



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:33 PM UTC

PDB ID : 8DXO / pdb_00008dxo
EMDB ID : EMD-27771
Title : Structure of LRRC8C-LRRC8A(IL125) Chimera, Class 2
Authors : Takahashi, H.; Yamada, T.; Denton, J.S.; Strange, K.; Karakas, E.
Deposited on : 2022-08-02
Resolution : 3.60 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:

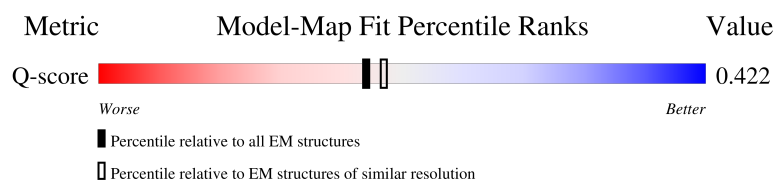
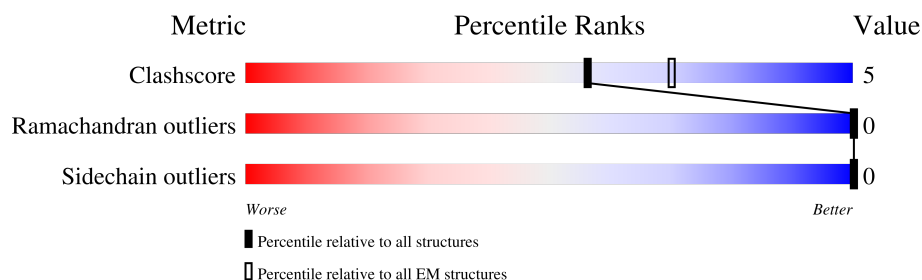
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 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	12797 (3.10 - 4.10)

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	
1	B	825	
1	C	825	
1	D	825	

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Mol	Chain	Length	Quality of chain
1	E	825	
1	F	825	
1	G	825	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17499 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	300	Total	C	N	O	S	0	0
			2497	1650	393	433	21		
1	E	301	Total	C	N	O	S	0	0
			2507	1656	396	434	21		
1	F	302	Total	C	N	O	S	0	0
			2516	1661	397	437	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
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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
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D	815	TYR	-	expression tag	UNP Q8TDW0
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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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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
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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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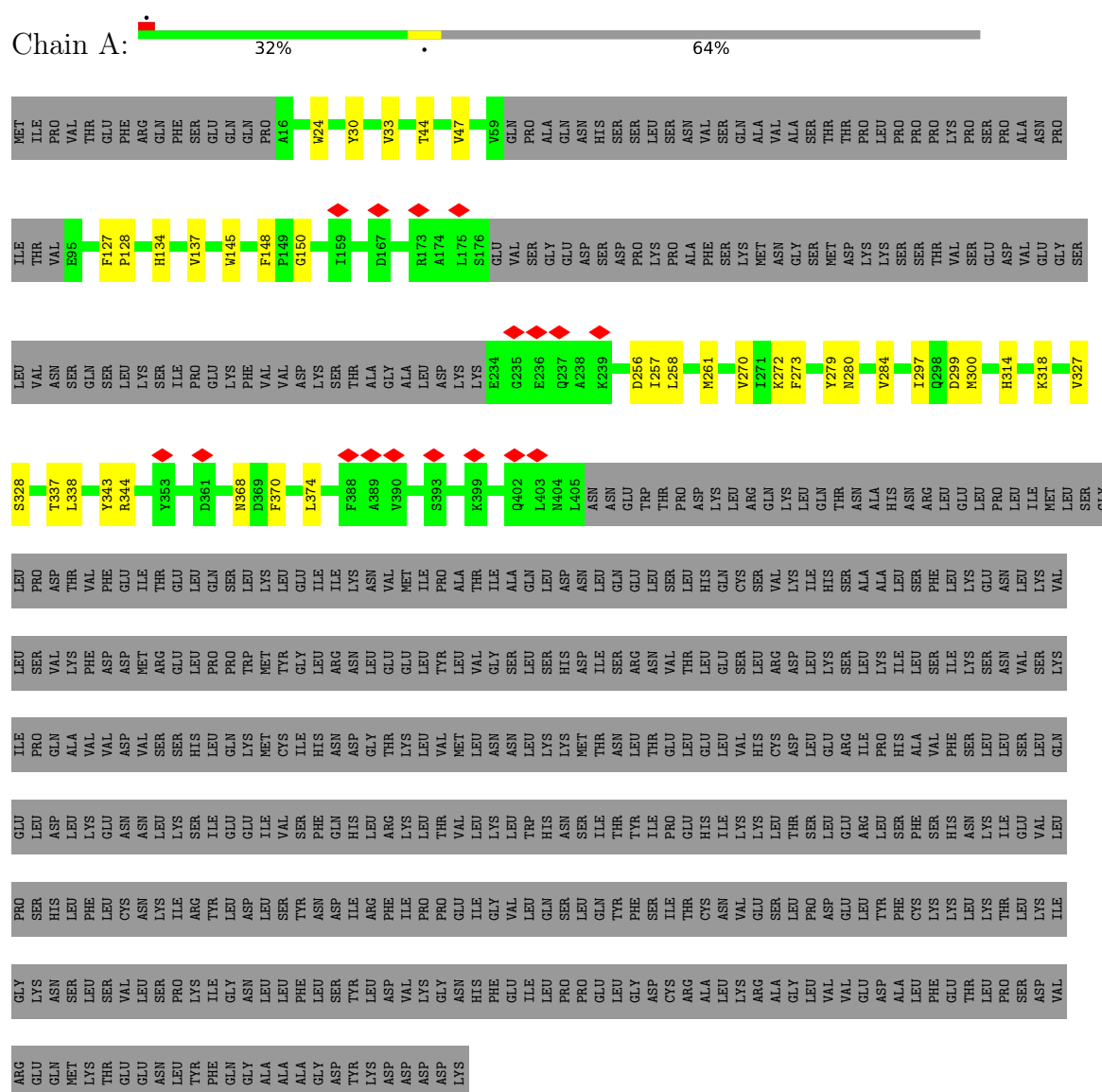
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G	817	ASP	-	expression tag	UNP Q8TDW0
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G	820	ASP	-	expression tag	UNP Q8TDW0
G	821	LYS	-	expression tag	UNP Q8TDW0

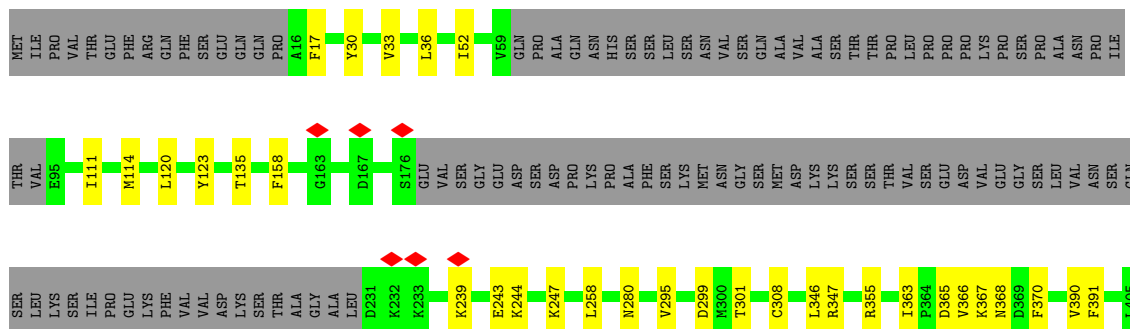
3 Residue-property plots

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 B: 32% 4% 64%



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

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

Chain D:

[illegible]

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

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



MET
ILE
PRO
VAL
THR
PHE
ARG
GLN
SER
PHE
GLU
GLN
GLN
PRO
ASP
A16
M35
L36
I52
V59
GLN
PRO
ALA
GLN
ASN
HIS
SER
SER
SER
LEU
SER
LYS
ASN
VAL
SER
SER
SER
GLN
ALA
VAL
ALA
SER
THR
THR
PRO
LEU
LEU
PRO
VAL
E95

L132
T135
L136
C141
T171
S176
GLU
VAL
SER
GLY
ASP
SER
SER
ASP
PRO
PRO
PRO
PHE
SER
LYS
ALA
SER
SER
L268
D299
C308
H314
V327
F351
R355
I363
L374
I377
V390
L405
ASN
ASN
GLU
TRP
THR
PRO
SER
LEU
LEU
VAL
VAL
SER
HIS
ASP
ASN
ASN
LEU
ILE
SER
GLN
GLN
CYS
VAL
LEU
THR
ILE
GLN
ASN
VAL

ASP
LYS
SER
THR
ALA
GLY
ALA
PRO
LEU
LEU
ILE
LEU
SER
SER
GLY
LEU
LEU
SER
ASP
PHE
THR
PHE
VAL
ASP
MET
ILE
GLU
GLU
LEU
LEU
GLN
SER
C308
H314
V327
F351
R355
I363
L374
I377
V390
L405
ASN
ASN
GLU
TRP
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PRO
SER
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ASP
PHE
THR
PHE
VAL
ASP
MET
ILE
GLU
GLU
LEU
LEU
GLN
SER
C308
H314
V327
F351
R355
I363
L374
I377
V390
L405
ASN
ASN
GLU
TRP
THR
PRO
SER
LEU
LEU
VAL
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SER
HIS
ASP
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CYS
VAL
LEU
THR
ILE
GLN
ASN
VAL

SER
ALA
SER
LEU
PHE
LEU
LEU
LYS
SER
VAL
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VAL
SER
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LEU
SER
ASP
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V390
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ASN
GLU
TRP
THR
PRO
SER
LEU
LEU
VAL
VAL
SER
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THR
PRO
SER
LEU
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VAL
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ASN
VAL

ARG
ILE
PRO
HIS
ALA
SER
VAL
PHE
SER
SER
LEU
LEU
SER
VAL
SER
GLY
LEU
LEU
SER
ASP
PHE
THR
PHE
VAL
ASP
MET
ILE
GLU
GLU
LEU
LEU
GLN
SER
C308
H314
V327
F351
R355
I363
L374
I377
V390
L405
ASN
ASN
GLU
TRP
THR
PRO
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F351
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● Molecule 1: Volume-regulated anion channel subunit LRRC8C,Volume-regulated anion channel subunit LRRC8A



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PHE
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V40
F41
L45
Q46
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L120
H134
C141
D167
E177
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D231
K239
A240
L241
F242
E243
F248
V252
E253
E254
G255
D256
Y262
Q265
L268
K272
I276
Y279
I287
C308
M312
R347

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

ASP TYR LYS ASP ASP ASP LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	132722	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	1.622	Depositor
Minimum map value	-0.969	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.12	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	0.30	0/3441
1	B	0.11	0/2568	0.30	0/3466
1	C	0.12	0/2574	0.31	0/3474
1	D	0.11	0/2565	0.28	0/3464
1	E	0.11	0/2574	0.30	0/3474
1	F	0.12	0/2583	0.32	0/3486
1	G	0.11	0/2557	0.32	0/3453
All	All	0.12	0/17969	0.30	0/24258

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	23	0
1	B	2501	0	2496	25	0
1	C	2507	0	2501	23	0
1	D	2497	0	2485	34	0
1	E	2507	0	2501	12	0
1	F	2516	0	2507	28	0
1	G	2490	0	2477	27	0
All	All	17499	0	17438	170	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 170 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:D:20:LEU:HD21	1:D:373:MET:HE1	1.62	0.78
1:D:158:PHE:CE2	1:D:373:MET:HE2	2.20	0.75
1:F:134:HIS:NE2	1:F:279:TYR:OH	2.20	0.75
1:C:355:ARG:NH2	1:C:365:ASP:OD1	2.21	0.73
1:E:355:ARG:NH2	1:E:363:ILE:O	2.25	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	292/825 (35%)	277 (95%)	15 (5%)	0	100	100
1	B	294/825 (36%)	272 (92%)	22 (8%)	0	100	100
1	C	295/825 (36%)	276 (94%)	19 (6%)	0	100	100
1	D	294/825 (36%)	274 (93%)	20 (7%)	0	100	100
1	E	295/825 (36%)	281 (95%)	14 (5%)	0	100	100
1	F	296/825 (36%)	272 (92%)	24 (8%)	0	100	100
1	G	293/825 (36%)	273 (93%)	20 (7%)	0	100	100
All	All	2059/5775 (36%)	1925 (94%)	134 (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	277/766 (36%)	277 (100%)	0	100	100
1	E	278/766 (36%)	278 (100%)	0	100	100
1	F	279/766 (36%)	279 (100%)	0	100	100
1	G	276/766 (36%)	276 (100%)	0	100	100
All	All	1940/5362 (36%)	1940 (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 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	314	HIS
1	E	305	ASN
1	G	398	ASN
1	F	402	GLN
1	B	237	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.

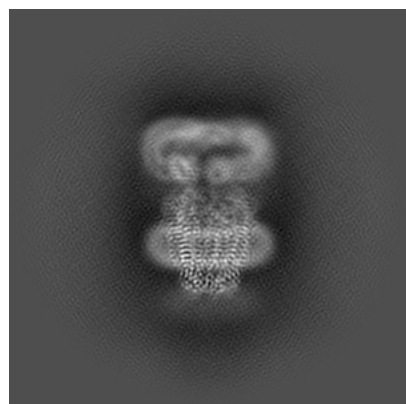
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27771. These allow visual inspection of the internal detail of the map and identification of artifacts.

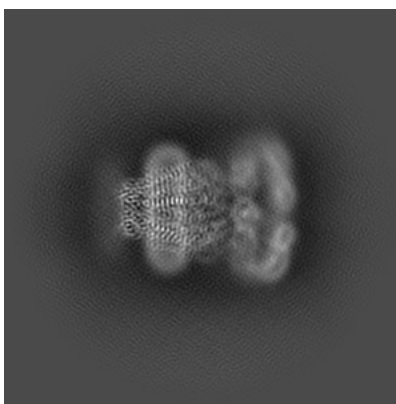
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

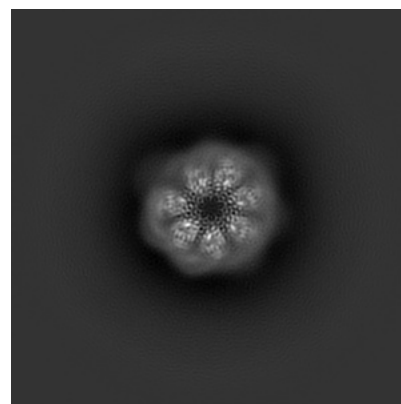
6.1.1 Primary map



X

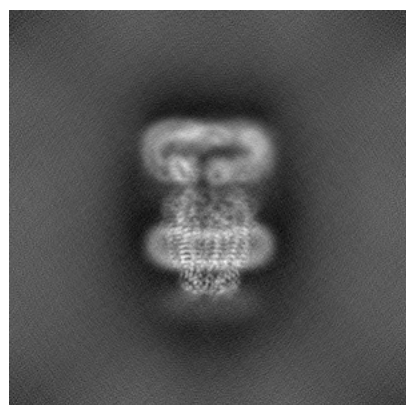


Y

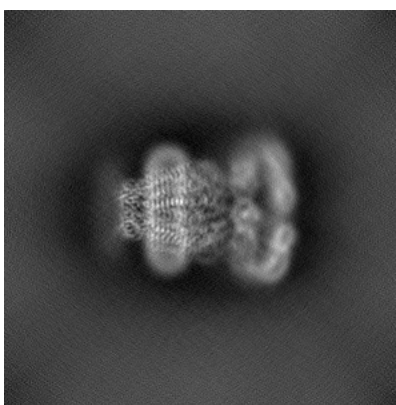


Z

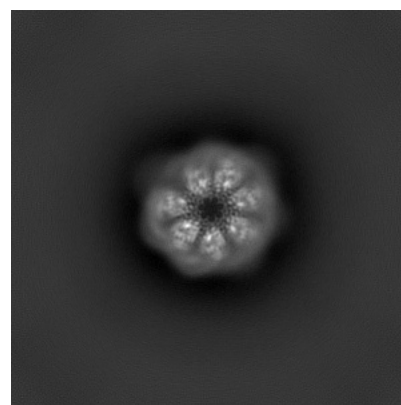
6.1.2 Raw map



X



Y

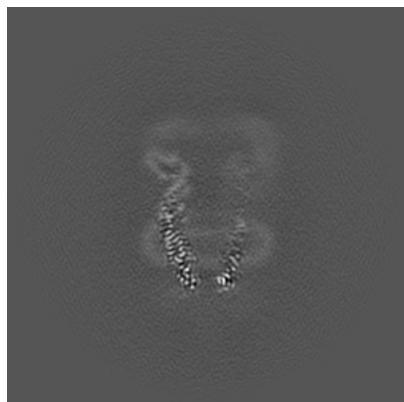


Z

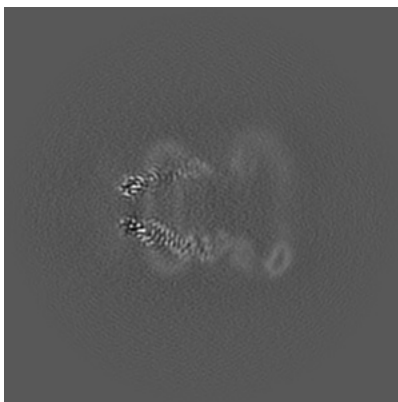
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

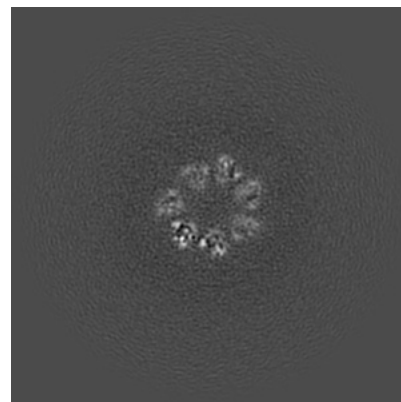
6.2.1 Primary map



X Index: 180

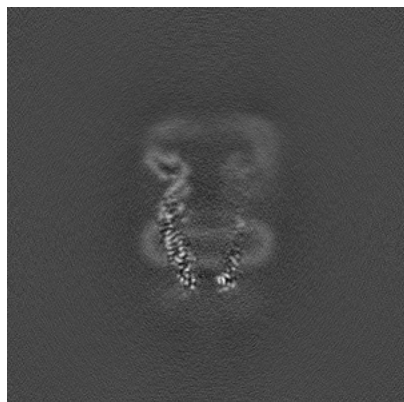


Y Index: 180

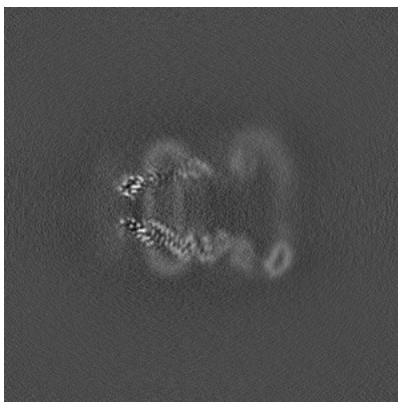


Z Index: 180

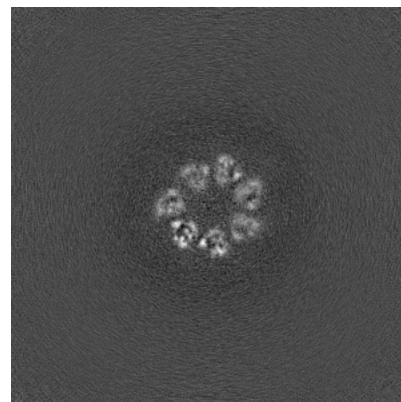
6.2.2 Raw map



X Index: 180



Y Index: 180

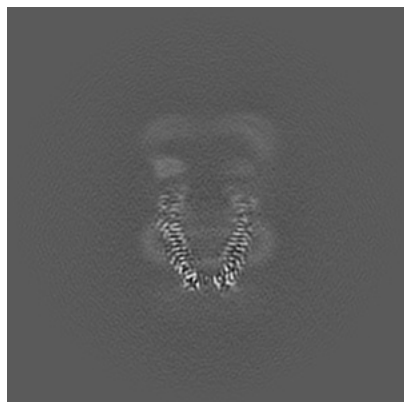


Z Index: 180

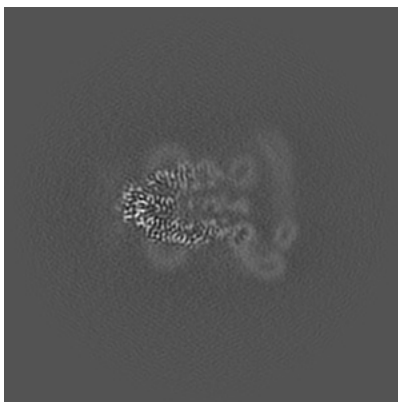
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

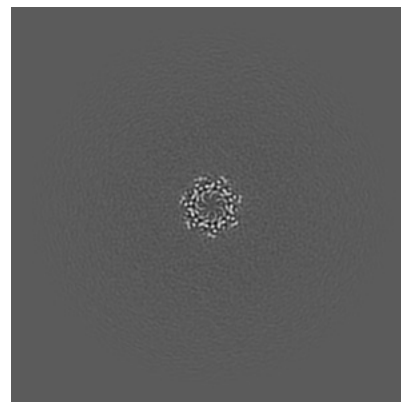
6.3.1 Primary map



X Index: 187

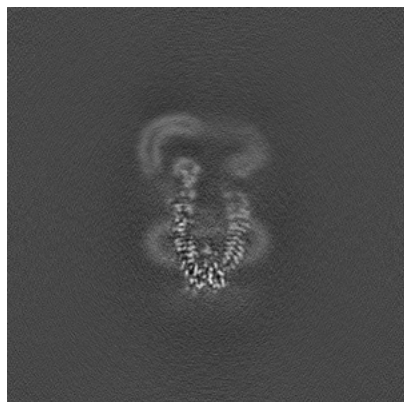


Y Index: 159

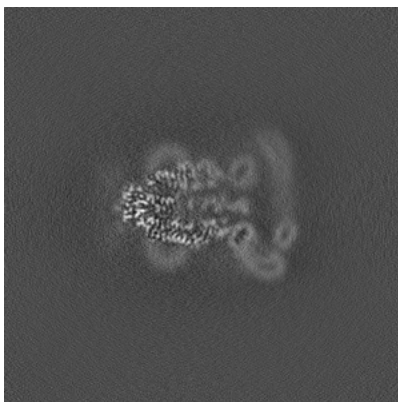


Z Index: 117

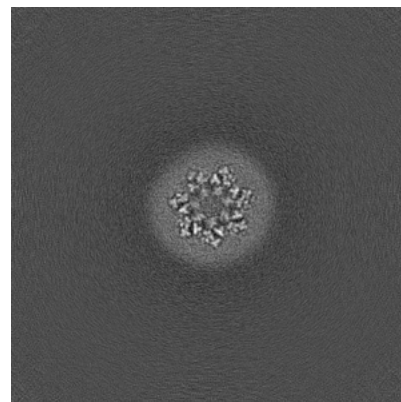
6.3.2 Raw map



X Index: 161



Y Index: 159



Z Index: 133

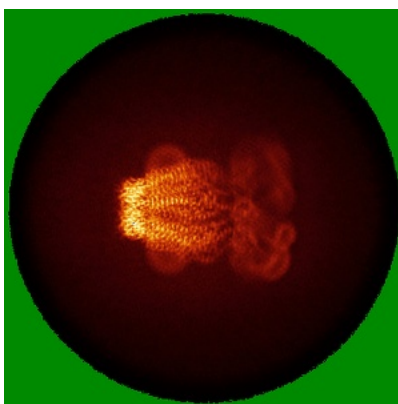
The images above show the largest variance slices of the map in three orthogonal directions.

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

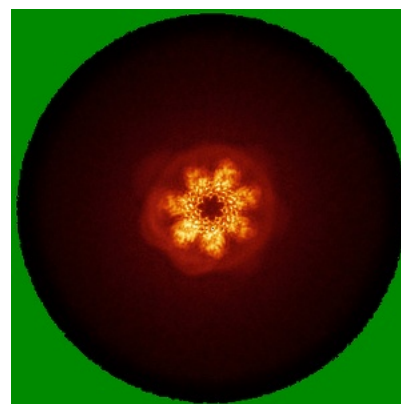
6.4.1 Primary map



X

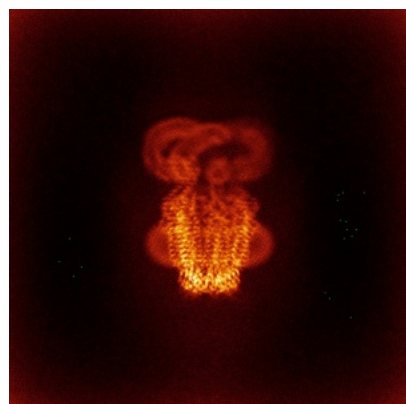


Y

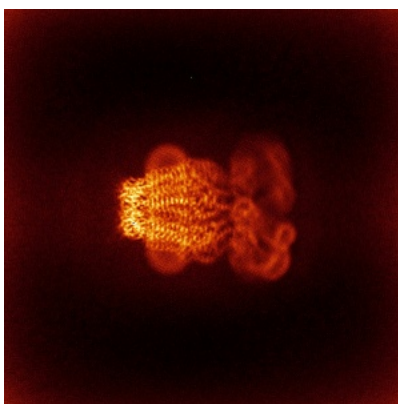


Z

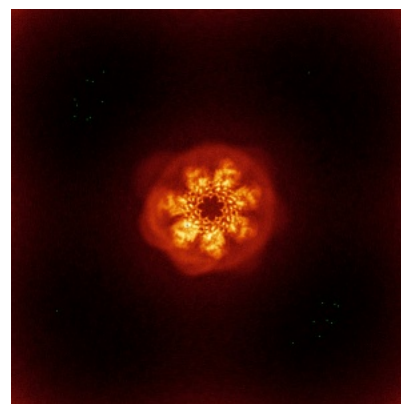
6.4.2 Raw map



X



Y

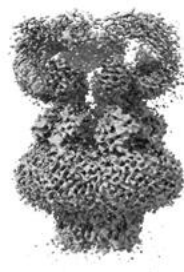


Z

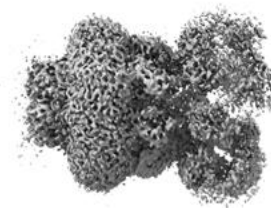
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

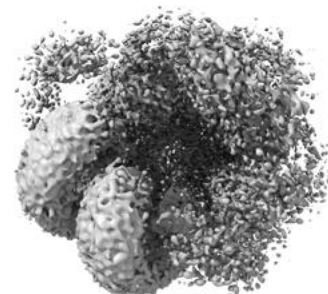
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

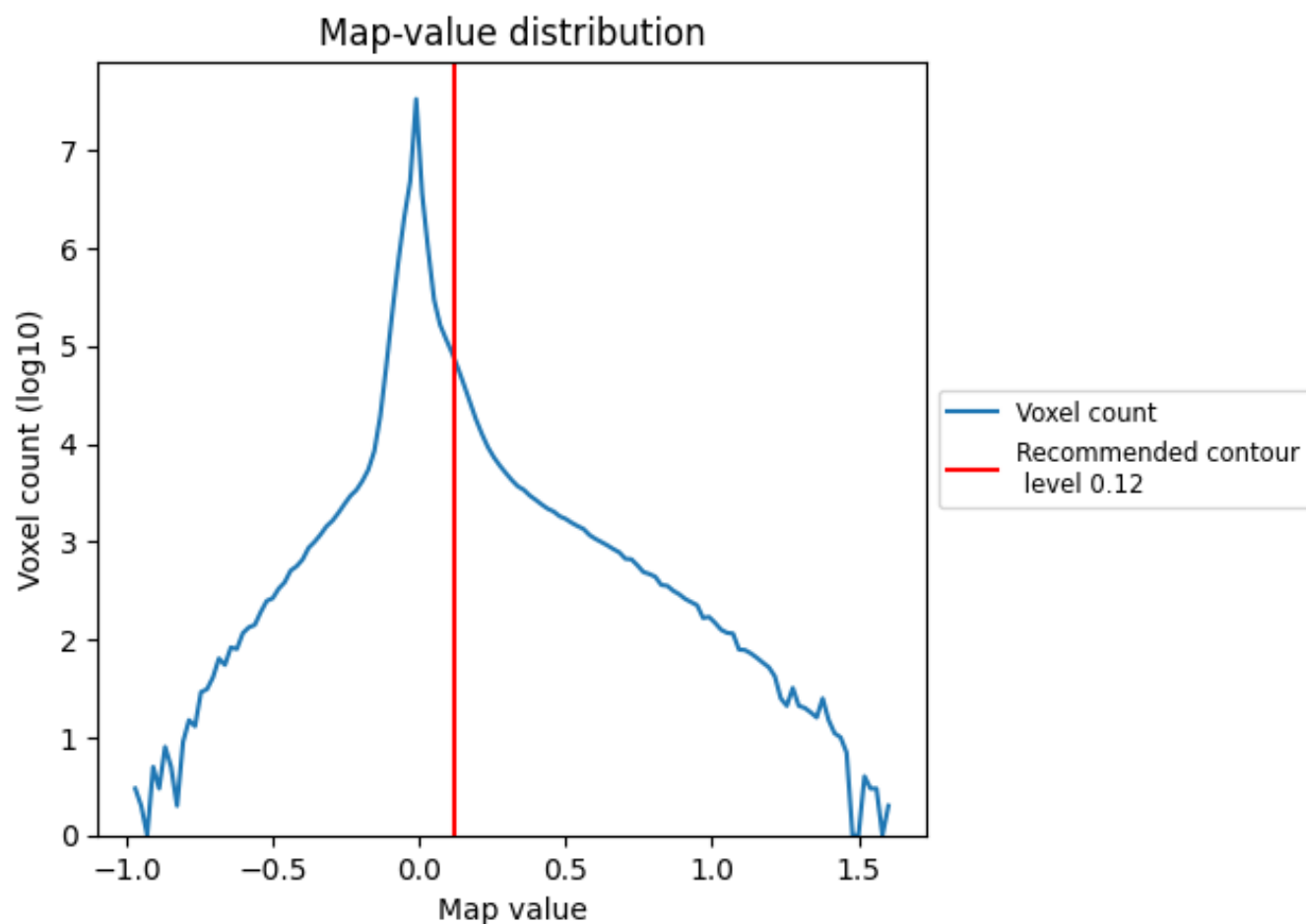
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

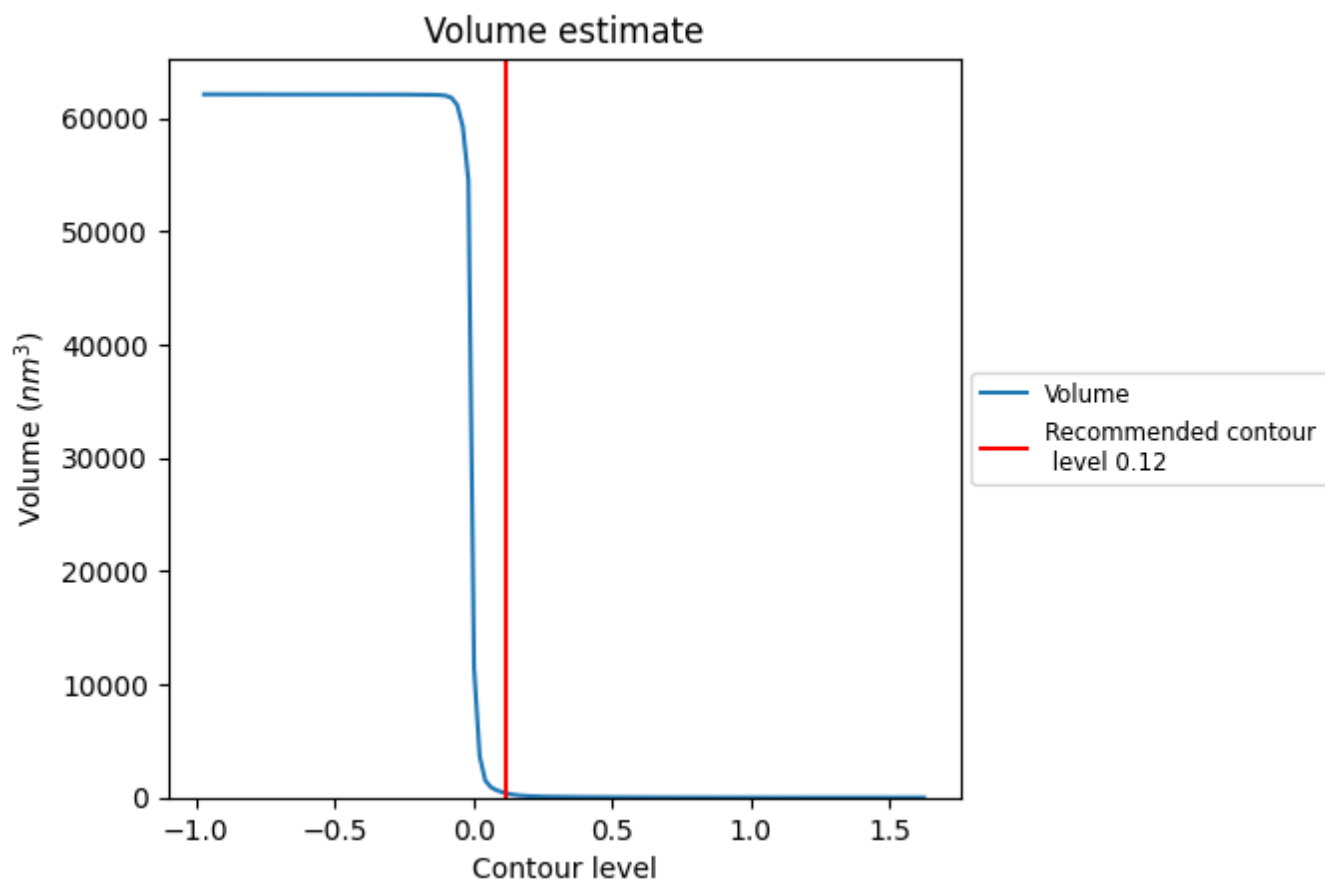
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

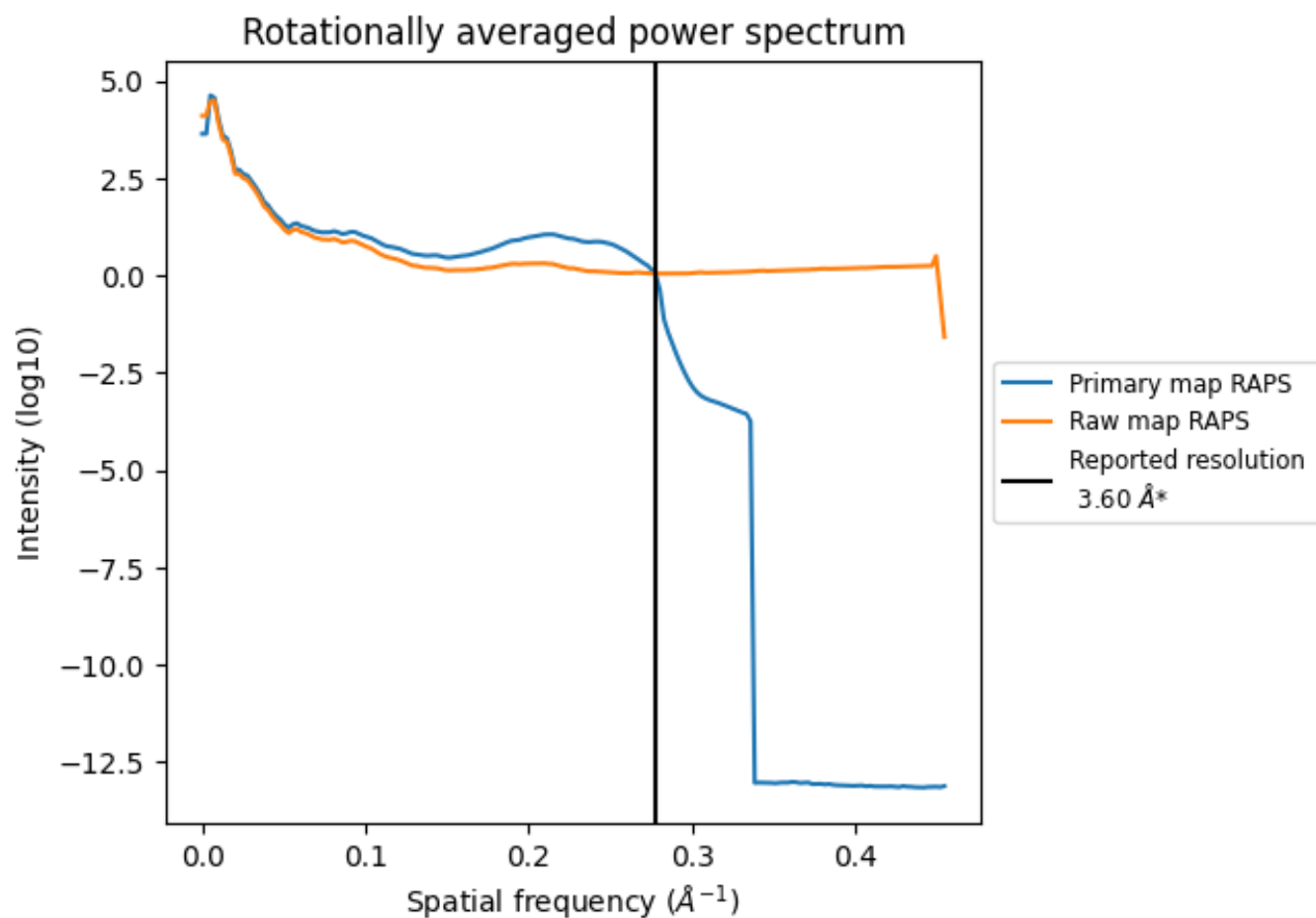
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 371 nm^3 ; this corresponds to an approximate mass of 335 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 ⓘ

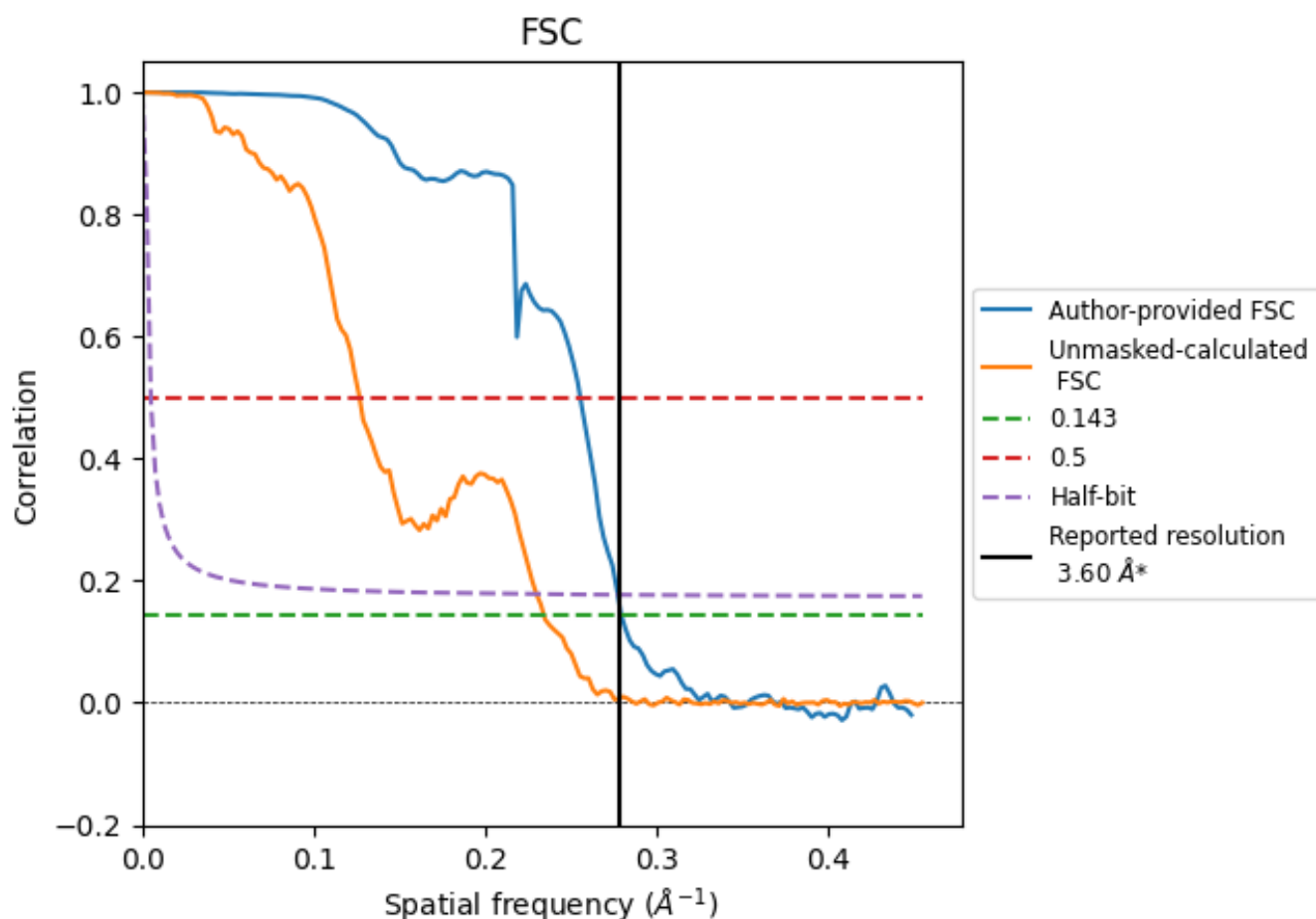


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

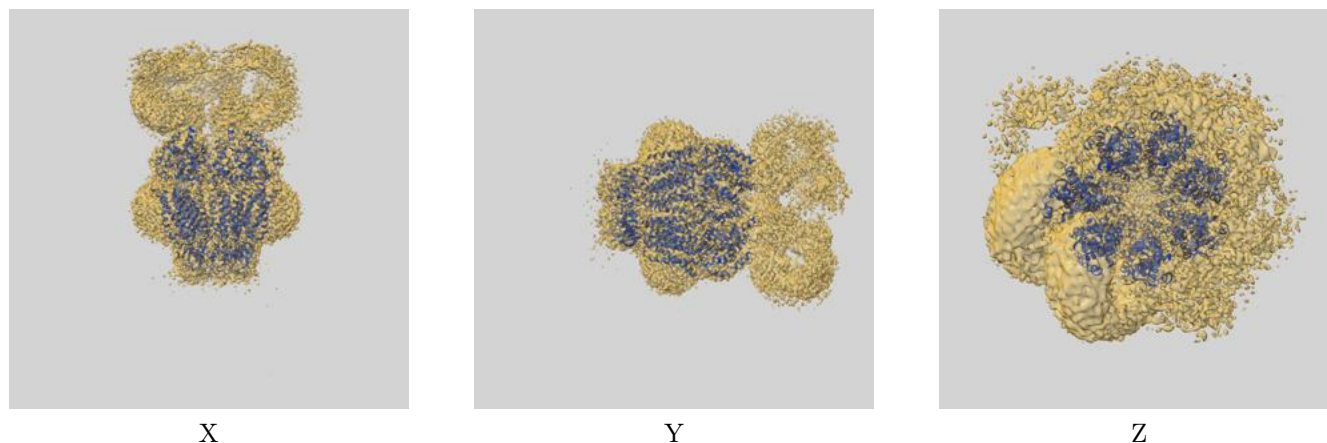
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.58	3.92	3.61
Unmasked-calculated*	4.27	7.90	4.35

*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 4.27 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

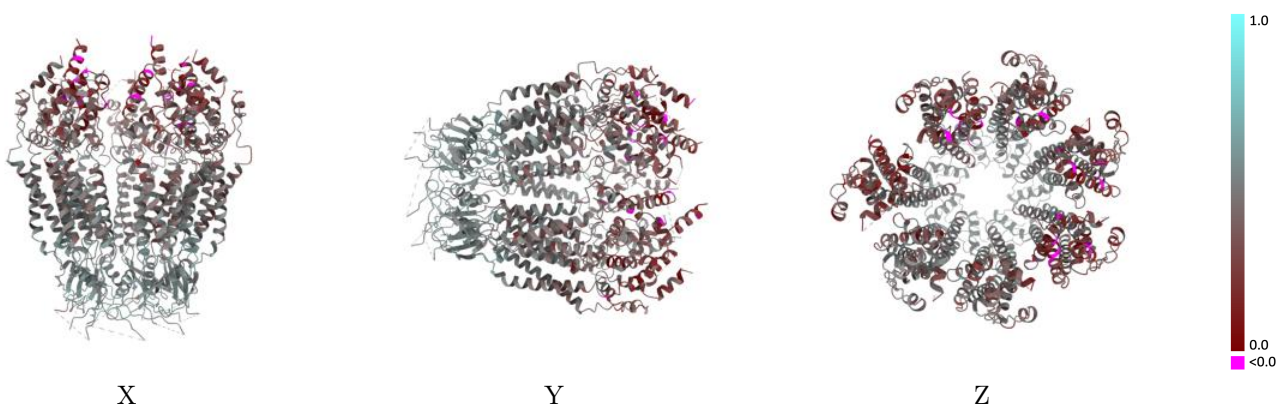
This section contains information regarding the fit between EMDB map EMD-27771 and PDB model 8DXO. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



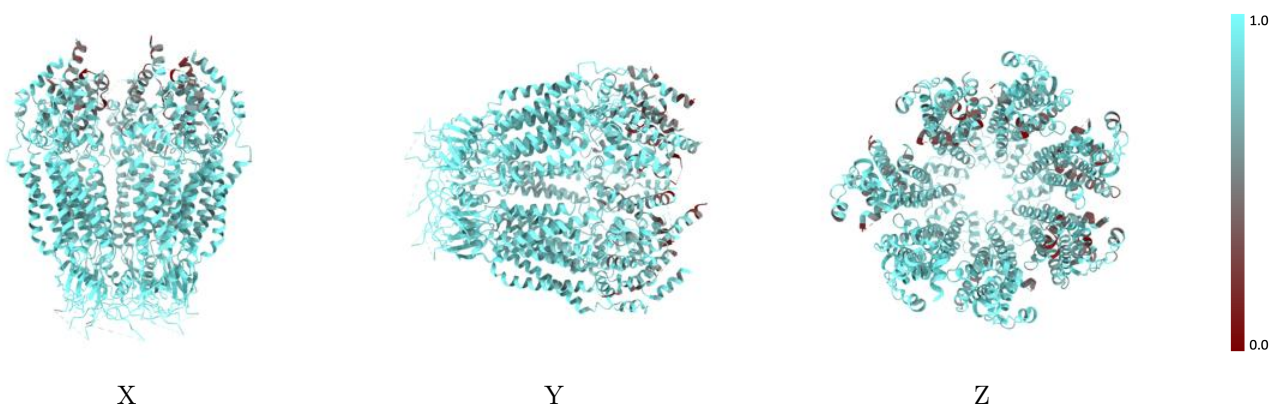
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



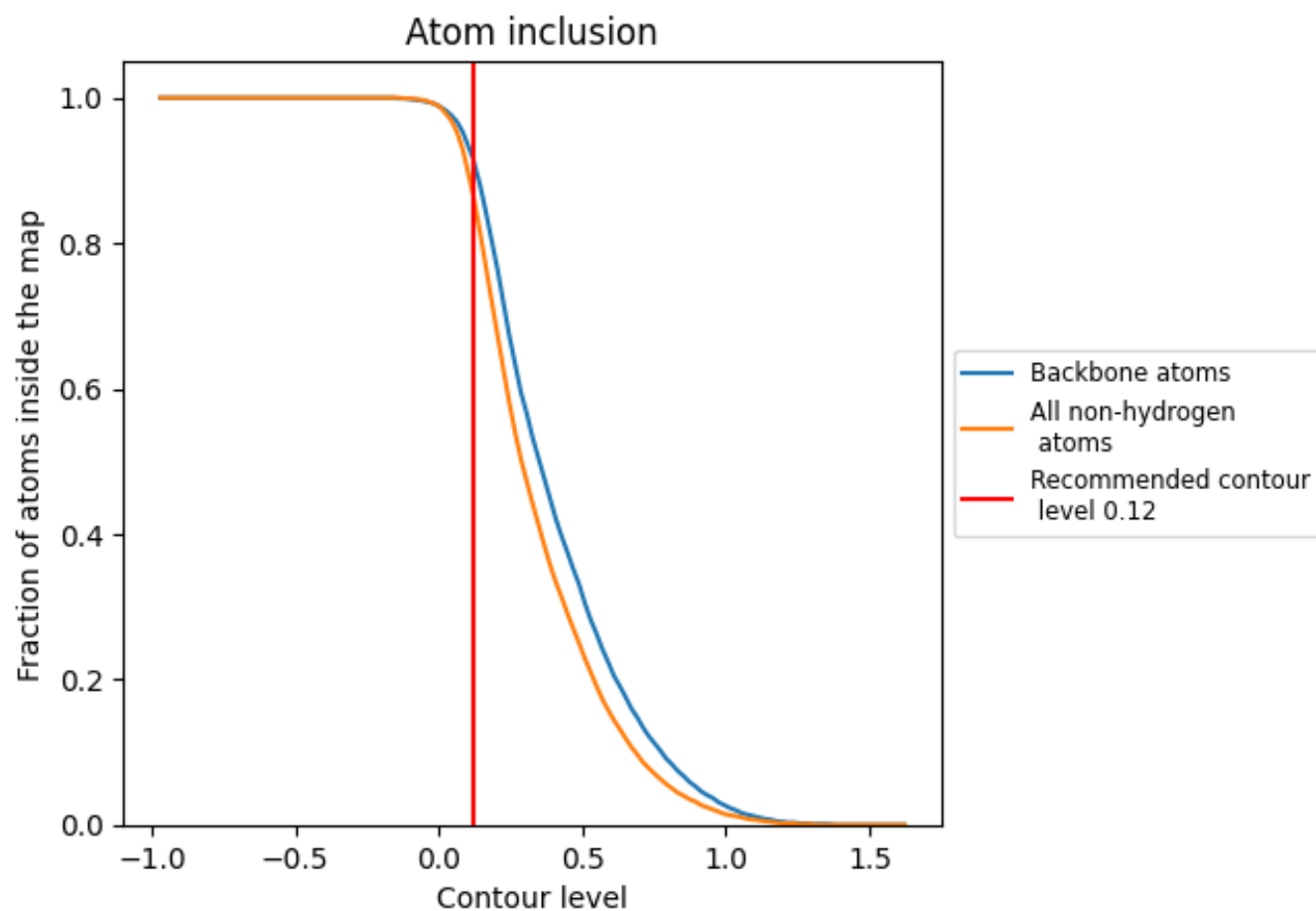
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 87% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8660	0.4220
A	0.8320	0.3910
B	0.8490	0.4100
C	0.8780	0.4330
D	0.8220	0.3950
E	0.8590	0.4020
F	0.9180	0.4660
G	0.9010	0.4590

1.0

0.0

<0.0