



## wwPDB EM Validation Summary Report ⓘ

Nov 23, 2022 – 02:01 AM JST

PDB ID : 7F92  
EMDB ID : EMD-31495  
Title : Structure of connexin43/Cx43/GJA1 gap junction intercellular channel in LMNG/CHS detergents at pH 8.0  
Authors : Lee, H.J.; Cha, H.J.; Jeong, H.; Lee, S.N.; Lee, C.W.; Woo, J.S.  
Deposited on : 2021-07-03  
Resolution : 3.10 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

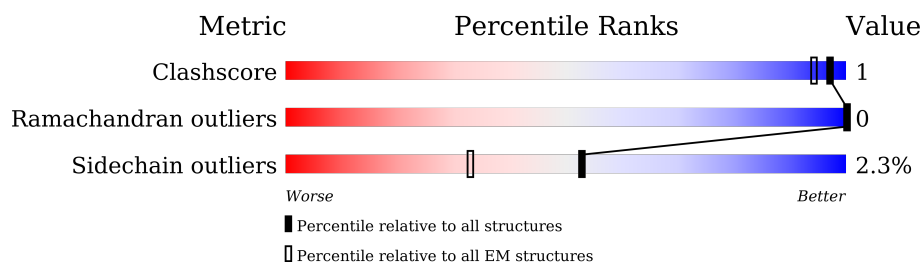
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	B	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	C	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	D	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	E	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	F	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	G	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>
1	H	382	<div> <div>7%</div> <div>49%</div> <div>49%</div> </div>

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Mol	Chain	Length	Quality of chain
1	I	382	
1	J	382	
1	K	382	
1	L	382	

## 2 Entry composition

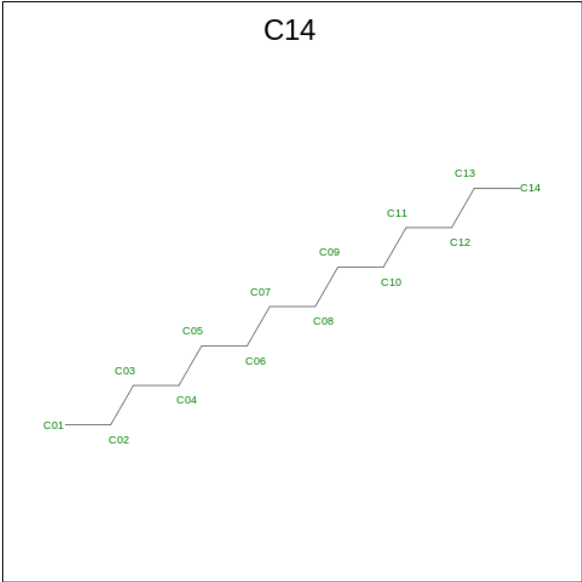
There are 3 unique types of molecules in this entry. The entry contains 21240 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Gap junction alpha-1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	B	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	C	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	D	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	E	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	F	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	G	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	H	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	I	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	J	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	K	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		
1	L	196	Total	C	N	O	S	0	0
			1594	1065	254	267	8		

- Molecule 2 is TETRADECANE (three-letter code: C14) (formula: C<sub>14</sub>H<sub>30</sub>).



Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	A	1	Total	C	0
			154	154	
2	B	1	Total	C	0
			154	154	
2	B	1	Total	C	0
			154	154	
2	B	1	Total	C	0
			154	154	

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Mol	Chain	Residues	Atoms	AltConf
2	B	1	Total C 154 154	0
2	B	1	Total C 154 154	0
2	B	1	Total C 154 154	0
2	B	1	Total C 154 154	0
2	B	1	Total C 154 154	0
2	B	1	Total C 154 154	0
2	B	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	C	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0

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Mol	Chain	Residues	Atoms	AltConf
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	D	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	E	1	Total C 154 154	0
2	F	1	Total C 154 154	0

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Mol	Chain	Residues	Atoms	AltConf
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	F	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0
2	G	1	Total C 154 154	0

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Mol	Chain	Residues	Atoms	AltConf
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	H	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0
2	I	1	Total C 154 154	0

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Mol	Chain	Residues	Atoms	AltConf
2	I	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	J	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0

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Mol	Chain	Residues	Atoms	AltConf
2	K	1	Total C 154 154	0
2	K	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0
2	L	1	Total C 154 154	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	AltConf
3	A	22	Total O 22 22	0
3	B	21	Total O 21 21	0
3	C	23	Total O 23 23	0
3	D	22	Total O 22 22	0
3	E	21	Total O 21 21	0
3	F	23	Total O 23 23	0

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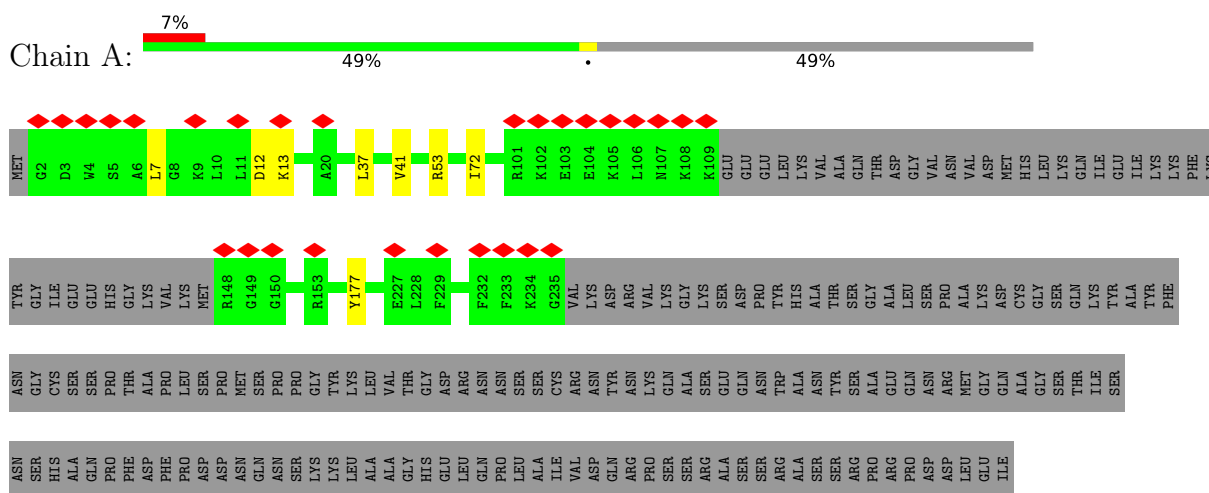
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Mol	Chain	Residues	Atoms		AltConf
3	G	23	Total 23	O 23	0
3	H	22	Total 22	O 22	0
3	I	21	Total 21	O 21	0
3	J	23	Total 23	O 23	0
3	K	22	Total 22	O 22	0
3	L	21	Total 21	O 21	0

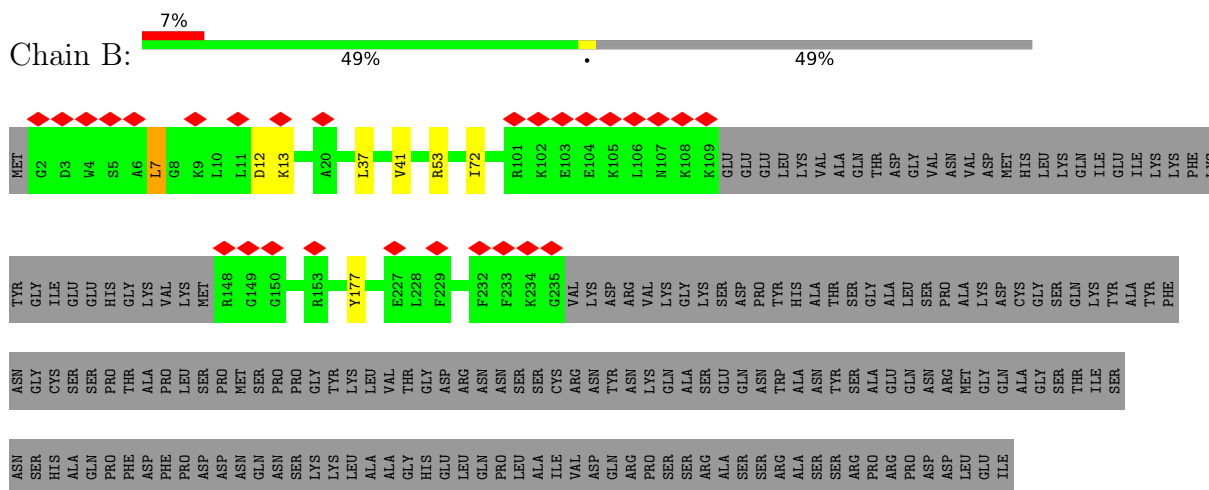
### 3 Residue-property plots [i](#)

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 alpha-1 protein

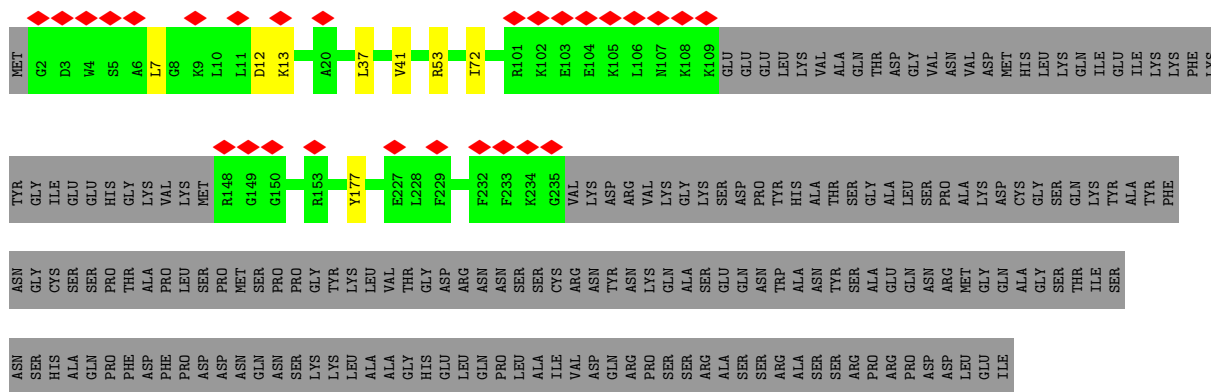


#### • Molecule 1: Gap junction alpha-1 protein

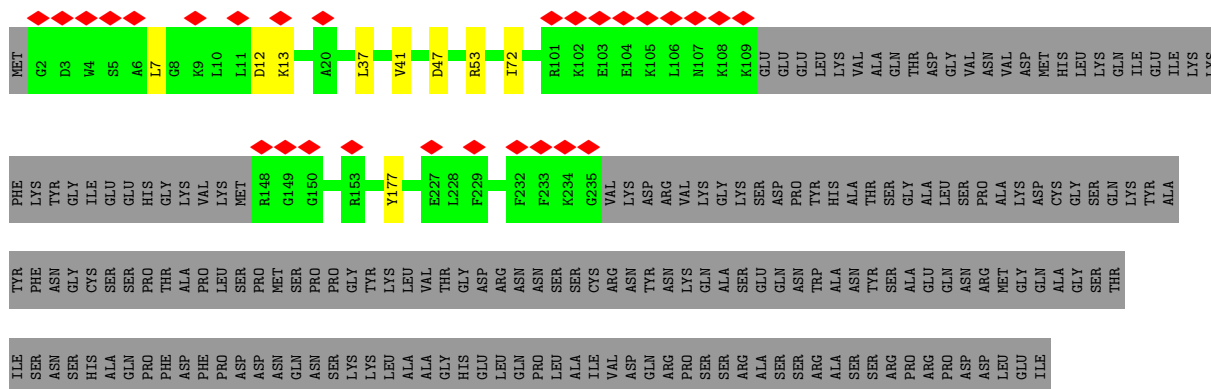


#### • Molecule 1: Gap junction alpha-1 protein

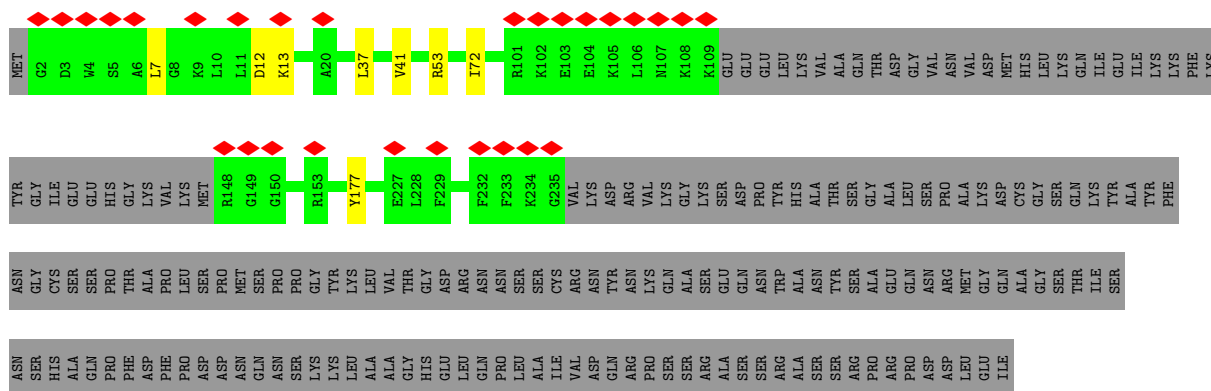




• Molecule 1: Gap junction alpha-1 protein

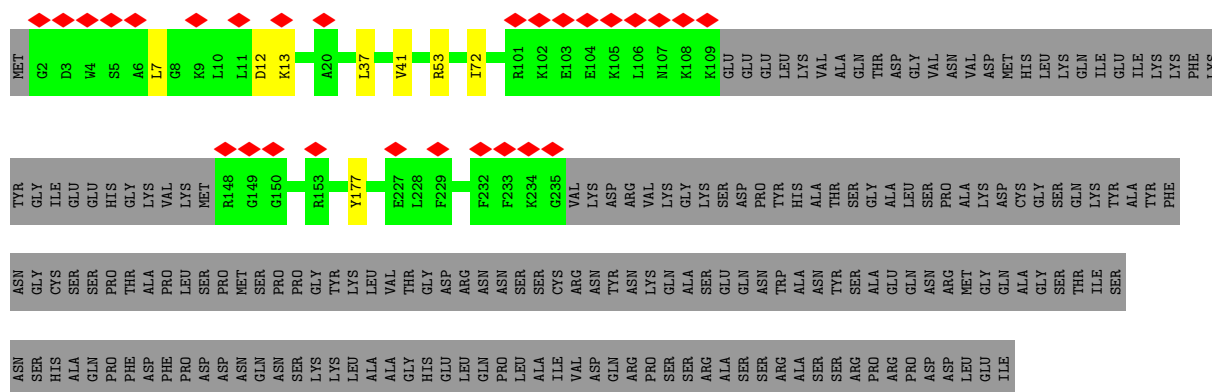


• Molecule 1: Gap junction alpha-1 protein

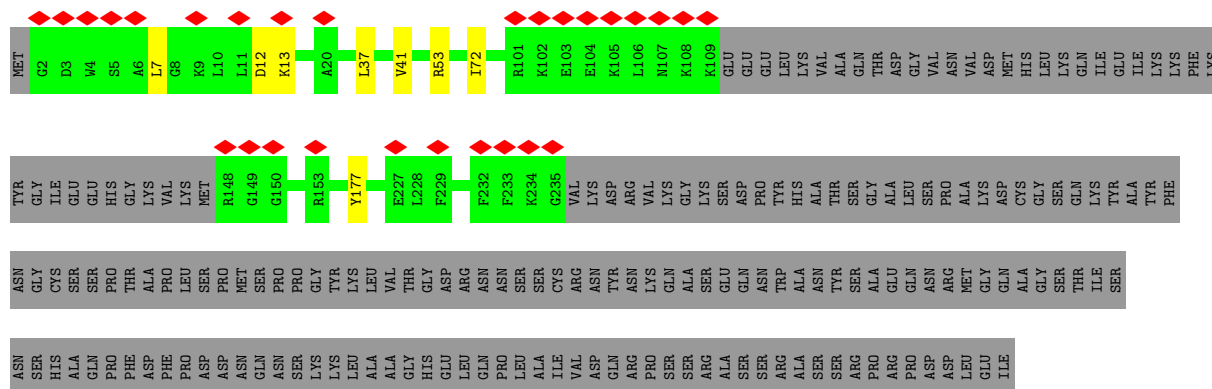


• Molecule 1: Gap junction alpha-1 protein

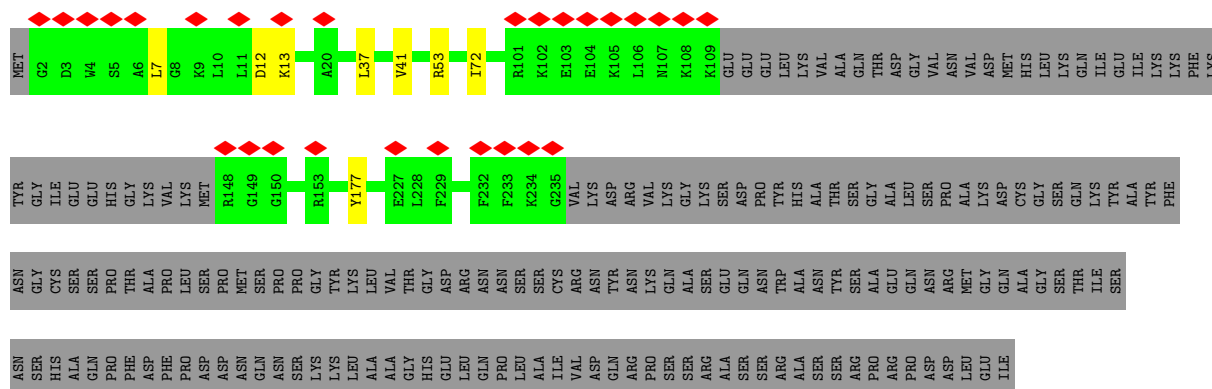




• Molecule 1: Gap junction alpha-1 protein

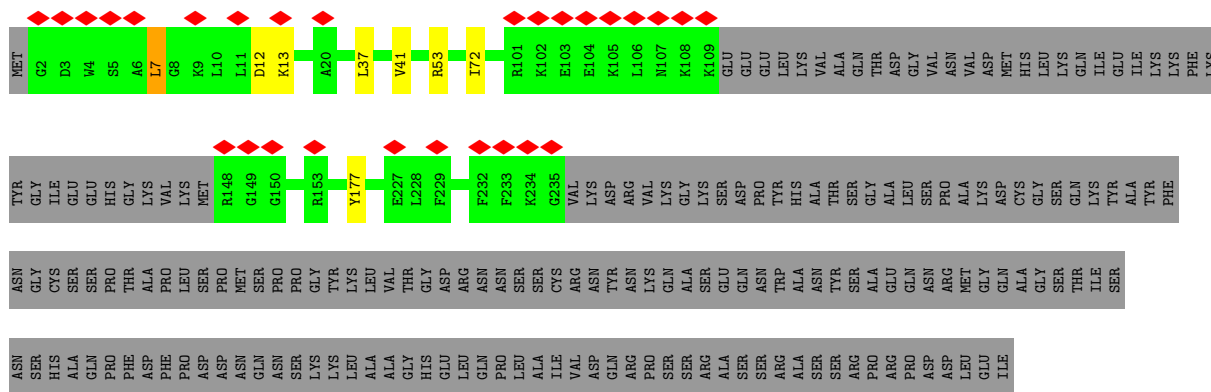


• Molecule 1: Gap junction alpha-1 protein

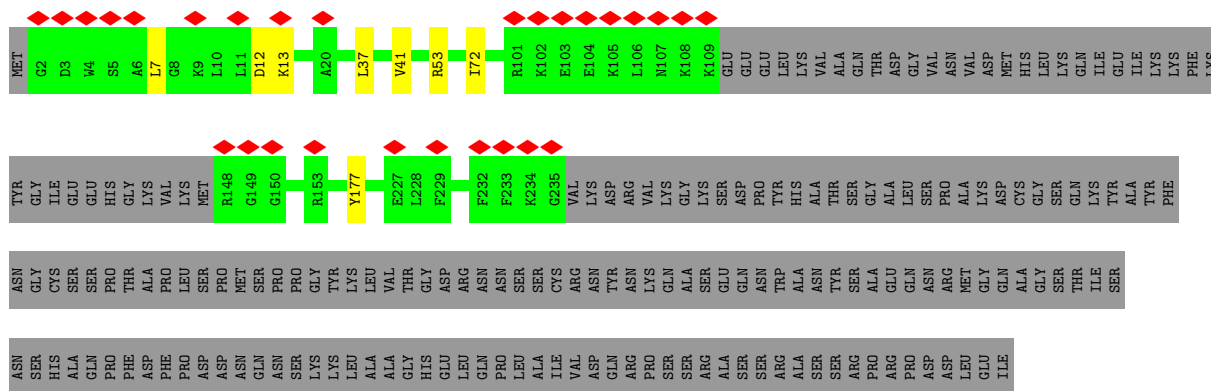


• Molecule 1: Gap junction alpha-1 protein

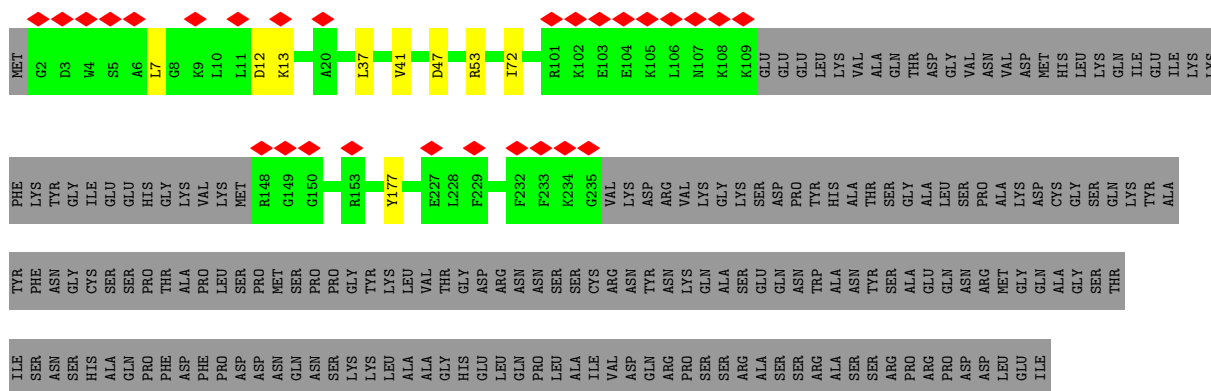




- Molecule 1: Gap junction alpha-1 protein



- Molecule 1: Gap junction alpha-1 protein



- Molecule 1: Gap junction alpha-1 protein





ASN	GLY	ASN	TYR	MET
SER	CYS	G2	GLY	G2
HIS	ILE	D3	ILE	D3
ALA	SER	W4	GLU	W4
GLN	SER	S5	HIS	S5
PRO	THR	A6	GLY	A6
PHE	ALA	L7	LYS	L7
ASP	PRO	G8	VAL	G8
PHE	PRO	K9	LYS	K9
PRO	LEU	L10	LYS	L10
ASP	ASP	L11	MET	L11
ASN	ASN	D12	PRO	D12
ASN	GLN	K13	SER	K13
ASN	ASN	A20	PRO	A20
ASN	ASN	L37	LYS	L37
ASN	ASN	V41	LEU	V41
ASN	ASN	R53	VAL	R53
ASN	ASN	I72	ASP	I72
ASN	ASN	R101	LYS	R101
ASN	ASN	K102	LYS	K102
ASN	ASN	E103	LYS	E103
ASN	ASN	E104	LYS	E104
ASN	ASN	K105	LYS	K105
ASN	ASN	L106	LYS	L106
ASN	ASN	N107	LYS	N107
ASN	ASN	K108	LYS	K108
ASN	ASN	K109	LYS	K109
ASN	ASN	GLU	GLU	GLU
ASN	ASN	GLU	GLU	GLU
ASN	ASN	GLU	GLU	GLU
ASN	ASN	LEU	LEU	LEU
ASN	ASN	LYS	LYS	LYS
ASN	ASN	VAL	VAL	VAL
ASN	ASN	ALA	ALA	ALA
ASN	ASN	GLN	GLN	GLN
ASN	ASN	THR	THR	THR
ASN	ASN	ASP	ASP	ASP
ASN	ASN	GLY	GLY	GLY
ASN	ASN	VAL	VAL	VAL
ASN	ASN	ASN	ASN	ASN
ASN	ASN	ASP	ASP	ASP
ASN	ASN	GLN	GLN	GLN
ASN	ASN	VAL	VAL	VAL
ASN	ASN	ASP	ASP	ASP
ASN	ASN	GLY	GLY	GLY
ASN	ASN	LYS	LYS	LYS
ASN	ASN	SER	SER	SER
ASN	ASN	ASP	ASP	ASP
ASN	ASN	PRO	PRO	PRO
ASN	ASN	TYR	TYR	TYR
ASN	ASN	HIS	HIS	HIS
ASN	ASN	ALA	ALA	ALA
ASN	ASN	THR	THR	THR
ASN	ASN	GLY	GLY	GLY
ASN	ASN	ALA	ALA	ALA
ASN	ASN	LEU	LEU	LEU
ASN	ASN	SER	SER	SER
ASN	ASN	PRO	PRO	PRO
ASN	ASN	ASP	ASP	ASP
ASN	ASN	GLN	GLN	GLN
ASN	ASN	VAL	VAL	VAL
ASN	ASN	ALA	ALA	ALA
ASN	ASN	GLY	GLY	GLY
ASN	ASN	SER	SER	SER
ASN	ASN	THR	THR	THR
ASN	ASN	ILE	ILE	ILE
ASN	ASN	TYR	TYR	TYR
ASN	ASN	PHE	PHE	PHE
ASN	ASN	LYS	LYS	LYS

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21689	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.204	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.032	Depositor
Map size ( $\text{\AA}$ )	270.0, 270.0, 270.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.675, 0.675, 0.675	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: C14

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	0.40	0/1637	0.54	0/2218
1	B	0.40	0/1637	0.54	0/2218
1	C	0.41	0/1637	0.54	0/2218
1	D	0.41	0/1637	0.54	0/2218
1	E	0.40	0/1637	0.54	0/2218
1	F	0.41	0/1637	0.54	0/2218
1	G	0.41	0/1637	0.54	0/2218
1	H	0.41	0/1637	0.54	0/2218
1	I	0.40	0/1637	0.54	0/2218
1	J	0.41	0/1637	0.54	0/2218
1	K	0.40	0/1637	0.54	0/2218
1	L	0.40	0/1637	0.54	0/2218
All	All	0.41	0/19644	0.54	0/26616

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	1594	0	1626	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1594	0	1626	3	0
1	C	1594	0	1626	2	0
1	D	1594	0	1626	3	0
1	E	1594	0	1626	2	0
1	F	1594	0	1626	2	0
1	G	1594	0	1626	2	0
1	H	1594	0	1626	2	0
1	I	1594	0	1626	3	0
1	J	1594	0	1626	2	0
1	K	1594	0	1626	3	0
1	L	1594	0	1626	2	0
2	A	154	0	330	0	0
2	B	154	0	330	0	0
2	C	154	0	330	0	0
2	D	154	0	330	0	0
2	E	154	0	330	0	0
2	F	154	0	330	0	0
2	G	154	0	330	0	0
2	H	154	0	330	0	0
2	I	154	0	330	0	0
2	J	154	0	330	0	0
2	K	154	0	330	0	0
2	L	154	0	330	0	0
3	A	22	0	0	0	0
3	B	21	0	0	0	0
3	C	23	0	0	0	0
3	D	22	0	0	0	0
3	E	21	0	0	0	0
3	F	23	0	0	0	0
3	G	23	0	0	0	0
3	H	22	0	0	0	0
3	I	21	0	0	0	0
3	J	23	0	0	0	0
3	K	22	0	0	0	0
3	L	21	0	0	0	0
All	All	21240	0	23472	28	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 1.

The worst 5 of 28 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:37:LEU:HA	1:B:41:VAL:HG22	1.93	0.51
1:I:37:LEU:HA	1:I:41:VAL:HG22	1.93	0.51
1:J:37:LEU:HA	1:J:41:VAL:HG22	1.93	0.51
1:C:37:LEU:HA	1:C:41:VAL:HG22	1.93	0.50
1:K:37:LEU:HA	1:K:41:VAL:HG22	1.93	0.50

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	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	B	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	C	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	D	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	E	192/382 (50%)	187 (97%)	5 (3%)	0	100	100
1	F	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	G	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	H	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	I	192/382 (50%)	187 (97%)	5 (3%)	0	100	100
1	J	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	K	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
1	L	192/382 (50%)	186 (97%)	6 (3%)	0	100	100
All	All	2304/4584 (50%)	2234 (97%)	70 (3%)	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	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	B	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	C	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	D	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	E	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	F	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	G	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	H	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	I	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	J	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	K	175/333 (53%)	171 (98%)	4 (2%)	50	77
1	L	175/333 (53%)	171 (98%)	4 (2%)	50	77
All	All	2100/3996 (53%)	2052 (98%)	48 (2%)	53	77

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	7	LEU
1	I	53	ARG
1	H	12	ASP
1	I	7	LEU
1	J	12	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	49	GLN
1	I	49	GLN
1	L	49	GLN
1	J	49	GLN

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Mol	Chain	Res	Type
1	D	49	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

132 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	C14	G	402	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	G	407	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	I	402	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	K	404	-	13,13,13	0.28	0	12,12,12	0.85	0
2	C14	F	401	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	L	402	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	C	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	G	410	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	J	403	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	D	406	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	D	409	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	I	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	F	402	-	13,13,13	0.22	0	12,12,12	0.98	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	C14	B	405	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	G	401	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	K	405	-	13,13,13	0.17	0	12,12,12	1.01	0
2	C14	A	406	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	L	407	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	H	409	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	A	402	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	F	411	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	C	409	-	13,13,13	0.24	0	12,12,12	0.88	0
2	C14	L	409	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	J	407	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	D	402	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	F	403	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	G	403	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	E	405	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	G	411	-	13,13,13	0.27	0	12,12,12	0.84	0
2	C14	B	402	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	H	407	-	13,13,13	0.21	0	12,12,12	0.94	0
2	C14	C	404	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	I	403	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	L	410	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	L	403	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	F	406	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	E	409	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	L	401	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	J	402	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	H	405	-	13,13,13	0.17	0	12,12,12	1.01	0
2	C14	E	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	F	410	-	13,13,13	0.24	0	12,12,12	0.88	0
2	C14	E	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	K	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	I	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	C	405	-	13,13,13	0.18	0	12,12,12	1.02	0
2	C14	F	407	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	I	406	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	C	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	A	410	-	13,13,13	0.27	0	12,12,12	0.82	0
2	C14	F	405	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	H	404	-	13,13,13	0.27	0	12,12,12	0.84	0
2	C14	D	407	-	13,13,13	0.21	0	12,12,12	0.94	0
2	C14	H	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	A	403	-	13,13,13	0.21	0	12,12,12	0.94	0
2	C14	J	404	-	13,13,13	0.27	0	12,12,12	0.85	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	C14	G	409	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	A	401	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	H	406	-	13,13,13	0.28	0	12,12,12	0.79	0
2	C14	A	404	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	K	402	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	L	405	-	13,13,13	0.27	0	12,12,12	0.84	0
2	C14	C	402	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	J	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	D	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	H	401	-	13,13,13	0.22	0	12,12,12	0.97	0
2	C14	H	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	J	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	C	406	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	D	403	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	J	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	B	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	C	403	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	E	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	B	406	-	13,13,13	0.28	0	12,12,12	0.81	0
2	C14	D	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	A	411	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	B	403	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	A	409	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	B	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	K	403	-	13,13,13	0.27	0	12,12,12	0.82	0
2	C14	L	408	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	B	407	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	H	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	D	404	-	13,13,13	0.27	0	12,12,12	0.85	0
2	C14	K	407	-	13,13,13	0.21	0	12,12,12	0.94	0
2	C14	C	407	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	H	403	-	13,13,13	0.27	0	12,12,12	0.82	0
2	C14	D	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	E	404	-	13,13,13	0.27	0	12,12,12	0.84	0
2	C14	E	402	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	L	406	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	F	408	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	G	404	-	13,13,13	0.26	0	12,12,12	0.89	0
2	C14	J	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	K	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	D	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	H	402	-	13,13,13	0.27	0	12,12,12	0.86	0
2	C14	A	408	-	13,13,13	0.22	0	12,12,12	0.97	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	C14	E	407	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	F	409	-	13,13,13	0.26	0	12,12,12	0.89	0
2	C14	G	405	-	13,13,13	0.24	0	12,12,12	0.88	0
2	C14	I	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	J	406	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	C	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	L	404	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	I	405	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	I	409	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	I	407	-	13,13,13	0.21	0	12,12,12	0.95	0
2	C14	J	405	-	13,13,13	0.18	0	12,12,12	1.01	0
2	C14	B	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	G	408	-	13,13,13	0.22	0	12,12,12	0.97	0
2	C14	K	408	-	13,13,13	0.26	0	12,12,12	0.90	0
2	C14	A	407	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	F	404	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	G	406	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	K	406	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	L	411	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	E	410	-	13,13,13	0.26	0	12,12,12	0.86	0
2	C14	B	404	-	13,13,13	0.27	0	12,12,12	0.84	0
2	C14	I	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	E	406	-	13,13,13	0.28	0	12,12,12	0.80	0
2	C14	E	403	-	13,13,13	0.27	0	12,12,12	0.81	0
2	C14	B	409	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	J	409	-	13,13,13	0.24	0	12,12,12	0.88	0
2	C14	C	401	-	13,13,13	0.22	0	12,12,12	0.98	0
2	C14	K	409	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	B	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	K	411	-	13,13,13	0.27	0	12,12,12	0.83	0
2	C14	A	405	-	13,13,13	0.24	0	12,12,12	0.89	0
2	C14	D	405	-	13,13,13	0.17	0	12,12,12	1.01	0
2	C14	I	404	-	13,13,13	0.27	0	12,12,12	0.85	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	C14	G	402	-	-	5/11/11/11	-
2	C14	G	407	-	-	2/11/11/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	C14	I	402	-	-	2/11/11/11	-
2	C14	K	404	-	-	3/11/11/11	-
2	C14	F	401	-	-	2/11/11/11	-
2	C14	L	402	-	-	3/11/11/11	-
2	C14	C	411	-	-	2/11/11/11	-
2	C14	G	410	-	-	4/11/11/11	-
2	C14	J	403	-	-	4/11/11/11	-
2	C14	D	406	-	-	5/11/11/11	-
2	C14	D	409	-	-	1/11/11/11	-
2	C14	I	408	-	-	2/11/11/11	-
2	C14	F	402	-	-	3/11/11/11	-
2	C14	B	405	-	-	2/11/11/11	-
2	C14	G	401	-	-	2/11/11/11	-
2	C14	K	405	-	-	2/11/11/11	-
2	C14	A	406	-	-	4/11/11/11	-
2	C14	L	407	-	-	5/11/11/11	-
2	C14	H	409	-	-	1/11/11/11	-
2	C14	A	402	-	-	5/11/11/11	-
2	C14	F	411	-	-	4/11/11/11	-
2	C14	C	409	-	-	1/11/11/11	-
2	C14	L	409	-	-	2/11/11/11	-
2	C14	J	407	-	-	1/11/11/11	-
2	C14	D	402	-	-	2/11/11/11	-
2	C14	F	403	-	-	2/11/11/11	-
2	C14	G	403	-	-	1/11/11/11	-
2	C14	E	405	-	-	2/11/11/11	-
2	C14	G	411	-	-	3/11/11/11	-
2	C14	B	402	-	-	2/11/11/11	-
2	C14	H	407	-	-	1/11/11/11	-
2	C14	C	404	-	-	3/11/11/11	-
2	C14	I	403	-	-	4/11/11/11	-
2	C14	L	410	-	-	1/11/11/11	-
2	C14	L	403	-	-	2/11/11/11	-
2	C14	F	406	-	-	2/11/11/11	-
2	C14	E	409	-	-	1/11/11/11	-
2	C14	L	401	-	-	2/11/11/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	C14	J	402	-	-	2/11/11/11	-
2	C14	H	405	-	-	2/11/11/11	-
2	C14	E	411	-	-	2/11/11/11	-
2	C14	F	410	-	-	1/11/11/11	-
2	C14	E	401	-	-	3/11/11/11	-
2	C14	K	410	-	-	4/11/11/11	-
2	C14	I	411	-	-	2/11/11/11	-
2	C14	C	405	-	-	2/11/11/11	-
2	C14	F	407	-	-	5/11/11/11	-
2	C14	I	406	-	-	5/11/11/11	-
2	C14	C	408	-	-	2/11/11/11	-
2	C14	A	410	-	-	4/11/11/11	-
2	C14	F	405	-	-	3/11/11/11	-
2	C14	H	404	-	-	3/11/11/11	-
2	C14	D	407	-	-	1/11/11/11	-
2	C14	H	411	-	-	2/11/11/11	-
2	C14	A	403	-	-	1/11/11/11	-
2	C14	J	404	-	-	3/11/11/11	-
2	C14	G	409	-	-	2/11/11/11	-
2	C14	A	401	-	-	2/11/11/11	-
2	C14	H	406	-	-	5/11/11/11	-
2	C14	A	404	-	-	2/11/11/11	-
2	C14	K	402	-	-	2/11/11/11	-
2	C14	L	405	-	-	3/11/11/11	-
2	C14	C	402	-	-	2/11/11/11	-
2	C14	J	410	-	-	4/11/11/11	-
2	C14	D	410	-	-	4/11/11/11	-
2	C14	H	401	-	-	3/11/11/11	-
2	C14	H	408	-	-	2/11/11/11	-
2	C14	J	411	-	-	2/11/11/11	-
2	C14	C	406	-	-	5/11/11/11	-
2	C14	D	403	-	-	4/11/11/11	-
2	C14	J	408	-	-	2/11/11/11	-
2	C14	B	410	-	-	4/11/11/11	-
2	C14	C	403	-	-	4/11/11/11	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	C14	E	408	-	-	2/11/11/11	-
2	C14	B	406	-	-	5/11/11/11	-
2	C14	D	401	-	-	3/11/11/11	-
2	C14	A	411	-	-	3/11/11/11	-
2	C14	B	403	-	-	4/11/11/11	-
2	C14	A	409	-	-	2/11/11/11	-
2	C14	B	401	-	-	3/11/11/11	-
2	C14	K	403	-	-	4/11/11/11	-
2	C14	L	408	-	-	1/11/11/11	-
2	C14	B	407	-	-	1/11/11/11	-
2	C14	H	410	-	-	4/11/11/11	-
2	C14	D	404	-	-	3/11/11/11	-
2	C14	K	407	-	-	1/11/11/11	-
2	C14	C	407	-	-	1/11/11/11	-
2	C14	H	403	-	-	4/11/11/11	-
2	C14	D	411	-	-	2/11/11/11	-
2	C14	E	404	-	-	3/11/11/11	-
2	C14	E	402	-	-	2/11/11/11	-
2	C14	L	406	-	-	2/11/11/11	-
2	C14	F	408	-	-	1/11/11/11	-
2	C14	G	404	-	-	2/11/11/11	-
2	C14	J	401	-	-	3/11/11/11	-
2	C14	K	401	-	-	3/11/11/11	-
2	C14	D	408	-	-	2/11/11/11	-
2	C14	H	402	-	-	2/11/11/11	-
2	C14	A	408	-	-	3/11/11/11	-
2	C14	E	407	-	-	1/11/11/11	-
2	C14	F	409	-	-	2/11/11/11	-
2	C14	G	405	-	-	1/11/11/11	-
2	C14	I	410	-	-	4/11/11/11	-
2	C14	J	406	-	-	5/11/11/11	-
2	C14	C	410	-	-	4/11/11/11	-
2	C14	L	404	-	-	4/11/11/11	-
2	C14	I	405	-	-	2/11/11/11	-
2	C14	I	409	-	-	1/11/11/11	-
2	C14	I	407	-	-	1/11/11/11	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	C14	J	405	-	-	2/11/11/11	-
2	C14	B	408	-	-	2/11/11/11	-
2	C14	G	408	-	-	3/11/11/11	-
2	C14	K	408	-	-	2/11/11/11	-
2	C14	A	407	-	-	2/11/11/11	-
2	C14	F	404	-	-	4/11/11/11	-
2	C14	G	406	-	-	4/11/11/11	-
2	C14	K	406	-	-	5/11/11/11	-
2	C14	L	411	-	-	4/11/11/11	-
2	C14	E	410	-	-	4/11/11/11	-
2	C14	B	404	-	-	3/11/11/11	-
2	C14	I	401	-	-	3/11/11/11	-
2	C14	E	406	-	-	5/11/11/11	-
2	C14	E	403	-	-	4/11/11/11	-
2	C14	B	409	-	-	1/11/11/11	-
2	C14	J	409	-	-	1/11/11/11	-
2	C14	C	401	-	-	3/11/11/11	-
2	C14	K	409	-	-	1/11/11/11	-
2	C14	B	411	-	-	2/11/11/11	-
2	C14	K	411	-	-	2/11/11/11	-
2	C14	A	405	-	-	1/11/11/11	-
2	C14	D	405	-	-	2/11/11/11	-
2	C14	I	404	-	-	3/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 348 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	C14	C10-C11-C12-C13
2	B	405	C14	C10-C11-C12-C13
2	C	405	C14	C10-C11-C12-C13
2	D	405	C14	C10-C11-C12-C13
2	E	405	C14	C10-C11-C12-C13

There are no ring outliers.

No monomer is involved in short contacts.

## 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.

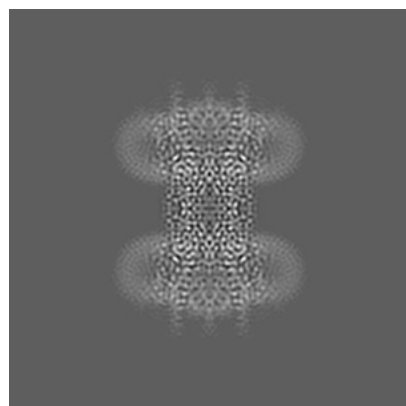
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31495. These allow visual inspection of the internal detail of the map and identification of artifacts.

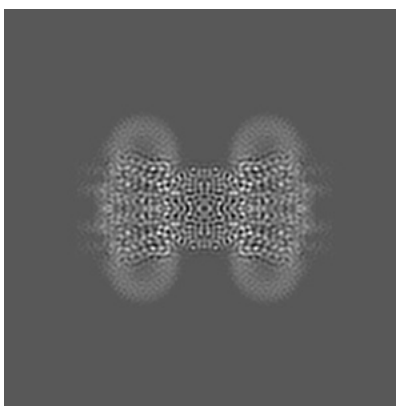
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

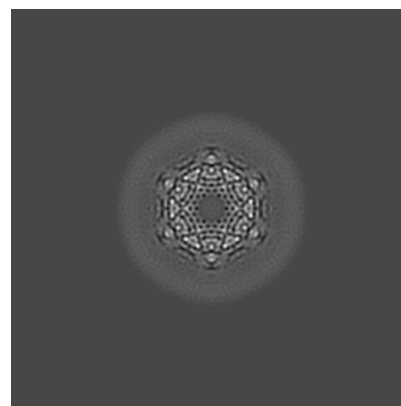
#### 6.1.1 Primary map



X

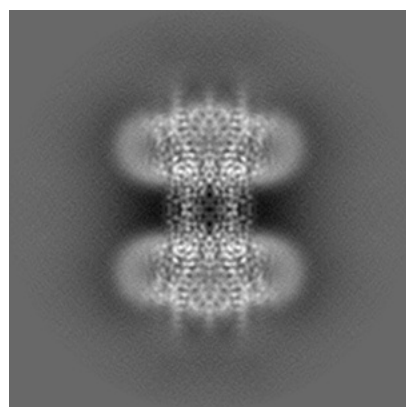


Y

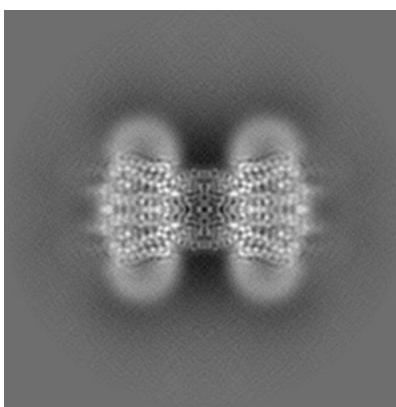


Z

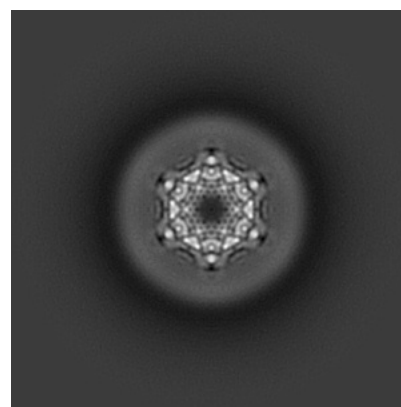
#### 6.1.2 Raw map



X



Y



Z

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

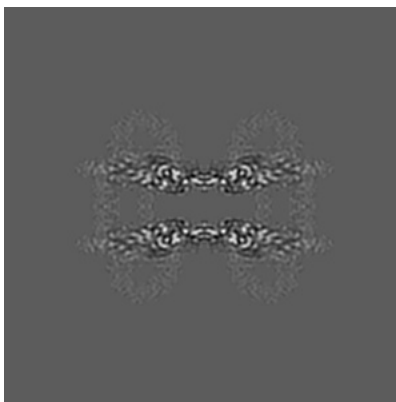


## 6.2 Central slices [i](#)

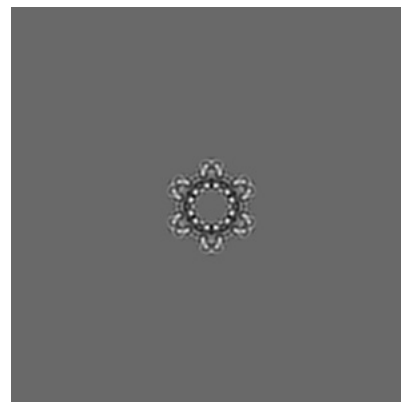
### 6.2.1 Primary map



X Index: 200

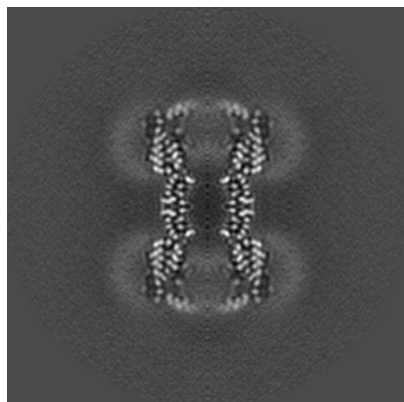


Y Index: 200

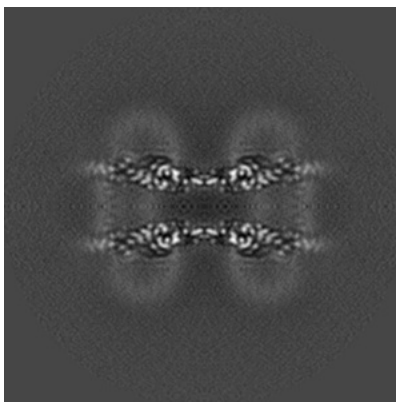


Z Index: 200

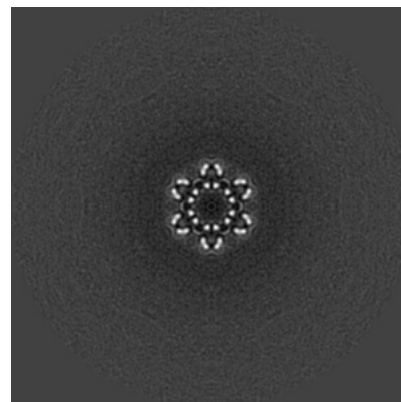
### 6.2.2 Raw map



X Index: 200



Y Index: 200

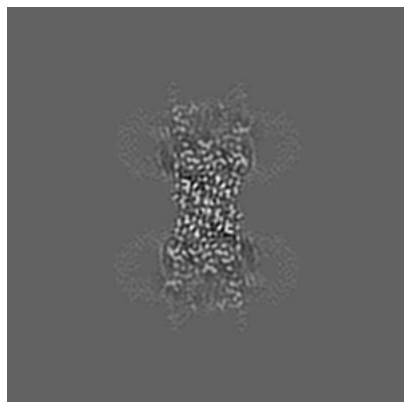


Z Index: 200

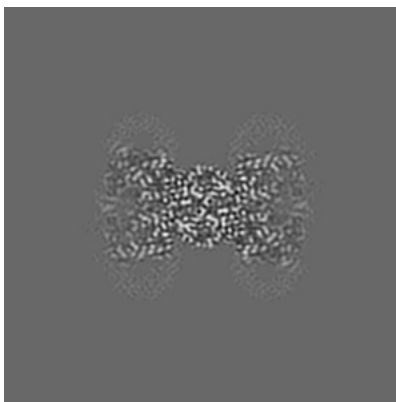
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

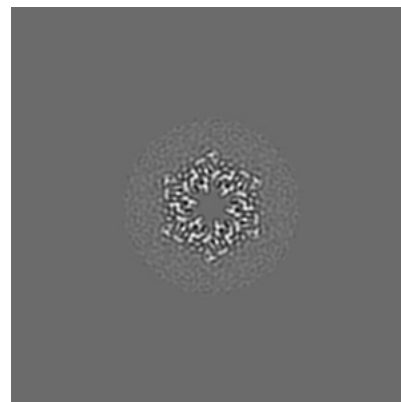
### 6.3.1 Primary map



X Index: 224

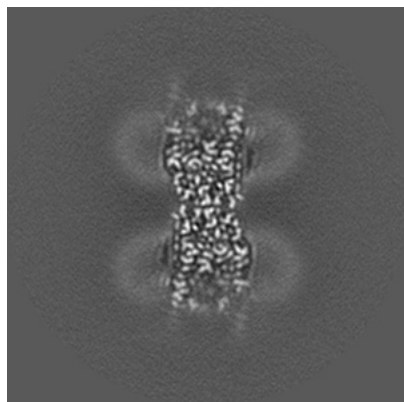


Y Index: 222

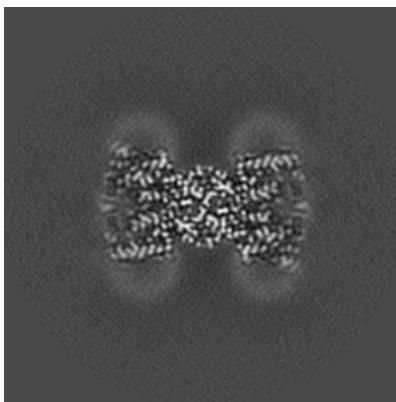


Z Index: 238

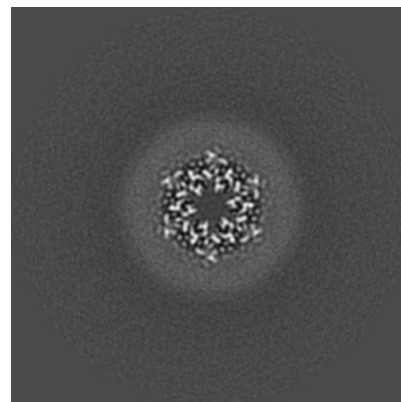
### 6.3.2 Raw map



X Index: 175



Y Index: 222

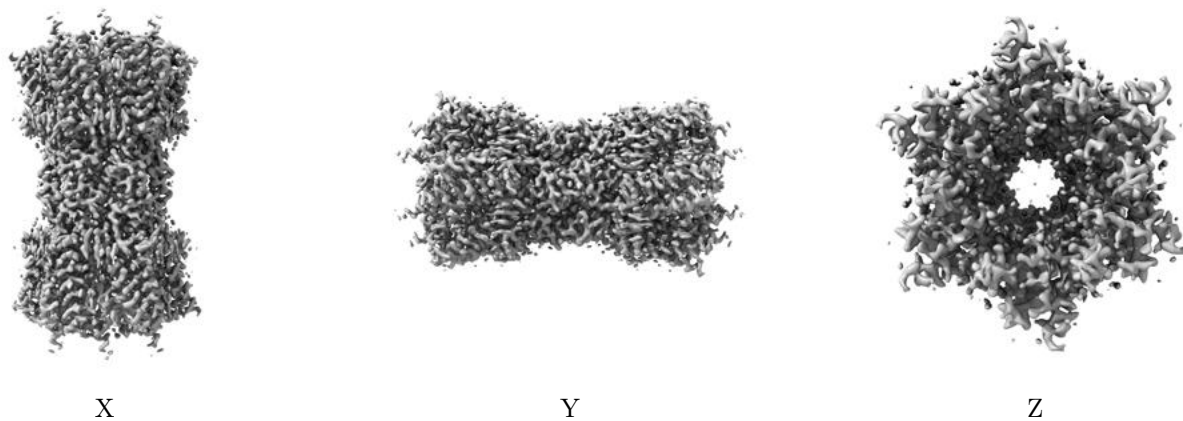


Z Index: 162

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

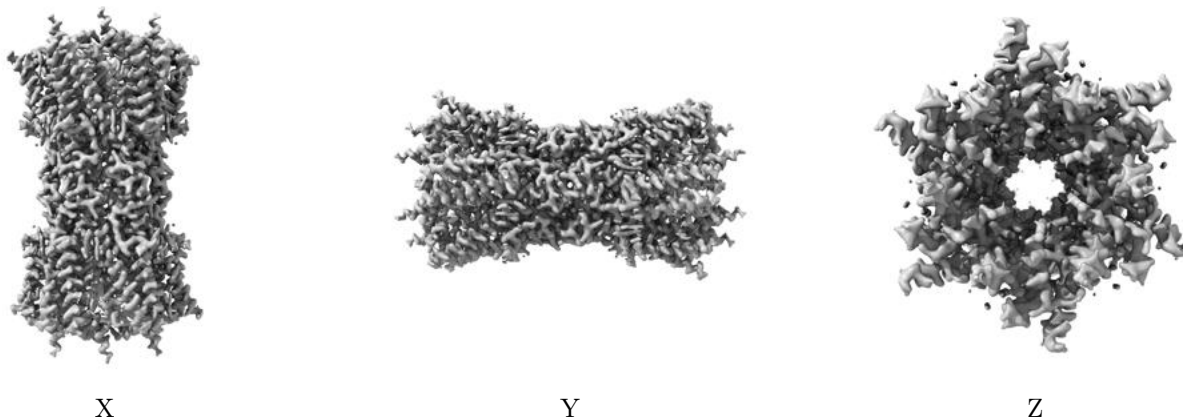
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.032. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

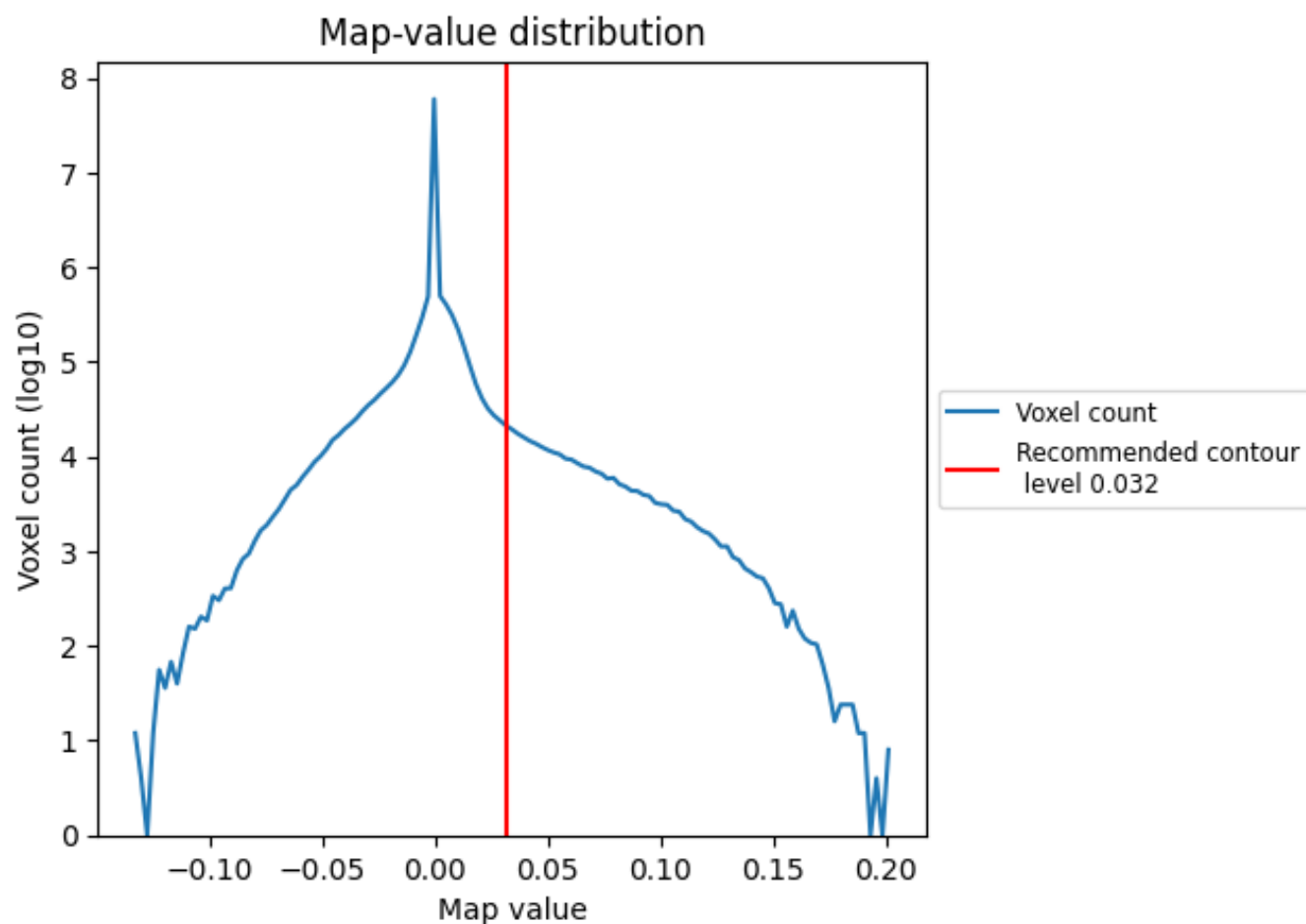
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

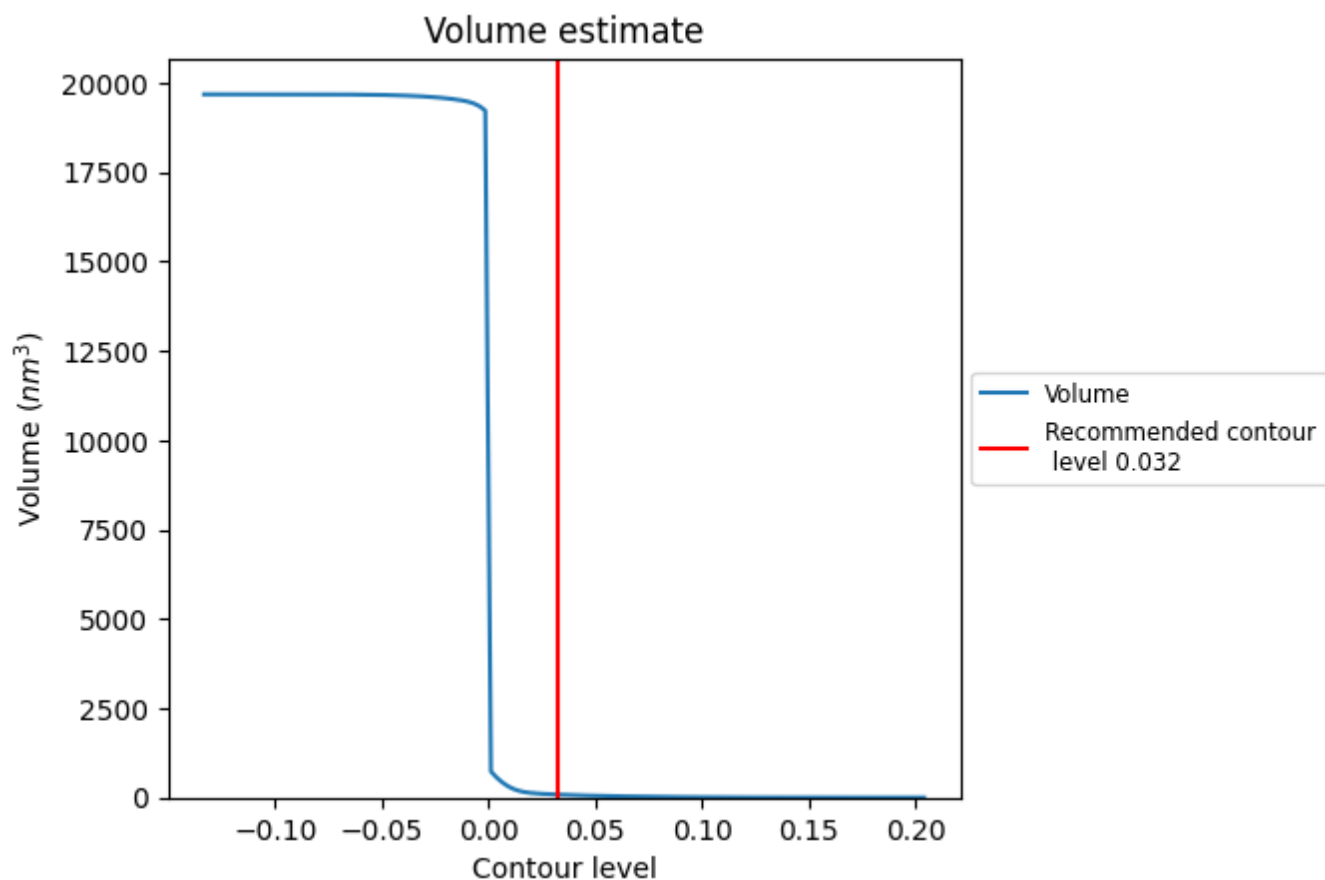
This section contains the results of statistical analysis of the map.

### 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.

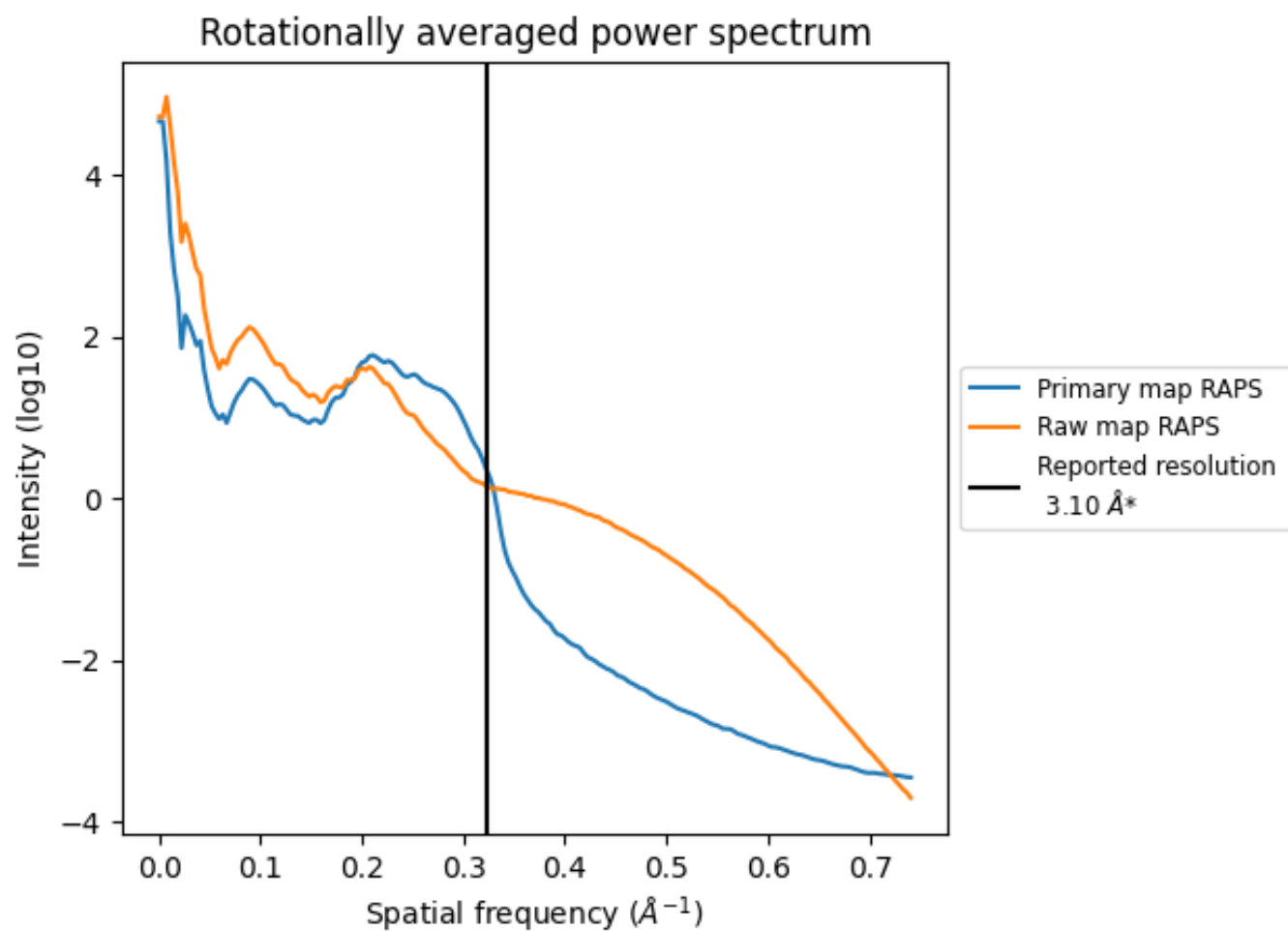
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84  $\text{nm}^3$ ; this corresponds to an approximate mass of 76 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 ⓘ

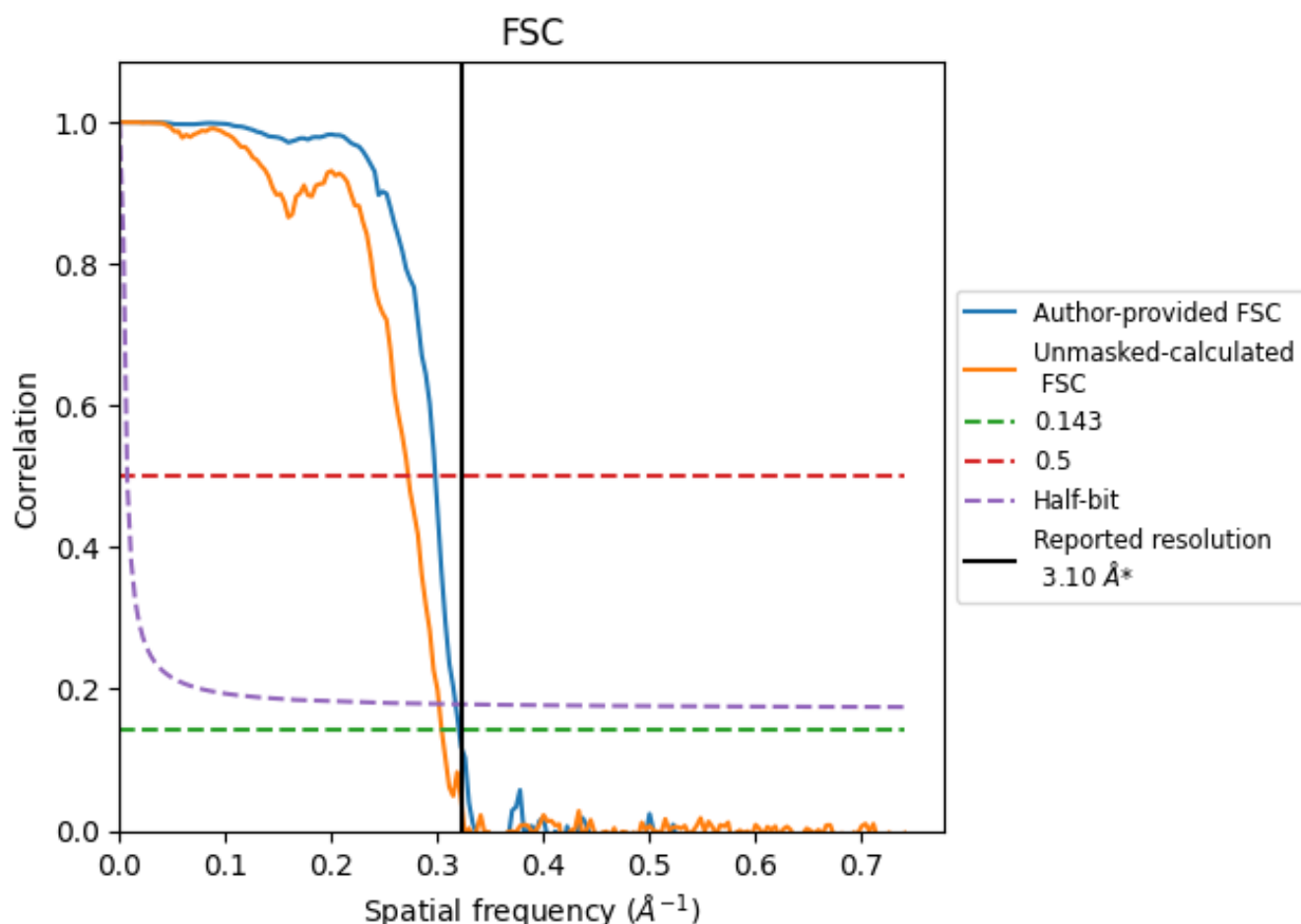


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 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 0.323 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.36	3.15
Unmasked-calculated*	3.29	3.67	3.32

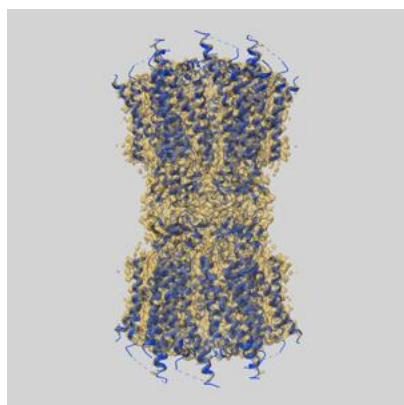
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



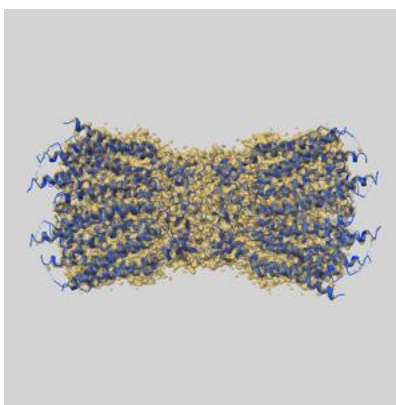
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31495 and PDB model 7F92. Per-residue inclusion information can be found in section 3 on page 13.

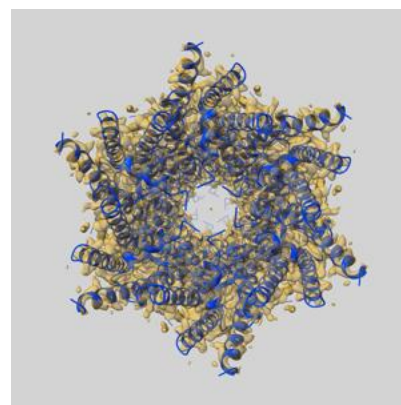
### 9.1 Map-model overlay [i](#)



X



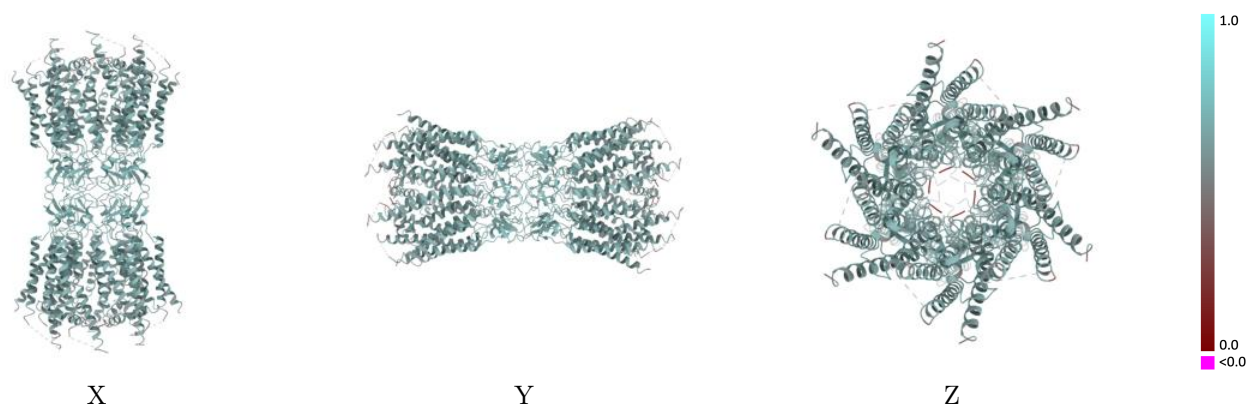
Y



Z

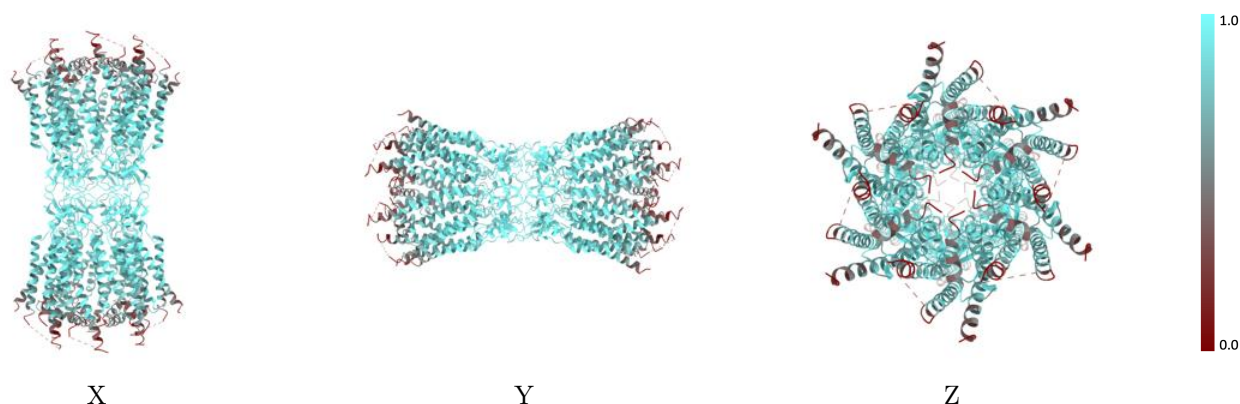
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



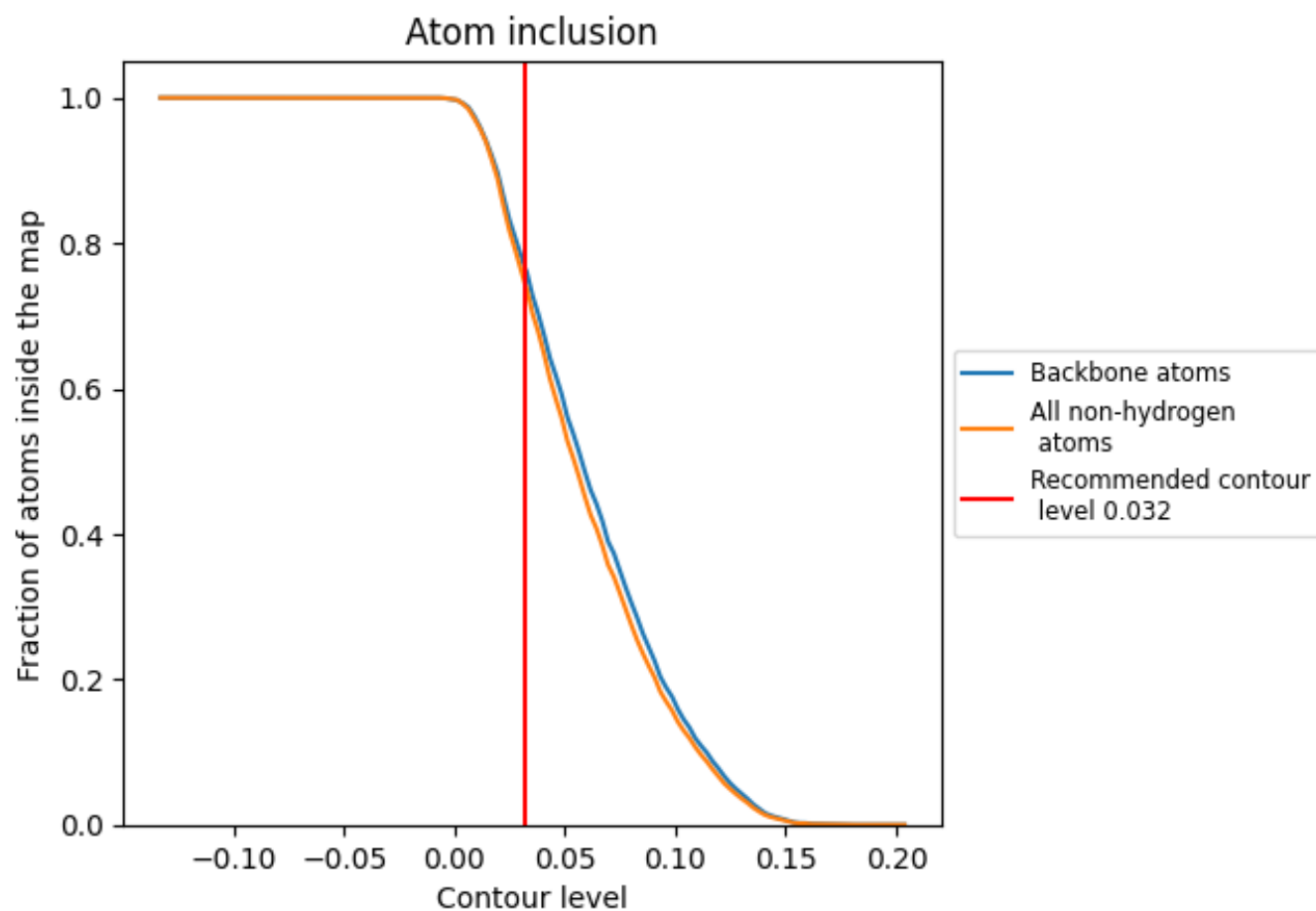
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.032).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 74% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7432</div>	<div><div></div>0.6140</div>
A	<div><div></div>0.7462</div>	<div><div></div>0.6130</div>
B	<div><div></div>0.7497</div>	<div><div></div>0.6140</div>
C	<div><div></div>0.7462</div>	<div><div></div>0.6140</div>
D	<div><div></div>0.7462</div>	<div><div></div>0.6140</div>
E	<div><div></div>0.7497</div>	<div><div></div>0.6140</div>
F	<div><div></div>0.7456</div>	<div><div></div>0.6130</div>
G	<div><div></div>0.7456</div>	<div><div></div>0.6140</div>
H	<div><div></div>0.7462</div>	<div><div></div>0.6140</div>
I	<div><div></div>0.7497</div>	<div><div></div>0.6140</div>
J	<div><div></div>0.7456</div>	<div><div></div>0.6130</div>
K	<div><div></div>0.7462</div>	<div><div></div>0.6130</div>
L	<div><div></div>0.7497</div>	<div><div></div>0.6140</div>

1.0

0.0

<0.0