



Full wwPDB EM Validation Report ⓘ

Dec 17, 2023 – 12:16 AM JST

PDB ID : 8I8R
EMDB ID : EMD-35250
Title : Cryo-EM Structure of OmpC3-MlaA Complex in MSP2N2 Nanodiscs
Authors : Yeow, J.; Luo, M.; Chng, S.S.
Deposited on : 2023-02-05
Resolution : 2.93 Å (reported)
Based on initial model : 5NUP

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.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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) : 2.36

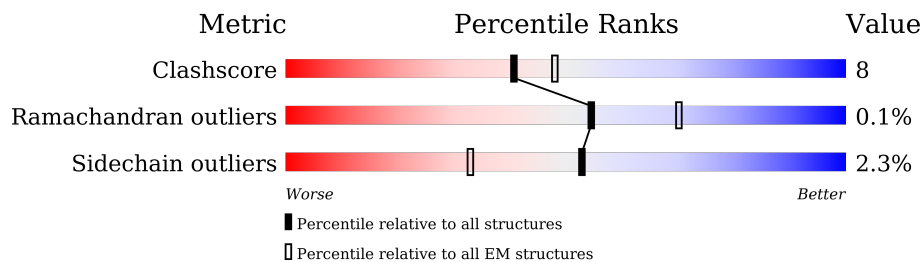
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.93 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 ≥ 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	346	
1	B	346	
1	C	346	
2	D	234	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 10151 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 Outer membrane porin C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	345	Total	C	N	O	S	0	0
			2709	1696	457	553	3		
1	B	345	Total	C	N	O	S	0	0
			2709	1696	457	553	3		
1	C	345	Total	C	N	O	S	0	0
			2709	1696	457	553	3		

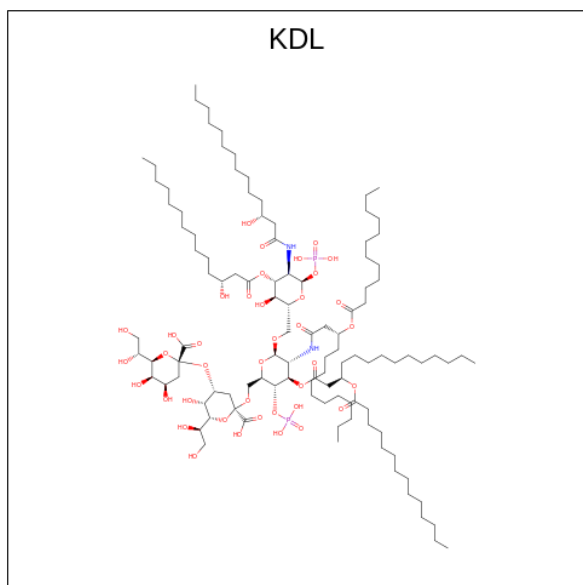
- Molecule 2 is a protein called Intermembrane phospholipid transport system lipoprotein MlaA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	197	Total	C	N	O	S	0	0
			1565	1015	261	281	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	188	CYS	GLN	engineered mutation	UNP P76506

- Molecule 3 is (2 {R},4 {R},5 {R},6 {R})-6-[(1 {R})-1,2-bis(oxidanyl)ethyl]-2-[(2 {R},4 {R},5 {R},6 {R})-6-[(1 {R})-1,2-bis(oxidanyl)ethyl]-2-carboxy-2-[(2 {R},3 {S},4 {R},5 {R},6 {R})-5-[(3 {R})-3-dodecanoyloxytetradecanoyl]amino]-6-[(2 {R},3 {S},4 {R},5 {R},6 {R})-3-oxidanyl-5-[(3 {R})-3-oxidanyltetradecanoyl]amino]-4-[(3 {R})-3-oxidanyltetradecanoyl]oxy-6-phosphonoxy-oxan-2-yl]methoxy]-3-phosphonoxy-4-[(3 {R})-3-tetradecanoyloxytetradecanoyl]oxy-oxan-2-yl]methoxy]-5-oxidanyl-oxan-4-yl]oxy-4,5-bis(oxidanyl)oxane-2-carboxylic acid (three-letter code: KDL) (formula: C₁₁₀H₂₀₂N₂O₃₉P₂).

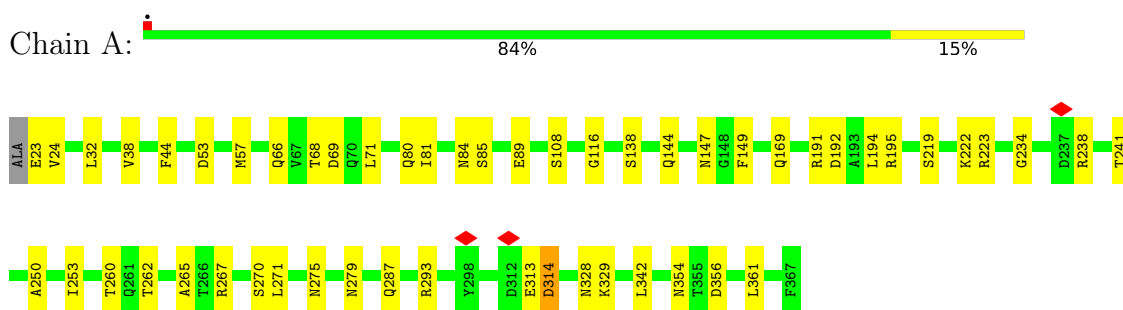


Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
3	A	1	Total 153	110	2	39	2	0
3	B	1	Total 153	110	2	39	2	0
3	C	1	Total 153	110	2	39	2	0

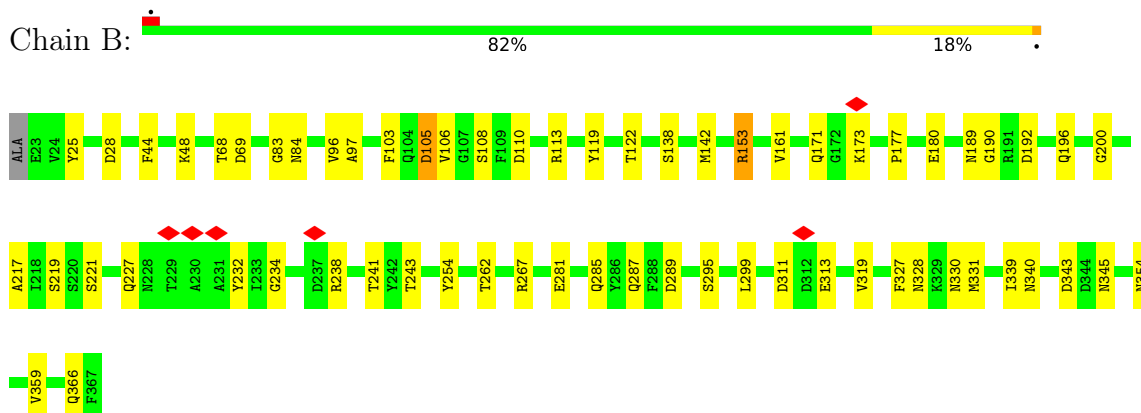
3 Residue-property plots

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

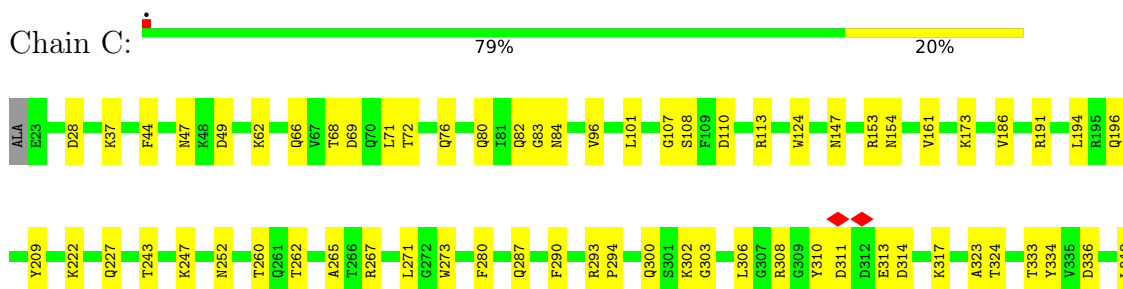
- Molecule 1: Outer membrane porin C



- Molecule 1: Outer membrane porin C

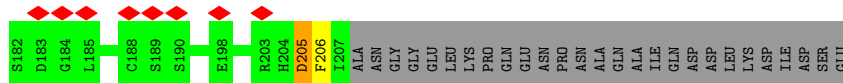
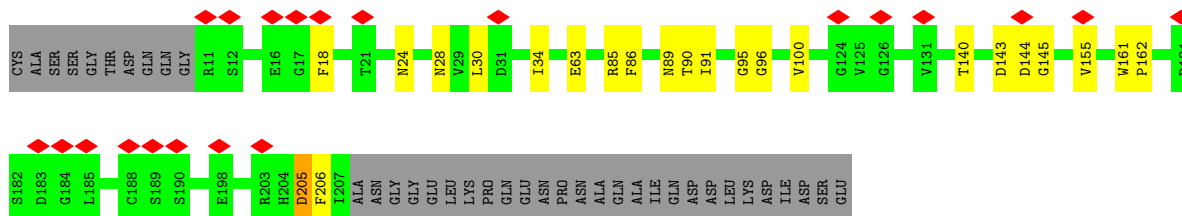
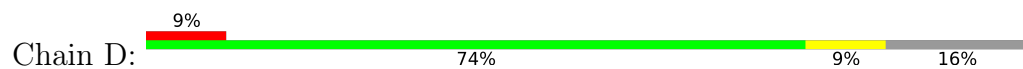


- Molecule 1: Outer membrane porin C





- Molecule 2: Intermembrane phospholipid transport system lipoprotein MlaA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	205487	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Patch CTF routine in cryoSPARC	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	90	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.517	Depositor
Minimum map value	-0.199	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.12	Depositor
Map size (\AA)	266.88, 266.88, 266.88	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.834, 0.834, 0.834	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.24	0/2768	0.46	0/3746
1	B	0.24	0/2768	0.46	0/3746
1	C	0.25	0/2768	0.46	0/3746
2	D	0.24	0/1617	0.44	0/2204
All	All	0.24	0/9921	0.46	0/13442

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2709	0	2483	37	0
1	B	2709	0	2483	47	0
1	C	2709	0	2483	42	0
2	D	1565	0	1468	16	0
3	A	153	0	0	10	0
3	B	153	0	0	19	0
3	C	153	0	0	6	0
All	All	10151	0	8917	143	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 8.

All (143) 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:173:LYS:HZ1	3:B:401:KDL:CBK	1.79	0.95
1:B:173:LYS:NZ	3:B:401:KDL:CBK	2.30	0.94
1:A:238:ARG:NH2	3:A:401:KDL:OHE	2.04	0.89
3:B:401:KDL:CFH	2:D:91:ILE:CD1	2.53	0.86
3:B:401:KDL:CFH	2:D:91:ILE:HD12	2.11	0.80
3:B:401:KDL:CFH	2:D:91:ILE:HD13	2.15	0.75
1:A:44:PHE:HE1	3:B:401:KDL:CDQ	2.04	0.71
1:B:173:LYS:HZ2	3:B:401:KDL:CBK	2.08	0.66
1:A:361:LEU:HD11	3:B:401:KDL:CDY	2.27	0.65
1:B:48:LYS:HB3	1:C:186:VAL:HB	1.78	0.64
1:B:285:GLN:HE21	1:B:295:SER:HB2	1.63	0.63
2:D:140:THR:H	2:D:144:ASP:HB2	1.64	0.62
1:A:262:THR:HB	1:A:265:ALA:HB3	1.81	0.62
1:B:142:MET:SD	1:B:171:GLN:NE2	2.74	0.61
1:B:330:ASN:HB3	1:B:366:GLN:HB2	1.84	0.60
2:D:89:ASN:HB3	2:D:96:GLY:HA2	1.83	0.59
1:C:71:LEU:HD21	1:C:101:LEU:HD22	1.85	0.59
1:C:280:PHE:HB3	1:C:300:GLN:HE21	1.67	0.58
1:C:302:LYS:HA	1:C:314:ASP:HA	1.86	0.58
1:A:192:ASP:OD1	1:A:192:ASP:N	2.35	0.58
1:A:361:LEU:CD1	3:B:401:KDL:CDZ	2.82	0.58
1:A:147:ASN:ND2	1:C:83:GLY:O	2.36	0.58
1:A:260:THR:HB	1:A:279:ASN:HB2	1.86	0.58
1:C:311:ASP:N	1:C:311:ASP:OD1	2.38	0.57
1:B:108:SER:N	1:B:153:ARG:O	2.38	0.56
1:B:119:TYR:HA	1:B:122:THR:HG22	1.88	0.56
1:A:66:GLN:NE2	1:A:68:THR:O	2.33	0.56
1:B:138:SER:O	1:B:267:ARG:NH2	2.39	0.55
1:A:223:ARG:NH2	1:A:234:GLY:O	2.40	0.55
1:B:311:ASP:OD1	1:B:311:ASP:N	2.35	0.55
1:B:83:GLY:O	1:C:147:ASN:ND2	2.40	0.54
1:B:110:ASP:OD1	1:B:110:ASP:N	2.40	0.54
1:B:105:ASP:N	1:B:105:ASP:OD1	2.40	0.54
1:A:361:LEU:HD11	3:B:401:KDL:CDZ	2.38	0.53
1:A:23:GLU:N	1:A:32:LEU:O	2.42	0.53
1:A:238:ARG:HH22	3:A:401:KDL:CFL	2.21	0.53
1:C:310:TYR:HB3	1:C:313:GLU:HG3	1.90	0.53
1:B:238:ARG:NH1	3:B:401:KDL:OHE	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:401:KDL:CFG	2:D:91:ILE:HD12	2.38	0.53
1:A:38:VAL:HG22	1:A:57:MET:HG2	1.92	0.52
1:C:68:THR:OG1	1:C:69:ASP:N	2.43	0.52
1:C:124:TRP:HB3	1:C:247:LYS:HG3	1.91	0.52
1:B:44:PHE:HE1	3:C:401:KDL:CDQ	2.23	0.52
2:D:24:ASN:OD1	2:D:28:ASN:ND2	2.43	0.52
3:B:401:KDL:CFG	2:D:91:ILE:CD1	2.88	0.51
1:B:254:TYR:HB3	1:B:285:GLN:HB2	1.91	0.51
1:B:97:ALA:H	1:B:113:ARG:HB3	1.76	0.51
1:C:110:ASP:N	1:C:110:ASP:OD1	2.44	0.51
2:D:30:LEU:HG	2:D:34:ILE:HD13	1.92	0.50
2:D:140:THR:O	2:D:145:GLY:N	2.43	0.50
1:B:217:ALA:HB3	1:B:243:THR:HB	1.92	0.50
1:C:324:THR:HG23	1:C:334:TYR:HB3	1.93	0.50
1:A:314:ASP:HB3	1:A:342:LEU:HD21	1.93	0.49
1:B:327:PHE:N	1:B:331:MET:O	2.39	0.49
1:C:96:VAL:HA	1:C:113:ARG:HG2	1.94	0.49
1:C:333:THR:HG22	1:C:363:LEU:HB3	1.95	0.49
1:B:44:PHE:HB2	1:B:359:VAL:HG13	1.95	0.49
1:C:173:LYS:HZ1	3:C:401:KDL:CBK	2.25	0.48
3:A:401:KDL:CDS	1:C:44:PHE:HE1	2.27	0.48
1:C:66:GLN:OE1	1:C:72:THR:OG1	2.32	0.48
1:C:317:LYS:H	1:C:342:LEU:HD23	1.78	0.48
1:A:84:ASN:HB2	1:B:189:ASN:HD22	1.79	0.48
1:B:103:PHE:HB2	1:B:106:VAL:HG22	1.96	0.48
1:C:194:LEU:O	1:C:267:ARG:NH1	2.47	0.48
1:B:343:ASP:OD1	1:B:343:ASP:N	2.46	0.47
1:C:28:ASP:N	1:C:28:ASP:OD1	2.38	0.47
1:C:62:LYS:HG3	1:C:76:GLN:HG3	1.96	0.47
1:A:354:ASN:ND2	1:A:356:ASP:OD1	2.48	0.47
1:C:69:ASP:N	1:C:69:ASP:OD1	2.44	0.47
1:B:219:SER:HB3	1:B:241:THR:HB	1.96	0.47
1:A:138:SER:HA	1:A:144:GLN:HB3	1.96	0.46
1:A:329:LYS:NZ	1:B:28:ASP:OD1	2.49	0.46
1:C:262:THR:HB	1:C:265:ALA:HB3	1.97	0.46
2:D:63:GLU:HB3	2:D:86:PHE:HB2	1.97	0.46
1:A:194:LEU:HG	1:A:267:ARG:HD3	1.97	0.46
1:B:196:GLN:O	1:B:227:GLN:NE2	2.49	0.46
1:B:96:VAL:HA	1:B:113:ARG:HG2	1.97	0.46
1:C:293:ARG:N	1:C:324:THR:O	2.47	0.46
1:B:173:LYS:NZ	3:B:401:KDL:CBI	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:ASN:OD1	1:A:328:ASN:N	2.48	0.45
1:B:319:VAL:HG13	1:B:339:ILE:HB	1.98	0.45
1:A:85:SER:HB2	1:A:89:GLU:HG3	1.97	0.45
1:A:241:THR:HG23	1:A:262:THR:HG22	1.98	0.45
1:B:328:ASN:OD1	1:B:328:ASN:N	2.44	0.45
1:A:222:LYS:HE3	3:A:401:KDL:O4	2.16	0.45
1:B:84:ASN:O	1:C:191:ARG:NH2	2.46	0.45
1:A:191:ARG:HG3	1:A:195:ARG:HG3	1.99	0.44
1:A:24:VAL:HG12	1:B:25:TYR:HB2	1.98	0.44
1:C:354:ASN:HD22	1:C:358:ILE:HD11	1.83	0.44
1:A:287:GLN:OE1	1:A:293:ARG:NH1	2.50	0.44
1:B:192:ASP:N	1:B:192:ASP:OD1	2.50	0.44
1:C:267:ARG:HG2	1:C:273:TRP:CD1	2.53	0.44
1:A:361:LEU:CD1	3:B:401:KDL:CEA	2.95	0.44
1:B:103:PHE:HZ	2:D:100:VAL:HG13	1.80	0.44
1:C:47:ASN:HD21	1:C:49:ASP:HB2	1.83	0.44
1:B:68:THR:OG1	1:B:69:ASP:N	2.50	0.44
1:B:177:PRO:HA	1:B:190:GLY:HA3	1.99	0.44
1:C:252:ASN:HB3	1:C:287:GLN:HB3	2.00	0.44
1:B:281:GLU:HB3	1:B:299:LEU:HG	2.00	0.43
1:B:289:ASP:N	1:B:289:ASP:OD1	2.46	0.43
1:C:108:SER:N	1:C:153:ARG:O	2.49	0.43
3:A:401:KDL:OBF	3:A:401:KDL:OBJ	2.35	0.43
1:C:80:GLN:HE21	1:C:82:GLN:HE21	1.66	0.43
1:C:243:THR:HG23	1:C:260:THR:HG22	2.00	0.43
1:C:303:GLY:HA3	1:C:306:LEU:HD11	1.99	0.43
1:A:69:ASP:N	1:A:69:ASP:OD1	2.49	0.43
1:C:271:LEU:HD22	1:C:308:ARG:HH12	1.82	0.43
1:A:68:THR:HG23	1:A:71:LEU:H	1.84	0.43
1:B:354:ASN:N	1:B:354:ASN:OD1	2.47	0.43
1:C:107:GLY:HA2	1:C:154:ASN:HA	1.99	0.43
1:C:294:PRO:HA	1:C:323:ALA:HA	2.01	0.43
1:A:194:LEU:HD21	1:A:270:SER:HA	2.00	0.43
1:B:173:LYS:HZ2	3:B:401:KDL:CBI	2.32	0.43
3:A:401:KDL:OEC	3:A:401:KDL:OED	2.35	0.42
1:A:238:ARG:HH12	3:A:401:KDL:CFL	2.33	0.42
1:A:44:PHE:CE1	3:B:401:KDL:CDQ	2.93	0.42
1:C:37:LYS:HE3	1:C:366:GLN:HG2	2.01	0.42
2:D:205:ASP:HB3	2:D:206:PHE:H	1.53	0.42
1:A:250:ALA:O	1:A:253:ILE:HG12	2.20	0.42
1:B:232:TYR:O	1:B:234:GLY:N	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:401:KDL:OET	3:A:401:KDL:OAQ	2.36	0.42
1:B:313:GLU:OE1	1:B:345:ASN:ND2	2.50	0.42
1:B:241:THR:HG23	1:B:262:THR:HG22	2.01	0.42
3:A:401:KDL:CDS	1:C:44:PHE:CE1	3.03	0.42
2:D:86:PHE:O	2:D:90:THR:OG1	2.30	0.42
1:C:345:ASN:OD1	1:C:345:ASN:N	2.52	0.42
3:C:401:KDL:OEC	3:C:401:KDL:OED	2.37	0.41
1:C:173:LYS:NZ	3:C:401:KDL:CBK	2.83	0.41
3:C:401:KDL:OCA	3:C:401:KDL:OBW	2.38	0.41
3:A:401:KDL:OCA	3:A:401:KDL:OBW	2.38	0.41
3:B:401:KDL:OAQ	3:B:401:KDL:OET	2.37	0.41
1:C:196:GLN:O	1:C:227:GLN:NE2	2.52	0.41
3:C:401:KDL:OBJ	3:C:401:KDL:OBF	2.38	0.41
1:A:57:MET:N	1:A:81:ILE:O	2.52	0.41
1:A:116:GLY:HA2	1:A:169:GLN:HE22	1.85	0.41
2:D:90:THR:HA	2:D:95:GLY:HA2	2.02	0.41
1:B:340:ASN:ND2	1:B:354:ASN:O	2.53	0.41
2:D:161:TRP:CD1	2:D:162:PRO:HD3	2.55	0.41
1:B:171:GLN:HB3	1:B:200:GLY:H	1.84	0.41
3:B:401:KDL:OBJ	3:B:401:KDL:OBF	2.39	0.41
1:B:200:GLY:HA3	1:B:221:SER:HA	2.03	0.41
1:A:149:PHE:HD1	1:A:149:PHE:HA	1.79	0.40
1:C:68:THR:OG1	1:C:69:ASP:OD1	2.39	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	343/346 (99%)	335 (98%)	8 (2%)	0	100 100
1	B	343/346 (99%)	328 (96%)	15 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	343/346 (99%)	337 (98%)	6 (2%)	0	100	100
2	D	195/234 (83%)	193 (99%)	1 (0%)	1 (0%)	29	60
All	All	1224/1272 (96%)	1193 (98%)	30 (2%)	1 (0%)	54	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	155	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	275/275 (100%)	267 (97%)	8 (3%)	42	73
1	B	275/275 (100%)	270 (98%)	5 (2%)	59	82
1	C	275/275 (100%)	269 (98%)	6 (2%)	52	78
2	D	162/196 (83%)	158 (98%)	4 (2%)	47	76
All	All	987/1021 (97%)	964 (98%)	23 (2%)	53	78

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ASP
1	A	80	GLN
1	A	108	SER
1	A	219	SER
1	A	271	LEU
1	A	275	ASN
1	A	313	GLU
1	A	314	ASP
1	B	105	ASP
1	B	153	ARG
1	B	161	VAL

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Mol	Chain	Res	Type
1	B	180	GLU
1	B	287	GLN
1	C	84	ASN
1	C	161	VAL
1	C	209	TYR
1	C	222	LYS
1	C	290	PHE
1	C	336	ASP
2	D	18	PHE
2	D	85	ARG
2	D	143	ASP
2	D	205	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	ASN
1	A	174	ASN
1	A	258	GLN
1	A	340	ASN
1	B	171	GLN
1	B	174	ASN
1	B	227	GLN
1	C	82	GLN
1	C	88	ASN
2	D	56	ASN
2	D	178	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

3 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
3	KDL	A	401	-	153,156,156	1.94	31 (20%)	184,201,201	1.66	36 (19%)
3	KDL	C	401	-	153,156,156	1.87	30 (19%)	184,201,201	1.64	33 (17%)
3	KDL	B	401	-	153,156,156	1.94	30 (19%)	184,201,201	1.72	33 (17%)

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	KDL	A	401	-	-	94/156/234/234	0/4/4/4
3	KDL	C	401	-	-	76/156/234/234	0/4/4/4
3	KDL	B	401	-	-	87/156/234/234	0/4/4/4

All (91) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	KDL	OBW-CBP	6.91	1.51	1.42
3	C	401	KDL	OBW-CBP	6.86	1.51	1.42
3	A	401	KDL	OBW-CBP	6.79	1.51	1.42
3	A	401	KDL	OBH-CBA	6.62	1.51	1.42
3	B	401	KDL	OBH-CBA	6.55	1.51	1.42
3	C	401	KDL	OBH-CBA	6.52	1.51	1.42
3	B	401	KDL	C2-N2	6.19	1.55	1.45
3	A	401	KDL	C2-N2	6.08	1.55	1.45
3	B	401	KDL	C7-N2	5.85	1.46	1.34
3	A	401	KDL	C7-N2	5.69	1.46	1.34
3	B	401	KDL	OAQ-CAP	5.65	1.53	1.44
3	A	401	KDL	OAQ-CAP	5.59	1.53	1.44
3	A	401	KDL	CDO-NAO	5.32	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	KDL	CDO-NAO	5.32	1.45	1.34
3	C	401	KDL	OAQ-CAP	5.29	1.52	1.44
3	C	401	KDL	C2-N2	5.24	1.54	1.45
3	C	401	KDL	C7-N2	5.23	1.45	1.34
3	C	401	KDL	CDO-NAO	5.17	1.45	1.34
3	B	401	KDL	PHC-O4	4.95	1.68	1.59
3	A	401	KDL	PHC-O4	4.82	1.68	1.59
3	C	401	KDL	PHC-O4	4.79	1.68	1.59
3	B	401	KDL	CEF-CEE	4.74	1.60	1.50
3	A	401	KDL	CEF-CEE	4.58	1.59	1.50
3	C	401	KDL	CEF-CEE	4.34	1.59	1.50
3	A	401	KDL	O5-C1	4.31	1.52	1.41
3	B	401	KDL	O5-C1	4.19	1.52	1.41
3	C	401	KDL	O5-C1	4.06	1.52	1.41
3	B	401	KDL	OAU-CAL	4.01	1.52	1.41
3	B	401	KDL	OAQ-CEE	4.00	1.45	1.34
3	A	401	KDL	OAU-CAL	3.95	1.51	1.41
3	A	401	KDL	OAQ-CEE	3.94	1.45	1.34
3	C	401	KDL	OFZ-CGN	3.91	1.45	1.34
3	A	401	KDL	OFZ-CGN	3.91	1.45	1.34
3	B	401	KDL	OFZ-CGN	3.87	1.45	1.34
3	C	401	KDL	OAU-CAL	3.81	1.51	1.41
3	C	401	KDL	OAQ-CEE	3.68	1.44	1.34
3	A	401	KDL	C3-C2	-3.56	1.47	1.53
3	B	401	KDL	OFJ-CGB	3.50	1.44	1.34
3	A	401	KDL	OFJ-CGB	3.44	1.44	1.34
3	B	401	KDL	C3-C2	-3.33	1.47	1.53
3	A	401	KDL	CBQ-CBR	-3.30	1.48	1.53
3	B	401	KDL	C8-C7	3.29	1.59	1.51
3	C	401	KDL	OFJ-CGB	3.24	1.43	1.34
3	C	401	KDL	C8-C7	3.22	1.59	1.51
3	C	401	KDL	C3-C2	-3.15	1.47	1.53
3	A	401	KDL	C8-C7	2.98	1.58	1.51
3	A	401	KDL	PHG-OAM	2.95	1.64	1.59
3	B	401	KDL	CBQ-CBR	-2.88	1.48	1.53
3	C	401	KDL	PHG-OAM	2.86	1.64	1.59
3	B	401	KDL	PHG-OAM	2.86	1.64	1.59
3	C	401	KDL	CBQ-CBR	-2.85	1.48	1.53
3	B	401	KDL	CGC-CGB	2.80	1.58	1.50
3	B	401	KDL	CAN-NAO	2.78	1.50	1.45
3	A	401	KDL	CGC-CGB	2.77	1.58	1.50
3	A	401	KDL	CAN-NAO	2.68	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	401	KDL	CGP-CGN	2.61	1.58	1.50
3	A	401	KDL	CGP-CGN	2.60	1.58	1.50
3	B	401	KDL	CGP-CGN	2.55	1.58	1.50
3	A	401	KDL	O7-C7	-2.54	1.18	1.23
3	A	401	KDL	OBD-CBC	2.53	1.51	1.43
3	B	401	KDL	OEC-CDO	-2.49	1.18	1.23
3	A	401	KDL	OBW-CBV	2.47	1.47	1.44
3	A	401	KDL	OEC-CDO	-2.46	1.18	1.23
3	C	401	KDL	CGC-CGB	2.45	1.57	1.50
3	C	401	KDL	OBD-CBC	2.44	1.51	1.43
3	B	401	KDL	O7-C7	-2.42	1.18	1.23
3	B	401	KDL	OBD-CBC	2.42	1.50	1.43
3	C	401	KDL	OEC-CDO	-2.42	1.18	1.23
3	C	401	KDL	O7-C7	-2.41	1.18	1.23
3	C	401	KDL	CFL-CFK	2.40	1.55	1.50
3	C	401	KDL	O3-CFK	2.38	1.41	1.34
3	C	401	KDL	CAN-NAO	2.35	1.49	1.45
3	A	401	KDL	O3-CFK	2.33	1.40	1.34
3	B	401	KDL	OAU-CAT	2.31	1.49	1.44
3	A	401	KDL	OBH-CBG	2.27	1.47	1.44
3	A	401	KDL	OAU-CAT	2.23	1.49	1.44
3	B	401	KDL	O3-CFK	2.23	1.40	1.34
3	C	401	KDL	OBJ-CBI	-2.22	1.38	1.43
3	B	401	KDL	OBJ-CBI	-2.22	1.38	1.43
3	B	401	KDL	OBH-CBG	2.18	1.47	1.44
3	C	401	KDL	OFJ-CEW	-2.18	1.41	1.46
3	C	401	KDL	OBH-CBG	2.17	1.47	1.44
3	A	401	KDL	CFL-CFK	2.16	1.55	1.50
3	B	401	KDL	CFL-CFK	2.15	1.55	1.50
3	B	401	KDL	OET-CEG	-2.13	1.37	1.43
3	C	401	KDL	OAU-CAT	2.12	1.49	1.44
3	A	401	KDL	OET-CEG	-2.07	1.37	1.43
3	B	401	KDL	OBW-CBV	2.06	1.47	1.44
3	A	401	KDL	OFJ-CEW	-2.04	1.41	1.46
3	A	401	KDL	OBJ-CBI	-2.04	1.39	1.43
3	C	401	KDL	OET-CEG	-2.03	1.37	1.43

All (102) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	KDL	CBQ-CBR-CBT	8.13	118.78	110.84
3	A	401	KDL	CDP-CDO-NAO	6.92	125.39	116.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	KDL	CDP-CDO-NAO	6.71	125.12	116.33
3	C	401	KDL	CDP-CDO-NAO	6.08	124.30	116.33
3	B	401	KDL	OAQ-CEE-CEF	5.66	121.87	111.46
3	A	401	KDL	OAQ-CEE-CEF	5.49	121.55	111.46
3	B	401	KDL	OFJ-CGB-CGC	5.31	122.94	111.50
3	A	401	KDL	OFJ-CGB-CGC	5.26	122.83	111.50
3	B	401	KDL	CBQ-CBR-CBT	5.21	115.94	110.84
3	A	401	KDL	CAN-NAO-CDO	5.17	130.51	122.90
3	B	401	KDL	CAN-NAO-CDO	4.98	130.24	122.90
3	A	401	KDL	OBW-CBV-CBT	4.97	115.58	108.52
3	C	401	KDL	O3-CFK-CFL	4.76	120.20	111.46
3	B	401	KDL	OBW-CBP-CBQ	4.51	117.74	111.24
3	C	401	KDL	OBW-CBP-CBQ	4.44	117.64	111.24
3	B	401	KDL	C8-C7-N2	4.43	122.13	116.33
3	C	401	KDL	OAQ-CEE-CEF	4.41	119.57	111.46
3	B	401	KDL	OAU-CAT-CAV	4.35	115.44	106.67
3	B	401	KDL	O3-CFK-CFL	4.35	119.45	111.46
3	A	401	KDL	C1-O5-C5	4.30	122.12	113.69
3	A	401	KDL	O3-CFK-CFL	4.25	119.27	111.46
3	A	401	KDL	OFZ-CGN-CGP	4.01	120.14	111.50
3	A	401	KDL	OEC-CDO-NAO	-3.91	116.35	122.95
3	C	401	KDL	CAV-O1-C1	3.89	121.34	113.74
3	C	401	KDL	OFJ-CGB-CGC	3.89	119.89	111.50
3	A	401	KDL	OAU-CAT-CAV	3.82	114.37	106.67
3	B	401	KDL	O7-C7-C8	-3.69	116.10	121.50
3	C	401	KDL	OEC-CDO-NAO	-3.69	116.73	122.95
3	C	401	KDL	CAN-NAO-CDO	3.66	128.29	122.90
3	C	401	KDL	OFJ-CEW-C8	3.66	113.84	106.65
3	B	401	KDL	CBP-CBQ-CBR	3.65	118.05	110.66
3	B	401	KDL	OEC-CDO-NAO	-3.64	116.80	122.95
3	B	401	KDL	OFZ-CGN-CGP	3.61	119.28	111.50
3	B	401	KDL	CAV-O1-C1	3.60	120.78	113.74
3	C	401	KDL	OFZ-CGN-CGP	3.55	119.16	111.50
3	C	401	KDL	OBH-CBA-CBB	3.42	116.17	111.24
3	A	401	KDL	OBH-CBA-CBB	3.42	116.17	111.24
3	B	401	KDL	C2-N2-C7	3.41	127.92	122.90
3	B	401	KDL	OBH-CBA-CBB	3.41	116.14	111.24
3	B	401	KDL	OES-CEE-CEF	-3.31	117.42	124.73
3	A	401	KDL	C2-N2-C7	3.26	127.70	122.90
3	B	401	KDL	C1-O5-C5	3.25	120.06	113.69
3	A	401	KDL	OES-CEE-CEF	-3.13	117.81	124.73
3	A	401	KDL	OBW-CBP-CBQ	3.12	115.73	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	KDL	CAL-OAU-CAT	3.11	119.78	113.69
3	C	401	KDL	C1-O5-C5	3.00	119.58	113.69
3	C	401	KDL	CBG-CBE-CBC	2.99	116.03	109.66
3	C	401	KDL	CBX-CBV-CBT	-2.97	109.11	114.03
3	A	401	KDL	CAV-O1-C1	2.97	119.53	113.74
3	B	401	KDL	CBX-CBV-CBT	-2.93	109.18	114.03
3	A	401	KDL	O7-C7-C8	-2.90	117.25	121.50
3	B	401	KDL	CBB-CBA-CAX	-2.90	104.52	111.19
3	C	401	KDL	OAU-CAT-CAV	2.84	112.41	106.67
3	C	401	KDL	O1-CAV-CAT	2.83	114.28	109.05
3	B	401	KDL	CBG-CBE-CBC	2.82	115.66	109.66
3	C	401	KDL	CBP-CBQ-CBR	2.81	116.35	110.66
3	A	401	KDL	CBP-OBW-CBV	2.80	120.71	114.20
3	A	401	KDL	CAL-OAU-CAT	2.76	119.11	113.69
3	A	401	KDL	CBQ-CBR-CBT	2.76	113.54	110.84
3	A	401	KDL	C8-C7-N2	2.71	119.87	116.33
3	B	401	KDL	OAM-CAL-CAN	2.67	113.22	108.40
3	B	401	KDL	CAP-OAQ-CEE	2.66	121.95	117.53
3	B	401	KDL	CAL-OAU-CAT	2.65	118.88	113.69
3	A	401	KDL	OAM-CAL-CAN	2.62	113.15	108.40
3	A	401	KDL	O5-C5-C4	2.62	115.28	109.75
3	A	401	KDL	C1-C2-N2	2.61	115.50	111.00
3	B	401	KDL	OBW-CBV-CBT	2.57	112.17	108.52
3	C	401	KDL	CBR-CBT-CBV	2.57	115.56	110.41
3	A	401	KDL	CBB-CBA-CAX	-2.52	105.40	111.19
3	A	401	KDL	CBG-CBE-CBC	2.50	114.98	109.66
3	C	401	KDL	O7-C7-N2	-2.50	118.74	122.95
3	C	401	KDL	CBB-CBA-CAX	-2.49	105.46	111.19
3	B	401	KDL	OFJ-CEW-CEX	2.44	114.10	107.10
3	A	401	KDL	OFJ-CEW-CEX	2.41	114.04	107.10
3	C	401	KDL	OES-CEE-CEF	-2.37	119.50	124.73
3	A	401	KDL	OBD-CBP-CBQ	2.36	113.41	107.31
3	B	401	KDL	C1-C2-N2	2.35	115.06	111.00
3	B	401	KDL	OEC-CDO-CDP	-2.34	118.07	121.50
3	A	401	KDL	CBX-CBV-CBT	-2.29	110.23	114.03
3	C	401	KDL	C8-C7-N2	2.28	119.31	116.33
3	C	401	KDL	OFZ-CFM-CFN	2.27	113.63	107.10
3	C	401	KDL	OFY-CFK-CFL	-2.27	119.71	124.73
3	C	401	KDL	O5-C5-C4	2.27	114.53	109.75
3	A	401	KDL	CAL-CAN-NAO	-2.27	107.10	111.00
3	B	401	KDL	O5-C5-C4	2.25	114.50	109.75
3	C	401	KDL	CBQ-CBP-CBM	-2.24	106.03	111.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	KDL	CAL-CAN-NAO	-2.21	107.19	111.00
3	A	401	KDL	OEC-CDO-CDP	-2.21	118.26	121.50
3	B	401	KDL	CBI-CBG-CBE	-2.20	110.38	114.03
3	A	401	KDL	CBP-CBQ-CBR	2.20	115.11	110.66
3	A	401	KDL	OFZ-CFM-CFN	2.20	113.41	107.10
3	B	401	KDL	OFZ-CFM-CFN	2.15	113.28	107.10
3	C	401	KDL	OBW-CBV-CBT	2.12	111.53	108.52
3	A	401	KDL	CAP-OAQ-CEE	2.12	121.06	117.53
3	C	401	KDL	C2-N2-C7	-2.11	119.78	122.90
3	B	401	KDL	CBP-OBW-CBV	2.11	119.11	114.20
3	B	401	KDL	OFJ-CGB-OGA	-2.07	118.69	123.70
3	C	401	KDL	CAP-OAQ-CEE	2.07	120.97	117.53
3	A	401	KDL	OFJ-CGB-OGA	-2.06	118.72	123.70
3	A	401	KDL	OFY-CFK-CFL	-2.06	120.19	124.73
3	A	401	KDL	O5-C1-C2	2.05	114.59	110.58
3	C	401	KDL	CBA-OBH-CBG	2.03	118.93	114.20

There are no chirality outliers.

All (257) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	KDL	N2-C7-C8-CEW
3	A	401	KDL	O7-C7-C8-CEW
3	A	401	KDL	CAL-CAN-NAO-CDO
3	A	401	KDL	OAY-CAX-CBA-O6
3	A	401	KDL	CAX-CBA-O6-C6
3	A	401	KDL	CBB-CBA-O6-C6
3	A	401	KDL	OBH-CBA-O6-C6
3	A	401	KDL	CBE-CBG-CBI-CBK
3	A	401	KDL	CBE-CBG-CBI-OBJ
3	A	401	KDL	OBH-CBG-CBI-CBK
3	A	401	KDL	OBH-CBG-CBI-OBJ
3	A	401	KDL	OBN-CBM-CBP-OBW
3	A	401	KDL	OBW-CBV-CBX-OBY
3	A	401	KDL	CEF-CEE-OAQ-CAP
3	A	401	KDL	CEE-CEF-CEG-CEH
3	A	401	KDL	CEE-CEF-CEG-OET
3	A	401	KDL	OFJ-CEW-CEX-CEY
3	A	401	KDL	CEX-CEW-OFJ-CGB
3	A	401	KDL	CFK-CFL-CFM-OFZ
3	A	401	KDL	CFN-CFM-OFZ-CGN
3	A	401	KDL	OGA-CGB-OFJ-CEW

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Mol	Chain	Res	Type	Atoms
3	A	401	KDL	C4-O4-PHC-OHE
3	B	401	KDL	CAL-CAN-NAO-CDO
3	B	401	KDL	CAT-CAV-O1-C1
3	B	401	KDL	OAY-CAX-CBA-O6
3	B	401	KDL	OAY-CAX-CBA-OBH
3	B	401	KDL	CAX-CBA-O6-C6
3	B	401	KDL	CBB-CBA-O6-C6
3	B	401	KDL	OBN-CBM-CBP-CBQ
3	B	401	KDL	OBN-CBM-CBP-OBD
3	B	401	KDL	OBN-CBM-CBP-OBW
3	B	401	KDL	OBO-CBM-CBP-CBQ
3	B	401	KDL	CEF-CEE-OAQ-CAP
3	B	401	KDL	CEE-CEF-CEG-CEH
3	B	401	KDL	CEE-CEF-CEG-OET
3	B	401	KDL	CEX-CEW-OFJ-CGB
3	B	401	KDL	CFK-CFL-CFM-OFZ
3	B	401	KDL	CFL-CFM-CFN-CFO
3	B	401	KDL	CFN-CFM-OFZ-CGN
3	B	401	KDL	CGC-CGB-OFJ-CEW
3	B	401	KDL	OGA-CGB-OFJ-CEW
3	B	401	KDL	OGO-CGN-OFZ-CFM
3	B	401	KDL	C4-O4-PHC-OHE
3	C	401	KDL	C7-C8-CEW-CEX
3	C	401	KDL	C7-C8-CEW-OFJ
3	C	401	KDL	CAN-CAP-OAQ-CEE
3	C	401	KDL	CAT-CAV-O1-C1
3	C	401	KDL	OAY-CAX-CBA-O6
3	C	401	KDL	OAY-CAX-CBA-OBH
3	C	401	KDL	CBB-CBA-O6-C6
3	C	401	KDL	OBN-CBM-CBP-OBD
3	C	401	KDL	CEF-CEE-OAQ-CAP
3	C	401	KDL	C8-CEW-CEX-CEY
3	C	401	KDL	OFJ-CEW-CEX-CEY
3	C	401	KDL	CFK-CFL-CFM-CFN
3	C	401	KDL	CFK-CFL-CFM-OFZ
3	C	401	KDL	CFN-CFM-OFZ-CGN
3	C	401	KDL	CGC-CGB-OFJ-CEW
3	C	401	KDL	C4-O4-PHC-OHE
3	A	401	KDL	OES-CEE-OAQ-CAP
3	A	401	KDL	OGO-CGN-OFZ-CFM
3	B	401	KDL	OES-CEE-OAQ-CAP
3	C	401	KDL	OES-CEE-OAQ-CAP

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Mol	Chain	Res	Type	Atoms
3	C	401	KDL	OGA-CGB-OFJ-CEW
3	C	401	KDL	OGO-CGN-OFZ-CFM
3	A	401	KDL	CGC-CGB-OFJ-CEW
3	A	401	KDL	CGP-CGN-OFZ-CFM
3	B	401	KDL	CGP-CGN-OFZ-CFM
3	C	401	KDL	CGP-CGN-OFZ-CFM
3	A	401	KDL	CDP-CDO-NAO-CAN
3	B	401	KDL	CDP-CDO-NAO-CAN
3	C	401	KDL	CDP-CDO-NAO-CAN
3	B	401	KDL	CGV-CGW-CGX-CGY
3	A	401	KDL	OEC-CDO-NAO-CAN
3	B	401	KDL	OEC-CDO-NAO-CAN
3	C	401	KDL	OEC-CDO-NAO-CAN
3	A	401	KDL	CAN-CAP-OAQ-CEE
3	B	401	KDL	CAN-CAP-OAQ-CEE
3	B	401	KDL	CDT-CDU-CDV-CDW
3	B	401	KDL	C4-C5-C6-O6
3	A	401	KDL	CDT-CDU-CDV-CDW
3	A	401	KDL	C4-C5-C6-O6
3	C	401	KDL	CGV-CGW-CGX-CGY
3	A	401	KDL	CGB-CGC-CGD-CGE
3	A	401	KDL	CGV-CGW-CGX-CGY
3	C	401	KDL	CDT-CDU-CDV-CDW
3	A	401	KDL	C8-CEW-CEX-CEY
3	A	401	KDL	CFL-CFM-CFN-CFO
3	B	401	KDL	O5-C5-C6-O6
3	B	401	KDL	CFN-CFO-CFP-CFQ
3	B	401	KDL	CGB-CGC-CGD-CGE
3	B	401	KDL	CGU-CGV-CGW-CGX
3	A	401	KDL	CDS-CDT-CDU-CDV
3	A	401	KDL	CEK-CEL-CEM-CEN
3	B	401	KDL	CDS-CDT-CDU-CDV
3	B	401	KDL	CGH-CGI-CGJ-CGK
3	A	401	KDL	CFD-CFE-CFF-CFG
3	B	401	KDL	CFB-CFC-CFD-CFE
3	C	401	KDL	CFN-CFO-CFP-CFQ
3	C	401	KDL	CGU-CGV-CGW-CGX
3	B	401	KDL	CEK-CEL-CEM-CEN
3	C	401	KDL	CDV-CDW-CDX-CDY
3	C	401	KDL	CEN-CEO-CEP-CEQ
3	A	401	KDL	CGD-CGE-CGF-CGG
3	A	401	KDL	CBE-CBC-OB-OBP

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Mol	Chain	Res	Type	Atoms
3	C	401	KDL	CGQ-CGR-CGS-CGT
3	B	401	KDL	C5-C6-O6-CBA
3	B	401	KDL	CFC-CFD-CFE-CFF
3	C	401	KDL	CEH-CEI-CEJ-CEK
3	C	401	KDL	CGD-CGE-CGF-CGG
3	A	401	KDL	CGC-CGD-CGE-CGF
3	A	401	KDL	CEY-CEZ-CFA-CFB
3	C	401	KDL	CEX-CEY-CEZ-CFA
3	B	401	KDL	CEZ-CFA-CFB-CFC
3	C	401	KDL	CFA-CFB-CFC-CFD
3	C	401	KDL	CGS-CGT-CGU-CGV
3	B	401	KDL	CGC-CGD-CGE-CGF
3	A	401	KDL	OAU-CAT-CAV-O1
3	A	401	KDL	CGS-CGT-CGU-CGV
3	A	401	KDL	O5-C5-C6-O6
3	B	401	KDL	OAU-CAT-CAV-O1
3	C	401	KDL	CGH-CGI-CGJ-CGK
3	A	401	KDL	CFC-CFD-CFE-CFF
3	C	401	KDL	C4-C5-C6-O6
3	A	401	KDL	CEN-CEO-CEP-CEQ
3	A	401	KDL	CEZ-CFA-CFB-CFC
3	A	401	KDL	CEJ-CEK-CEL-CEM
3	A	401	KDL	CFB-CFC-CFD-CFE
3	A	401	KDL	CGH-CGI-CGJ-CGK
3	C	401	KDL	CGW-CGX-CGY-CGZ
3	C	401	KDL	CEI-CEJ-CEK-CEL
3	B	401	KDL	OFY-CFK-O3-C3
3	B	401	KDL	CEF-CEG-CEH-CEI
3	B	401	KDL	CGN-CGP-CGQ-CGR
3	B	401	KDL	CFL-CFK-O3-C3
3	C	401	KDL	CFL-CFK-O3-C3
3	C	401	KDL	CDU-CDV-CDW-CDX
3	C	401	KDL	OFY-CFK-O3-C3
3	A	401	KDL	CGP-CGQ-CGR-CGS
3	C	401	KDL	CFB-CFC-CFD-CFE
3	B	401	KDL	CFD-CFE-CFF-CFG
3	C	401	KDL	OAU-CAT-CAV-O1
3	A	401	KDL	OFZ-CFM-CFN-CFO
3	B	401	KDL	OFJ-CEW-CEX-CEY
3	B	401	KDL	OFZ-CFM-CFN-CFO
3	A	401	KDL	CFN-CFO-CFP-CFQ
3	B	401	KDL	CGE-CGF-CGG-CGH

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Mol	Chain	Res	Type	Atoms
3	B	401	KDL	CGD-CGE-CGF-CGG
3	A	401	KDL	CAT-CAV-O1-C1
3	C	401	KDL	CDX-CDY-CDZ-CEA
3	B	401	KDL	CFE-CFF-CFG-CFH
3	B	401	KDL	OET-CEG-CEH-CEI
3	C	401	KDL	CDW-CDX-CDY-CDZ
3	A	401	KDL	C5-C6-O6-CBA
3	C	401	KDL	C5-C6-O6-CBA
3	B	401	KDL	CGS-CGT-CGU-CGV
3	A	401	KDL	CFE-CFF-CFG-CFH
3	C	401	KDL	CGF-CGG-CGH-CGI
3	A	401	KDL	CEF-CEG-CEH-CEI
3	B	401	KDL	CDP-CDQ-CDR-CDS
3	C	401	KDL	CFC-CFD-CFE-CFF
3	A	401	KDL	CFL-CFK-O3-C3
3	C	401	KDL	CGY-CGZ-CHA-CHB
3	A	401	KDL	CFA-CFB-CFC-CFD
3	C	401	KDL	O5-C5-C6-O6
3	C	401	KDL	CFD-CFE-CFF-CFG
3	C	401	KDL	CDR-CDS-CDT-CDU
3	A	401	KDL	CGF-CGG-CGH-CGI
3	A	401	KDL	OFY-CFK-O3-C3
3	C	401	KDL	CEK-CEL-CEM-CEN
3	C	401	KDL	CGB-CGC-CGD-CGE
3	A	401	KDL	CGE-CGF-CGG-CGH
3	C	401	KDL	CDS-CDT-CDU-CDV
3	C	401	KDL	CGP-CGQ-CGR-CGS
3	B	401	KDL	CFM-CFN-CFO-CFP
3	B	401	KDL	CFA-CFB-CFC-CFD
3	C	401	KDL	CGC-CGD-CGE-CGF
3	A	401	KDL	OAZ-CAX-CBA-O6
3	B	401	KDL	OAZ-CAX-CBA-O6
3	C	401	KDL	OAZ-CAX-CBA-O6
3	A	401	KDL	CDO-CDP-CDQ-OED
3	B	401	KDL	CDO-CDP-CDQ-OED
3	C	401	KDL	CDO-CDP-CDQ-OED
3	A	401	KDL	CGW-CGX-CGY-CGZ
3	B	401	KDL	CGF-CGG-CGH-CGI
3	B	401	KDL	CFK-CFL-CFM-CFN
3	A	401	KDL	CFP-CFQ-CFR-CFS
3	C	401	KDL	CFE-CFF-CFG-CFH
3	C	401	KDL	CDQ-CDR-CDS-CDT

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Mol	Chain	Res	Type	Atoms
3	A	401	KDL	CDO-CDP-CDQ-CDR
3	B	401	KDL	CDO-CDP-CDQ-CDR
3	C	401	KDL	CDO-CDP-CDQ-CDR
3	B	401	KDL	CGW-CGX-CGY-CGZ
3	B	401	KDL	CFO-CFP-CFQ-CFR
3	B	401	KDL	OBH-CBA-O6-C6
3	B	401	KDL	C8-CEW-CEX-CEY
3	B	401	KDL	O7-C7-C8-CEW
3	C	401	KDL	CGN-CGP-CGQ-CGR
3	A	401	KDL	CEG-CEH-CEI-CEJ
3	A	401	KDL	CEW-CEX-CEY-CEZ
3	B	401	KDL	CEG-CEH-CEI-CEJ
3	C	401	KDL	CGJ-CGK-CGL-CGM
3	B	401	KDL	CGJ-CGK-CGL-CGM
3	B	401	KDL	N2-C7-C8-CEW
3	A	401	KDL	CAR-CAT-CAV-O1
3	A	401	KDL	OET-CEG-CEH-CEI
3	B	401	KDL	OED-CDQ-CDR-CDS
3	A	401	KDL	OBJ-CBI-CBK-OBL
3	B	401	KDL	CGQ-CGR-CGS-CGT
3	B	401	KDL	CBE-CBC-OBD-CBP
3	A	401	KDL	C1-C2-N2-C7
3	B	401	KDL	C1-C2-N2-C7
3	C	401	KDL	CAR-CAT-CAV-O1
3	C	401	KDL	CEL-CEM-CEN-CEO
3	C	401	KDL	CFP-CFQ-CFR-CFS
3	B	401	KDL	CAR-CAT-CAV-O1
3	A	401	KDL	CGJ-CGK-CGL-CGM
3	B	401	KDL	CEW-CEX-CEY-CEZ
3	A	401	KDL	CGQ-CGR-CGS-CGT
3	C	401	KDL	C2-C1-O1-CAV
3	C	401	KDL	CAX-CBA-O6-C6
3	A	401	KDL	CFR-CFS-CFT-CFU
3	A	401	KDL	C8-CEW-OFJ-CGB
3	A	401	KDL	CGI-CGJ-CGK-CGL
3	A	401	KDL	OBO-CBM-CBP-CBQ
3	A	401	KDL	C3-C2-N2-C7
3	B	401	KDL	C3-C2-N2-C7
3	B	401	KDL	CDX-CDY-CDZ-CEA
3	A	401	KDL	CFM-CFN-CFO-CFP
3	C	401	KDL	CAL-CAN-NAO-CDO
3	A	401	KDL	CGT-CGU-CGV-CGW

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Mol	Chain	Res	Type	Atoms
3	A	401	KDL	CEX-CEY-CEZ-CFA
3	A	401	KDL	OAZ-CAX-CBA-OBH
3	B	401	KDL	OBO-CBM-CBP-OBD
3	B	401	KDL	OBO-CBM-CBP-OBW
3	C	401	KDL	CBE-CBC-OBD-CBP
3	A	401	KDL	CBQ-CBP-OBD-CBC
3	A	401	KDL	C4-O4-PHC-OHF
3	C	401	KDL	CAL-OAM-PHG-OHJ
3	A	401	KDL	CFK-CFL-CFM-CFN
3	A	401	KDL	CDR-CDS-CDT-CDU
3	B	401	KDL	OAQ-CEE-CEF-CEG
3	B	401	KDL	CAP-CAN-NAO-CDO
3	B	401	KDL	CEH-CEI-CEJ-CEK
3	B	401	KDL	CGX-CGY-CGZ-CHA
3	B	401	KDL	OFY-CFK-CFL-CFM
3	C	401	KDL	OBH-CBA-O6-C6
3	C	401	KDL	CFR-CFS-CFT-CFU
3	A	401	KDL	CAP-CAN-NAO-CDO
3	A	401	KDL	OFJ-CGB-CGC-CGD
3	C	401	KDL	OGA-CGB-CGC-CGD
3	A	401	KDL	OED-CDQ-CDR-CDS
3	B	401	KDL	OFJ-CGB-CGC-CGD
3	C	401	KDL	OFJ-CGB-CGC-CGD
3	B	401	KDL	CEL-CEM-CEN-CEO
3	A	401	KDL	CEL-CEM-CEN-CEO
3	A	401	KDL	CDX-CDY-CDZ-CEA

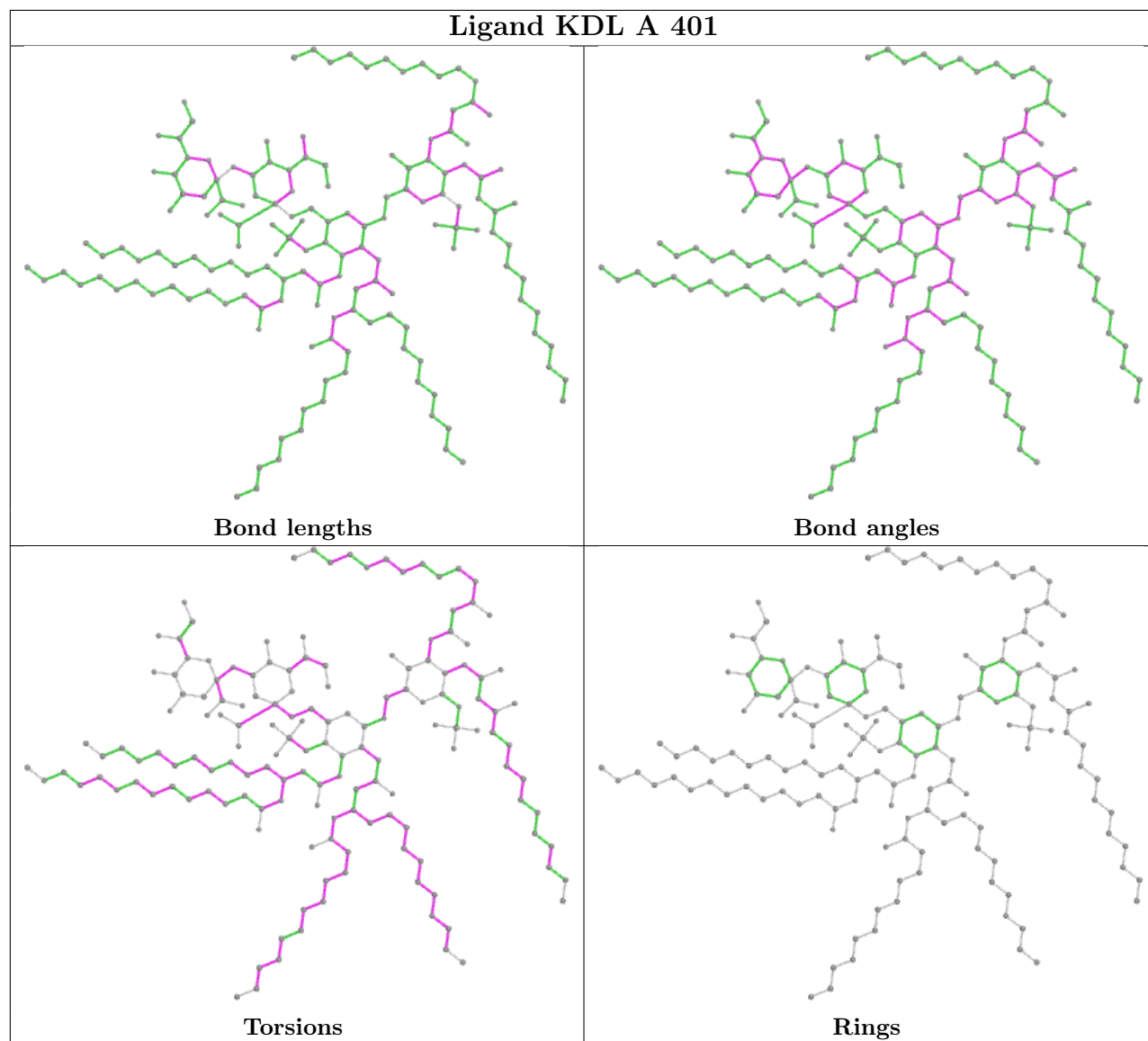
There are no ring outliers.

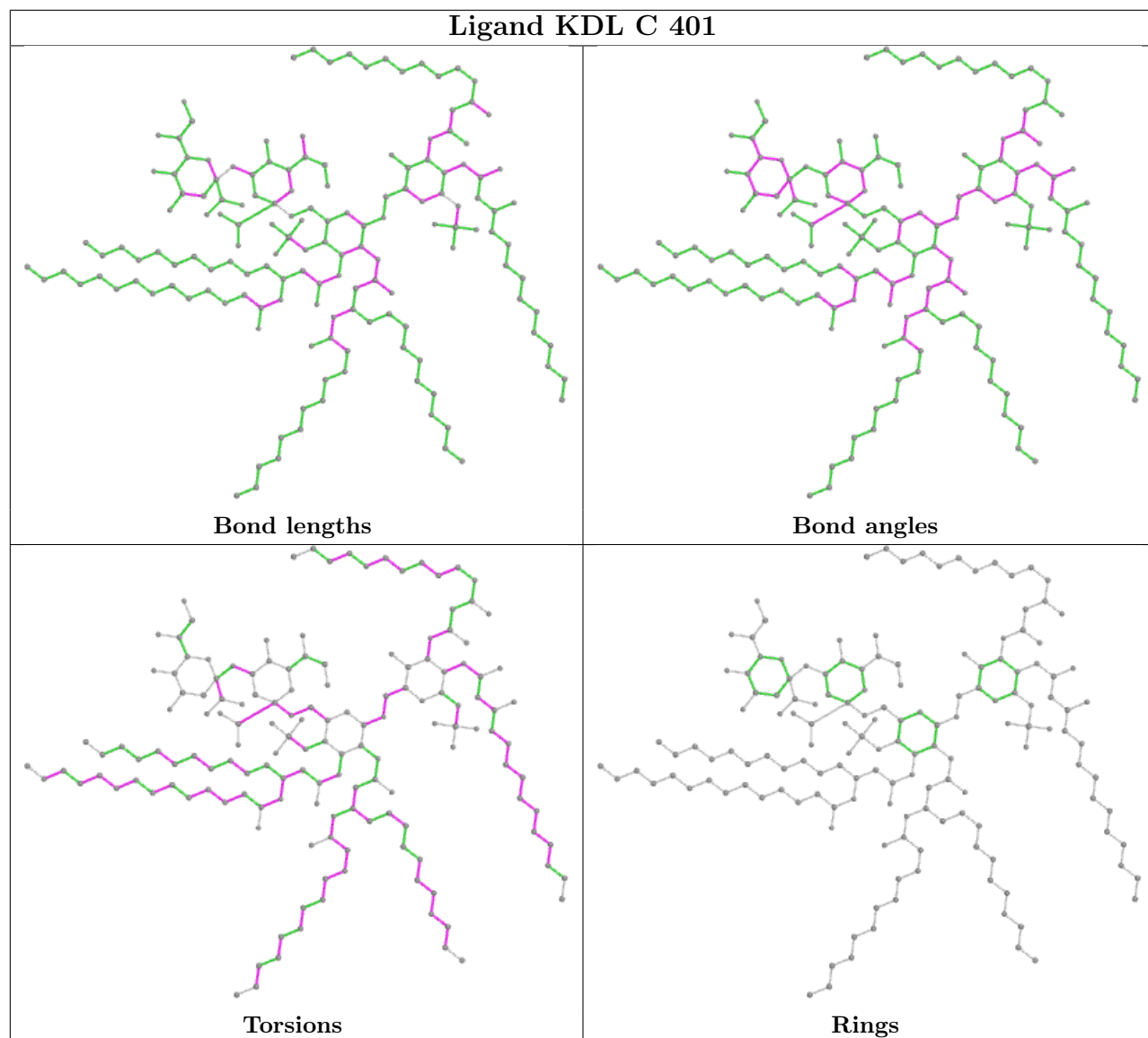
3 monomers are involved in 35 short contacts:

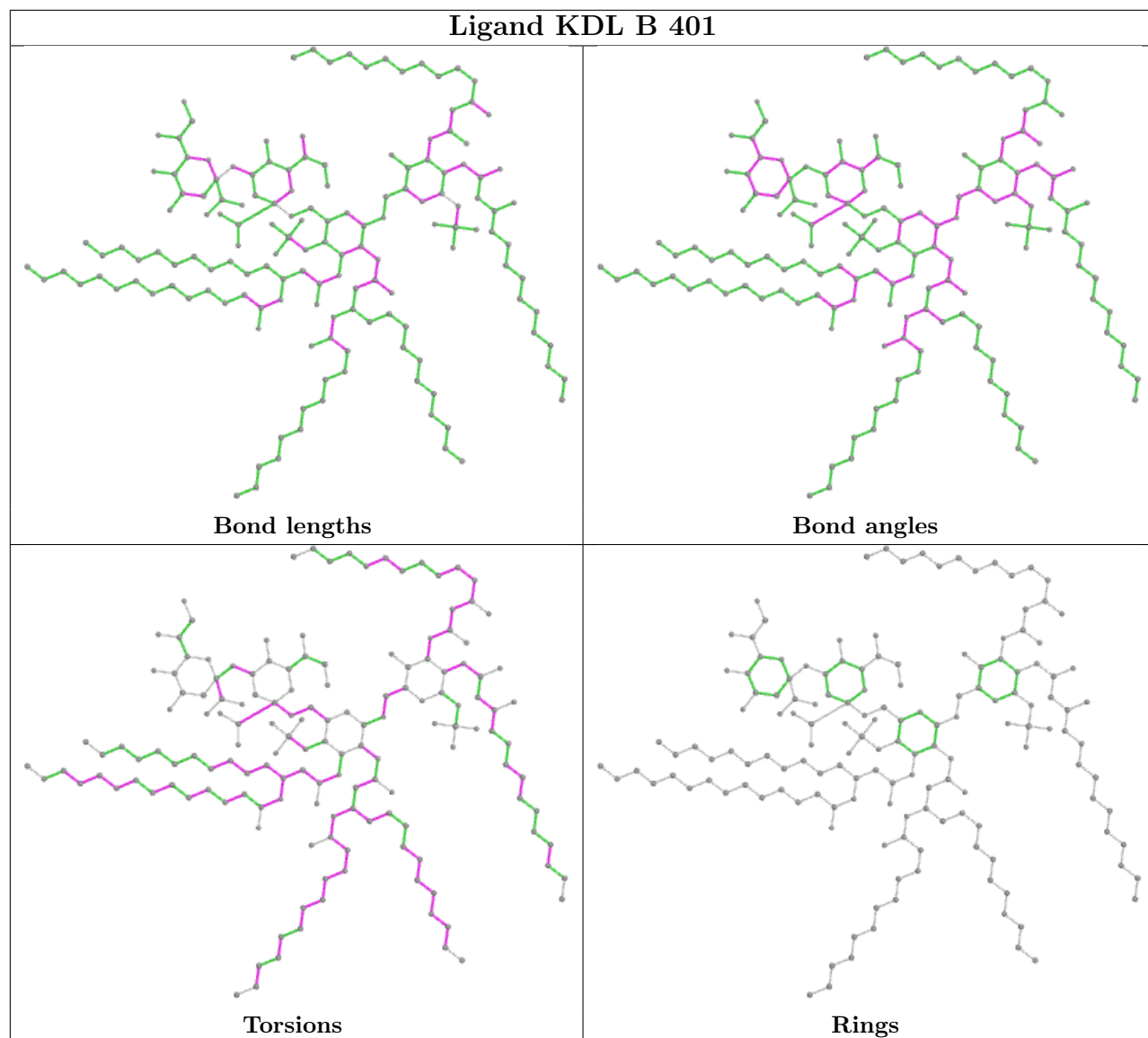
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	KDL	10	0
3	C	401	KDL	6	0
3	B	401	KDL	19	0

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

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







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.

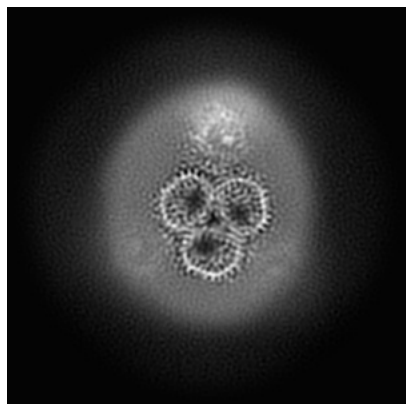
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35250. These allow visual inspection of the internal detail of the map and identification of artifacts.

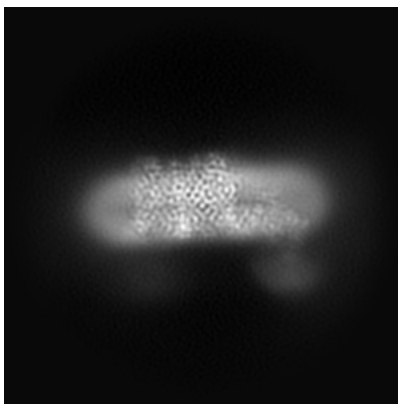
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

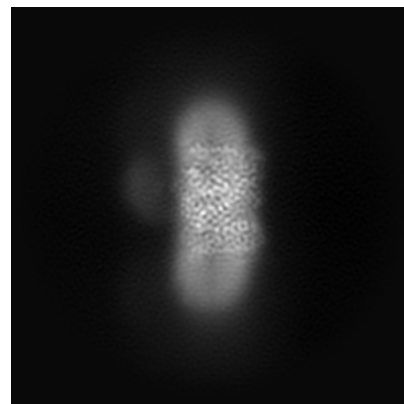
6.1.1 Primary map



X

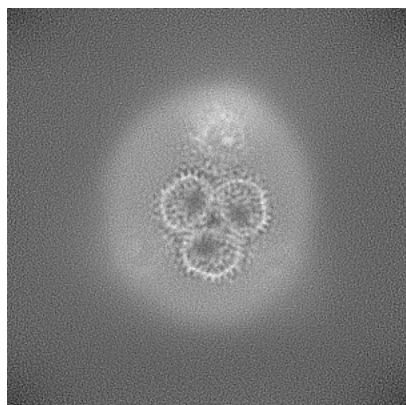


Y

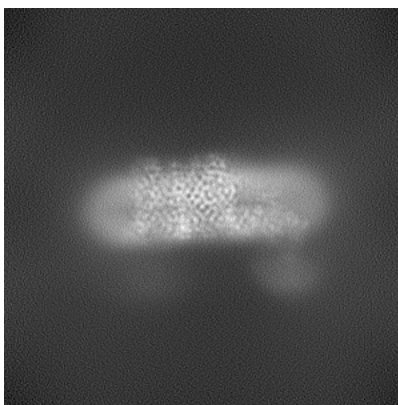


Z

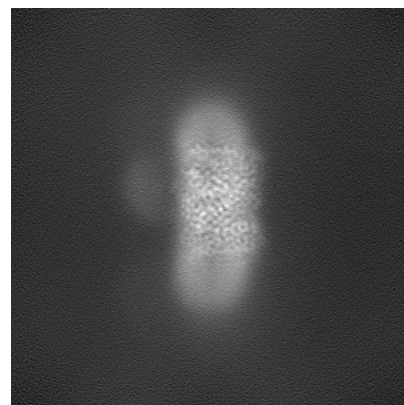
6.1.2 Raw map



X



Y

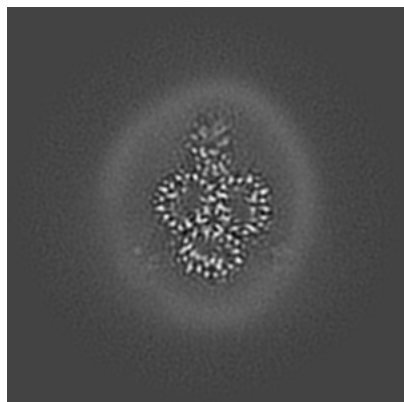


Z

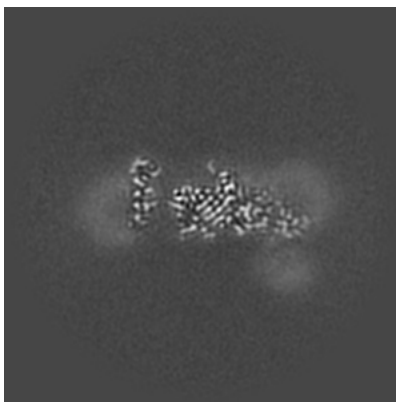
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

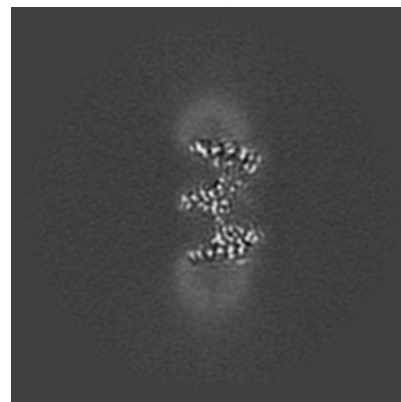
6.2.1 Primary map



X Index: 160

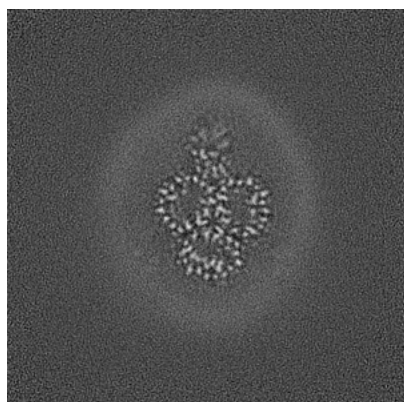


Y Index: 160

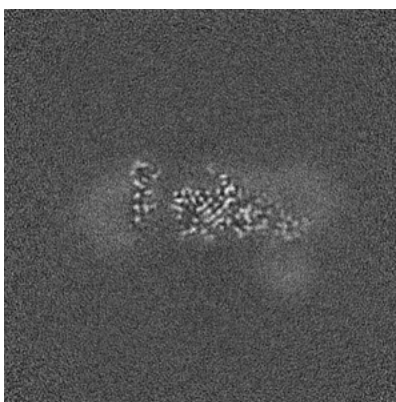


Z Index: 160

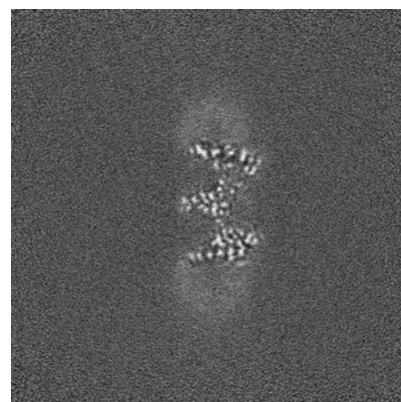
6.2.2 Raw map



X Index: 160



Y Index: 160

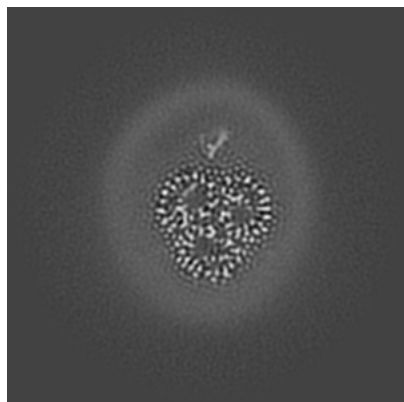


Z Index: 160

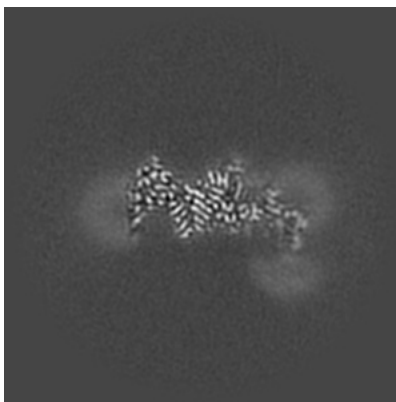
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

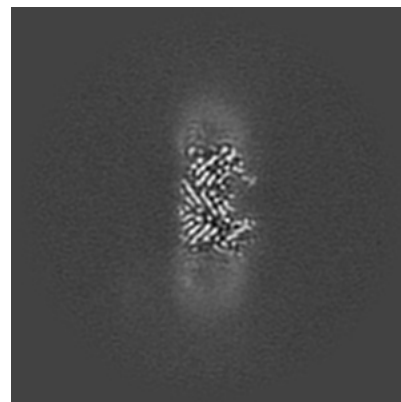
6.3.1 Primary map



X Index: 171

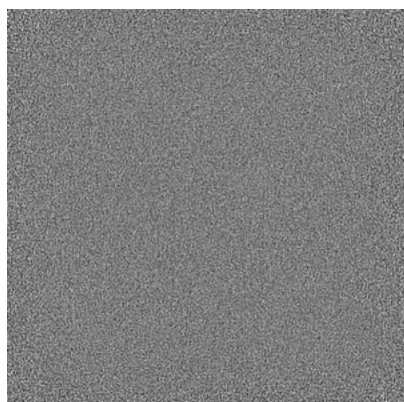


Y Index: 172

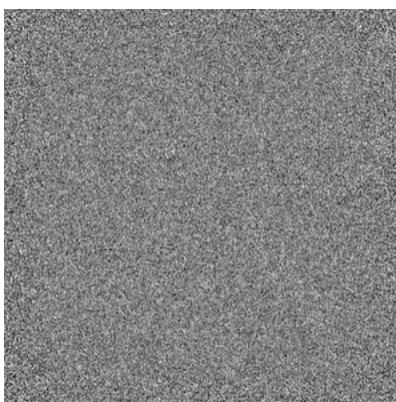


Z Index: 142

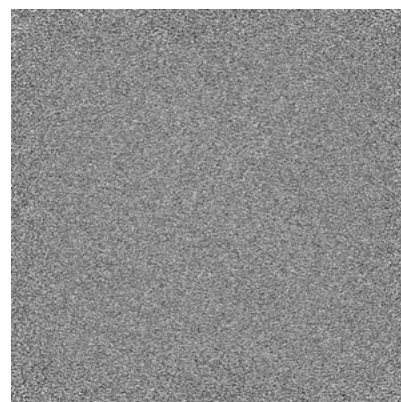
6.3.2 Raw map



X Index: 0



Y Index: 0

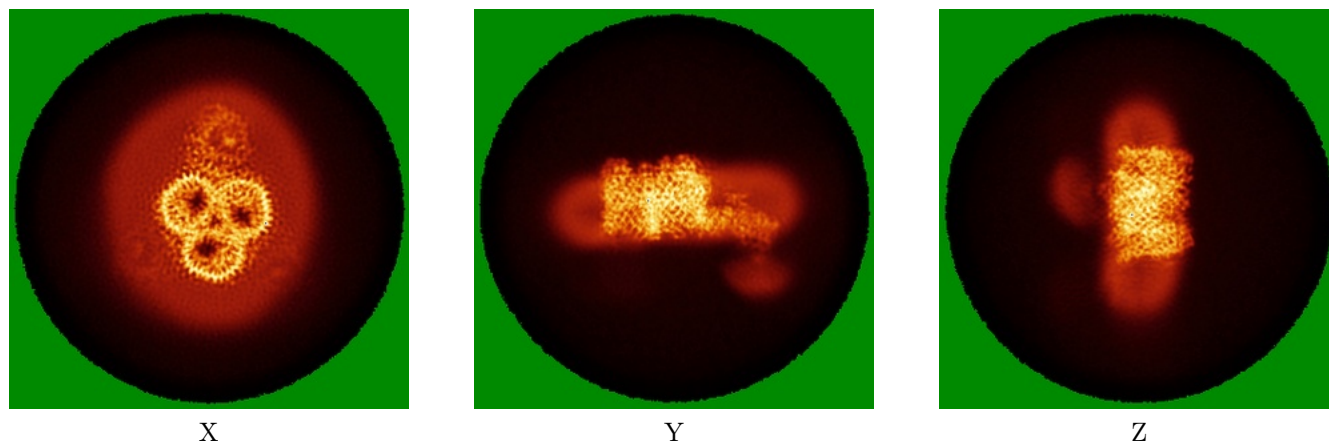


Z Index: 0

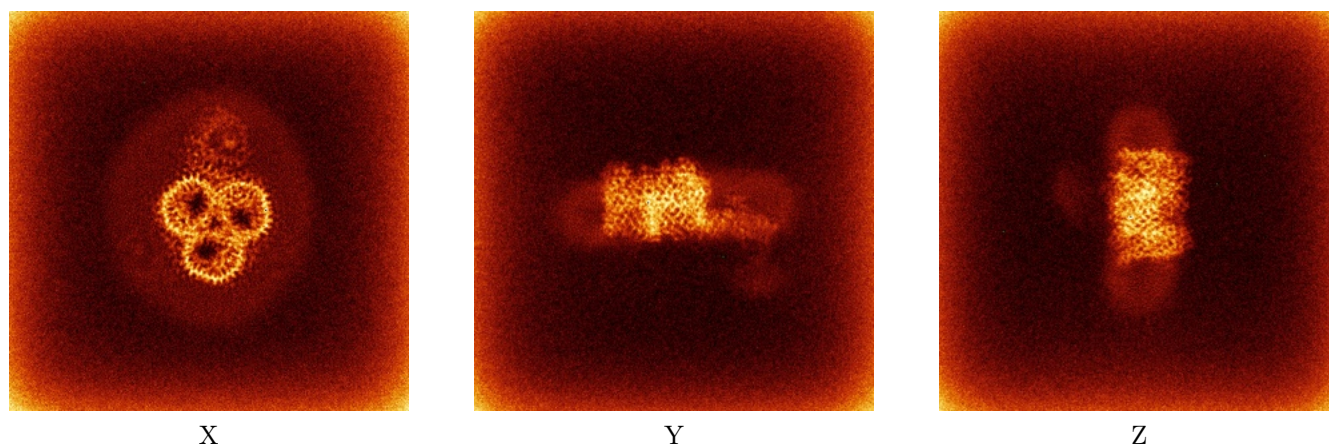
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



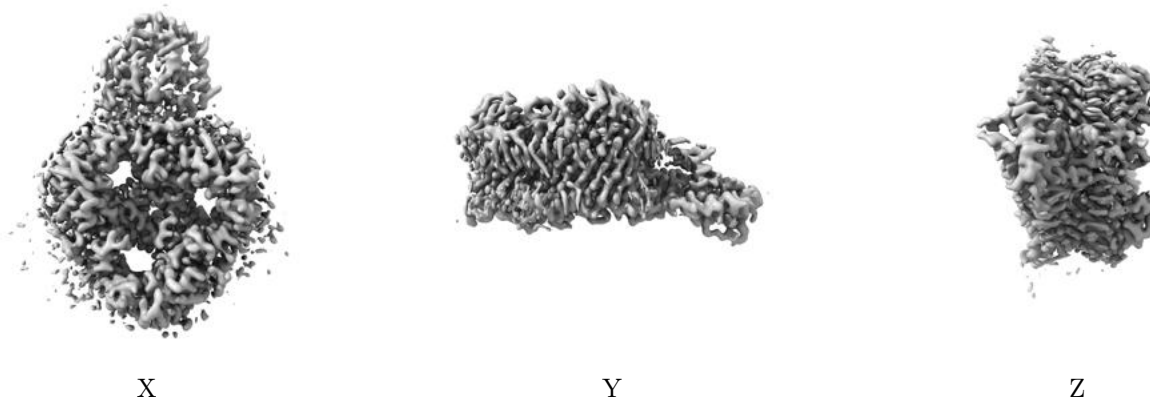
6.4.2 Raw map



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

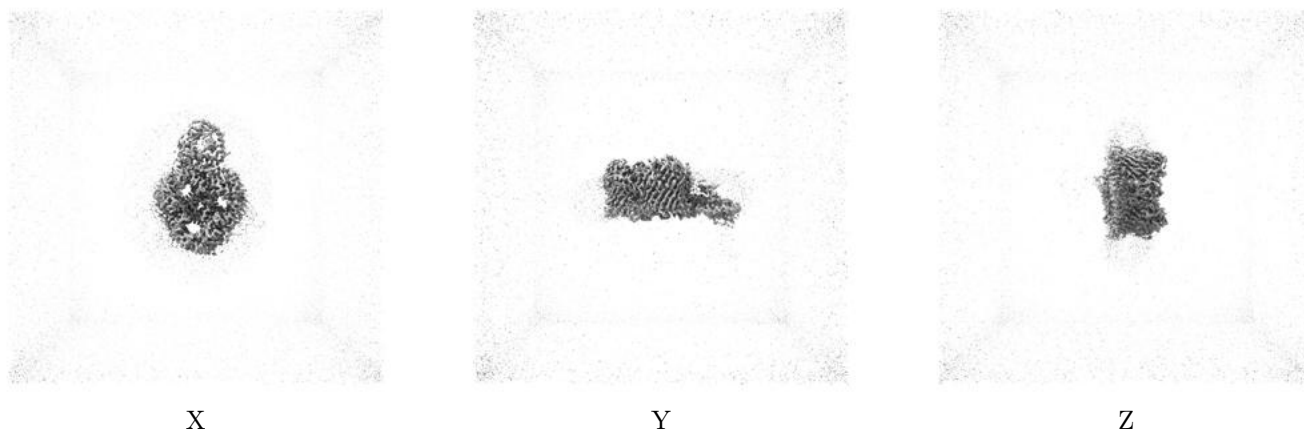
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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.

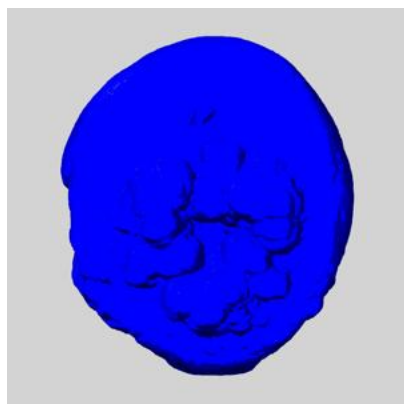
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

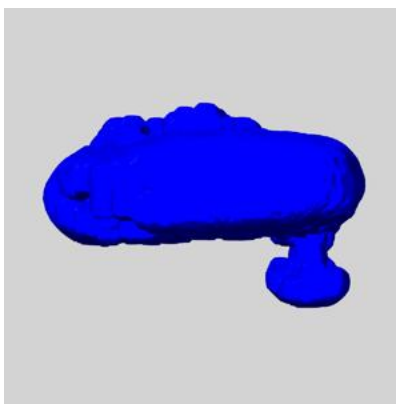
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

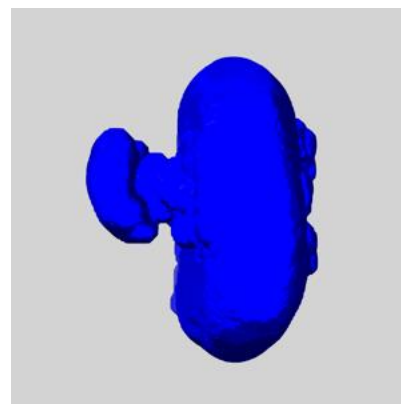
6.6.1 emd_35250_msk_1.map [i](#)



X



Y

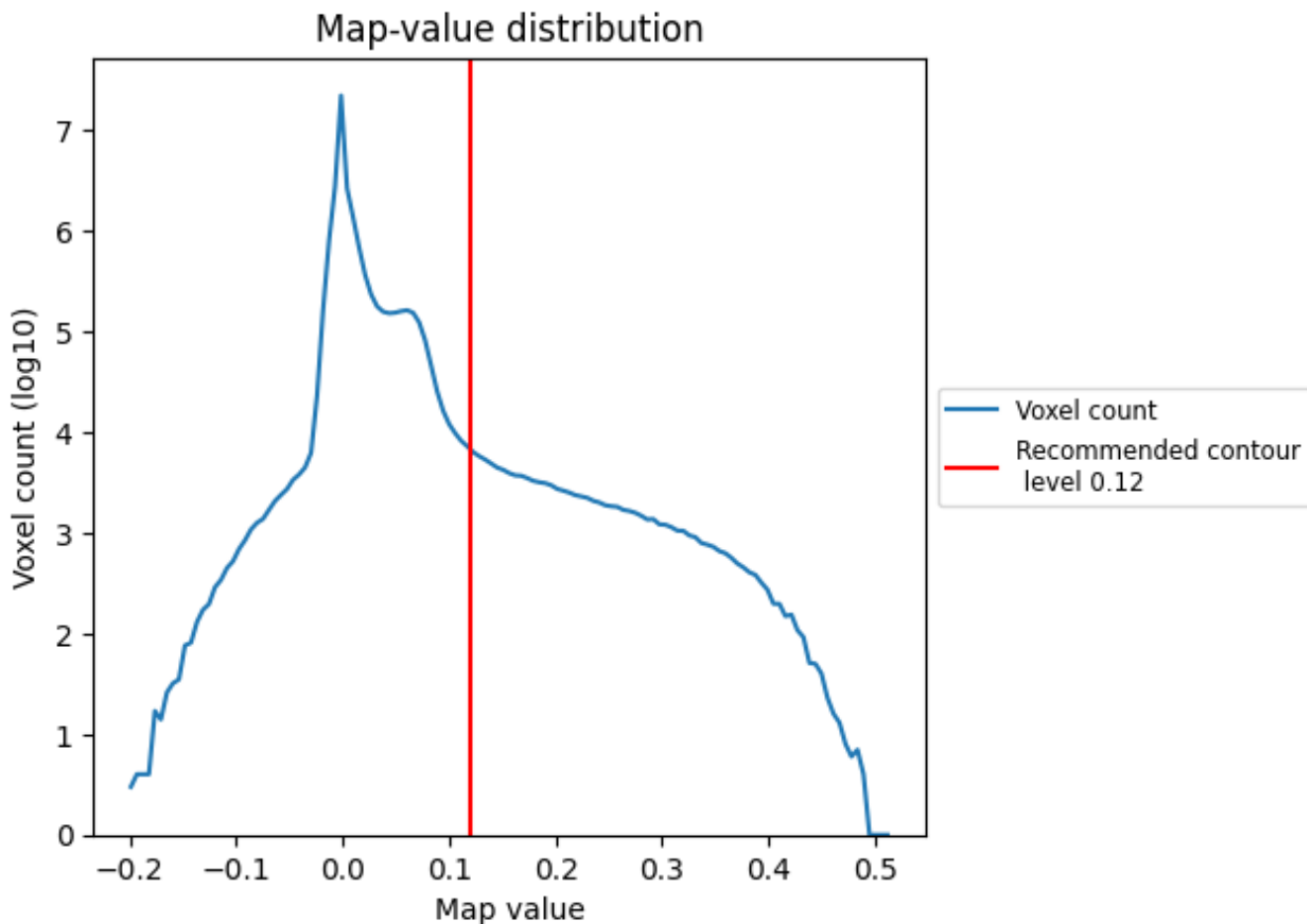


Z

7 Map analysis [i](#)

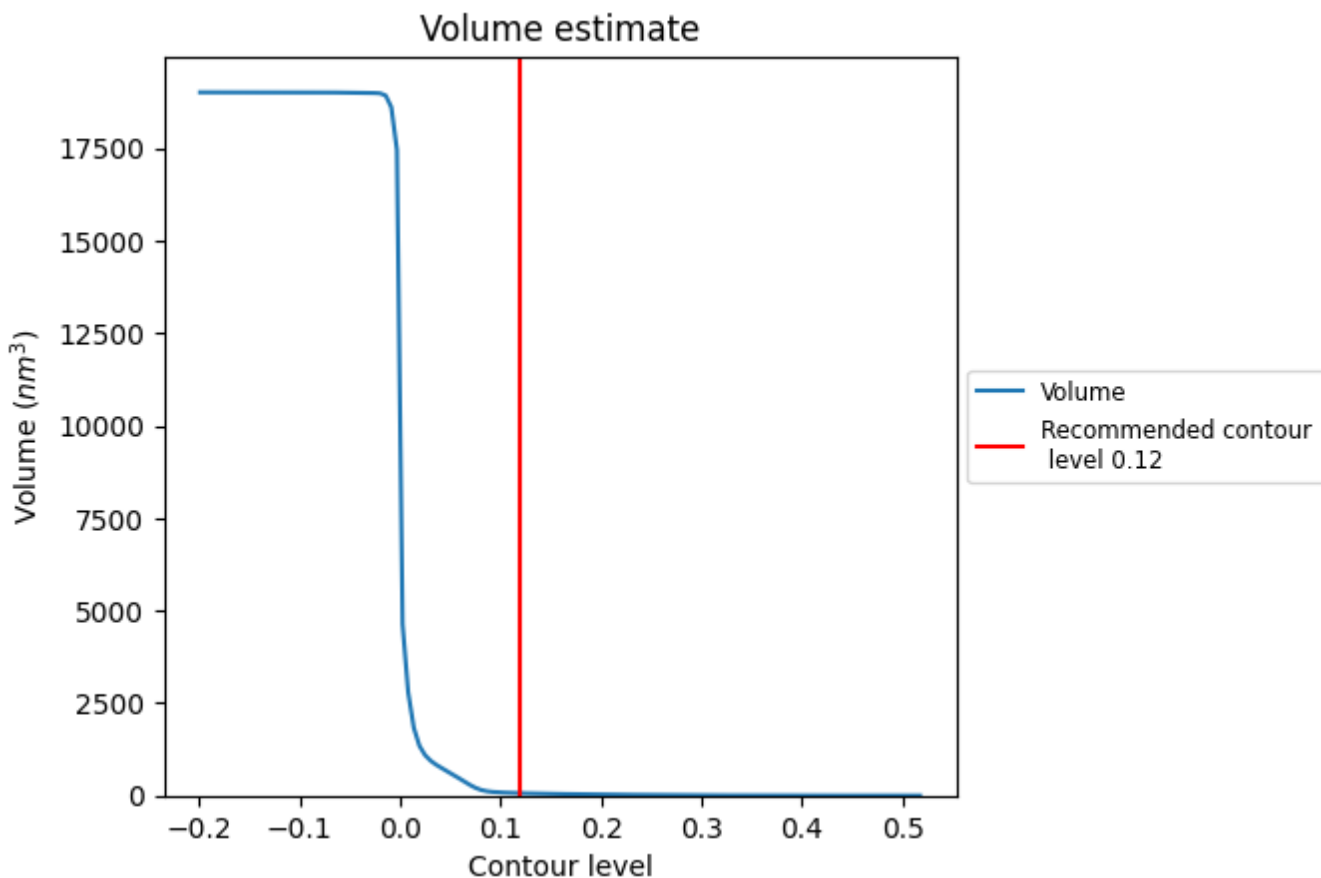
This section contains the results of statistical analysis of the map.

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.

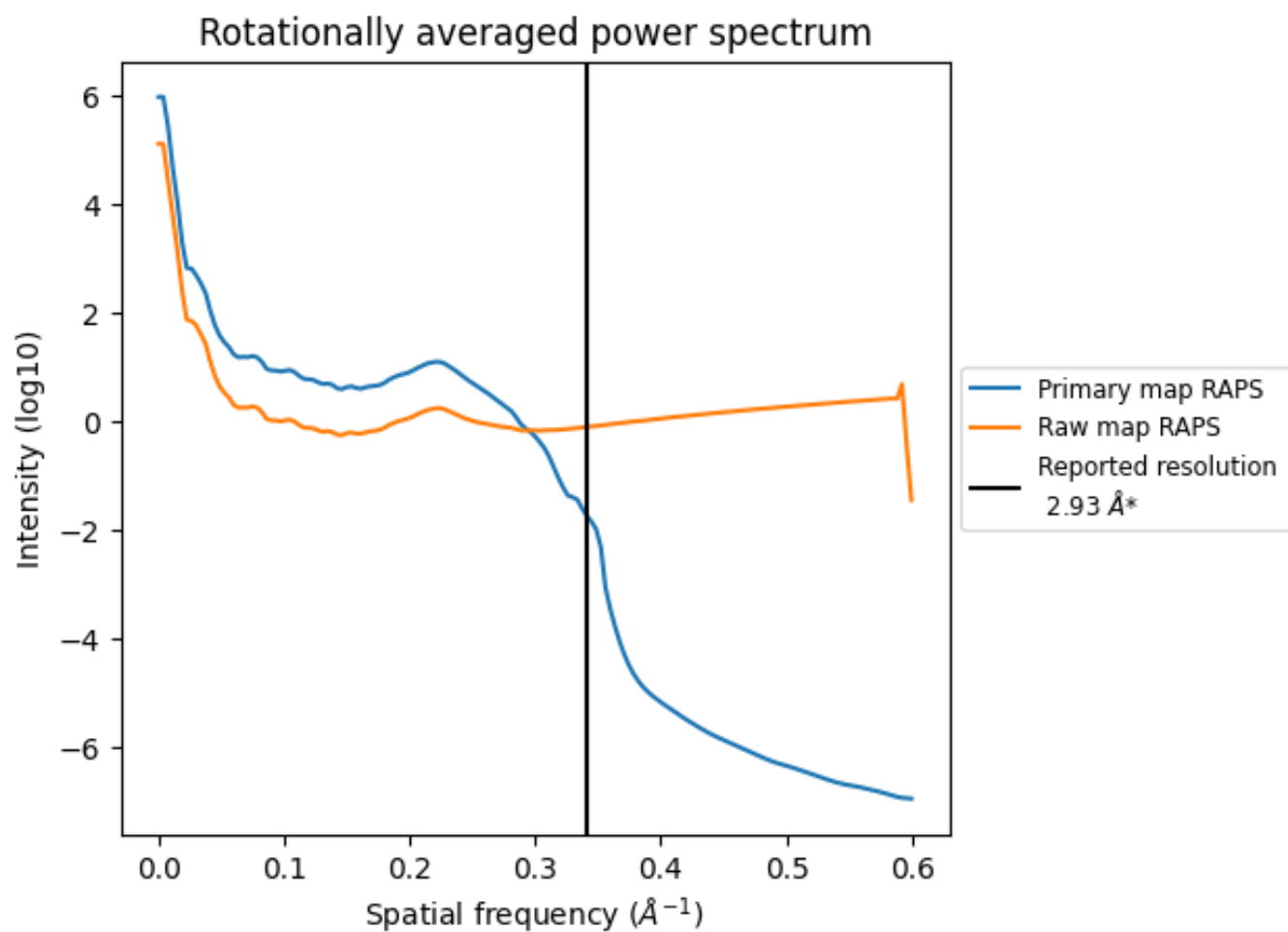
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 64 nm^3 ; this corresponds to an approximate mass of 58 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

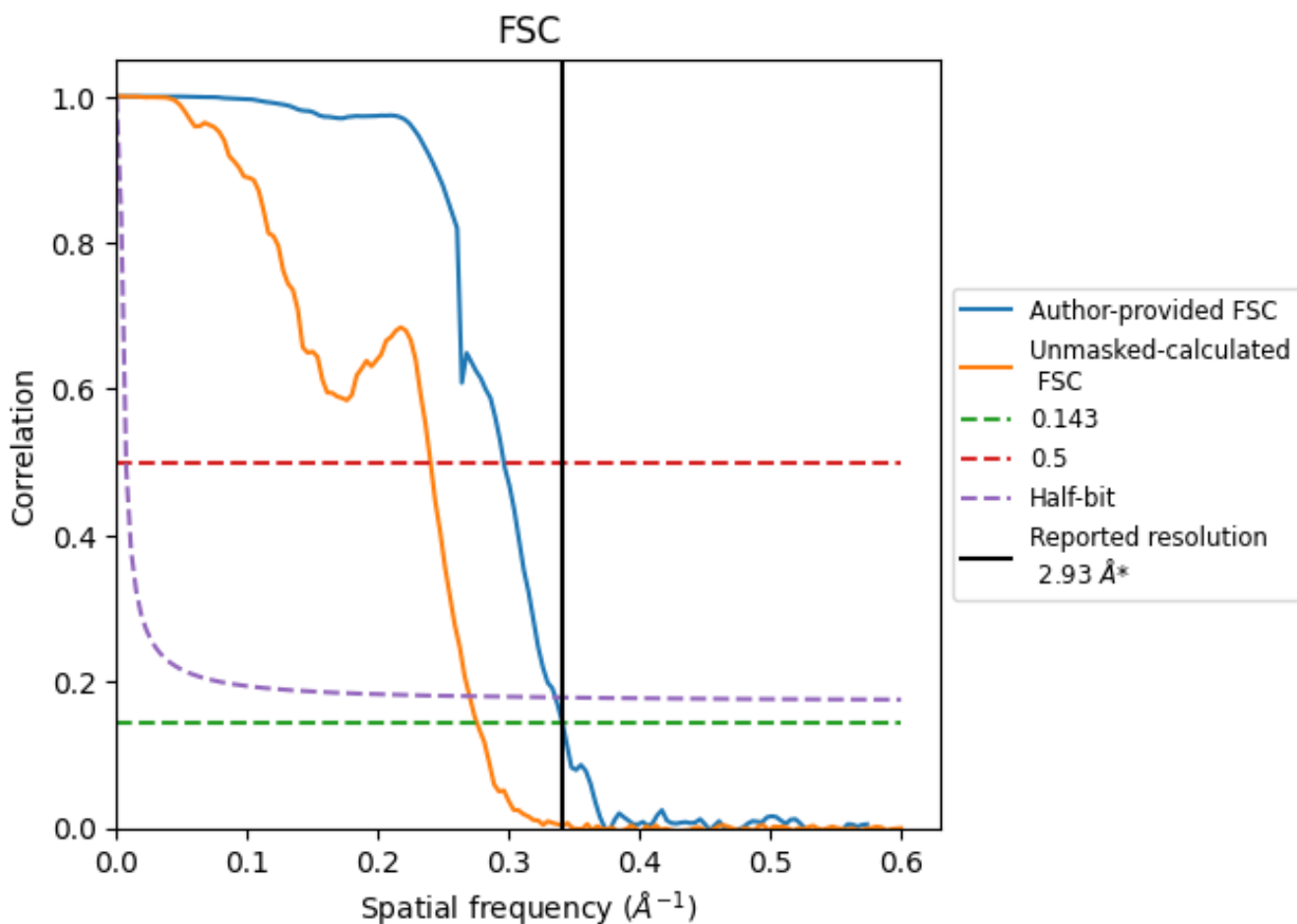


*Reported resolution corresponds to spatial frequency of 0.341 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.341 Å⁻¹

8.2 Resolution estimates [i](#)

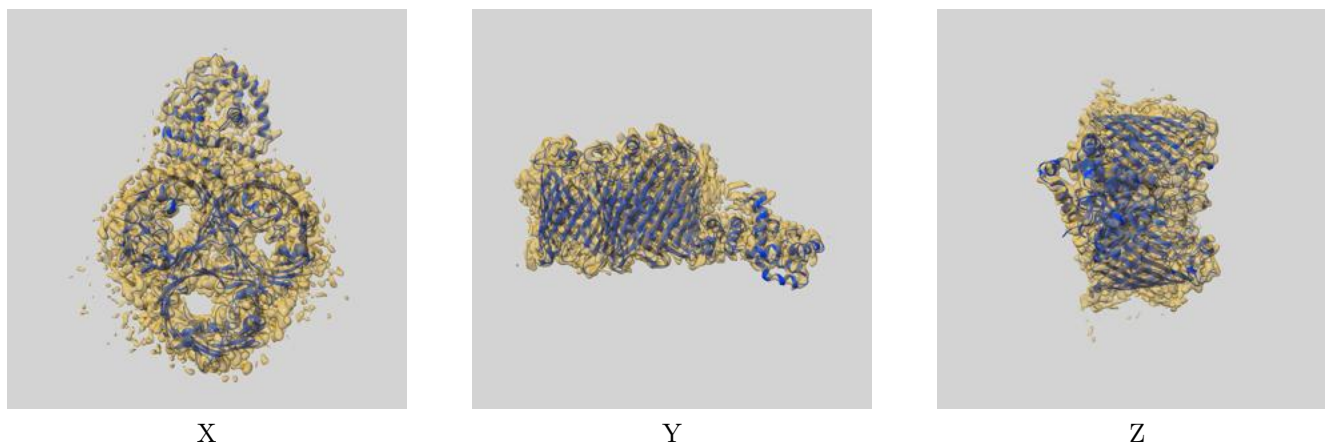
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	2.93	3.38	2.98
Unmasked-calculated*	3.63	4.17	3.71

*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 3.63 differs from the reported value 2.93 by more than 10 %

9 Map-model fit [i](#)

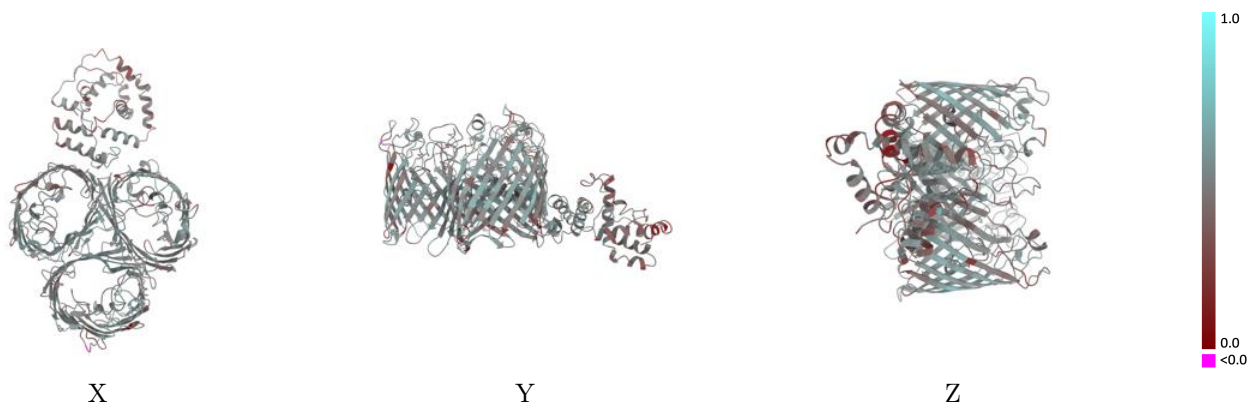
This section contains information regarding the fit between EMDB map EMD-35250 and PDB model 8I8R. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



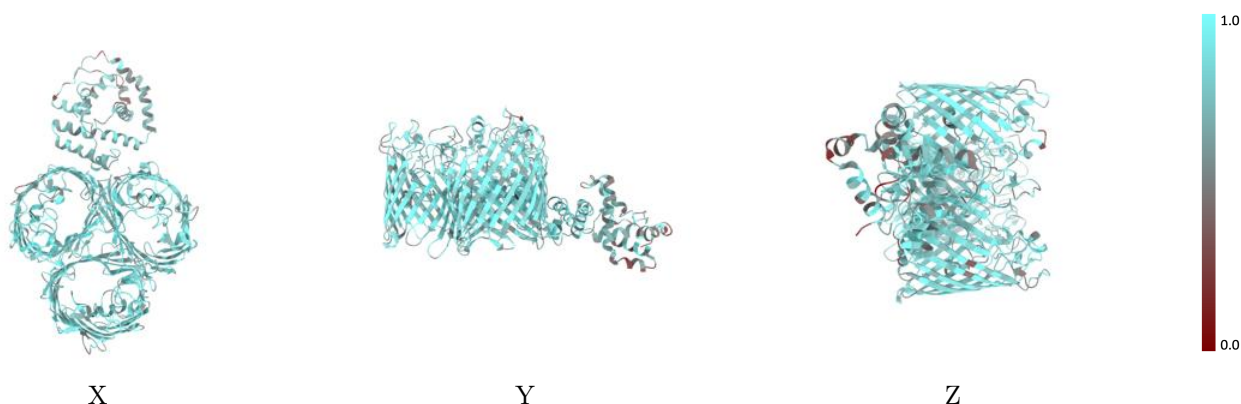
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



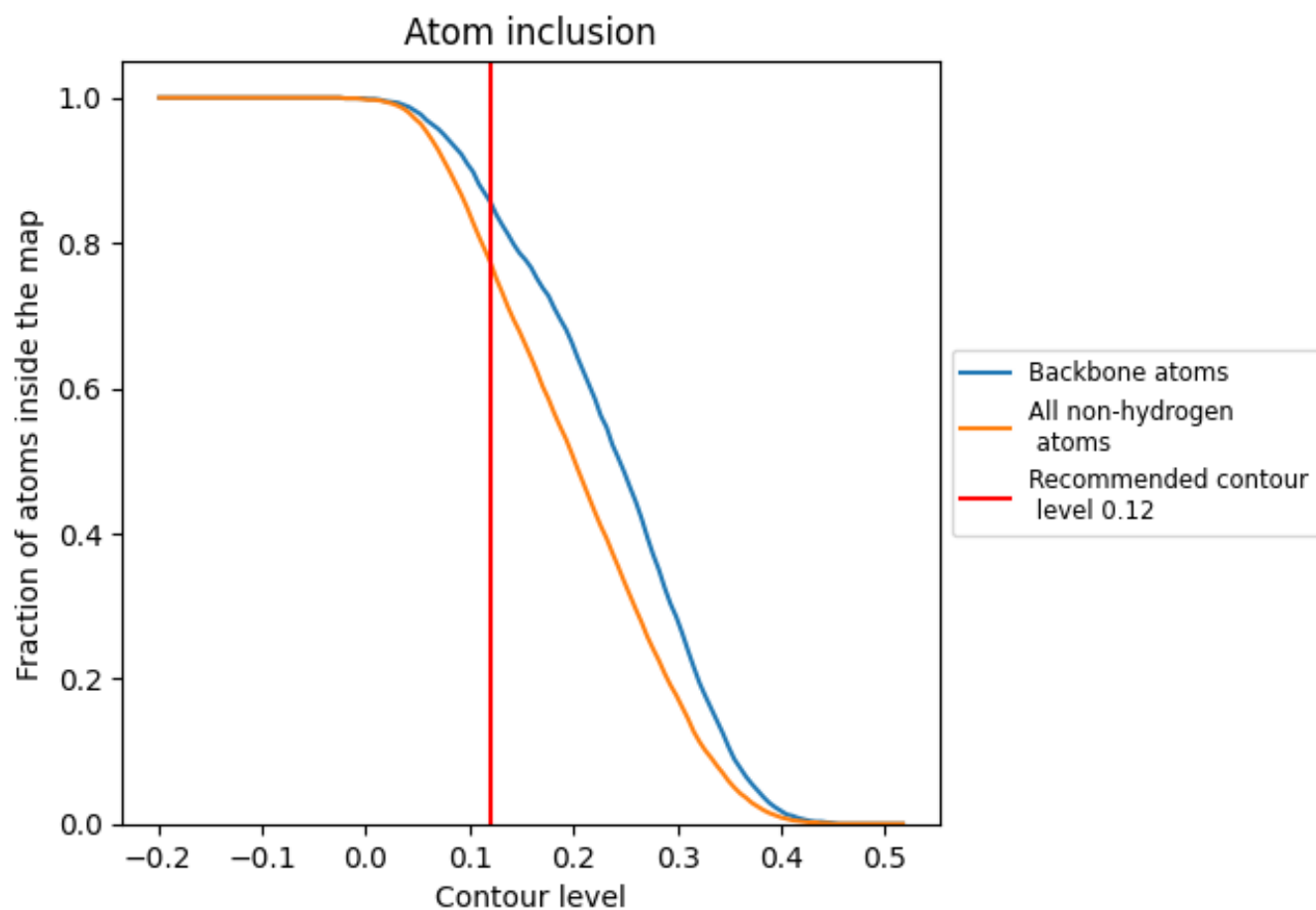
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).











9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7730	 0.4770
A	 0.7970	 0.4880
B	 0.7930	 0.4880
C	 0.7820	 0.4860
D	 0.6760	 0.4220

