



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:35 AM UTC

PDB ID : 8DXP / pdb_00008dxp
EMDB ID : EMD-27772
Title : Structure of LRRC8C-LRRC8A(IL125) Chimera, Class 3
Authors : Takahashi, H.; Yamada, T.; Denton, J.S.; Strange, K.; Karakas, E.
Deposited on : 2022-08-02
Resolution : 3.70 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:

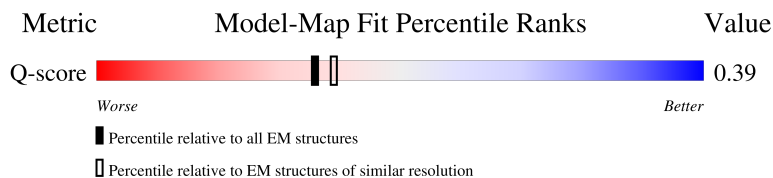
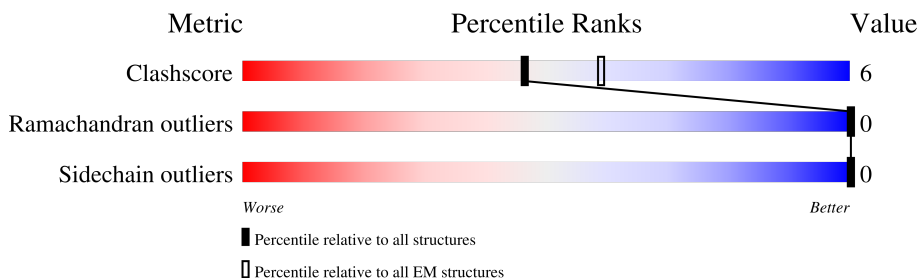
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.70 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	11569 (3.20 - 4.20)

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	825	9% 31% 5% 64%
1	B	825	6% 31% 5% 64%
1	C	825	31% 6% 64%
1	D	825	5% 32% • 64%

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Mol	Chain	Length	Quality of chain
1	E	825	 32%5%64%
1	F	825	 30%6%64%
1	G	825	 31%5%64%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17465 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 Volume-regulated anion channel subunit LRRC8C, Volume-regulated anion channel subunit LRRC8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	298	Total	C	N	O	S	0	0
			2481	1640	391	429	21		
1	B	300	Total	C	N	O	S	0	0
			2501	1653	395	432	21		
1	C	301	Total	C	N	O	S	0	0
			2507	1656	396	434	21		
1	D	298	Total	C	N	O	S	0	0
			2481	1640	391	429	21		
1	E	300	Total	C	N	O	S	0	0
			2498	1651	395	431	21		
1	F	301	Total	C	N	O	S	0	0
			2507	1656	396	434	21		
1	G	299	Total	C	N	O	S	0	0
			2490	1645	392	432	21		

There are 147 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	177G	GLY	-	linker	UNP Q8IWT6
A	?	-	LYS	deletion	UNP Q8TDW0
A	803	GLU	-	expression tag	UNP Q8TDW0
A	804	ASN	-	expression tag	UNP Q8TDW0
A	805	LEU	-	expression tag	UNP Q8TDW0
A	806	TYR	-	expression tag	UNP Q8TDW0
A	807	PHE	-	expression tag	UNP Q8TDW0
A	808	GLN	-	expression tag	UNP Q8TDW0
A	809	GLY	-	expression tag	UNP Q8TDW0
A	810	ALA	-	expression tag	UNP Q8TDW0
A	811	ALA	-	expression tag	UNP Q8TDW0
A	812	ALA	-	expression tag	UNP Q8TDW0
A	813	GLY	-	expression tag	UNP Q8TDW0
A	814	ASP	-	expression tag	UNP Q8TDW0
A	815	TYR	-	expression tag	UNP Q8TDW0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	816	LYS	-	expression tag	UNP Q8TDW0
A	817	ASP	-	expression tag	UNP Q8TDW0
A	818	ASP	-	expression tag	UNP Q8TDW0
A	819	ASP	-	expression tag	UNP Q8TDW0
A	820	ASP	-	expression tag	UNP Q8TDW0
A	821	LYS	-	expression tag	UNP Q8TDW0
B	176H	GLY	-	linker	UNP Q8IWT6
B	?	-	LYS	deletion	UNP Q8TDW0
B	803	GLU	-	expression tag	UNP Q8TDW0
B	804	ASN	-	expression tag	UNP Q8TDW0
B	805	LEU	-	expression tag	UNP Q8TDW0
B	806	TYR	-	expression tag	UNP Q8TDW0
B	807	PHE	-	expression tag	UNP Q8TDW0
B	808	GLN	-	expression tag	UNP Q8TDW0
B	809	GLY	-	expression tag	UNP Q8TDW0
B	810	ALA	-	expression tag	UNP Q8TDW0
B	811	ALA	-	expression tag	UNP Q8TDW0
B	812	ALA	-	expression tag	UNP Q8TDW0
B	813	GLY	-	expression tag	UNP Q8TDW0
B	814	ASP	-	expression tag	UNP Q8TDW0
B	815	TYR	-	expression tag	UNP Q8TDW0
B	816	LYS	-	expression tag	UNP Q8TDW0
B	817	ASP	-	expression tag	UNP Q8TDW0
B	818	ASP	-	expression tag	UNP Q8TDW0
B	819	ASP	-	expression tag	UNP Q8TDW0
B	820	ASP	-	expression tag	UNP Q8TDW0
B	821	LYS	-	expression tag	UNP Q8TDW0
C	177G	GLY	-	linker	UNP Q8IWT6
C	?	-	LYS	deletion	UNP Q8TDW0
C	803	GLU	-	expression tag	UNP Q8TDW0
C	804	ASN	-	expression tag	UNP Q8TDW0
C	805	LEU	-	expression tag	UNP Q8TDW0
C	806	TYR	-	expression tag	UNP Q8TDW0
C	807	PHE	-	expression tag	UNP Q8TDW0
C	808	GLN	-	expression tag	UNP Q8TDW0
C	809	GLY	-	expression tag	UNP Q8TDW0
C	810	ALA	-	expression tag	UNP Q8TDW0
C	811	ALA	-	expression tag	UNP Q8TDW0
C	812	ALA	-	expression tag	UNP Q8TDW0
C	813	GLY	-	expression tag	UNP Q8TDW0
C	814	ASP	-	expression tag	UNP Q8TDW0
C	815	TYR	-	expression tag	UNP Q8TDW0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	816	LYS	-	expression tag	UNP Q8TDW0
C	817	ASP	-	expression tag	UNP Q8TDW0
C	818	ASP	-	expression tag	UNP Q8TDW0
C	819	ASP	-	expression tag	UNP Q8TDW0
C	820	ASP	-	expression tag	UNP Q8TDW0
C	821	LYS	-	expression tag	UNP Q8TDW0
D	178F	GLY	-	linker	UNP Q8IWT6
D	?	-	LYS	deletion	UNP Q8TDW0
D	803	GLU	-	expression tag	UNP Q8TDW0
D	804	ASN	-	expression tag	UNP Q8TDW0
D	805	LEU	-	expression tag	UNP Q8TDW0
D	806	TYR	-	expression tag	UNP Q8TDW0
D	807	PHE	-	expression tag	UNP Q8TDW0
D	808	GLN	-	expression tag	UNP Q8TDW0
D	809	GLY	-	expression tag	UNP Q8TDW0
D	810	ALA	-	expression tag	UNP Q8TDW0
D	811	ALA	-	expression tag	UNP Q8TDW0
D	812	ALA	-	expression tag	UNP Q8TDW0
D	813	GLY	-	expression tag	UNP Q8TDW0
D	814	ASP	-	expression tag	UNP Q8TDW0
D	815	TYR	-	expression tag	UNP Q8TDW0
D	816	LYS	-	expression tag	UNP Q8TDW0
D	817	ASP	-	expression tag	UNP Q8TDW0
D	818	ASP	-	expression tag	UNP Q8TDW0
D	819	ASP	-	expression tag	UNP Q8TDW0
D	820	ASP	-	expression tag	UNP Q8TDW0
D	821	LYS	-	expression tag	UNP Q8TDW0
E	177G	GLY	-	linker	UNP Q8IWT6
E	?	-	LYS	deletion	UNP Q8TDW0
E	803	GLU	-	expression tag	UNP Q8TDW0
E	804	ASN	-	expression tag	UNP Q8TDW0
E	805	LEU	-	expression tag	UNP Q8TDW0
E	806	TYR	-	expression tag	UNP Q8TDW0
E	807	PHE	-	expression tag	UNP Q8TDW0
E	808	GLN	-	expression tag	UNP Q8TDW0
E	809	GLY	-	expression tag	UNP Q8TDW0
E	810	ALA	-	expression tag	UNP Q8TDW0
E	811	ALA	-	expression tag	UNP Q8TDW0
E	812	ALA	-	expression tag	UNP Q8TDW0
E	813	GLY	-	expression tag	UNP Q8TDW0
E	814	ASP	-	expression tag	UNP Q8TDW0
E	815	TYR	-	expression tag	UNP Q8TDW0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	816	LYS	-	expression tag	UNP Q8TDW0
E	817	ASP	-	expression tag	UNP Q8TDW0
E	818	ASP	-	expression tag	UNP Q8TDW0
E	819	ASP	-	expression tag	UNP Q8TDW0
E	820	ASP	-	expression tag	UNP Q8TDW0
E	821	LYS	-	expression tag	UNP Q8TDW0
F	178F	GLY	-	linker	UNP Q8IWT6
F	?	-	LYS	deletion	UNP Q8TDW0
F	803	GLU	-	expression tag	UNP Q8TDW0
F	804	ASN	-	expression tag	UNP Q8TDW0
F	805	LEU	-	expression tag	UNP Q8TDW0
F	806	TYR	-	expression tag	UNP Q8TDW0
F	807	PHE	-	expression tag	UNP Q8TDW0
F	808	GLN	-	expression tag	UNP Q8TDW0
F	809	GLY	-	expression tag	UNP Q8TDW0
F	810	ALA	-	expression tag	UNP Q8TDW0
F	811	ALA	-	expression tag	UNP Q8TDW0
F	812	ALA	-	expression tag	UNP Q8TDW0
F	813	GLY	-	expression tag	UNP Q8TDW0
F	814	ASP	-	expression tag	UNP Q8TDW0
F	815	TYR	-	expression tag	UNP Q8TDW0
F	816	LYS	-	expression tag	UNP Q8TDW0
F	817	ASP	-	expression tag	UNP Q8TDW0
F	818	ASP	-	expression tag	UNP Q8TDW0
F	819	ASP	-	expression tag	UNP Q8TDW0
F	820	ASP	-	expression tag	UNP Q8TDW0
F	821	LYS	-	expression tag	UNP Q8TDW0
G	178F	GLY	-	linker	UNP Q8IWT6
G	?	-	LYS	deletion	UNP Q8TDW0
G	803	GLU	-	expression tag	UNP Q8TDW0
G	804	ASN	-	expression tag	UNP Q8TDW0
G	805	LEU	-	expression tag	UNP Q8TDW0
G	806	TYR	-	expression tag	UNP Q8TDW0
G	807	PHE	-	expression tag	UNP Q8TDW0
G	808	GLN	-	expression tag	UNP Q8TDW0
G	809	GLY	-	expression tag	UNP Q8TDW0
G	810	ALA	-	expression tag	UNP Q8TDW0
G	811	ALA	-	expression tag	UNP Q8TDW0
G	812	ALA	-	expression tag	UNP Q8TDW0
G	813	GLY	-	expression tag	UNP Q8TDW0
G	814	ASP	-	expression tag	UNP Q8TDW0
G	815	TYR	-	expression tag	UNP Q8TDW0

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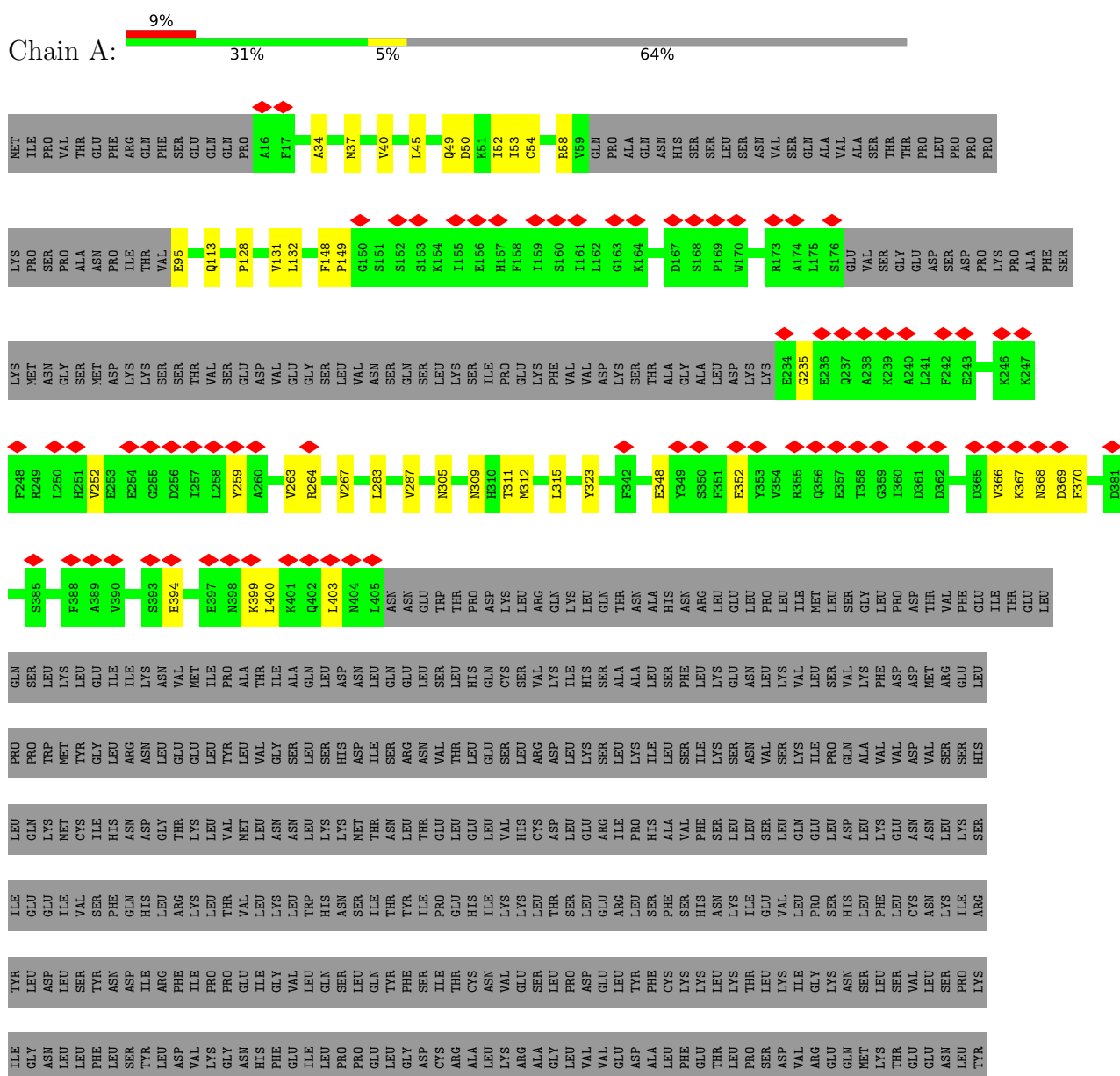
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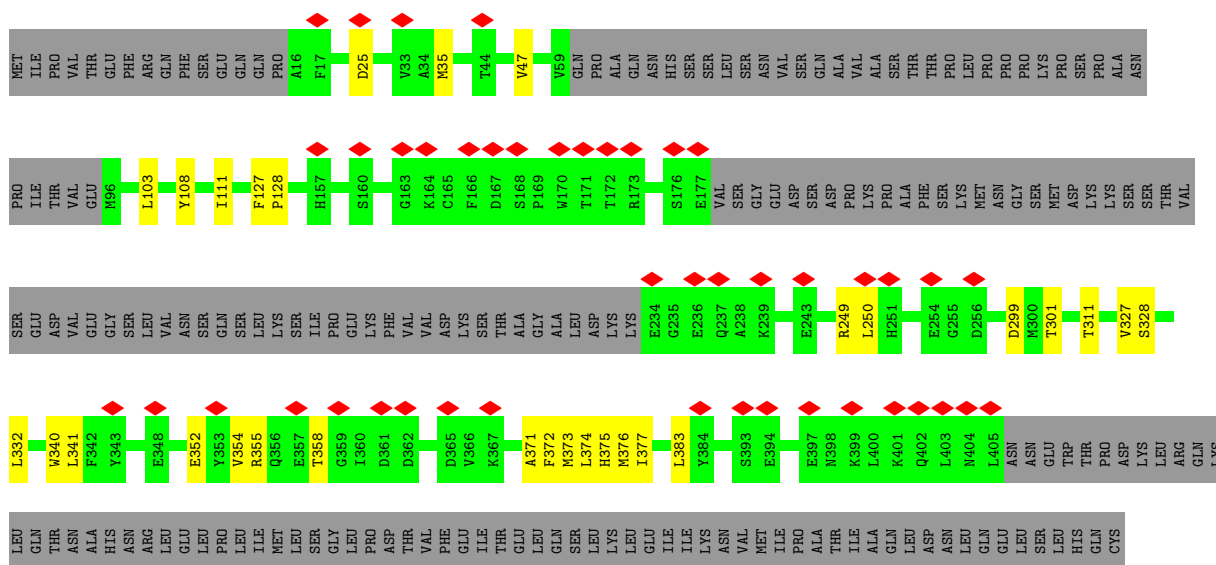
Chain	Residue	Modelled	Actual	Comment	Reference
G	816	LYS	-	expression tag	UNP Q8TDW0
G	817	ASP	-	expression tag	UNP Q8TDW0
G	818	ASP	-	expression tag	UNP Q8TDW0
G	819	ASP	-	expression tag	UNP Q8TDW0
G	820	ASP	-	expression tag	UNP Q8TDW0
G	821	LYS	-	expression tag	UNP Q8TDW0

3 Residue-property plots

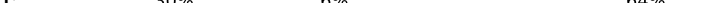
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

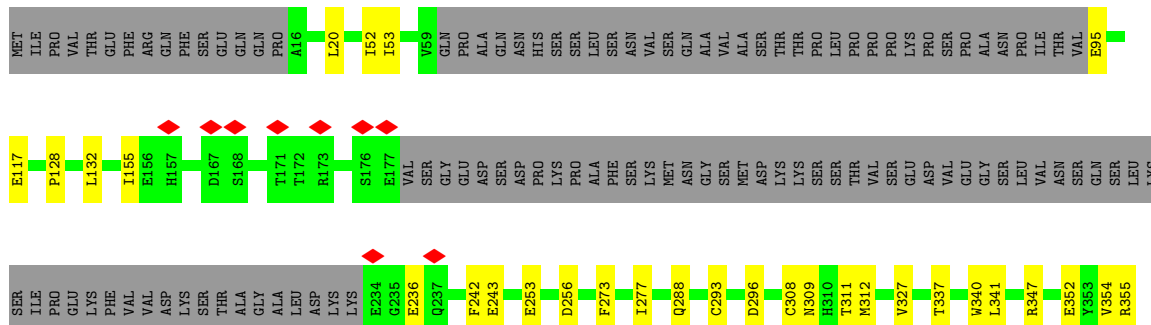
- Molecule 1: Volume-regulated anion channel subunit LRRC8C, Volume-regulated anion channel subunit LRRC8A







- Chain F:  30% 6% 64%



LYS	LEU	PHE	LYS	VAL	PHE	VAL	PHE	VAL	Q356
THR	SER	LEU	GLU	VAL	ASP	VAL	ASP	PHE	
GLU	VAL	CYS	ASN	ASN	CYS	ASN	ASP	GLU	D362
GLU	LEU	ASN	ASN	VAL	ASN	VAL	MET	THR	
LEU	SER	LYS	LEU	SER	LYS	SER	ARG	GLU	V366
LYS	PRO	ILE	ARG	SER	ILE	SER	GLU	LEU	K367
THR	PRO	ARG	TYR	SER	HIS	HIS	LEU	LEU	N368
PHE	ILE	TYR	TYR	ILE	TYR	ILE	PHO	GLN	
GLY	GLY	GLU	GLU	GLN	GLN	GLN	SER	SER	F372
GLY	GLY	ASP	ASP	GLU	ASP	GLU	THR	LEU	
ALA	LEU	LEU	ILE	MET	MET	LYS	LYS	LYS	K373
ALA	LEU	SER	VAL	CYS	CYS	TYR	TYR	LEU	M376
ALA	PHE	TYR	SER	ILE	ILE	GLY	GLY	GLU	D377
GLY	LEU	ASN	PHE	HIS	HIS	LEU	ARG	ILE	D378
ASP	SER	ASN	GLN	ASN	ASN	ASN	ASN	LYS	Q379
TYR	TYR	TYR	HIS	ASP	ASP	ILE	ASN	LYS	V380
LYS	LEU	ARG	LEU	GLY	GLY	LEU	LEU	ASN	D381
ASP	ASP	PHE	ARG	THR	THR	GLU	GLU	MET	
ASP	VAL	ILE	LYS	LYS	LYS	GLU	MET	ILE	K386
ASP	LYS	PRO	LEU	LEU	LEU	LEU	LEU	ILE	
ASP	GLY	PRO	THR	VAL	VAL	TYR	TYR	PRO	S393
LYS	ASN	GLU	VAL	MET	ASN	LEU	LEU	ALA	L400
	HIS	ILE	LEU	LEU	ILE	GLY	VAL	THR	
	PHE	GLY	LYS	ASN	ASN	ASN	SER	ALA	
	GLU	VAL	LEU	ASN	LEU	LEU	LEU	GLN	M404
	ILE	LEU	THR	LEU	LYS	LEU	SER	LEU	L405
	LEU	GLN	HIS	LYS	LYS	SER	SER	ASP	ASN
	PRO	SER	ASN	MET	ASN	HIS	ASN	ASN	GLU
	PRO	LEU	SER	LYS	THR	ILE	SER	GLN	THR
	GLU	GLN	GLN	THR	ASN	ASN	SER	GLN	THR
	LEU	TYR	THR	ASN	THR	ARG	GLU	THR	THR
	GLY	PHE	TYR	LEU	THR	ASN	LEU	PRO	PRO
	ASP	SER	ILE	THR	ILE	GLU	VAL	SER	ASP
	CYS	ILE	THR	GLU	GLU	VAL	SER	LEU	LYS
	ARG	THR	CYS	LEU	LEU	THR	ARG	LYS	GLN
	ALA	THR	LEU	CYS	ASP	VAL	ALA	ASN	ASN
	GLY	LEU	THR	THR	ASP	VAL	VAL	ARG	ASN
	LEU	PRO	SER	GLU	LEU	ILE	LEU	SER	ARG
	LEU	PRO	LEU	GLU	LEU	GLU	GLU	PHO	GLU
	VAL	ASP	ASN	GLU	GLU	GLU	LEU	LEU	GLU
	VAL	GLU	ASN	ARG	ARG	ILE	SER	LYS	PRO
	GLU	GLU	LEU	GLU	GLU	PRO	LYS	GLU	LEU
	ASP	TYR	LEU	PRO	TYR	ASN	ASN	ASN	ILE
	ALA	PHE	SER	HIS	SER	LYS	ALA	ASN	MET
	LEU	CYS	PHE	ALA	ILE	ILE	LEU	ARG	LEU
	LEU	LYS	SER	ALA	THR	THR	SER	LEU	LEU
	PHE	LYS	THR	VAL	ASN	HIS	PHO	GLU	GLU
	GLU	LYS	HIS	PHE	ILE	ILE	LEU	SER	GLY
	THR	LEU	ASN	SER	LEU	LYS	LYS	VAL	GLY
	LEU	LYS	ASN	SER	LEU	THR	SER	SER	LEU
	PRO	THR	ILE	LEU	LEU	ASN	VAL	VAL	PRO
	SER	LEU	ILE	SER	GLU	THR	ASN	GLN	ASP
	ASP	LYS	VAL	SER	LYS	VAL	VAL	VAL	LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	100772	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.405	Depositor
Minimum map value	-0.785	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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	0.12	0/2548	0.32	0/3441
1	B	0.13	0/2568	0.33	0/3466
1	C	0.13	0/2574	0.32	0/3474
1	D	0.12	0/2548	0.32	0/3441
1	E	0.12	0/2565	0.29	0/3462
1	F	0.14	0/2574	0.34	0/3474
1	G	0.13	0/2557	0.33	0/3453
All	All	0.13	0/17934	0.32	0/24211

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2481	0	2471	41	0
1	B	2501	0	2496	33	0
1	C	2507	0	2501	35	0
1	D	2481	0	2471	22	0
1	E	2498	0	2495	25	0
1	F	2507	0	2501	38	0
1	G	2490	0	2477	35	0
All	All	17465	0	17412	211	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 211 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:B:374:LEU:O	1:B:377:ILE:HG22	1.81	0.81
1:E:170:TRP:CZ2	1:E:395:VAL:HG11	2.20	0.76
1:A:45:LEU:O	1:A:45:LEU:HD23	1.86	0.75
1:A:283:LEU:O	1:A:283:LEU:HD12	1.87	0.75
1:E:53:ILE:HD12	1:F:113:GLN:OE1	1.88	0.73

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	292/825 (35%)	277 (95%)	15 (5%)	0	100	100
1	B	294/825 (36%)	262 (89%)	32 (11%)	0	100	100
1	C	295/825 (36%)	282 (96%)	13 (4%)	0	100	100
1	D	292/825 (35%)	276 (94%)	16 (6%)	0	100	100
1	E	294/825 (36%)	278 (95%)	16 (5%)	0	100	100
1	F	295/825 (36%)	274 (93%)	21 (7%)	0	100	100
1	G	293/825 (36%)	274 (94%)	19 (6%)	0	100	100
All	All	2055/5775 (36%)	1923 (94%)	132 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	275/766 (36%)	275 (100%)	0	100	100
1	B	277/766 (36%)	277 (100%)	0	100	100
1	C	278/766 (36%)	278 (100%)	0	100	100
1	D	275/766 (36%)	275 (100%)	0	100	100
1	E	277/766 (36%)	277 (100%)	0	100	100
1	F	278/766 (36%)	278 (100%)	0	100	100
1	G	276/766 (36%)	276 (100%)	0	100	100
All	All	1936/5362 (36%)	1936 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	280	ASN
1	G	309	ASN
1	D	251	HIS
1	D	309	ASN
1	E	49	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.

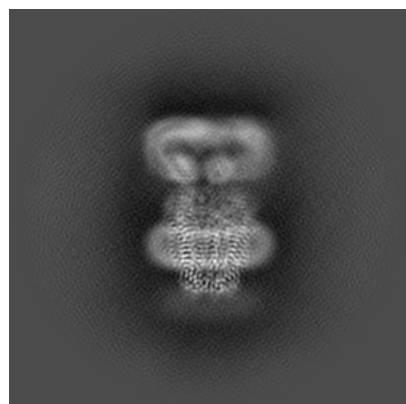
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27772. These allow visual inspection of the internal detail of the map and identification of artifacts.

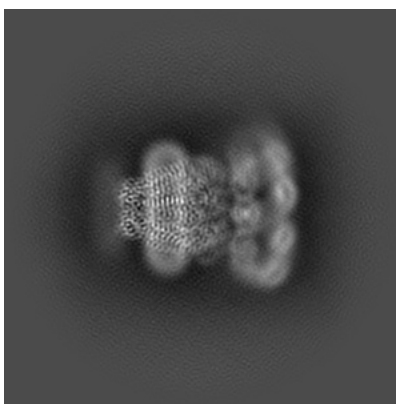
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

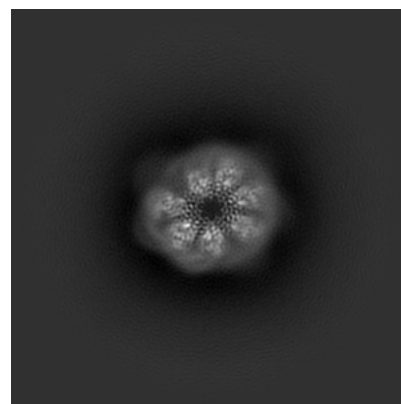
6.1.1 Primary map



X

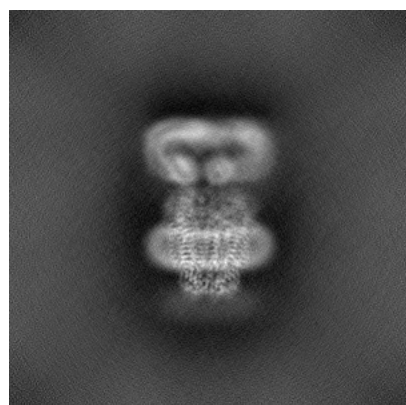


Y

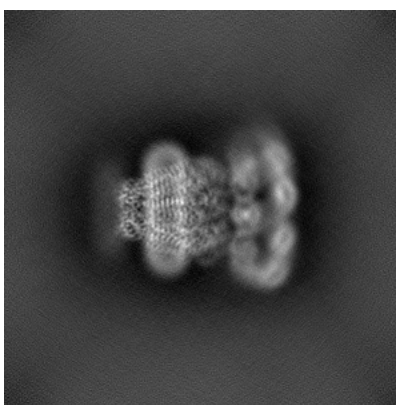


Z

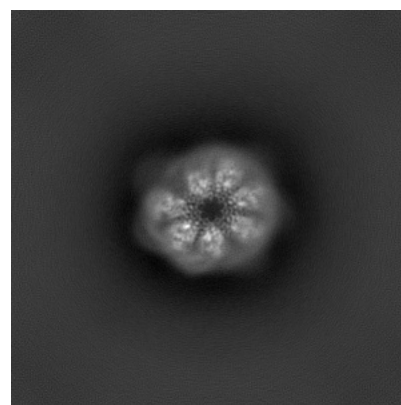
6.1.2 Raw map



X



Y



Z

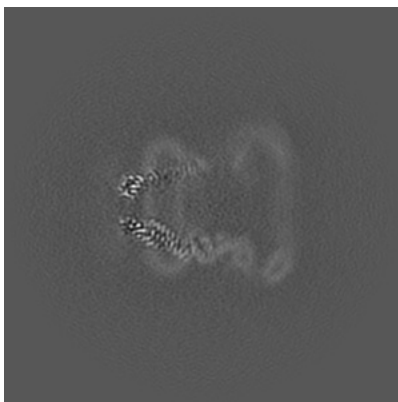
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

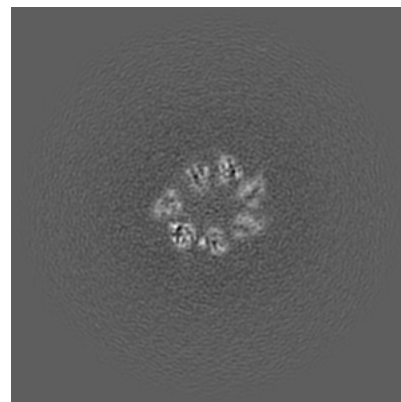
6.2.1 Primary map



X Index: 180



Y Index: 180

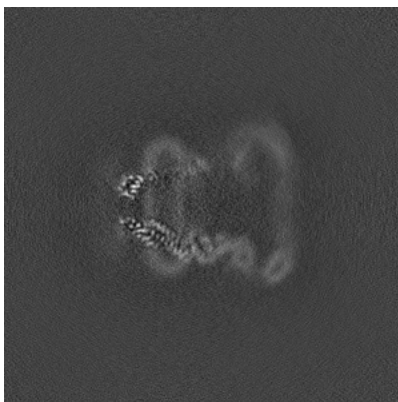


Z Index: 180

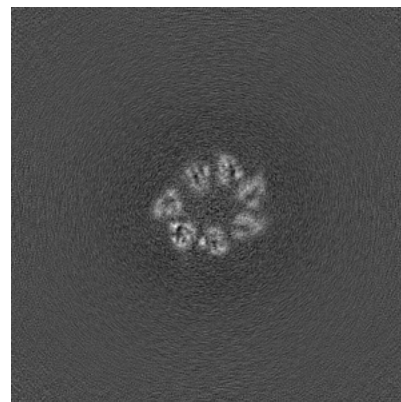
6.2.2 Raw map



X Index: 180



Y Index: 180

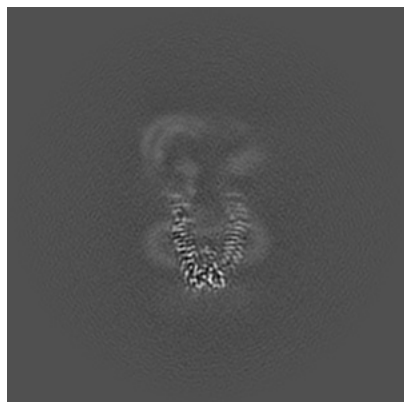


Z Index: 180

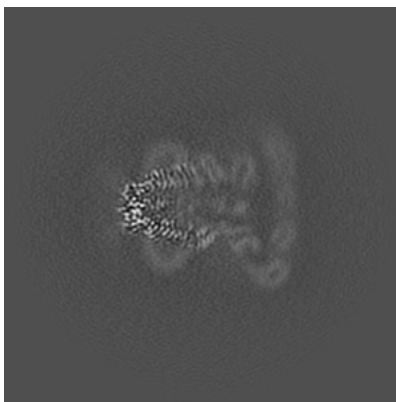
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

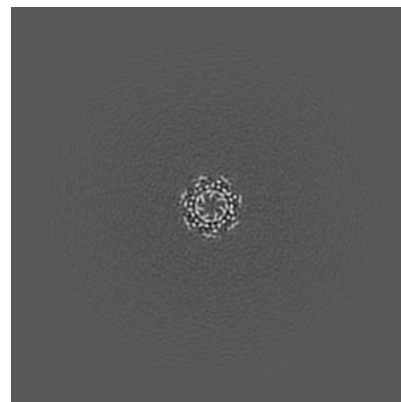
6.3.1 Primary map



X Index: 161

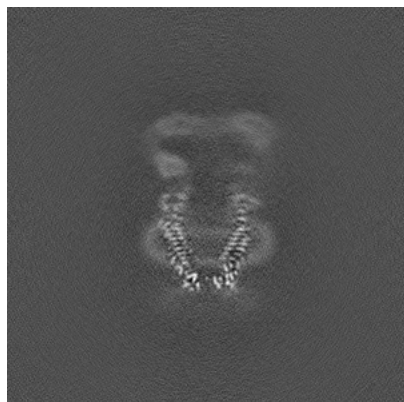


Y Index: 163

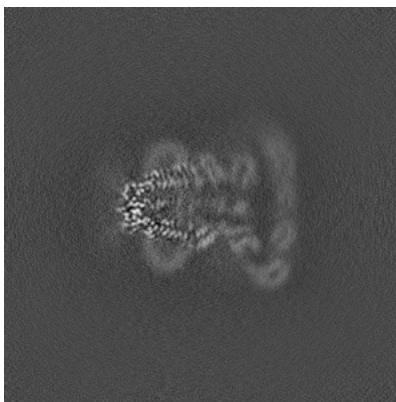


Z Index: 116

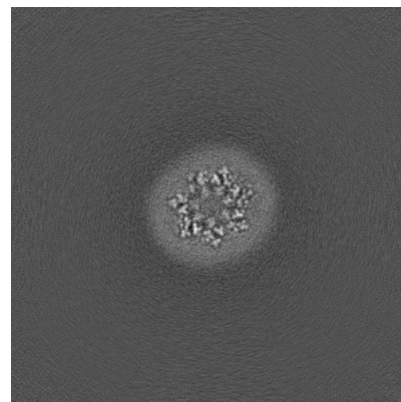
6.3.2 Raw map



X Index: 187



Y Index: 163

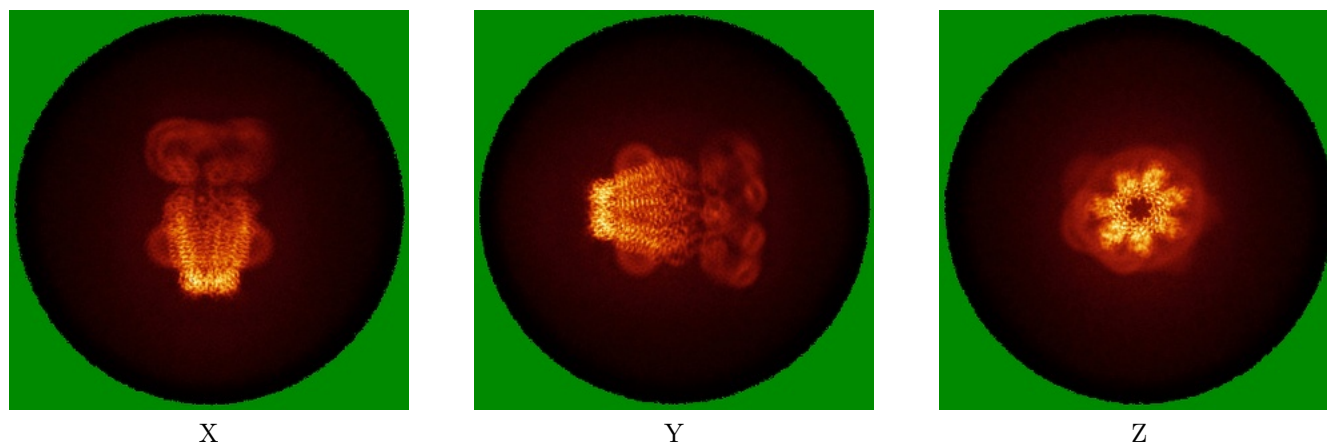


Z Index: 133

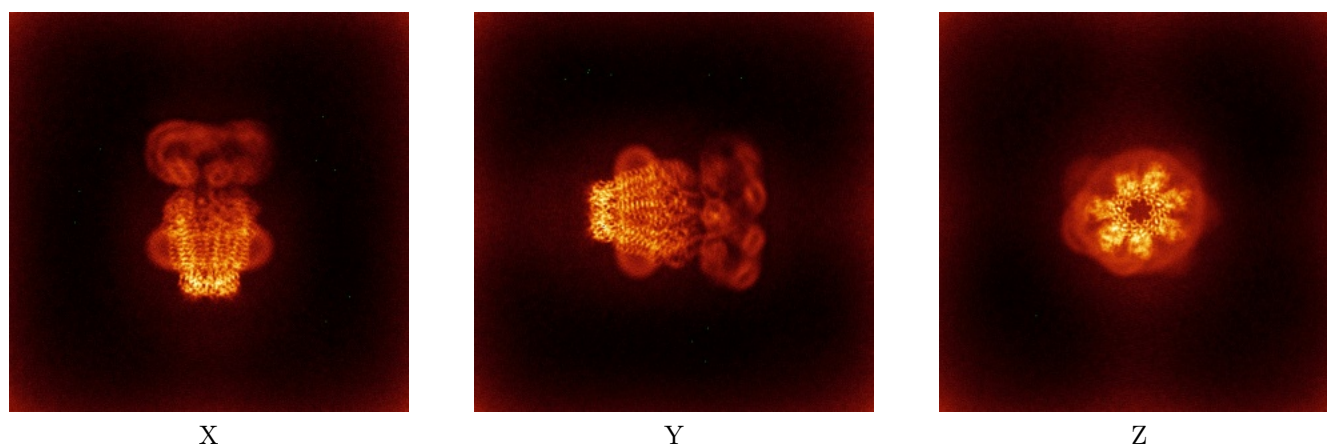
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

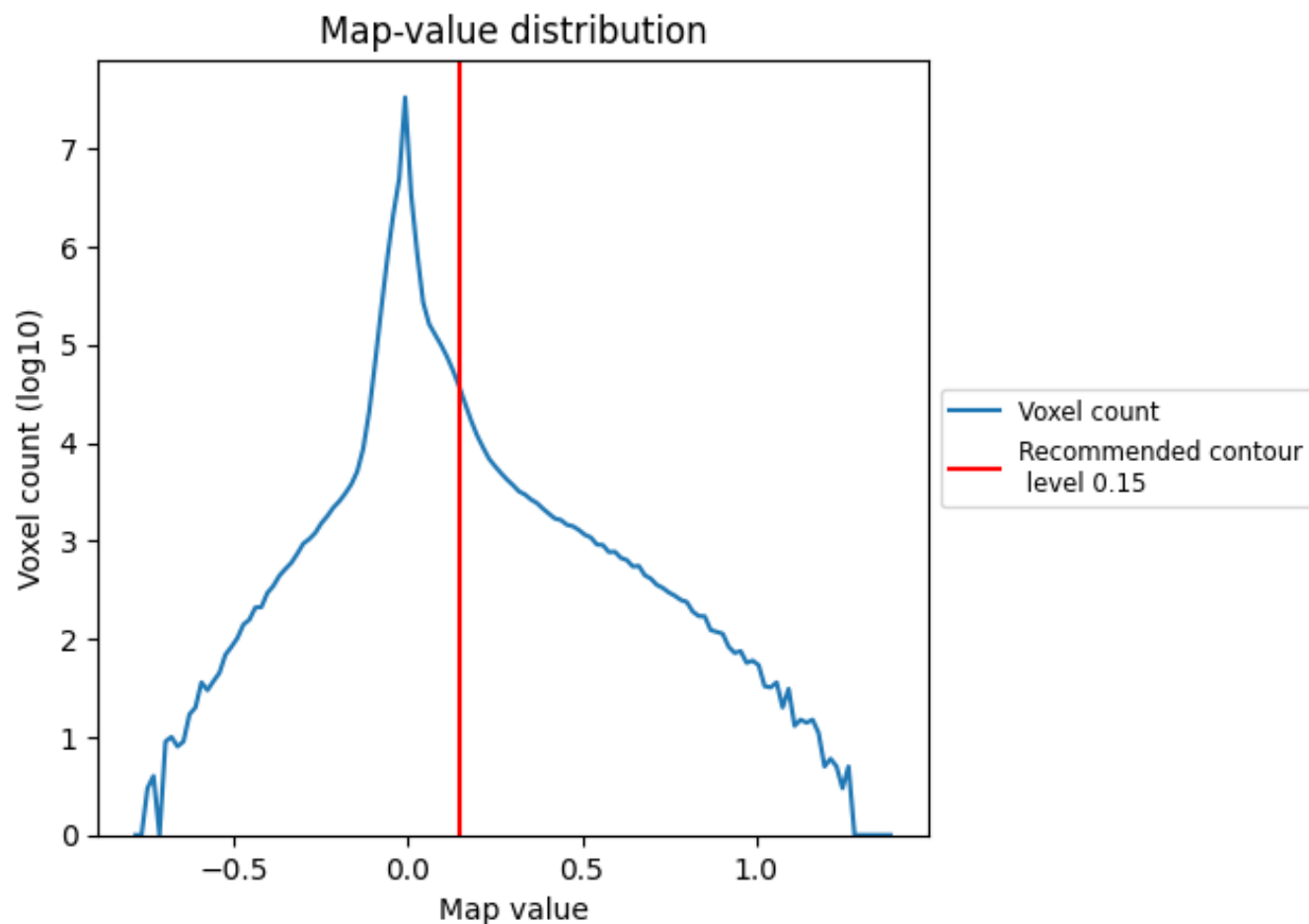
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

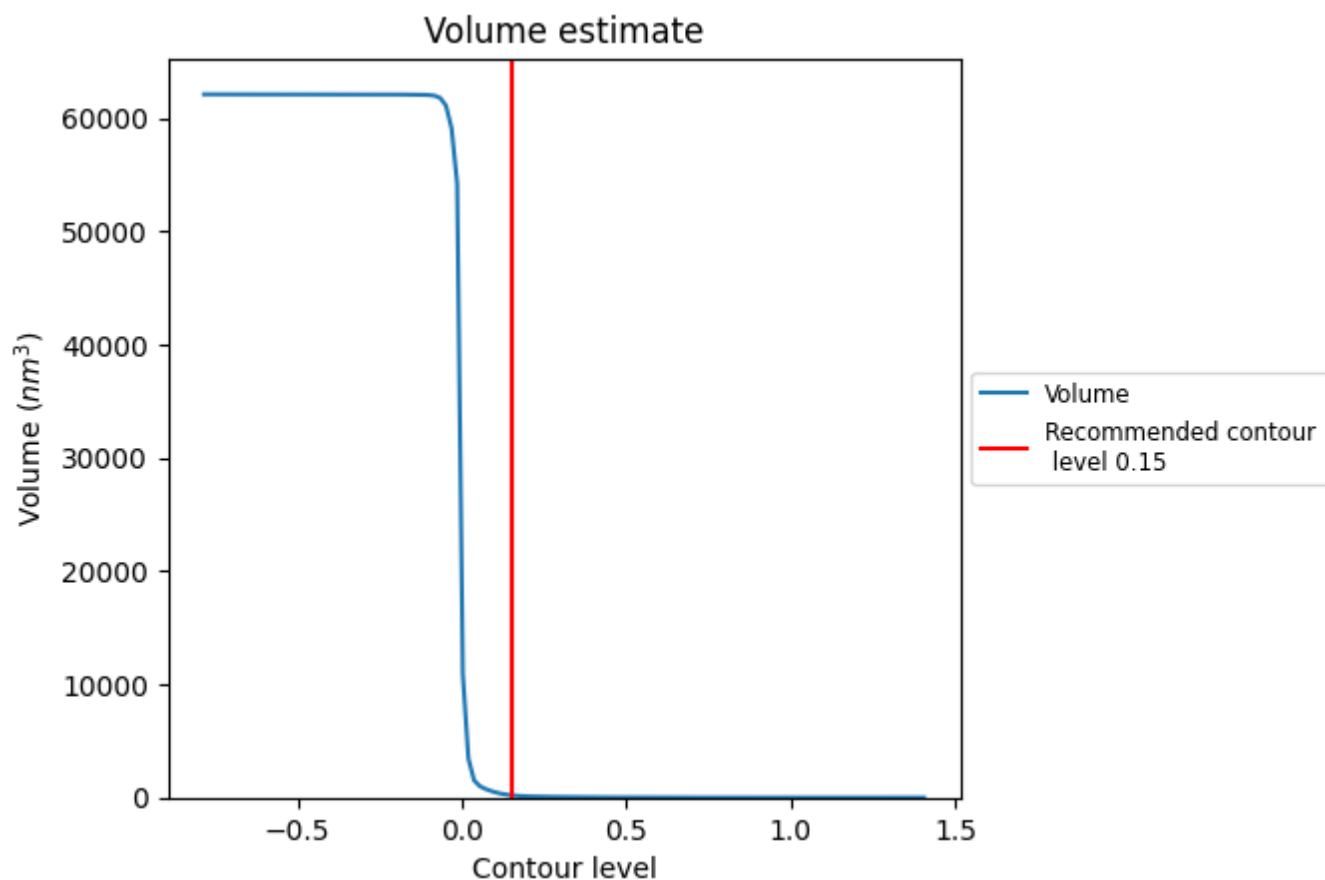
This section contains the results of statistical analysis of the map.

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.

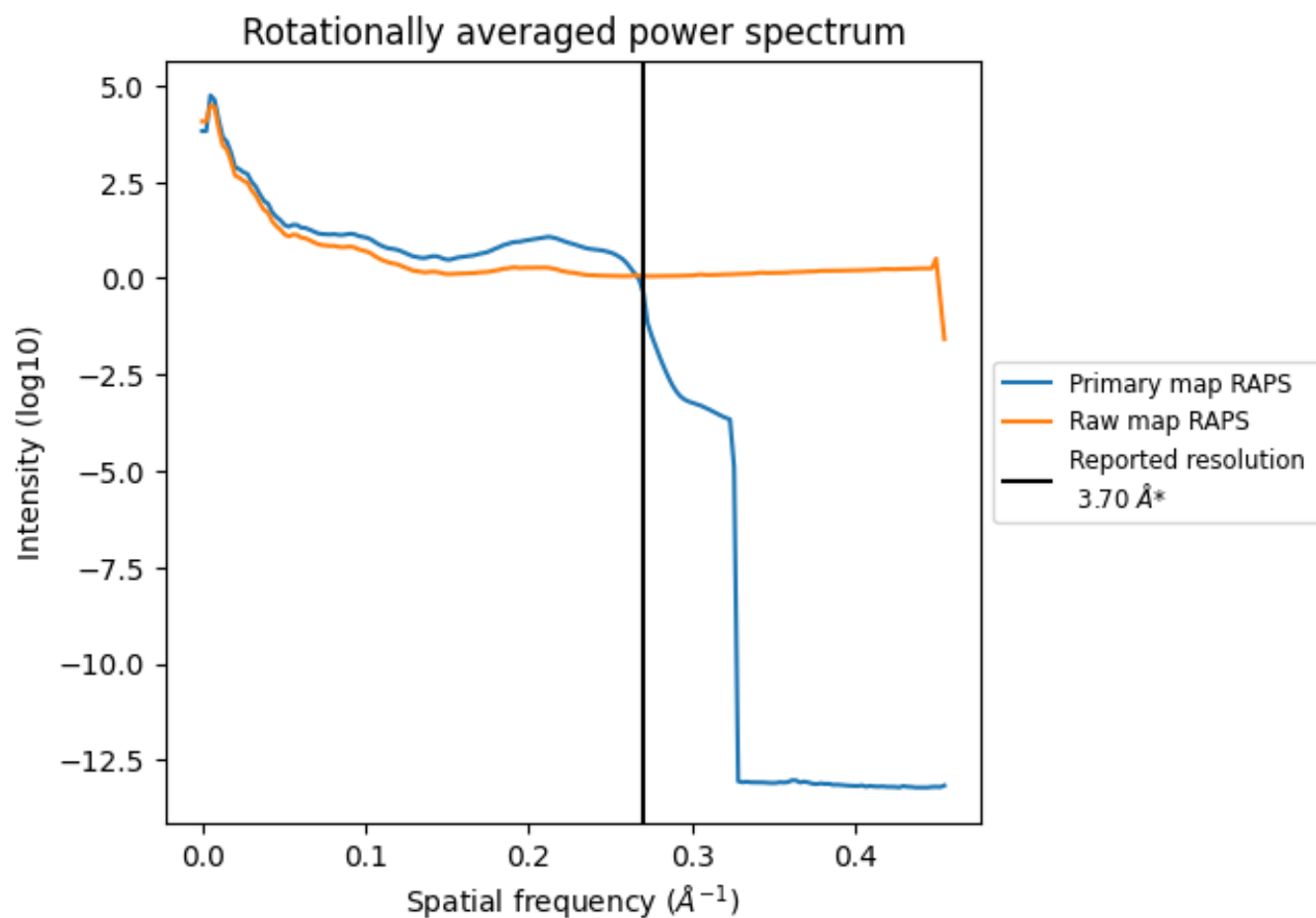
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 204 nm³; this corresponds to an approximate mass of 185 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 ⓘ

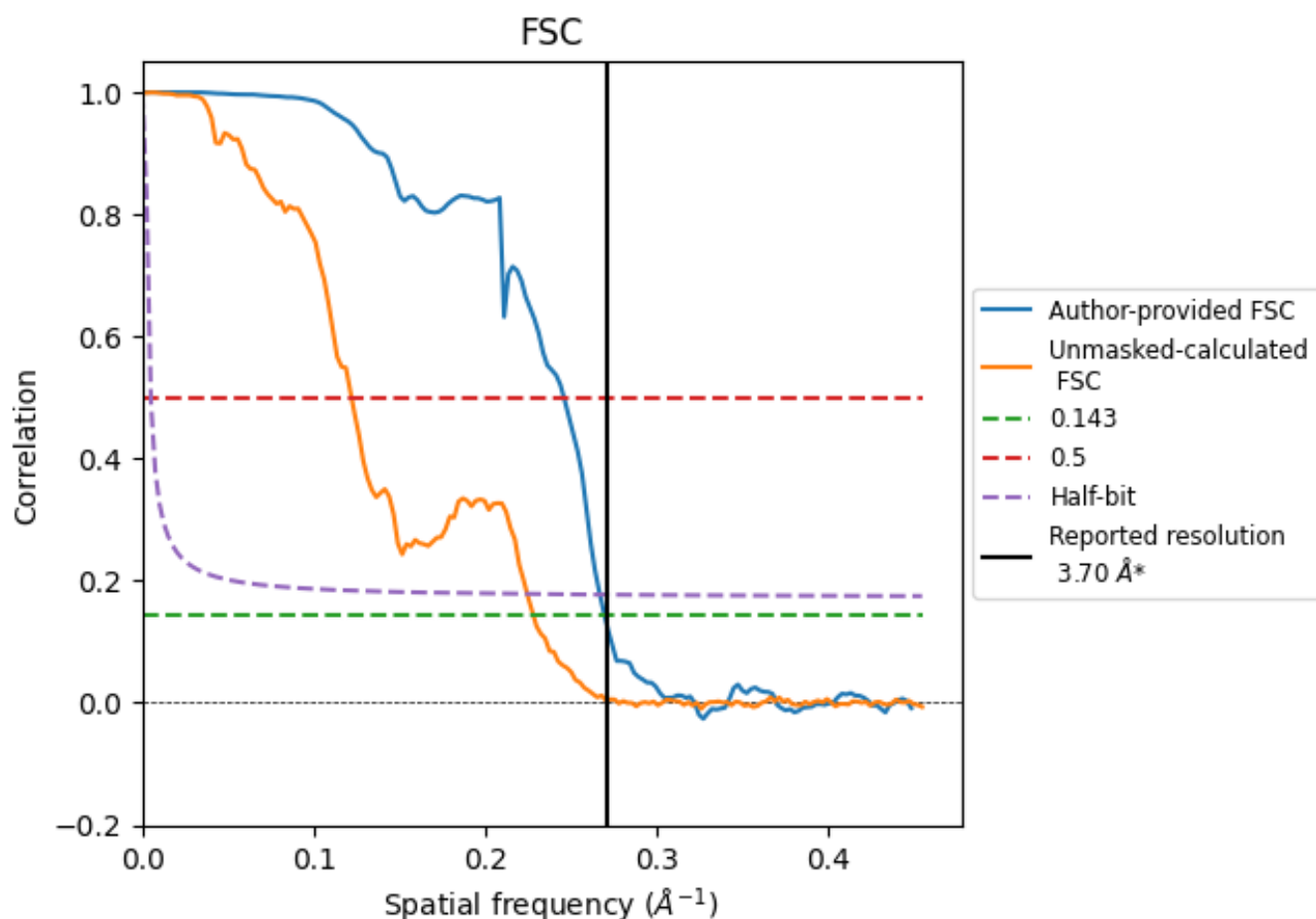


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

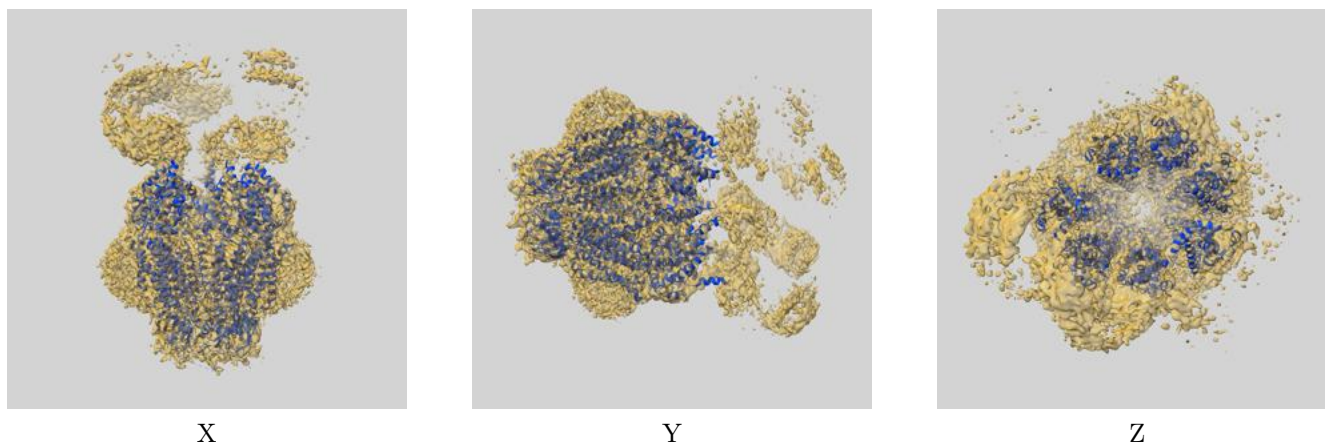
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.71	4.07	3.75
Unmasked-calculated*	4.39	8.20	4.46

*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 4.39 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

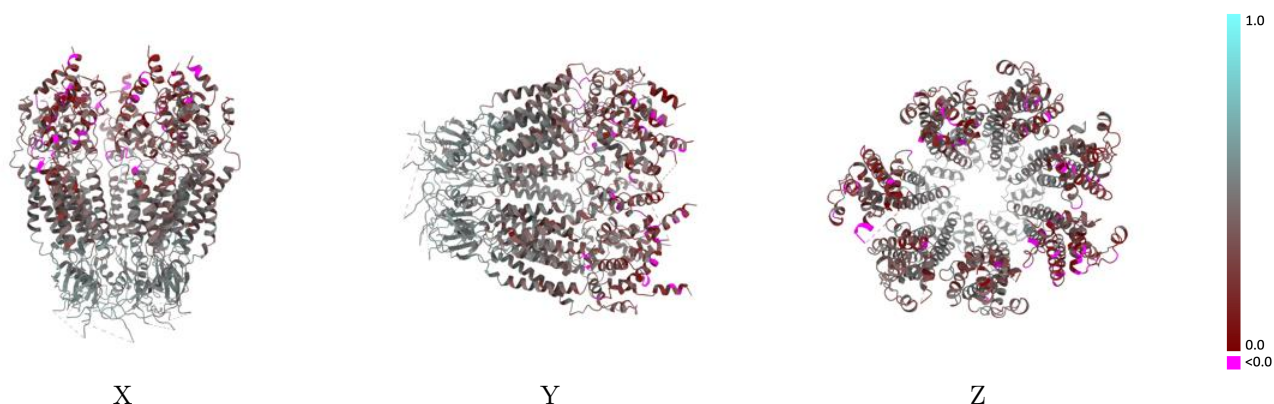
This section contains information regarding the fit between EMDB map EMD-27772 and PDB model 8DXP. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



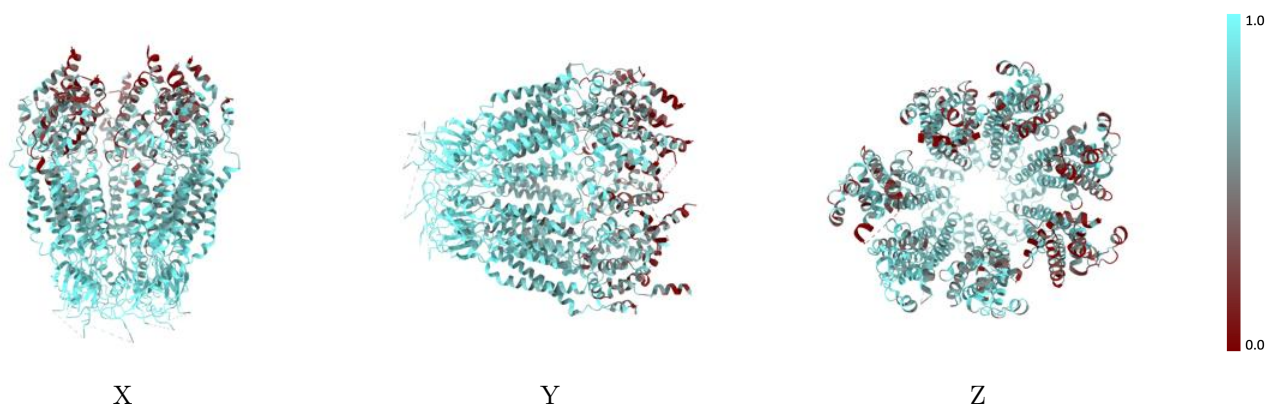
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



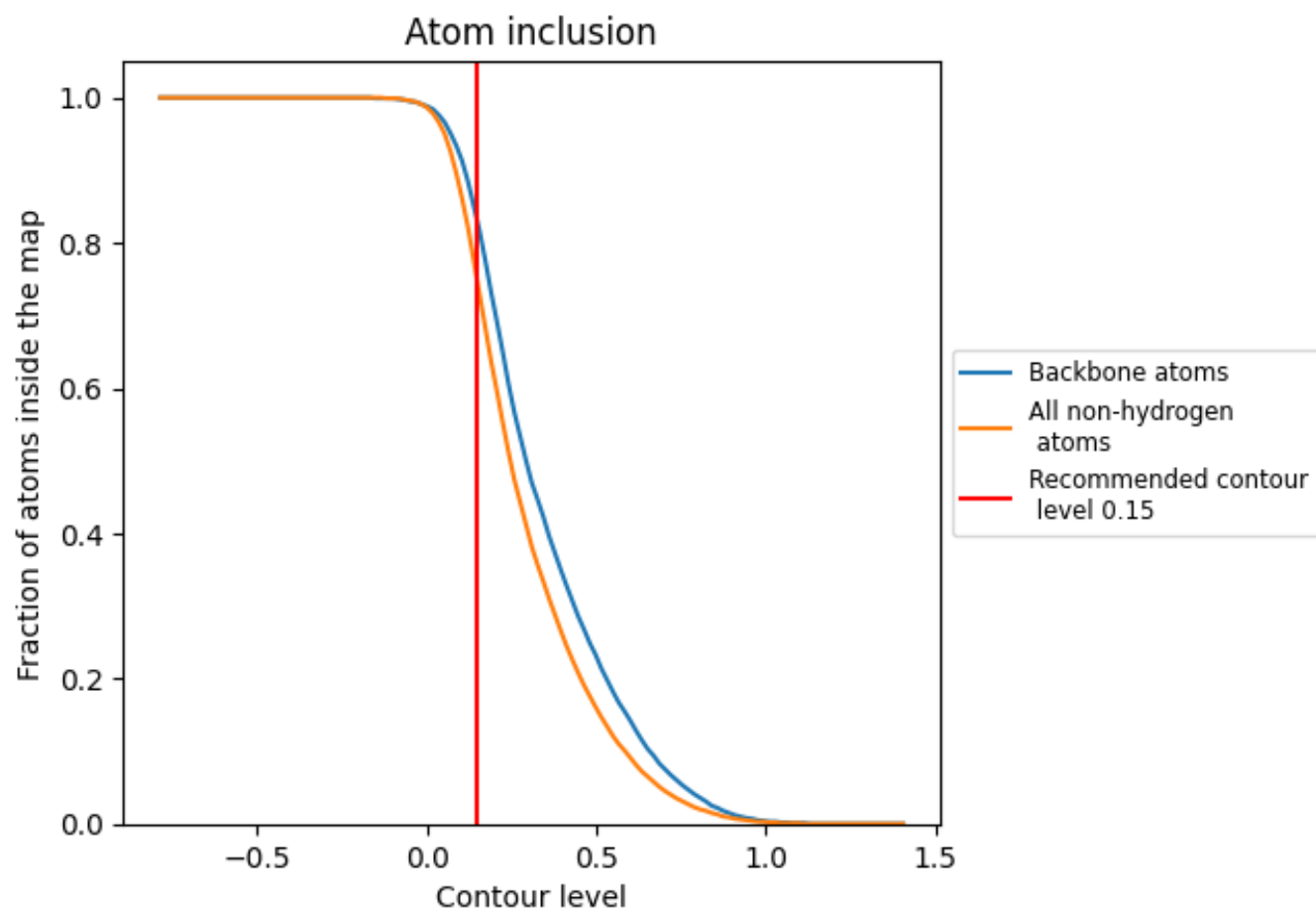
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 75% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7480	0.3900
A	0.6550	0.3340
B	0.7200	0.3830
C	0.7740	0.4090
D	0.7020	0.3780
E	0.7410	0.3710
F	0.8440	0.4360
G	0.7970	0.4210

1.0

0.0

<0.0