



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:21 AM UTC

PDB ID : 8PR3 / pdb_00008pr3
EMDB ID : EMD-17833
Title : Cytoplasmic dynein-1 heavy chain bound to JIP3-RH1
Authors : Singh, K.; Lau, C.K.; Manigrasso, G.; Gassmann, R.; Carter, A.P.
Deposited on : 2023-07-12
Resolution : 3.90 Å(reported)
Based on initial model : 7Z8G

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

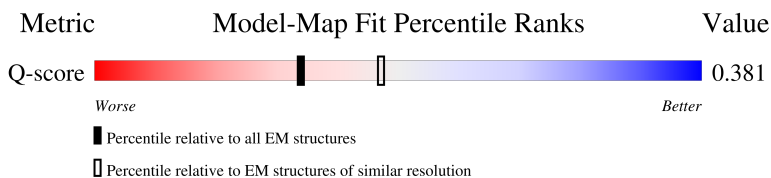
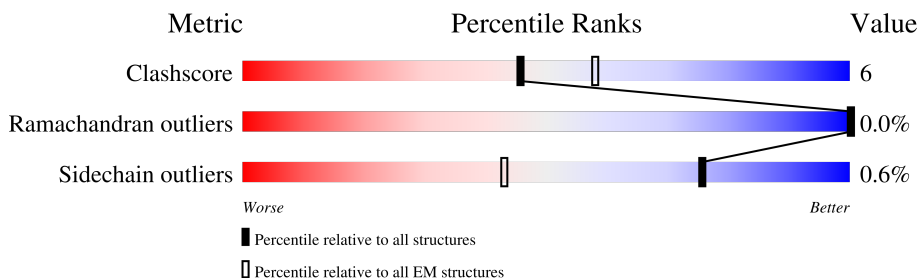
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	B	581	
1	C	581	
2	f	4646	
2	m	4646	

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Mol	Chain	Length	Quality of chain
3	h	612	51%9%39%
3	o	612	48%13%39%
4	E	492	97%
4	F	492	97%
4	j	492	7%50%11%39%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 17888 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 C-Jun-amino-terminal kinase-interacting protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	105	Total	C	N	O	S	0	0
			880	548	148	181	3		
1	C	106	Total	C	N	O	S	0	0
			886	551	149	183	3		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	SER	-	expression tag	UNP Q9UPT6
B	-5	ASN	-	expression tag	UNP Q9UPT6
B	-4	ILE	-	expression tag	UNP Q9UPT6
B	-3	GLU	-	expression tag	UNP Q9UPT6
B	-2	PHE	-	expression tag	UNP Q9UPT6
B	-1	LEU	-	expression tag	UNP Q9UPT6
B	0	LYS	-	expression tag	UNP Q9UPT6
B	561	GLY	-	expression tag	UNP Q9UPT6
B	562	SER	-	expression tag	UNP Q9UPT6
B	563	GLY	-	expression tag	UNP Q9UPT6
B	564	SER	-	expression tag	UNP Q9UPT6
B	565	GLY	-	expression tag	UNP Q9UPT6
B	566	ARG	-	expression tag	UNP Q9UPT6
B	567	TRP	-	expression tag	UNP Q9UPT6
B	568	SER	-	expression tag	UNP Q9UPT6
B	569	HIS	-	expression tag	UNP Q9UPT6
B	570	PRO	-	expression tag	UNP Q9UPT6
B	571	GLN	-	expression tag	UNP Q9UPT6
B	572	PHE	-	expression tag	UNP Q9UPT6
B	573	GLU	-	expression tag	UNP Q9UPT6
B	574	LYS	-	expression tag	UNP Q9UPT6
C	-6	SER	-	expression tag	UNP Q9UPT6
C	-5	ASN	-	expression tag	UNP Q9UPT6
C	-4	ILE	-	expression tag	UNP Q9UPT6
C	-3	GLU	-	expression tag	UNP Q9UPT6
C	-2	PHE	-	expression tag	UNP Q9UPT6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	LEU	-	expression tag	UNP Q9UPT6
C	0	LYS	-	expression tag	UNP Q9UPT6
C	561	GLY	-	expression tag	UNP Q9UPT6
C	562	SER	-	expression tag	UNP Q9UPT6
C	563	GLY	-	expression tag	UNP Q9UPT6
C	564	SER	-	expression tag	UNP Q9UPT6
C	565	GLY	-	expression tag	UNP Q9UPT6
C	566	ARG	-	expression tag	UNP Q9UPT6
C	567	TRP	-	expression tag	UNP Q9UPT6
C	568	SER	-	expression tag	UNP Q9UPT6
C	569	HIS	-	expression tag	UNP Q9UPT6
C	570	PRO	-	expression tag	UNP Q9UPT6
C	571	GLN	-	expression tag	UNP Q9UPT6
C	572	PHE	-	expression tag	UNP Q9UPT6
C	573	GLU	-	expression tag	UNP Q9UPT6
C	574	LYS	-	expression tag	UNP Q9UPT6

- Molecule 2 is a protein called Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	f	420	Total	C	N	O	S	0	0
			3449	2195	616	626	12		
2	m	523	Total	C	N	O	S	0	0
			4321	2746	784	778	13		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	1567	GLU	ARG	engineered mutation	UNP Q14204
f	1610	GLU	LYS	engineered mutation	UNP Q14204
m	1567	GLU	ARG	engineered mutation	UNP Q14204
m	1610	GLU	LYS	engineered mutation	UNP Q14204

- Molecule 3 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	371	Total	C	N	O	S	0	0
			2897	1820	508	554	15		
3	o	371	Total	C	N	O	S	0	0
			2897	1820	508	554	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	484	SER	THR	conflict	UNP Q13409
h	499	GLY	ASP	conflict	UNP Q13409
o	484	SER	THR	conflict	UNP Q13409
o	499	GLY	ASP	conflict	UNP Q13409

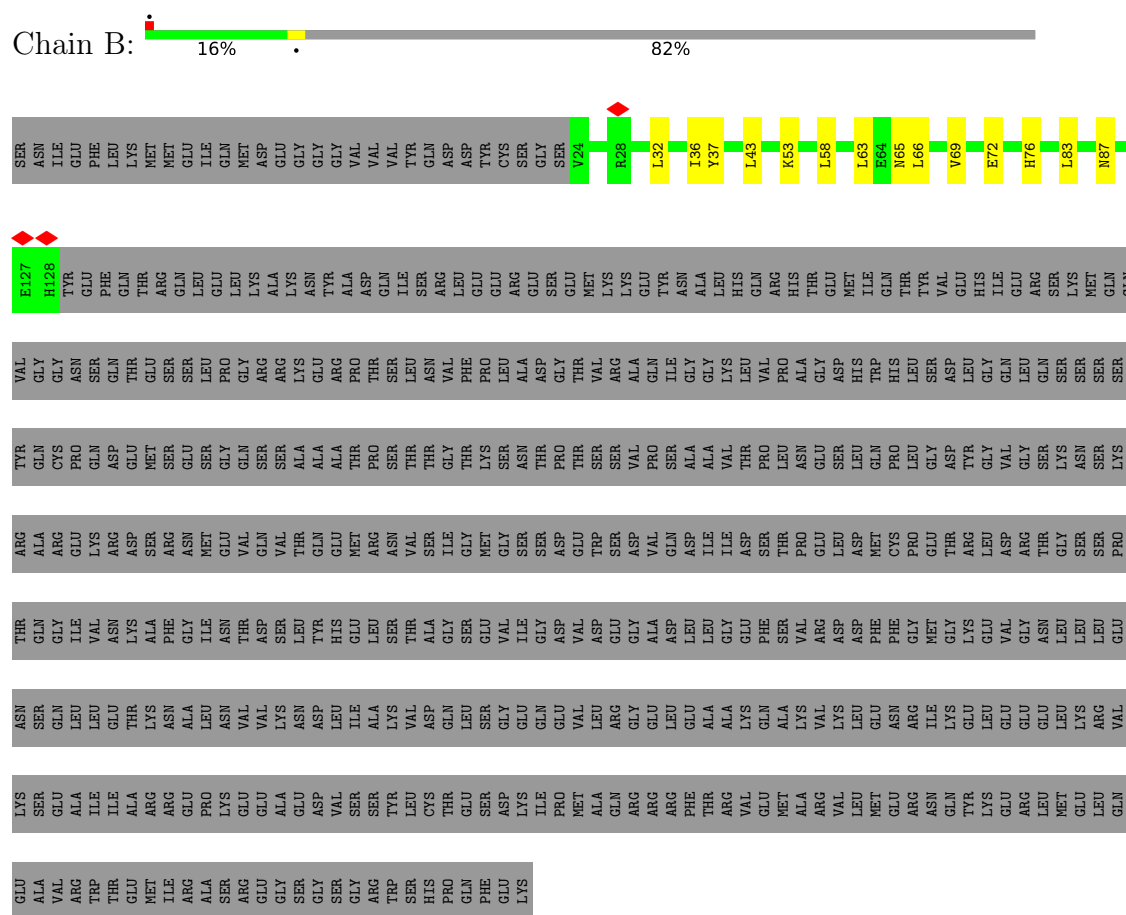
- Molecule 4 is a protein called Cytoplasmic dynein 1 light intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	j	299	Total 2428	C 1561	N 407	O 449	S 11	0	0
4	E	13	Total 65	C 39	N 13	O 13		0	0
4	F	13	Total 65	C 39	N 13	O 13		0	0

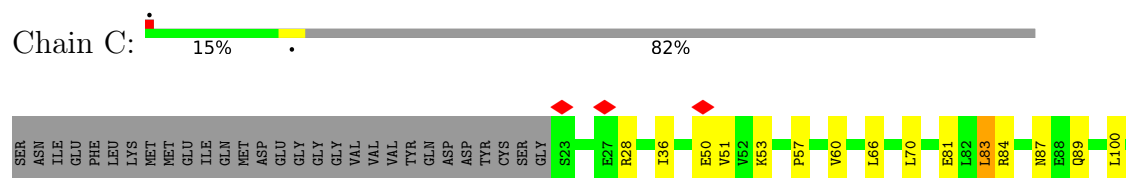
3 Residue-property plots

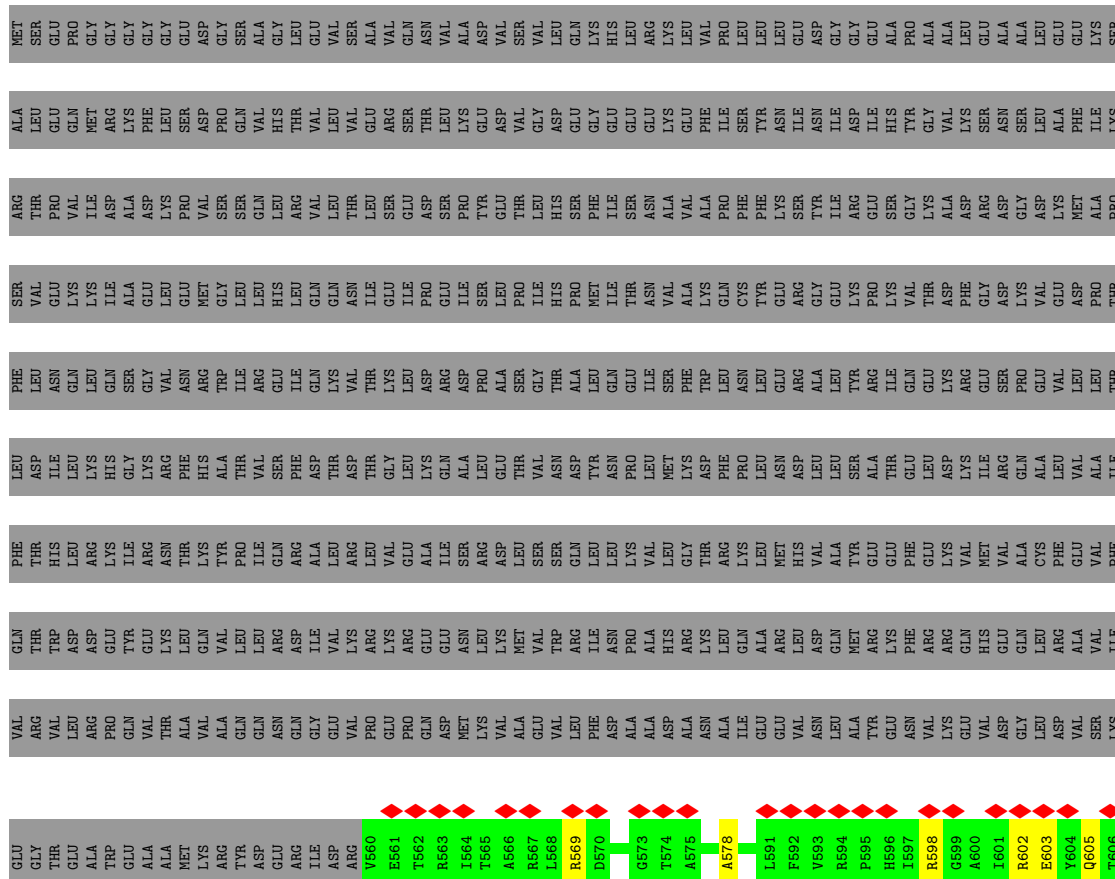
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: C-Jun-amino-terminal kinase-interacting protein 3



- Molecule 1: C-Jun-amino-terminal kinase-interacting protein 3

















- Molecule 3: Cytoplasmic dynein 1 intermediate chain 2

Chain h:



ASP	PHE	PRO	PRO	ARG	GLU	ILE	GLU	VAL	THR	THR	THR	LYS	GLU	THR	GLN	THR	PRO	PRO	LYS	GLU	ASP	GLU	GLU	GLU	VAL	VAL	ALA	ALA	PRO	PRO	LYS	PRO	PRO	ILE	GLU	GLU	PRO	GLU	ASN	ASP	SER	LYS	ALA	ALA	PRO	PRO	PRO	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible][illegible]

Category	Value	Color
W483	10	Green
K489	10	Green
D496	10	Red
D603	10	Green
V504	10	Green
M505	10	Green
L513	10	Green
D518	10	Green
G519	10	Green
M520	10	Green
G521	10	Green
R522	10	Green
L523	10	Green
D524	10	Green
L525	10	Green
F539	10	Green
M544	10	Green
L547	10	Green
M548	10	Green
R549	10	Green
V550	10	Green
R551	10	Green
W552	10	Green
E558	10	Green
F559	10	Green
D563	10	Green
S564	10	Green
D572	10	Green
E605	10	Red
A606	10	Red
A607	10	Red
T608	10	Red
ARG	10	Grey
ILE	10	Grey
PRO	10	Grey
ALA	10	Grey

- Molecule 3: Cytoplasmic dynein 1 intermediate chain 2

Chain o:



ASP PRO PRO PRO PRO ARG GLU ILE VAL THR THR THR THR GLU GLN GLN GLU GLU ASP ASP ASP VAL VAL VAL VAL PRO PRO PRO PRO ILE GLU GLU GLU THR THR LEU LYS LYS ASP ASP GLU GLU ASN ASP SER LYS LYS ALA ALA PRO PRO PRO PRO

GU	LEU	THR	GLU	GLU	GLY	LYS	GLN	GLN	LEU	HIS	SER	GLU	PHE	PHE	ASP	HIS	SER	THR	ARG	ILE	VAL	GLU	ARG	ALA	LEU	SER	SER	GLN	ILE	ASN	ILE	PHE	PHE	TYR	ASP	SER	GLY	ARG	ASP	LEU	GLU	GLY	ILE	GLN	GLY	ALA	K238	L239
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R264	D260	W261	E267	V270	D284	V289	W292	K296	T297	T298	C305	Q306	V309	M310	S311	L321	T326	Q330	L333	K340	P343	R346	L349	A352	H356	V361	T366	H370	S376	T377	T378	G379	K381	L381	S385
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Year	Q393	H400	V422	Y431	T432	H436	L442	H449	Q450	G451	P452	S475	F476	D477	M487	H488	K489	P490	L491	D496	M497	A498	D503	F504	M505	A512	G521	L528	D631	T532	I539	L547	V550	R557	D563	Q567	D572			
1993	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100		
1994	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
1995	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
1996	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
1997	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
1998	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
1999	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
2000	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
2001	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
2002	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
2003	100	100	100	100																																				

E575	I595	R599	A602	T608	ARG
Q576	N596	A600	E603		ILE
I577		D601	E604		PRO
			E605		ALA

- Molecule 4: Cytoplasmic dynein 1 light intermediate chain 2

97%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37297	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.023	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	296.52002, 296.52002, 296.52002	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.30	0/889	0.71	0/1194
1	C	0.30	0/895	0.78	0/1202
2	f	0.25	0/3512	0.55	3/4739 (0.1%)
2	m	0.26	0/4391	0.61	4/5912 (0.1%)
3	h	0.27	0/2976	0.46	1/4058 (0.0%)
3	o	0.30	0/2976	0.50	0/4058
4	E	0.78	0/64	1.38	1/88 (1.1%)
4	F	0.48	0/64	1.15	1/88 (1.1%)
4	j	0.20	0/2483	0.54	0/3352
All	All	0.27	0/18250	0.57	10/24691 (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
2	f	0	1
2	m	0	1
All	All	0	2

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	f	662	MET	CB-CG-SD	6.29	131.58	112.70
2	m	357	LEU	CA-CB-CG	6.29	138.30	116.30
2	m	393	LEU	CA-CB-CG	6.21	138.02	116.30
4	E	437	LEU	N-CA-C	6.11	117.74	111.14
4	F	434	ASN	N-CA-C	-5.49	105.38	111.36

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	f	1003	ARG	Sidechain
2	m	339	PHE	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	880	0	857	13	0
1	C	886	0	862	14	0
2	f	3449	0	3509	42	0
2	m	4321	0	4434	49	0
3	h	2897	0	2749	35	0
3	o	2897	0	2749	46	0
4	E	65	0	28	2	0
4	F	65	0	28	1	0
4	j	2428	0	2430	33	0
All	All	17888	0	17646	219	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 6.

The worst 5 of 219 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)
3:o:296:LYS:HD2	3:o:298:THR:OG1	1.79	0.82
3:o:601:ASP:O	3:o:604:GLU:HG2	1.89	0.73
3:o:600:ALA:O	3:o:603:GLU:HG2	1.90	0.72
2:f:994:LEU:HD12	2:f:1020:ARG:HD3	1.76	0.67
3:h:305:CYS:SG	3:h:306:GLN:N	2.70	0.64

There are no symmetry-related clashes.

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	B	103/581 (18%)	101 (98%)	2 (2%)	0	100	100
1	C	104/581 (18%)	102 (98%)	2 (2%)	0	100	100
2	f	416/4646 (9%)	402 (97%)	14 (3%)	0	100	100
2	m	515/4646 (11%)	509 (99%)	6 (1%)	0	100	100
3	h	369/612 (60%)	357 (97%)	12 (3%)	0	100	100
3	o	369/612 (60%)	355 (96%)	14 (4%)	0	100	100
4	E	11/492 (2%)	11 (100%)	0	0	100	100
4	F	11/492 (2%)	9 (82%)	2 (18%)	0	100	100
4	j	295/492 (60%)	280 (95%)	14 (5%)	1 (0%)	36	69
All	All	2193/13154 (17%)	2126 (97%)	66 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	j	353	GLU

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	B	99/514 (19%)	99 (100%)	0	100	100
1	C	100/514 (20%)	98 (98%)	2 (2%)	48	65
2	f	377/4125 (9%)	374 (99%)	3 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	m	467/4125 (11%)	465 (100%)	2 (0%)	84	83
3	h	316/531 (60%)	315 (100%)	1 (0%)	86	85
3	o	316/531 (60%)	313 (99%)	3 (1%)	70	75
4	j	268/422 (64%)	267 (100%)	1 (0%)	84	83
All	All	1943/10762 (18%)	1931 (99%)	12 (1%)	76	80

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	m	576	LYS
2	m	836	LEU
3	o	436	HIS
3	o	381	ILE
2	f	755	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
2	m	708	GLN
3	o	345	GLN
3	o	596	ASN
3	h	242	ASN
2	f	1002	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 [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.

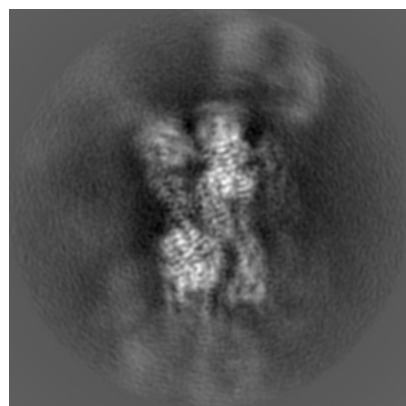
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17833. These allow visual inspection of the internal detail of the map and identification of artifacts.

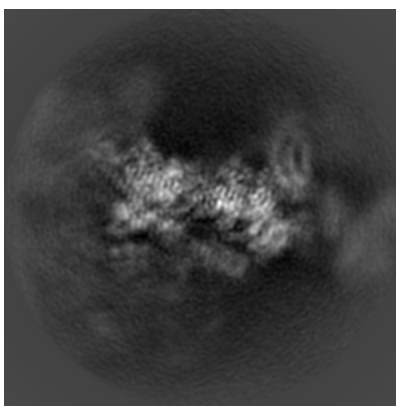
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

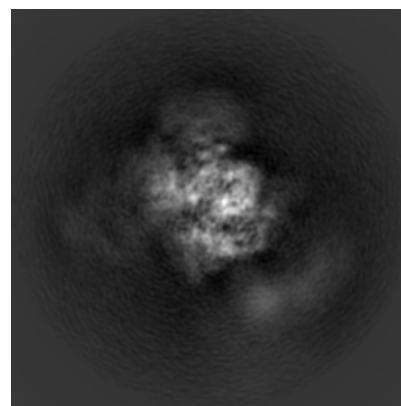
6.1.1 Primary map



X

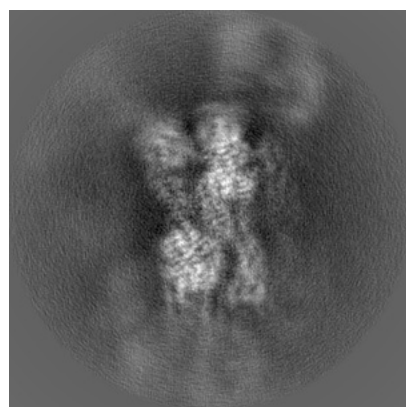


Y

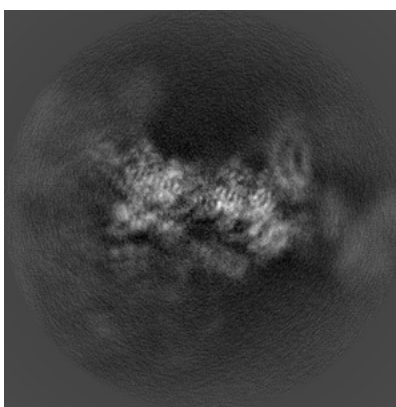


Z

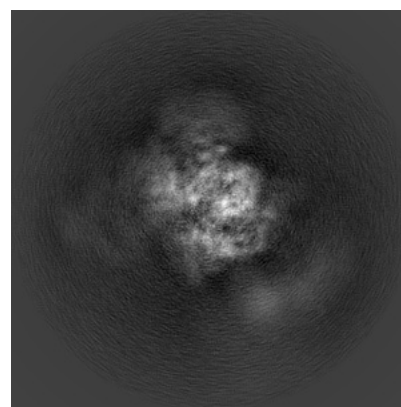
6.1.2 Raw map



X



Y

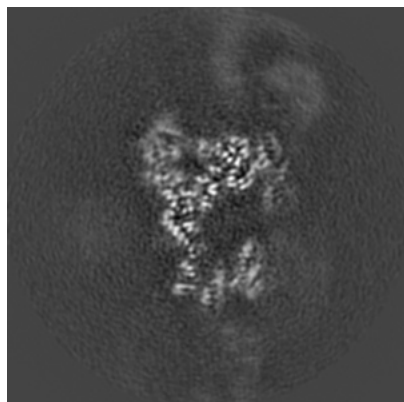


Z

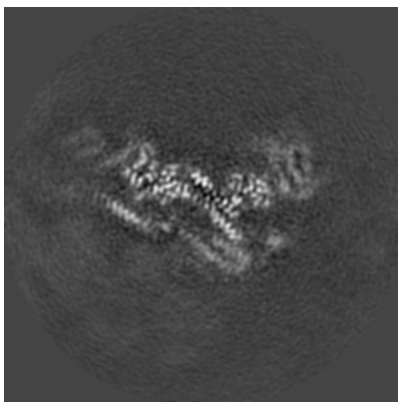
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

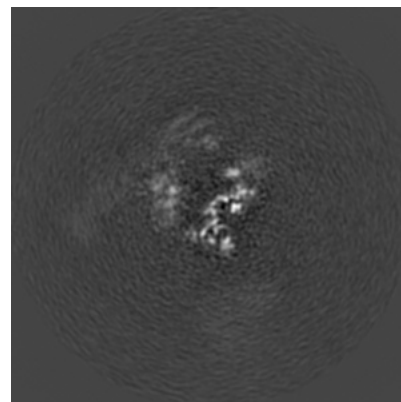
6.2.1 Primary map



X Index: 140

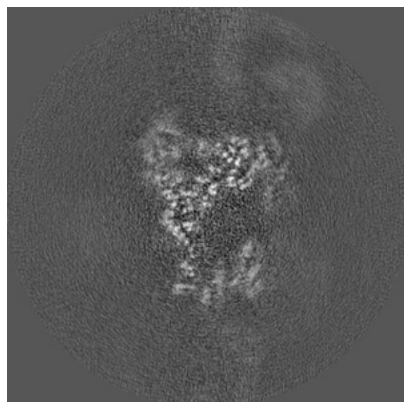


Y Index: 140

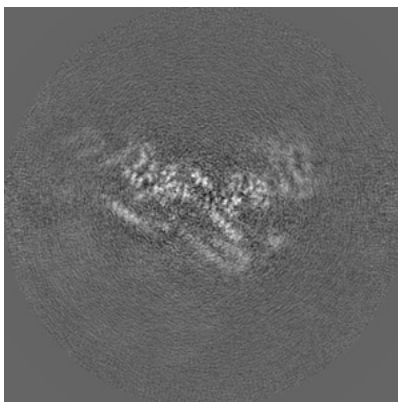


Z Index: 140

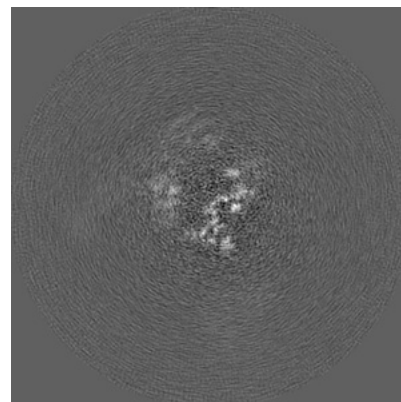
6.2.2 Raw map



X Index: 140



Y Index: 140

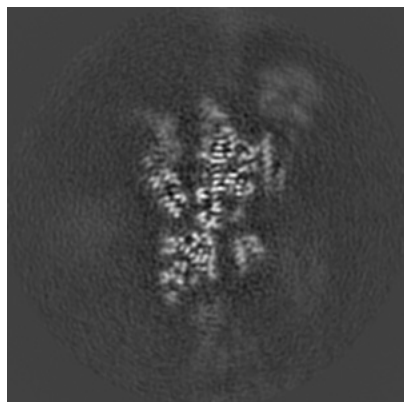


Z Index: 140

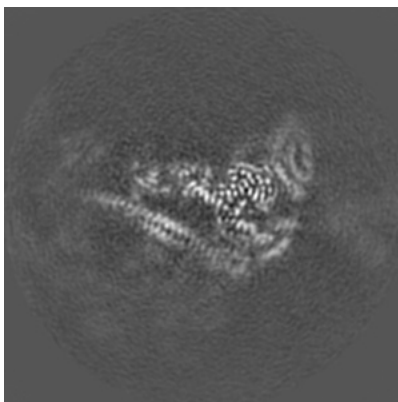
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

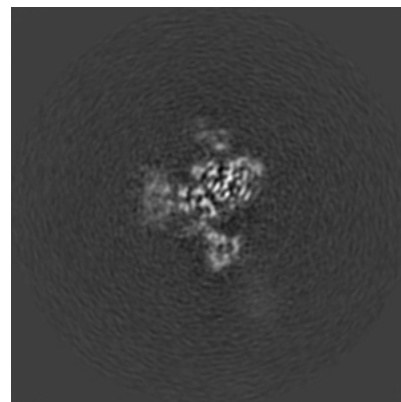
6.3.1 Primary map



X Index: 149

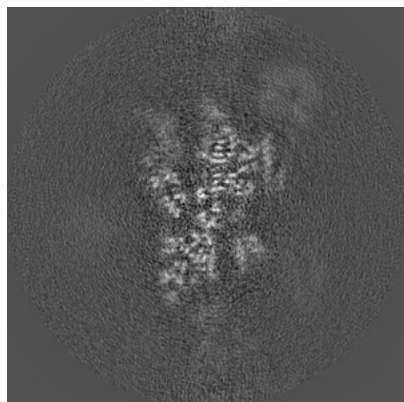


Y Index: 146

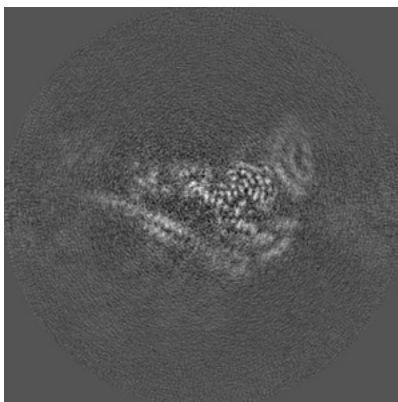


Z Index: 158

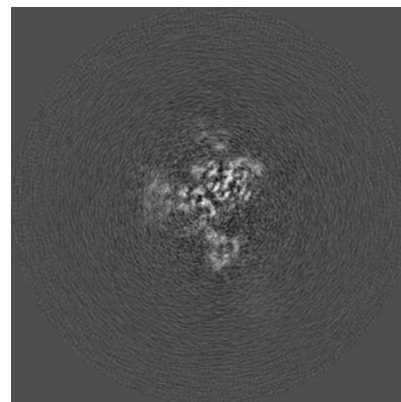
6.3.2 Raw map



X Index: 149



Y Index: 146

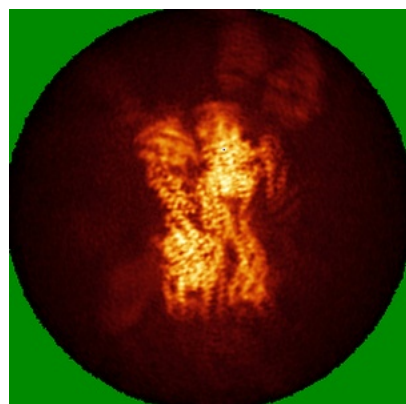


Z Index: 158

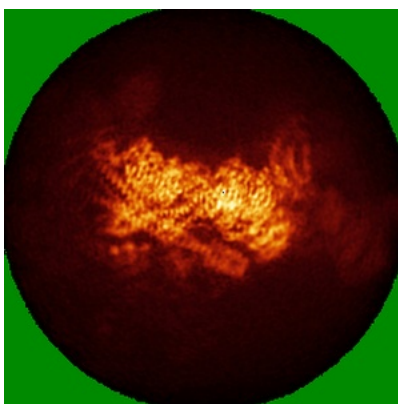
The images above show the largest variance slices of the map in three orthogonal directions.

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

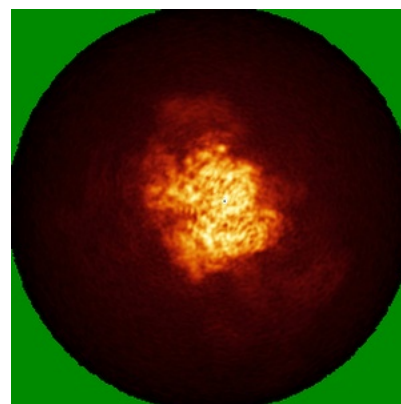
6.4.1 Primary map



X

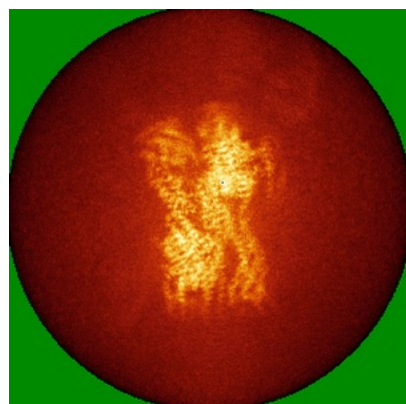


Y

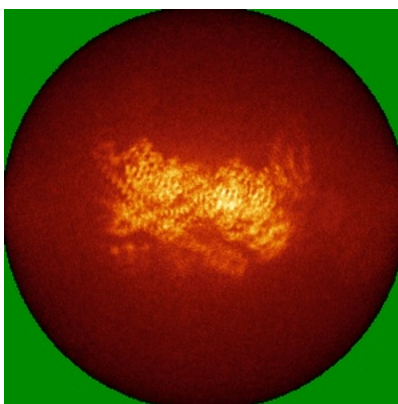


Z

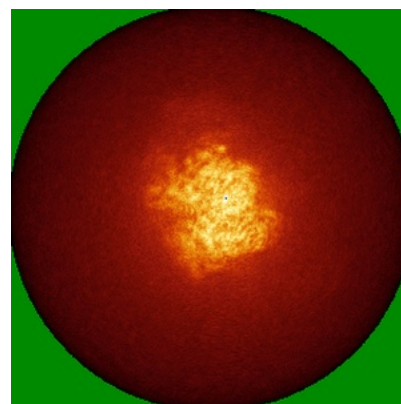
6.4.2 Raw map



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



The images above show the 3D surface view of the map at the recommended contour level 0.004. 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



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.

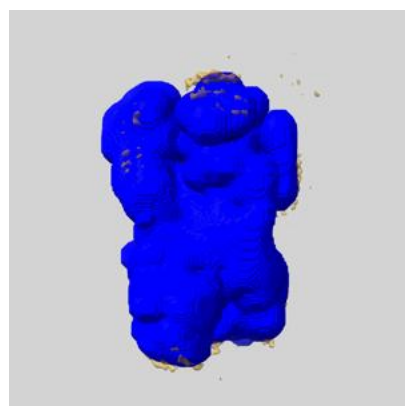
6.6 Mask visualisation [i](#)

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

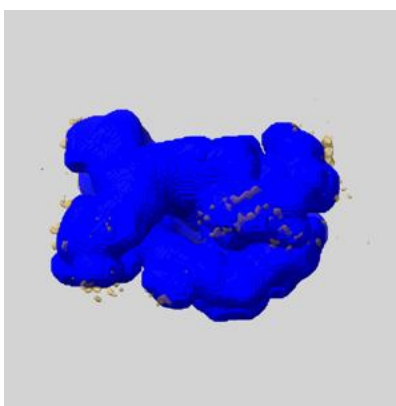
A mask typically either:

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

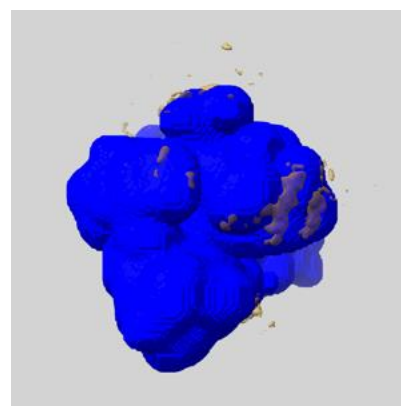
6.6.1 emd_17833_msk_1.map [i](#)



X



Y

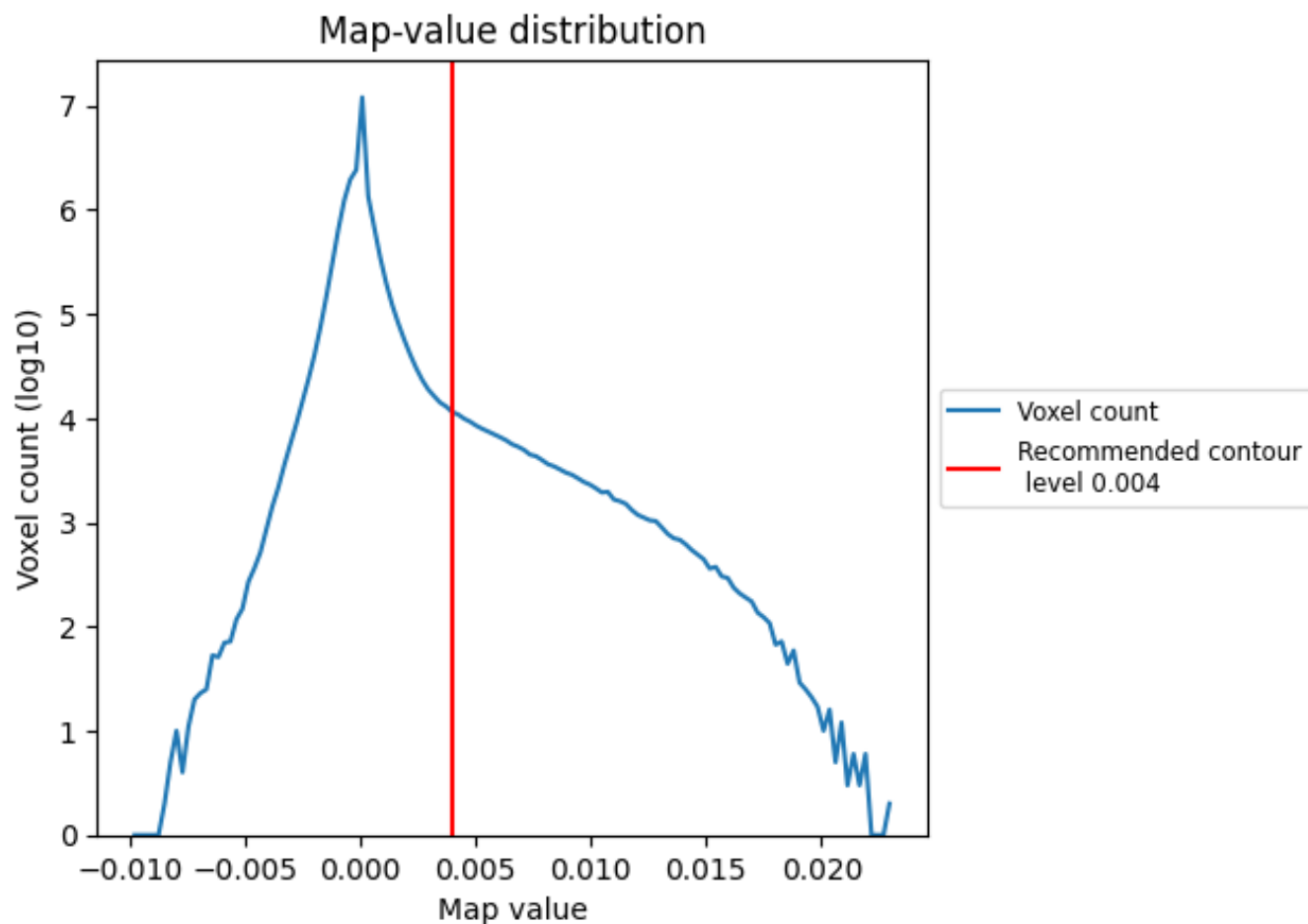


Z

7 Map analysis [i](#)

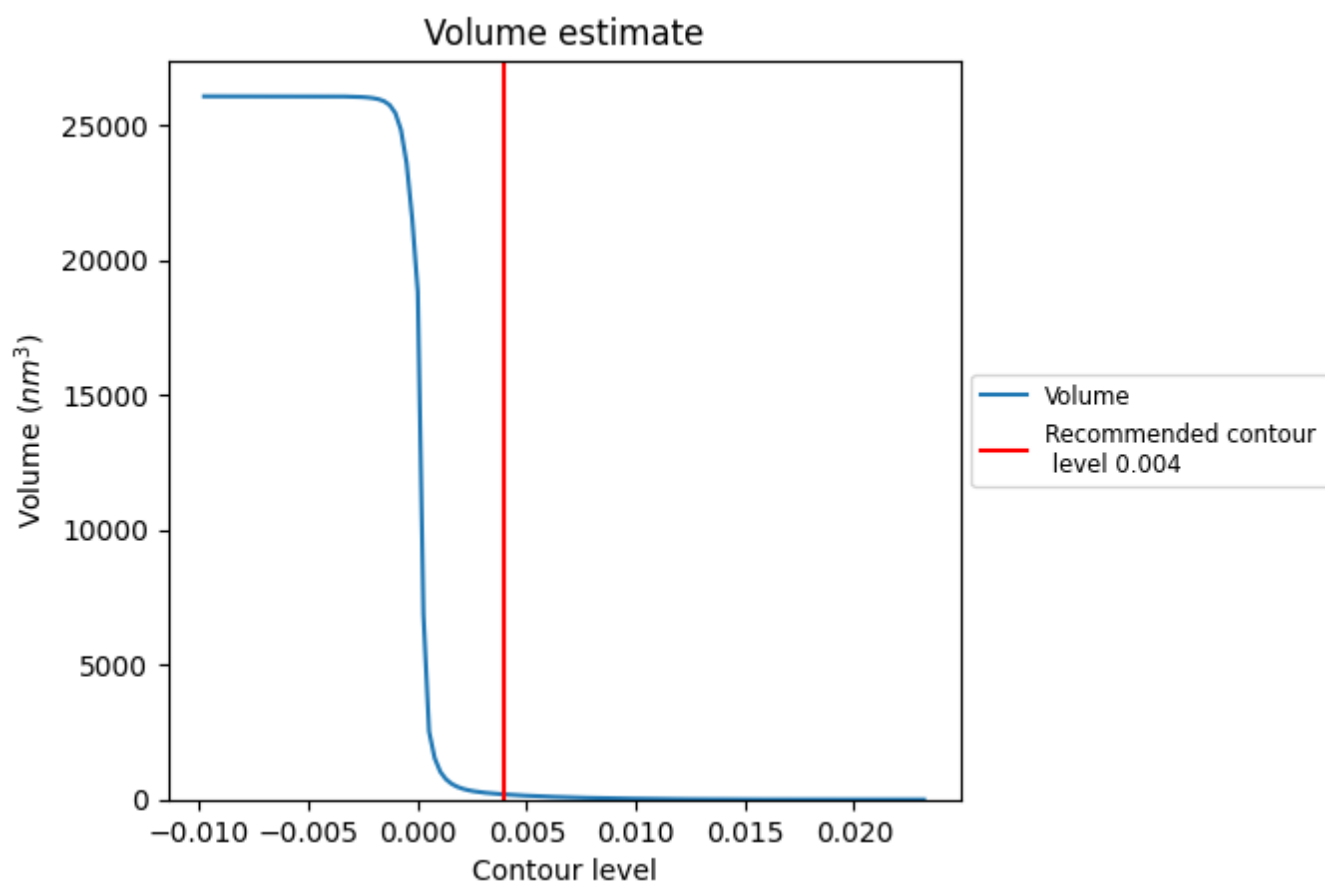
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

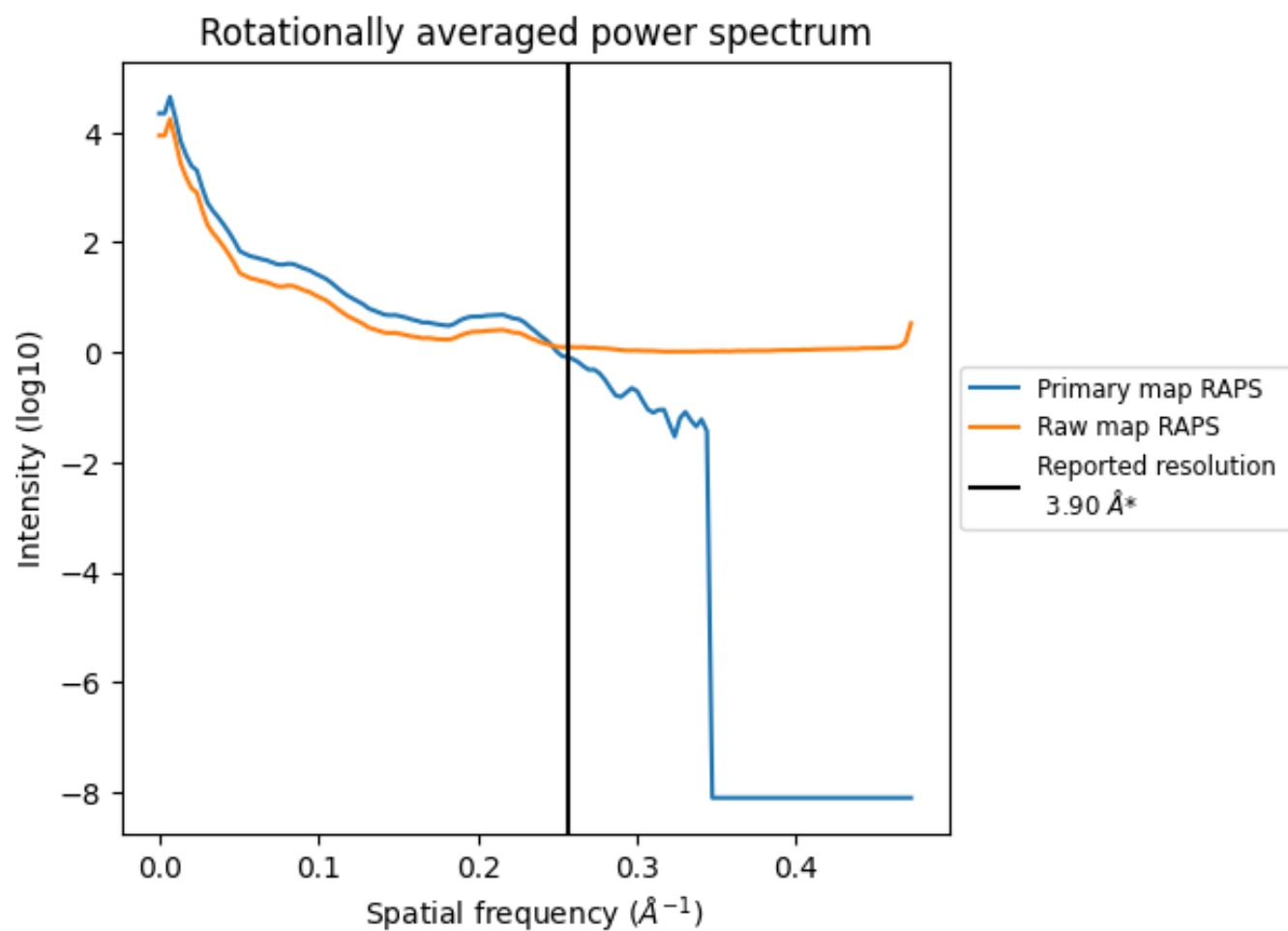
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 192 nm³; this corresponds to an approximate mass of 173 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 ⓘ

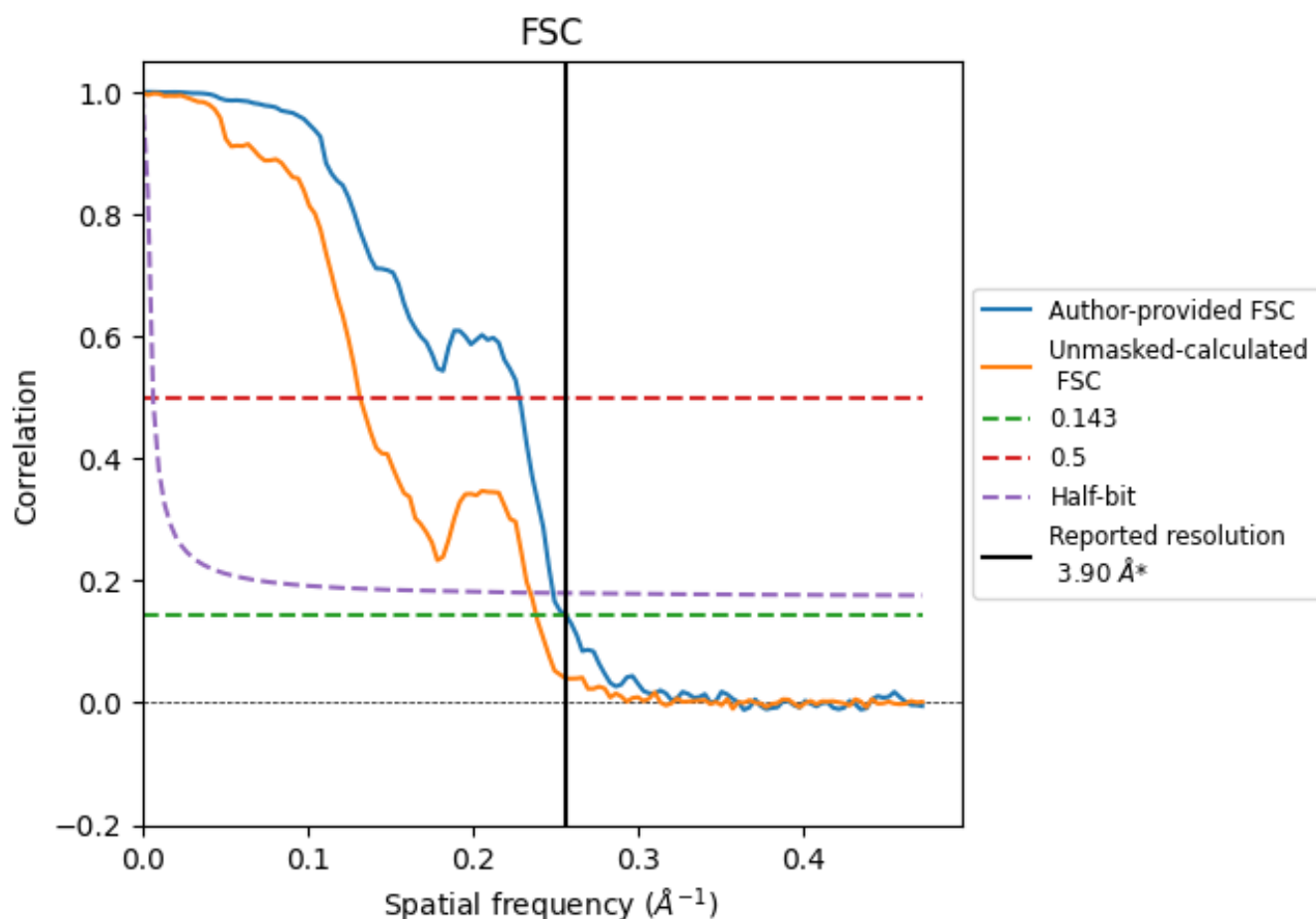


*Reported resolution corresponds to spatial frequency of $0.256 \text{ \AA}^{-1}$

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 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

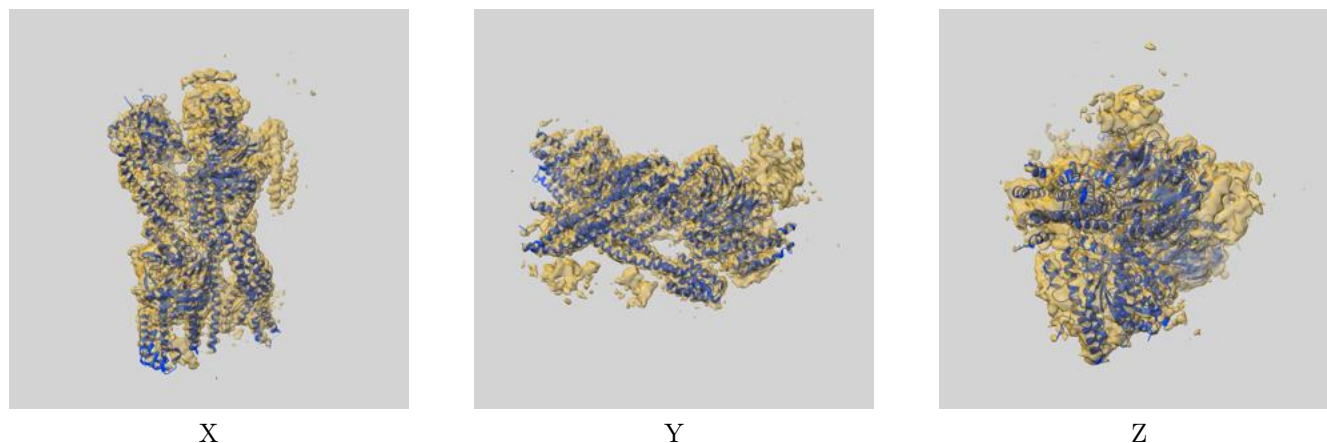
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.90	4.38	4.02
Unmasked-calculated*	4.19	7.59	4.26

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

9 Map-model fit [i](#)

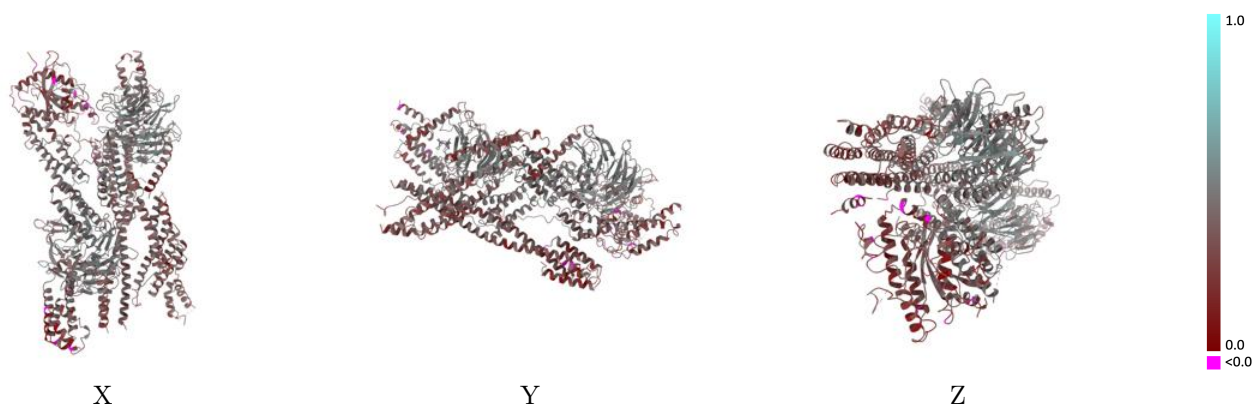
This section contains information regarding the fit between EMDB map EMD-17833 and PDB model 8PR3. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



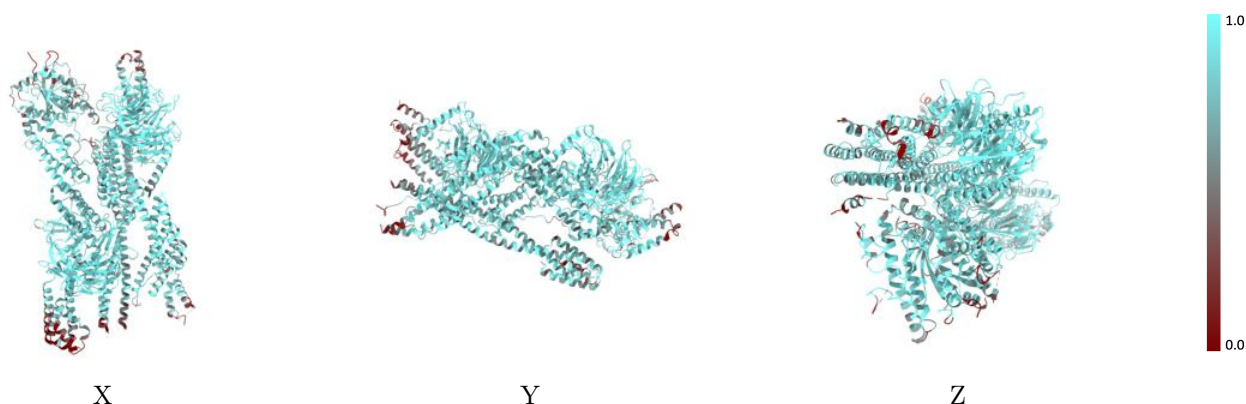
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



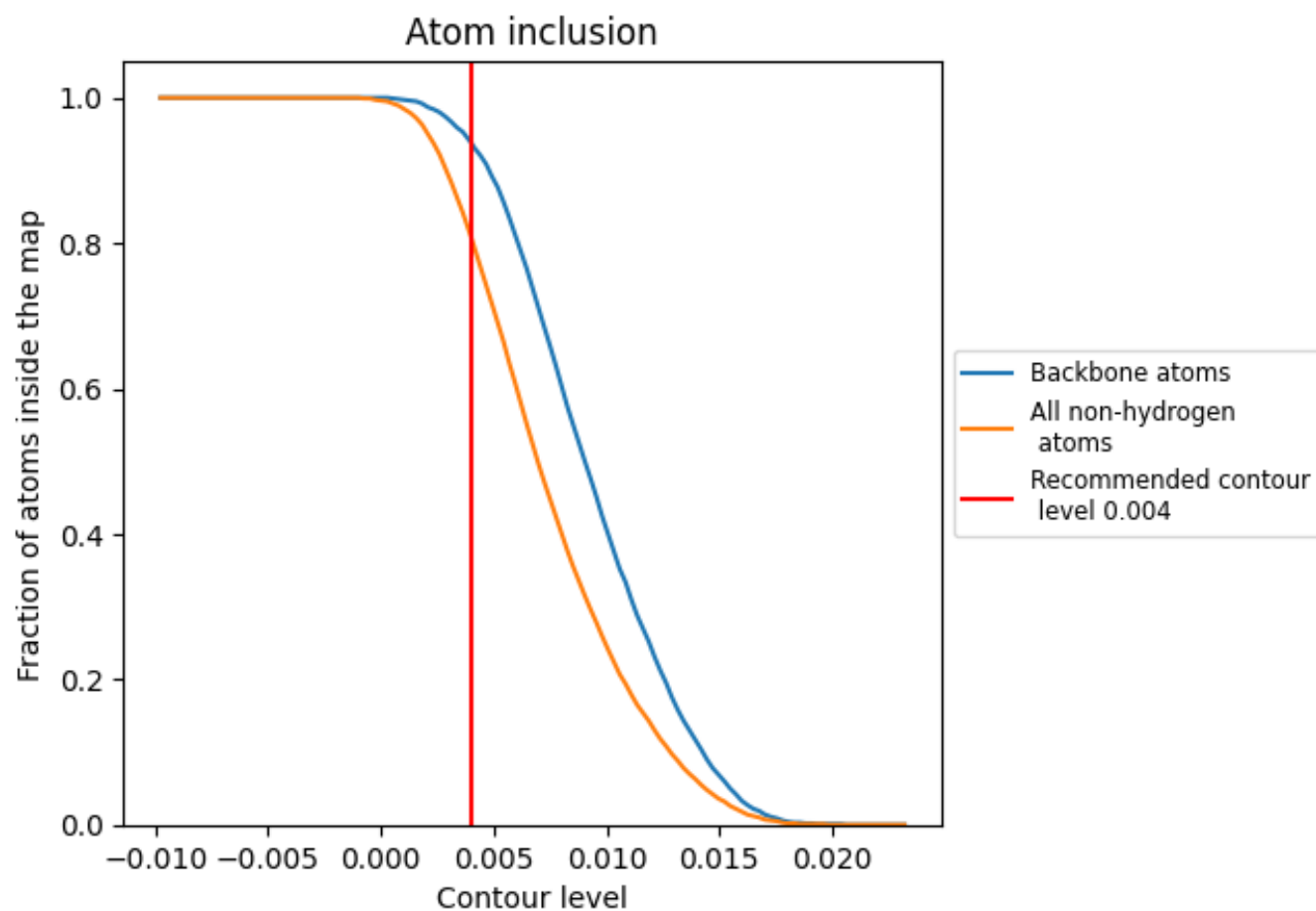
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 81% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8080	0.3810
B	0.7310	0.3200
C	0.7190	0.3170
E	0.4920	0.2580
F	0.3390	0.2010
f	0.7450	0.3840
h	0.9090	0.4490
j	0.7290	0.2850
m	0.8080	0.3670
o	0.9150	0.4550

1.0

0.0

<0.0