



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:39 AM UTC

PDB ID : 8XGE / pdb_00008xge
EMDB ID : EMD-38319
Title : Human Cx36/GJD2 gap junction channel in porcine brain lipids.
Authors : Cho, H.J.; Lee, H.H.
Deposited on : 2023-12-15
Resolution : 2.89 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

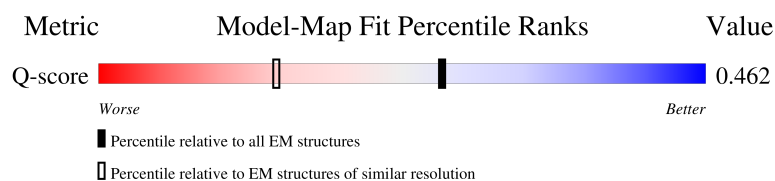
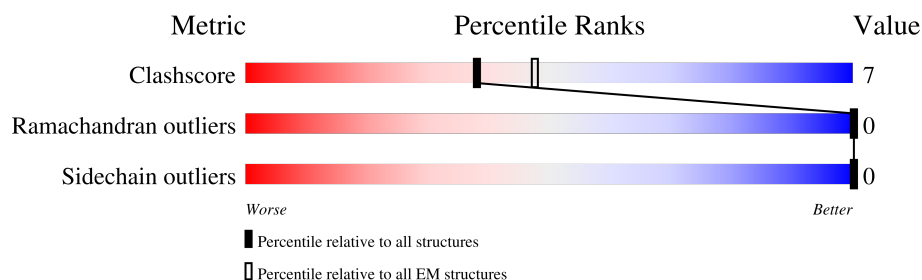
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	12148 (2.39 - 3.39)

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	331	
1	B	331	
1	C	331	
1	D	331	

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Mol	Chain	Length	Quality of chain
1	E	331	 48% . 50%
1	F	331	 48% . 50%
1	G	331	 48% . 50%
1	H	331	 48% . 50%
1	I	331	 48% . 50%
1	J	331	 48% . 50%
1	K	331	 48% . 50%
1	L	331	 48% . 50%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 32388 atoms, of which 16008 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 Gap junction delta-2 protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	C	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	B	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	D	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	E	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	F	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	G	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	H	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	I	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	J	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	K	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0
1	L	166	Total 2664	C 876	H 1334	N 212	O 229	S 13	0	0

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	322	SER	-	linker	UNP Q9UKL4
A	323	ARG	-	linker	UNP Q9UKL4
A	324	ASP	-	expression tag	UNP Q9UKL4
A	325	TYR	-	expression tag	UNP Q9UKL4
A	326	LYS	-	expression tag	UNP Q9UKL4
A	327	ASP	-	expression tag	UNP Q9UKL4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	328	ASP	-	expression tag	UNP Q9UKL4
A	329	ASP	-	expression tag	UNP Q9UKL4
A	330	ASP	-	expression tag	UNP Q9UKL4
A	331	LYS	-	expression tag	UNP Q9UKL4
C	322	SER	-	linker	UNP Q9UKL4
C	323	ARG	-	linker	UNP Q9UKL4
C	324	ASP	-	expression tag	UNP Q9UKL4
C	325	TYR	-	expression tag	UNP Q9UKL4
C	326	LYS	-	expression tag	UNP Q9UKL4
C	327	ASP	-	expression tag	UNP Q9UKL4
C	328	ASP	-	expression tag	UNP Q9UKL4
C	329	ASP	-	expression tag	UNP Q9UKL4
C	330	ASP	-	expression tag	UNP Q9UKL4
C	331	LYS	-	expression tag	UNP Q9UKL4
B	322	SER	-	linker	UNP Q9UKL4
B	323	ARG	-	linker	UNP Q9UKL4
B	324	ASP	-	expression tag	UNP Q9UKL4
B	325	TYR	-	expression tag	UNP Q9UKL4
B	326	LYS	-	expression tag	UNP Q9UKL4
B	327	ASP	-	expression tag	UNP Q9UKL4
B	328	ASP	-	expression tag	UNP Q9UKL4
B	329	ASP	-	expression tag	UNP Q9UKL4
B	330	ASP	-	expression tag	UNP Q9UKL4
B	331	LYS	-	expression tag	UNP Q9UKL4
D	322	SER	-	linker	UNP Q9UKL4
D	323	ARG	-	linker	UNP Q9UKL4
D	324	ASP	-	expression tag	UNP Q9UKL4
D	325	TYR	-	expression tag	UNP Q9UKL4
D	326	LYS	-	expression tag	UNP Q9UKL4
D	327	ASP	-	expression tag	UNP Q9UKL4
D	328	ASP	-	expression tag	UNP Q9UKL4
D	329	ASP	-	expression tag	UNP Q9UKL4
D	330	ASP	-	expression tag	UNP Q9UKL4
D	331	LYS	-	expression tag	UNP Q9UKL4
E	322	SER	-	linker	UNP Q9UKL4
E	323	ARG	-	linker	UNP Q9UKL4
E	324	ASP	-	expression tag	UNP Q9UKL4
E	325	TYR	-	expression tag	UNP Q9UKL4
E	326	LYS	-	expression tag	UNP Q9UKL4
E	327	ASP	-	expression tag	UNP Q9UKL4
E	328	ASP	-	expression tag	UNP Q9UKL4
E	329	ASP	-	expression tag	UNP Q9UKL4

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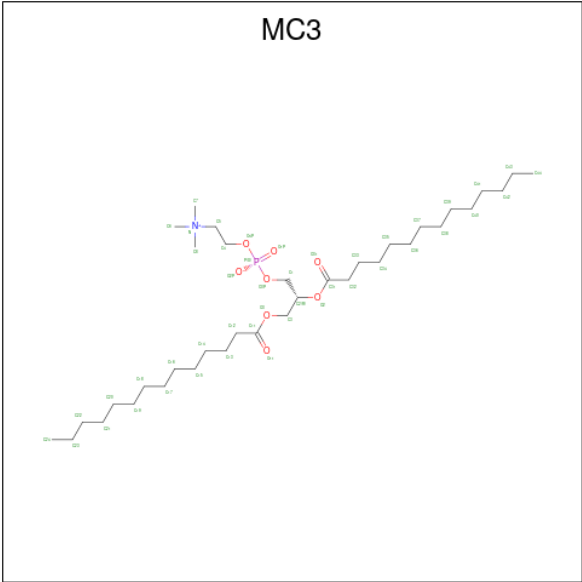
Chain	Residue	Modelled	Actual	Comment	Reference
E	330	ASP	-	expression tag	UNP Q9UKL4
E	331	LYS	-	expression tag	UNP Q9UKL4
F	322	SER	-	linker	UNP Q9UKL4
F	323	ARG	-	linker	UNP Q9UKL4
F	324	ASP	-	expression tag	UNP Q9UKL4
F	325	TYR	-	expression tag	UNP Q9UKL4
F	326	LYS	-	expression tag	UNP Q9UKL4
F	327	ASP	-	expression tag	UNP Q9UKL4
F	328	ASP	-	expression tag	UNP Q9UKL4
F	329	ASP	-	expression tag	UNP Q9UKL4
F	330	ASP	-	expression tag	UNP Q9UKL4
F	331	LYS	-	expression tag	UNP Q9UKL4
G	322	SER	-	linker	UNP Q9UKL4
G	323	ARG	-	linker	UNP Q9UKL4
G	324	ASP	-	expression tag	UNP Q9UKL4
G	325	TYR	-	expression tag	UNP Q9UKL4
G	326	LYS	-	expression tag	UNP Q9UKL4
G	327	ASP	-	expression tag	UNP Q9UKL4
G	328	ASP	-	expression tag	UNP Q9UKL4
G	329	ASP	-	expression tag	UNP Q9UKL4
G	330	ASP	-	expression tag	UNP Q9UKL4
G	331	LYS	-	expression tag	UNP Q9UKL4
H	322	SER	-	linker	UNP Q9UKL4
H	323	ARG	-	linker	UNP Q9UKL4
H	324	ASP	-	expression tag	UNP Q9UKL4
H	325	TYR	-	expression tag	UNP Q9UKL4
H	326	LYS	-	expression tag	UNP Q9UKL4
H	327	ASP	-	expression tag	UNP Q9UKL4
H	328	ASP	-	expression tag	UNP Q9UKL4
H	329	ASP	-	expression tag	UNP Q9UKL4
H	330	ASP	-	expression tag	UNP Q9UKL4
H	331	LYS	-	expression tag	UNP Q9UKL4
I	322	SER	-	linker	UNP Q9UKL4
I	323	ARG	-	linker	UNP Q9UKL4
I	324	ASP	-	expression tag	UNP Q9UKL4
I	325	TYR	-	expression tag	UNP Q9UKL4
I	326	LYS	-	expression tag	UNP Q9UKL4
I	327	ASP	-	expression tag	UNP Q9UKL4
I	328	ASP	-	expression tag	UNP Q9UKL4
I	329	ASP	-	expression tag	UNP Q9UKL4
I	330	ASP	-	expression tag	UNP Q9UKL4
I	331	LYS	-	expression tag	UNP Q9UKL4

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Chain	Residue	Modelled	Actual	Comment	Reference
J	322	SER	-	linker	UNP Q9UKL4
J	323	ARG	-	linker	UNP Q9UKL4
J	324	ASP	-	expression tag	UNP Q9UKL4
J	325	TYR	-	expression tag	UNP Q9UKL4
J	326	LYS	-	expression tag	UNP Q9UKL4
J	327	ASP	-	expression tag	UNP Q9UKL4
J	328	ASP	-	expression tag	UNP Q9UKL4
J	329	ASP	-	expression tag	UNP Q9UKL4
J	330	ASP	-	expression tag	UNP Q9UKL4
J	331	LYS	-	expression tag	UNP Q9UKL4
K	322	SER	-	linker	UNP Q9UKL4
K	323	ARG	-	linker	UNP Q9UKL4
K	324	ASP	-	expression tag	UNP Q9UKL4
K	325	TYR	-	expression tag	UNP Q9UKL4
K	326	LYS	-	expression tag	UNP Q9UKL4
K	327	ASP	-	expression tag	UNP Q9UKL4
K	328	ASP	-	expression tag	UNP Q9UKL4
K	329	ASP	-	expression tag	UNP Q9UKL4
K	330	ASP	-	expression tag	UNP Q9UKL4
K	331	LYS	-	expression tag	UNP Q9UKL4
L	322	SER	-	linker	UNP Q9UKL4
L	323	ARG	-	linker	UNP Q9UKL4
L	324	ASP	-	expression tag	UNP Q9UKL4
L	325	TYR	-	expression tag	UNP Q9UKL4
L	326	LYS	-	expression tag	UNP Q9UKL4
L	327	ASP	-	expression tag	UNP Q9UKL4
L	328	ASP	-	expression tag	UNP Q9UKL4
L	329	ASP	-	expression tag	UNP Q9UKL4
L	330	ASP	-	expression tag	UNP Q9UKL4
L	331	LYS	-	expression tag	UNP Q9UKL4

- Molecule 2 is 1,2-DIMYRISTOYL-RAC-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: MC3) (formula: C₃₆H₇₂NO₈P).



Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	C	0
			12	12	
2	A	1	Total	C	0
			9	9	
2	A	1	Total	C	0
			9	9	
2	A	1	Total	C	0
			5	5	
2	C	1	Total	C	0
			12	12	
2	C	1	Total	C	0
			9	9	
2	C	1	Total	C	0
			9	9	
2	C	1	Total	C	0
			5	5	
2	B	1	Total	C	0
			12	12	
2	B	1	Total	C	0
			9	9	
2	B	1	Total	C	0
			9	9	
2	B	1	Total	C	0
			5	5	
2	D	1	Total	C	0
			12	12	
2	D	1	Total	C	0
			9	9	

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Mol	Chain	Residues	Atoms	AltConf
2	D	1	Total C 9 9	0
2	D	1	Total C 5 5	0
2	E	1	Total C 12 12	0
2	E	1	Total C 9 9	0
2	E	1	Total C 9 9	0
2	E	1	Total C 5 5	0
2	F	1	Total C 12 12	0
2	F	1	Total C 9 9	0
2	F	1	Total C 9 9	0
2	F	1	Total C 5 5	0
2	G	1	Total C 12 12	0
2	G	1	Total C 9 9	0
2	G	1	Total C 9 9	0
2	G	1	Total C 5 5	0
2	H	1	Total C 12 12	0
2	H	1	Total C 9 9	0
2	H	1	Total C 9 9	0
2	H	1	Total C 5 5	0
2	I	1	Total C 12 12	0
2	I	1	Total C 9 9	0
2	I	1	Total C 9 9	0

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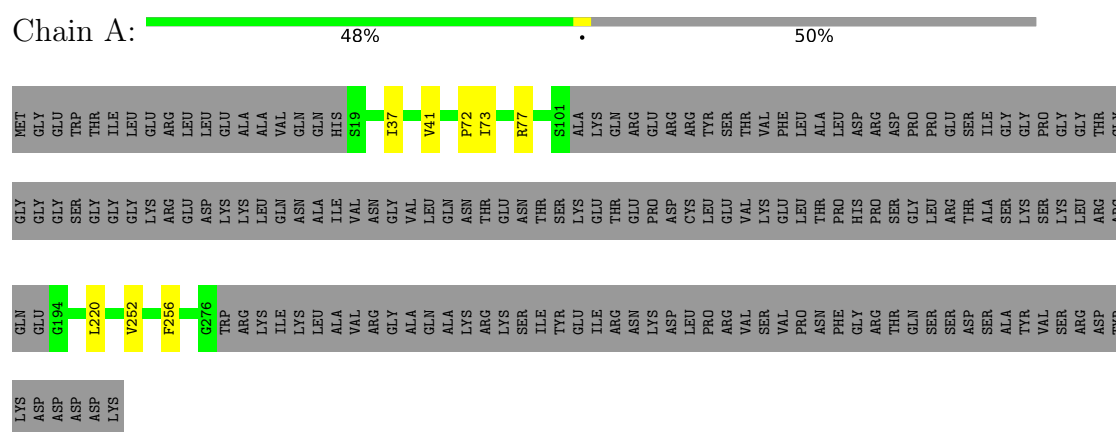
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Mol	Chain	Residues	Atoms	AltConf
2	I	1	Total C 5 5	0
2	J	1	Total C 12 12	0
2	J	1	Total C 9 9	0
2	J	1	Total C 9 9	0
2	J	1	Total C 5 5	0
2	K	1	Total C 12 12	0
2	K	1	Total C 9 9	0
2	K	1	Total C 9 9	0
2	K	1	Total C 5 5	0
2	L	1	Total C 12 12	0
2	L	1	Total C 9 9	0
2	L	1	Total C 9 9	0
2	L	1	Total C 5 5	0

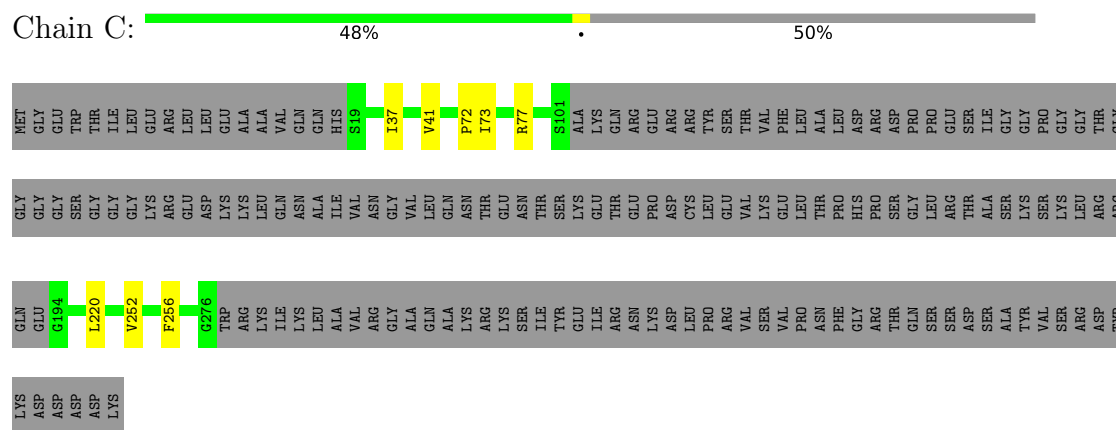
3 Residue-property plots

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.

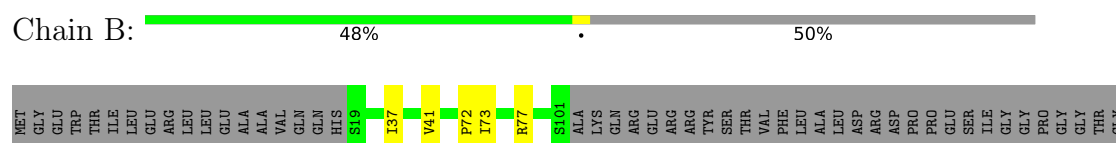
• Molecule 1: Gap junction delta-2 protein

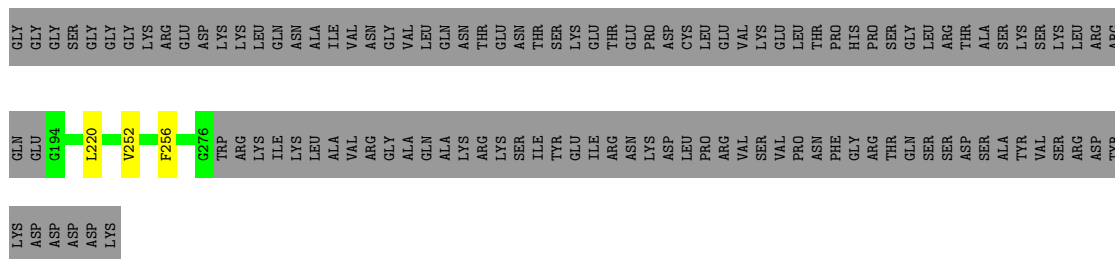


• Molecule 1: Gap junction delta-2 protein

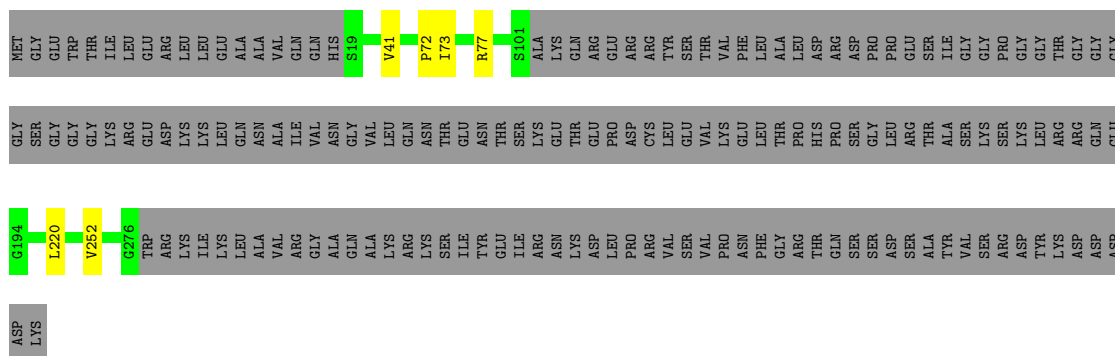


• Molecule 1: Gap junction delta-2 protein

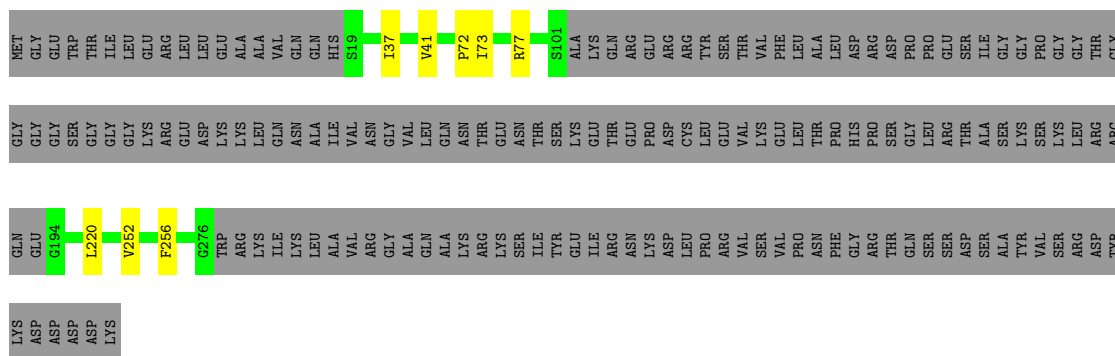




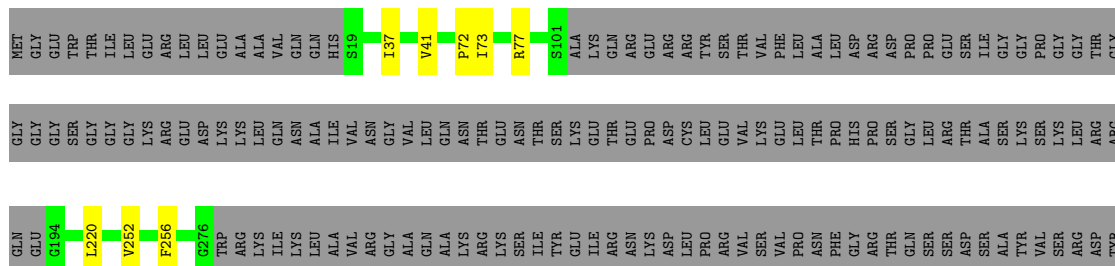
- Molecule 1: Gap junction delta-2 protein



- Molecule 1: Gap junction delta-2 protein



- Molecule 1: Gap junction delta-2 protein



LYS
ASP
ASP
ASP
ASP
LYS

• Molecule 1: Gap junction delta-2 protein



MET GLY GLU TRP THR ILE LEU GLU ARG ASP VAL GLN GLN HIS S19 V41 P72 I73 R77 S101 ALA LYS GLN ARG GLU PRO ARG ARG CYS ARG TYR SER THR VAL PHE LEU LEU ALA LEU ASP ARG ARG ASP PRO PRO GLU SER ILE GLY PRO GLY THR GLY GLY

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

G194 L220 V252 G276 TRP ARG ARG ILE LYS LEU ALA ALA ARG GLY ALA GLN ALA GLN VAL ASN VAL LEU ARG LYS SER ILE TYR GLU ILE ARG ASN LYS ASP LEU PRO ASP CYS VAL SER VAL PRO ASN PHE GLY THR ARG THR GLN SER ASP LEU TYR VAL SER ARG ASP

ASP
LYS

• Molecule 1: Gap junction delta-2 protein



MET GLY GLU TRP THR ILE LEU GLU ARG ASP VAL GLN GLN HIS S19 I37 V41 P72 I73 R77 S101 ALA LYS GLN ARG GLU PRO ARG ARG CYS ARG TYR SER THR VAL PHE LEU LEU ALA LEU ASP ARG ARG ASP PRO PRO GLU SER ILE GLY PRO GLY THR GLY GLY

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

GLN GLU G194 L220 V252 F256 G276 TRP ARG LYS ILE LYS LEU ALA ALA VAL ARG VAL ASN GLN ALA ALA LYS ARG THR SER TYR ILE TYR SER LYS ILE ARG GLN ASP PRO ARG VAL SER VAL ASN PHE GLY THR ARG GLN SER LEU SER ASP SER TYR VAL SER ARG TYR

LYS
ASP
ASP
ASP
ASP
LYS

• Molecule 1: Gap junction delta-2 protein



MET GLY GLU TRP THR ILE LEU GLU ARG ASP VAL GLN GLN HIS S19 I37 V41 P72 I73 R77 S101 ALA LYS GLN ARG GLU PRO ARG ARG CYS ARG TYR SER THR VAL PHE LEU LEU ALA LEU ASP ARG ARG ASP PRO PRO GLU SER ILE GLY PRO GLY THR GLY GLY

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

GLN GLU G194 L220 V252 F256 G276 TRP ARG LYS ILE LYS LEU ALA ALA VAL ARG VAL ASN GLN ALA ALA LYS ARG THR SER TYR ILE TYR SER LYS ILE ARG GLN ASP PRO ARG VAL SER VAL ASN PHE GLY THR ARG GLN SER LEU SER ASP SER TYR VAL SER ARG TYR

LYS
ASP
ASP
ASP
ASP
LYS

• Molecule 1: Gap junction delta-2 protein

LYS	GLN	GLY
ASP	GLU	GLY
ASP	G194	GLY
ASP	L220	SER
ASP	V252	GLY
LYS	F256	GLY
	K276	LYS
	TRP	ARG
	ARG	LYS
	LYS	LEU
	ILE	GLN
	LYS	ASN
	LEU	ALA
	ALA	ILE
	VAL	VAL
	ARG	ASN
	GLY	GLY
	ALA	VAL
	GLN	LEU
	ALA	GLN
	LYS	ASN
	ARG	THR
	LYS	GLU
	SER	ASN
	ILE	THR
	TYR	SER
	GLU	LYS
	ILE	GLU
	ARG	THR
	ASN	GLU
	LYS	PRO
	ASP	ASP
	LEU	CYS
	PRO	LEU
	ARG	GLU
	VAL	VAL
	SER	LYS
	VAL	GLU
	PRO	LEU
	PHE	THR
	ASN	THR
	GLY	HIS
	THR	PRO
	ARG	SER
	GLN	GLY
	SER	LEU
	SER	ARG
	ASP	THR
	SER	ALA
	ALA	SER
	TYR	LYS
	VAL	SER
	SER	LYS
	ARG	LEU
	THR	ARG
	TYR	ARG

Chain K: 48% 50%

Lys	GLN	GLY	Met
ASP	GLU	GLY	GLY
ASP	G194	GLY	GLY
ASP	L220	SER	TRP
ASP		GLY	ILE
Lys	V252	GLY	LEU
	F256	LYS	LEU
	G276	ARG	LEU
		ASP	LEU
		LYS	GLU
		LYS	ALA
		LEU	ALA
		GLN	VAL
		ASN	GLN
		THR	ASN
		GLY	THR
		ALA	GLU
		ALA	VAL
		GLN	LEU
		LYS	GLN
		ARG	ASN
		LYS	THR
		SER	GLU
		ILE	ASN
		TTR	THR
		GLU	SER
		ILE	LYS
		ARG	LYS
		ASN	GLN
		LYS	ARG
		ASP	GLU
		LEU	ARG
		PRO	ARG
		VAL	TYR
		SER	THR
		VAL	VAL
		PRO	VAL
		ASN	THR
		PHE	ALA
		GLY	LEU
		ARG	ASP
		THR	ASP
		GLN	PRO
		SER	PRO
		SER	GLU
		THR	THR
		SER	ILE
		ALA	GLY
		SER	PRO
		LYS	PRO
		LYS	GLY
		LEU	GLY
		ARG	THR
		ARG	GLY

Chain L: 48% . 50%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	177311	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 ($e^-/\text{\AA}^2$)	34.41	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0015	Depositor
Map size (Å)	250.2, 250.2, 250.2	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MC3

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	0/1362	0.30	0/1852
1	B	0.13	0/1362	0.30	0/1852
1	C	0.13	0/1362	0.30	0/1852
1	D	0.13	0/1362	0.30	0/1852
1	E	0.13	0/1362	0.30	0/1852
1	F	0.13	0/1362	0.30	0/1852
1	G	0.13	0/1362	0.29	0/1852
1	H	0.13	0/1362	0.30	0/1852
1	I	0.13	0/1362	0.30	0/1852
1	J	0.13	0/1362	0.30	0/1852
1	K	0.13	0/1362	0.30	0/1852
1	L	0.13	0/1362	0.30	0/1852
All	All	0.13	0/16344	0.30	0/22224

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

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	1330	1334	1333	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1330	1334	1333	21	0
1	C	1330	1334	1333	21	0
1	D	1330	1334	1333	21	0
1	E	1330	1334	1333	22	0
1	F	1330	1334	1333	22	0
1	G	1330	1334	1333	21	0
1	H	1330	1334	1333	22	0
1	I	1330	1334	1333	22	0
1	J	1330	1334	1333	21	0
1	K	1330	1334	1333	21	0
1	L	1330	1334	1333	21	0
2	A	35	0	57	18	0
2	B	35	0	57	18	0
2	C	35	0	57	18	0
2	D	35	0	57	19	0
2	E	35	0	57	19	0
2	F	35	0	57	19	0
2	G	35	0	57	19	0
2	H	35	0	57	19	0
2	I	35	0	57	19	0
2	J	35	0	57	18	0
2	K	35	0	57	18	0
2	L	35	0	57	18	0
All	All	16380	16008	16680	244	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 7.

The worst 5 of 244 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:73:ILE:CD1	2:E:401:MC3:C37	2.08	1.32
1:H:73:ILE:CD1	2:H:401:MC3:C37	2.08	1.32
1:A:73:ILE:CD1	2:A:401:MC3:C37	2.08	1.31
1:B:73:ILE:CD1	2:B:401:MC3:C37	2.08	1.31
1:J:73:ILE:CD1	2:J:401:MC3:C37	2.08	1.31

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	B	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	C	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	D	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	E	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	F	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	G	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	H	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	I	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	J	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	K	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
1	L	162/331 (49%)	160 (99%)	2 (1%)	0	100	100
All	All	1944/3972 (49%)	1920 (99%)	24 (1%)	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	150/289 (52%)	150 (100%)	0	100	100
1	B	150/289 (52%)	150 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	150/289 (52%)	150 (100%)	0	100	100
1	D	150/289 (52%)	150 (100%)	0	100	100
1	E	150/289 (52%)	150 (100%)	0	100	100
1	F	150/289 (52%)	150 (100%)	0	100	100
1	G	150/289 (52%)	150 (100%)	0	100	100
1	H	150/289 (52%)	150 (100%)	0	100	100
1	I	150/289 (52%)	150 (100%)	0	100	100
1	J	150/289 (52%)	150 (100%)	0	100	100
1	K	150/289 (52%)	150 (100%)	0	100	100
1	L	150/289 (52%)	150 (100%)	0	100	100
All	All	1800/3468 (52%)	1800 (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. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	75	HIS
1	G	75	HIS

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](#)

48 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	MC3	D	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	D	404	-	4,4,45	0.28	0	3,3,53	0.42	0
2	MC3	A	404	-	4,4,45	0.28	0	3,3,53	0.43	0
2	MC3	B	402	-	8,8,45	0.17	0	7,7,53	0.66	0
2	MC3	I	403	-	8,8,45	0.18	0	7,7,53	0.62	0
2	MC3	A	402	-	8,8,45	0.16	0	7,7,53	0.66	0
2	MC3	B	404	-	4,4,45	0.29	0	3,3,53	0.42	0
2	MC3	C	404	-	4,4,45	0.28	0	3,3,53	0.42	0
2	MC3	C	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	B	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	J	403	-	8,8,45	0.18	0	7,7,53	0.62	0
2	MC3	F	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	G	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	D	402	-	8,8,45	0.17	0	7,7,53	0.66	0
2	MC3	L	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	I	404	-	4,4,45	0.29	0	3,3,53	0.43	0
2	MC3	C	402	-	8,8,45	0.16	0	7,7,53	0.67	0
2	MC3	H	404	-	4,4,45	0.28	0	3,3,53	0.42	0
2	MC3	H	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	J	404	-	4,4,45	0.29	0	3,3,53	0.43	0
2	MC3	L	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	L	404	-	4,4,45	0.28	0	3,3,53	0.42	0
2	MC3	B	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	K	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	E	402	-	8,8,45	0.17	0	7,7,53	0.67	0
2	MC3	K	402	-	8,8,45	0.17	0	7,7,53	0.66	0
2	MC3	D	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	E	403	-	8,8,45	0.18	0	7,7,53	0.62	0
2	MC3	F	404	-	4,4,45	0.29	0	3,3,53	0.43	0
2	MC3	F	402	-	8,8,45	0.17	0	7,7,53	0.66	0
2	MC3	G	404	-	4,4,45	0.28	0	3,3,53	0.42	0
2	MC3	H	402	-	8,8,45	0.17	0	7,7,53	0.66	0
2	MC3	G	402	-	8,8,45	0.17	0	7,7,53	0.66	0
2	MC3	I	402	-	8,8,45	0.16	0	7,7,53	0.66	0
2	MC3	E	404	-	4,4,45	0.29	0	3,3,53	0.42	0
2	MC3	H	403	-	8,8,45	0.18	0	7,7,53	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	K	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	L	402	-	8,8,45	0.16	0	7,7,53	0.66	0
2	MC3	E	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	I	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	J	402	-	8,8,45	0.16	0	7,7,53	0.66	0
2	MC3	F	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	K	404	-	4,4,45	0.28	0	3,3,53	0.42	0
2	MC3	G	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	A	403	-	8,8,45	0.19	0	7,7,53	0.62	0
2	MC3	C	403	-	8,8,45	0.18	0	7,7,53	0.62	0
2	MC3	J	401	-	11,11,45	0.20	0	10,10,53	0.60	0
2	MC3	A	401	-	11,11,45	0.20	0	10,10,53	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	D	401	-	-	1/9/9/49	-
2	MC3	D	404	-	-	0/2/2/49	-
2	MC3	A	404	-	-	0/2/2/49	-
2	MC3	B	402	-	-	0/6/6/49	-
2	MC3	I	403	-	-	0/6/6/49	-
2	MC3	A	402	-	-	0/6/6/49	-
2	MC3	B	404	-	-	0/2/2/49	-
2	MC3	C	404	-	-	0/2/2/49	-
2	MC3	C	401	-	-	1/9/9/49	-
2	MC3	B	401	-	-	1/9/9/49	-
2	MC3	J	403	-	-	0/6/6/49	-
2	MC3	F	403	-	-	0/6/6/49	-
2	MC3	G	401	-	-	1/9/9/49	-
2	MC3	D	402	-	-	0/6/6/49	-
2	MC3	L	401	-	-	1/9/9/49	-
2	MC3	I	404	-	-	0/2/2/49	-
2	MC3	C	402	-	-	0/6/6/49	-
2	MC3	H	404	-	-	0/2/2/49	-
2	MC3	H	401	-	-	1/9/9/49	-
2	MC3	J	404	-	-	0/2/2/49	-
2	MC3	L	403	-	-	0/6/6/49	-
2	MC3	L	404	-	-	0/2/2/49	-
2	MC3	B	403	-	-	0/6/6/49	-
2	MC3	K	403	-	-	0/6/6/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	E	402	-	-	0/6/6/49	-
2	MC3	K	402	-	-	0/6/6/49	-
2	MC3	D	403	-	-	0/6/6/49	-
2	MC3	E	403	-	-	0/6/6/49	-
2	MC3	F	404	-	-	0/2/2/49	-
2	MC3	F	402	-	-	0/6/6/49	-
2	MC3	G	404	-	-	0/2/2/49	-
2	MC3	H	402	-	-	0/6/6/49	-
2	MC3	G	402	-	-	0/6/6/49	-
2	MC3	I	402	-	-	0/6/6/49	-
2	MC3	E	404	-	-	0/2/2/49	-
2	MC3	H	403	-	-	0/6/6/49	-
2	MC3	K	401	-	-	1/9/9/49	-
2	MC3	L	402	-	-	0/6/6/49	-
2	MC3	E	401	-	-	1/9/9/49	-
2	MC3	I	401	-	-	1/9/9/49	-
2	MC3	J	402	-	-	0/6/6/49	-
2	MC3	F	401	-	-	1/9/9/49	-
2	MC3	K	404	-	-	0/2/2/49	-
2	MC3	G	403	-	-	0/6/6/49	-
2	MC3	A	403	-	-	0/6/6/49	-
2	MC3	C	403	-	-	0/6/6/49	-
2	MC3	J	401	-	-	1/9/9/49	-
2	MC3	A	401	-	-	1/9/9/49	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	401	MC3	C39-C40-C41-C42
2	I	401	MC3	C39-C40-C41-C42
2	B	401	MC3	C39-C40-C41-C42
2	H	401	MC3	C39-C40-C41-C42
2	A	401	MC3	C39-C40-C41-C42

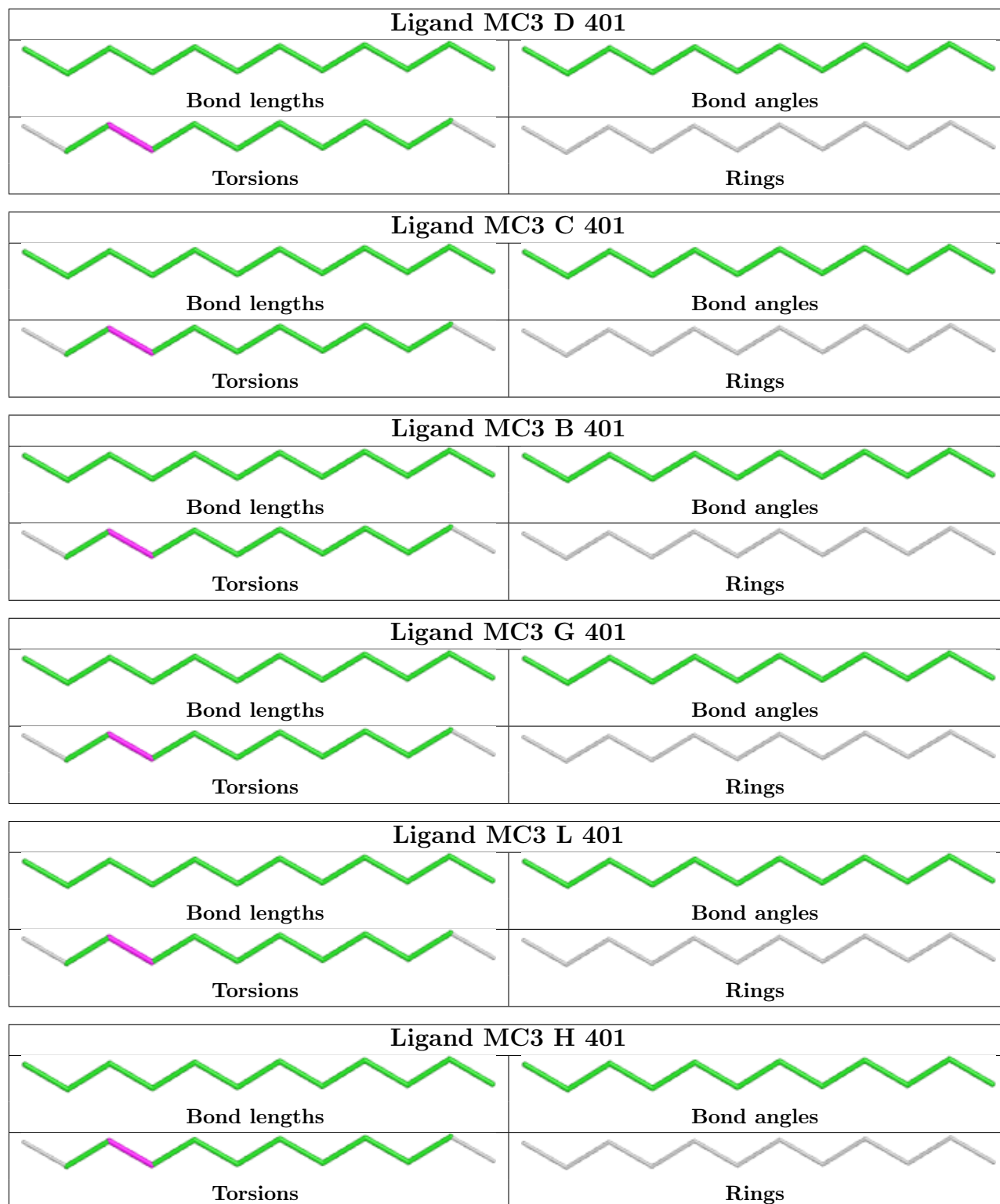
There are no ring outliers.

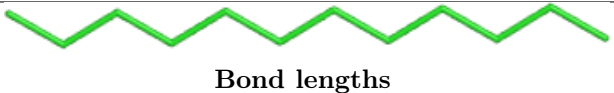
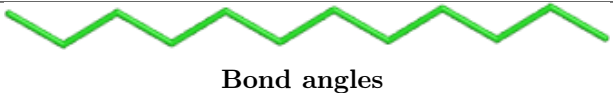
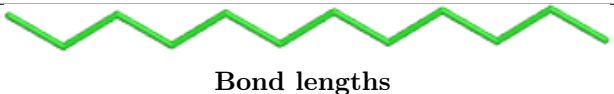
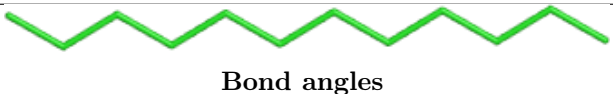
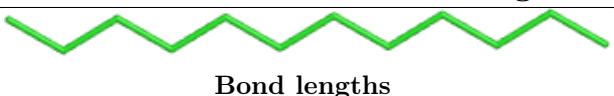
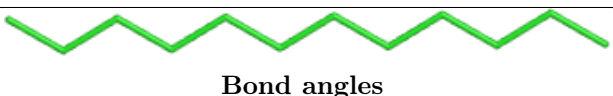
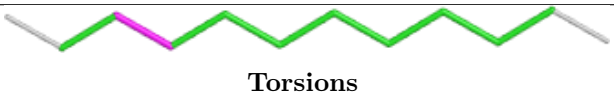
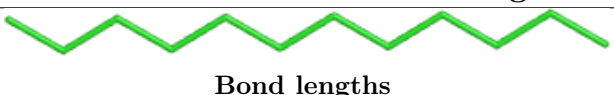
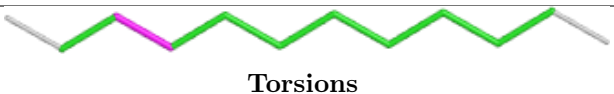
36 monomers are involved in 222 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	MC3	12	0
2	B	402	MC3	4	0
2	I	403	MC3	3	0
2	A	402	MC3	4	0
2	C	401	MC3	11	0
2	B	401	MC3	11	0
2	J	403	MC3	3	0
2	F	403	MC3	3	0
2	G	401	MC3	12	0
2	D	402	MC3	4	0
2	L	401	MC3	11	0
2	C	402	MC3	4	0
2	H	401	MC3	12	0
2	L	403	MC3	3	0
2	B	403	MC3	3	0
2	K	403	MC3	3	0
2	E	402	MC3	4	0
2	K	402	MC3	4	0
2	D	403	MC3	3	0
2	E	403	MC3	3	0
2	F	402	MC3	4	0
2	H	402	MC3	4	0
2	G	402	MC3	4	0
2	I	402	MC3	4	0
2	H	403	MC3	3	0
2	K	401	MC3	11	0
2	L	402	MC3	4	0
2	E	401	MC3	12	0
2	I	401	MC3	12	0
2	J	402	MC3	4	0
2	F	401	MC3	12	0
2	G	403	MC3	3	0
2	A	403	MC3	3	0
2	C	403	MC3	3	0
2	J	401	MC3	11	0
2	A	401	MC3	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



Ligand MC3 K 401			
 Bond lengths		 Bond angles	
 Torsions		 Rings	
Ligand MC3 E 401			
 Bond lengths		 Bond angles	
 Torsions		 Rings	
Ligand MC3 I 401			
 Bond lengths		 Bond angles	
 Torsions		 Rings	
Ligand MC3 F 401			
 Bond lengths		 Bond angles	
 Torsions		 Rings	
Ligand MC3 J 401			
 Bond lengths		 Bond angles	
 Torsions		 Rings	
Ligand MC3 A 401			
 Bond lengths		 Bond angles	
 Torsions		 Rings	

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

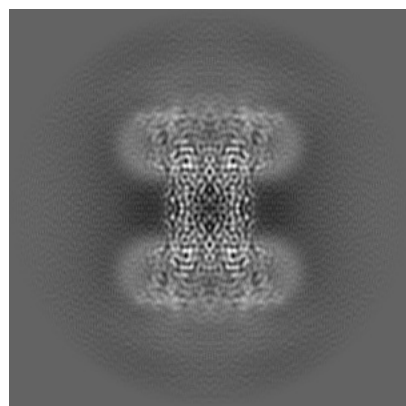
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38319. These allow visual inspection of the internal detail of the map and identification of artifacts.

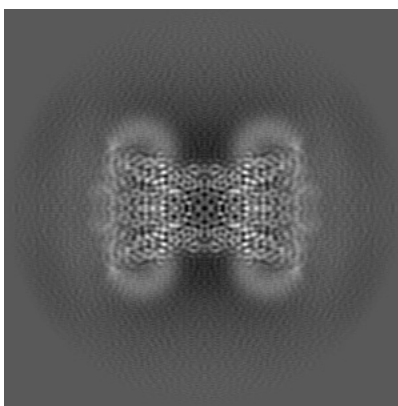
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

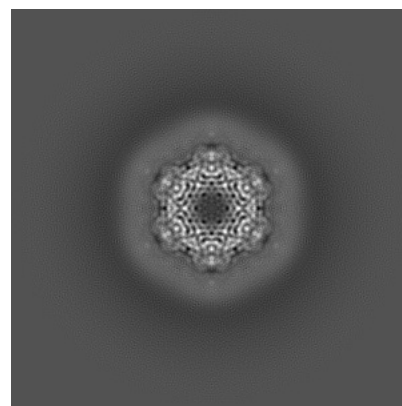
6.1.1 Primary map



X

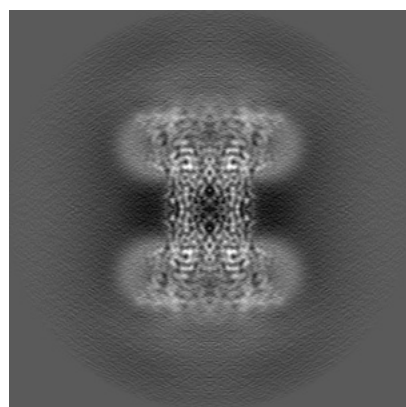


Y

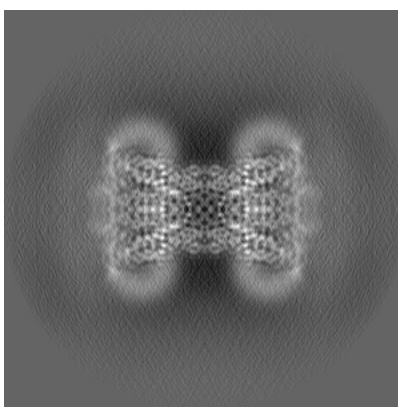


Z

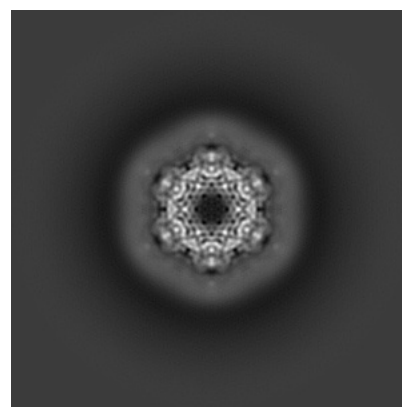
6.1.2 Raw map



X



Y

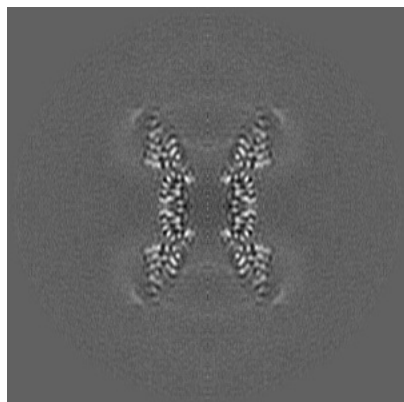


Z

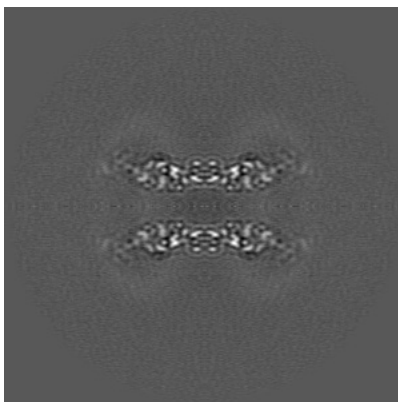
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

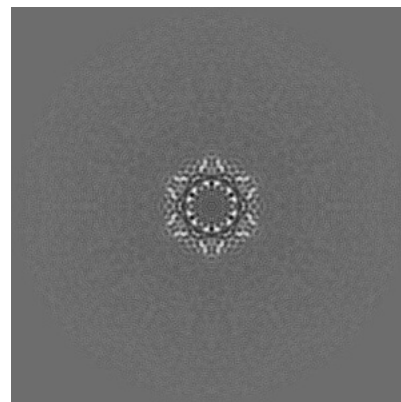
6.2.1 Primary map



X Index: 150

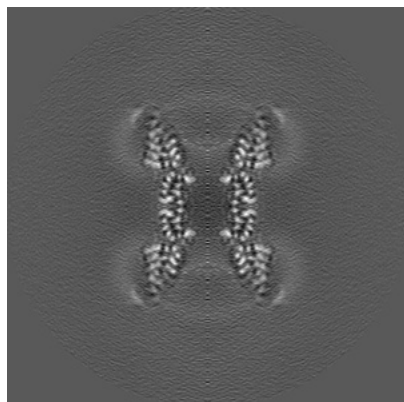


Y Index: 150

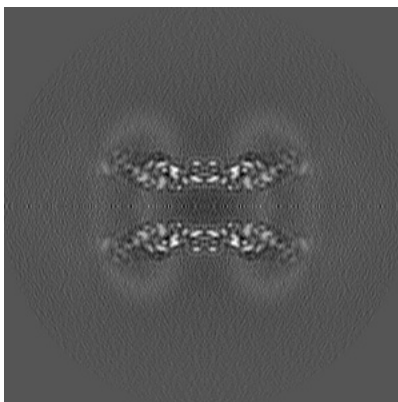


Z Index: 150

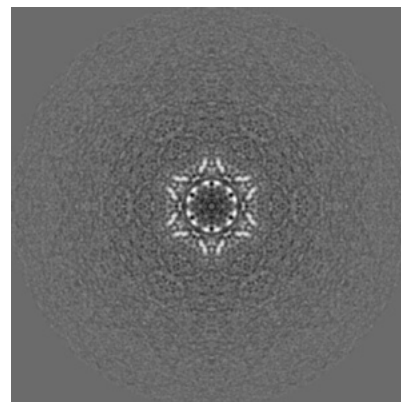
6.2.2 Raw map



X Index: 150



Y Index: 150

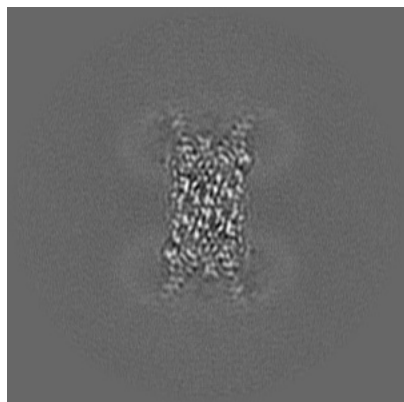


Z Index: 150

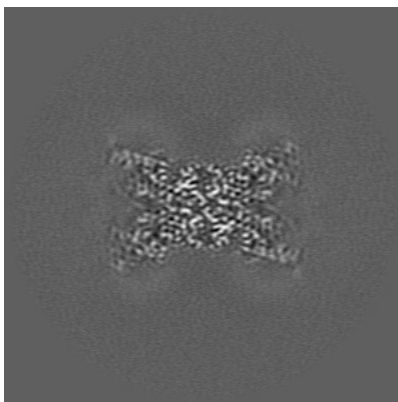
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

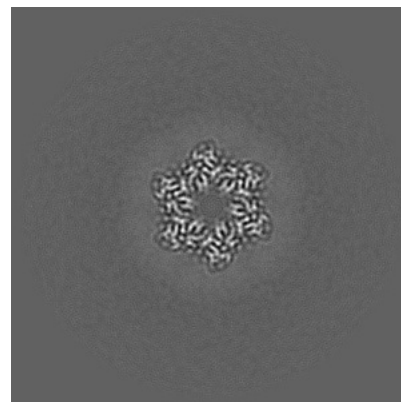
6.3.1 Primary map



X Index: 170

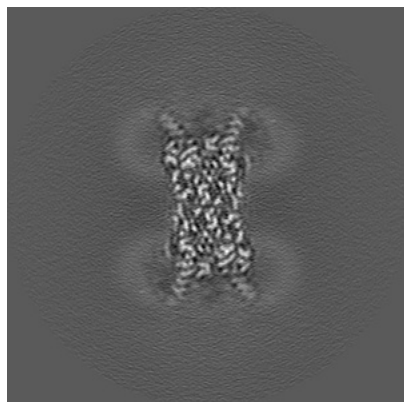


Y Index: 132

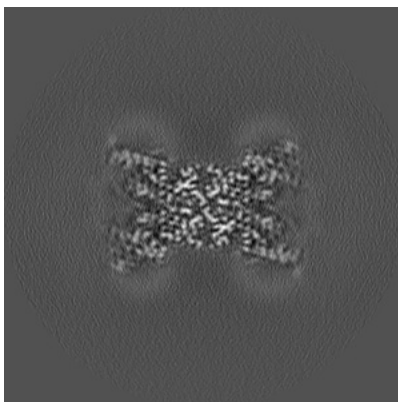


Z Index: 181

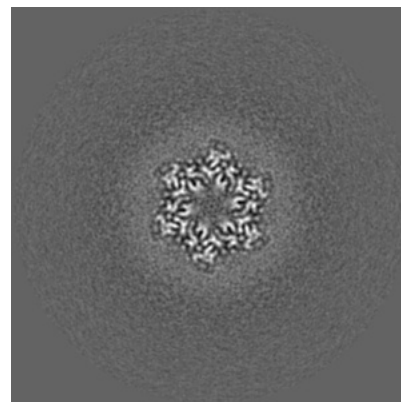
6.3.2 Raw map



X Index: 129



Y Index: 132

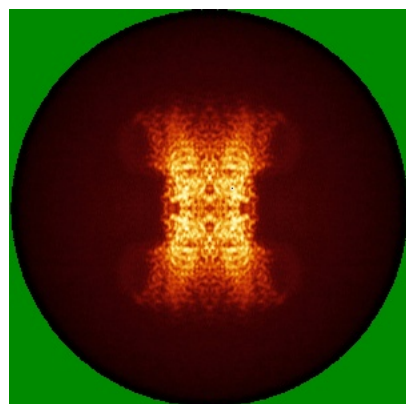


Z Index: 119

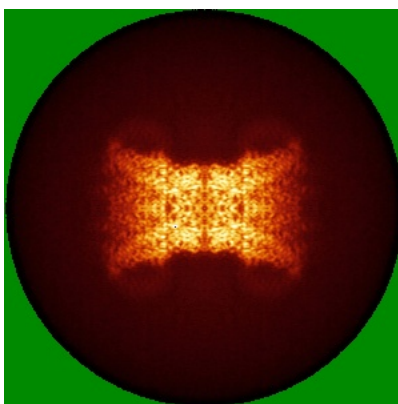
The images above show the largest variance slices of the map in three orthogonal directions.

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

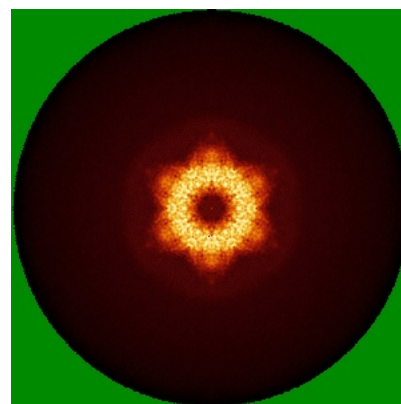
6.4.1 Primary map



X

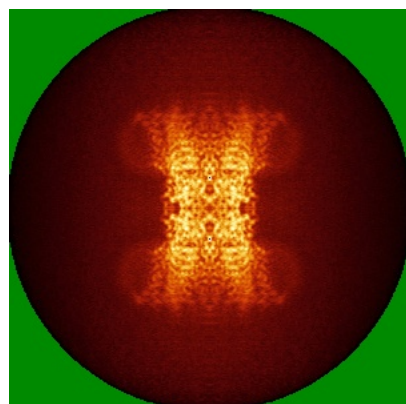


Y

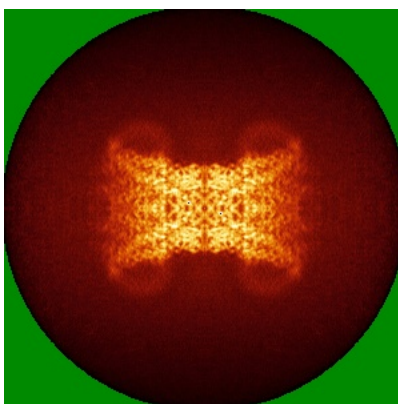


Z

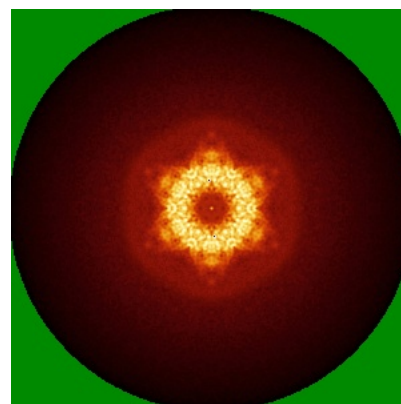
6.4.2 Raw map



X



Y

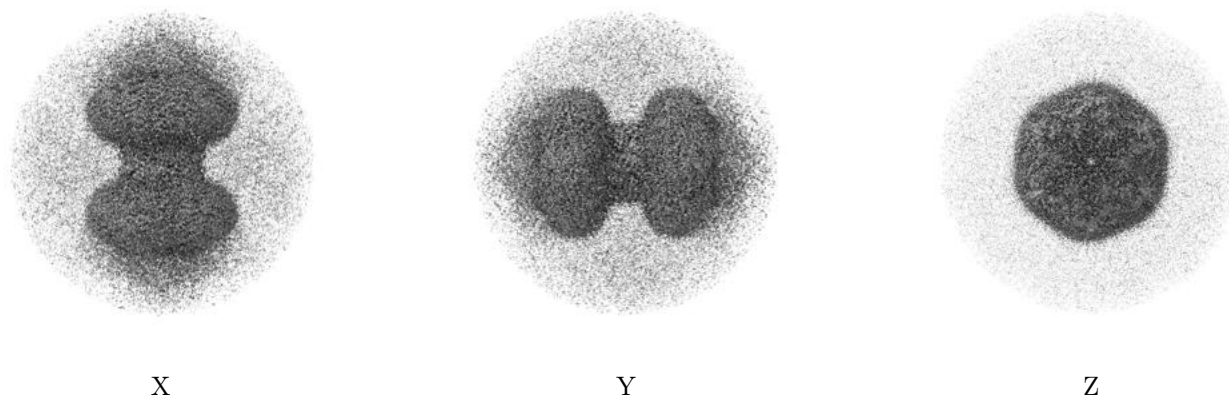


Z

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.

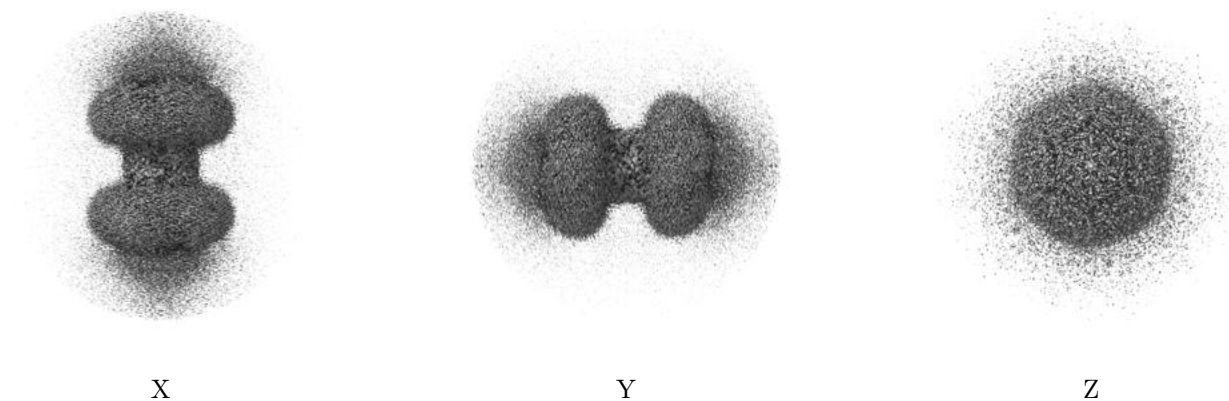
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0015. 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.

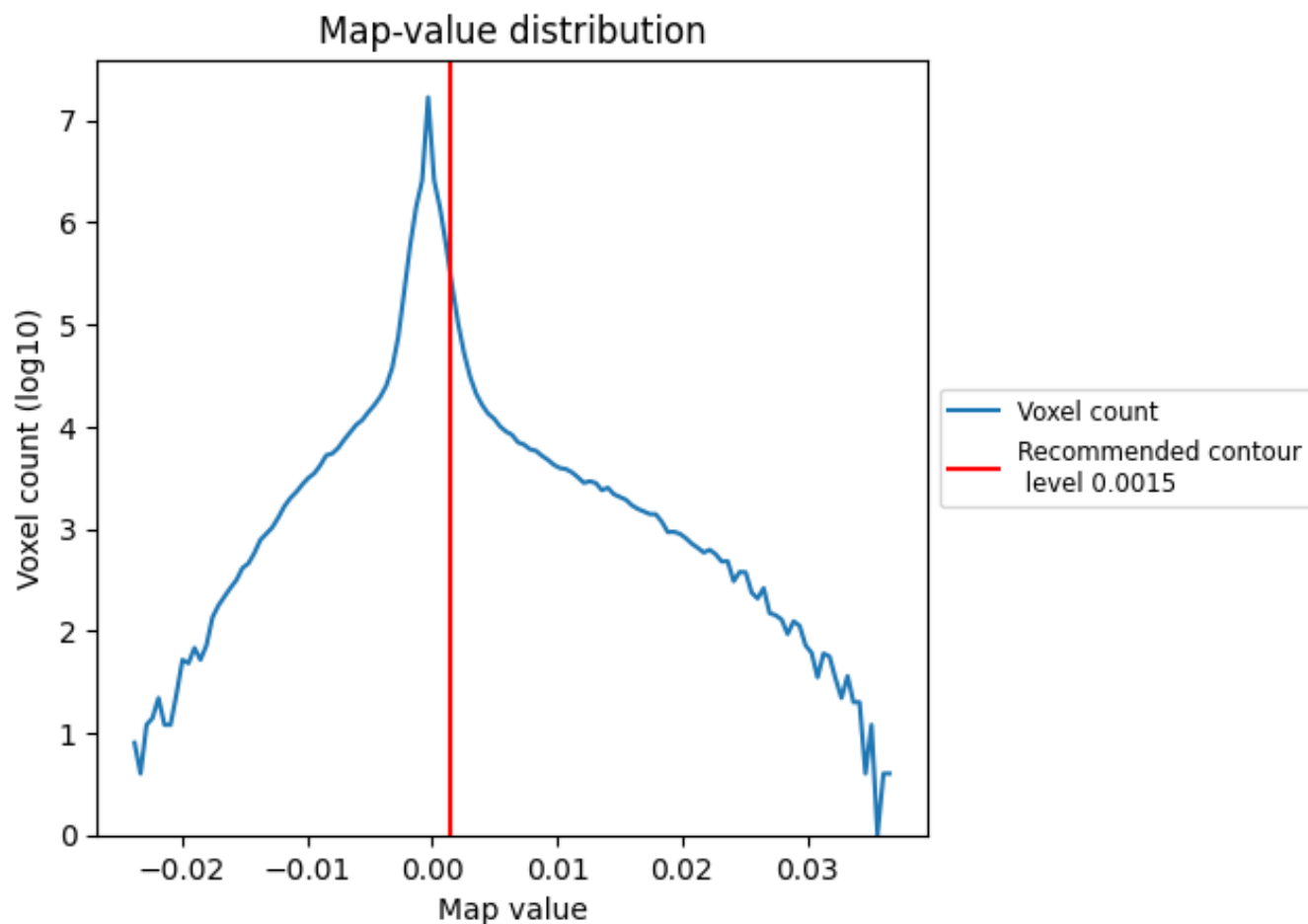
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

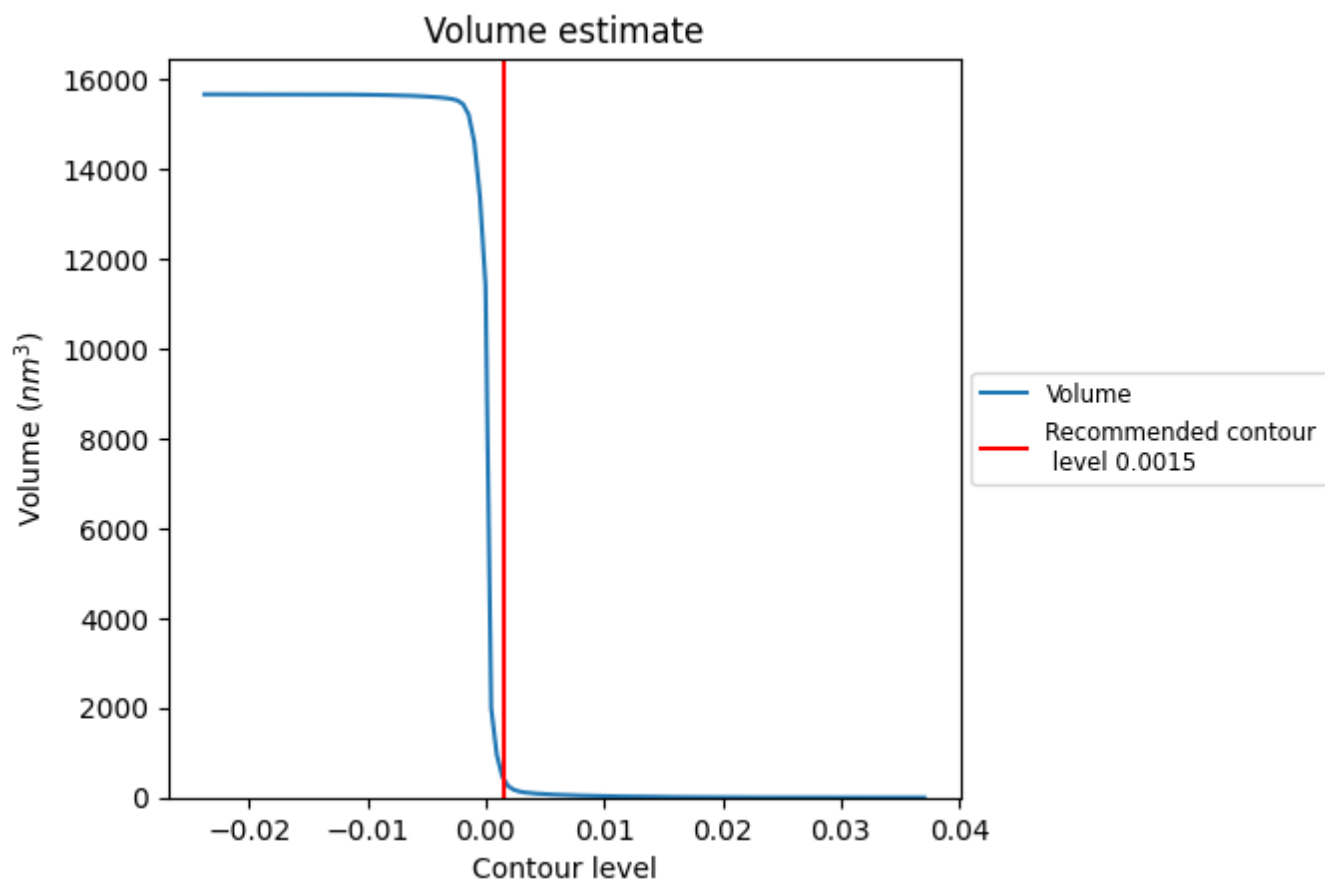
This section contains the results of statistical analysis of the map.

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.

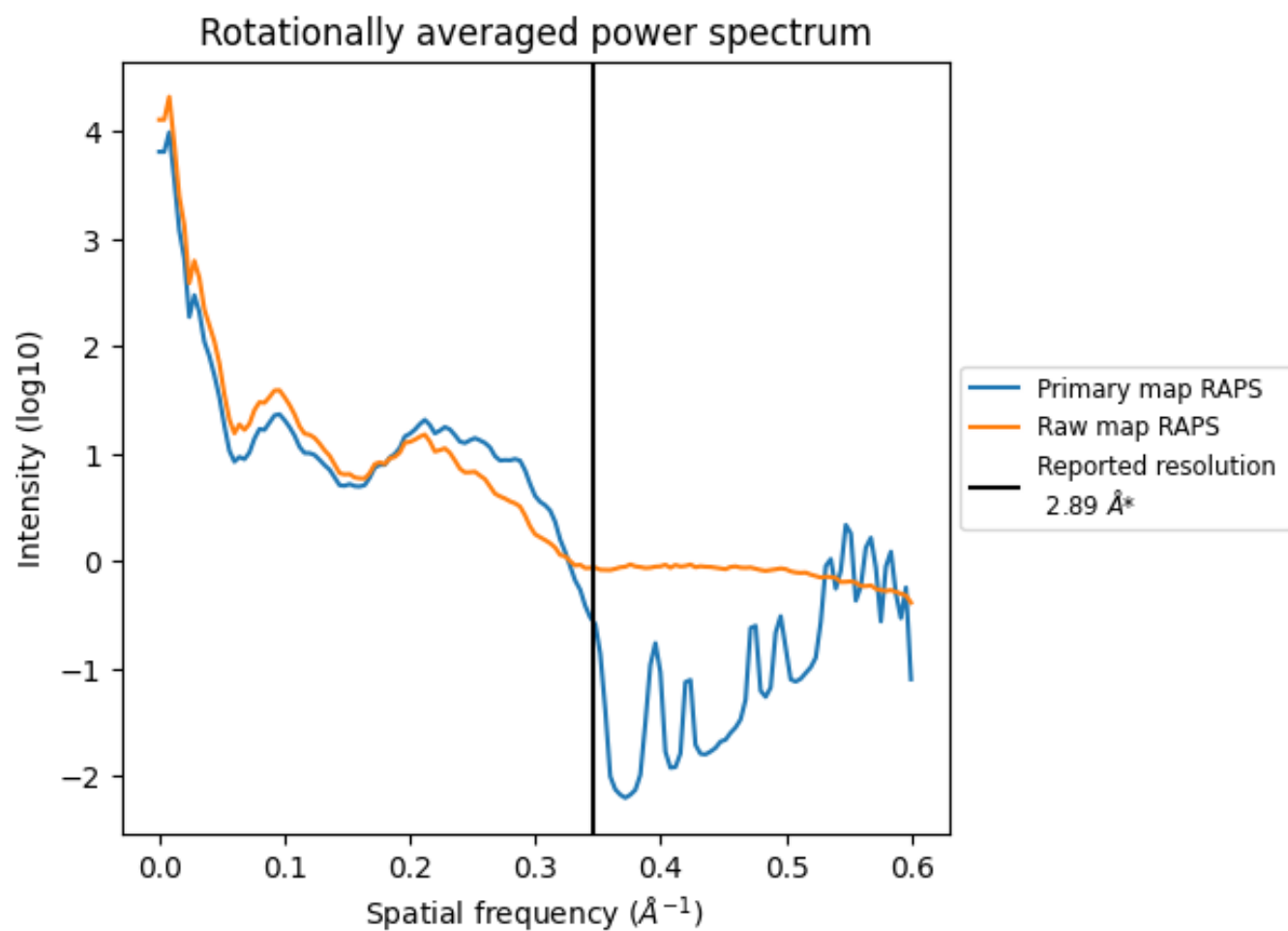
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 422 nm^3 ; this corresponds to an approximate mass of 381 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 ⓘ

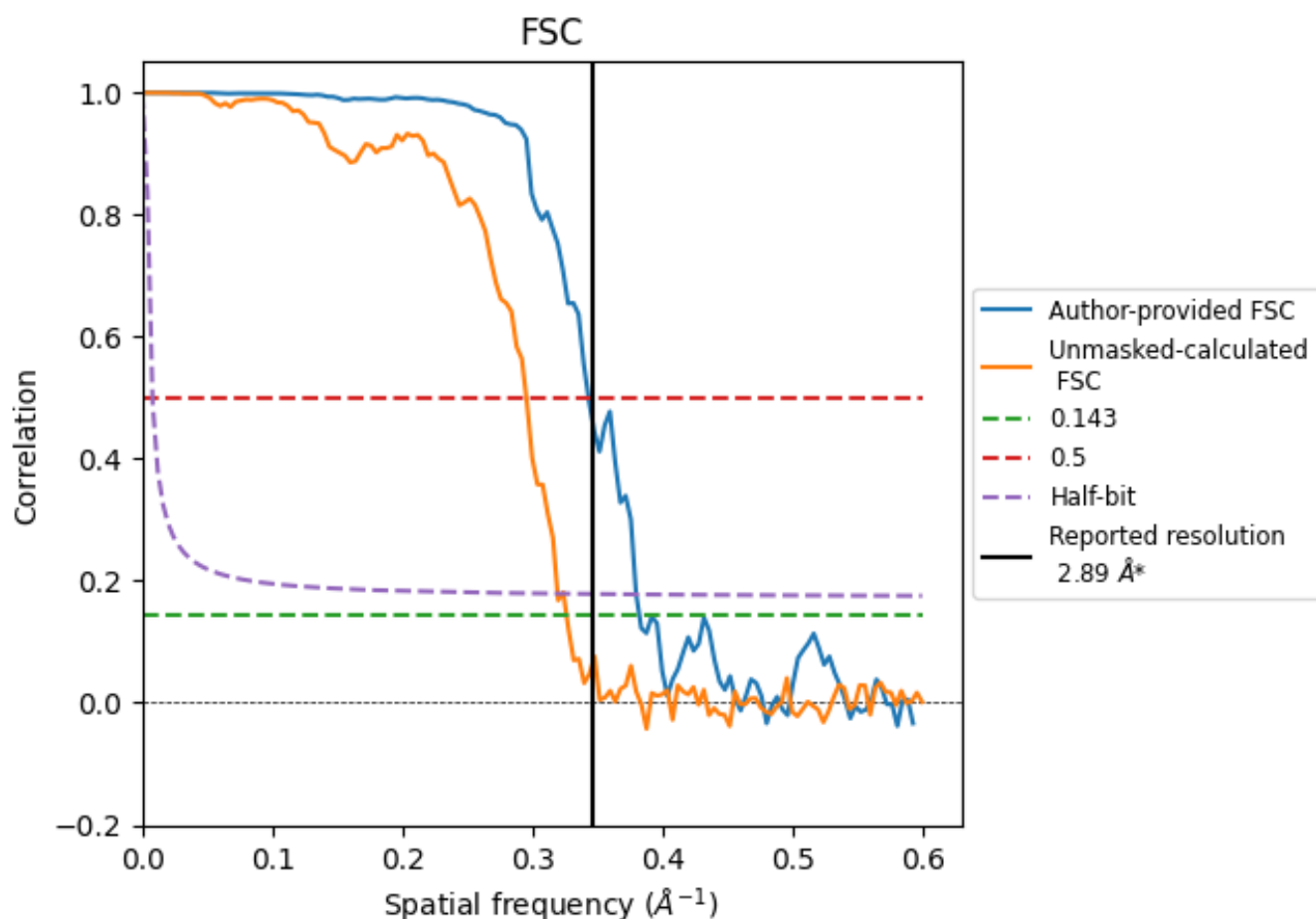


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

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 0.346 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

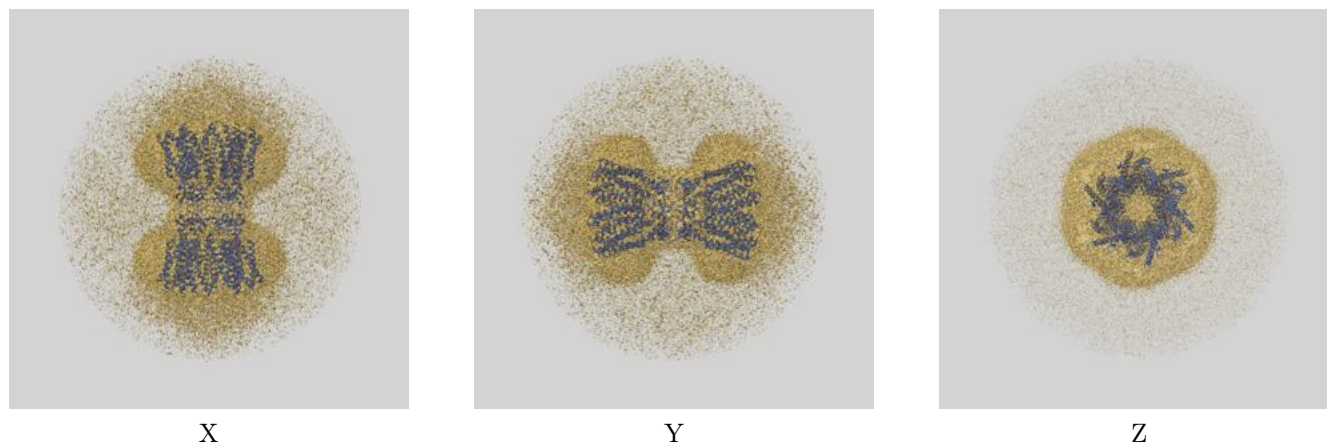
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.62	2.92	2.63
Unmasked-calculated*	3.07	3.39	3.13

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

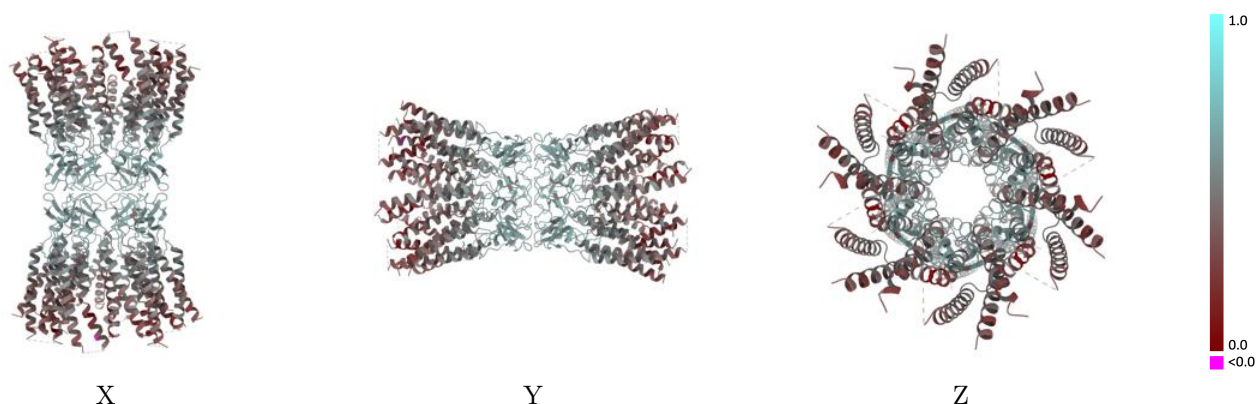
This section contains information regarding the fit between EMDB map EMD-38319 and PDB model 8XGE. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



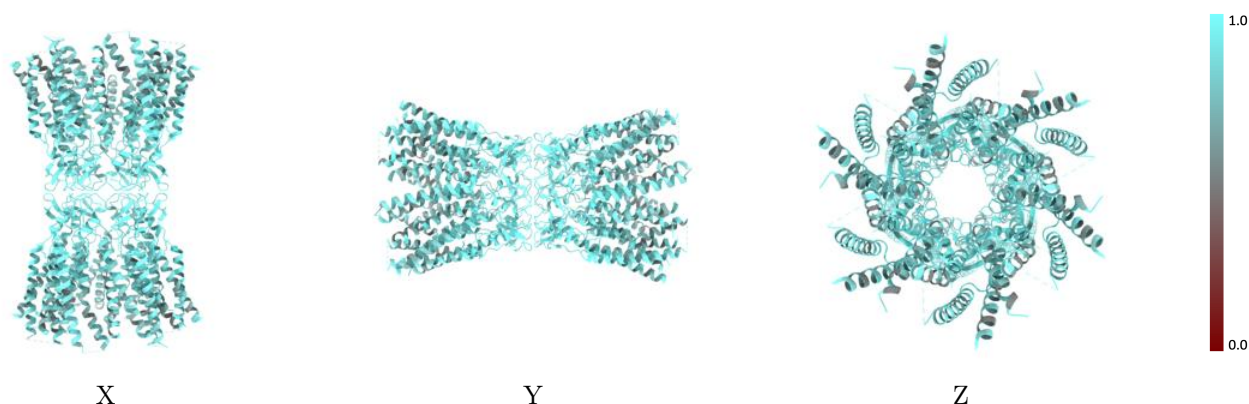
The images above show the 3D surface view of the map at the recommended contour level 0.0015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



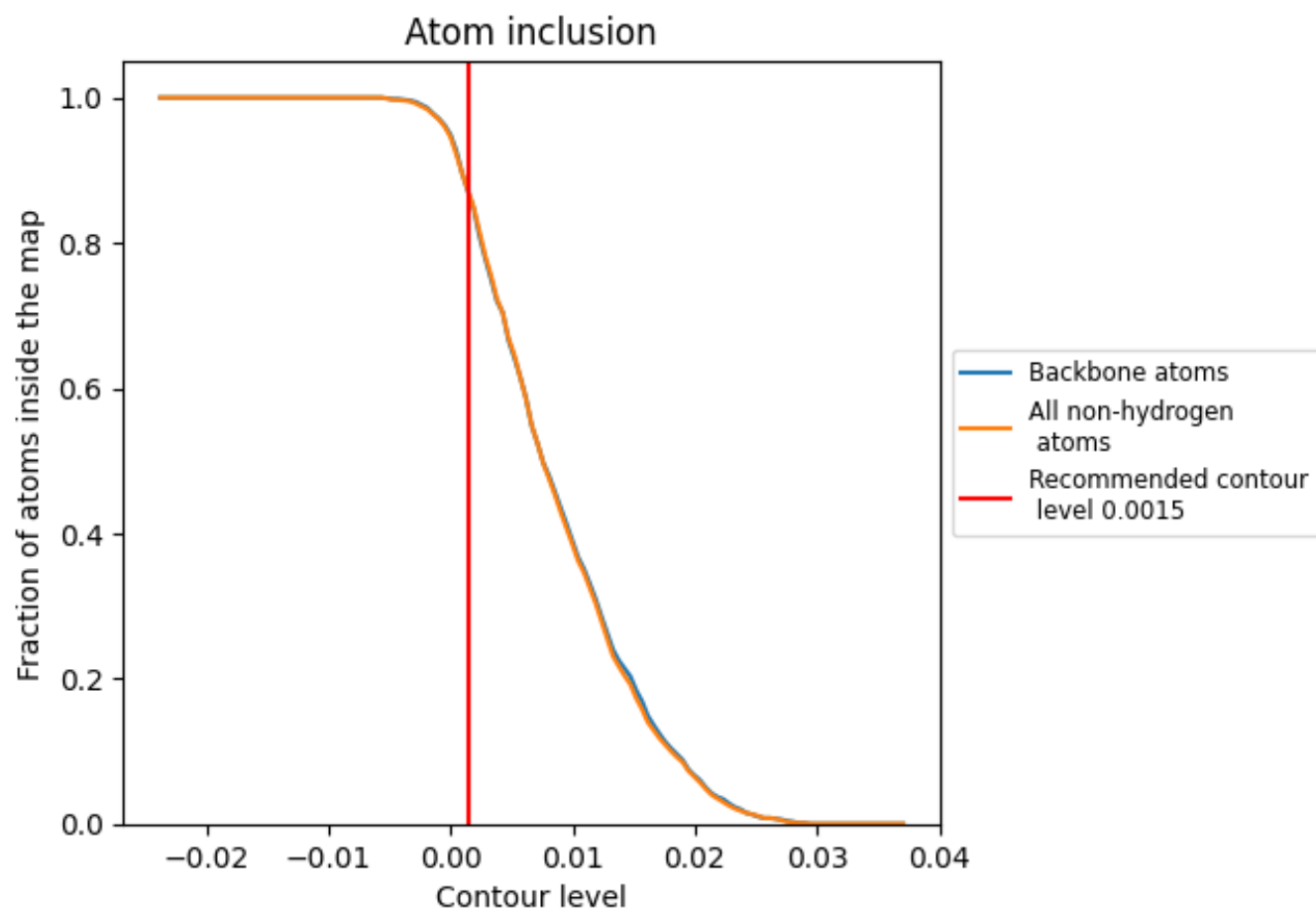
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% 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 (0.0015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8680	0.4620
A	0.8710	0.4590
B	0.8740	0.4570
C	0.8760	0.4620
D	0.8740	0.4590
E	0.8740	0.4570
F	0.8750	0.4580
G	0.8740	0.4680
H	0.8750	0.4680
I	0.8750	0.4680
J	0.8710	0.4620
K	0.8750	0.4570
L	0.8760	0.4650

1.0

0.0

<0.0