Full wwPDB EM Validation Report

Aug 17, 2026 – 09:22 PM EDT

PDB ID	:	9PIK / pdb_00009pik
EMDB ID	:	EMD-71670
Title	:	Structure of the two-pore domain, outwardly rectifying potassium (TOK1) from Candida albicans, overall structure
Authors	:	Durocher, B.; Manville, R.W.; Yan, R.; Yu, Z.; Abbott, G.W.; Miller, A.N.
Deposited on	:	2025-07-10
Resolution	:	2.62 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

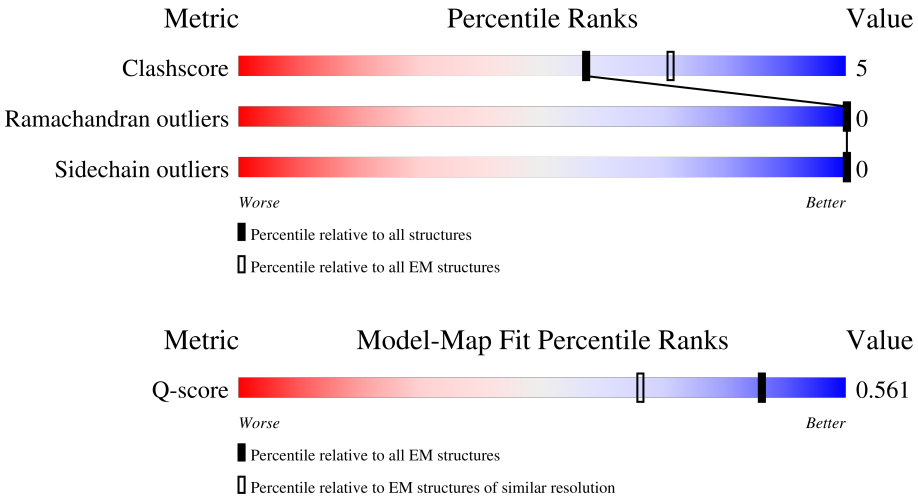
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.62 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	8810 (2.12 - 3.12)

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 <=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	795	57% 6% 36%
1	B	795	58% 6% 36%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8439 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 TOK potassium channel.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	505	Total	C	N	O	S	0	0
			4000	2644	638	694	24		
1	B	505	Total	C	N	O	S	0	0
			4000	2644	638	694	24		

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	742	VAL	-	expression tag	UNP C0IRA7
A	743	ASP	-	expression tag	UNP C0IRA7
A	744	GLY	-	expression tag	UNP C0IRA7
A	745	LEU	-	expression tag	UNP C0IRA7
A	746	GLU	-	expression tag	UNP C0IRA7
A	747	VAL	-	expression tag	UNP C0IRA7
A	748	LEU	-	expression tag	UNP C0IRA7
A	749	PHE	-	expression tag	UNP C0IRA7
A	750	GLN	-	expression tag	UNP C0IRA7
A	751	GLY	-	expression tag	UNP C0IRA7
A	752	PRO	-	expression tag	UNP C0IRA7
A	753	THR	-	expression tag	UNP C0IRA7
A	754	ALA	-	expression tag	UNP C0IRA7
A	755	ALA	-	expression tag	UNP C0IRA7
A	756	ALA	-	expression tag	UNP C0IRA7
A	757	VAL	-	expression tag	UNP C0IRA7
A	758	GLY	-	expression tag	UNP C0IRA7
A	759	SER	-	expression tag	UNP C0IRA7
A	760	GLY	-	expression tag	UNP C0IRA7
A	761	GLY	-	expression tag	UNP C0IRA7
A	762	LEU	-	expression tag	UNP C0IRA7
A	763	GLU	-	expression tag	UNP C0IRA7
A	764	GLY	-	expression tag	UNP C0IRA7
A	765	GLY	-	expression tag	UNP C0IRA7
A	766	GLY	-	expression tag	UNP C0IRA7
A	767	GLY	-	expression tag	UNP C0IRA7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	768	TRP	-	expression tag	UNP C0IRA7
A	769	SER	-	expression tag	UNP C0IRA7
A	770	HIS	-	expression tag	UNP C0IRA7
A	771	PRO	-	expression tag	UNP C0IRA7
A	772	GLN	-	expression tag	UNP C0IRA7
A	773	PHE	-	expression tag	UNP C0IRA7
A	774	GLU	-	expression tag	UNP C0IRA7
A	775	LYS	-	expression tag	UNP C0IRA7
A	776	GLY	-	expression tag	UNP C0IRA7
A	777	GLY	-	expression tag	UNP C0IRA7
A	778	GLY	-	expression tag	UNP C0IRA7
A	779	SER	-	expression tag	UNP C0IRA7
A	780	GLY	-	expression tag	UNP C0IRA7
A	781	GLY	-	expression tag	UNP C0IRA7
A	782	GLY	-	expression tag	UNP C0IRA7
A	783	SER	-	expression tag	UNP C0IRA7
A	784	GLY	-	expression tag	UNP C0IRA7
A	785	GLY	-	expression tag	UNP C0IRA7
A	786	GLY	-	expression tag	UNP C0IRA7
A	787	SER	-	expression tag	UNP C0IRA7
A	788	TRP	-	expression tag	UNP C0IRA7
A	789	SER	-	expression tag	UNP C0IRA7
A	790	HIS	-	expression tag	UNP C0IRA7
A	791	PRO	-	expression tag	UNP C0IRA7
A	792	GLN	-	expression tag	UNP C0IRA7
A	793	PHE	-	expression tag	UNP C0IRA7
A	794	GLU	-	expression tag	UNP C0IRA7
A	795	LYS	-	expression tag	UNP C0IRA7
B	742	VAL	-	expression tag	UNP C0IRA7
B	743	ASP	-	expression tag	UNP C0IRA7
B	744	GLY	-	expression tag	UNP C0IRA7
B	745	LEU	-	expression tag	UNP C0IRA7
B	746	GLU	-	expression tag	UNP C0IRA7
B	747	VAL	-	expression tag	UNP C0IRA7
B	748	LEU	-	expression tag	UNP C0IRA7
B	749	PHE	-	expression tag	UNP C0IRA7
B	750	GLN	-	expression tag	UNP C0IRA7
B	751	GLY	-	expression tag	UNP C0IRA7
B	752	PRO	-	expression tag	UNP C0IRA7
B	753	THR	-	expression tag	UNP C0IRA7
B	754	ALA	-	expression tag	UNP C0IRA7
B	755	ALA	-	expression tag	UNP C0IRA7

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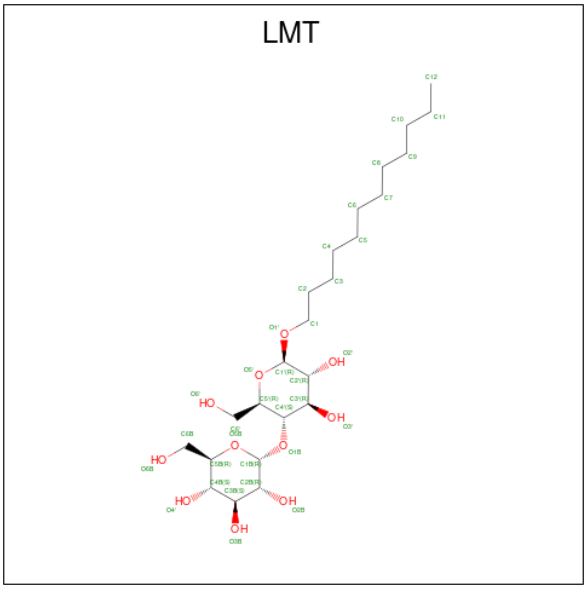
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Chain	Residue	Modelled	Actual	Comment	Reference
B	756	ALA	-	expression tag	UNP C0IRA7
B	757	VAL	-	expression tag	UNP C0IRA7
B	758	GLY	-	expression tag	UNP C0IRA7
B	759	SER	-	expression tag	UNP C0IRA7
B	760	GLY	-	expression tag	UNP C0IRA7
B	761	GLY	-	expression tag	UNP C0IRA7
B	762	LEU	-	expression tag	UNP C0IRA7
B	763	GLU	-	expression tag	UNP C0IRA7
B	764	GLY	-	expression tag	UNP C0IRA7
B	765	GLY	-	expression tag	UNP C0IRA7
B	766	GLY	-	expression tag	UNP C0IRA7
B	767	GLY	-	expression tag	UNP C0IRA7
B	768	TRP	-	expression tag	UNP C0IRA7
B	769	SER	-	expression tag	UNP C0IRA7
B	770	HIS	-	expression tag	UNP C0IRA7
B	771	PRO	-	expression tag	UNP C0IRA7
B	772	GLN	-	expression tag	UNP C0IRA7
B	773	PHE	-	expression tag	UNP C0IRA7
B	774	GLU	-	expression tag	UNP C0IRA7
B	775	LYS	-	expression tag	UNP C0IRA7
B	776	GLY	-	expression tag	UNP C0IRA7
B	777	GLY	-	expression tag	UNP C0IRA7
B	778	GLY	-	expression tag	UNP C0IRA7
B	779	SER	-	expression tag	UNP C0IRA7
B	780	GLY	-	expression tag	UNP C0IRA7
B	781	GLY	-	expression tag	UNP C0IRA7
B	782	GLY	-	expression tag	UNP C0IRA7
B	783	SER	-	expression tag	UNP C0IRA7
B	784	GLY	-	expression tag	UNP C0IRA7
B	785	GLY	-	expression tag	UNP C0IRA7
B	786	GLY	-	expression tag	UNP C0IRA7
B	787	SER	-	expression tag	UNP C0IRA7
B	788	TRP	-	expression tag	UNP C0IRA7
B	789	SER	-	expression tag	UNP C0IRA7
B	790	HIS	-	expression tag	UNP C0IRA7
B	791	PRO	-	expression tag	UNP C0IRA7
B	792	GLN	-	expression tag	UNP C0IRA7
B	793	PHE	-	expression tag	UNP C0IRA7
B	794	GLU	-	expression tag	UNP C0IRA7
B	795	LYS	-	expression tag	UNP C0IRA7

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
2	A	3	Total K 3 3	0

- Molecule 3 is DODECYL-BETA-D-MALTOSIDE (CCD ID: LMT) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total C 12 12	0
3	A	1	Total C 12 12	0
3	A	1	Total C 6 6	0
3	A	1	Total C 5 5	0
3	A	1	Total C 9 9	0
3	A	1	Total C 9 9	0
3	A	1	Total C 7 7	0
3	A	1	Total C 12 12	0
3	A	1	Total C 12 12	0
3	A	1	Total C 12 12	0
3	A	1	Total C 12 12	0

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Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total C 11 11	0
3	A	1	Total C 7 7	0
3	A	1	Total C 7 7	0
3	A	1	Total C 9 9	0
3	A	1	Total C 12 12	0
3	A	1	Total C 6 6	0
3	A	1	Total C 11 11	0
3	A	1	Total C 10 10	0
3	A	1	Total C 6 6	0
3	A	1	Total C 8 8	0
3	A	1	Total C 11 11	0
3	A	1	Total C 12 12	0
3	B	1	Total C 12 12	0
3	B	1	Total C 12 12	0
3	B	1	Total C 12 12	0
3	B	1	Total C 6 6	0
3	B	1	Total C 5 5	0
3	B	1	Total C 9 9	0
3	B	1	Total C 9 9	0
3	B	1	Total C 7 7	0
3	B	1	Total C 12 12	0

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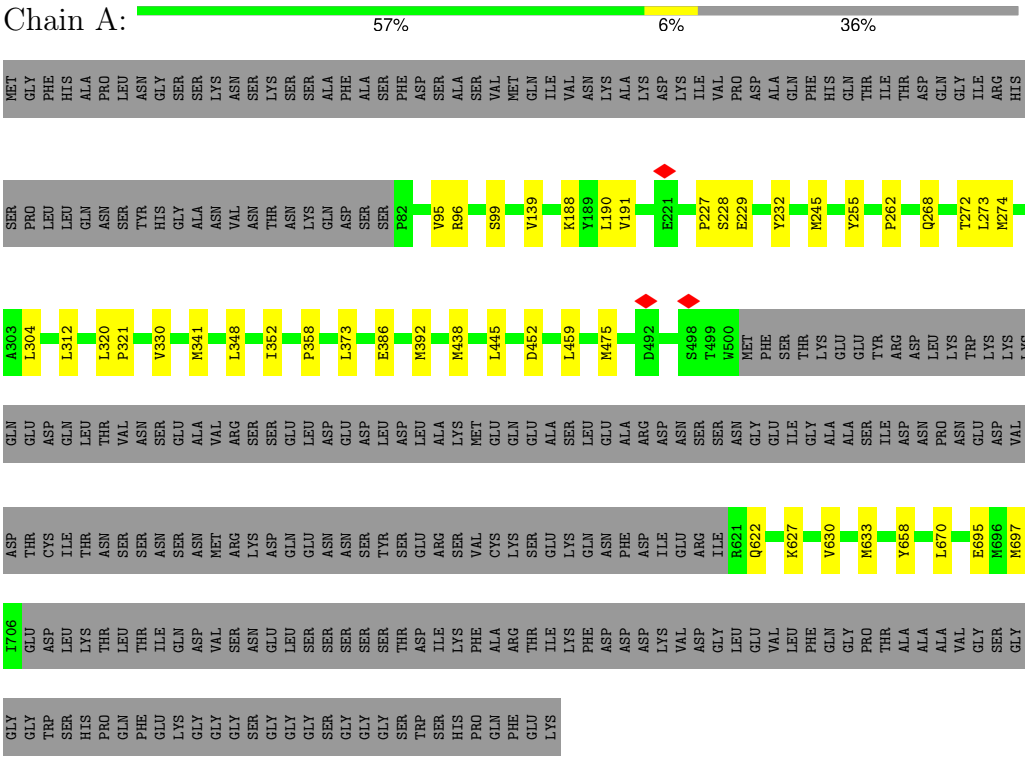
Mol	Chain	Residues	Atoms	AltConf
3	B	1	Total C 12 12	0
3	B	1	Total C 12 12	0
3	B	1	Total C 12 12	0
3	B	1	Total C 11 11	0
3	B	1	Total C 7 7	0
3	B	1	Total C 7 7	0
3	B	1	Total C 9 9	0
3	B	1	Total C 12 12	0
3	B	1	Total C 6 6	0
3	B	1	Total C 11 11	0
3	B	1	Total C 10 10	0
3	B	1	Total C 6 6	0
3	B	1	Total C 8 8	0
3	B	1	Total C 11 11	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.

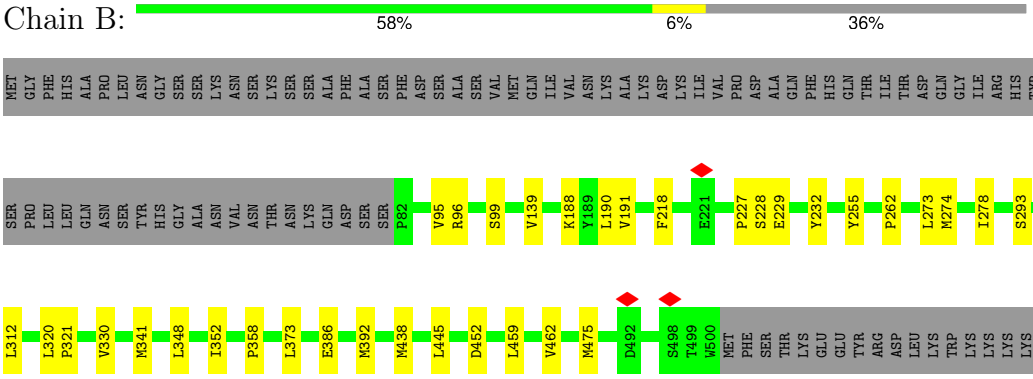
• Molecule 1: TOK potassium channel

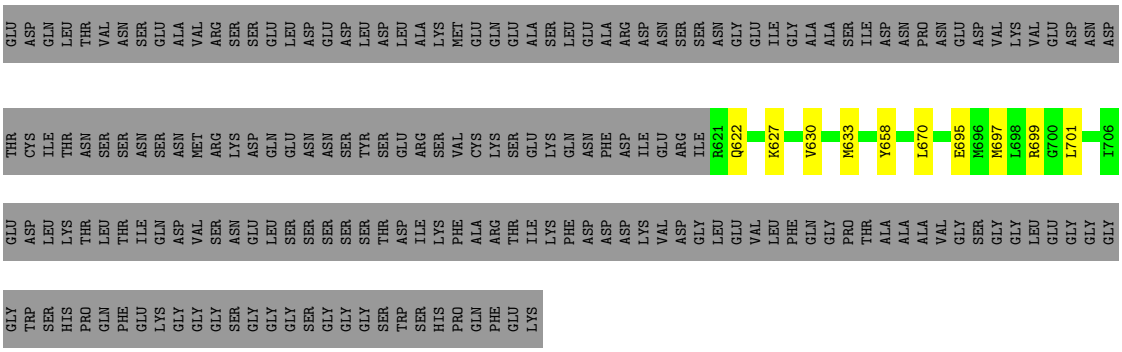
Chain A:



• Molecule 1: TOK potassium channel

Chain B:




GLU ASP GLN LEU THR VAL ASN SER GLU ALA VAL ARG SER SER GLU LEU ASP GLU ASP LEU ASP LEU ALA LYS MET GLU GLN GLU ALA SER LEU GLU ALA ARG ASP ASN SER SER ASN GLY GLU ILE GLY ALA ALA SER ILE ASP ASN PRO ASN GLU ASP VAL LYS VAL GLU ASP ASN
THR CYS ILE THR ASN SER SER ASN SER ASN MET ARG LYS ASP GLN GLU ASN ASN SER TYR SER GLU ARG SER VAL CYS LYS SER GLU LYS GLN ASN PHE ASP ILE GLU ARG ILE
B621 Q622 K627 V630 M633 Y658 L670 E695 M696 M697 L698 R699 G700 L701 L706
GLU ASP LEU LYS THR LEU THR ILE GLN ASP VAL SER ASN GLU LEU SER SER SER SER THR ASP ILE LYS PHE ALA ARG THR ILE LYS PHE ASP ASP ASP LYS VAL ASP GLY LEU GLU VAL LEU PHE GLN GLY PRO THR ALA ALA ALA VAL GLY SER GLY GLY LEU GLU GLY GLY GLY
GLY TRP SER HIS PRO GLN PHE GLU LYS GLY GLY GLY SER GLY GLY GLY GLY SER TRP SER HIS PRO GLN PHE GLU LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	378494	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.591	Depositor
Minimum map value	-0.618	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	264.64, 264.64, 264.64	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.827, 0.827, 0.827	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.21	0/4100	0.28	0/5567
1	B	0.21	0/4100	0.28	0/5567
All	All	0.21	0/8200	0.28	0/11134

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	4000	0	4117	41	0
1	B	4000	0	4117	41	0
2	A	3	0	0	0	0
3	A	218	0	383	5	0
3	B	218	0	383	3	0
All	All	8439	0	9000	83	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.

All (83) 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:96:ARG:CZ	1:B:99:SER:HB3	1.63	1.28
1:A:96:ARG:CZ	1:A:99:SER:HB3	1.63	1.27
1:A:96:ARG:NH2	1:A:99:SER:HB3	1.65	1.12
1:B:96:ARG:NH2	1:B:99:SER:HB3	1.65	1.10
1:A:273:LEU:HD22	1:A:352:ILE:CD1	1.84	1.08
1:B:273:LEU:HD22	1:B:352:ILE:CD1	1.84	1.06
1:A:633:MET:SD	1:A:697:MET:HE1	1.99	1.03
1:B:96:ARG:NH2	1:B:99:SER:CB	2.22	1.02
1:A:96:ARG:NH2	1:A:99:SER:CB	2.22	1.02
1:B:633:MET:SD	1:B:697:MET:HE1	1.99	1.01
1:A:273:LEU:HD22	1:A:352:ILE:HD11	1.55	0.87
1:B:273:LEU:HD22	1:B:352:ILE:HD11	1.55	0.86
1:A:312:LEU:CD2	1:A:341:MET:HE3	2.11	0.80
1:B:312:LEU:CD2	1:B:341:MET:HE3	2.11	0.79
1:B:232:TYR:CD1	1:B:459:LEU:HD13	2.22	0.75
1:A:96:ARG:NH2	1:A:99:SER:HB2	2.02	0.75
1:B:96:ARG:NH2	1:B:99:SER:HB2	2.02	0.74
1:A:232:TYR:CD1	1:A:459:LEU:HD13	2.22	0.74
1:B:312:LEU:HD21	1:B:341:MET:HE3	1.69	0.73
1:A:312:LEU:HD21	1:A:341:MET:HE3	1.69	0.73
1:A:96:ARG:CZ	1:A:99:SER:CB	2.55	0.72
1:B:273:LEU:HD22	1:B:352:ILE:HD13	1.73	0.70
1:A:273:LEU:HD22	1:A:352:ILE:HD13	1.73	0.68
1:B:96:ARG:CZ	1:B:99:SER:CB	2.55	0.67
1:A:348:LEU:HD12	1:A:352:ILE:HD12	1.81	0.63
1:B:348:LEU:HD12	1:B:352:ILE:HD12	1.81	0.62
1:B:227:PRO:HB2	1:B:232:TYR:CE2	2.35	0.62
1:A:227:PRO:HB2	1:A:232:TYR:CE2	2.35	0.62
1:A:630:VAL:HG11	1:A:701:LEU:HD21	1.82	0.62
1:B:630:VAL:HG11	1:B:701:LEU:HD21	1.82	0.61
1:A:95:VAL:HG12	1:A:358:PRO:HB2	1.84	0.59
1:B:95:VAL:HG12	1:B:358:PRO:HB2	1.84	0.58
1:B:445:LEU:HB3	1:B:475:MET:HG3	1.86	0.58
1:B:373:LEU:HD11	1:B:670:LEU:HB3	1.86	0.57
1:B:633:MET:SD	1:B:697:MET:CE	2.86	0.57
1:A:373:LEU:HD11	1:A:670:LEU:HB3	1.86	0.57
1:A:445:LEU:HB3	1:A:475:MET:HG3	1.86	0.56
1:B:228:SER:O	1:B:232:TYR:HD2	1.89	0.56
1:A:228:SER:O	1:A:232:TYR:HD2	1.89	0.56
1:A:139:VAL:HG21	1:A:304:LEU:HD22	1.88	0.55
1:A:348:LEU:HD12	1:A:352:ILE:CD1	2.37	0.54
1:B:139:VAL:HG21	1:B:304:LEU:HD22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:MET:HE2	1:A:670:LEU:HD23	1.89	0.54
1:B:348:LEU:HD12	1:B:352:ILE:CD1	2.37	0.54
1:B:392:MET:HE2	1:B:670:LEU:HD23	1.89	0.53
1:A:255:TYR:CE1	1:A:262:PRO:HG3	2.44	0.52
1:B:255:TYR:CE1	1:B:262:PRO:HG3	2.44	0.52
1:A:633:MET:SD	1:A:697:MET:CE	2.86	0.52
1:A:320:LEU:HD13	1:B:452:ASP:HB3	1.92	0.51
1:A:452:ASP:HB3	1:B:320:LEU:HD13	1.92	0.51
1:B:293:SER:HB2	3:B:812:LMT:H52	1.93	0.50
1:A:293:SER:HB2	3:A:914:LMT:H52	1.94	0.49
1:B:188:LYS:HE2	1:B:190:LEU:HB2	1.94	0.49
1:A:188:LYS:HE2	1:A:190:LEU:HB2	1.94	0.48
1:B:627:LYS:HE3	1:B:701:LEU:HD22	1.95	0.48
1:A:321:PRO:HG3	1:A:330:VAL:HG21	1.95	0.48
1:B:321:PRO:HG3	1:B:330:VAL:HG21	1.94	0.48
1:A:627:LYS:HE3	1:A:701:LEU:HD22	1.95	0.47
1:A:386:GLU:HG3	1:A:658:TYR:CE2	2.50	0.47
3:A:923:LMT:H51	3:B:821:LMT:H51	1.96	0.47
1:B:386:GLU:HG3	1:B:658:TYR:CE2	2.50	0.46
1:B:229:GLU:OE1	1:B:302:SER:N	2.50	0.45
1:B:228:SER:O	1:B:232:TYR:CD2	2.70	0.44
1:A:229:GLU:OE1	1:A:302:SER:N	2.50	0.44
1:B:188:LYS:HG3	1:B:191:VAL:HG22	2.00	0.43
1:A:188:LYS:HG3	1:A:191:VAL:HG22	2.00	0.43
1:A:228:SER:O	1:A:232:TYR:CD2	2.70	0.42
3:A:924:LMT:H71	3:A:924:LMT:H41	1.86	0.42
1:A:438:MET:HE1	3:A:921:LMT:H81	2.01	0.42
1:A:622:GLN:H	1:A:622:GLN:CD	2.28	0.41
1:B:438:MET:HE1	3:B:819:LMT:H81	2.01	0.41
1:A:348:LEU:CD1	1:A:352:ILE:HD12	2.50	0.41
3:A:925:LMT:H82	3:A:925:LMT:H112	1.83	0.41
1:B:274:MET:HE3	1:B:278:ILE:HD11	2.03	0.41
1:B:348:LEU:CD1	1:B:352:ILE:HD12	2.50	0.41
1:B:622:GLN:H	1:B:622:GLN:CD	2.28	0.41
1:B:695:GLU:O	1:B:699:ARG:HG2	2.21	0.41
1:A:695:GLU:O	1:A:699:ARG:HG2	2.21	0.41
1:B:232:TYR:HB2	1:B:462:VAL:HG21	2.03	0.40
1:A:274:MET:HE3	1:A:278:ILE:HD11	2.03	0.40
1:B:218:PHE:CD2	1:B:227:PRO:HG3	2.56	0.40
1:A:245:MET:HE3	1:A:245:MET:HB3	1.96	0.40
1:A:268:GLN:O	1:A:272:THR:HG23	2.22	0.40

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	501/795 (63%)	493 (98%)	8 (2%)	0	100	100
1	B	501/795 (63%)	493 (98%)	8 (2%)	0	100	100
All	All	1002/1590 (63%)	986 (98%)	16 (2%)	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	439/691 (64%)	439 (100%)	0	100	100
1	B	439/691 (64%)	439 (100%)	0	100	100
All	All	878/1382 (64%)	878 (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. There are no such sidechains identified.

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)

Of 49 ligands modelled in this entry, 3 are monoatomic - leaving 46 for Mogul analysis.

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	$\#\|Z\| > 2$
3	LMT	B	819	-	10,10,36	0.29	0	9,9,47	0.35	0
3	LMT	A	909	-	8,8,36	0.30	0	7,7,47	0.28	0
3	LMT	A	912	-	11,11,36	0.26	0	10,10,47	0.29	0
3	LMT	B	816	-	8,8,36	0.30	0	7,7,47	0.32	0
3	LMT	A	904	-	11,11,36	0.26	0	10,10,47	0.29	0
3	LMT	A	922	-	9,9,36	0.29	0	8,8,47	0.33	0
3	LMT	B	822	-	7,7,36	0.13	0	6,6,47	0.14	0
3	LMT	A	926	-	11,11,36	0.28	0	10,10,47	0.34	0
3	LMT	B	803	-	11,11,36	0.26	0	10,10,47	0.30	0
3	LMT	B	812	-	11,11,36	0.27	0	10,10,47	0.32	0
3	LMT	A	905	-	11,11,36	0.26	0	10,10,47	0.30	0
3	LMT	B	801	-	11,11,36	0.28	0	10,10,47	0.35	0
3	LMT	A	924	-	7,7,36	0.13	0	6,6,47	0.14	0
3	LMT	A	914	-	11,11,36	0.27	0	10,10,47	0.32	0
3	LMT	B	811	-	11,11,36	0.26	0	10,10,47	0.29	0
3	LMT	A	910	-	6,6,36	0.31	0	5,5,47	0.35	0
3	LMT	B	821	-	5,5,36	0.32	0	4,4,47	0.33	0
3	LMT	B	815	-	6,6,36	0.28	0	5,5,47	0.21	0
3	LMT	B	804	-	5,5,36	0.28	0	4,4,47	0.18	0
3	LMT	B	805	-	4,4,36	0.33	0	3,3,47	0.39	0
3	LMT	A	916	-	6,6,36	0.27	0	5,5,47	0.21	0
3	LMT	B	808	-	6,6,36	0.32	0	5,5,47	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	LMT	A	923	-	5,5,36	0.32	0	4,4,47	0.33	0
3	LMT	A	917	-	6,6,36	0.28	0	5,5,47	0.21	0
3	LMT	A	925	-	10,10,36	0.16	0	9,9,47	0.10	0
3	LMT	A	908	-	8,8,36	0.29	0	7,7,47	0.33	0
3	LMT	B	810	-	11,11,36	0.26	0	10,10,47	0.29	0
3	LMT	A	915	-	10,10,36	0.28	0	9,9,47	0.33	0
3	LMT	B	809	-	11,11,36	0.27	0	10,10,47	0.29	0
3	LMT	B	820	-	9,9,36	0.29	0	8,8,47	0.33	0
3	LMT	B	818	-	5,5,36	0.11	0	4,4,47	0.12	0
3	LMT	A	911	-	11,11,36	0.27	0	10,10,47	0.29	0
3	LMT	B	802	-	11,11,36	0.25	0	10,10,47	0.29	0
3	LMT	B	813	-	10,10,36	0.28	0	9,9,47	0.33	0
3	LMT	A	919	-	11,11,36	0.27	0	10,10,47	0.32	0
3	LMT	B	806	-	8,8,36	0.29	0	7,7,47	0.33	0
3	LMT	A	920	-	5,5,36	0.11	0	4,4,47	0.12	0
3	LMT	A	907	-	4,4,36	0.33	0	3,3,47	0.39	0
3	LMT	A	906	-	5,5,36	0.28	0	4,4,47	0.18	0
3	LMT	B	814	-	6,6,36	0.27	0	5,5,47	0.21	0
3	LMT	B	823	-	10,10,36	0.17	0	9,9,47	0.10	0
3	LMT	A	921	-	10,10,36	0.28	0	9,9,47	0.35	0
3	LMT	B	807	-	8,8,36	0.29	0	7,7,47	0.28	0
3	LMT	A	913	-	11,11,36	0.25	0	10,10,47	0.29	0
3	LMT	A	918	-	8,8,36	0.30	0	7,7,47	0.32	0
3	LMT	B	817	-	11,11,36	0.27	0	10,10,47	0.32	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
3	LMT	B	819	-	-	2/8/8/61	-
3	LMT	A	909	-	-	1/6/6/61	-
3	LMT	A	912	-	-	4/9/9/61	-
3	LMT	B	816	-	-	2/6/6/61	-
3	LMT	A	904	-	-	2/9/9/61	-
3	LMT	A	922	-	-	4/7/7/61	-
3	LMT	B	822	-	-	3/5/5/61	-
3	LMT	A	926	-	-	2/9/9/61	-
3	LMT	B	803	-	-	1/9/9/61	-
3	LMT	B	812	-	-	2/9/9/61	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LMT	A	905	-	-	1/9/9/61	-
3	LMT	B	801	-	-	2/9/9/61	-
3	LMT	A	924	-	-	3/5/5/61	-
3	LMT	A	914	-	-	2/9/9/61	-
3	LMT	B	811	-	-	2/9/9/61	-
3	LMT	A	910	-	-	3/4/4/61	-
3	LMT	B	821	-	-	2/3/3/61	-
3	LMT	B	815	-	-	0/4/4/61	-
3	LMT	B	804	-	-	0/3/3/61	-
3	LMT	B	805	-	-	0/2/2/61	-
3	LMT	A	916	-	-	2/4/4/61	-
3	LMT	B	808	-	-	3/4/4/61	-
3	LMT	A	923	-	-	2/3/3/61	-
3	LMT	A	917	-	-	0/4/4/61	-
3	LMT	A	925	-	-	4/8/8/61	-
3	LMT	A	908	-	-	1/6/6/61	-
3	LMT	B	810	-	-	4/9/9/61	-
3	LMT	A	915	-	-	0/8/8/61	-
3	LMT	B	809	-	-	1/9/9/61	-
3	LMT	B	820	-	-	4/7/7/61	-
3	LMT	B	818	-	-	0/3/3/61	-
3	LMT	A	911	-	-	1/9/9/61	-
3	LMT	B	802	-	-	2/9/9/61	-
3	LMT	B	813	-	-	0/8/8/61	-
3	LMT	A	919	-	-	0/9/9/61	-
3	LMT	B	806	-	-	1/6/6/61	-
3	LMT	A	920	-	-	0/3/3/61	-
3	LMT	A	907	-	-	0/2/2/61	-
3	LMT	A	906	-	-	0/3/3/61	-
3	LMT	B	814	-	-	2/4/4/61	-
3	LMT	B	823	-	-	4/8/8/61	-
3	LMT	A	921	-	-	2/8/8/61	-
3	LMT	B	807	-	-	1/6/6/61	-
3	LMT	A	913	-	-	2/9/9/61	-
3	LMT	A	918	-	-	2/6/6/61	-
3	LMT	B	817	-	-	0/9/9/61	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (76) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	924	LMT	C4-C5-C6-C7
3	B	822	LMT	C4-C5-C6-C7
3	A	925	LMT	C4-C5-C6-C7
3	A	925	LMT	C11-C10-C9-C8
3	B	823	LMT	C4-C5-C6-C7
3	B	823	LMT	C11-C10-C9-C8
3	A	908	LMT	C7-C8-C9-C10
3	B	806	LMT	C7-C8-C9-C10
3	A	922	LMT	C7-C8-C9-C10
3	A	925	LMT	C6-C7-C8-C9
3	B	820	LMT	C7-C8-C9-C10
3	B	823	LMT	C6-C7-C8-C9
3	A	926	LMT	C7-C8-C9-C10
3	B	801	LMT	C7-C8-C9-C10
3	A	912	LMT	C4-C5-C6-C7
3	B	810	LMT	C4-C5-C6-C7
3	A	918	LMT	C6-C7-C8-C9
3	B	816	LMT	C6-C7-C8-C9
3	A	921	LMT	C7-C8-C9-C10
3	B	819	LMT	C7-C8-C9-C10
3	A	914	LMT	C7-C8-C9-C10
3	A	922	LMT	C4-C5-C6-C7
3	B	812	LMT	C7-C8-C9-C10
3	B	820	LMT	C4-C5-C6-C7
3	A	918	LMT	C7-C8-C9-C10
3	B	816	LMT	C7-C8-C9-C10
3	A	925	LMT	C2-C3-C4-C5
3	B	823	LMT	C2-C3-C4-C5
3	A	924	LMT	C3-C4-C5-C6
3	B	822	LMT	C3-C4-C5-C6
3	A	923	LMT	C4-C5-C6-C7
3	B	821	LMT	C4-C5-C6-C7
3	B	808	LMT	C3-C4-C5-C6
3	A	910	LMT	C3-C4-C5-C6
3	A	924	LMT	C1-C2-C3-C4
3	B	822	LMT	C1-C2-C3-C4
3	A	916	LMT	C3-C4-C5-C6
3	B	814	LMT	C3-C4-C5-C6
3	A	904	LMT	C4-C5-C6-C7

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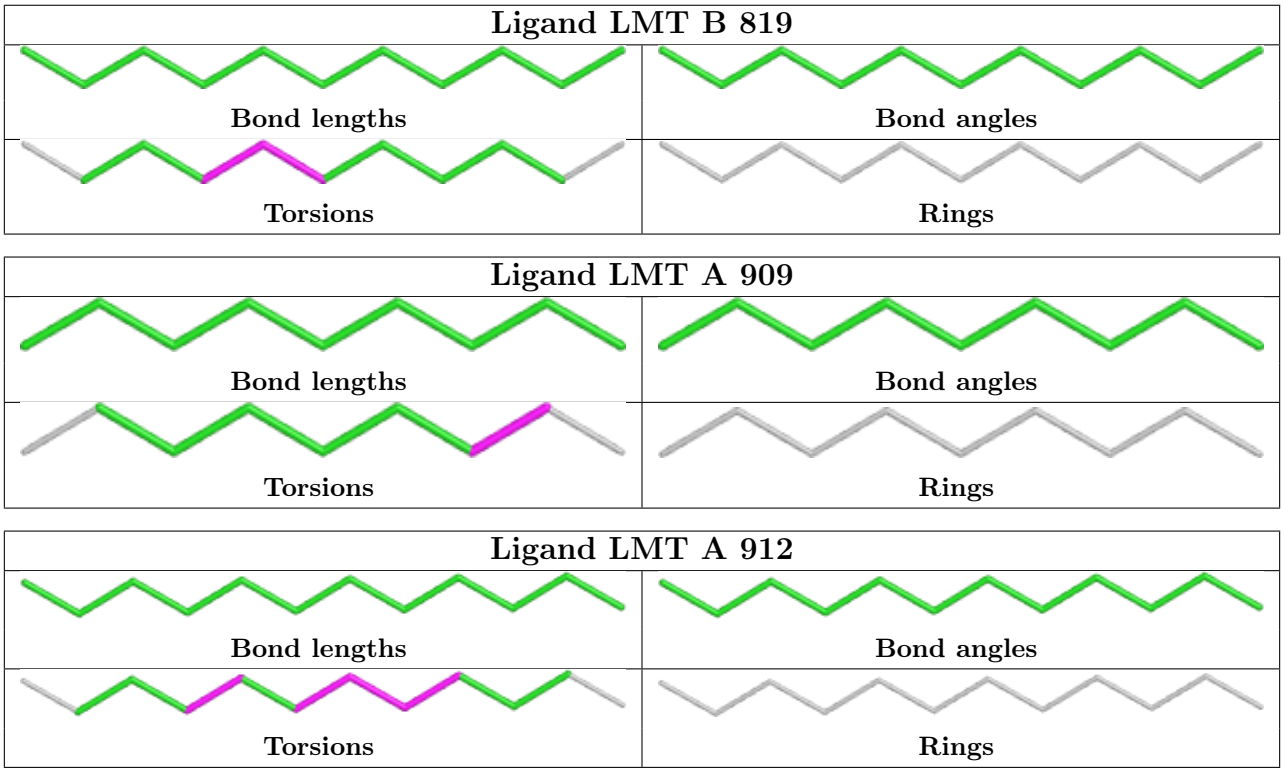
Mol	Chain	Res	Type	Atoms
3	B	802	LMT	C4-C5-C6-C7
3	B	803	LMT	C7-C8-C9-C10
3	A	905	LMT	C7-C8-C9-C10
3	A	913	LMT	C1-C2-C3-C4
3	B	811	LMT	C1-C2-C3-C4
3	A	910	LMT	C5-C6-C7-C8
3	B	808	LMT	C5-C6-C7-C8
3	B	811	LMT	C3-C4-C5-C6
3	A	913	LMT	C3-C4-C5-C6
3	B	814	LMT	C1-C2-C3-C4
3	A	916	LMT	C1-C2-C3-C4
3	A	911	LMT	C4-C5-C6-C7
3	B	809	LMT	C4-C5-C6-C7
3	A	912	LMT	C7-C8-C9-C10
3	B	810	LMT	C7-C8-C9-C10
3	A	923	LMT	C5-C6-C7-C8
3	B	821	LMT	C5-C6-C7-C8
3	A	910	LMT	C4-C5-C6-C7
3	B	808	LMT	C4-C5-C6-C7
3	A	926	LMT	C3-C4-C5-C6
3	B	801	LMT	C3-C4-C5-C6
3	A	922	LMT	C5-C6-C7-C8
3	B	820	LMT	C5-C6-C7-C8
3	B	819	LMT	C6-C7-C8-C9
3	A	921	LMT	C6-C7-C8-C9
3	A	914	LMT	C6-C7-C8-C9
3	B	812	LMT	C6-C7-C8-C9
3	A	909	LMT	C3-C4-C5-C6
3	B	807	LMT	C3-C4-C5-C6
3	B	802	LMT	C5-C6-C7-C8
3	A	904	LMT	C5-C6-C7-C8
3	A	912	LMT	C5-C6-C7-C8
3	B	810	LMT	C5-C6-C7-C8
3	A	922	LMT	C3-C4-C5-C6
3	B	820	LMT	C3-C4-C5-C6
3	B	810	LMT	C3-C4-C5-C6
3	A	912	LMT	C3-C4-C5-C6

There are no ring outliers.

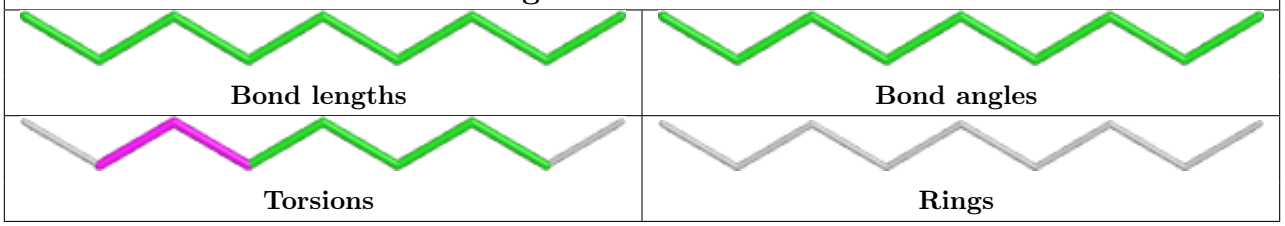
8 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	819	LMT	1	0
3	B	812	LMT	1	0
3	A	924	LMT	1	0
3	A	914	LMT	1	0
3	B	821	LMT	1	0
3	A	923	LMT	1	0
3	A	925	LMT	1	0
3	A	921	LMT	1	0

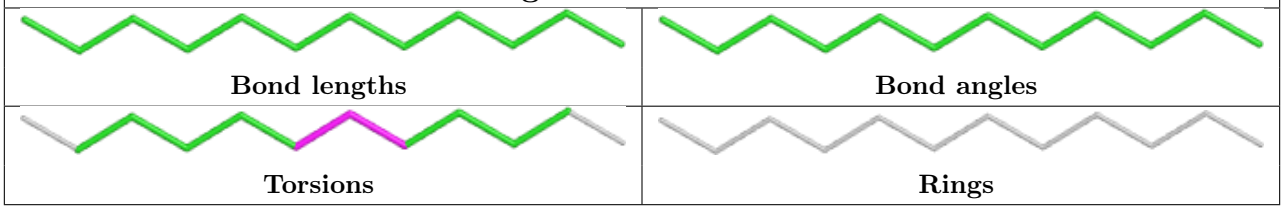
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.



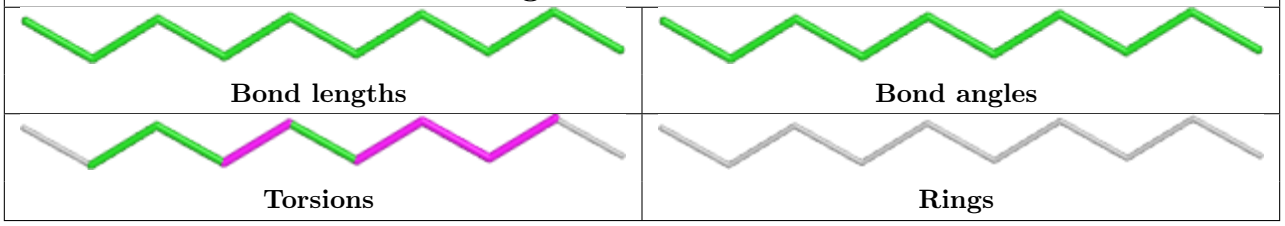
Ligand LMT B 816



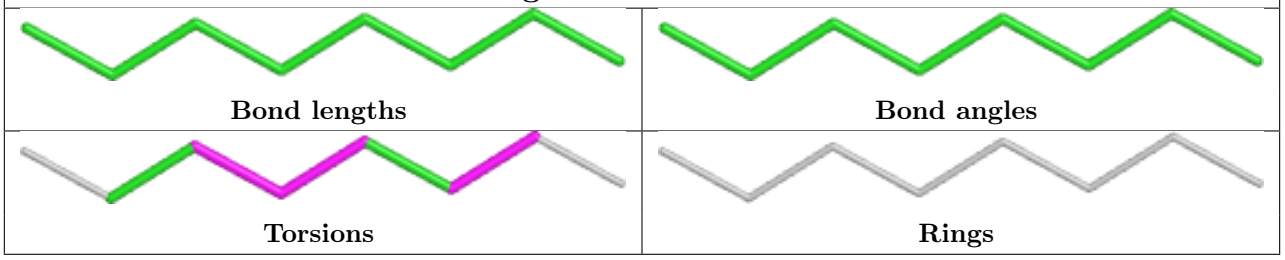
Ligand LMT A 904



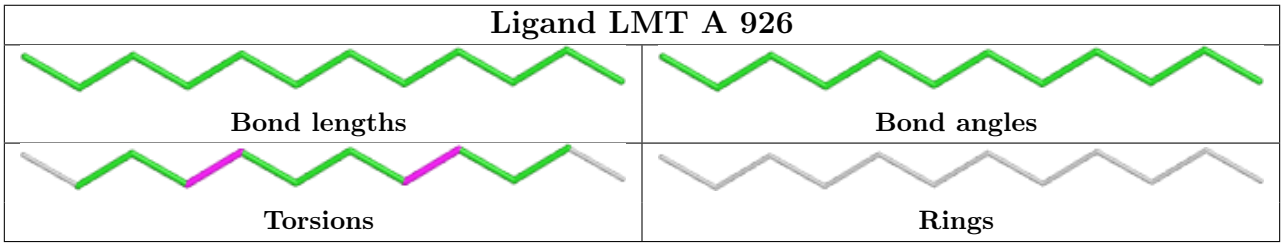
Ligand LMT A 922



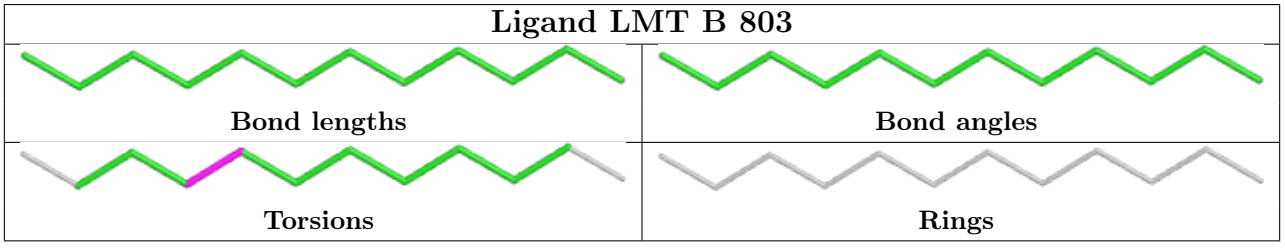
Ligand LMT B 822



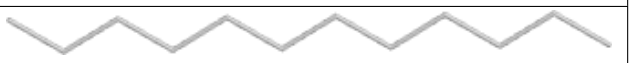
Ligand LMT A 926

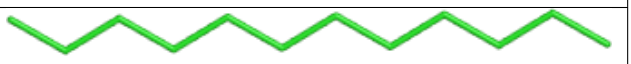


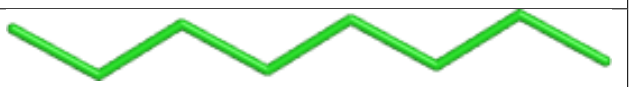
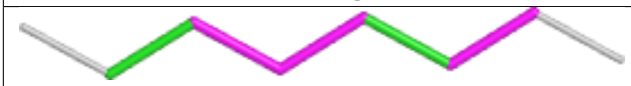
Ligand LMT B 803

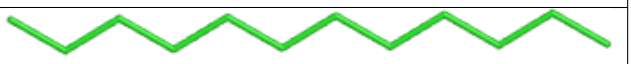
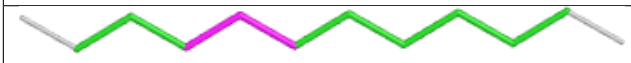


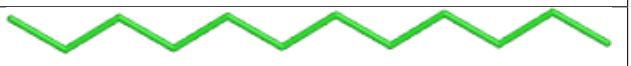
Ligand LMT B 812	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT A 905	
 Bond lengths	 Bond angles
 Torsions	 Rings

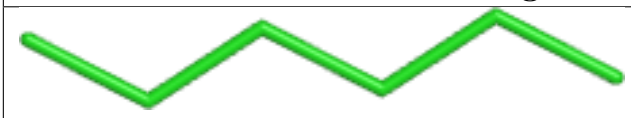
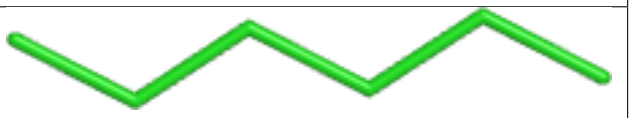
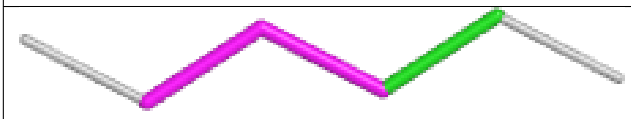
Ligand LMT B 801	
 Bond lengths	 Bond angles
 Torsions	 Rings

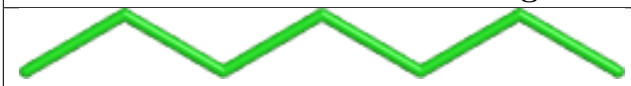
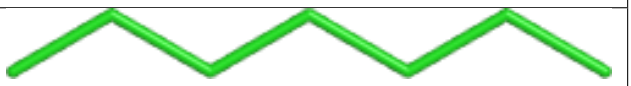
Ligand LMT A 924	
 Bond lengths	 Bond angles
 Torsions	 Rings

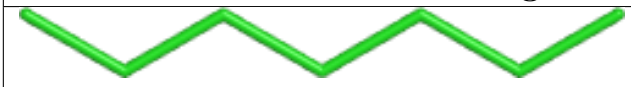
Ligand LMT A 914	
 Bond lengths	 Bond angles
 Torsions	 Rings

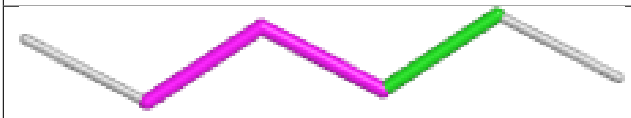
Ligand LMT B 811	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT A 910	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT B 821	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT A 916	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT B 808	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT A 923	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT A 925	
Bond lengths	Bond angles
Torsions	Rings

Ligand LMT A 908	
Bond lengths	Bond angles
Torsions	Rings

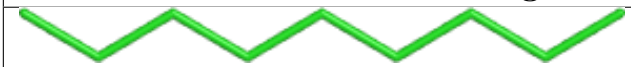
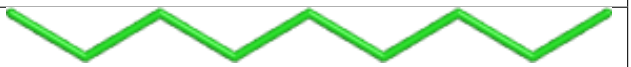
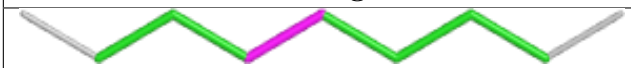
Ligand LMT B 810	
Bond lengths	Bond angles
Torsions	Rings

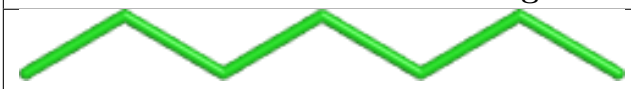
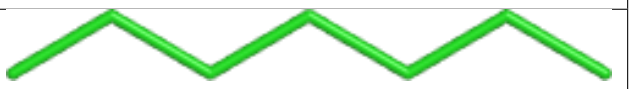
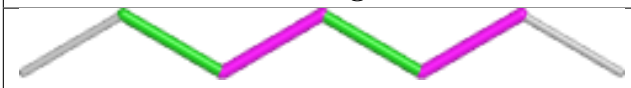
Ligand LMT B 809	
Bond lengths	Bond angles
Torsions	Rings

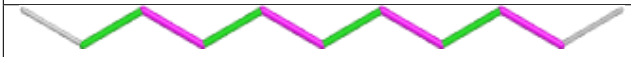
Ligand LMT B 820	
Bond lengths	Bond angles
Torsions	Rings

Ligand LMT A 911	
Bond lengths	Bond angles
Torsions	Rings

Ligand LMT B 802	
 Bond lengths	 Bond angles
 Torsions	 Rings

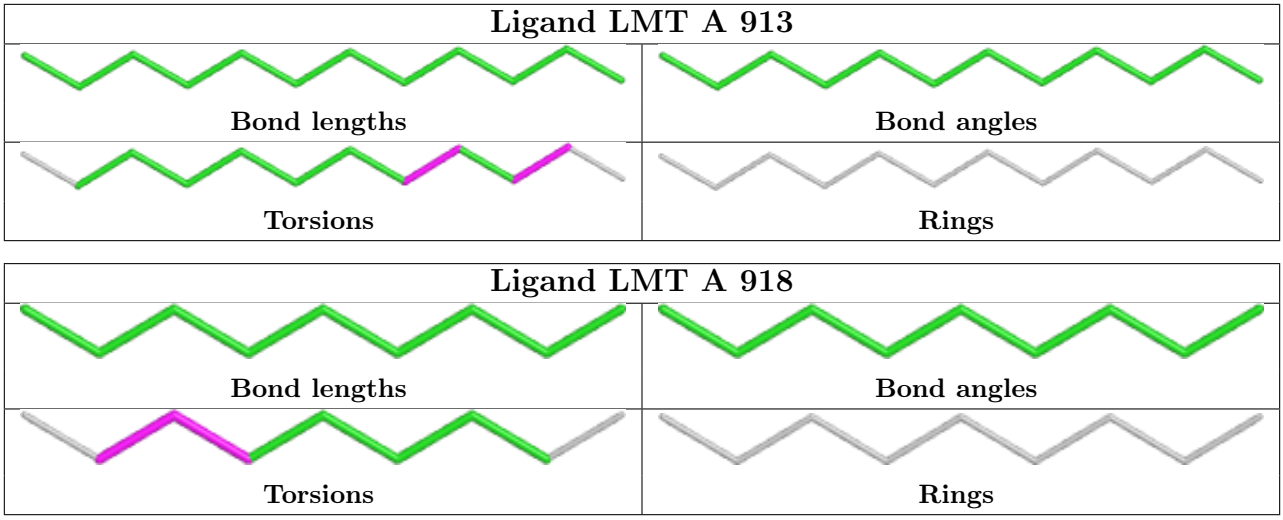
Ligand LMT B 806	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT B 814	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT B 823	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT A 921	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LMT B 807	
 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.

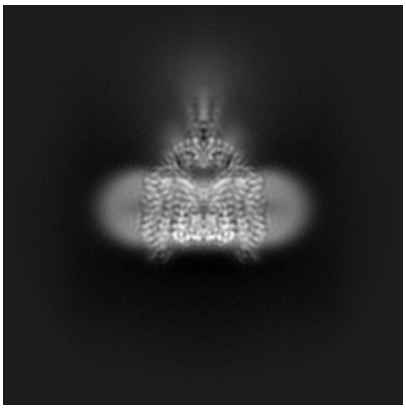
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-71670. These allow visual inspection of the internal detail of the map and identification of artifacts.

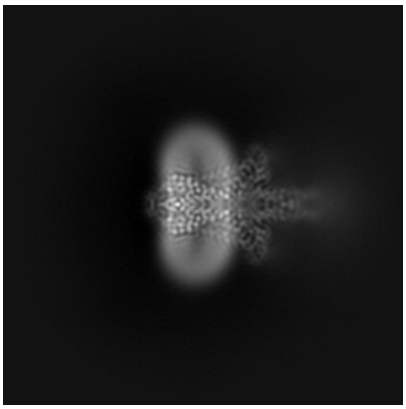
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

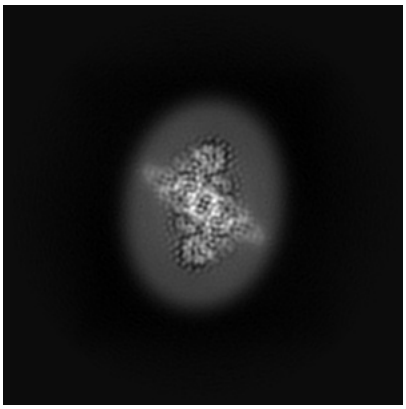
6.1.1 Primary map



X

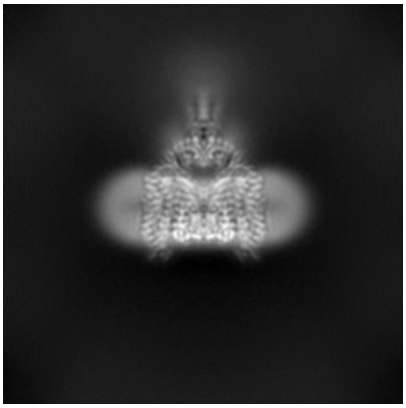


Y

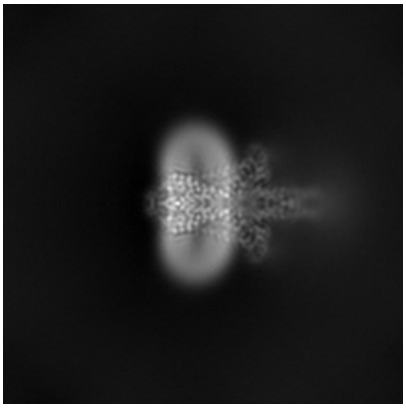


Z

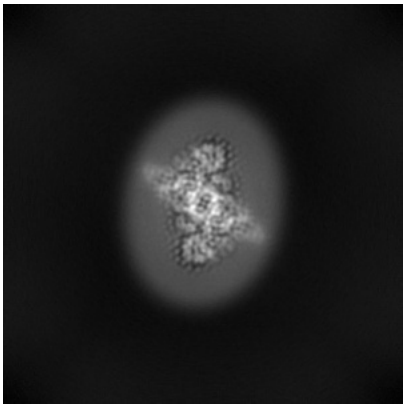
6.1.2 Raw map



X



Y

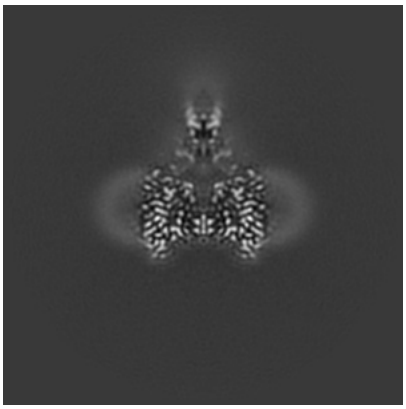


Z

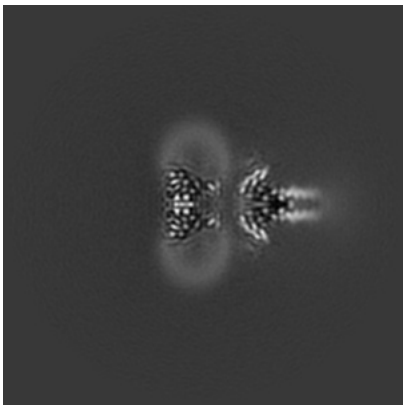
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

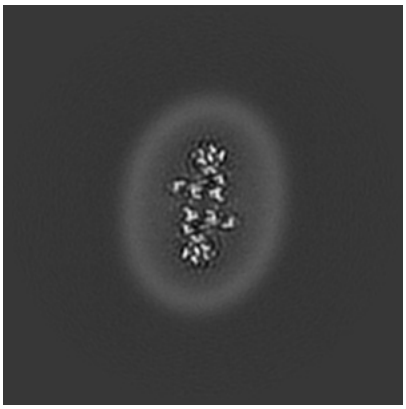
6.2.1 Primary map



X Index: 160

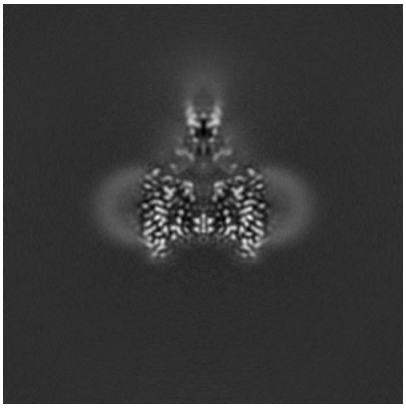


Y Index: 160

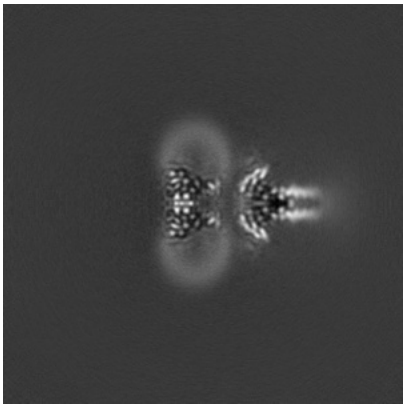


Z Index: 160

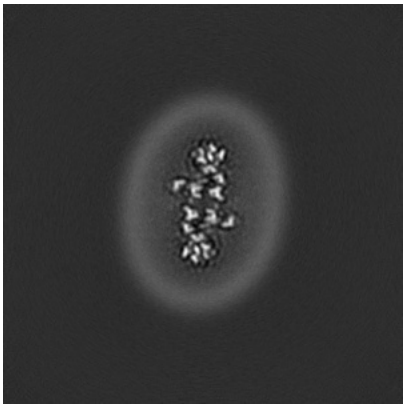
6.2.2 Raw map



X Index: 160



Y Index: 160

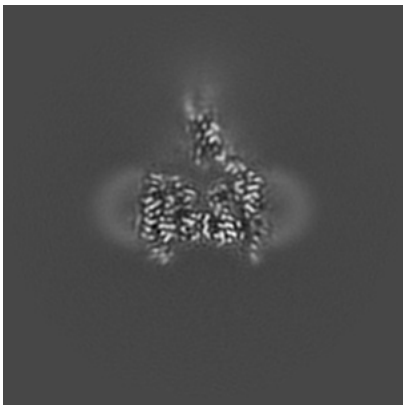


Z Index: 160

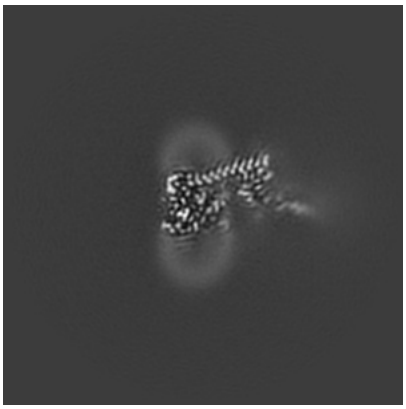
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

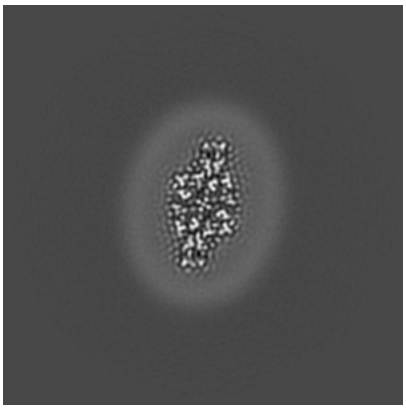
6.3.1 Primary map



X Index: 156

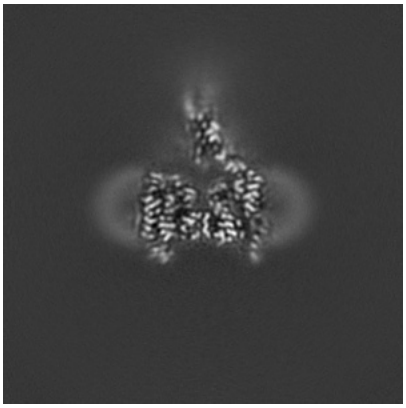


Y Index: 147

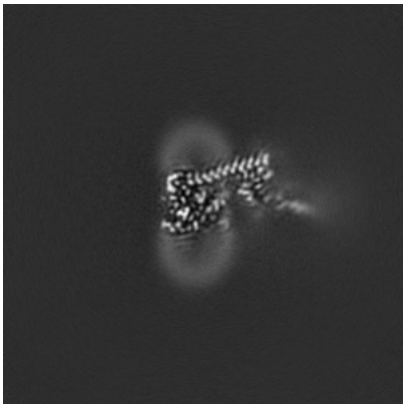


Z Index: 142

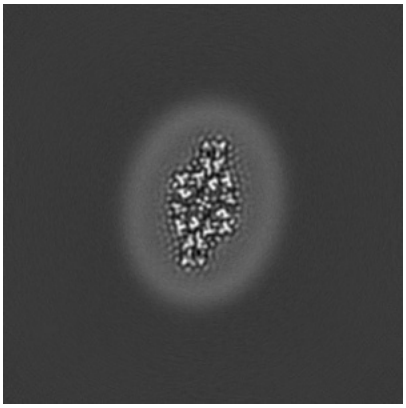
6.3.2 Raw map



X Index: 156



Y Index: 147

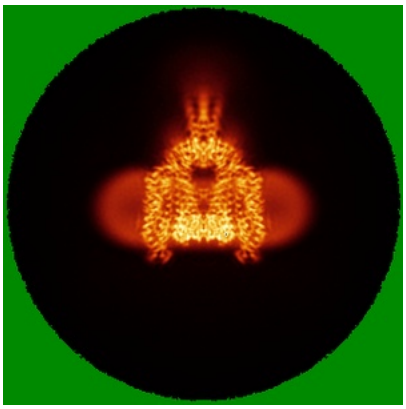


Z Index: 142

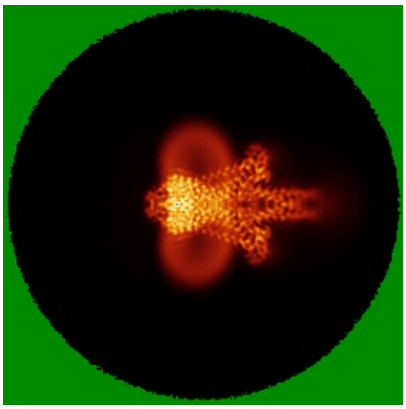
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

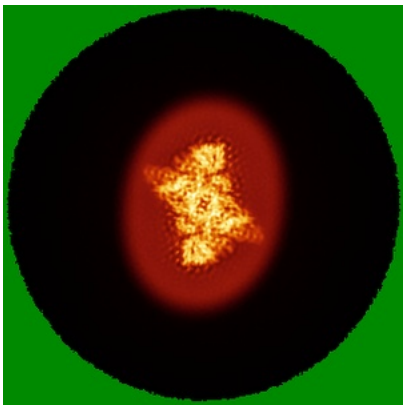
6.4.1 Primary map



X

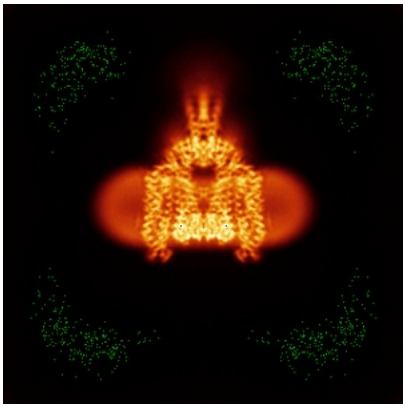


Y

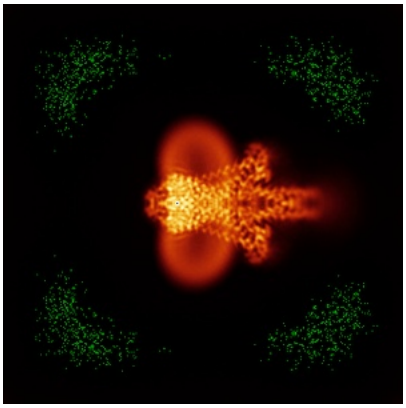


Z

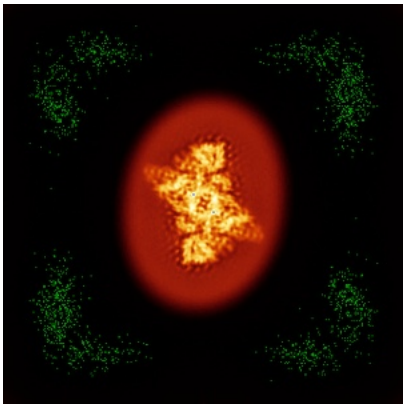
6.4.2 Raw map



X



Y

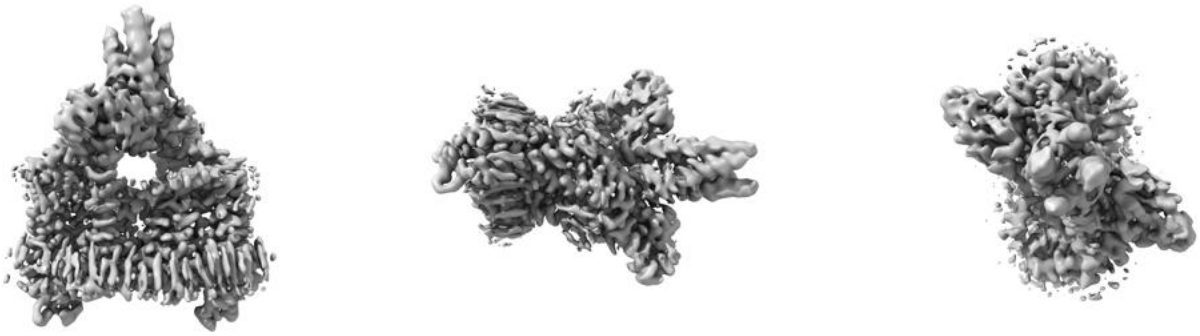


Z

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 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

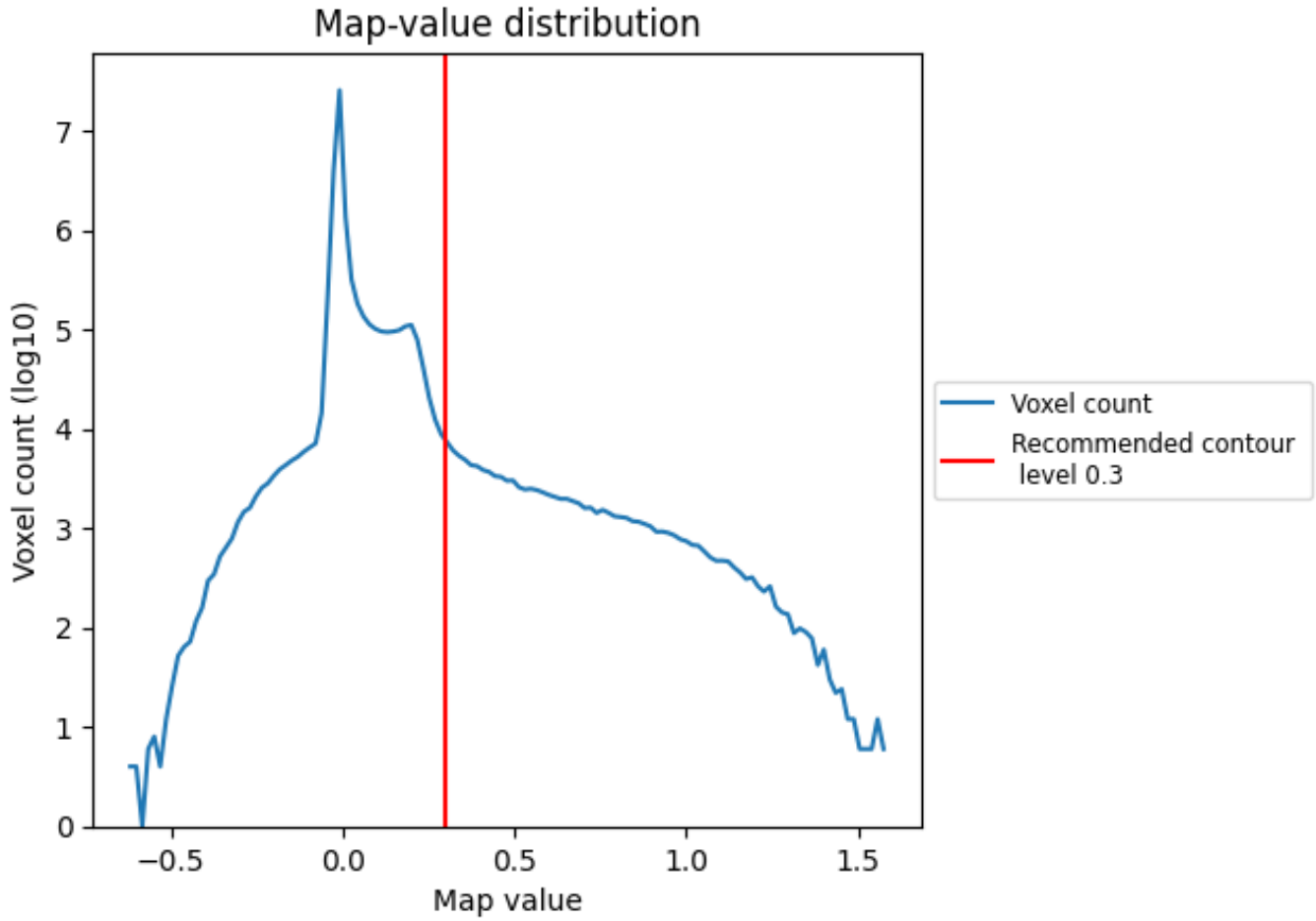
6.6 Mask visualisation (i)

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

7 Map analysis

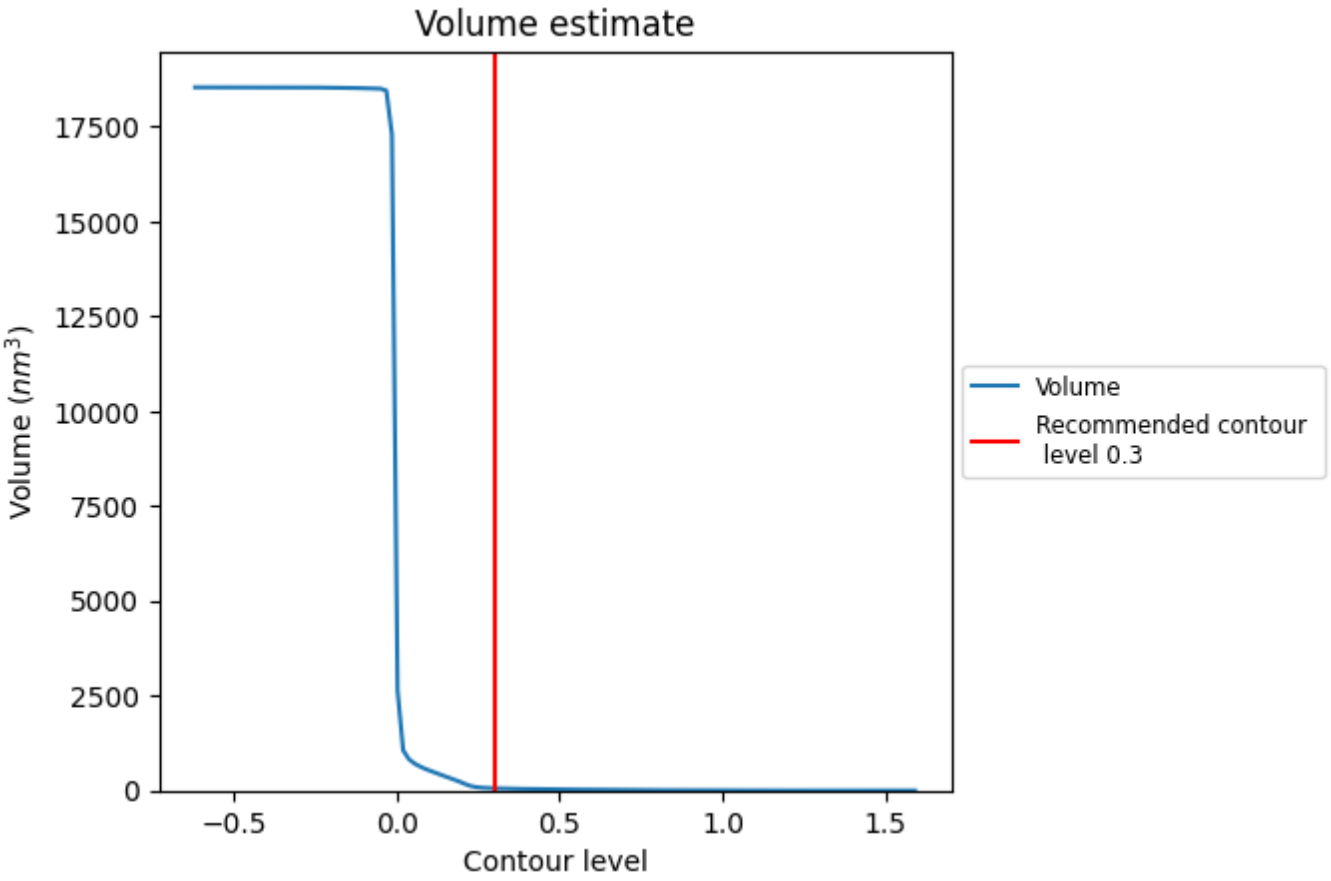
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

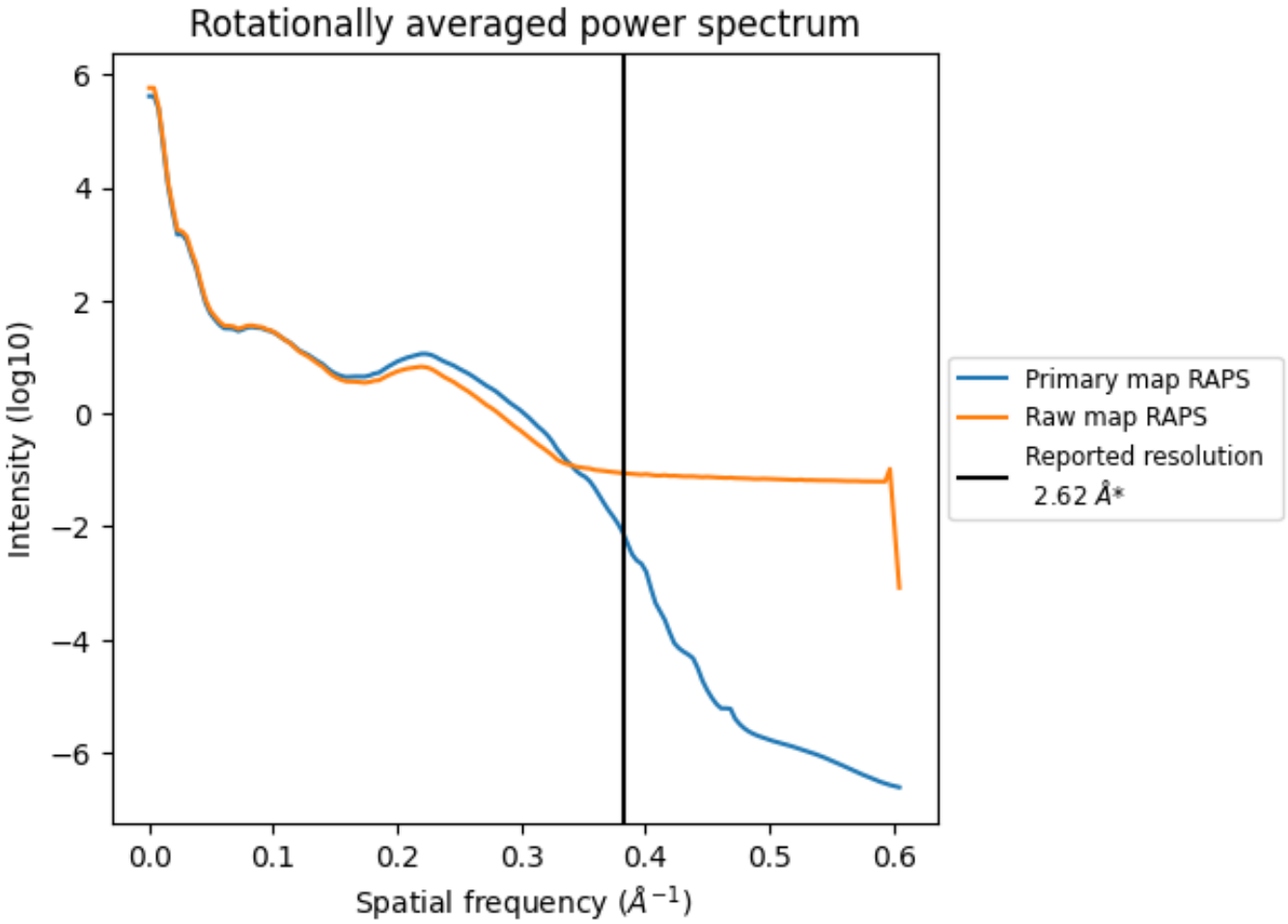
7.2 Volume estimate (i)



The volume at the recommended contour level is 60 nm^3; this corresponds to an approximate mass of 54 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 (i)

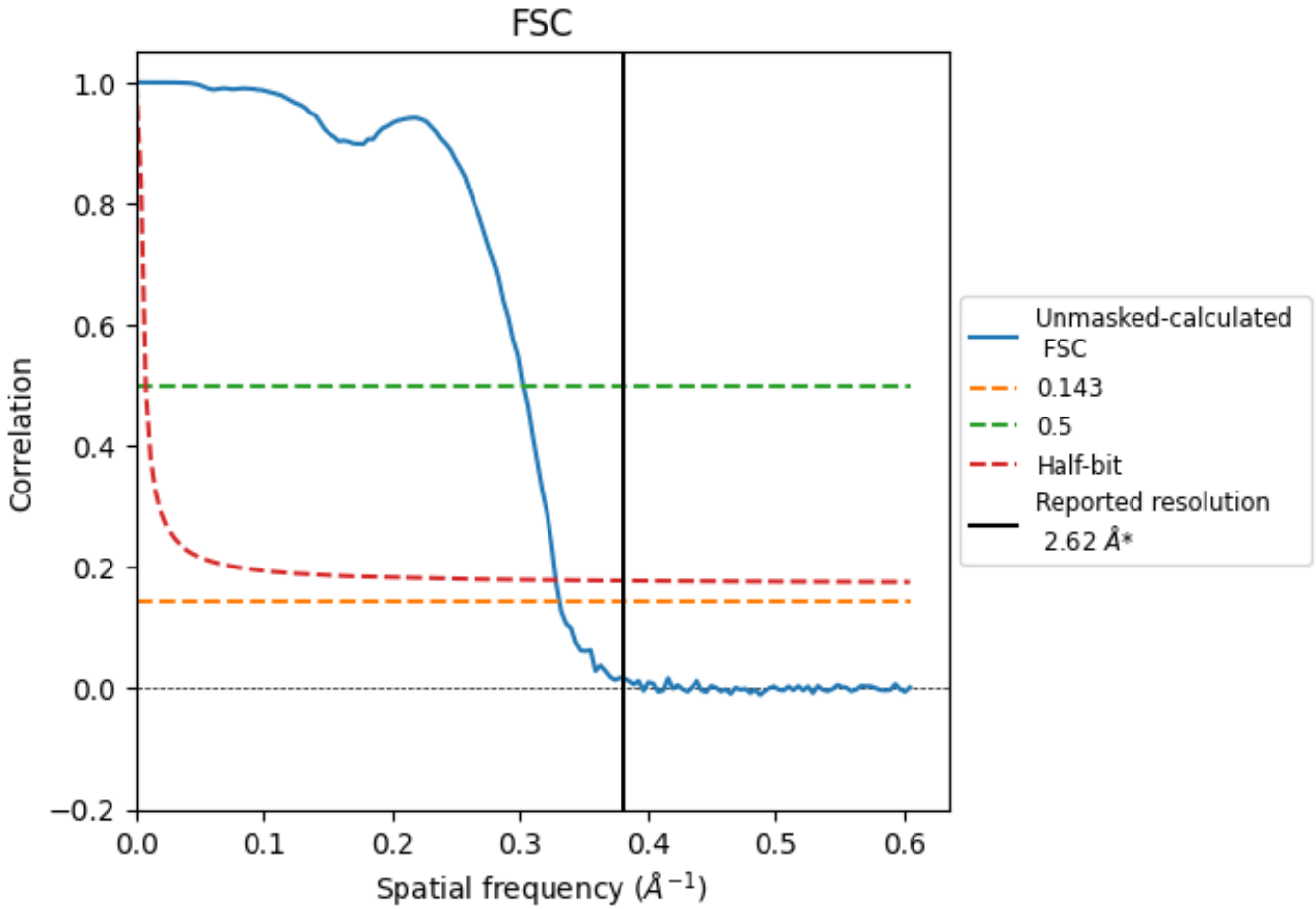


*Reported resolution corresponds to spatial frequency of 0.382 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.382 Å^{-1}

8.2 Resolution estimates (i)

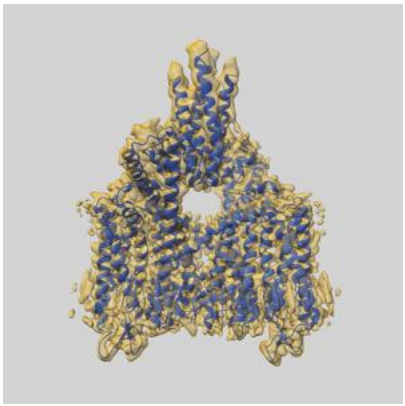
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.62	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.02	3.31	3.05

*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 3.02 differs from the reported value 2.62 by more than 10 %

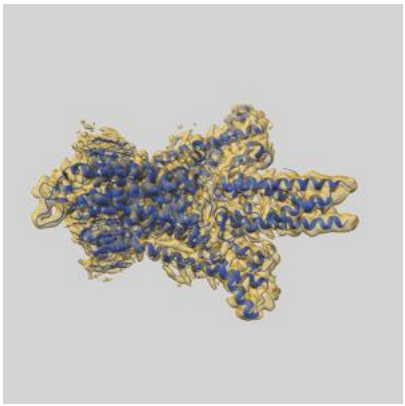
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-71670 and PDB model 9PIK. Per-residue inclusion information can be found in section 3 on page 9.

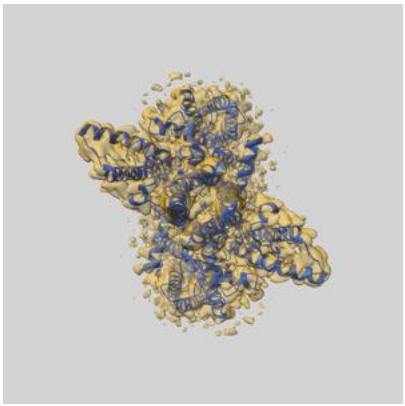
9.1 Map-model overlay



X



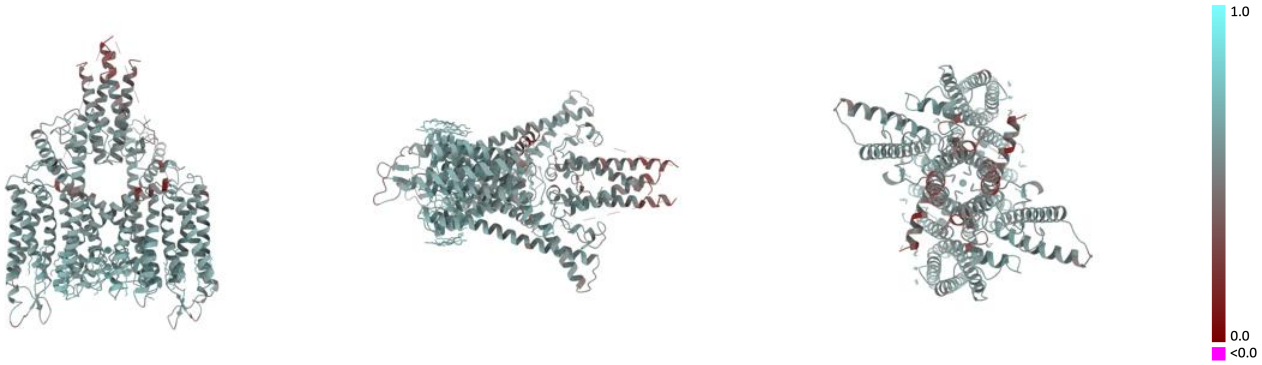
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 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.

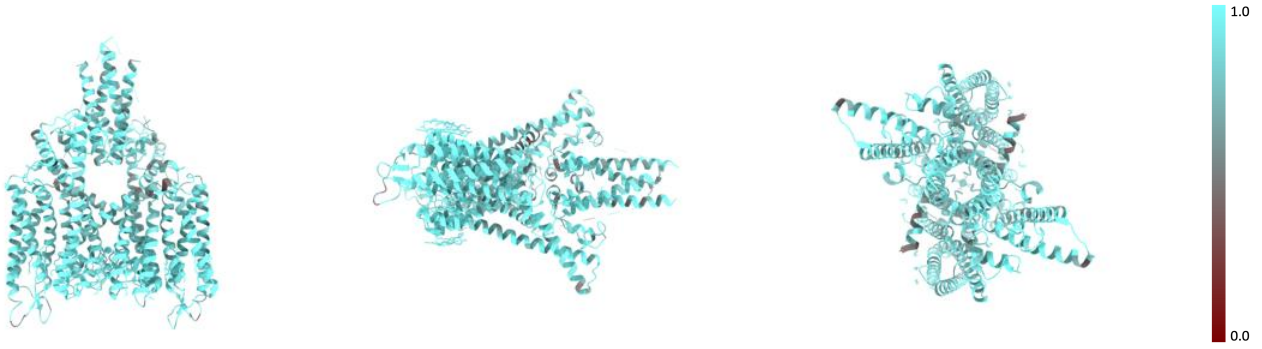
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

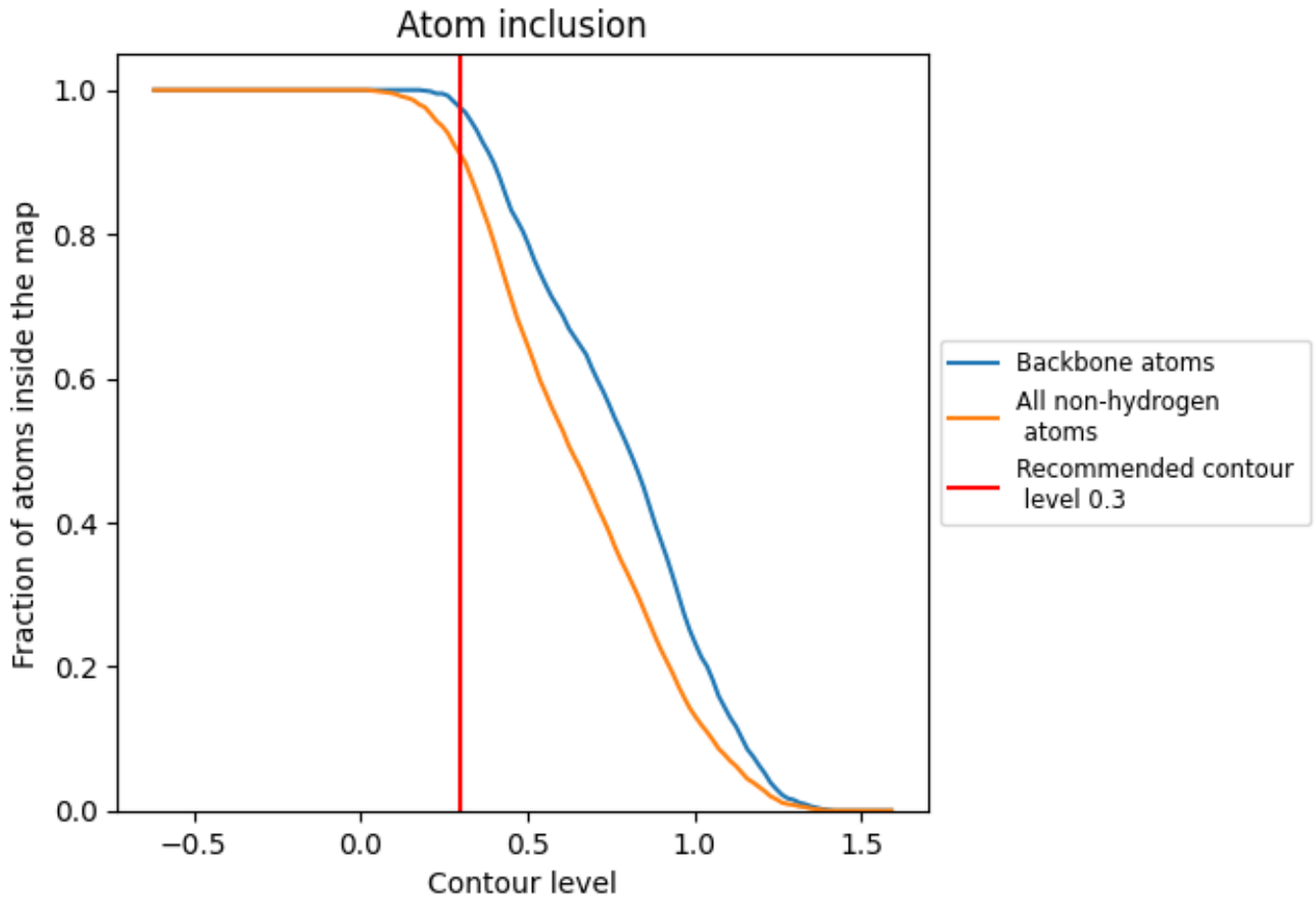
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.9100	0.5610
A	0.9100	0.5610
B	0.9100	0.5610