



wwPDB EM Validation Summary Report ⓘ

Sep 21, 2026 – 12:36 PM EDT

PDB ID : 38RK / pdb_000038rk
EMDB ID : EMD-79081
Title : Cryo-EM structure of the L274A mutant of the Arabidopsis thaliana mechanosensitive channel of small conductance-like protein 2 (MSL2) in DOPC lipid nanodiscs.
Authors : Angiulli, G.; Dong, L.; Walz, T.
Deposited on : 2026-09-15
Resolution : 2.80 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:

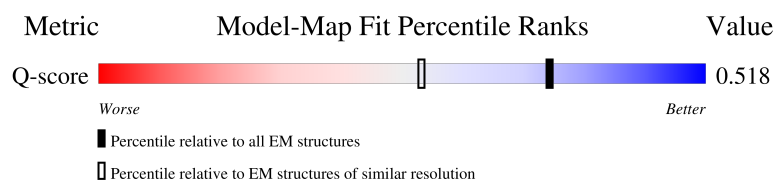
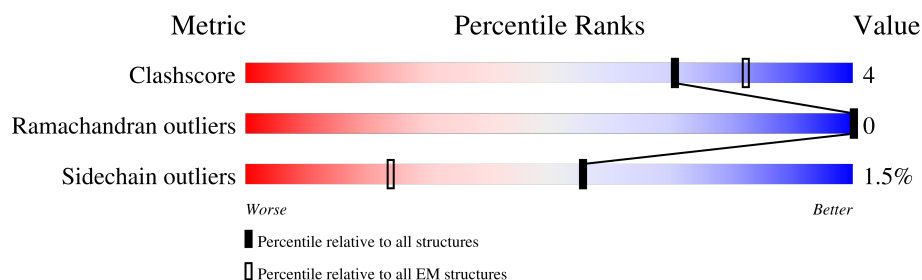
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	866	
1	B	866	
1	C	866	
1	D	866	

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Mol	Chain	Length	Quality of chain
1	E	866	 20% • 78%
1	F	866	 20% • 78%
1	G	866	 19% • 78%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11004 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 Mechanosensitive ion channel protein 2, chloroplastic, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		
1	B	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		
1	C	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		
1	D	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		
1	E	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		
1	F	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		
1	G	194	Total	C	N	O	S	0	0
			1572	1003	293	271	5		

There are 252 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	MET	-	initiating methionine	UNP Q56X46
A	274	ALA	LEU	engineered mutation	UNP Q56X46
A	674	SER	-	linker	UNP Q56X46
A	675	ASN	-	linker	UNP Q56X46
A	676	SER	-	linker	UNP Q56X46
A	677	LEU	-	linker	UNP Q56X46
A	678	GLU	-	linker	UNP Q56X46
A	679	VAL	-	linker	UNP Q56X46
A	680	LEU	-	linker	UNP Q56X46
A	681	PHE	-	linker	UNP Q56X46
A	682	GLN	-	linker	UNP Q56X46
A	683	GLY	-	linker	UNP Q56X46
A	684	PRO	-	linker	UNP Q56X46
A	685	THR	-	linker	UNP Q56X46
A	686	ALA	-	linker	UNP Q56X46

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Chain	Residue	Modelled	Actual	Comment	Reference
A	687	ALA	-	linker	UNP Q56X46
A	688	ALA	-	linker	UNP Q56X46
A	689	ALA	-	linker	UNP Q56X46
A	690	VAL	-	linker	UNP Q56X46
A	753	LEU	PHE	conflict	UNP P42212
A	754	THR	SER	conflict	UNP P42212
A	895	LYS	ALA	conflict	UNP P42212
A	920	LEU	HIS	conflict	UNP P42212
A	928	SER	-	expression tag	UNP P42212
A	929	GLY	-	expression tag	UNP P42212
A	930	GLY	-	expression tag	UNP P42212
A	931	GLY	-	expression tag	UNP P42212
A	932	THR	-	expression tag	UNP P42212
A	933	GLU	-	expression tag	UNP P42212
A	934	THR	-	expression tag	UNP P42212
A	935	SER	-	expression tag	UNP P42212
A	936	GLN	-	expression tag	UNP P42212
A	937	VAL	-	expression tag	UNP P42212
A	938	ALA	-	expression tag	UNP P42212
A	939	PRO	-	expression tag	UNP P42212
A	940	ALA	-	expression tag	UNP P42212
B	75	MET	-	initiating methionine	UNP Q56X46
B	274	ALA	LEU	engineered mutation	UNP Q56X46
B	674	SER	-	linker	UNP Q56X46
B	675	ASN	-	linker	UNP Q56X46
B	676	SER	-	linker	UNP Q56X46
B	677	LEU	-	linker	UNP Q56X46
B	678	GLU	-	linker	UNP Q56X46
B	679	VAL	-	linker	UNP Q56X46
B	680	LEU	-	linker	UNP Q56X46
B	681	PHE	-	linker	UNP Q56X46
B	682	GLN	-	linker	UNP Q56X46
B	683	GLY	-	linker	UNP Q56X46
B	684	PRO	-	linker	UNP Q56X46
B	685	THR	-	linker	UNP Q56X46
B	686	ALA	-	linker	UNP Q56X46
B	687	ALA	-	linker	UNP Q56X46
B	688	ALA	-	linker	UNP Q56X46
B	689	ALA	-	linker	UNP Q56X46
B	690	VAL	-	linker	UNP Q56X46
B	753	LEU	PHE	conflict	UNP P42212
B	754	THR	SER	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	895	LYS	ALA	conflict	UNP P42212
B	920	LEU	HIS	conflict	UNP P42212
B	928	SER	-	expression tag	UNP P42212
B	929	GLY	-	expression tag	UNP P42212
B	930	GLY	-	expression tag	UNP P42212
B	931	GLY	-	expression tag	UNP P42212
B	932	THR	-	expression tag	UNP P42212
B	933	GLU	-	expression tag	UNP P42212
B	934	THR	-	expression tag	UNP P42212
B	935	SER	-	expression tag	UNP P42212
B	936	GLN	-	expression tag	UNP P42212
B	937	VAL	-	expression tag	UNP P42212
B	938	ALA	-	expression tag	UNP P42212
B	939	PRO	-	expression tag	UNP P42212
B	940	ALA	-	expression tag	UNP P42212
C	75	MET	-	initiating methionine	UNP Q56X46
C	274	ALA	LEU	engineered mutation	UNP Q56X46
C	674	SER	-	linker	UNP Q56X46
C	675	ASN	-	linker	UNP Q56X46
C	676	SER	-	linker	UNP Q56X46
C	677	LEU	-	linker	UNP Q56X46
C	678	GLU	-	linker	UNP Q56X46
C	679	VAL	-	linker	UNP Q56X46
C	680	LEU	-	linker	UNP Q56X46
C	681	PHE	-	linker	UNP Q56X46
C	682	GLN	-	linker	UNP Q56X46
C	683	GLY	-	linker	UNP Q56X46
C	684	PRO	-	linker	UNP Q56X46
C	685	THR	-	linker	UNP Q56X46
C	686	ALA	-	linker	UNP Q56X46
C	687	ALA	-	linker	UNP Q56X46
C	688	ALA	-	linker	UNP Q56X46
C	689	ALA	-	linker	UNP Q56X46
C	690	VAL	-	linker	UNP Q56X46
C	753	LEU	PHE	conflict	UNP P42212
C	754	THR	SER	conflict	UNP P42212
C	895	LYS	ALA	conflict	UNP P42212
C	920	LEU	HIS	conflict	UNP P42212
C	928	SER	-	expression tag	UNP P42212
C	929	GLY	-	expression tag	UNP P42212
C	930	GLY	-	expression tag	UNP P42212
C	931	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	932	THR	-	expression tag	UNP P42212
C	933	GLU	-	expression tag	UNP P42212
C	934	THR	-	expression tag	UNP P42212
C	935	SER	-	expression tag	UNP P42212
C	936	GLN	-	expression tag	UNP P42212
C	937	VAL	-	expression tag	UNP P42212
C	938	ALA	-	expression tag	UNP P42212
C	939	PRO	-	expression tag	UNP P42212
C	940	ALA	-	expression tag	UNP P42212
D	75	MET	-	initiating methionine	UNP Q56X46
D	274	ALA	LEU	engineered mutation	UNP Q56X46
D	674	SER	-	linker	UNP Q56X46
D	675	ASN	-	linker	UNP Q56X46
D	676	SER	-	linker	UNP Q56X46
D	677	LEU	-	linker	UNP Q56X46
D	678	GLU	-	linker	UNP Q56X46
D	679	VAL	-	linker	UNP Q56X46
D	680	LEU	-	linker	UNP Q56X46
D	681	PHE	-	linker	UNP Q56X46
D	682	GLN	-	linker	UNP Q56X46
D	683	GLY	-	linker	UNP Q56X46
D	684	PRO	-	linker	UNP Q56X46
D	685	THR	-	linker	UNP Q56X46
D	686	ALA	-	linker	UNP Q56X46
D	687	ALA	-	linker	UNP Q56X46
D	688	ALA	-	linker	UNP Q56X46
D	689	ALA	-	linker	UNP Q56X46
D	690	VAL	-	linker	UNP Q56X46
D	753	LEU	PHE	conflict	UNP P42212
D	754	THR	SER	conflict	UNP P42212
D	895	LYS	ALA	conflict	UNP P42212
D	920	LEU	HIS	conflict	UNP P42212
D	928	SER	-	expression tag	UNP P42212
D	929	GLY	-	expression tag	UNP P42212
D	930	GLY	-	expression tag	UNP P42212
D	931	GLY	-	expression tag	UNP P42212
D	932	THR	-	expression tag	UNP P42212
D	933	GLU	-	expression tag	UNP P42212
D	934	THR	-	expression tag	UNP P42212
D	935	SER	-	expression tag	UNP P42212
D	936	GLN	-	expression tag	UNP P42212
D	937	VAL	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	938	ALA	-	expression tag	UNP P42212
D	939	PRO	-	expression tag	UNP P42212
D	940	ALA	-	expression tag	UNP P42212
E	75	MET	-	initiating methionine	UNP Q56X46
E	274	ALA	LEU	engineered mutation	UNP Q56X46
E	674	SER	-	linker	UNP Q56X46
E	675	ASN	-	linker	UNP Q56X46
E	676	SER	-	linker	UNP Q56X46
E	677	LEU	-	linker	UNP Q56X46
E	678	GLU	-	linker	UNP Q56X46
E	679	VAL	-	linker	UNP Q56X46
E	680	LEU	-	linker	UNP Q56X46
E	681	PHE	-	linker	UNP Q56X46
E	682	GLN	-	linker	UNP Q56X46
E	683	GLY	-	linker	UNP Q56X46
E	684	PRO	-	linker	UNP Q56X46
E	685	THR	-	linker	UNP Q56X46
E	686	ALA	-	linker	UNP Q56X46
E	687	ALA	-	linker	UNP Q56X46
E	688	ALA	-	linker	UNP Q56X46
E	689	ALA	-	linker	UNP Q56X46
E	690	VAL	-	linker	UNP Q56X46
E	753	LEU	PHE	conflict	UNP P42212
E	754	THR	SER	conflict	UNP P42212
E	895	LYS	ALA	conflict	UNP P42212
E	920	LEU	HIS	conflict	UNP P42212
E	928	SER	-	expression tag	UNP P42212
E	929	GLY	-	expression tag	UNP P42212
E	930	GLY	-	expression tag	UNP P42212
E	931	GLY	-	expression tag	UNP P42212
E	932	THR	-	expression tag	UNP P42212
E	933	GLU	-	expression tag	UNP P42212
E	934	THR	-	expression tag	UNP P42212
E	935	SER	-	expression tag	UNP P42212
E	936	GLN	-	expression tag	UNP P42212
E	937	VAL	-	expression tag	UNP P42212
E	938	ALA	-	expression tag	UNP P42212
E	939	PRO	-	expression tag	UNP P42212
E	940	ALA	-	expression tag	UNP P42212
F	75	MET	-	initiating methionine	UNP Q56X46
F	274	ALA	LEU	engineered mutation	UNP Q56X46
F	674	SER	-	linker	UNP Q56X46

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Chain	Residue	Modelled	Actual	Comment	Reference
F	675	ASN	-	linker	UNP Q56X46
F	676	SER	-	linker	UNP Q56X46
F	677	LEU	-	linker	UNP Q56X46
F	678	GLU	-	linker	UNP Q56X46
F	679	VAL	-	linker	UNP Q56X46
F	680	LEU	-	linker	UNP Q56X46
F	681	PHE	-	linker	UNP Q56X46
F	682	GLN	-	linker	UNP Q56X46
F	683	GLY	-	linker	UNP Q56X46
F	684	PRO	-	linker	UNP Q56X46
F	685	THR	-	linker	UNP Q56X46
F	686	ALA	-	linker	UNP Q56X46
F	687	ALA	-	linker	UNP Q56X46
F	688	ALA	-	linker	UNP Q56X46
F	689	ALA	-	linker	UNP Q56X46
F	690	VAL	-	linker	UNP Q56X46
F	753	LEU	PHE	conflict	UNP P42212
F	754	THR	SER	conflict	UNP P42212
F	895	LYS	ALA	conflict	UNP P42212
F	920	LEU	HIS	conflict	UNP P42212
F	928	SER	-	expression tag	UNP P42212
F	929	GLY	-	expression tag	UNP P42212
F	930	GLY	-	expression tag	UNP P42212
F	931	GLY	-	expression tag	UNP P42212
F	932	THR	-	expression tag	UNP P42212
F	933	GLU	-	expression tag	UNP P42212
F	934	THR	-	expression tag	UNP P42212
F	935	SER	-	expression tag	UNP P42212
F	936	GLN	-	expression tag	UNP P42212
F	937	VAL	-	expression tag	UNP P42212
F	938	ALA	-	expression tag	UNP P42212
F	939	PRO	-	expression tag	UNP P42212
F	940	ALA	-	expression tag	UNP P42212
G	75	MET	-	initiating methionine	UNP Q56X46
G	274	ALA	LEU	engineered mutation	UNP Q56X46
G	674	SER	-	linker	UNP Q56X46
G	675	ASN	-	linker	UNP Q56X46
G	676	SER	-	linker	UNP Q56X46
G	677	LEU	-	linker	UNP Q56X46
G	678	GLU	-	linker	UNP Q56X46
G	679	VAL	-	linker	UNP Q56X46
G	680	LEU	-	linker	UNP Q56X46

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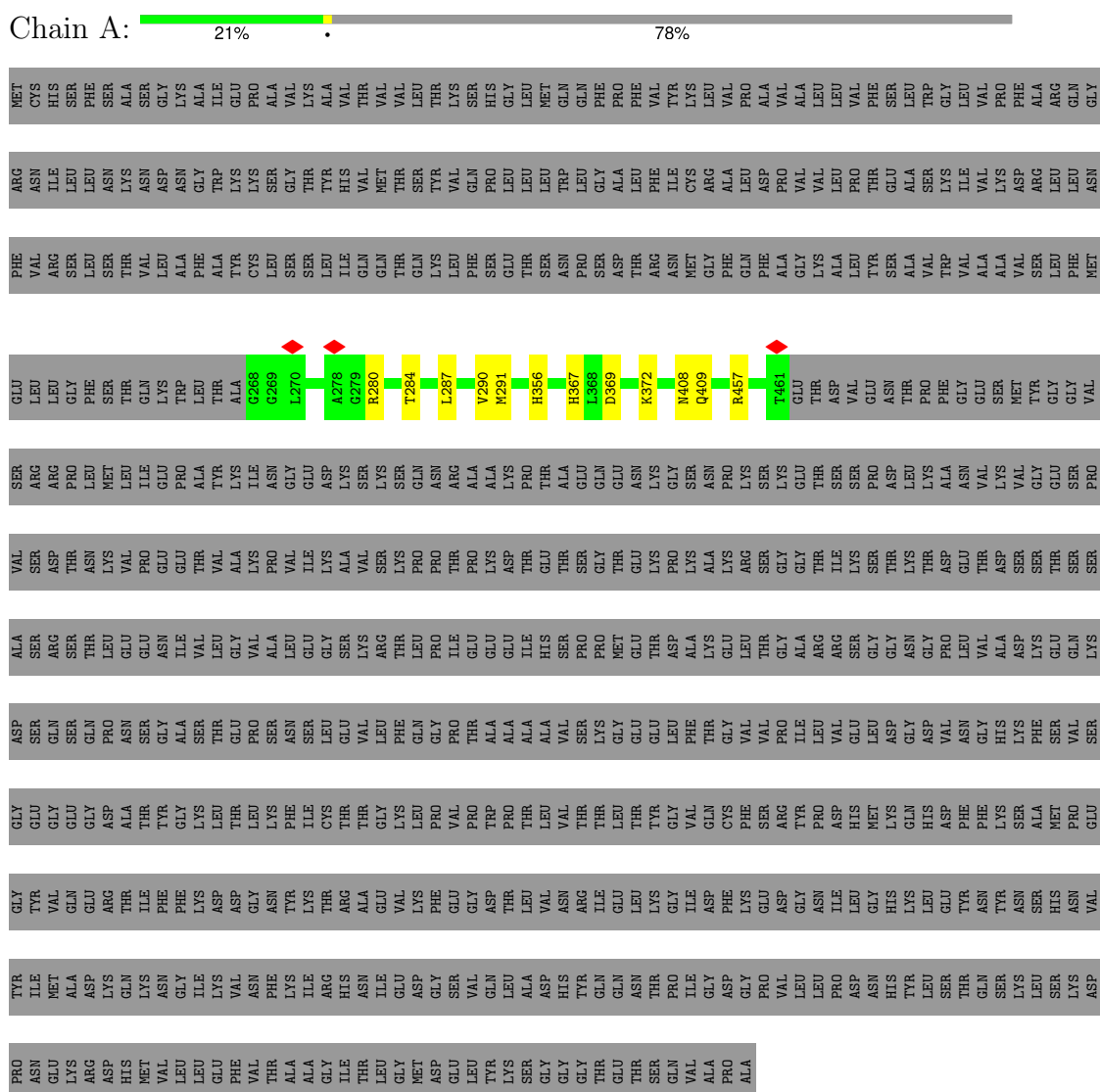
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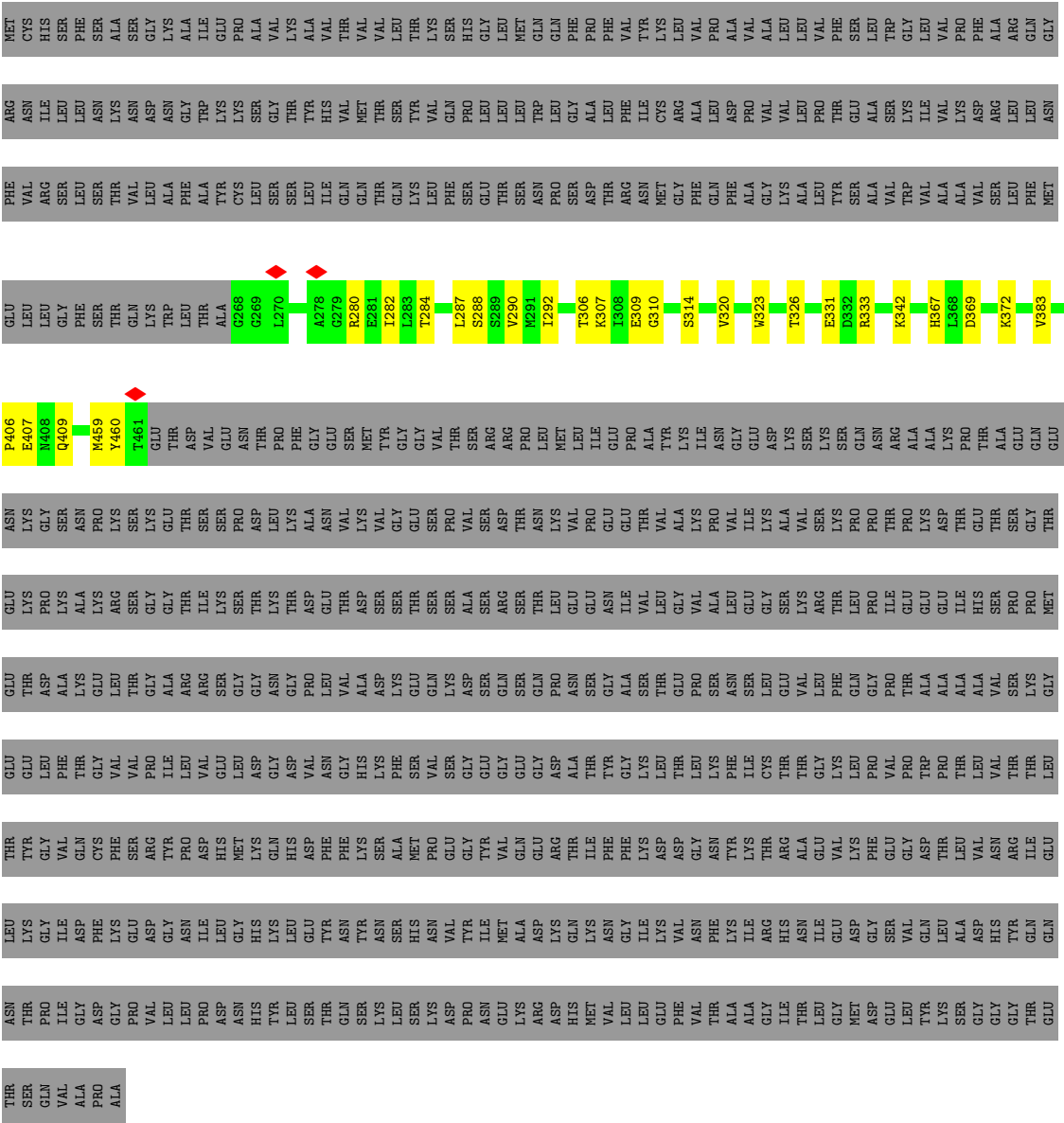
Chain	Residue	Modelled	Actual	Comment	Reference
G	681	PHE	-	linker	UNP Q56X46
G	682	GLN	-	linker	UNP Q56X46
G	683	GLY	-	linker	UNP Q56X46
G	684	PRO	-	linker	UNP Q56X46
G	685	THR	-	linker	UNP Q56X46
G	686	ALA	-	linker	UNP Q56X46
G	687	ALA	-	linker	UNP Q56X46
G	688	ALA	-	linker	UNP Q56X46
G	689	ALA	-	linker	UNP Q56X46
G	690	VAL	-	linker	UNP Q56X46
G	753	LEU	PHE	conflict	UNP P42212
G	754	THR	SER	conflict	UNP P42212
G	895	LYS	ALA	conflict	UNP P42212
G	920	LEU	HIS	conflict	UNP P42212
G	928	SER	-	expression tag	UNP P42212
G	929	GLY	-	expression tag	UNP P42212
G	930	GLY	-	expression tag	UNP P42212
G	931	GLY	-	expression tag	UNP P42212
G	932	THR	-	expression tag	UNP P42212
G	933	GLU	-	expression tag	UNP P42212
G	934	THR	-	expression tag	UNP P42212
G	935	SER	-	expression tag	UNP P42212
G	936	GLN	-	expression tag	UNP P42212
G	937	VAL	-	expression tag	UNP P42212
G	938	ALA	-	expression tag	UNP P42212
G	939	PRO	-	expression tag	UNP P42212
G	940	ALA	-	expression tag	UNP P42212

3 Residue-property plots

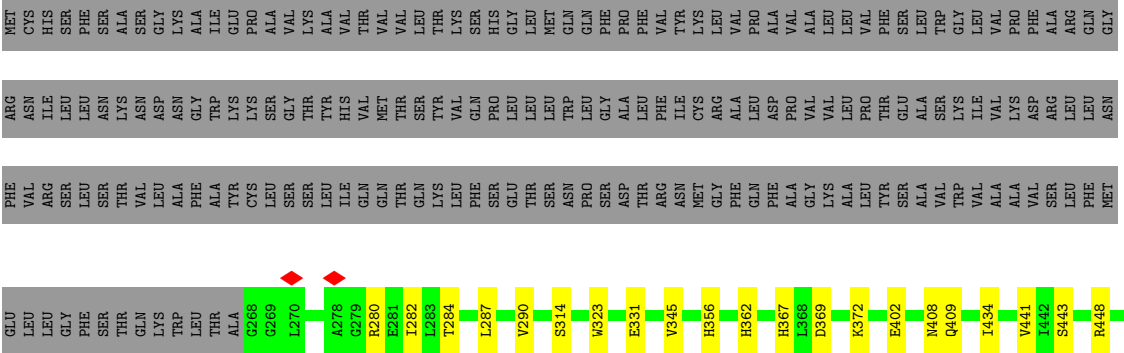
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Mechanosensitive ion channel protein 2, chloroplastic, Green fluorescent protein





● Molecule 1: Mechanosensitive ion channel protein 2, chloroplatic,Green fluorescent protein



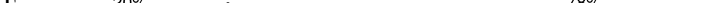
[illegible]

- Molecule 1: Mechanosensitive ion channel protein 2, chloroplastic, Green fluorescent protein

Chain E: 20% 78%

LEU	PRO	ASN	PRO	ASN	LEU	ARG	THR	THR	ASP	GLU	PHE	ARG	MET
ASP	HIS	ILE	ASP	HIS	GLU	SER	ILE	SER	VAL	LEU	VAL	ASN	CYS
ASN	MET	GLY	MET	GLY	GLY	GLY	SER	PRO	ASN	GLY	ARG	ILE	HIS
HIS	LYS	HIS	LYS	ASP	GLY	ASP	THR	ASP	THR	PHE	LEU	LEU	PHE
THR	GLN	LYS	GLN	GLY	ASN	ASN	LYS	LEU	PRO	SER	SER	ASN	SER
LEU	HIS	GLU	ASP	VAL	PRO	PRO	THR	ASP	PHE	THR	THR	LYS	ALA
GLU	ASP	THR	GLY	ASN	GLY	GLU	GLU	ALA	GLY	GLN	LEU	ASN	SER
GLN	PHE	ASN	GLY	VAL	LEU	VAL	THR	VAL	SER	TRP	ALA	ASN	LYS
SER	LYS	THR	HIS	HIS	ALA	ASP	ASP	ASP	THR	LEU	PHE	GLY	ALA
LYS	SER	ASN	PHE	LYS	ASP	SER	SER	VAL	TYR	THR	ALA	TRP	ILE
LEU	ALA	SER	LYS	PHE	GLY	GLY	GLY	GLY	GLY	ALA	TYR	LYS	PRO
SER	MET	HIS	MET	THR	GLN	GLN	THR	THR	VAL	G268	CYS	LYS	ASN
ASN	PRO	ASN	PRO	GLY	GLY	GLN	SER	PRO	VAL	G269	LEU	SER	ALA
VAL	GLY	VAL	GLY	GLY	GLY	GLY	ASP	ALA	VAL	L270	SER	GLY	VAL
PRO	GLY	TYR	GLY	GLY	ASP	SER	SER	VAL	SER	L270	SER	THR	LYS
ASN	ILE	ILE	TYR	GLY	SER	SER	SER	SER	ARG	A278	LEU	TYR	ALA
GLU	MET	MET	VAL	GLY	GLN	ARG	ARG	ASP	ARG	G279	ILE	HIS	VAL
LYS	ALA	ALA	GLN	GLY	GLY	SER	THR	THR	PRO	R280	GLN	THR	THR
ARG	ASP	ASP	GLY	GLY	GLY	THR	THR	ASN	VAL	E281	THR	MET	VAL
ASP	LYS	LYS	ARG	ASP	PRO	PRO	LEU	LYS	MET	I282	GLN	THR	VAL
HIS	GLN	GLN	ASN	ALA	ASN	ASN	GLY	VAL	LEU	L283	GLN	SER	LEU
MET	LYS	LYS	ILE	THR	SER	SER	GLY	PRO	ILE	T284	LYS	TYR	THR
VAL	PHE	ASN	PHE	THR	GLY	GLY	ASN	GLY	GLY				
LEU	PHE	LYS	PHE	LYS	GLY	ALA	ILE	GLY	VAL	L287	PHE	GLN	SER
LEU	ILE	ILE	LYS	THR	THR	THR	VAL	VAL	ALA	V290	GLU	LEU	GLY
PHE	VAL	VAL	ASP	THR	LEU	GLY	GLY	ALA	LYS	M291	THR	LEU	LEU
VAL	GLY	ASN	GLY	LEU	PRO	PRO	VAL	LYS	ILE		SER	LEU	MET
THR	ASN	PHE	ASN	LYS	LYS	SER	ALA	PHO	ASN	K307	ASN	TRP	GLN
ALA	LYS	LYS	TYR	PHE	ASN	ASN	LEU	VAL	GLY		PRO	LEU	GLN
ALA	ILE	ILE	LYS	ILE	SER	SER	GLY	ILE	GLY	G310	SER	GLY	PHE
GLY	ARG	ARG	THR	THR	LEU	GLY	LYS	ALA	ASP		THR	ALA	PRO
ILE	HIS	HIS	ARG	THR	GLY	GLY	SER	ALA	LYS	V320	THR	LEU	PHE
THR	ASN	ASN	ALA	ALA	THR	VAL	LYS	VAL	SER		ARG	PHE	VAL
LEU	ILE	ILE	GLY	GLY	GLY	LEU	ARG	SER	LYS	W323	ASN	ILE	TYR
GLY	GLY	GLU	VAL	VAL	LYS	PHE	THR	THR	LYS		MET	CYS	LYS
MET	ASP	ASP	VAL	LEU	LEU	GLN	LEU	PRO	GLN	T326	GLY	ARG	LEU
ASP	GLY	GLY	PHE	PRO	PRO	GLY	ILE	THR	ASN		PHE	ALA	VAL
GLU	SER	SER	GLY	VAL	THR	THR	THR	THR	ARG	H356	GLN	LEU	PRO
LEU	VAL	VAL	GLY	PRO	THR	THR	GLY	PRO	ALA		PHE	ASP	ALA
TYR	GLN	GLN	ASP	TRP	ALA	ALA	GLU	LYS	ASP	H367	ALA	PRO	VAL
LYS	THR	THR	THR	PRO	PRO	ALA	GLU	ASP	LYS	L368	GLY	VAL	ALA
SER	ALA	ALA	THR	THR	ALA	ALA	ILE	THR	PRO	D369	LYS	VAL	LEU
GLY	ASP	ASP	VAL	VAL	ALA	HIS	GLY	LEU	THR		ALA	LEU	LEU
GLY	HIS	HIS	ASN	VAL	VAL	SER	SER	THR	ALA	K372	LEU	PRO	VAL
GLY	THR	GLN	ILE	THR	THR	LYS	PRO	PRO	GLY		TYR	THR	PHE
THR	GLN	GLN	GLY	THR	GLY	GLY	GLY	GLY	GLN	V383	SER	GLY	SER
THR	ASN	ASN	LEU	THR	GLY	GLY	GLY	GLY	GLY		ALA	ALA	TRP
SER	THR	THR	LYS	TYR	GLY	GLY	THR	LYS	LYS	M408	VAL	ILE	GLY
GLN	PRO	PRO	ILE	VAL	GLY	LEU	ASP	ALA	SER	Q409	VAL	VAL	VAL
VAL	ILE	ILE	ILE	VAL	PHE	THR	ALA	LYS	GLY		ALA	VAL	VAL
ALA	GLY	GLY	ASP	GLN	THR	THR	LYS	ALA	ASN	I434	ALA	LYS	PRO
PRO	ASP	PHE	PHE	CYS	GLY	GLY	GLY	LYS	PRO	L449	VAL	ASP	PHE
PRO	GLY	LYS	VAL	PHE	VAL	VAL	LEU	ARG	LYS		VAL	ARG	ALA
GLY	PRO	PRO	VAL	SER	VAL	VAL	THR	SER	SER	L449	LEU	LEU	ARG
VAL	VAL	VAL	PRO	ARG	PRO	PRO	GLY	GLY	GLY	T461	PHE	LEU	GLY
ILE	THR	THR	THR	THR	ILE	THR	GLY	GLY	THR		MET	ASN	GLN

- Molecule 1: Mechanosensitive ion channel protein 2, chloroplastic, Green fluorescent protein

Chain F:  20% 78%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	81059	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.052	Depositor
Minimum map value	-0.326	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.191	Depositor
Map size (Å)	309.6, 309.6, 309.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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	0.13	0/1605	0.27	0/2177
1	B	0.13	0/1605	0.27	0/2177
1	C	0.13	0/1605	0.26	0/2177
1	D	0.13	0/1605	0.27	0/2177
1	E	0.13	0/1605	0.26	0/2177
1	F	0.13	0/1605	0.26	0/2177
1	G	0.14	0/1605	0.29	0/2177
All	All	0.13	0/11235	0.27	0/15239

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	1572	0	1626	10	0
1	B	1572	0	1626	14	0
1	C	1572	0	1626	12	0
1	D	1572	0	1626	16	0
1	E	1572	0	1626	12	0
1	F	1572	0	1626	9	0
1	G	1572	0	1626	16	0
All	All	11004	0	11382	79	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 4.

The worst 5 of 79 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:E:287:LEU:O	1:E:291:MET:HG3	1.94	0.67
1:B:460:TYR:OH	1:D:448:ARG:NH1	2.29	0.65
1:E:280:ARG:O	1:E:284:THR:OG1	2.17	0.62
1:D:280:ARG:O	1:D:284:THR:OG1	2.18	0.62
1:G:280:ARG:O	1:G:284:THR:OG1	2.18	0.62

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	192/866 (22%)	187 (97%)	5 (3%)	0	100	100
1	B	192/866 (22%)	187 (97%)	5 (3%)	0	100	100
1	C	192/866 (22%)	188 (98%)	4 (2%)	0	100	100
1	D	192/866 (22%)	186 (97%)	6 (3%)	0	100	100
1	E	192/866 (22%)	189 (98%)	3 (2%)	0	100	100
1	F	192/866 (22%)	187 (97%)	5 (3%)	0	100	100
1	G	192/866 (22%)	187 (97%)	5 (3%)	0	100	100
All	All	1344/6062 (22%)	1311 (98%)	33 (2%)	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	174/749 (23%)	174 (100%)	0	100	100
1	B	174/749 (23%)	172 (99%)	2 (1%)	65	87
1	C	174/749 (23%)	170 (98%)	4 (2%)	44	78
1	D	174/749 (23%)	169 (97%)	5 (3%)	37	73
1	E	174/749 (23%)	173 (99%)	1 (1%)	78	92
1	F	174/749 (23%)	171 (98%)	3 (2%)	53	83
1	G	174/749 (23%)	171 (98%)	3 (2%)	53	83
All	All	1218/5243 (23%)	1200 (98%)	18 (2%)	55	84

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	441	VAL
1	G	441	VAL
1	G	349	ARG
1	D	426	GLU
1	F	426	GLU

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	C	444	HIS
1	D	387	ASN
1	E	408	ASN
1	B	319	HIS
1	B	340	ASN

5.3.3 RNA ⓘ

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.

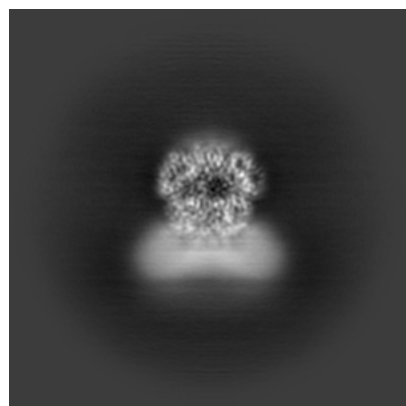
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-79081. These allow visual inspection of the internal detail of the map and identification of artifacts.

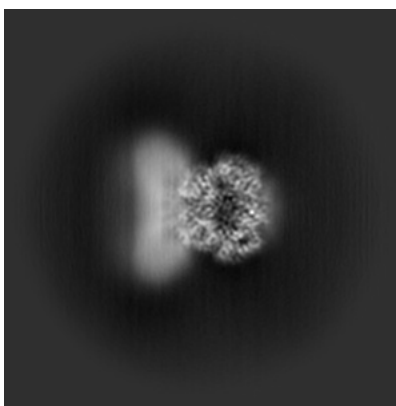
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

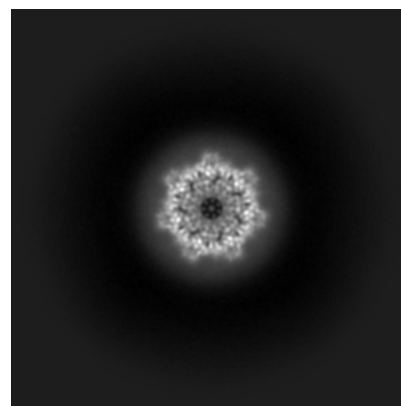
6.1.1 Primary map



X

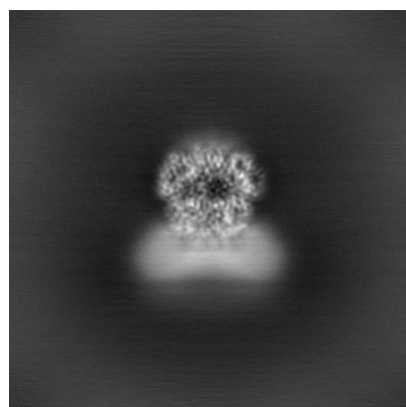


Y

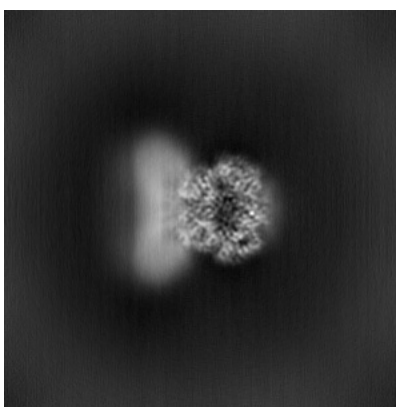


Z

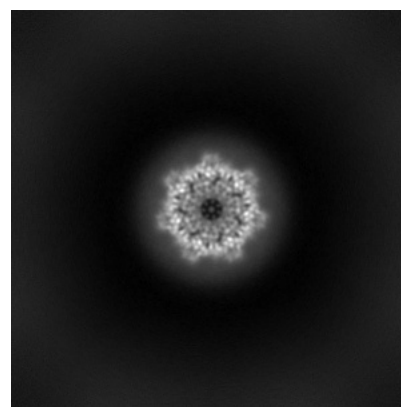
6.1.2 Raw map



X



Y

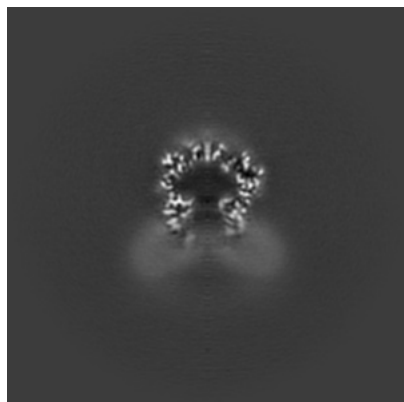


Z

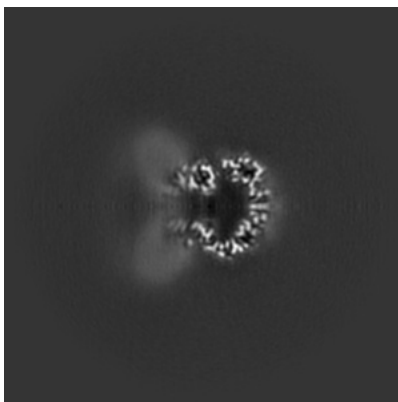
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

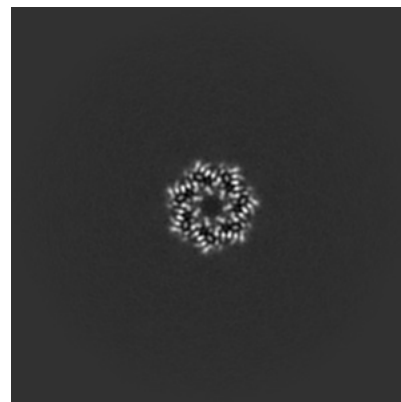
6.2.1 Primary map



X Index: 180

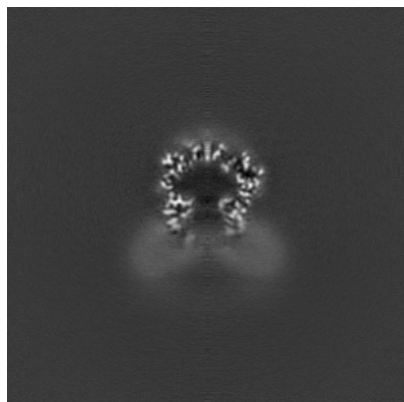


Y Index: 180

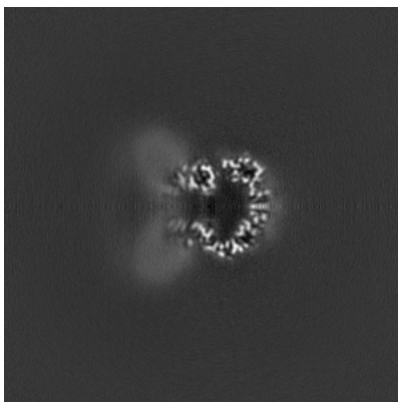


Z Index: 180

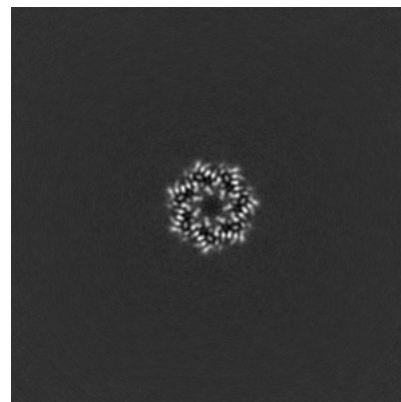
6.2.2 Raw map



X Index: 180



Y Index: 180

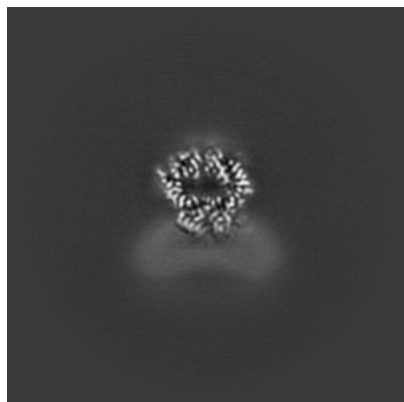


Z Index: 180

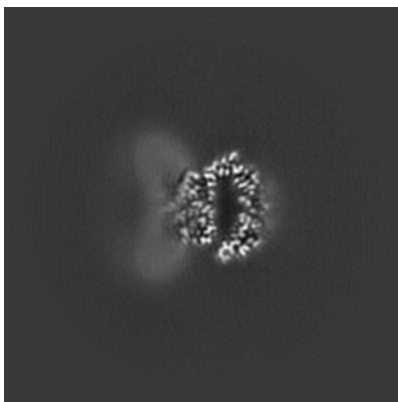
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

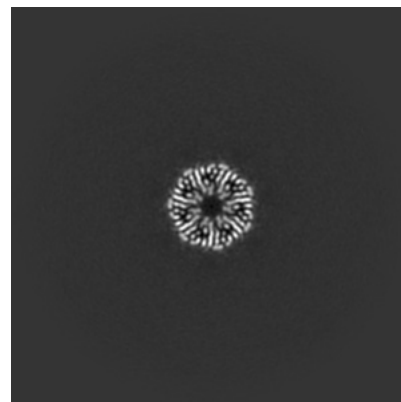
6.3.1 Primary map



X Index: 158

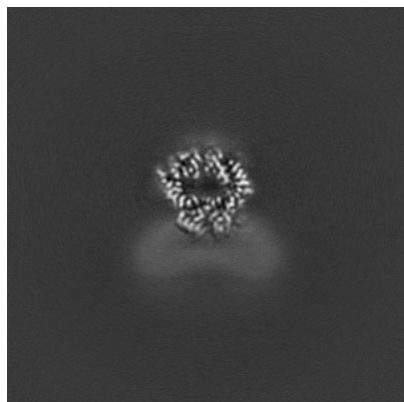


Y Index: 164

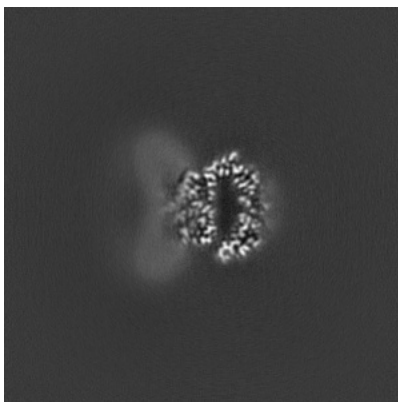


Z Index: 184

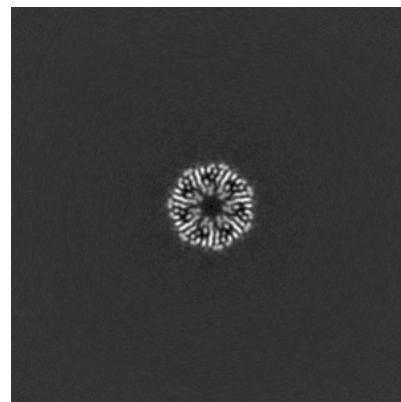
6.3.2 Raw map



X Index: 158



Y Index: 164

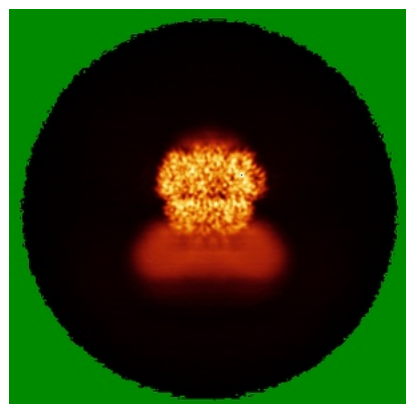


Z Index: 184

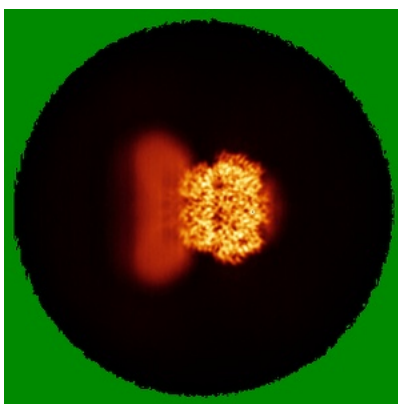
The images above show the largest variance slices of the map in three orthogonal directions.

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

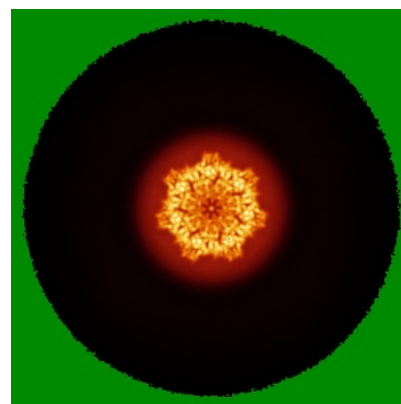
6.4.1 Primary map



X

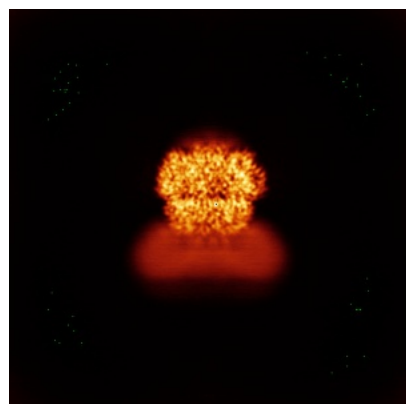


Y

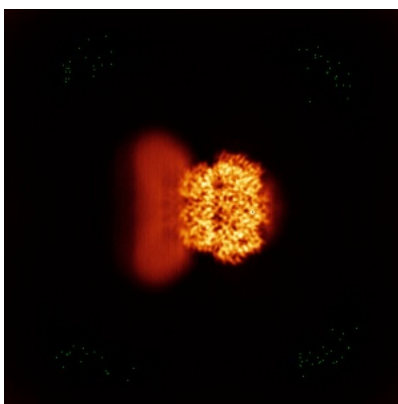


Z

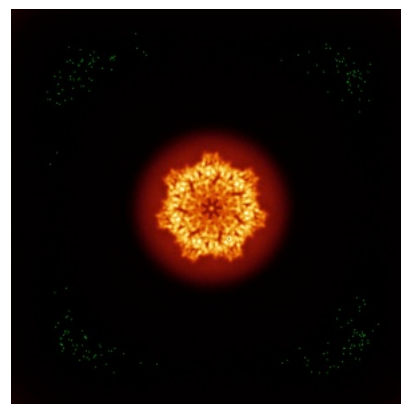
6.4.2 Raw map



X



Y

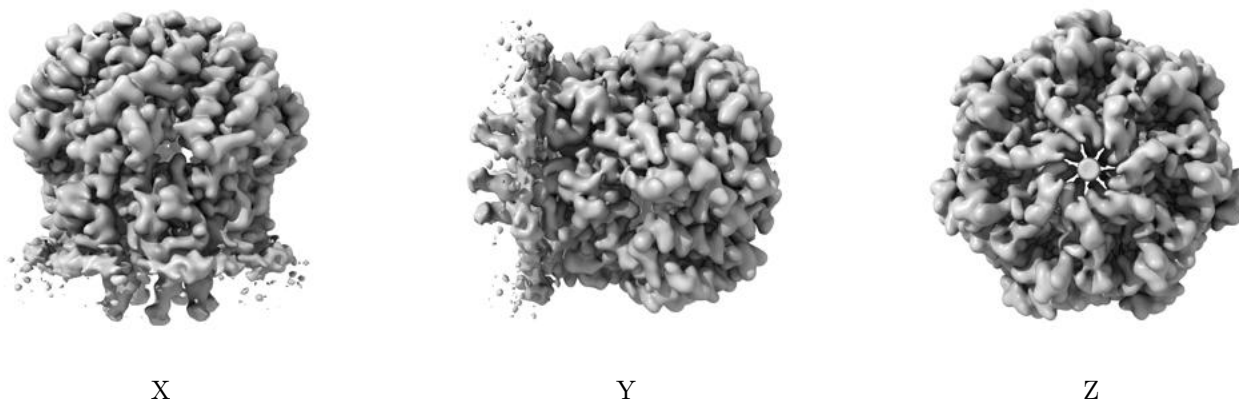


Z

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.

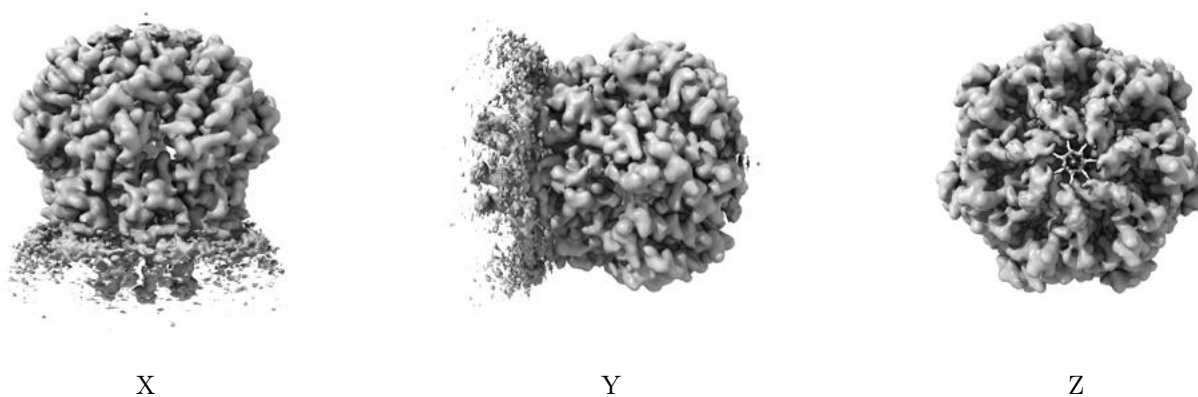
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.191. 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.

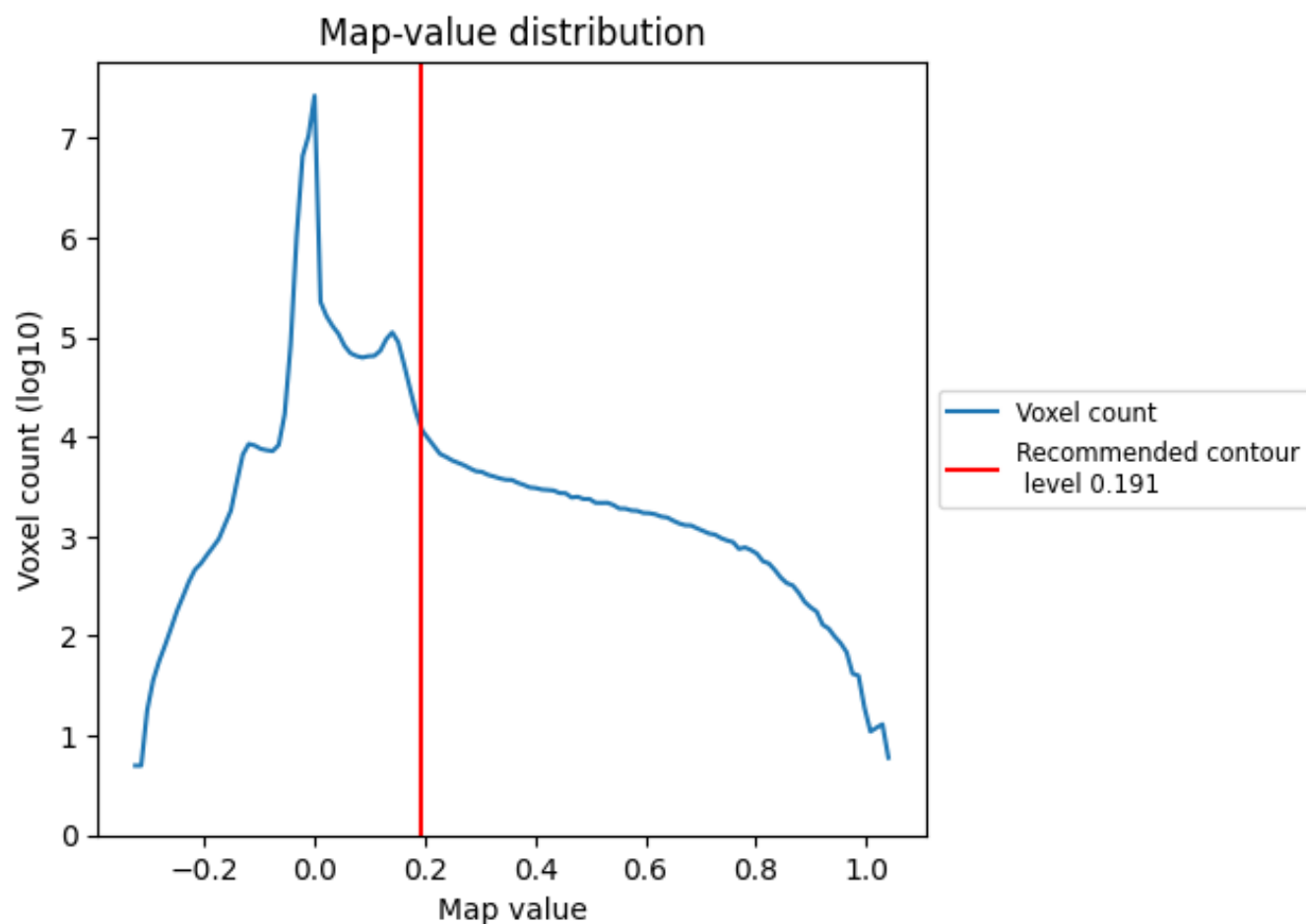
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

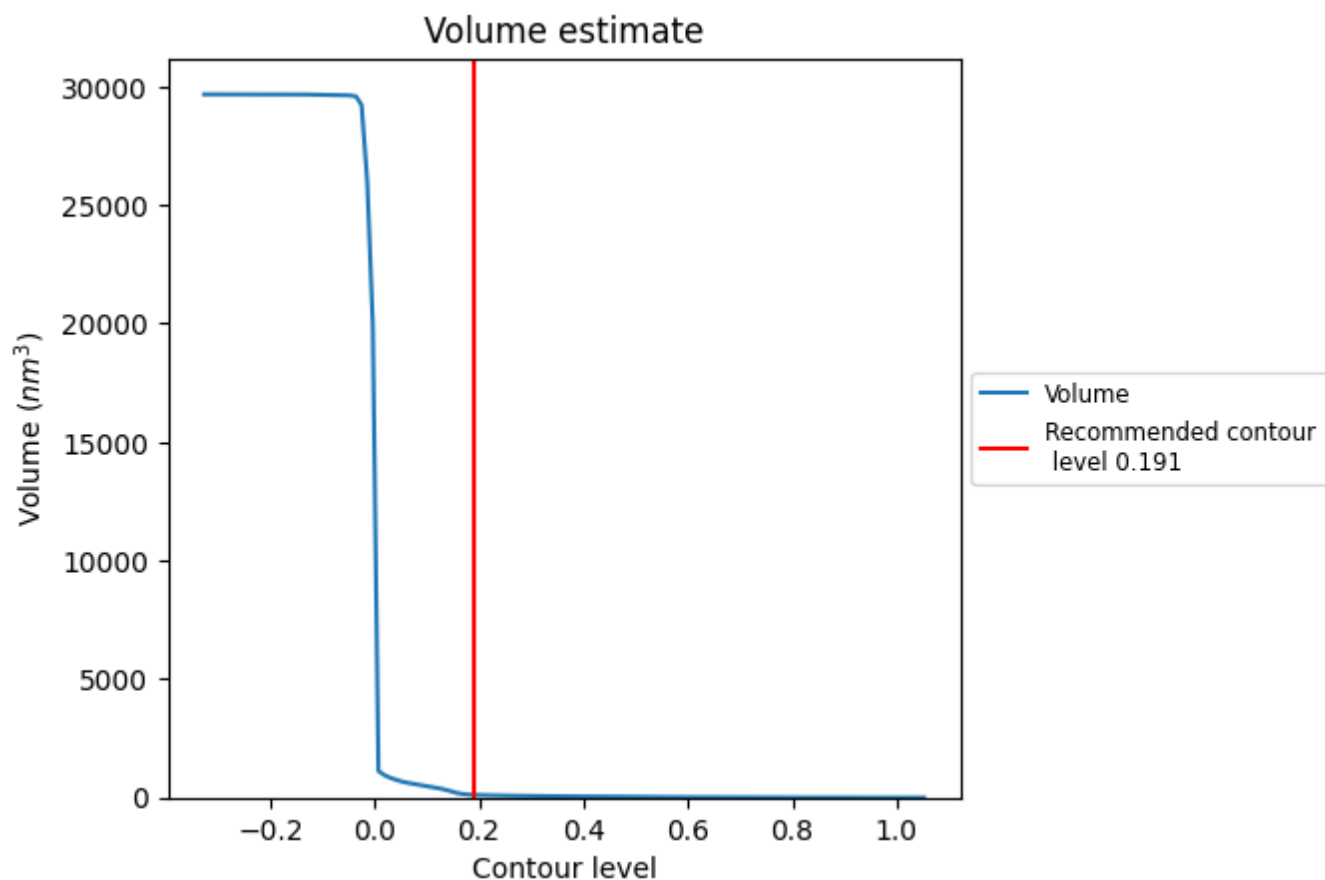
This section contains the results of statistical analysis of the map.

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.

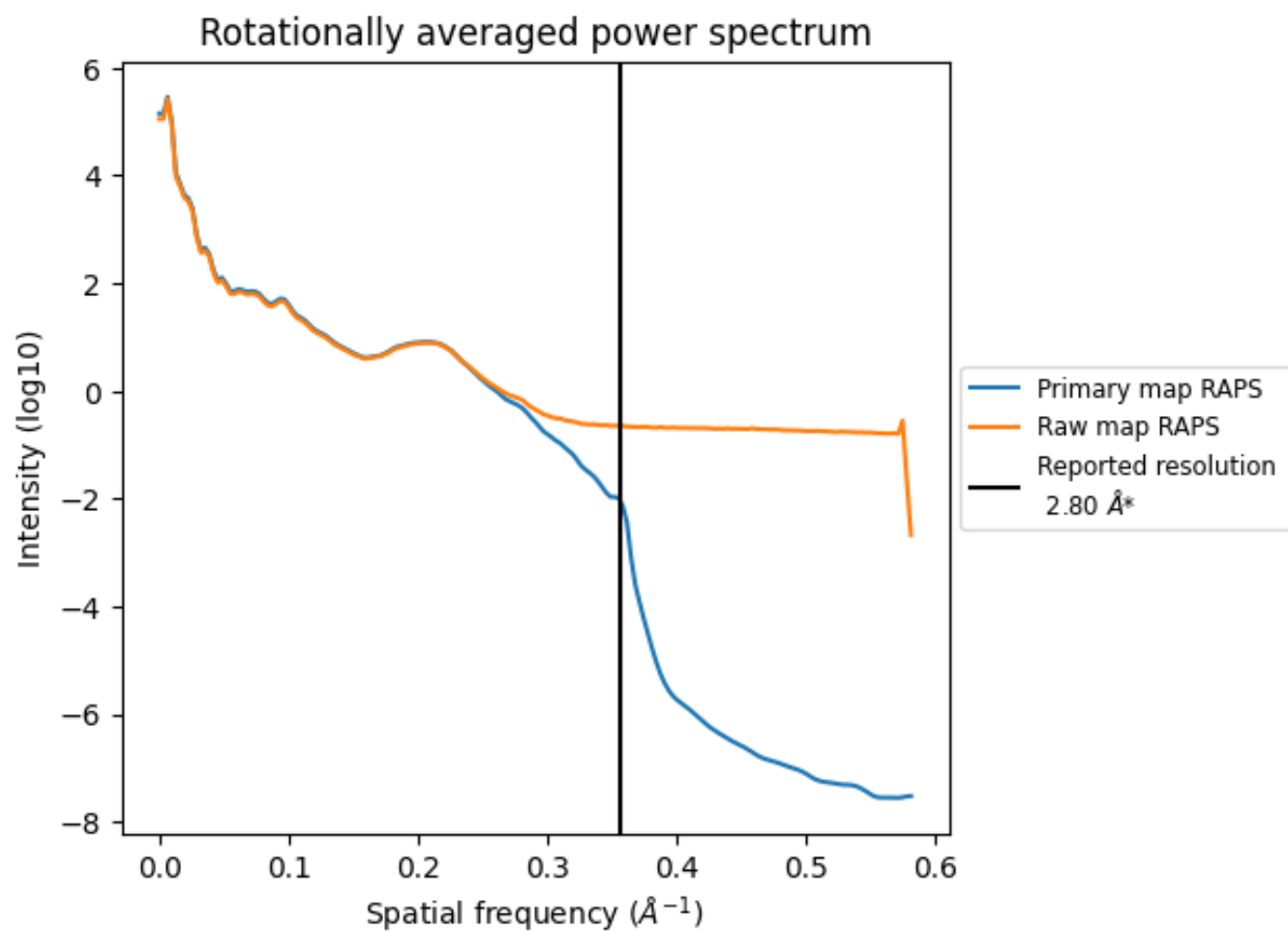
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 113 nm³; this corresponds to an approximate mass of 102 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 ⓘ

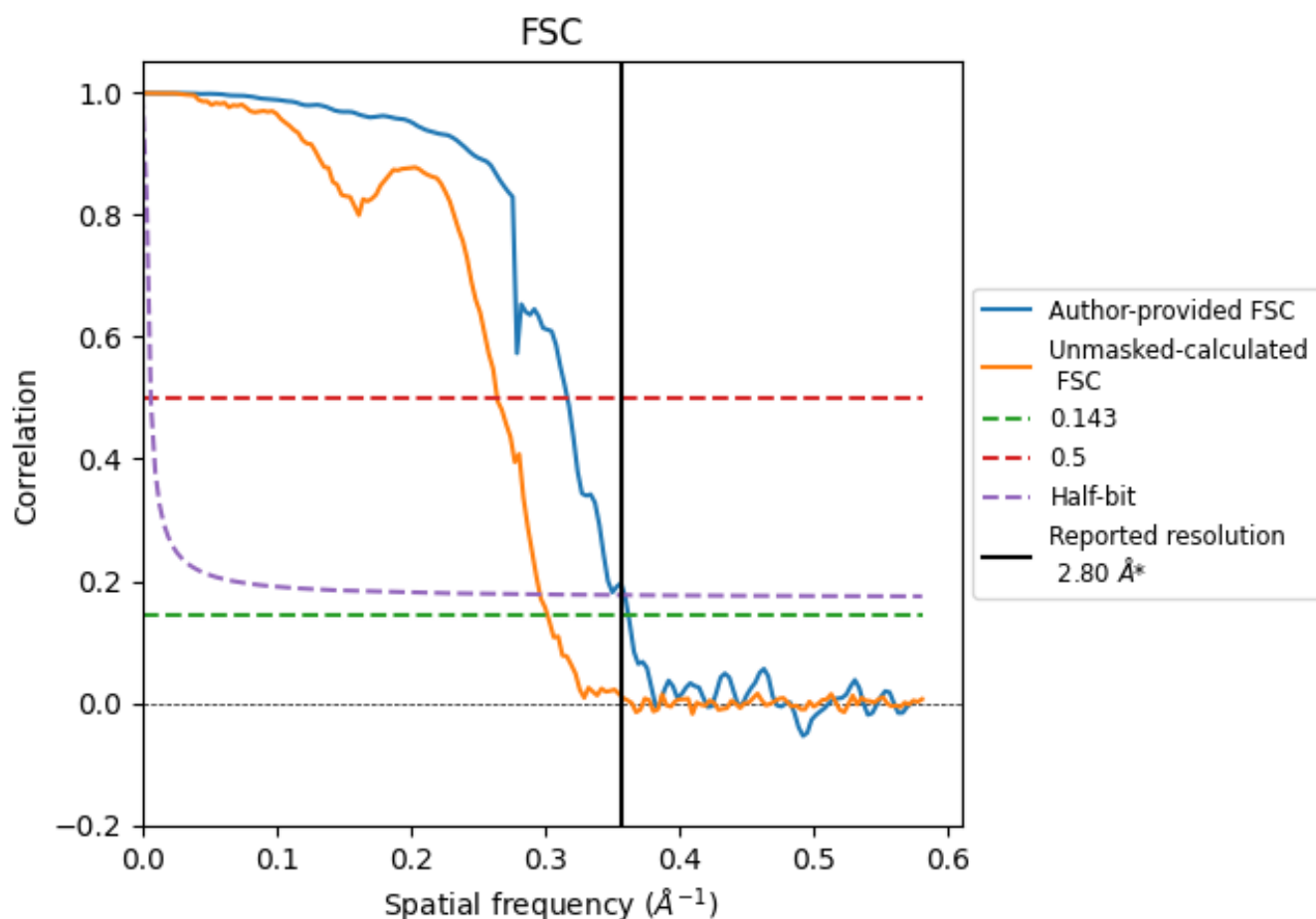


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 $0.357 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

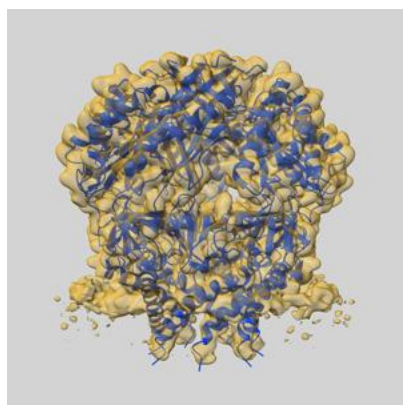
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.76	3.16	2.78
Unmasked-calculated*	3.31	3.78	3.37

*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 3.31 differs from the reported value 2.8 by more than 10 %

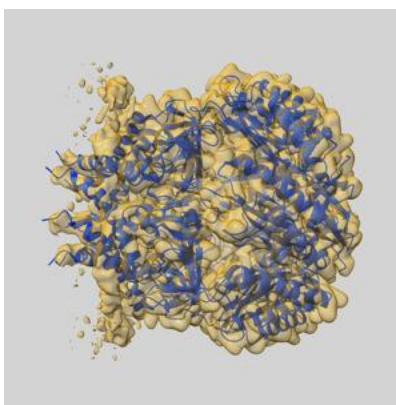
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-79081 and PDB model 38RK. Per-residue inclusion information can be found in section [3](#) on page [11](#).

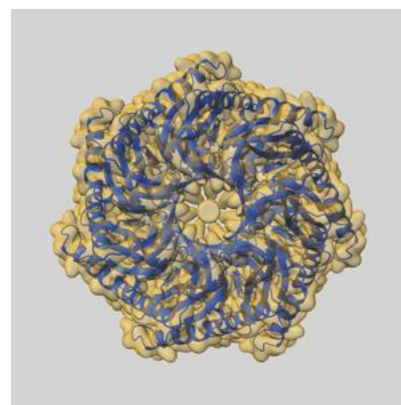
9.1 Map-model overlay [i](#)



X



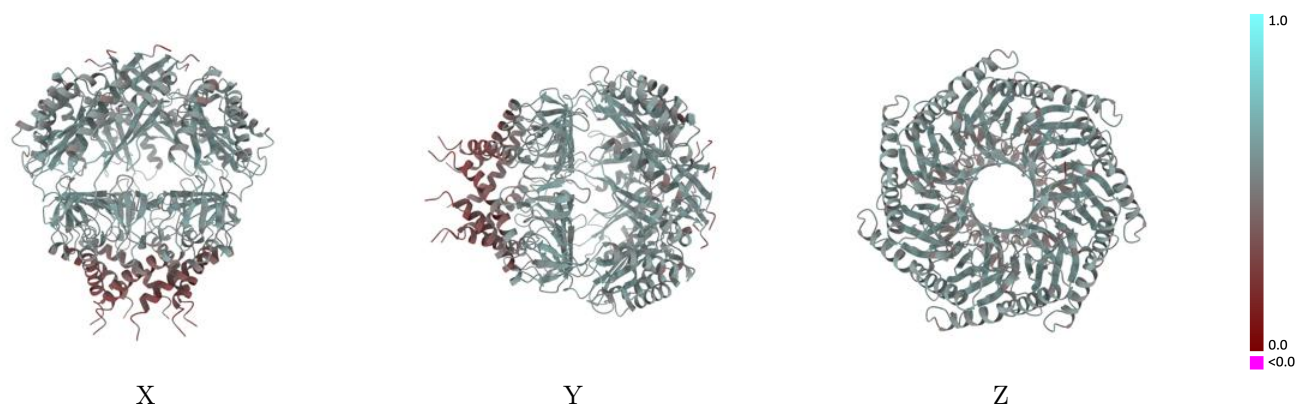
Y



Z

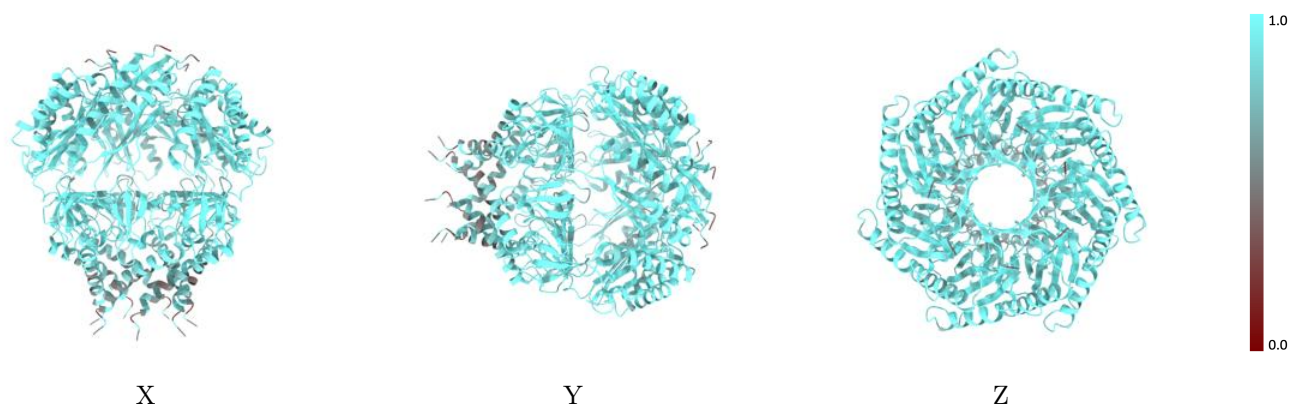
The images above show the 3D surface view of the map at the recommended contour level 0.191 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



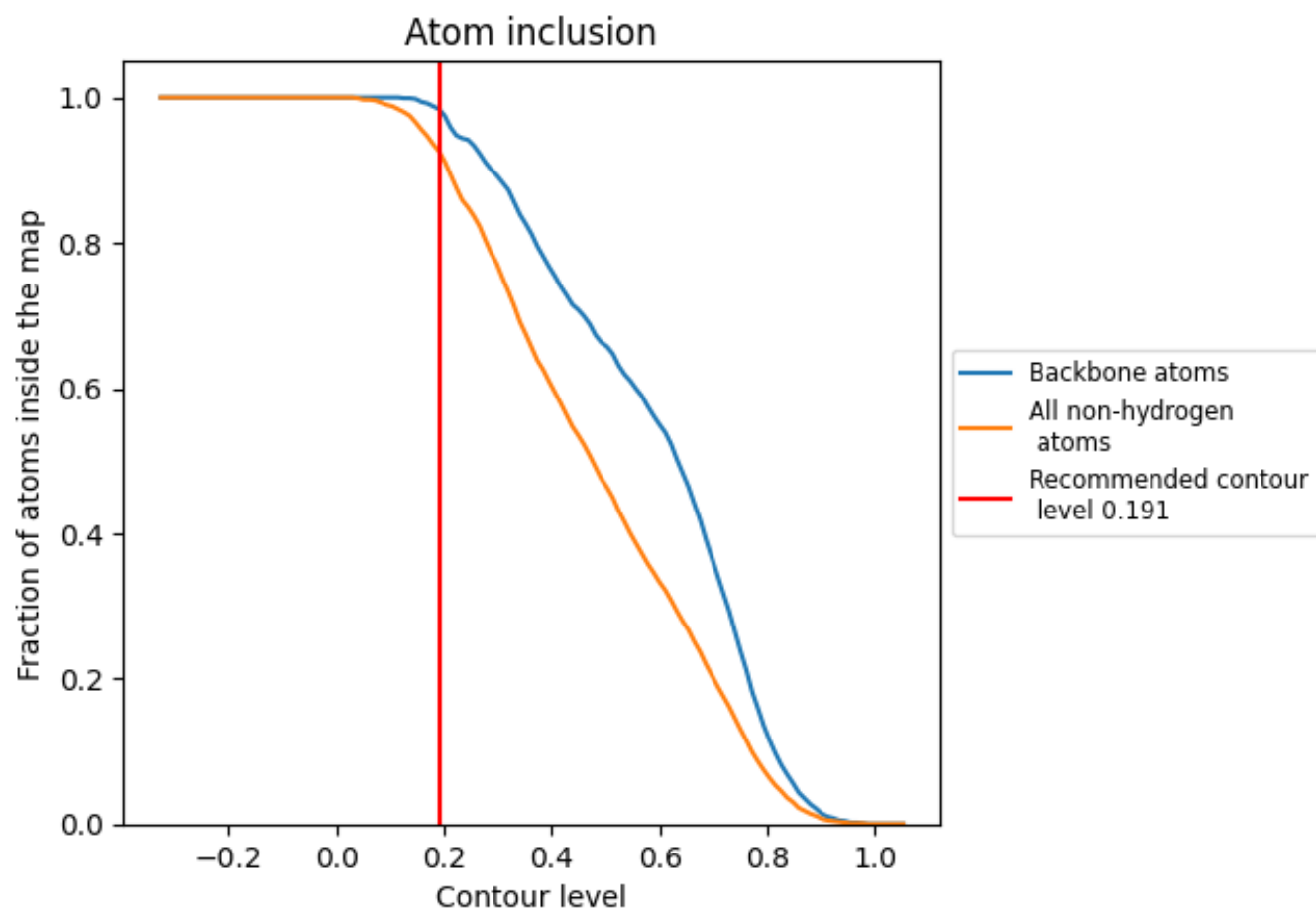
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.191).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% 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 (0.191) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9260	0.5180
A	0.9270	0.5170
B	0.9240	0.5170
C	0.9260	0.5170
D	0.9260	0.5190
E	0.9260	0.5190
F	0.9280	0.5180
G	0.9260	0.5160

1.0

0.0

<0.0