



wwPDB EM Validation Summary Report ⓘ

Sep 22, 2026 – 02:34 PM EDT

PDB ID : 38RX / pdb_000038rx
EMDB ID : EMD-79091
Title : Cryo-EM structure of wild-type Arabidopsis thaliana mechanosensitive channel of small conductance-like protein 2 (MSL2) in chloroplast lipid nanodiscs.
Authors : Angiulli, G.; Dong, L.; Walz, T.
Deposited on : 2026-09-15
Resolution : 2.40 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

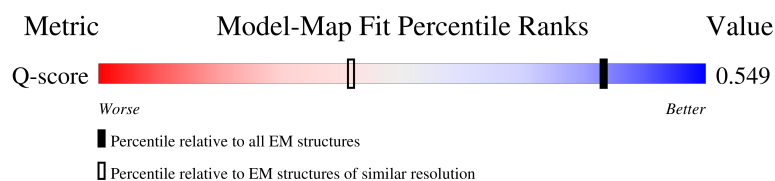
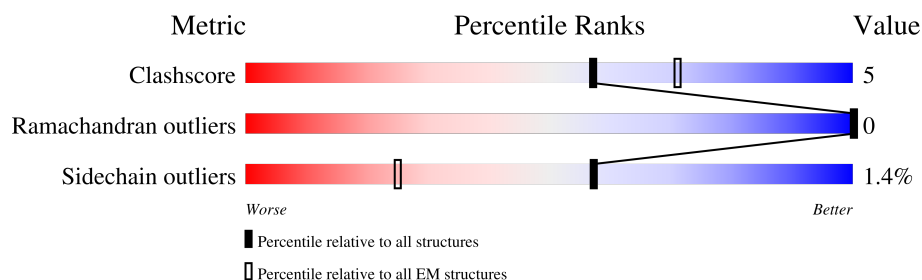
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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	5628 (1.90 - 2.90)

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	19% 78%
1	G	866	19% 78%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10934 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
			1562	995	293	269	5		
1	B	194	Total	C	N	O	S	0	0
			1562	995	293	269	5		
1	C	194	Total	C	N	O	S	0	0
			1562	995	293	269	5		
1	D	194	Total	C	N	O	S	0	0
			1562	995	293	269	5		
1	E	194	Total	C	N	O	S	0	0
			1562	995	293	269	5		
1	F	194	Total	C	N	O	S	0	0
			1562	995	293	269	5		
1	G	194	Total	C	N	O	S	0	0
			1562	995	293	269	5		

There are 245 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	MET	-	initiating methionine	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
A	687	ALA	-	linker	UNP Q56X46

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Chain	Residue	Modelled	Actual	Comment	Reference
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	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
B	895	LYS	ALA	conflict	UNP P42212
B	920	LEU	HIS	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
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	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
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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
C	932	THR	-	expression tag	UNP P42212
C	933	GLU	-	expression tag	UNP P42212
C	934	THR	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
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	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
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D	929	GLY	-	expression tag	UNP P42212
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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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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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	674	SER	-	linker	UNP Q56X46
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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F	690	VAL	-	linker	UNP Q56X46
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F	937	VAL	-	expression tag	UNP P42212
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F	939	PRO	-	expression tag	UNP P42212
F	940	ALA	-	expression tag	UNP P42212
G	75	MET	-	initiating methionine	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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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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

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

A horizontal bar chart with a green segment representing 20% and a grey segment representing 78%. The segments are separated by a small gap, and the percentages are labeled below the bar.

[illegible]

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

Response	Percentage
Yes	20%
No	78%

[illegible]

[illegible]

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

Chain D: 19% . 78%

ARG	THR	SER	PRO	SER	GLU	E407	GLU	PHE	ARG	MET
ILE	THR	GLY	PRO	THR	GLN	Q408	LEU	VAL	ASN	CYS
LEU	LEU	GLY	MET	THR	GLU	Q409	LEU	ARG	ILE	HIS
LEU	THR	GLU	GLU	GLY	ASN		GLY	SER	LEU	LEU
GLY	TYR	GLY	THR	LYS	LYS	D437	PHE	LEU	LEU	PHE
ILE	VAL	PHE	ASP	PRO	GLY		THR	SER	ASN	SER
ASP	GLN	THR	LYS	ALA	SER	R440	THR	THR	LYS	ALA
PHE	CYS	GLY	LYS	ALA	ASN		GLN	VAL	ASN	SER
GLY	PHE	VAL	GLU	ARG	PRO	S443	LYS	ALA	ASP	LYS
GLU	SER	VAL	THR	SER	SER	T463	LEU	PHE	GLY	ALA
ASP	ARG	PRO	GLY	GLY	GLU		THR	ALA	TRP	ILE
GLY	TYR	ILE	ALA	GLY	GLU		ALA	TYR	LYS	GLU
ASN	PRO	LEU	ARG	THR	THR	ASP	G269	CYS	LYS	PRO
ILE	ASP	VAL	ARG	ILE	SER	VAL	G269	LEU	SER	ALA
LEU	HIS	GLU	SER	LYS	GLU			SER	THR	VAL
GLY	MET	LEU	GLY	SER	PRO	ASN	V273	SER	GLY	LYS
LYS	LYS	ASP	GLY	THR	ASP	THR		LEU	TYR	ALA
HIS	GLN	GLY	ASN	LYS	LEU	PRO	A278	ILE	HIS	VAL
LEU	HIS	ASP	GLY	THR	LYS	PHE	G279	GLN	VAL	THR
GLU	ASP	VAL	PRO	THR	ALA	GLY	R280	GLN	MET	VAL
TYR	PHE	ASN	LEU	GLU	ASN	GLU	E281	THR	THR	VAL
ASN	PHE	GLY	VAL	THR	VAL	SER	T282	GLN	SER	LEU
TYR	LYS	HIS	ALA	ASP	LYS	MET	L283	LYS	TYR	THR
ASN	SER	LYS	ASP	ASP	VAL	TYR	T284	LEU	VAL	LYS
SER	ALA	PHE	LYS	GLY	VAL	GLY	M285	PHE	GLN	SER
HIS	MET	THR	GLY	THR	GLU	GLY	F286	SER	PRO	HIS
ASN	GLN	SER	GLN	SER	SER	VAL	L287	GLU	LEU	GLY
VAL	PRO	VAL	LYS	SER	PRO	THR		LEU	LEU	GLY
TYR	GLY	GLY	ASP	ALA	VAL	SER	M291	SER	LEU	MET
ILE	TYR	GLU	SER	SER	SER	ARG		ASN	TRP	GLN
MET	VAL	GLY	GLN	ARG	ASP	ARG	R296	PRO	LEU	GLN
ALA	GLN	GLY	SER	THR	THR	LEU		SER	GLY	PHE
ASP	GLU	GLY	GLN	THR	ASN	PRO	L300	ASP	ALA	PRO
LYS	ARG	ASP	PRO	LEU	LYS	MET		THR	LEU	PHE
GLN	THR	ALA	ASN	GLU	VAL	LEU	T308	ARG	PHE	VAL
ILE	ILE	THR	SER	GLU	PRO	ILE	E309	TYR	ILE	TYR
ASN	PHE	TYR	GLY	ASN	GLU	GLU		CYS	ARG	LYS
GLY	PHE	GLY	ALA	ILE	GLU	PRO	V313	GLY	ARG	LEU
ILE	LYS	LYS	SER	VAL	THR	ALA		PHE	ALA	VAL
LYS	ASP	LEU	THR	LEU	VAL	TYR	G321	GLN	LEU	PRO
VAL	ASP	THR	GLU	GLY	ALA	LYS	W322	PHE	ASP	ALA
ASN	GLY	LEU	PRO	VAL	LYS	ILE		ALA	PRO	VAL
ASP	ASN	LYS	SER	ALA	PRO	ASN	T326	GLY	VAL	VAL
PHE	ASN	LYS	ASN	ALA	VAL	GLY		LYS	VAL	LEU
ILE	LYS	ILE	SER	GLU	ILE	GLU	T338	ALA	LEU	LEU
ARG	THR	CYS	LEU	GLY	LYS	ASP	F339	LEU	PRO	VAL
HIS	ARG	THR	GLU	SER	ALA	LYS		TYR	THR	PHE
ASN	ALA	THR	VAL	LYS	VAL	LYS	N340	SER	GLU	SER
ILE	GLU	GLY	LEU	ARG	SER	LYS	H341	ALA	ALA	LEU
GLY	VAL	LYS	PHE	THR	LYS	SER	F342	VAL	SER	TRP
ASP	LYS	PRO	GLN	LEU	PRO	GLN	F343	TRP	LYS	GLY
GLY	PHE	LEU	GLY	THR	PRO	ASN		VAL	ILE	VAL
SER	GLU	VAL	PRO	ILE	THR	ARG	R349	ALA	VAL	VAL
VAL	GLY	PRO	THR	GLU	PRO	ALA		ALA	LYS	VAL
GLN	ASP	TRP	ALA	GLU	LYS	ALA	H356	VAL	ASP	PHE

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

GLN	VAL	ALA	PRO	ALA	GLY	VAL	GLN	LEU	ASP	PRO	GLY	H444	GLU	PHE	ARG	MET
ILE	GLY	ASP	ILE	ASP	ILE	GLN	ASP	PHE	ALA	LYS	SER	H445	LEU	VAL	ASN	CYS
GLY	GLY	ASP	GLY	GLY	PHE	CYS	GLY	VAL	LEU	LYS	PRO	L449	PHE	LEU	SER	ILE
PRO	VAL	PRO	VAL	THR	SER	SER	THR	VAL	THR	SER	SER	T461	THR	SER	ASN	PHE
VAL	ASP	GLY	ASP	GLY	GLY	ARG	GLY	LEU	GLY	GLY	GLY	GLU	THR	THR	LYS	ALA
LEU	ILE	TYR	ILE	ALA	THR	PRO	ALA	THR	GLY	GLY	GLY	THR	THR	GLN	VAL	THR
LEU	ASP	THR	VAL	ARG	ARG	ASP	THR	VAL	ASP	ILE	THR	VAL	ASP	LYS	ALA	GLY
ASP	GLY	ASP	GLY	GLY	SER	HIS	GLY	GLY	SER	LYS	SER	ASN	GLY	PHE	GLY	LYS
HIS	HIS	LYS	LYS	GLN	LYS	THR	LYS	ASP	THR	THR	ASP	THR	ALA	TYR	TRP	ILE
TYR	LYS	LYS	LYS	GLY	GLY	GLY	GLY	GLY	LYS	LYS	LEU	PRO	G268	CYS	LYS	GLU
LEU	LEU	GLY	GLY	ASP	ASP	ASP	THR	VAL	THR	ASP	ALA	GLY	A278	SER	GLY	PRO
SER	TYR	THR	THR	PHE	PHE	ASN	ASN	GLY	LEU	THR	VAL	SER	G279	LEU	THR	LYS
GLN	ASN	ASN	TYR	ASN	ASN	THR	LYS	HIS	VAL	ASP	LYS	MET	R280	ILE	TYR	ALA
SER	TYR	SER	ASN	LYS	LYS	THR	LYS	GLY	ALA	ASP	VAL	THR	L287	GLN	VAL	THR
LYS	LYS	SER	ASN	PRO	PRO	GLY	GLY	VAL	GLN	SER	SER	THR	M291	THR	THR	VAL
ASP	VAL	THR	VAL	GLY	GLY	GLY	GLY	SER	GLY	THR	PRO	THR	R296	GLN	SER	LEU
PRO	ASP	THR	GLY	ASP	ASP	GLY	ASP	ALA	LYS	SER	VAL	SER	L300	LEU	VAL	LYS
ASN	ASN	ILE	TYR	GLN	VAL	VAL	GLN	SER	ARG	SER	ARG	THR	R307	PHE	GLN	THR
LYS	ALA	ILE	ALA	GLY	GLY	GLY	GLY	GLY	ARG	THR	PRO	PRO	T306	GLY	PRO	GLY
ASP	LYS	ARG	GLY	PRO	ARG	GLY	GLY	LEU	SER	THR	ASN	MET	R307	SER	LEU	LEU
HIS	GLN	MET	THR	ASN	PHE	ASN	ILE	GLU	GLY	PRO	ILE	LEU	E309	ASN	TRP	GLN
VAL	LEU	LEU	LEU	GLY	GLY	GLY	ILE	ILE	GLY	GLY	GLY	GLU	V313	SER	GLY	LEU
LEU	LEU	LEU	LEU	LYS	LYS	LYS	LYS	VAL	SER	VAL	THR	ALA	G321	ASP	ALA	PRO
PHE	VAL	THR	THR	THR	THR	ASP	ASP	LEU	THR	LEU	VAL	TYR	G321	THR	LEU	VAL
VAL	ASP	GLY	ASP	GLY	ASP	GLY	GLY	THR	GLY	GLY	ALA	LYS	T326	ARG	PHE	TYR
THR	THR	PHE	THR	PRO	PRO	GLY	LYS	VAL	VAL	VAL	ILE	ASN	T326	ASN	ILE	TYR
ALA	ALA	LYS	LYS	SER	SER	ASN	LYS	ALA	ALA	PRO	PRO	ASN	I338	GLY	CYS	LYS
GLY	ALA	ILE	ILE	ASN	ASN	THR	THR	LEU	LEU	VAL	GLY	GLY	P339	PHE	ALA	VAL
GLY	GLY	THR	THR	SER	SER	ILE	GLY	GLY	GLY	ILE	ILE	GLU	N340	GLN	LEU	PRO
ILE	THR	THR	THR	LEU	LEU	CYS	THR	THR	GLY	LYS	LYS	ASP	F343	PHE	ASP	ALA
THR	THR	THR	THR	THR	THR	THR	THR	THR	GLY	GLY	GLY	ASP	F343	ALA	PRO	VAL
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	SER	H356	GLY	VAL	ALA
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ARG	THR	SER	SER	H356	LYS	VAL	LEU
MET	MET	MET	MET	MET	MET	MET	MET	MET	LEU	LEU	PRO	GLN	D379	ALA	PRO	VAL
ASP	ASP	GLY	GLY	GLY	PHE	PHE	GLY	GLY	GLY	PRO	PRO	ASN	E391	TYR	THR	THR
GLY	SER	SER	SER	GLY	GLY	GLY	GLY	VAL	PRO	ILE	THR	ARG	E391	SER	GLY	PHE</

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

MET	CYS	HIS	PHE	SER	ALA	SER	GLY	ALA	ILE	GLU	PRO	VAL	VAL	LYS	THR	LEU	LEU	MET	GLN	PHE	PHE	VAL	TRP	LYS	LEU	VAL	PRO	ALA	VAL	LEU	VAL	PHE	SER	LEU	GLY	VAL	ARG	GLN
ARG	ASN	ILE	LEU	ASN	LYS	ASN	ASP	GLY	TRP	LYS	LYS	SER	GLY	THR	TYR	HIS	VAL	MET	THR	SER	TYR	VAL	GLN	TRP	GLY	ALA	PHE	PHE	ILE	ARG	CYS	VAL	LEU	THR	PRO	VAL	LEU	ASN

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	302597	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	1.061	Depositor
Minimum map value	-0.322	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.145	Depositor
Map size (Å)	275.2, 275.2, 275.2	wwPDB
Map dimensions	320, 320, 320	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	0/1595	0.28	0/2163
1	B	0.12	0/1595	0.29	0/2163
1	C	0.12	0/1595	0.28	0/2163
1	D	0.12	0/1595	0.29	0/2163
1	E	0.12	0/1595	0.26	0/2163
1	F	0.12	0/1595	0.28	0/2163
1	G	0.13	0/1595	0.29	0/2163
All	All	0.12	0/11165	0.28	0/15141

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	1562	0	1595	14	0
1	B	1562	0	1595	15	0
1	C	1562	0	1595	10	0
1	D	1562	0	1595	17	0
1	E	1562	0	1595	17	0
1	F	1562	0	1595	22	0
1	G	1562	0	1595	17	0
All	All	10934	0	11165	105	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 5.

The worst 5 of 105 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:449:LEU:HB3	1:F:409:GLN:HE21	1.52	0.74
1:E:321:GLY:O	1:E:340:ASN:ND2	2.22	0.72
1:A:308:ILE:HG22	1:A:309:GLU:HG2	1.72	0.70
1:D:308:ILE:HG22	1:D:309:GLU:HG2	1.74	0.70
1:F:405:ILE:O	1:F:409:GLN:HA	1.91	0.69

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%)	182 (95%)	10 (5%)	0	100	100
1	B	192/866 (22%)	184 (96%)	8 (4%)	0	100	100
1	C	192/866 (22%)	184 (96%)	8 (4%)	0	100	100
1	D	192/866 (22%)	184 (96%)	8 (4%)	0	100	100
1	E	192/866 (22%)	183 (95%)	9 (5%)	0	100	100
1	F	192/866 (22%)	183 (95%)	9 (5%)	0	100	100
1	G	192/866 (22%)	183 (95%)	9 (5%)	0	100	100
All	All	1344/6062 (22%)	1283 (96%)	61 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	170/750 (23%)	168 (99%)	2 (1%)	63	81
1	B	170/750 (23%)	167 (98%)	3 (2%)	51	73
1	C	170/750 (23%)	166 (98%)	4 (2%)	43	65
1	D	170/750 (23%)	167 (98%)	3 (2%)	51	73
1	E	170/750 (23%)	168 (99%)	2 (1%)	63	81
1	F	170/750 (23%)	169 (99%)	1 (1%)	78	89
1	G	170/750 (23%)	168 (99%)	2 (1%)	63	81
All	All	1190/5250 (23%)	1173 (99%)	17 (1%)	57	79

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	443	SER
1	G	443	SER
1	C	349	ARG
1	C	422	SER
1	D	300	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	424	HIS
1	F	424	HIS
1	D	424	HIS
1	D	408	ASN
1	E	424	HIS

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.

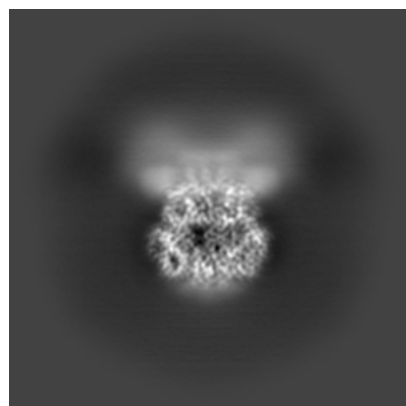
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-79091. These allow visual inspection of the internal detail of the map and identification of artifacts.

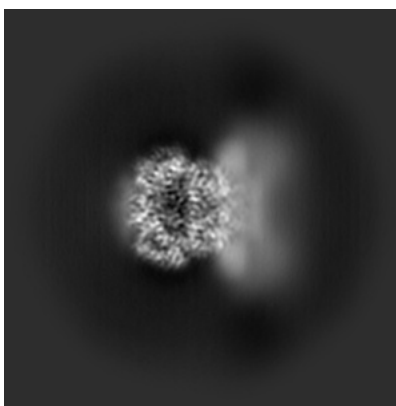
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

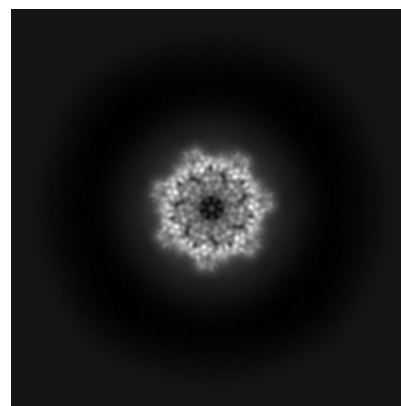
6.1.1 Primary map



X

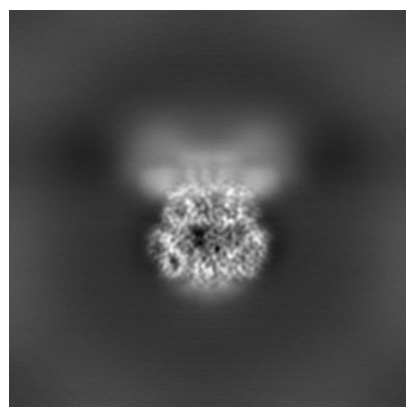


Y

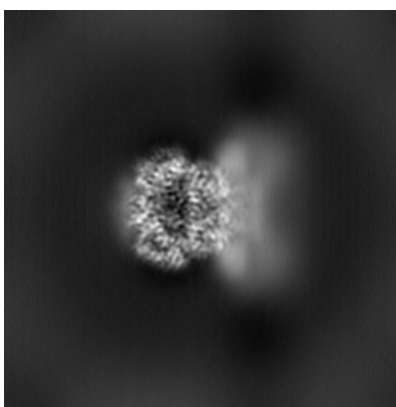


Z

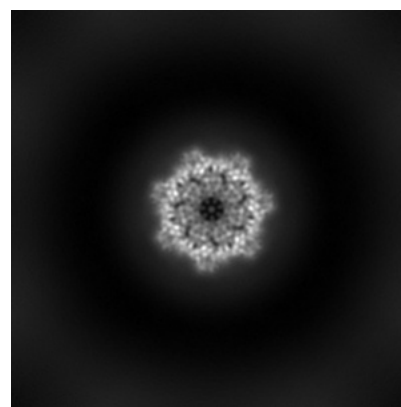
6.1.2 Raw map



X



Y

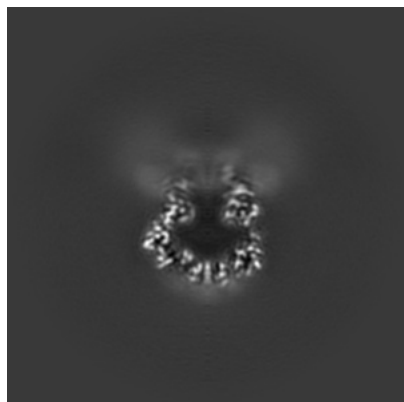


Z

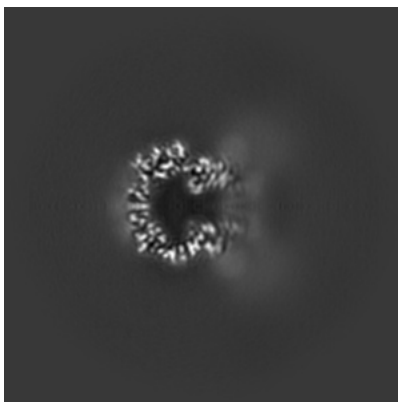
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

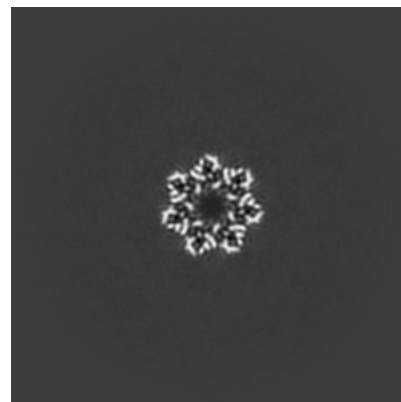
6.2.1 Primary map



X Index: 160

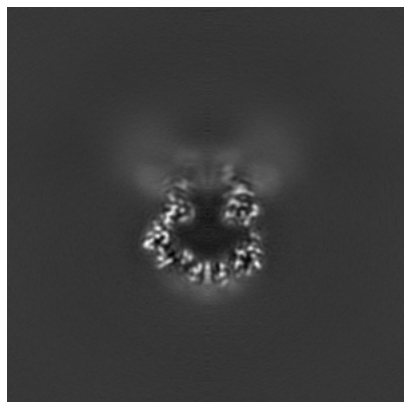


Y Index: 160

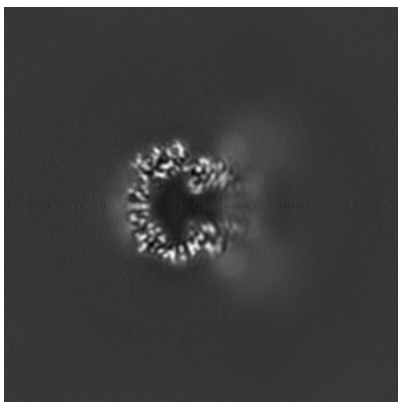


Z Index: 160

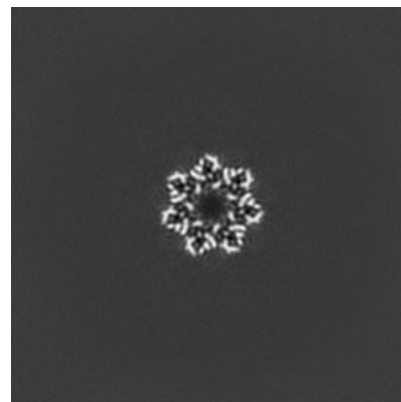
6.2.2 Raw map



X Index: 160



Y Index: 160

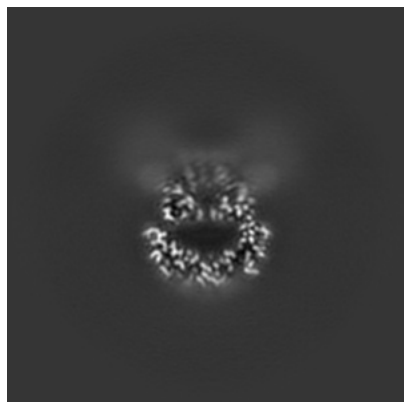


Z Index: 160

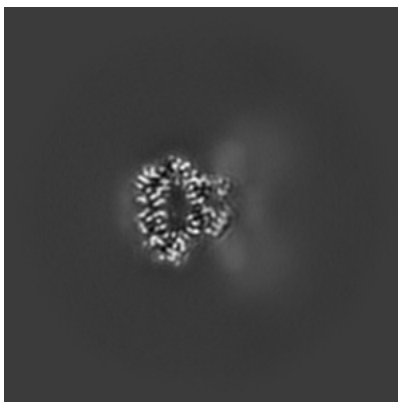
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

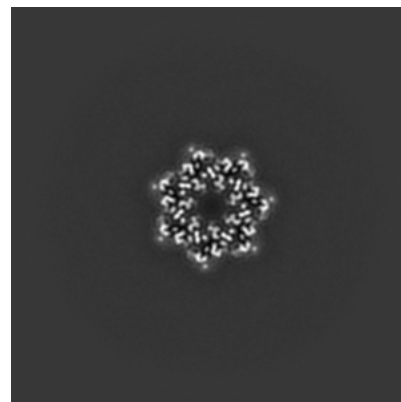
6.3.1 Primary map



X Index: 149

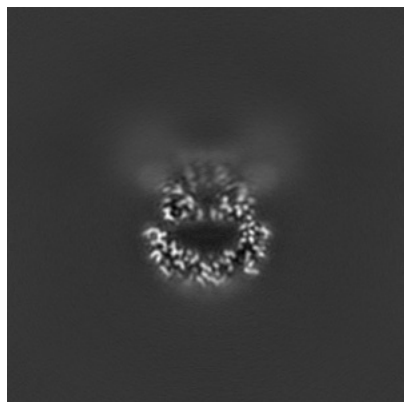


Y Index: 136

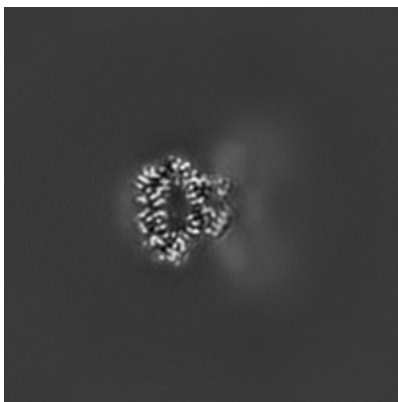


Z Index: 123

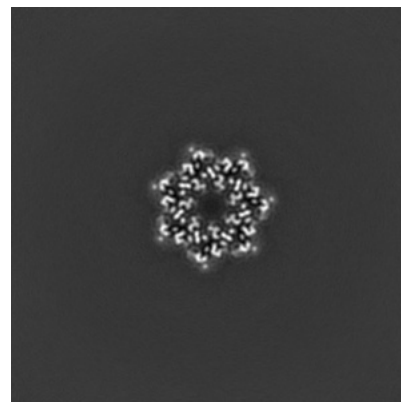
6.3.2 Raw map



X Index: 149



Y Index: 136

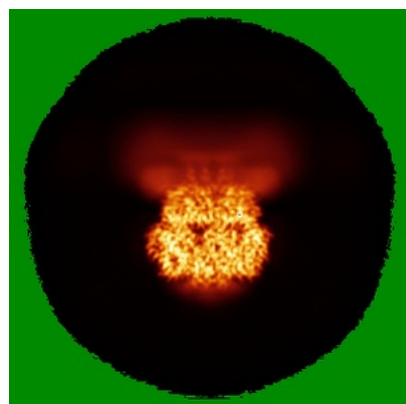


Z Index: 123

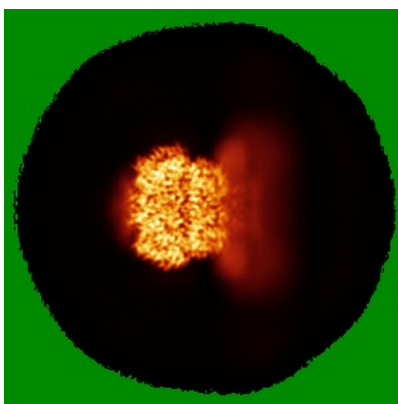
The images above show the largest variance slices of the map in three orthogonal directions.

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

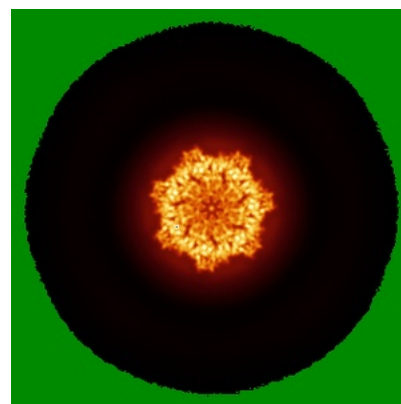
6.4.1 Primary map



X

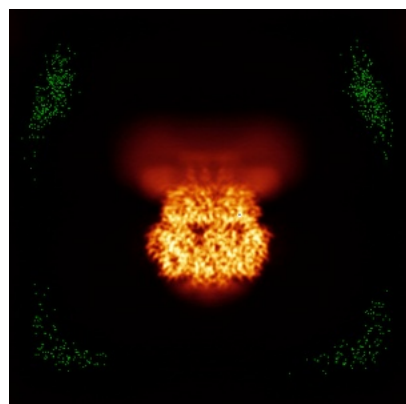


Y

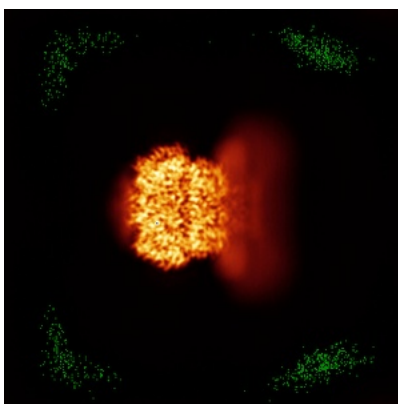


Z

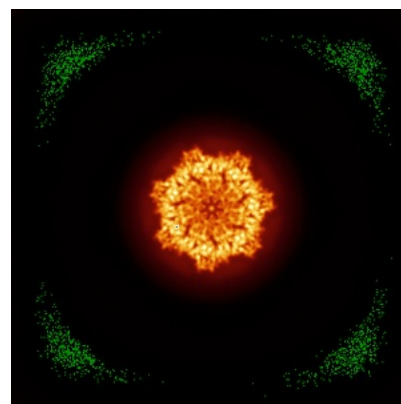
6.4.2 Raw map



X



Y

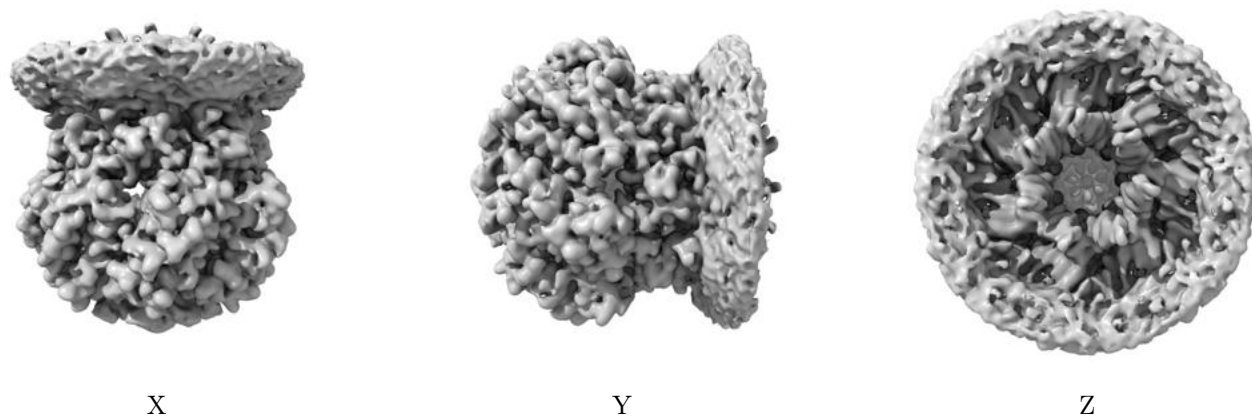


Z

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.

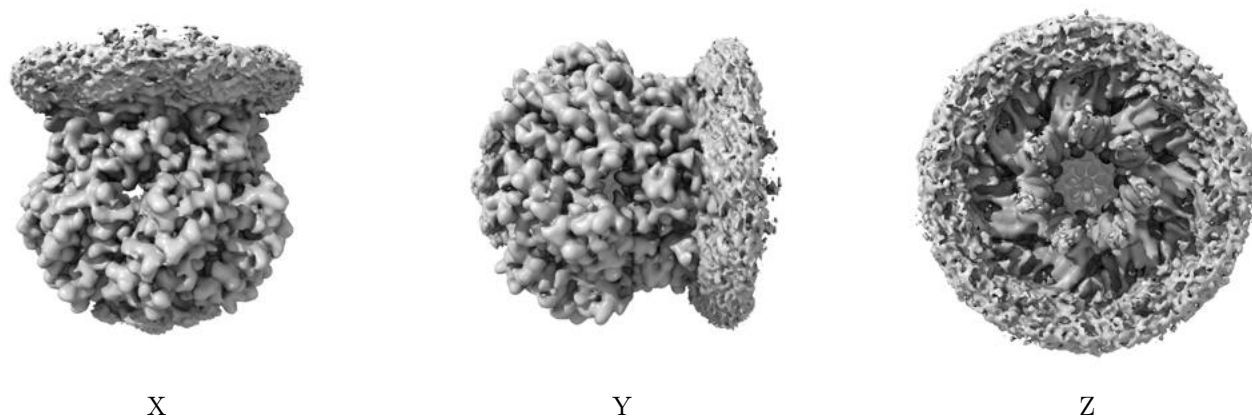
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.145. 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.

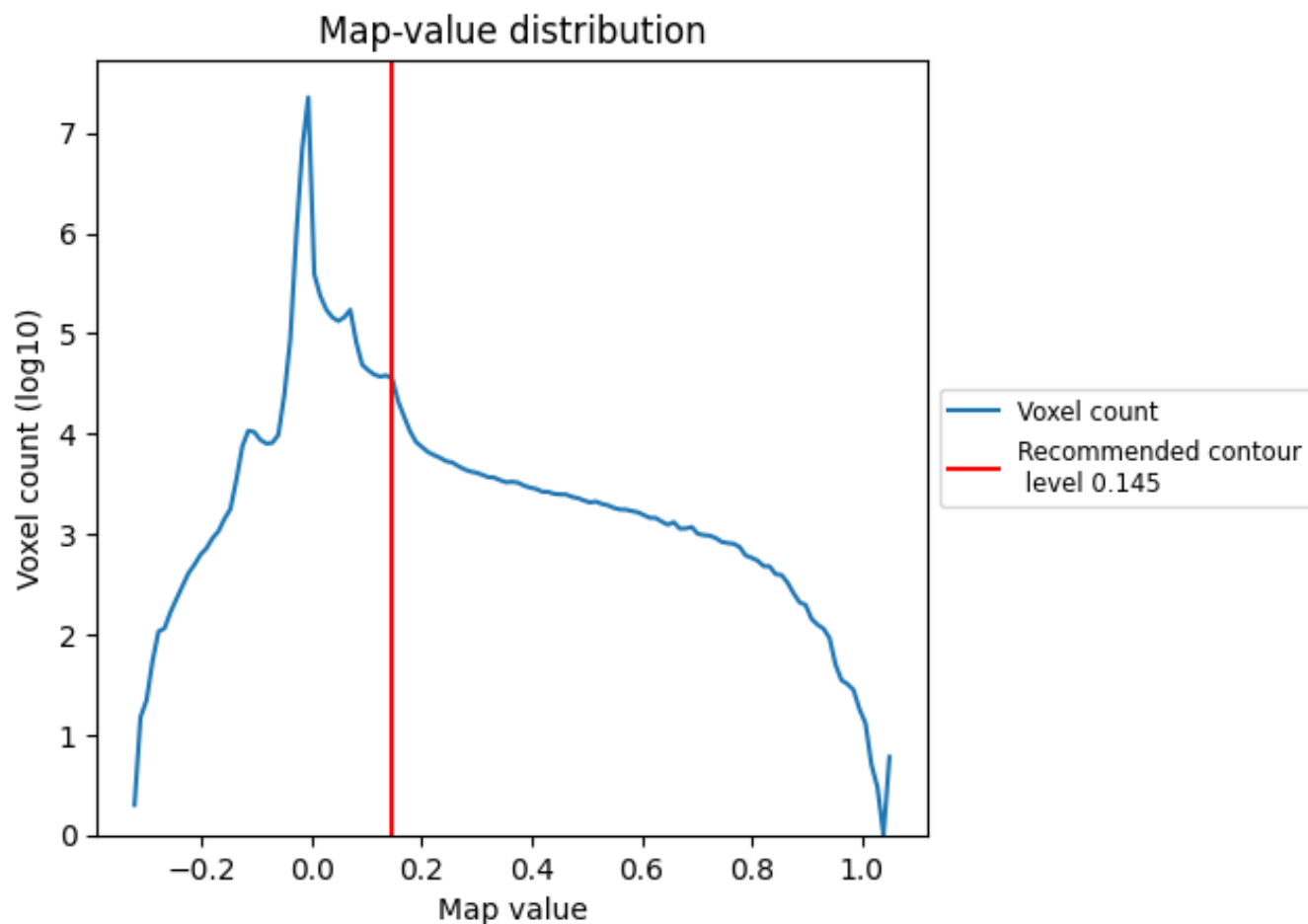
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

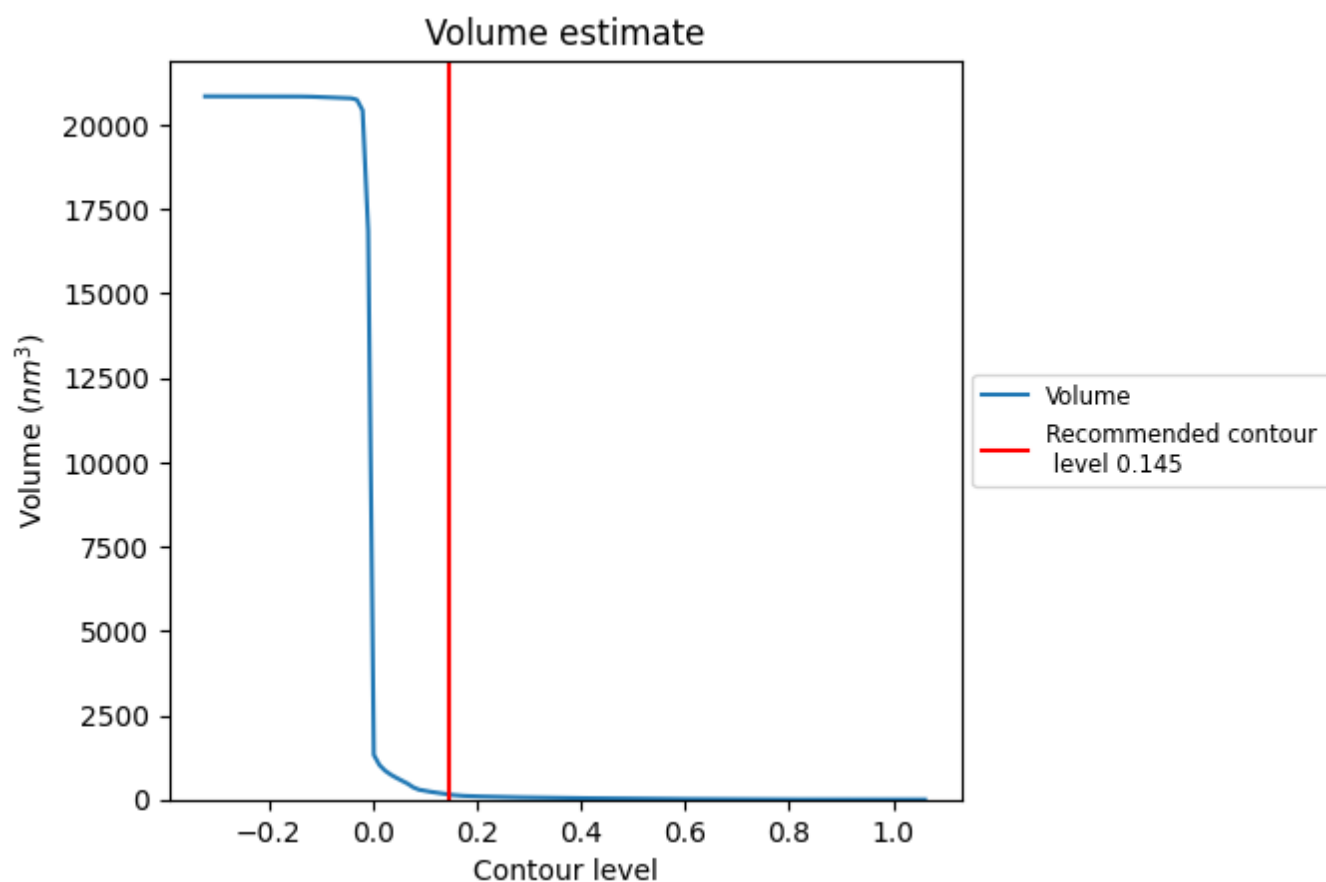
This section contains the results of statistical analysis of the map.

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.

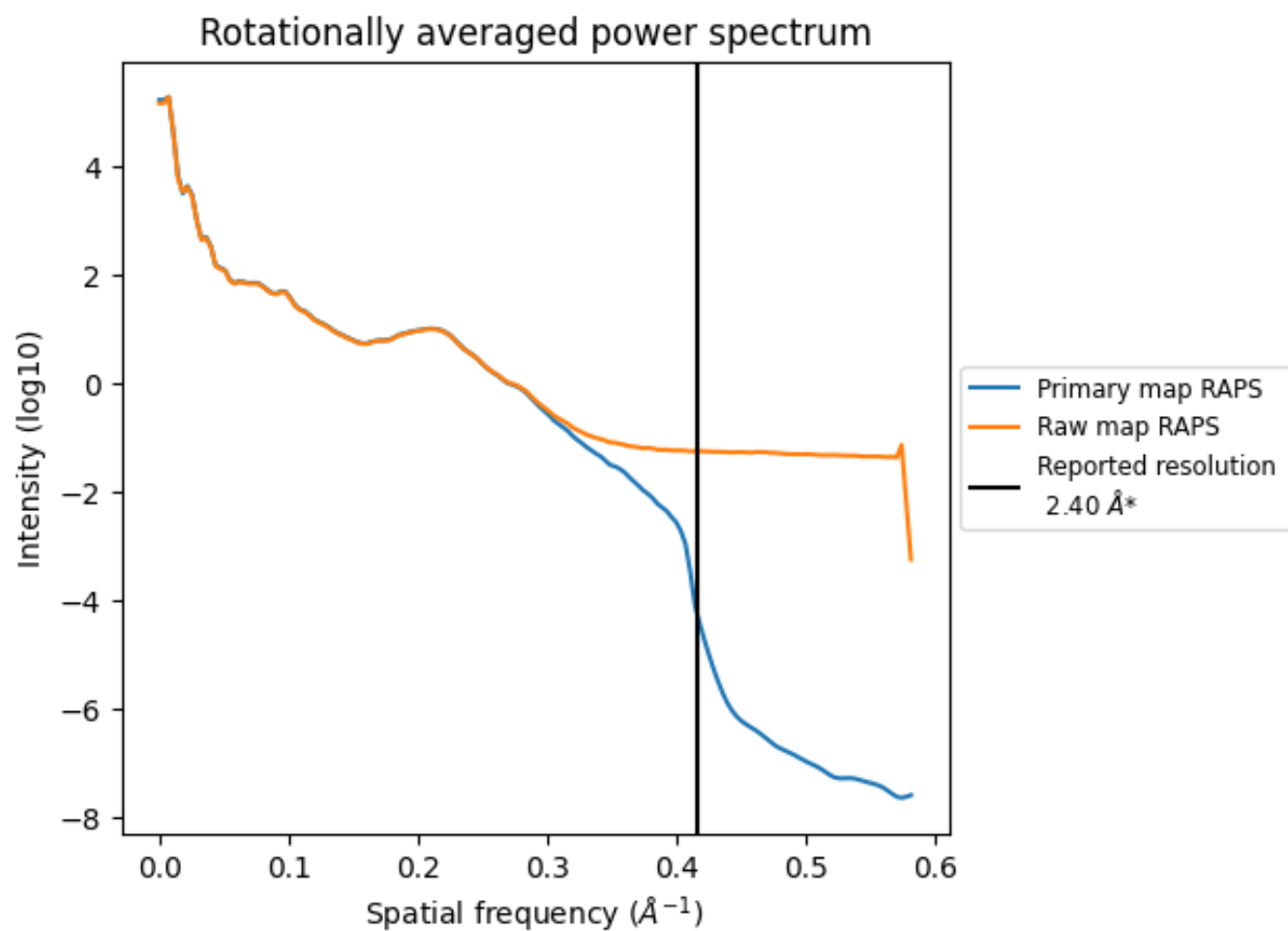
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 154 nm^3 ; this corresponds to an approximate mass of 139 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 ⓘ

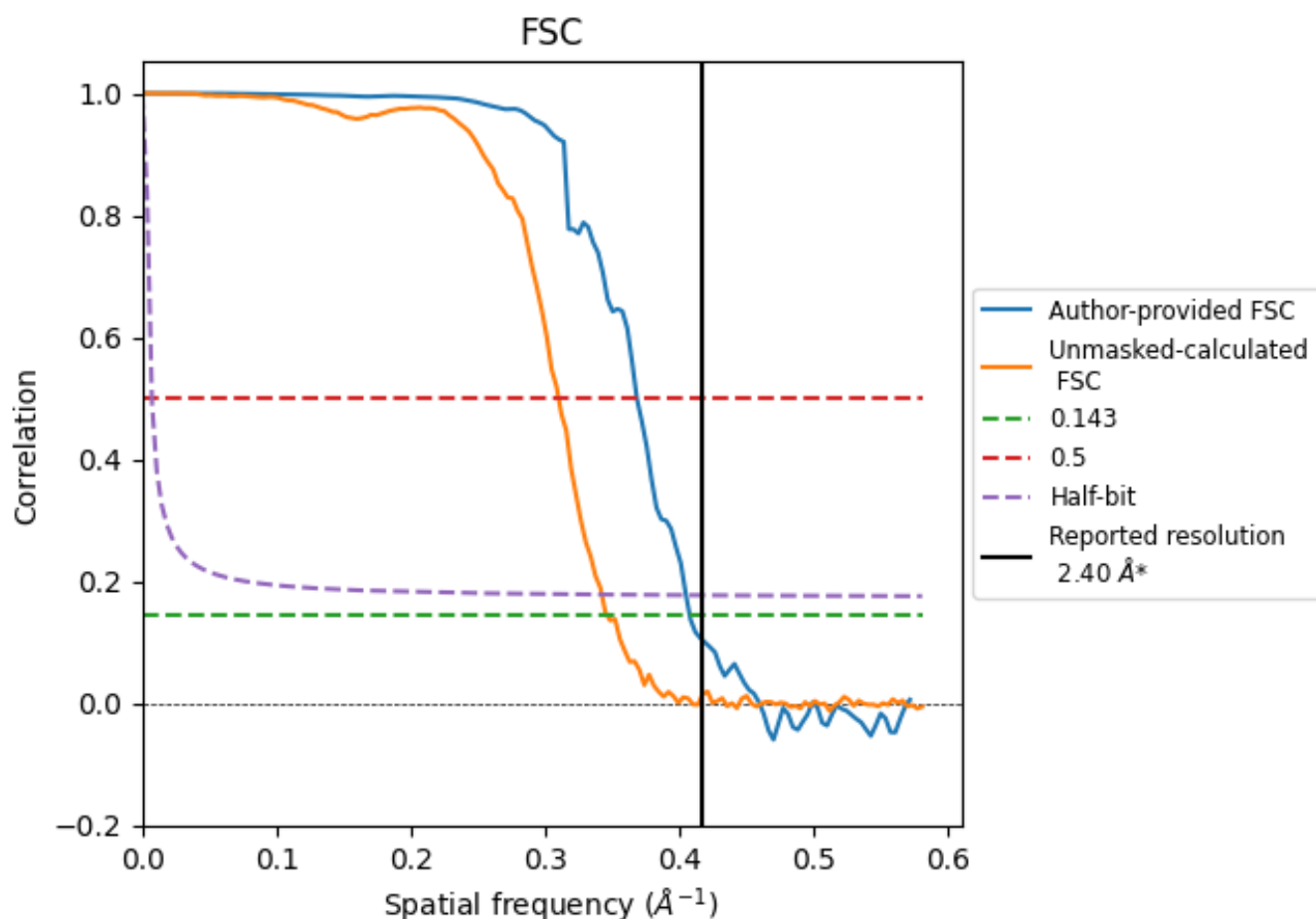


*Reported resolution corresponds to spatial frequency of 0.417 $\text{\AA}^{-1}$

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 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

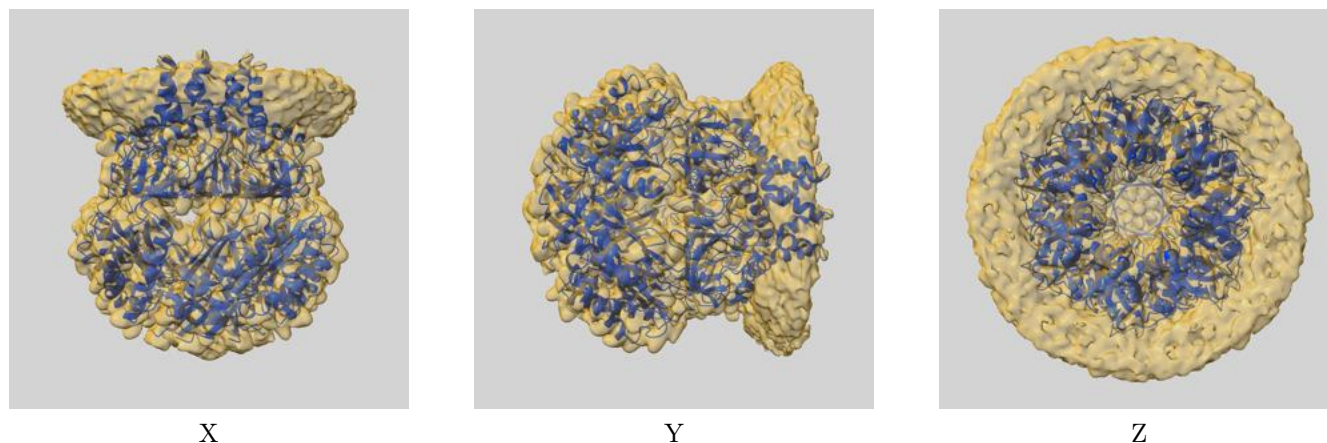
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.45	2.71	2.47
Unmasked-calculated*	2.88	3.22	2.92

*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 2.88 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

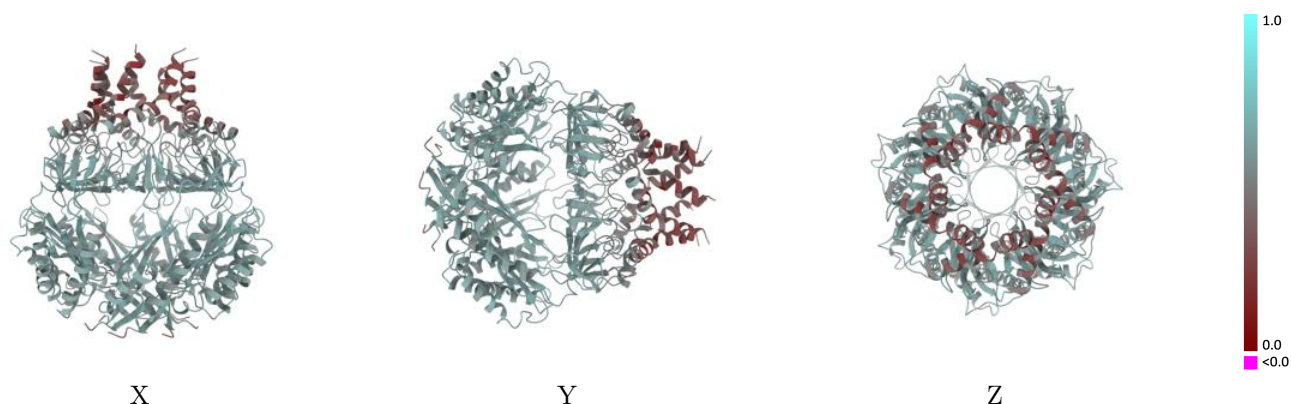
This section contains information regarding the fit between EMDB map EMD-79091 and PDB model 38RX. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



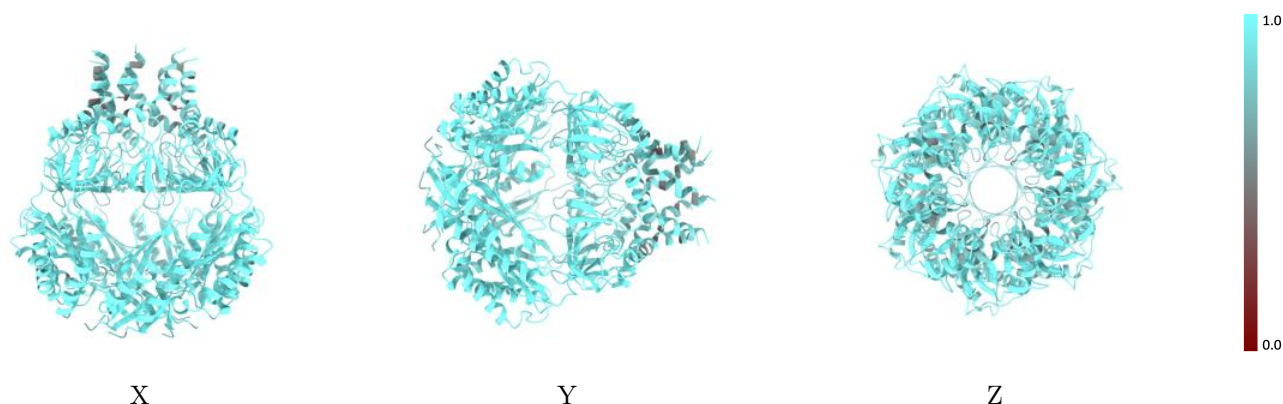
The images above show the 3D surface view of the map at the recommended contour level 0.145 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



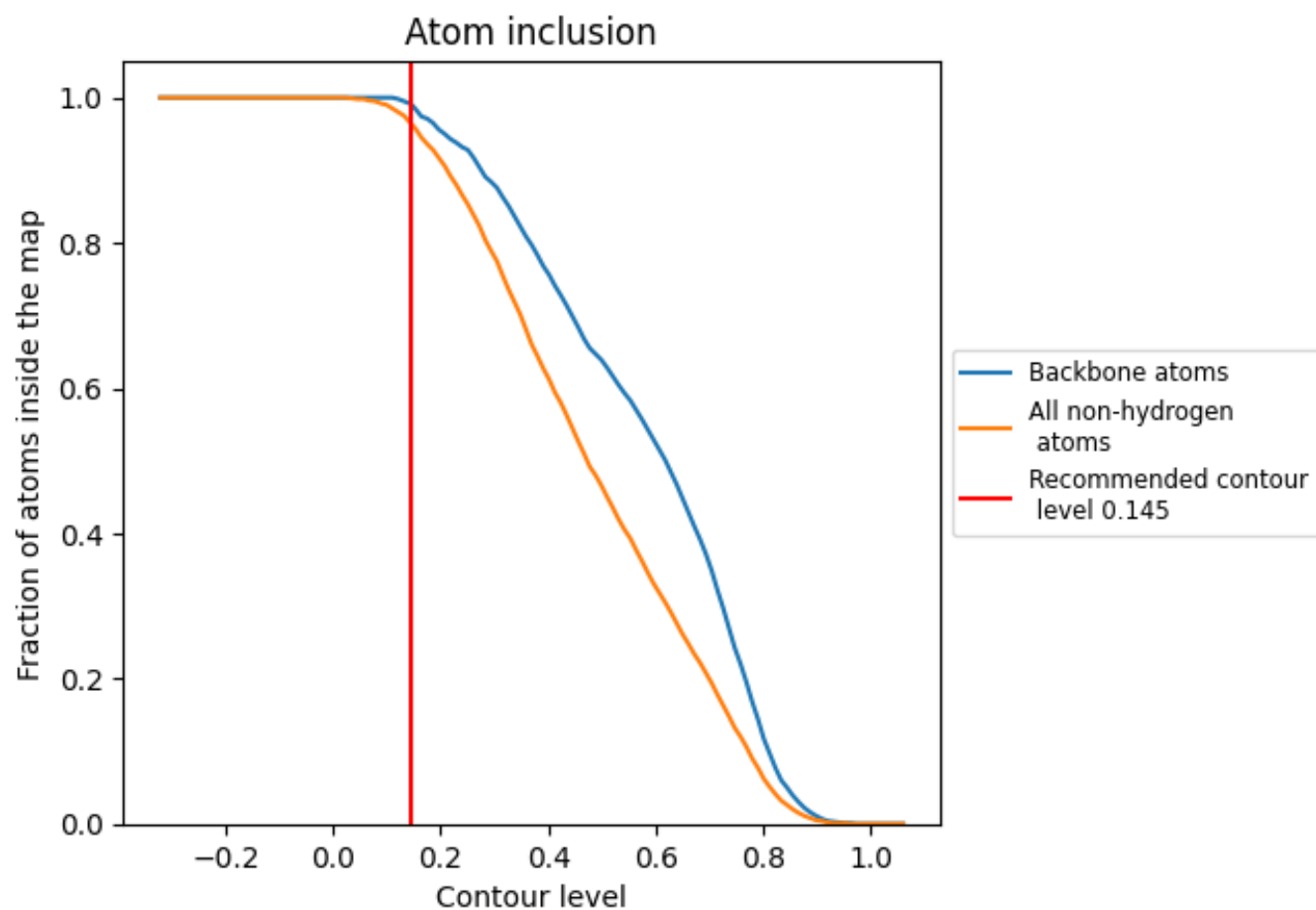
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.145).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 96% 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 (0.145) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9640	0.5490
A	0.9670	0.5490
B	0.9660	0.5510
C	0.9630	0.5480
D	0.9650	0.5500
E	0.9660	0.5490
F	0.9610	0.5490
G	0.9640	0.5480

1.0

0.0

<0.0