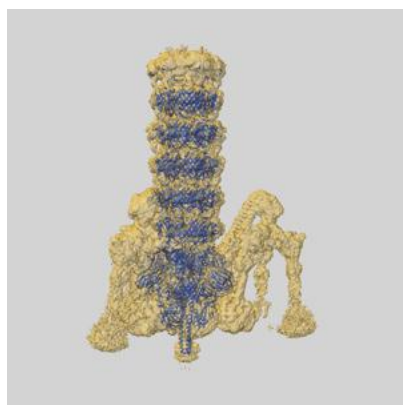
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	2.88	3.30	2.93
Unmasked-calculated*	4.15	7.37	4.22

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.15 differs from the reported value 2.88 by more than 10 %

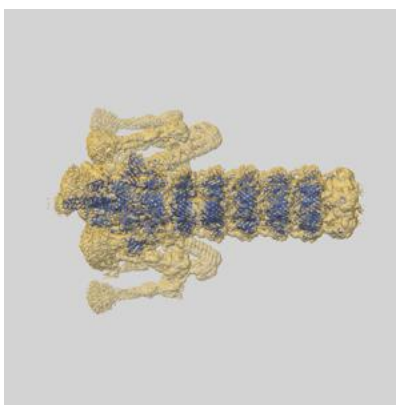
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61074 and PDB model 9J1K. Per-residue inclusion information can be found in section [3](#) on page [8](#).

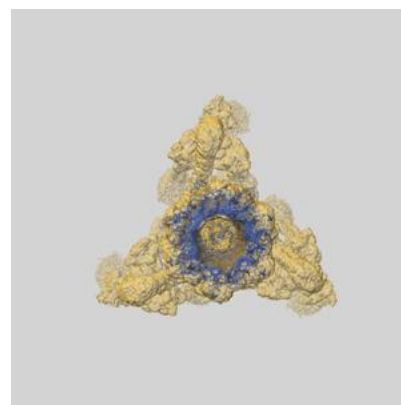
9.1 Map-model overlay [i](#)



X



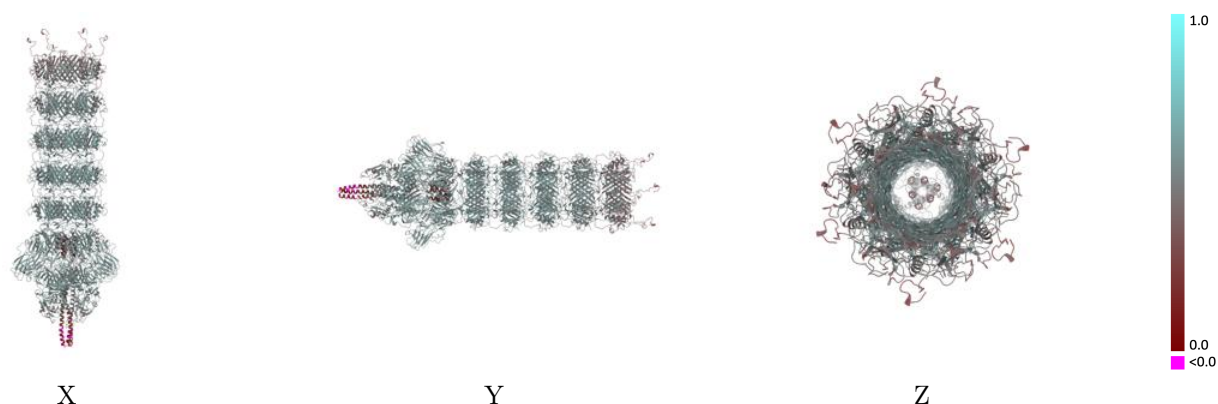
Y



Z

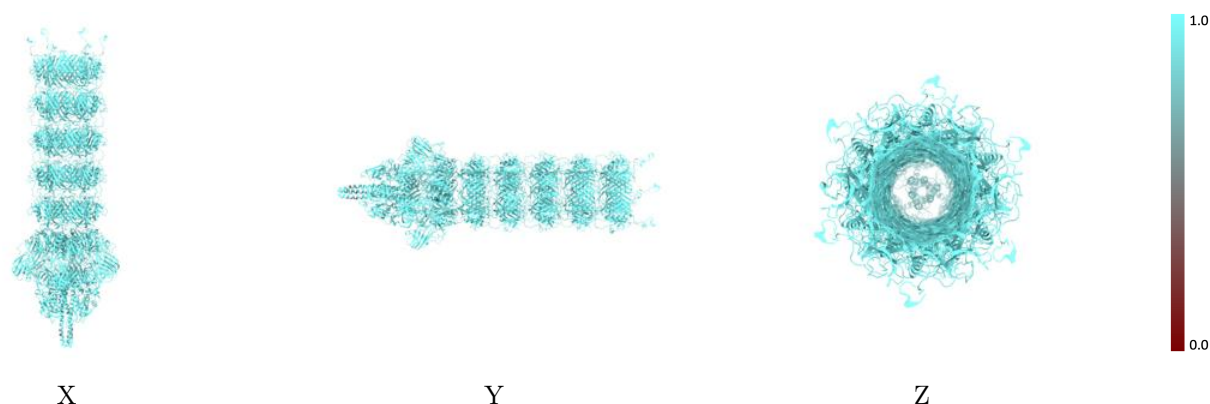
The images above show the 3D surface view of the map at the recommended contour level 0.23 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



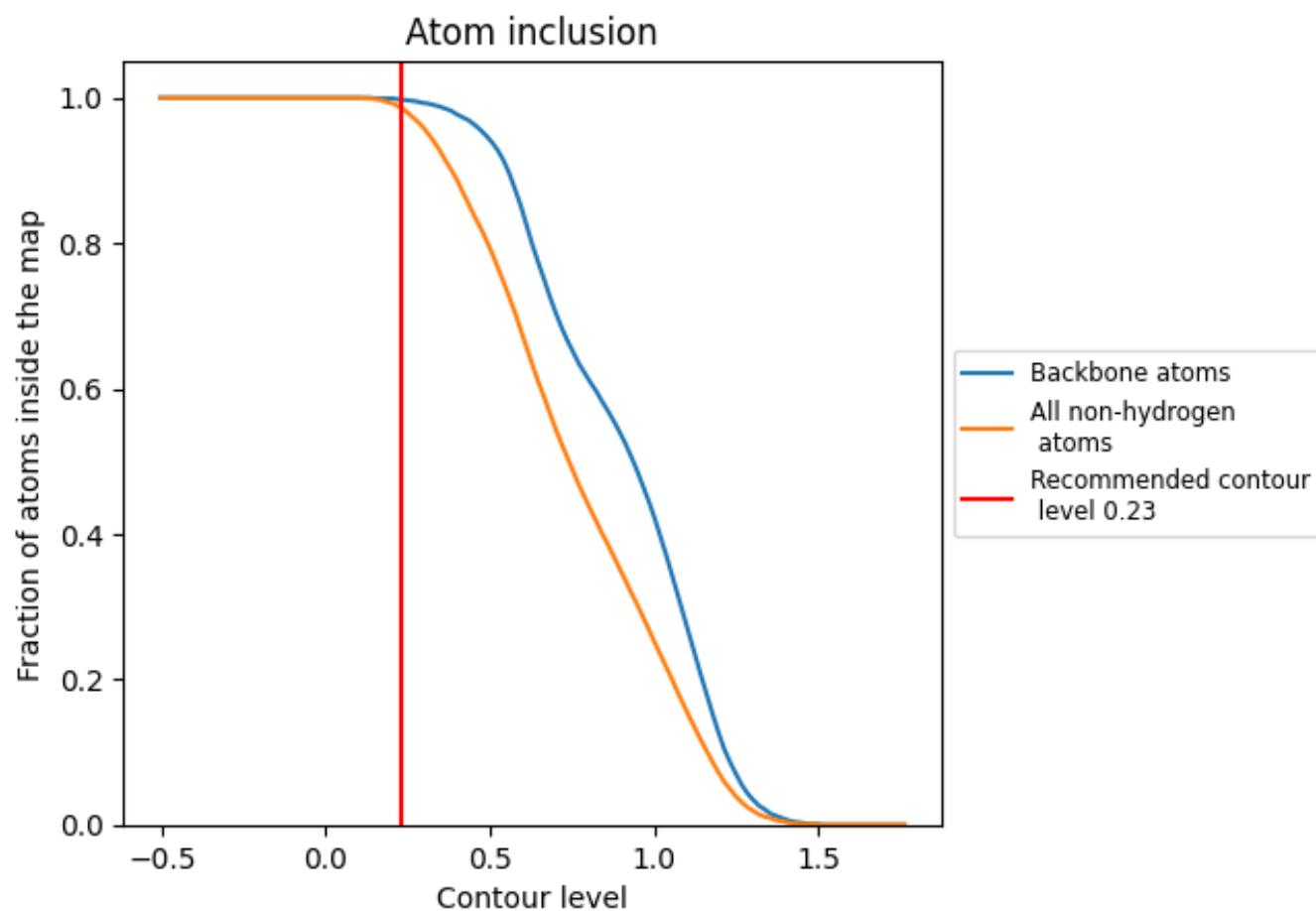
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.23).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9860	 0.5150
A	 0.9860	 0.5450
B	 0.9890	 0.5370
C	 0.9870	 0.5060
D	 0.9870	 0.5440
E	 0.9880	 0.5380
F	 0.9880	 0.5060
G	 0.9870	 0.5380
H	 0.9810	 0.4390
I	 0.9880	 0.5390
J	 0.9850	 0.4420
K	 0.9880	 0.5460
L	 0.9830	 0.5020
M	 0.9750	 0.3240
N	 0.9820	 0.4370
O	 0.9820	 0.4420
P	 0.9880	 0.5440
Q	 0.9830	 0.5020
R	 0.9800	 0.3280
S	 0.9820	 0.5420
T	 0.9860	 0.5360
U	 0.9870	 0.5080
V	 0.9850	 0.4380
W	 0.9870	 0.5340
X	 0.9910	 0.5440
Y	 0.9870	 0.5440
Z	 0.9890	 0.5370
a	 0.9850	 0.5420
b	 0.9890	 0.5370
c	 0.9880	 0.5120
d	 0.9850	 0.4400
e	 0.9870	 0.5080
f	 0.9890	 0.5410
g	 0.9870	 0.5350
h	 0.9820	 0.4390



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Chain	Atom inclusion	Q-score
i	 0.9850	 0.4360
j	 0.9890	 0.5460
k	 0.9910	 0.5450
l	 0.9820	 0.5010
m	 0.9850	 0.3190
n	 0.9840	 0.5410
o	 0.9860	 0.5360
p	 0.9900	 0.5070
q	 0.9820	 0.4410
r	 0.9870	 0.5350
s	 0.9920	 0.5440