



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:37 PM UTC

PDB ID : 8DXN / pdb_00008dxn
EMDB ID : EMD-27770
Title : Structure of LRRC8C-LRRC8A(IL125) Chimera, Class 1
Authors : Takahashi, H.; Yamada, T.; Denton, J.S.; Strange, K.; Karakas, E.
Deposited on : 2022-08-02
Resolution : 3.40 Å(reported)

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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

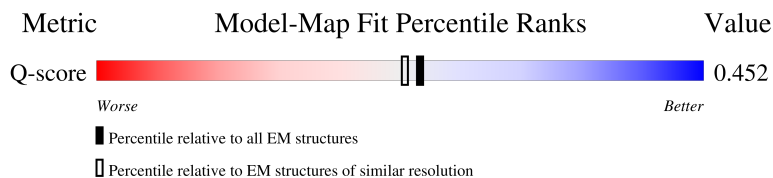
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	825	
1	B	825	
1	C	825	
1	D	825	

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Mol	Chain	Length	Quality of chain
1	E	825	33% 64%
1	F	825	32% 5% 63%
1	G	825	31% 5% 64%

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
C	815	TYR	-	expression tag	UNP Q8TDW0

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

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

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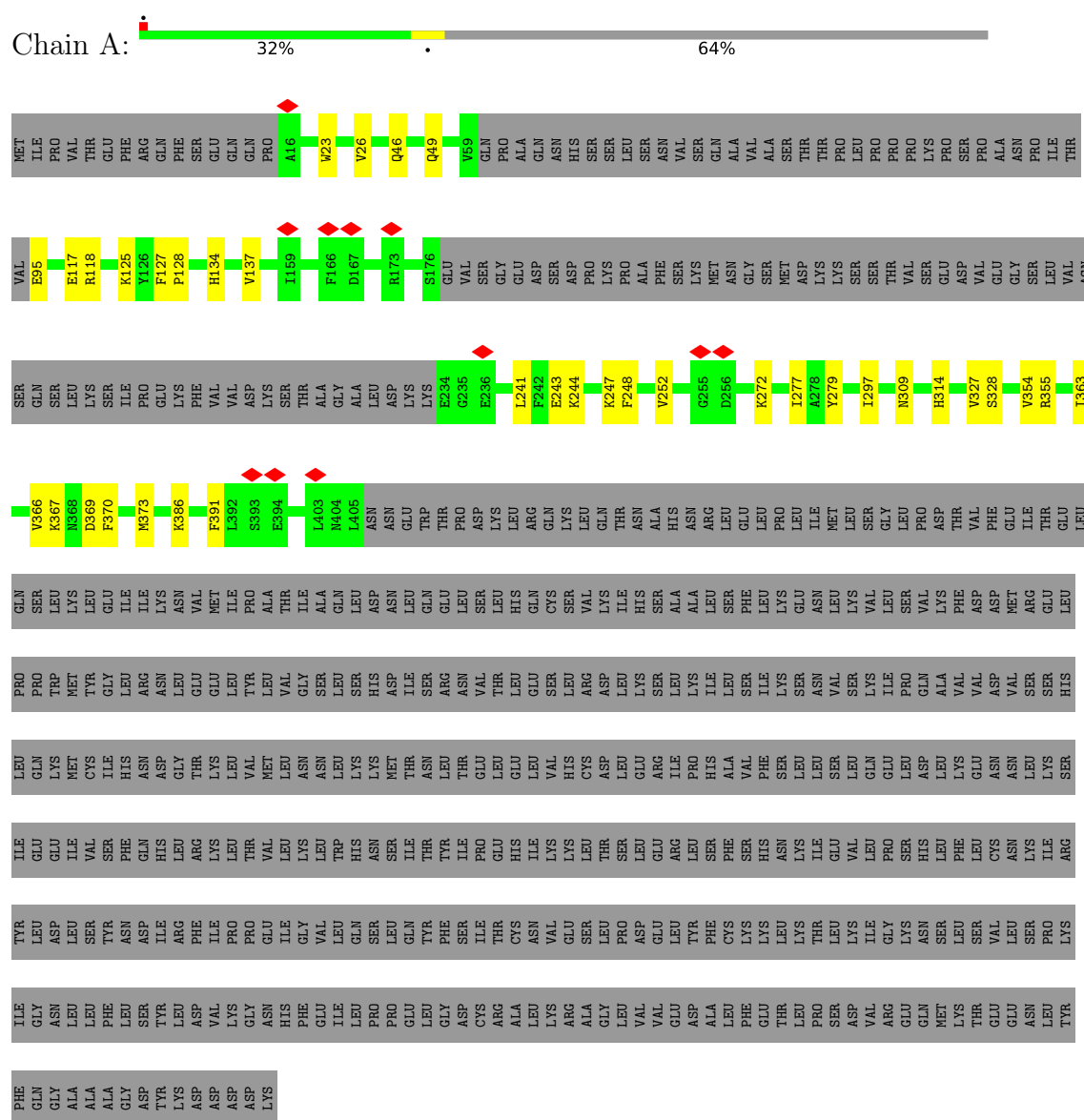
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Chain	Residue	Modelled	Actual	Comment	Reference
G	816	LYS	-	expression tag	UNP Q8TDW0
G	817	ASP	-	expression tag	UNP Q8TDW0
G	818	ASP	-	expression tag	UNP Q8TDW0
G	819	ASP	-	expression tag	UNP Q8TDW0
G	820	ASP	-	expression tag	UNP Q8TDW0
G	821	LYS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

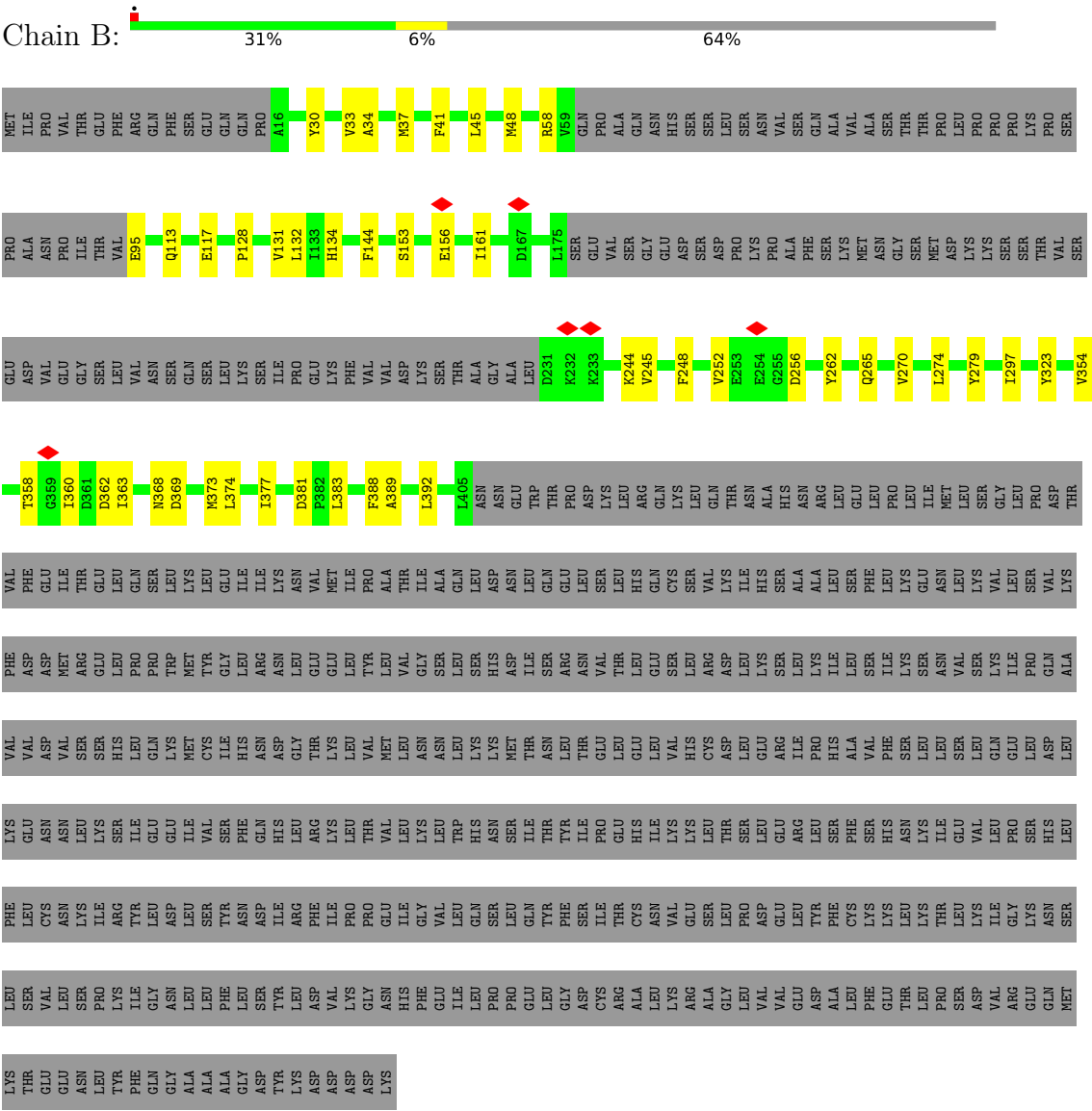
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

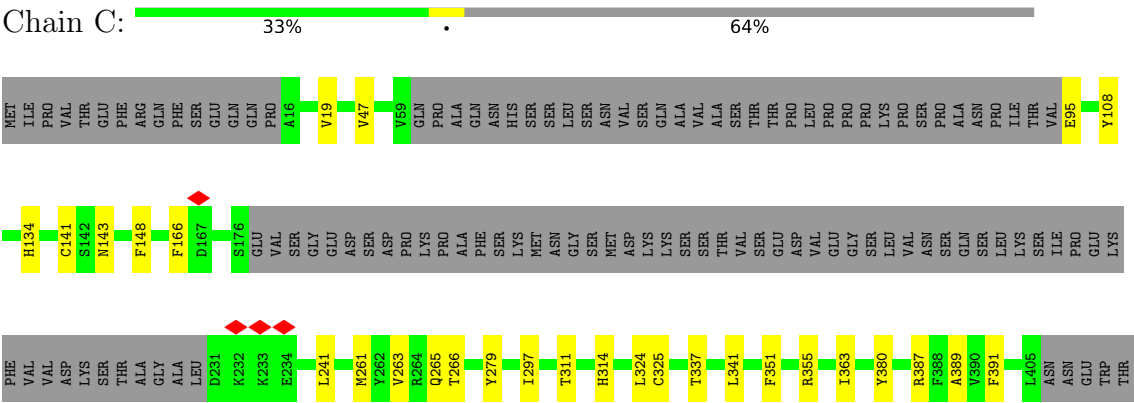
- Molecule 1: Volume-regulated anion channel subunit LRRC8C, Volume-regulated anion channel subunit LRRC8A



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



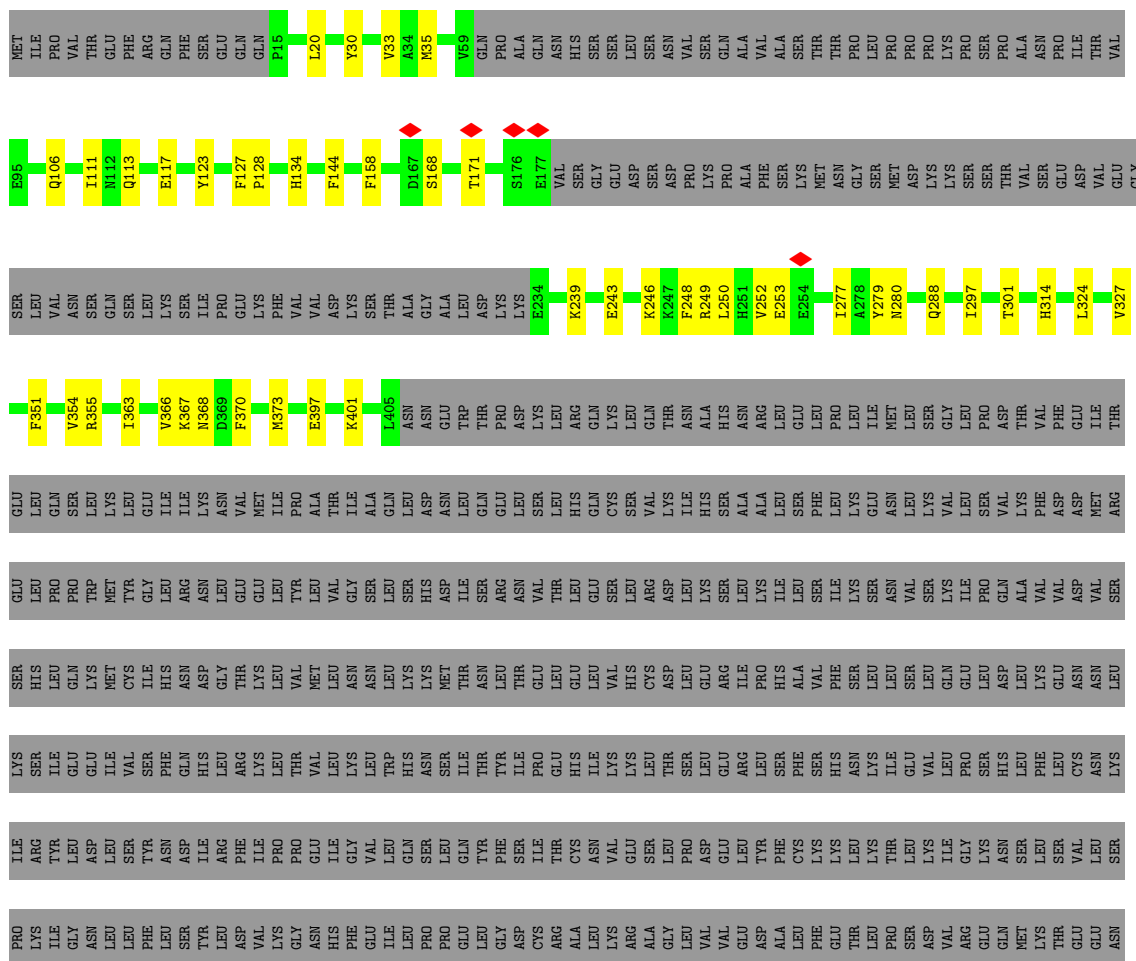
- Molecule 1: Volume-regulated anion channel subunit LRRC8C,Volume-regulated anion channel subunit LRRC8A



[illegible]

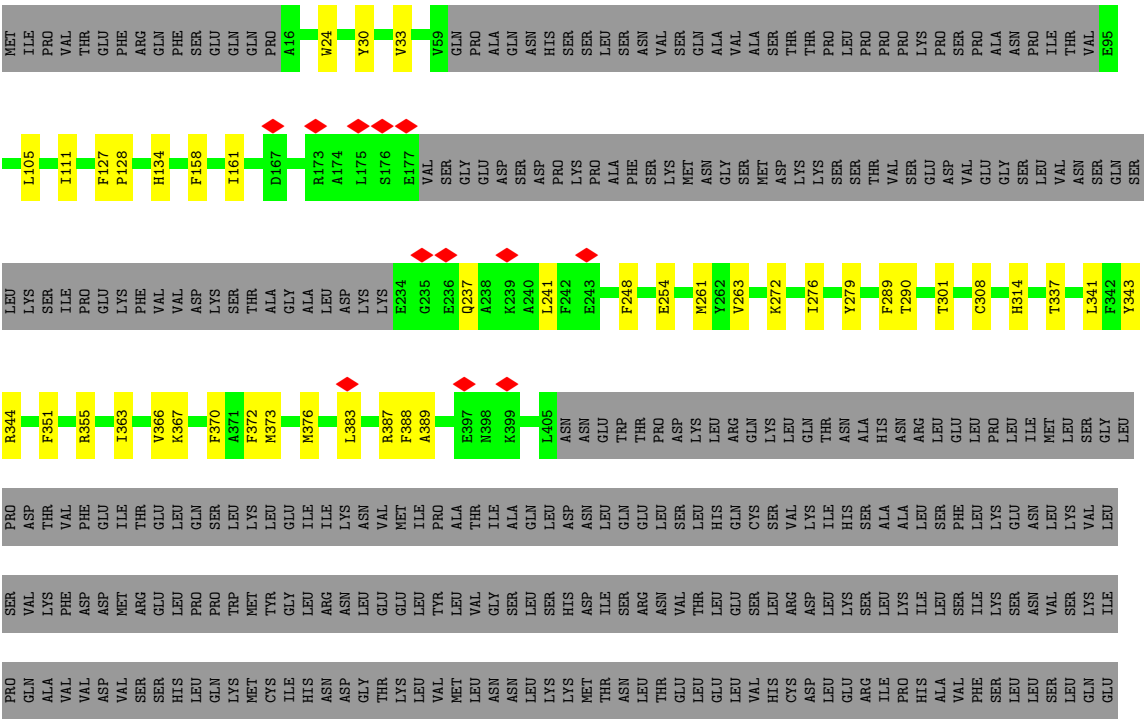
- Molecule 1: Volume-regulated anion channel subunit LRRC8C, Volume-regulated anion channel subunit LRRC8A

Chain D: 31% 5% 64%





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



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

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	203011	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	2.151	Depositor
Minimum map value	-1.235	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.15	0/2548	0.33	0/3441
1	B	0.15	0/2568	0.36	0/3466
1	C	0.15	0/2574	0.33	0/3474
1	D	0.15	0/2565	0.34	0/3464
1	E	0.14	0/2574	0.31	0/3474
1	F	0.15	0/2583	0.33	0/3486
1	G	0.13	0/2557	0.31	0/3453
All	All	0.15	0/17969	0.33	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	25	0
1	B	2501	0	2496	37	0
1	C	2507	0	2501	20	0
1	D	2497	0	2485	33	0
1	E	2507	0	2501	19	0
1	F	2516	0	2507	24	0
1	G	2490	0	2477	30	0
All	All	17499	0	17438	176	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 176 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:ILE:HG23	1:B:392:LEU:HD11	1.62	0.80
1:A:134:HIS:NE2	1:A:279:TYR:OH	2.17	0.75
1:G:134:HIS:NE2	1:G:279:TYR:OH	2.23	0.72
1:G:351:PHE:O	1:G:355:ARG:NE	2.25	0.69
1:E:134:HIS:NE2	1:E:279:TYR:OH	2.25	0.68

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%)	278 (95%)	14 (5%)	0	100	100
1	B	294/825 (36%)	261 (89%)	33 (11%)	0	100	100
1	C	295/825 (36%)	275 (93%)	20 (7%)	0	100	100
1	D	294/825 (36%)	269 (92%)	25 (8%)	0	100	100
1	E	295/825 (36%)	282 (96%)	13 (4%)	0	100	100
1	F	296/825 (36%)	271 (92%)	25 (8%)	0	100	100
1	G	293/825 (36%)	276 (94%)	17 (6%)	0	100	100
All	All	2059/5775 (36%)	1912 (93%)	147 (7%)	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 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	294	ASN
1	G	305	ASN
1	G	404	ASN
1	E	314	HIS
1	F	113	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.

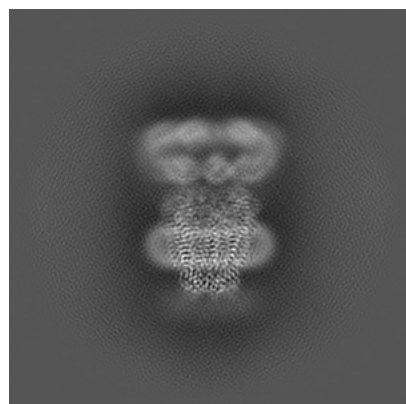
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27770. These allow visual inspection of the internal detail of the map and identification of artifacts.

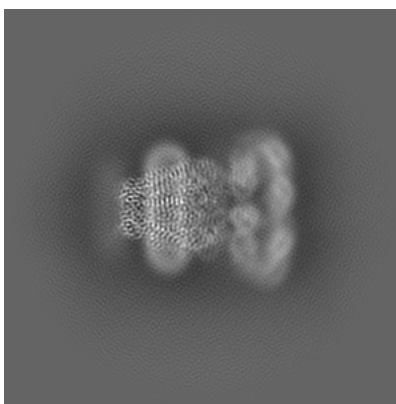
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

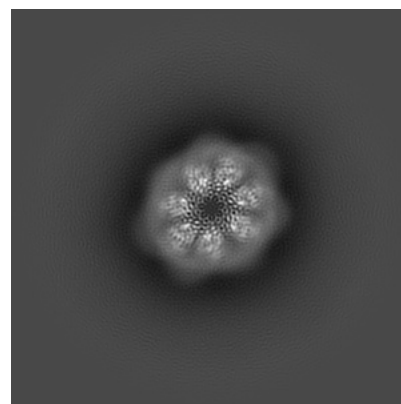
6.1.1 Primary map



X

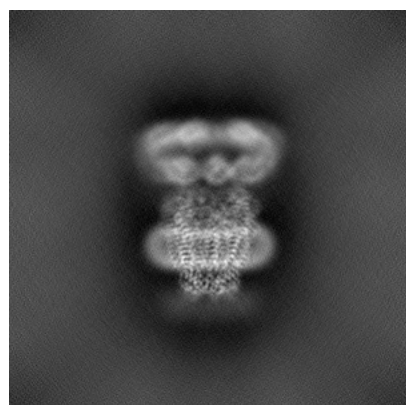


Y

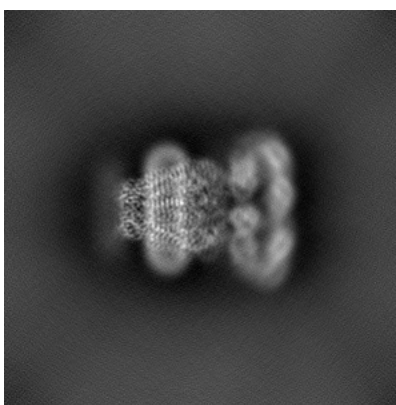


Z

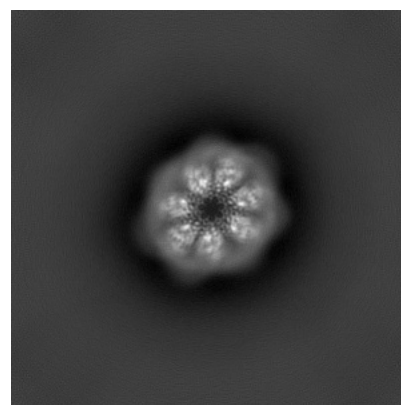
6.1.2 Raw map



X



Y

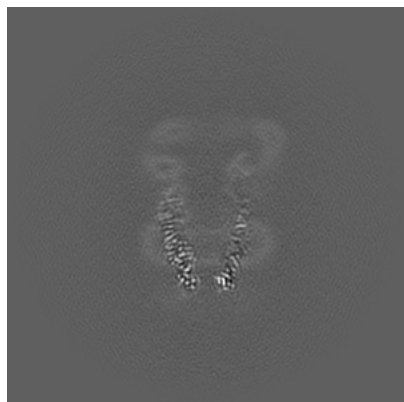


Z

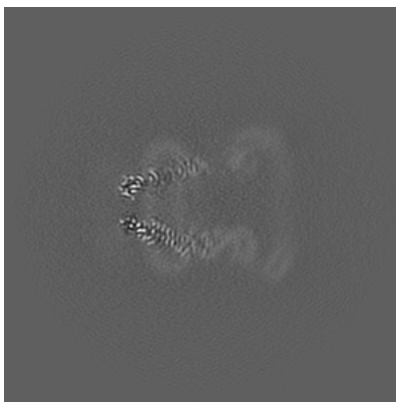
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

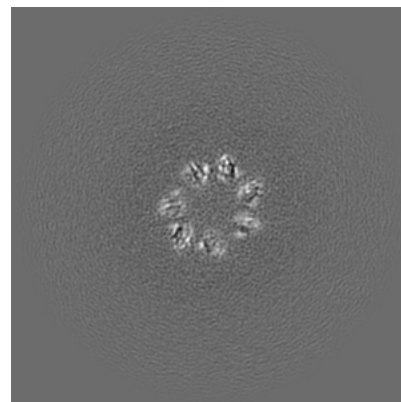
6.2.1 Primary map



X Index: 180

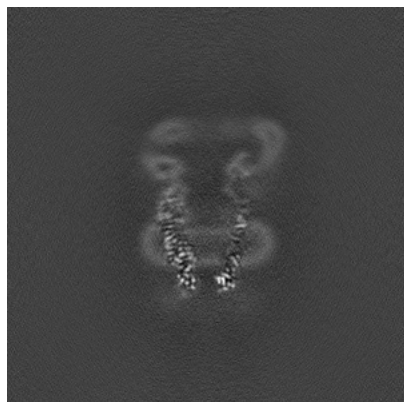


Y Index: 180

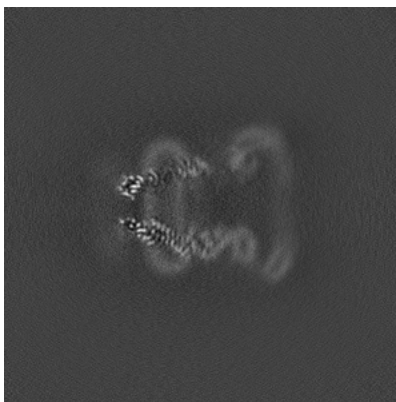


Z Index: 180

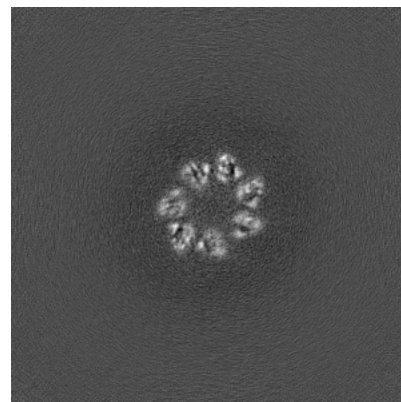
6.2.2 Raw map



X Index: 180



Y Index: 180

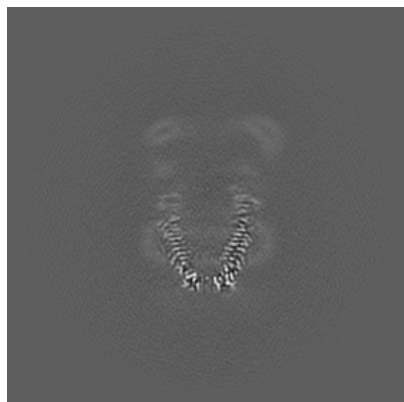


Z Index: 180

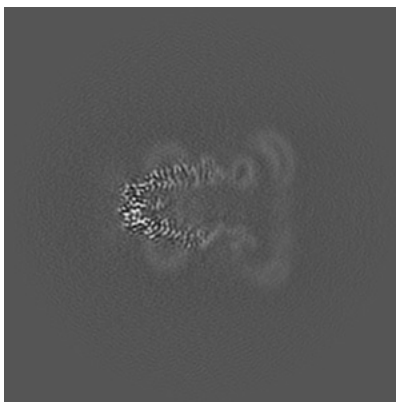
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

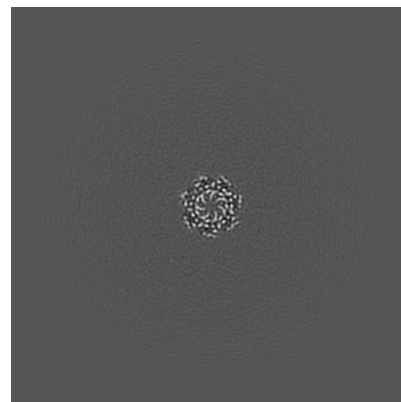
6.3.1 Primary map



X Index: 187

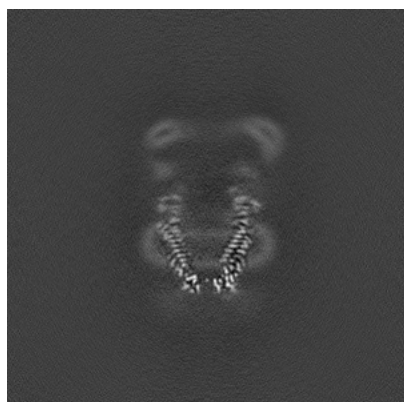


Y Index: 163

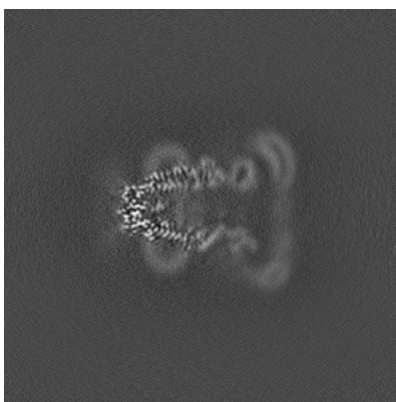


Z Index: 116

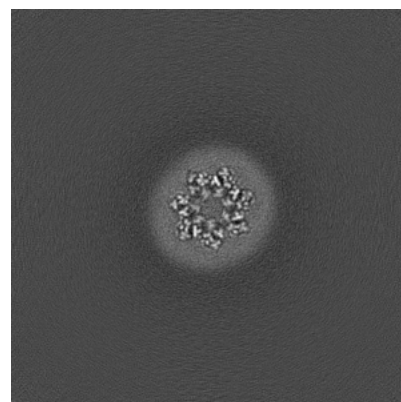
6.3.2 Raw map



X Index: 187



Y Index: 163



Z Index: 133

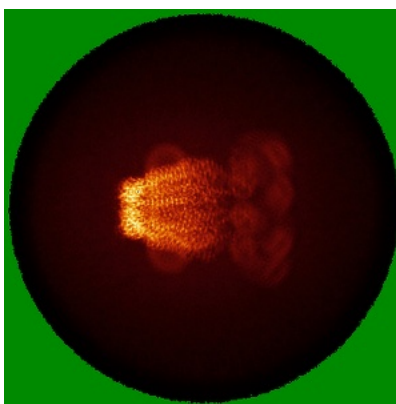
The images above show the largest variance slices of the map in three orthogonal directions.

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

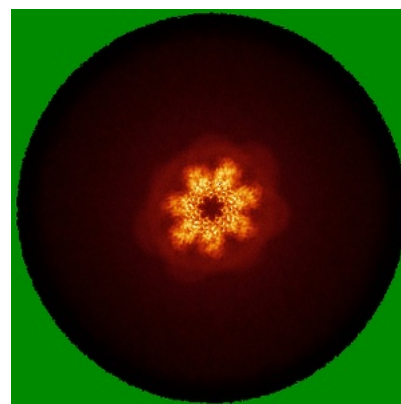
6.4.1 Primary map



X

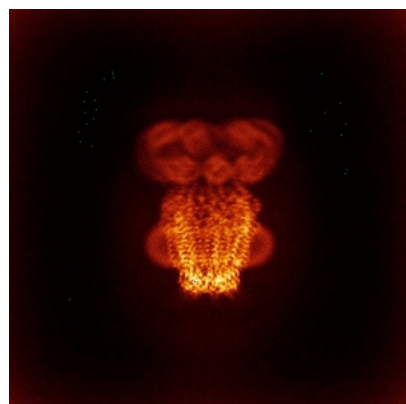


Y

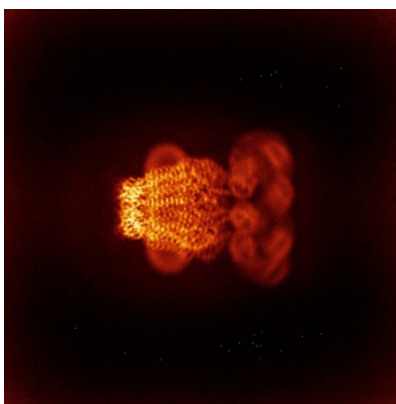


Z

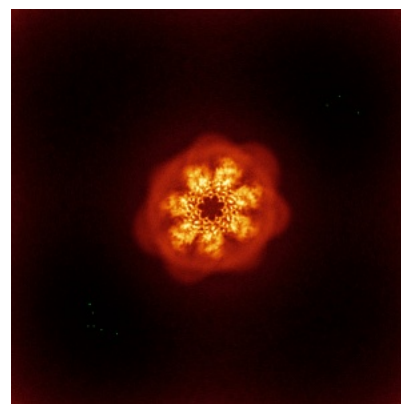
6.4.2 Raw map



X



Y



Z

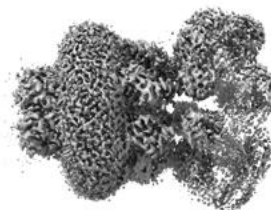
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

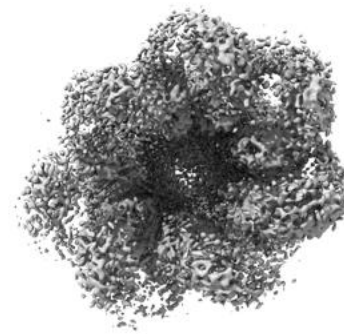
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

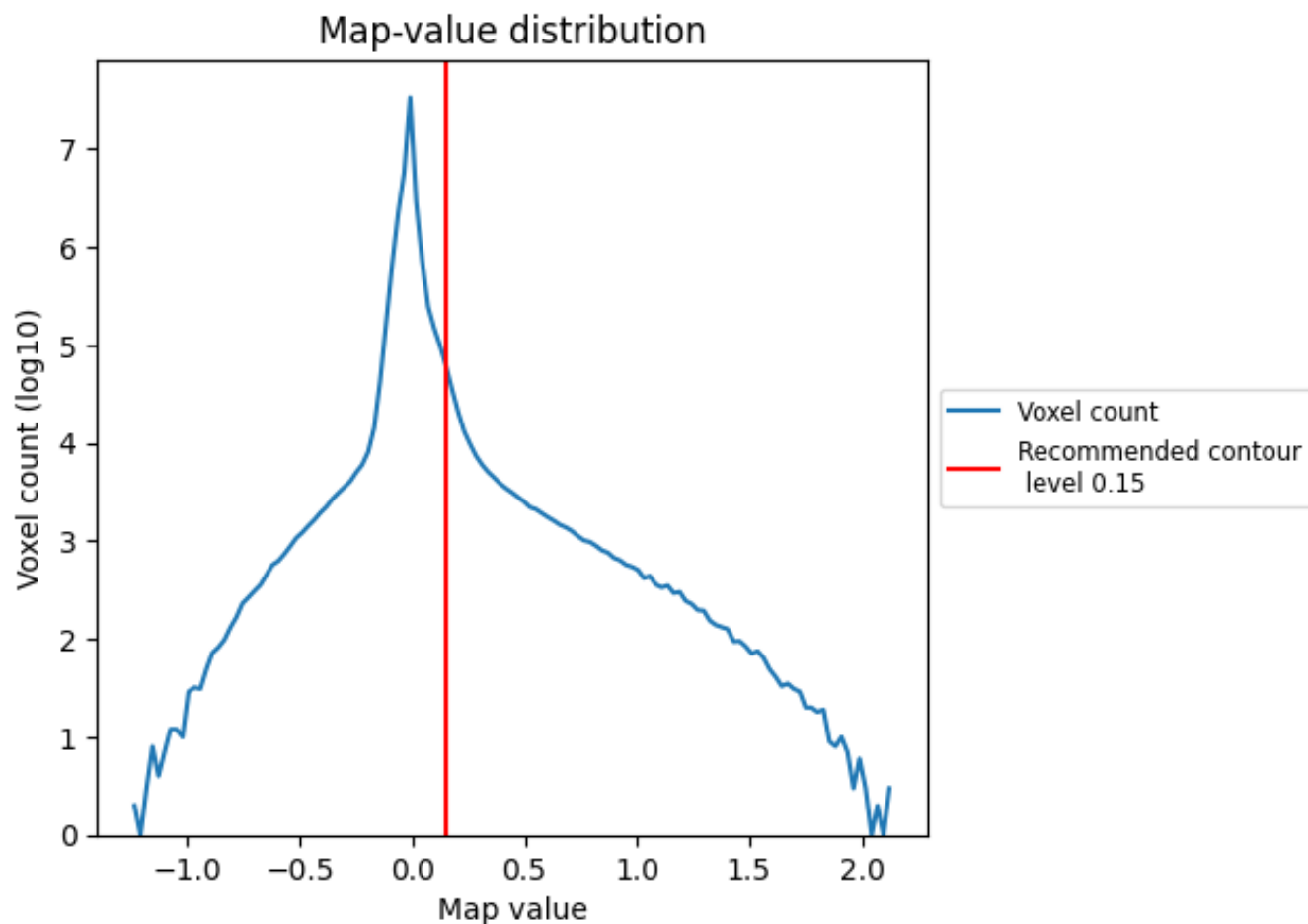
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

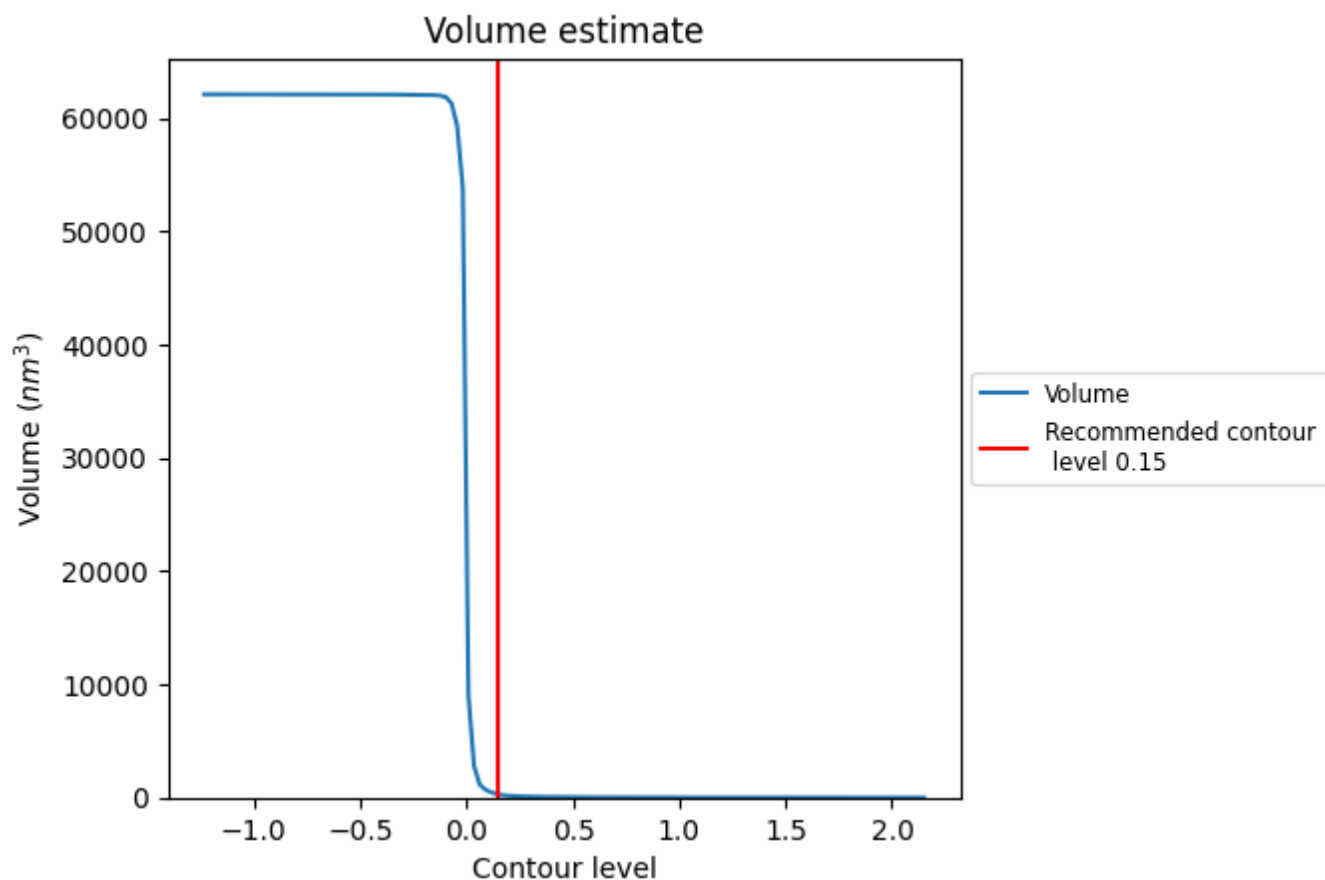
This section contains the results of statistical analysis of the map.

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.

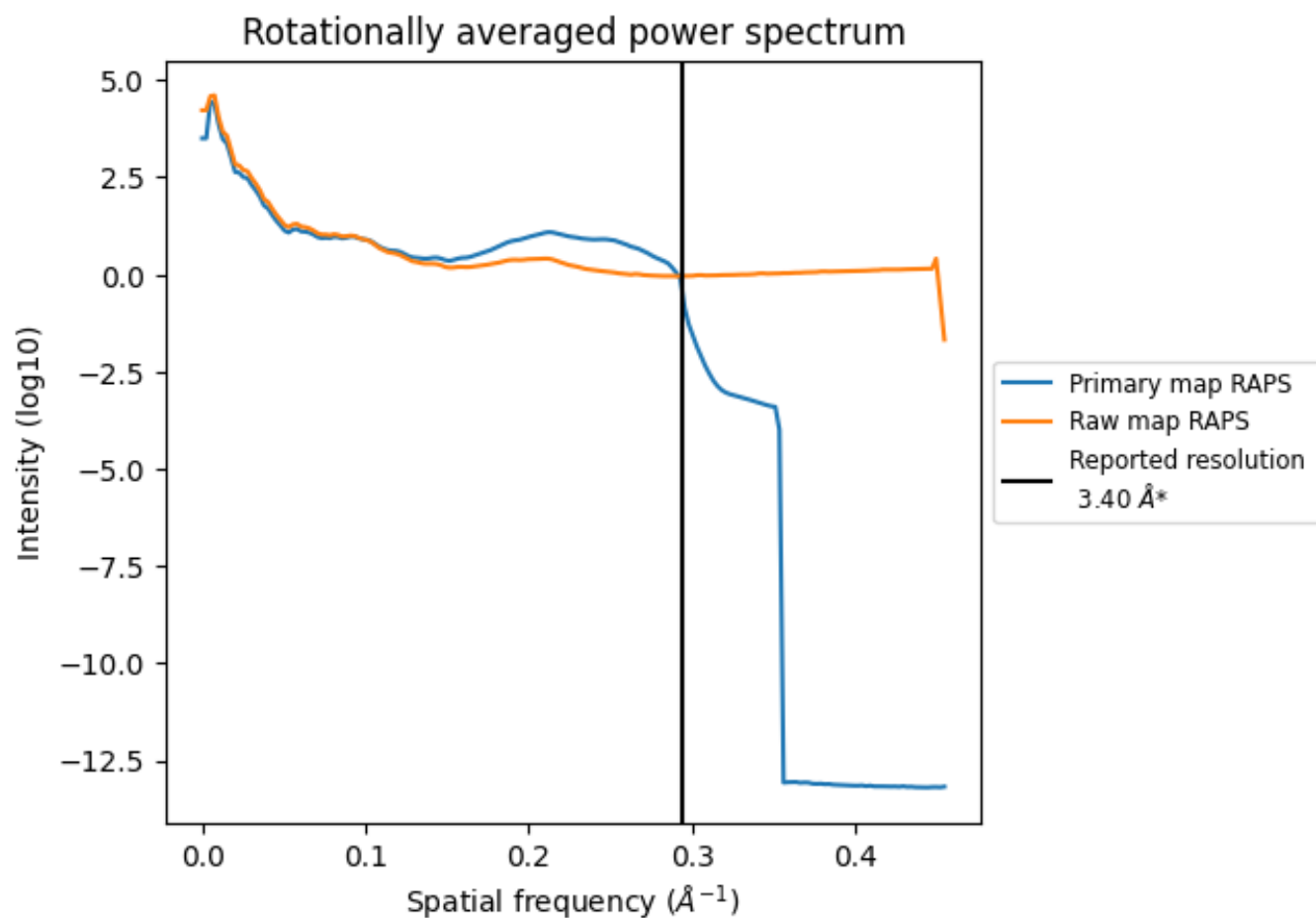
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 283 nm^3 ; this corresponds to an approximate mass of 255 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 ⓘ

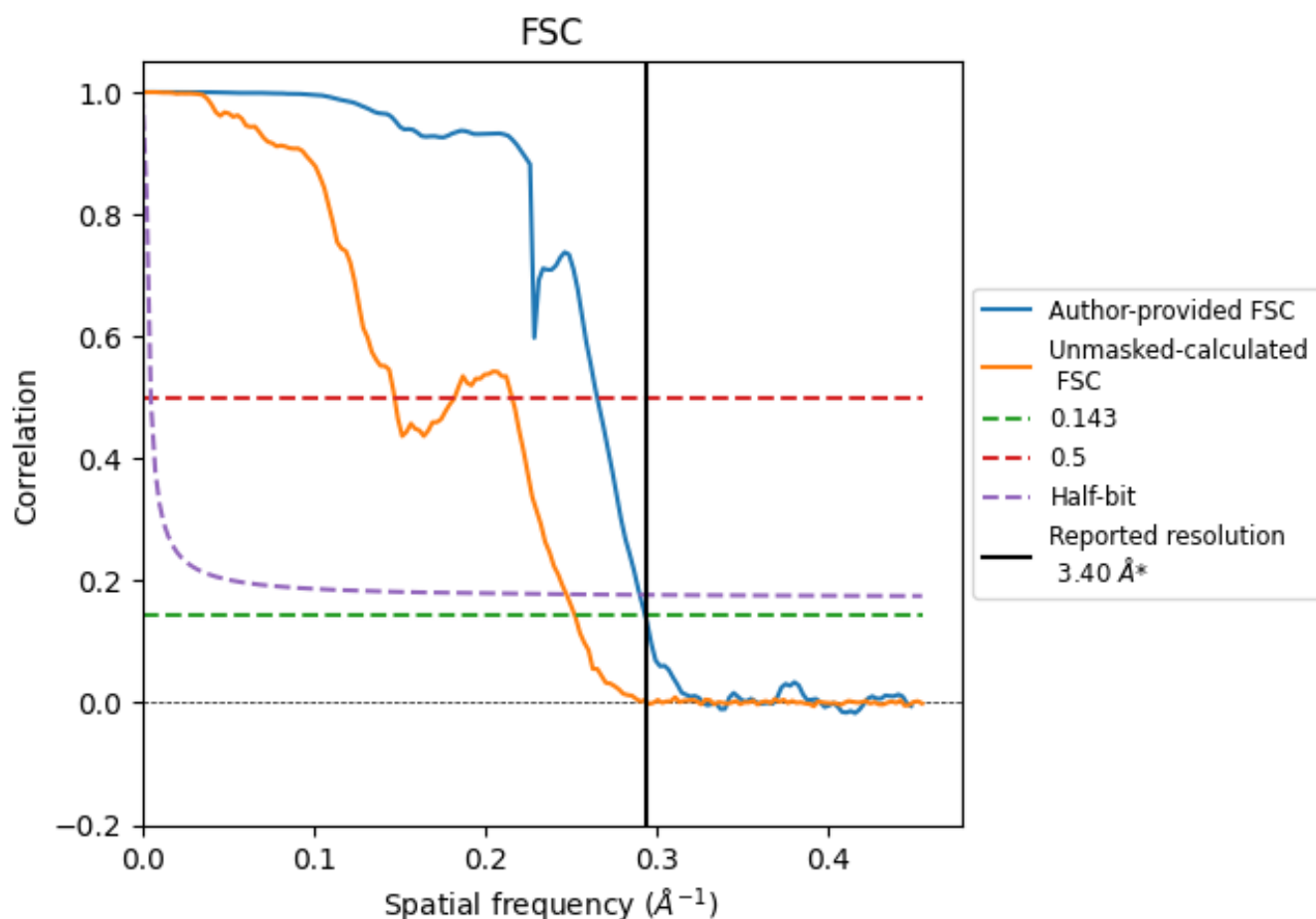


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

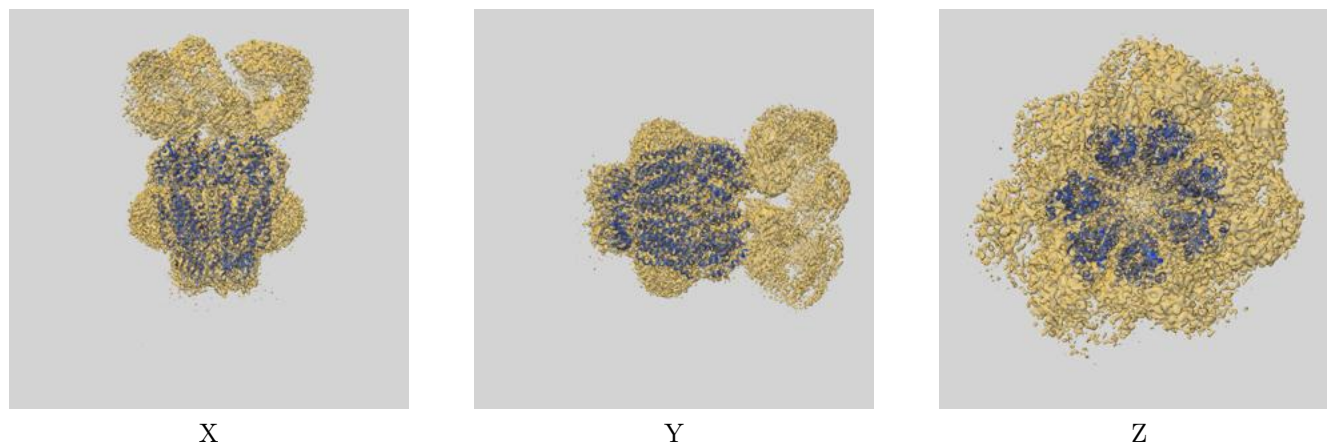
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.41	3.77	3.45
Unmasked-calculated*	3.97	6.80	4.05

*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 3.97 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

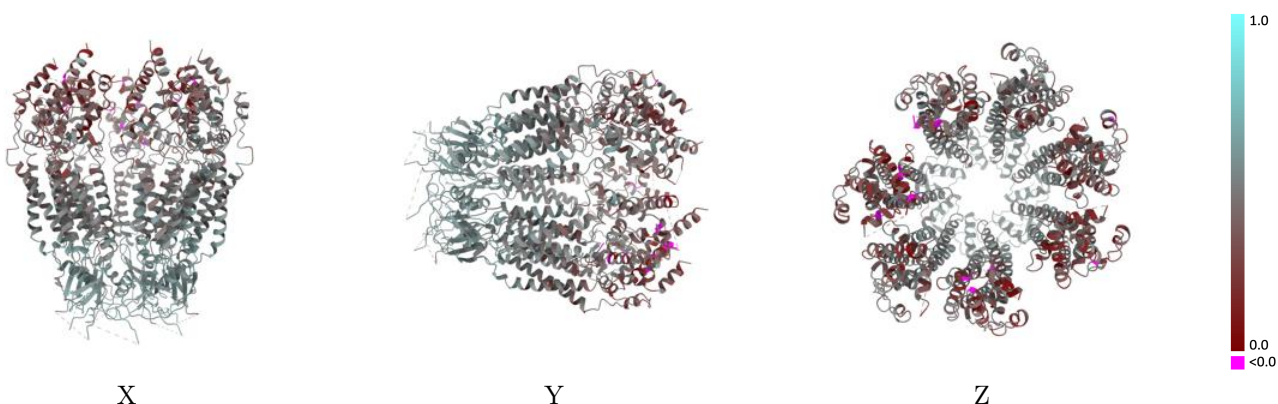
This section contains information regarding the fit between EMDB map EMD-27770 and PDB model 8DXN. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



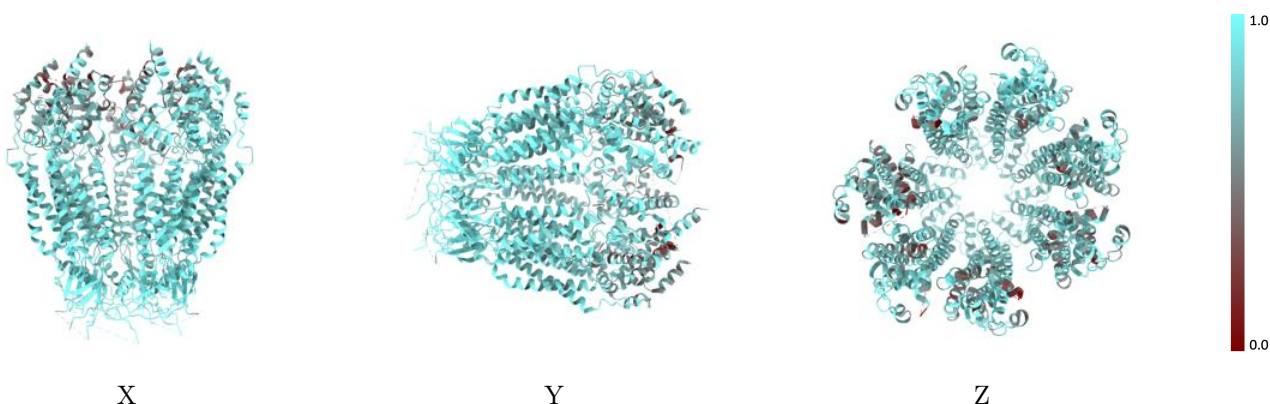
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



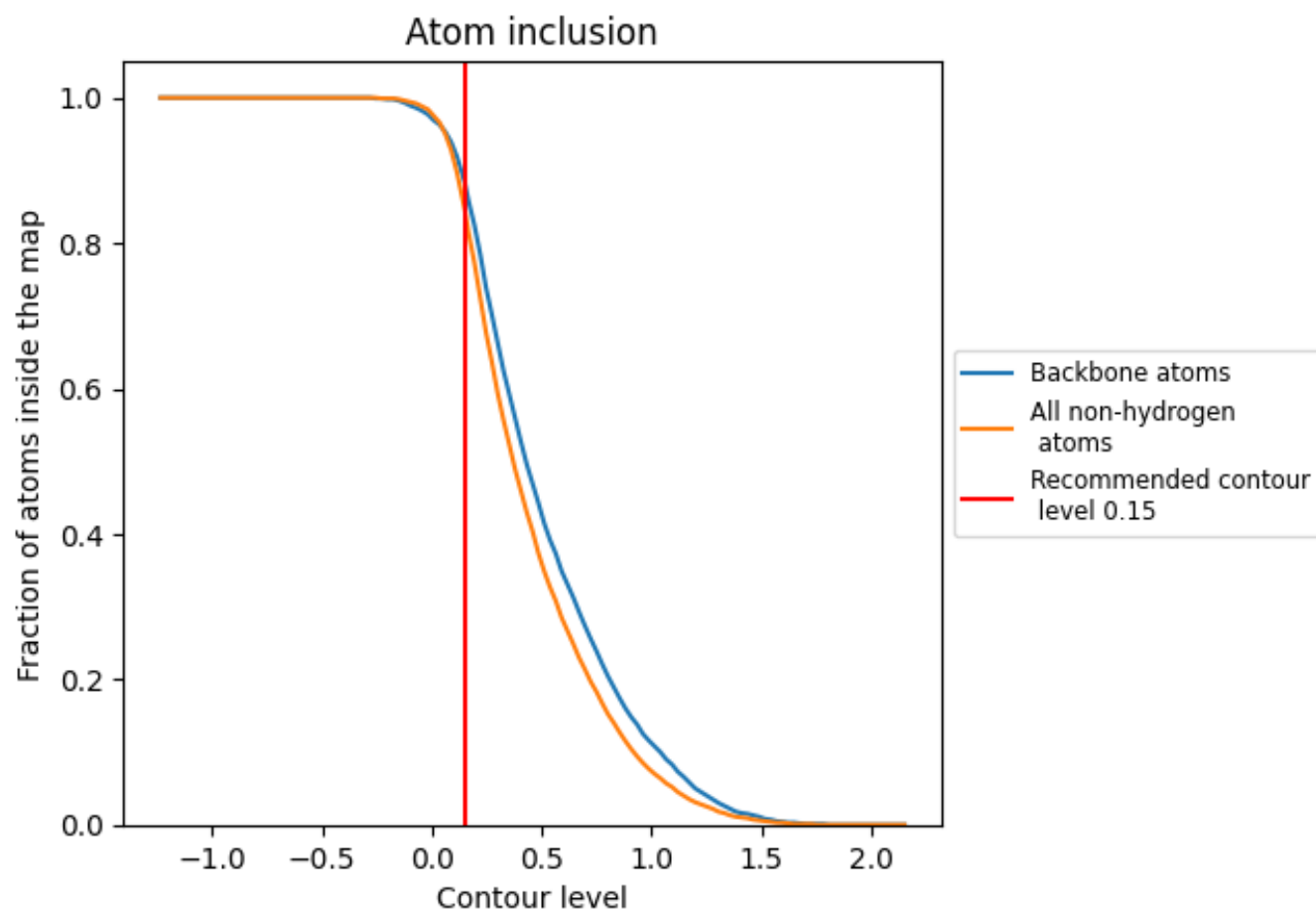
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8450	0.4520
A	0.8200	0.4260
B	0.8490	0.4580
C	0.8820	0.4870
D	0.8700	0.4630
E	0.8010	0.4180
F	0.8590	0.4730
G	0.8330	0.4370

1.0

0.0

<0.0