



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 04:14 AM UTC

PDB ID : 7NF8 / pdb_00007nf8
EMDB ID : EMD-12298
Title : Ovine (b0,+AT-rBAT)2 hetero-tetramer, asymmetric unit, rigid-body fitted
Authors : Lee, Y.; Kuehlbrandt, W.
Deposited on : 2021-02-05
Resolution : 2.83 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

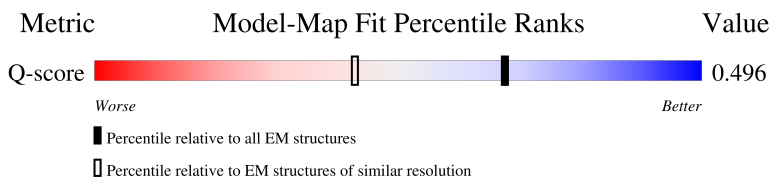
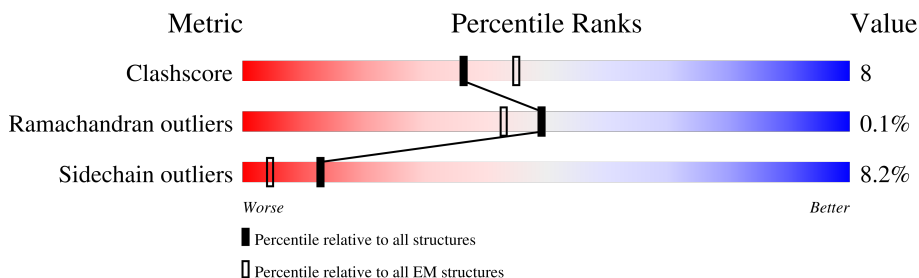
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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	11847 (2.33 - 3.33)

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	B	515	
2	A	686	
3	C	2	
3	D	2	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8817 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 B(0,+)-type amino acid transporter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	455	Total	C	N	O	S	0	0
			3506	2344	540	597	25		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	488	TRP	-	expression tag	UNP A0A6P3EL78
B	489	SER	-	expression tag	UNP A0A6P3EL78
B	490	HIS	-	expression tag	UNP A0A6P3EL78
B	491	PRO	-	expression tag	UNP A0A6P3EL78
B	492	GLN	-	expression tag	UNP A0A6P3EL78
B	493	PHE	-	expression tag	UNP A0A6P3EL78
B	494	GLU	-	expression tag	UNP A0A6P3EL78
B	495	LYS	-	expression tag	UNP A0A6P3EL78
B	496	GLY	-	expression tag	UNP A0A6P3EL78
B	497	GLY	-	expression tag	UNP A0A6P3EL78
B	498	GLY	-	expression tag	UNP A0A6P3EL78
B	499	SER	-	expression tag	UNP A0A6P3EL78
B	500	GLY	-	expression tag	UNP A0A6P3EL78
B	501	GLY	-	expression tag	UNP A0A6P3EL78
B	502	GLY	-	expression tag	UNP A0A6P3EL78
B	503	SER	-	expression tag	UNP A0A6P3EL78
B	504	GLY	-	expression tag	UNP A0A6P3EL78
B	505	GLY	-	expression tag	UNP A0A6P3EL78
B	506	SER	-	expression tag	UNP A0A6P3EL78
B	507	ALA	-	expression tag	UNP A0A6P3EL78
B	508	TRP	-	expression tag	UNP A0A6P3EL78
B	509	SER	-	expression tag	UNP A0A6P3EL78
B	510	HIS	-	expression tag	UNP A0A6P3EL78
B	511	PRO	-	expression tag	UNP A0A6P3EL78
B	512	GLN	-	expression tag	UNP A0A6P3EL78
B	513	PHE	-	expression tag	UNP A0A6P3EL78
B	514	GLU	-	expression tag	UNP A0A6P3EL78
B	515	LYS	-	expression tag	UNP A0A6P3EL78

- Molecule 2 is a protein called neutral and basic amino acid transport protein rBAT.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	623	5090	3250	868	948	24	0	0

There are 3 discrepancies between the modelled and reference sequences:

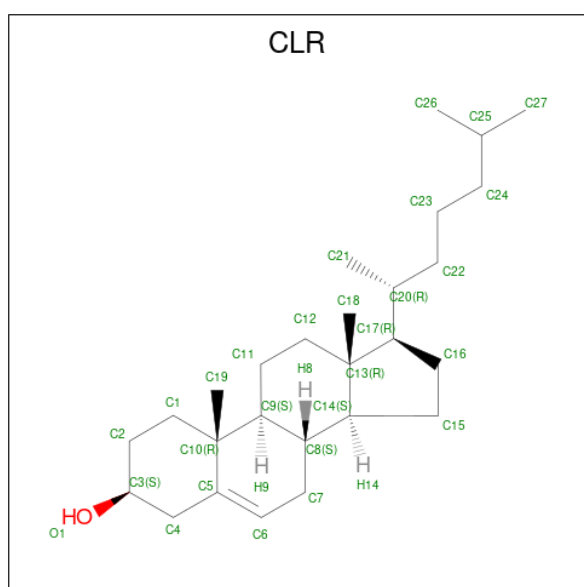
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A0A6P7DVK7
A	1	SER	-	expression tag	UNP A0A6P7DVK7
A	181	GLN	ARG	conflict	UNP A0A6P7DVK7

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



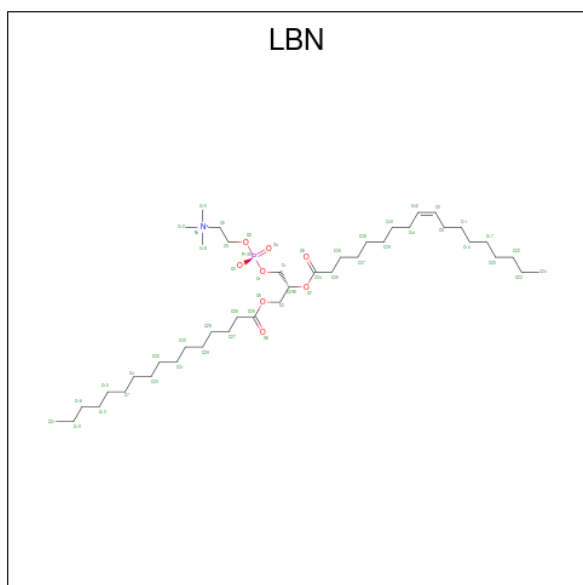
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	2	28	16	2	10	0	0
3	D	2	28	16	2	10	0	0

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			AltConf
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	

- Molecule 5 is 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (CCD ID: LBN) (formula: $C_{42}H_{82}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total	Ca	0
			1	1	

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

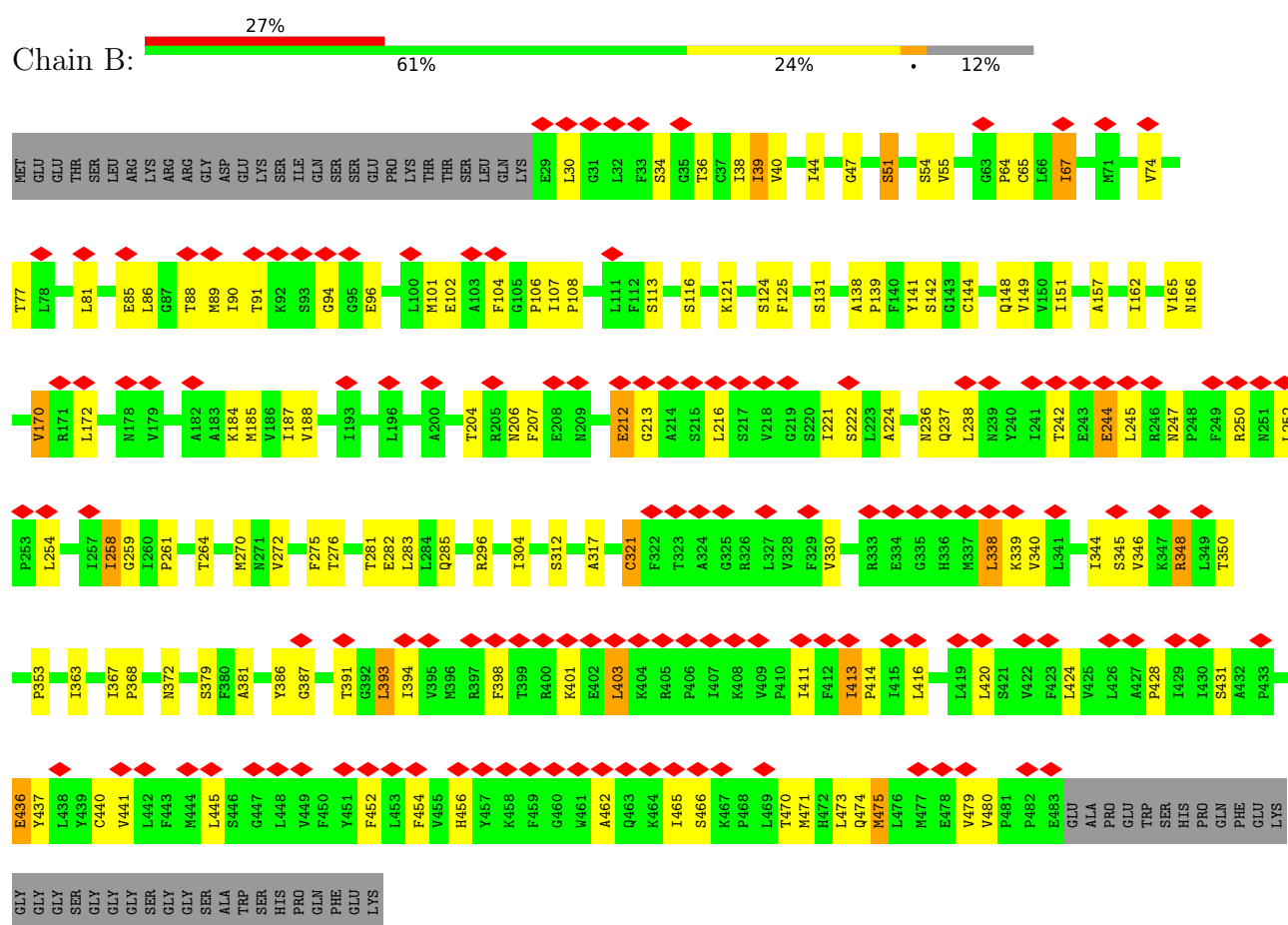


Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	

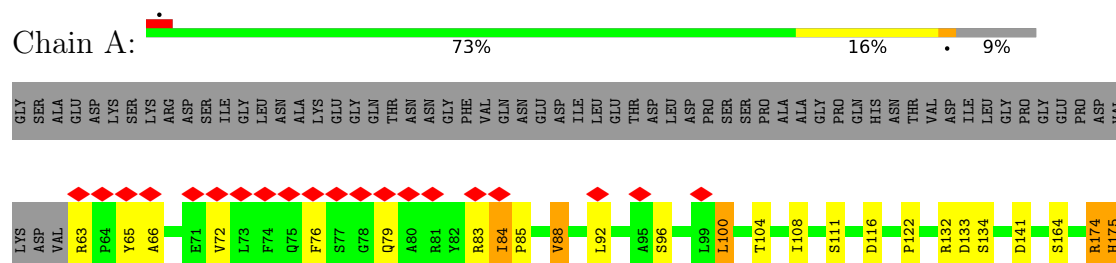
3 Residue-property plots

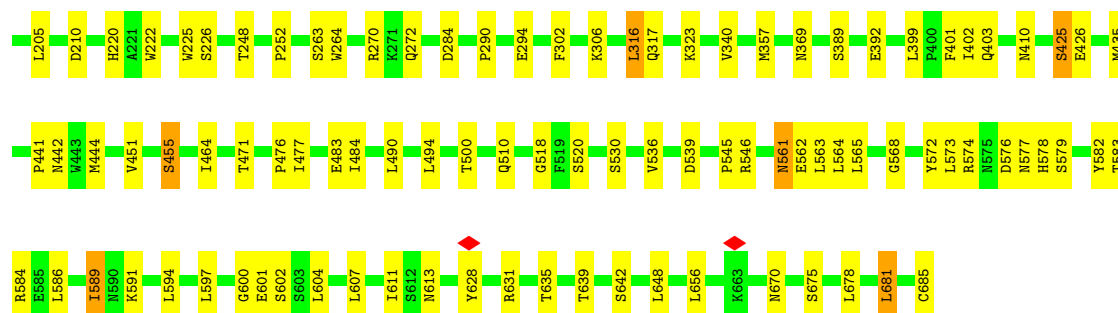
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: B(0,+)-type amino acid transporter 1



- Molecule 2: neutral and basic amino acid transport protein rBAT





- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	581697	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.186	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	351.53918, 351.53918, 351.53918	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09856, 1.09856, 1.09856	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: CA, LBN, CLR, NAG

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	B	0.20	0/3601	0.44	0/4915
2	A	0.29	0/5229	0.43	0/7098
All	All	0.25	0/8830	0.44	0/12013

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	174	ARG	Peptide

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	B	3506	0	3637	73	0
2	A	5090	0	4903	66	0
3	C	28	0	25	1	0
3	D	28	0	25	0	0
4	B	56	0	92	2	0
5	A	52	0	0	0	0
6	A	1	0	0	0	0
7	A	56	0	52	1	0
All	All	8817	0	8734	135	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 (135) 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)
2:A:464:ILE:HD11	2:A:597:LEU:HB3	1.63	0.79
2:A:565:LEU:O	2:A:584:ARG:NH1	2.17	0.77
1:B:107:ILE:HG13	1:B:108:PRO:HD3	1.66	0.76
2:A:410:ASN:H	2:A:442:ASN:HD21	1.35	0.74
2:A:435:MET:HE1	2:A:441:PRO:HG3	1.71	0.72
1:B:188:VAL:HG22	1:B:270:MET:HE1	1.74	0.69
2:A:220:HIS:HD2	2:A:222:TRP:H	1.39	0.68
2:A:65:TYR:HE1	2:A:72:VAL:HG21	1.57	0.68
1:B:345:SER:OG	1:B:348:ARG:O	2.14	0.66
2:A:578:HIS:HB3	2:A:600:GLY:HA3	1.77	0.65
1:B:452:PHE:HA	1:B:456:HIS:HB3	1.77	0.65
2:A:607:LEU:HB2	2:A:635:THR:HG23	1.79	0.65
1:B:206:ASN:ND2	1:B:275:PHE:O	2.29	0.65
1:B:339:LYS:HD2	1:B:339:LYS:H	1.63	0.63
1:B:47:GLY:O	1:B:51:SER:OG	2.11	0.63
2:A:563:LEU:HD21	2:A:681:LEU:HD21	1.81	0.63
1:B:242:THR:HG22	1:B:252:LEU:HD13	1.80	0.63
1:B:166:ASN:HD22	1:B:321:CYS:HB3	1.65	0.61
1:B:170:VAL:HG23	1:B:350:THR:HG22	1.82	0.61
1:B:474:GLN:NE2	1:B:479:VAL:O	2.28	0.61
1:B:89:MET:HE3	1:B:403:LEU:HD11	1.82	0.61
2:A:200:ILE:HG23	2:A:205:LEU:HB2	1.83	0.60
2:A:133:ASP:HB3	2:A:520:SER:HA	1.83	0.60
1:B:394:ILE:O	1:B:398:PHE:N	2.35	0.59
2:A:594:LEU:HD23	2:A:648:LEU:HD12	1.84	0.59
2:A:122:PRO:HB3	2:A:476:PRO:HG2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:389:SER:HB3	2:A:392:GLU:HB2	1.85	0.57
1:B:344:ILE:O	1:B:480:VAL:N	2.34	0.57
2:A:425:SER:HB2	2:A:572:TYR:OH	2.03	0.57
2:A:601:GLU:HG2	2:A:602:SER:H	1.68	0.57
2:A:628:TYR:HD1	2:A:631:ARG:HB2	1.68	0.57
1:B:471:MET:O	1:B:475:MET:N	2.37	0.57
1:B:261:PRO:HA	1:B:264:THR:HG22	1.87	0.57
1:B:282:GLU:OE2	1:B:296:ARG:NH1	2.38	0.56
1:B:101:MET:HE1	1:B:106:PRO:HB3	1.87	0.56
2:A:601:GLU:O	2:A:642:SER:HB2	2.05	0.56
2:A:510:GLN:NE2	2:A:530:SER:OG	2.39	0.56
1:B:30:LEU:HD12	1:B:244:GLU:HB3	1.87	0.55
1:B:471:MET:HB3	2:A:66:ALA:HA	1.88	0.55
2:A:369:ASN:HD21	2:A:403:GLN:NE2	2.07	0.53
1:B:471:MET:HA	1:B:474:GLN:HB3	1.90	0.52
1:B:30:LEU:HB3	1:B:34:SER:OG	2.10	0.52
1:B:281:THR:HG21	2:A:202:ASP:HA	1.91	0.52
1:B:54:SER:OG	1:B:372:ASN:ND2	2.43	0.52
1:B:184:LYS:HB2	1:B:312:SER:HB2	1.91	0.52
1:B:102:GLU:OE2	1:B:401:LYS:NZ	2.42	0.51
1:B:381:ALA:HB2	1:B:440:CYS:SG	2.50	0.51
2:A:132:ARG:NH1	2:A:518:GLY:O	2.44	0.51
2:A:84:ILE:HG22	2:A:85:PRO:HD3	1.93	0.51
1:B:338:LEU:HD22	1:B:340:VAL:HG12	1.93	0.51
1:B:39:ILE:HD11	1:B:259:GLY:HA3	1.92	0.50
1:B:387:GLY:O	1:B:391:THR:HG23	2.11	0.50
1:B:212:GLU:OE2	1:B:213:GLY:N	2.44	0.50
1:B:36:THR:HG21	1:B:258:ILE:HD11	1.94	0.50
2:A:290:PRO:O	2:A:294:GLU:HG2	2.12	0.50
2:A:471:THR:OG1	2:A:582:TYR:OH	2.22	0.50
2:A:568:GLY:O	2:A:584:ARG:NH2	2.44	0.50
2:A:63:ARG:HB3	2:A:76:PHE:HZ	1.78	0.49
4:B:601:CLR:H121	2:A:100:LEU:HD21	1.96	0.48
2:A:573:LEU:HD21	2:A:656:LEU:HD13	1.93	0.48
1:B:88:THR:O	1:B:91:THR:OG1	2.32	0.48
2:A:444:MET:HG3	2:A:477:ILE:HB	1.95	0.48
2:A:164:SER:OG	2:A:175:HIS:NE2	2.47	0.48
1:B:149:VAL:HG11	2:A:678:LEU:HD22	1.95	0.48
1:B:345:SER:HA	1:B:479:VAL:HA	1.97	0.47
2:A:369:ASN:HD21	2:A:403:GLN:HE21	1.63	0.47
2:A:225:TRP:CD1	7:A:705:NAG:H81	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:611:ILE:HG22	2:A:613:ASN:HB3	1.97	0.47
1:B:104:PHE:HB3	1:B:108:PRO:HG2	1.97	0.46
2:A:451:VAL:HG12	2:A:455:SER:HB2	1.96	0.46
2:A:399:LEU:HD12	2:A:402:ILE:HD12	1.97	0.46
1:B:367:ILE:HG12	4:B:601:CLR:H191	1.97	0.46
1:B:462:ALA:O	1:B:465:ILE:HG22	2.15	0.46
1:B:104:PHE:CB	1:B:108:PRO:HG2	2.45	0.46
1:B:411:ILE:O	1:B:414:PRO:HD2	2.16	0.46
1:B:441:VAL:O	1:B:445:LEU:HG	2.15	0.46
1:B:353:PRO:HD3	1:B:479:VAL:HG11	1.98	0.46
1:B:437:TYR:O	1:B:441:VAL:HG23	2.16	0.46
1:B:157:ALA:HB2	2:A:100:LEU:HB3	1.98	0.45
1:B:148:GLN:HE22	1:B:151:ILE:HD11	1.81	0.45
2:A:302:PHE:CZ	2:A:306:LYS:HE2	2.52	0.45
1:B:141:TYR:HE2	2:A:108:ILE:HG12	1.82	0.45
1:B:216:LEU:HD12	1:B:216:LEU:H	1.82	0.45
2:A:561:ASN:O	2:A:561:ASN:ND2	2.47	0.45
2:A:85:PRO:HA	2:A:88:VAL:HG12	1.99	0.44
1:B:39:ILE:HB	1:B:238:LEU:HD21	2.00	0.44
1:B:94:GLY:HA2	1:B:330:VAL:HG21	2.00	0.44
2:A:263:SER:O	2:A:263:SER:OG	2.31	0.44
1:B:185:MET:HE3	1:B:185:MET:HB3	1.89	0.44
2:A:483:GLU:HG2	2:A:484:ILE:HG23	2.00	0.44
1:B:424:LEU:HD23	1:B:424:LEU:HA	1.88	0.44
2:A:401:PHE:CD2	2:A:402:ILE:HG13	2.53	0.44
1:B:86:LEU:HD21	1:B:393:LEU:HB2	1.99	0.43
3:C:1:NAG:H62	3:C:2:NAG:O5	2.18	0.43
2:A:65:TYR:O	2:A:65:TYR:CG	2.71	0.43
1:B:121:LYS:HD3	1:B:121:LYS:HA	1.75	0.43
2:A:79:GLN:HE22	2:A:83:ARG:HD2	1.83	0.43
1:B:40:VAL:O	1:B:44:ILE:HG12	2.19	0.43
1:B:81:LEU:HD23	1:B:81:LEU:HA	1.78	0.43
2:A:317:GLN:HA	2:A:357:MET:HE2	2.00	0.43
2:A:613:ASN:O	2:A:613:ASN:ND2	2.52	0.43
1:B:55:VAL:HG23	1:B:224:ALA:HB1	2.01	0.43
1:B:125:PHE:HE1	1:B:317:ALA:HB1	1.84	0.43
2:A:92:LEU:HD12	2:A:92:LEU:HA	1.85	0.43
2:A:174:ARG:O	2:A:175:HIS:HB2	2.19	0.42
1:B:64:PRO:O	1:B:67:ILE:HG12	2.20	0.42
1:B:367:ILE:HB	1:B:368:PRO:HD3	2.01	0.42
1:B:436:GLU:H	1:B:436:GLU:HG3	1.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:GLU:HG2	1:B:393:LEU:HD21	2.02	0.42
2:A:252:PRO:HD2	2:A:264:TRP:CG	2.54	0.42
2:A:562:GLU:C	2:A:564:LEU:H	2.26	0.42
2:A:576:ASP:OD1	2:A:576:ASP:N	2.52	0.42
2:A:545:PRO:HG2	2:A:546:ARG:HG2	2.02	0.42
1:B:222:SER:OG	1:B:428:PRO:HG3	2.19	0.42
1:B:96:GLU:HG2	1:B:96:GLU:O	2.19	0.42
1:B:89:MET:HG3	1:B:90:ILE:HD12	2.02	0.41
2:A:586:LEU:HD12	2:A:586:LEU:HA	1.85	0.41
1:B:162:ILE:HD13	1:B:162:ILE:HA	1.92	0.41
1:B:138:ALA:N	1:B:139:PRO:HD2	2.36	0.41
2:A:270:ARG:HG2	2:A:272:GLN:HB2	2.02	0.41
2:A:316:LEU:HD12	2:A:316:LEU:HA	1.84	0.41
1:B:247:ASN:ND2	1:B:250:ARG:HB2	2.36	0.41
1:B:466:SER:O	1:B:470:THR:HG23	2.20	0.41
2:A:563:LEU:O	2:A:563:LEU:HD13	2.20	0.41
1:B:116:SER:O	1:B:116:SER:OG	2.38	0.40
1:B:282:GLU:HA	1:B:285:GLN:HG2	2.03	0.40
2:A:591:LYS:HE2	2:A:591:LYS:HB3	1.84	0.40
1:B:413:ILE:HG13	1:B:414:PRO:CD	2.51	0.40
1:B:236:ASN:ND2	1:B:386:TYR:OH	2.55	0.40
1:B:282:GLU:OE1	1:B:296:ARG:NH2	2.50	0.40
2:A:100:LEU:O	2:A:104:THR:HG22	2.22	0.40
2:A:586:LEU:HB3	2:A:589:ILE:HG13	2.02	0.40
2:A:604:LEU:HD23	2:A:639:THR:HB	2.04	0.40
2:A:323:LYS:HE3	2:A:323:LYS:HB2	1.86	0.40
2:A:494:LEU:HD23	2:A:494:LEU:HA	1.79	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	B	453/515 (88%)	436 (96%)	17 (4%)	0	100	100
2	A	621/686 (90%)	583 (94%)	37 (6%)	1 (0%)	43	62
All	All	1074/1201 (89%)	1019 (95%)	54 (5%)	1 (0%)	49	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	175	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	383/432 (89%)	338 (88%)	45 (12%)	5	11
2	A	560/612 (92%)	528 (94%)	32 (6%)	18	39
All	All	943/1044 (90%)	866 (92%)	77 (8%)	13	23

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	38	ILE
1	B	39	ILE
1	B	51	SER
1	B	65	CYS
1	B	67	ILE
1	B	74	VAL
1	B	77	THR
1	B	113	SER
1	B	124	SER
1	B	131	SER
1	B	142	SER
1	B	144	CYS
1	B	165	VAL
1	B	170	VAL
1	B	172	LEU

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Mol	Chain	Res	Type
1	B	187	ILE
1	B	204	THR
1	B	207	PHE
1	B	212	GLU
1	B	221	ILE
1	B	237	GLN
1	B	244	GLU
1	B	245	LEU
1	B	254	LEU
1	B	258	ILE
1	B	272	VAL
1	B	276	THR
1	B	283	LEU
1	B	304	ILE
1	B	321	CYS
1	B	338	LEU
1	B	346	VAL
1	B	348	ARG
1	B	363	ILE
1	B	379	SER
1	B	393	LEU
1	B	403	LEU
1	B	413	ILE
1	B	416	LEU
1	B	420	LEU
1	B	431	SER
1	B	436	GLU
1	B	454	PHE
1	B	473	LEU
1	B	475	MET
2	A	84	ILE
2	A	88	VAL
2	A	96	SER
2	A	100	LEU
2	A	111	SER
2	A	116	ASP
2	A	134	SER
2	A	141	ASP
2	A	191	LYS
2	A	210	ASP
2	A	226	SER
2	A	248	THR

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Mol	Chain	Res	Type
2	A	284	ASP
2	A	316	LEU
2	A	340	VAL
2	A	425	SER
2	A	426	GLU
2	A	455	SER
2	A	490	LEU
2	A	500	THR
2	A	536	VAL
2	A	539	ASP
2	A	561	ASN
2	A	574	ARG
2	A	577	ASN
2	A	579	SER
2	A	583	THR
2	A	589	ILE
2	A	670	ASN
2	A	675	SER
2	A	681	LEU
2	A	685	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	148	GLN
1	B	166	ASN
1	B	203	ASN
1	B	227	ASN
1	B	251	ASN
1	B	271	ASN
1	B	287	GLN
1	B	372	ASN
1	B	456	HIS
2	A	79	GLN
2	A	146	GLN
2	A	156	ASN
2	A	181	GLN
2	A	201	HIS
2	A	220	HIS
2	A	224	GLN
2	A	282	GLN
2	A	293	GLN

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Mol	Chain	Res	Type
2	A	301	GLN
2	A	335	GLN
2	A	345	GLN
2	A	366	GLN
2	A	369	ASN
2	A	370	GLN
2	A	442	ASN
2	A	466	ASN
2	A	510	GLN
2	A	516	ASN
2	A	534	HIS
2	A	575	ASN
2	A	577	ASN
2	A	598	ASN
2	A	606	ASN
2	A	679	ASN

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](#)

4 monosaccharides 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	NAG	C	1	2,3	14,14,15	0.35	0	17,19,21	0.48	0
3	NAG	C	2	3	14,14,15	0.31	0	17,19,21	0.54	0
3	NAG	D	1	2,3	14,14,15	0.28	0	17,19,21	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	D	2	3	14,14,15	0.25	0	17,19,21	0.43	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	NAG	C	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	3/6/23/26	0/1/1/1
3	NAG	D	1	2,3	-	4/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

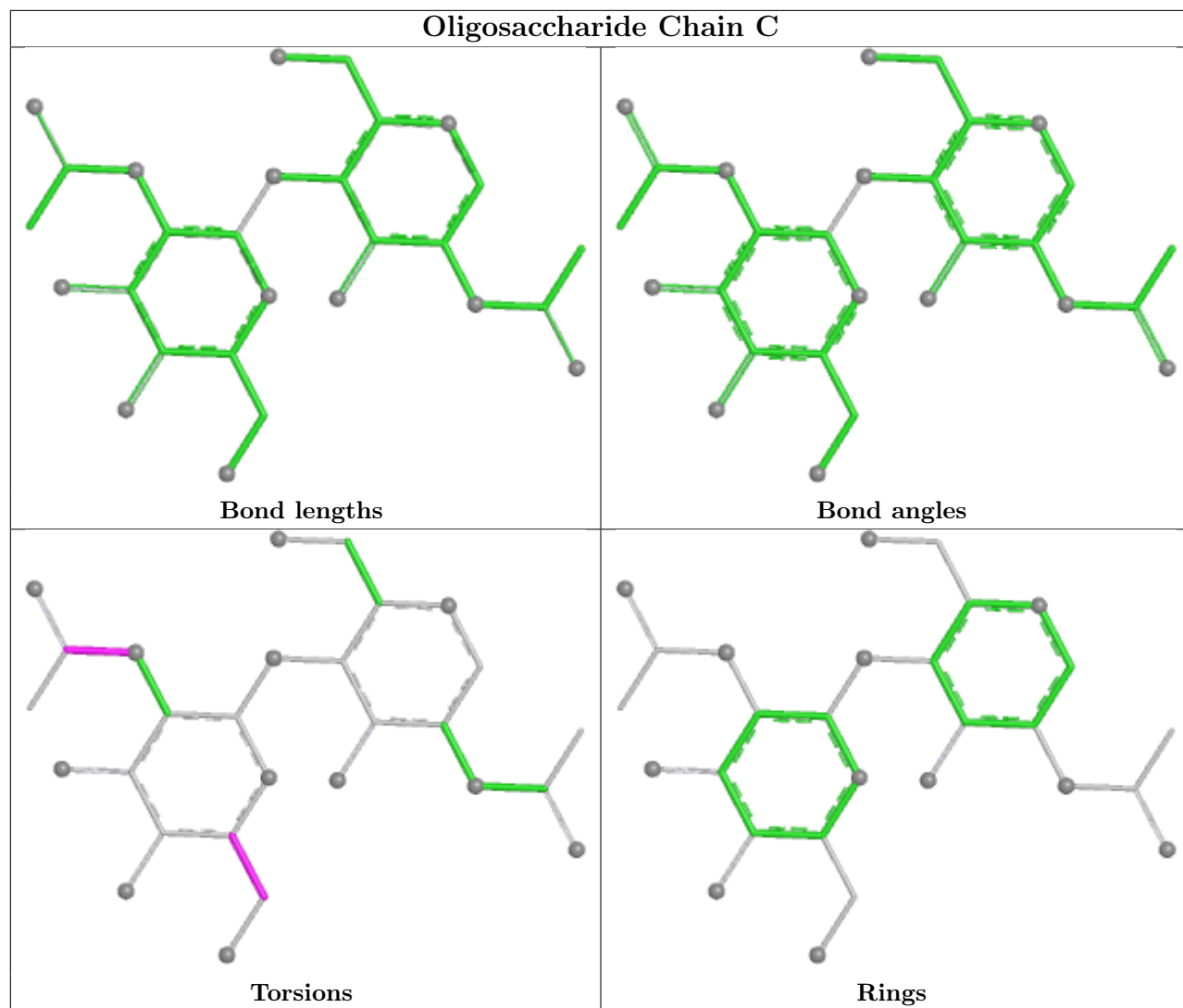
Mol	Chain	Res	Type	Atoms
3	D	2	NAG	O5-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
3	D	1	NAG	C8-C7-N2-C2
3	D	1	NAG	O7-C7-N2-C2
3	C	2	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6

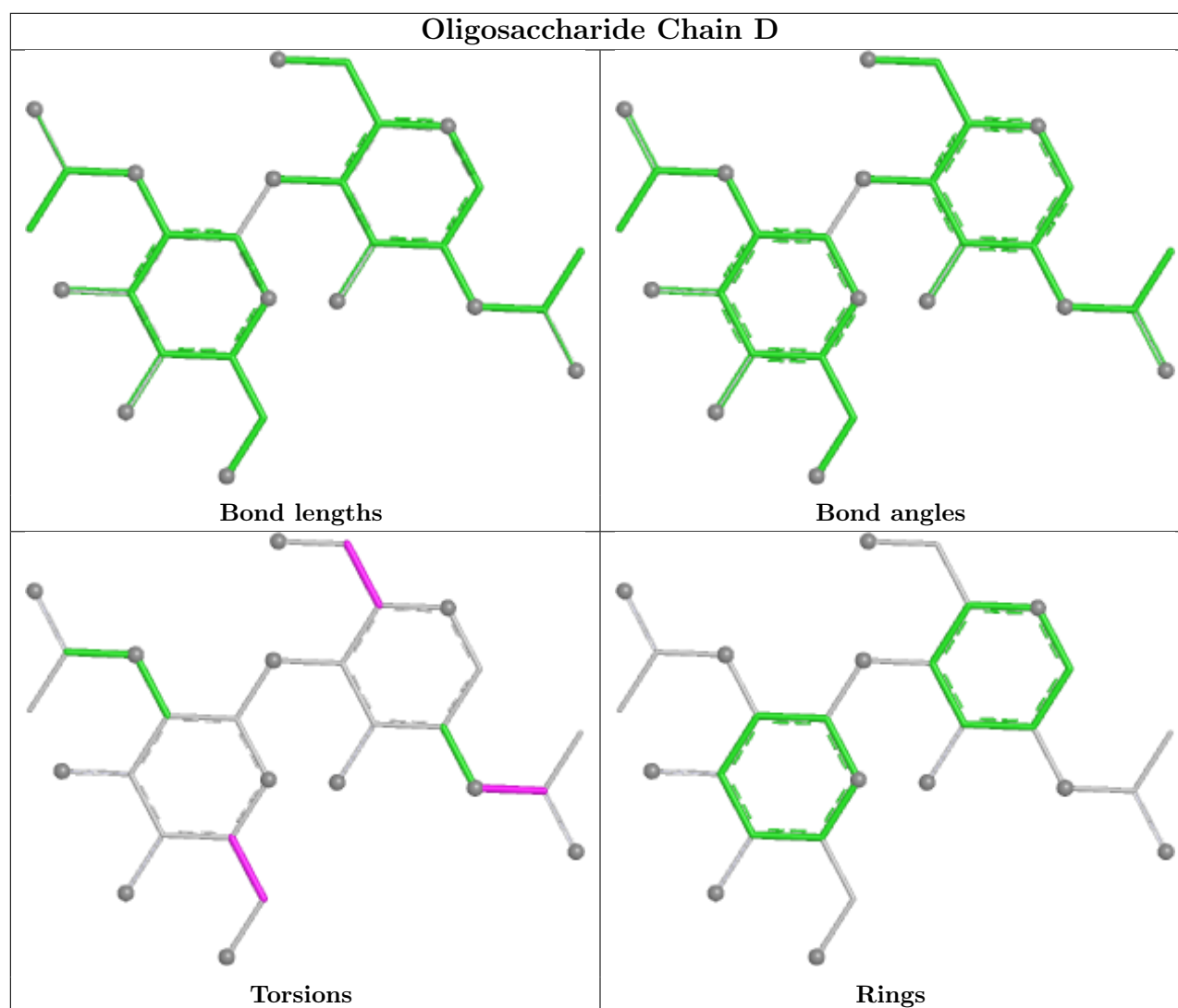
There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	NAG	1	0
3	C	1	NAG	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 oligosaccharide.





5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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	$\# Z > 2$
7	NAG	A	704	2	14,14,15	0.27	0	17,19,21	0.47	0
7	NAG	A	705	2	14,14,15	0.24	0	17,19,21	0.48	0
5	LBN	A	701	-	51,51,51	0.30	0	57,59,59	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CLR	B	602	-	31,31,31	0.28	0	48,48,48	0.39	0
4	CLR	B	601	-	31,31,31	0.28	0	48,48,48	0.45	0
7	NAG	A	706	2	14,14,15	0.22	0	17,19,21	0.40	0
7	NAG	A	703	2	14,14,15	0.25	0	17,19,21	0.45	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
7	NAG	A	704	2	-	2/6/23/26	0/1/1/1
7	NAG	A	705	2	-	0/6/23/26	0/1/1/1
5	LBN	A	701	-	-	10/55/55/55	-
4	CLR	B	602	-	-	4/10/68/68	0/4/4/4
4	CLR	B	601	-	-	0/10/68/68	0/4/4/4
7	NAG	A	706	2	-	2/6/23/26	0/1/1/1
7	NAG	A	703	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	701	LBN	C26-C25-O5-C3
5	A	701	LBN	O6-C25-O5-C3
7	A	706	NAG	C4-C5-C6-O6
7	A	706	NAG	O5-C5-C6-O6
7	A	704	NAG	O5-C5-C6-O6
4	B	602	CLR	C22-C23-C24-C25
7	A	703	NAG	C4-C5-C6-O6
5	A	701	LBN	C31-C32-C33-C4
5	A	701	LBN	C42-C5-C8-C11
5	A	701	LBN	C9-C6-N1-C15
5	A	701	LBN	C39-C40-C41-C42
7	A	703	NAG	O5-C5-C6-O6
4	B	602	CLR	C13-C17-C20-C22
4	B	602	CLR	C16-C17-C20-C22
5	A	701	LBN	C9-C6-N1-C18

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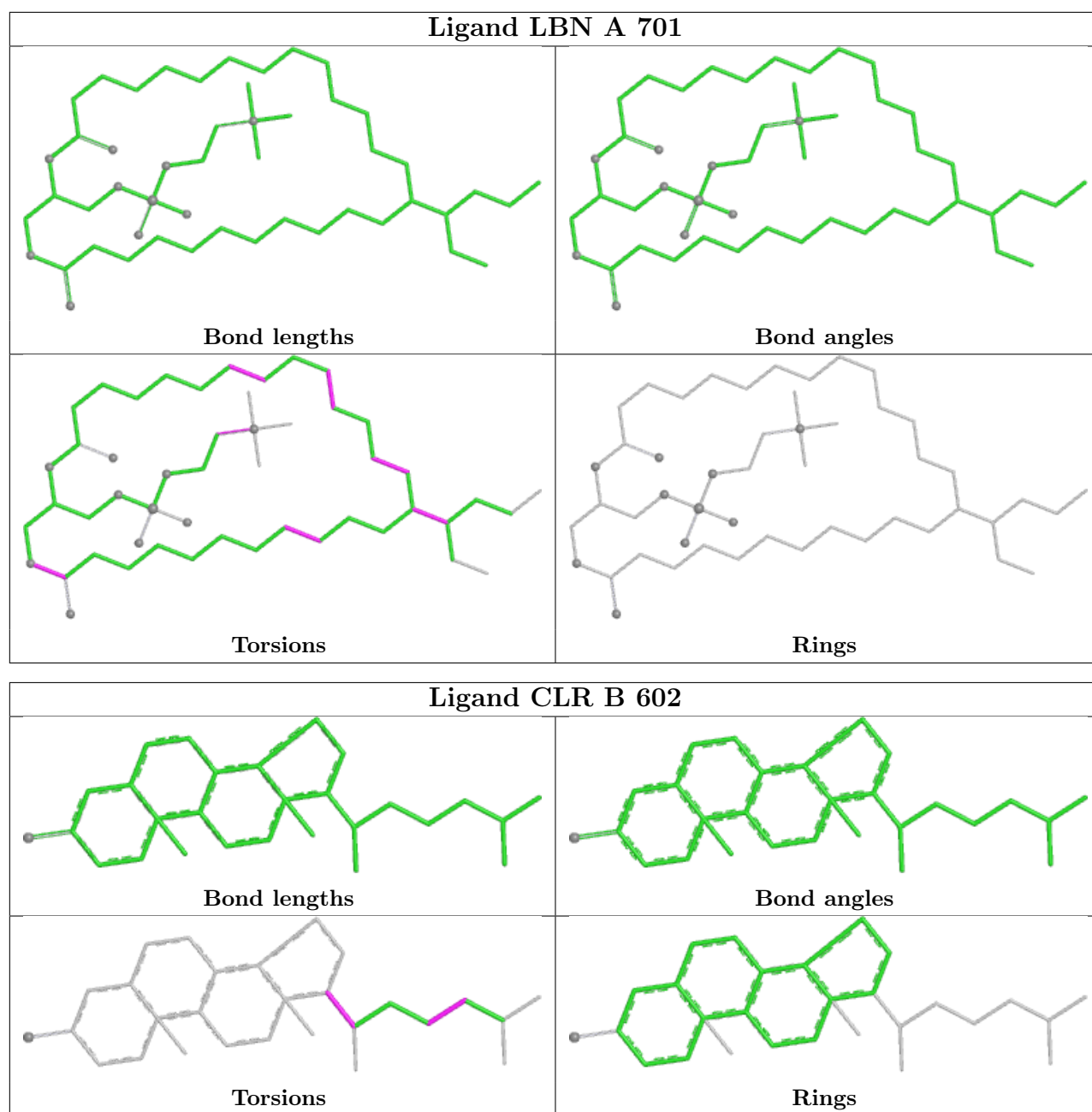
Mol	Chain	Res	Type	Atoms
4	B	602	CLR	C13-C17-C20-C21
5	A	701	LBN	C9-C6-N1-C12
5	A	701	LBN	C11-C14-C17-C20
7	A	704	NAG	C4-C5-C6-O6
5	A	701	LBN	C17-C20-C22-C23

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	705	NAG	1	0
4	B	601	CLR	2	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.

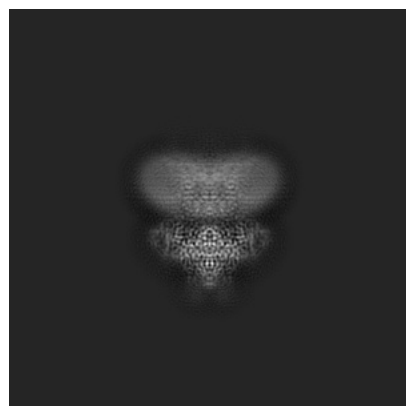
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12298. These allow visual inspection of the internal detail of the map and identification of artifacts.

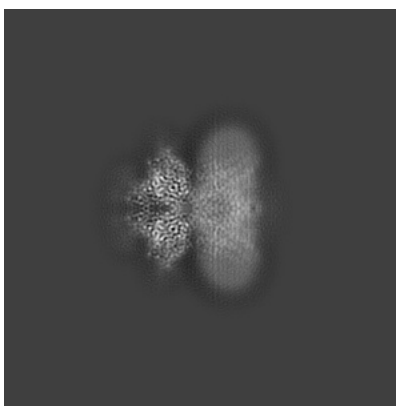
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

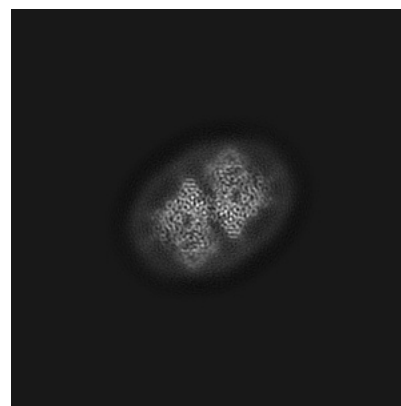
6.1.1 Primary map



X

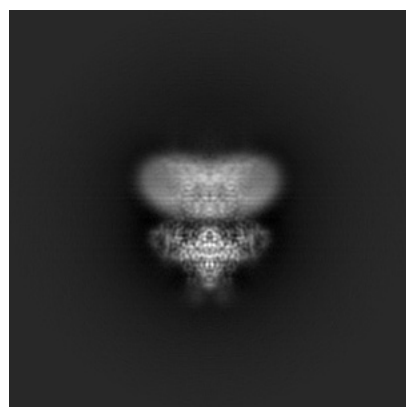


Y

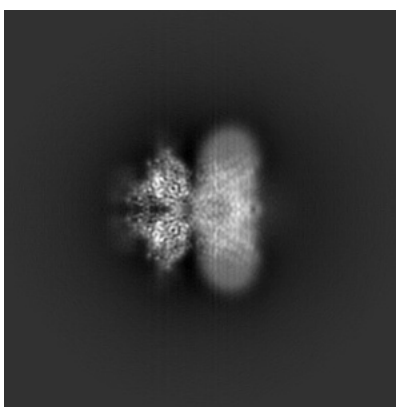


Z

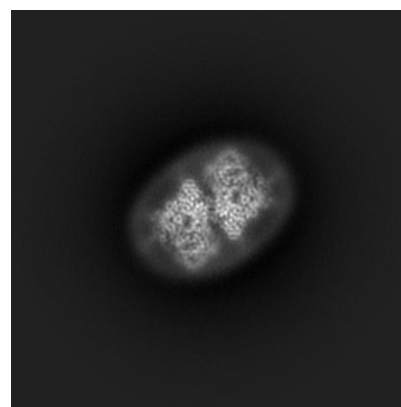
6.1.2 Raw map



X



Y

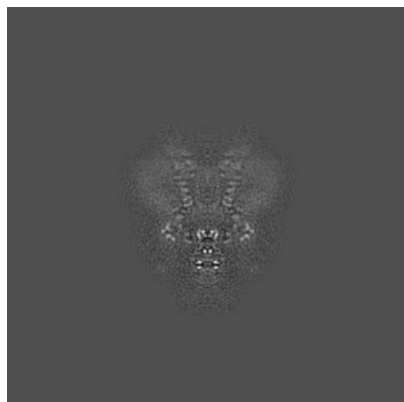


Z

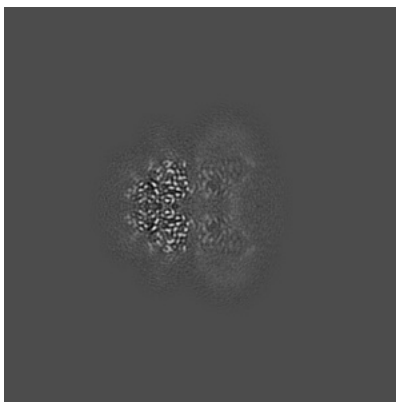
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

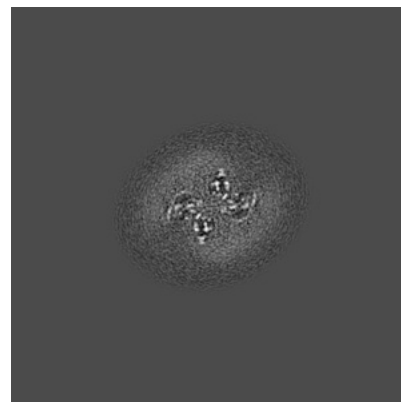
6.2.1 Primary map



X Index: 160



Y Index: 160

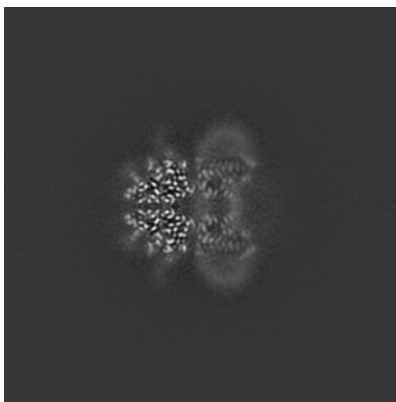


Z Index: 160

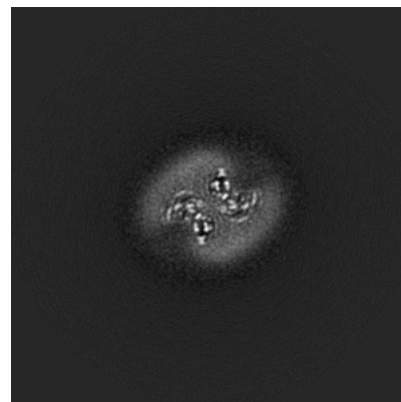
6.2.2 Raw map



X Index: 160



Y Index: 160

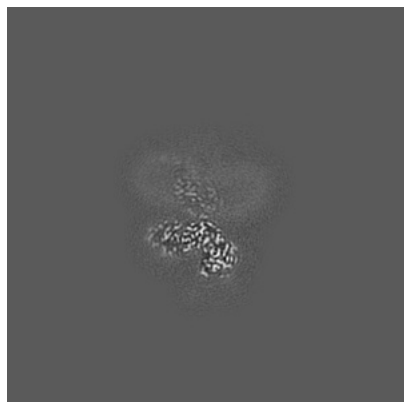


Z Index: 160

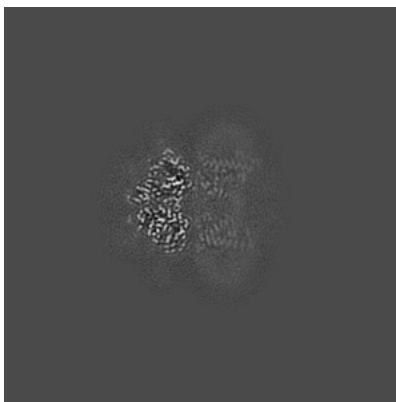
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

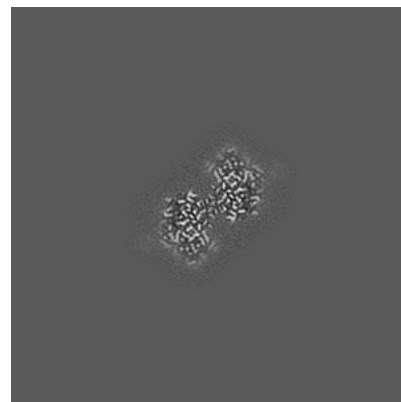
6.3.1 Primary map



X Index: 145

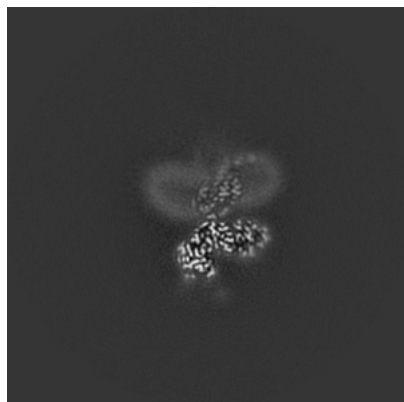


Y Index: 163

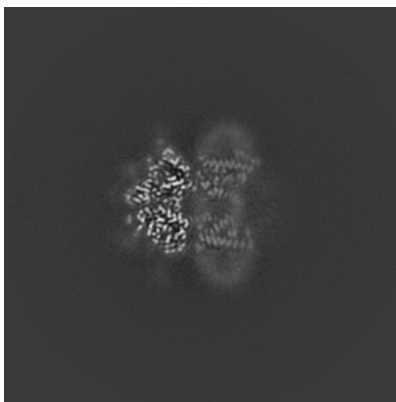


Z Index: 137

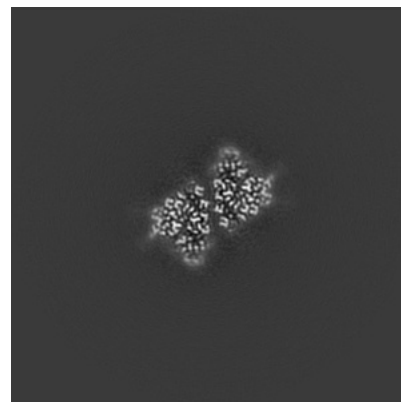
6.3.2 Raw map



X Index: 175



Y Index: 163

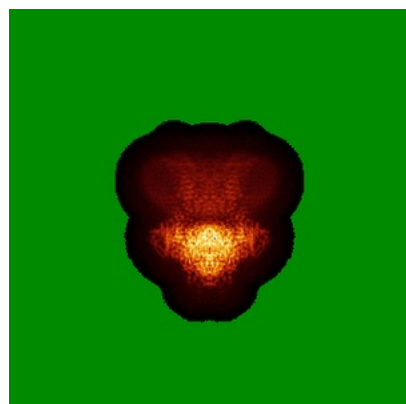


Z Index: 131

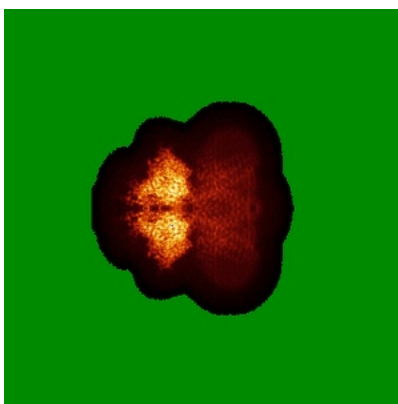
The images above show the largest variance slices of the map in three orthogonal directions.

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

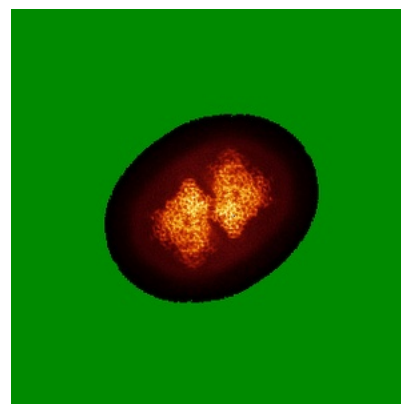
6.4.1 Primary map



X



Y

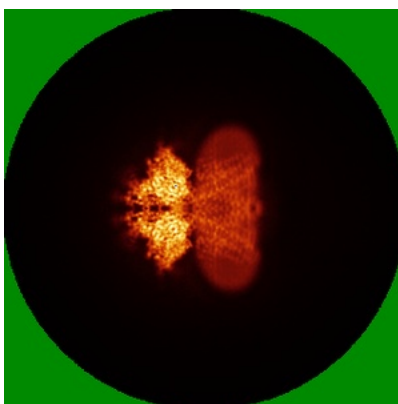


Z

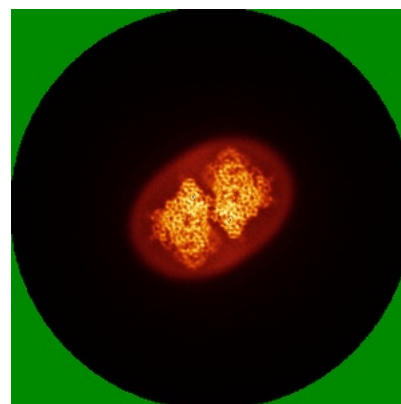
6.4.2 Raw map



X



Y



Z

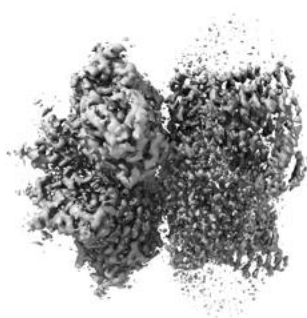
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

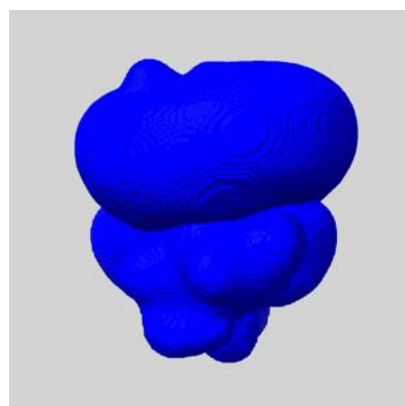
6.6 Mask visualisation [i](#)

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

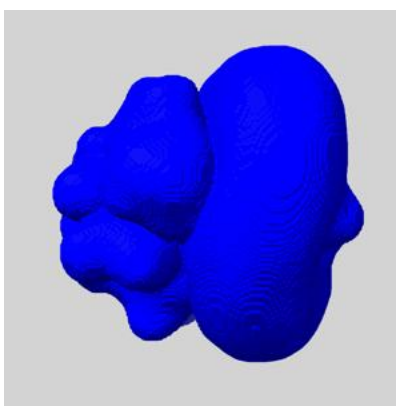
A mask typically either:

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

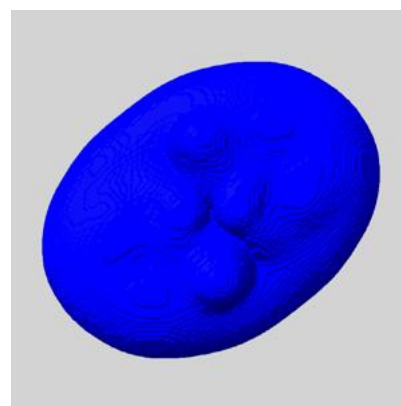
6.6.1 emd_12298_msk_1.map [i](#)



X



Y

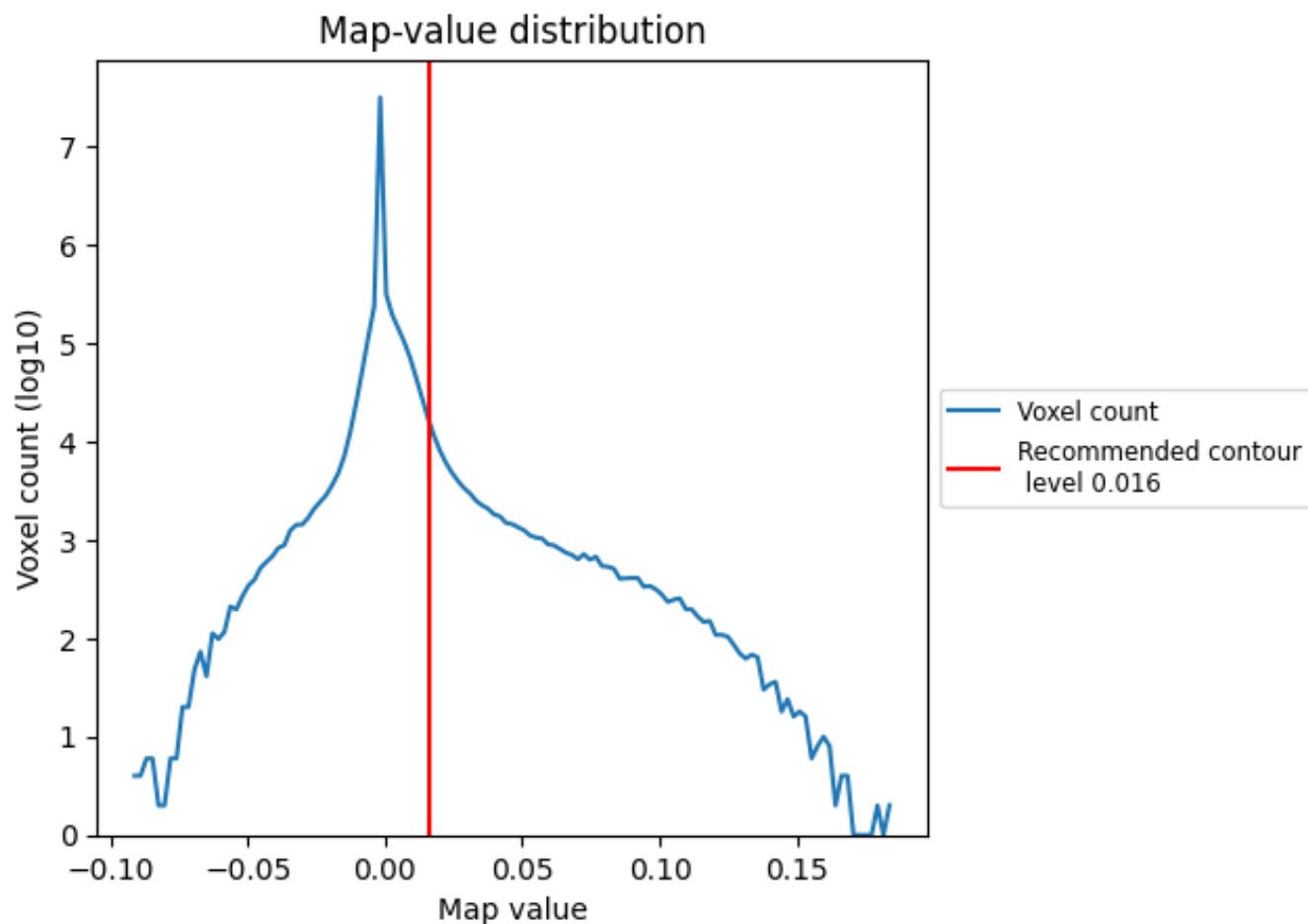


Z

7 Map analysis [i](#)

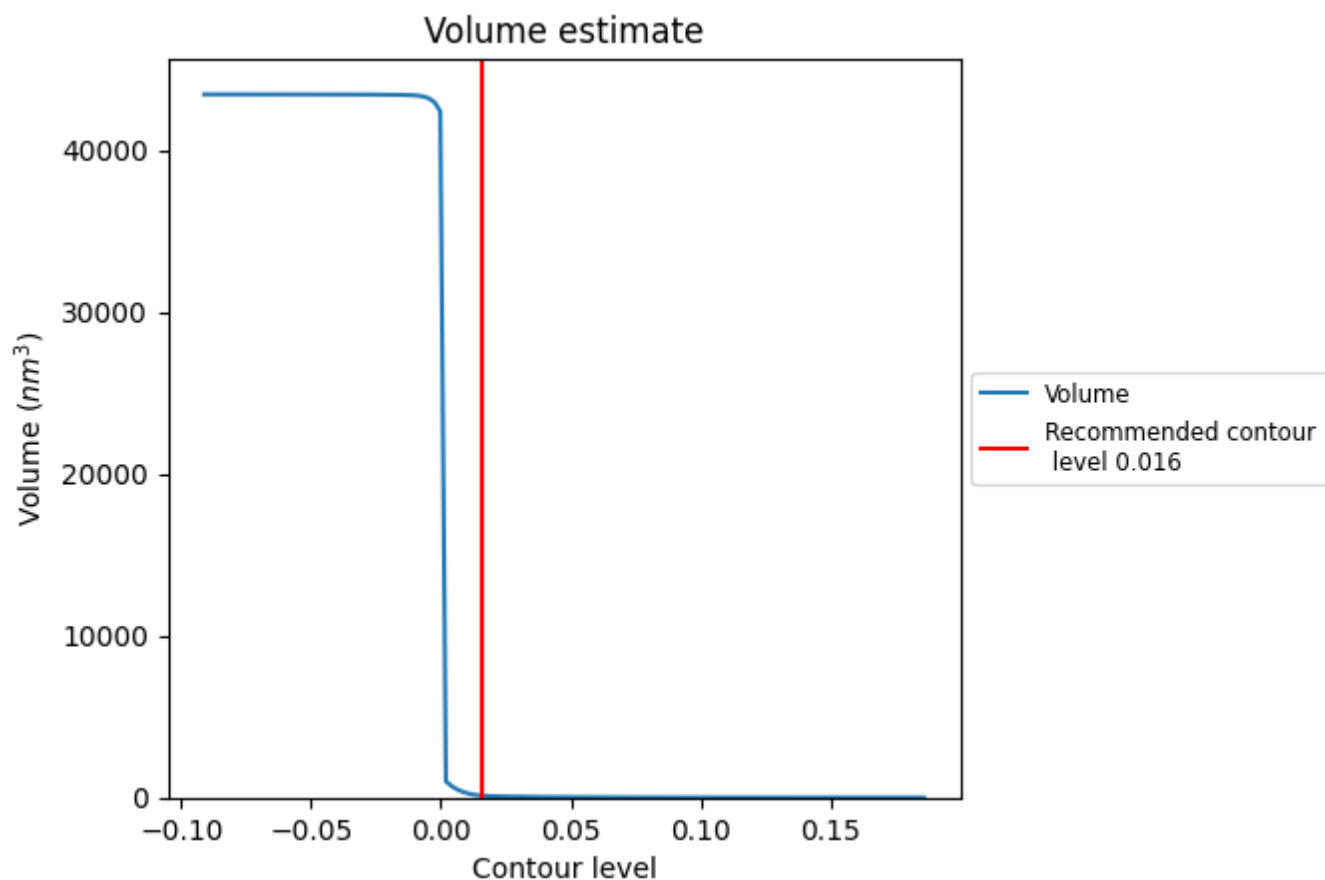
This section contains the results of statistical analysis of the map.

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.

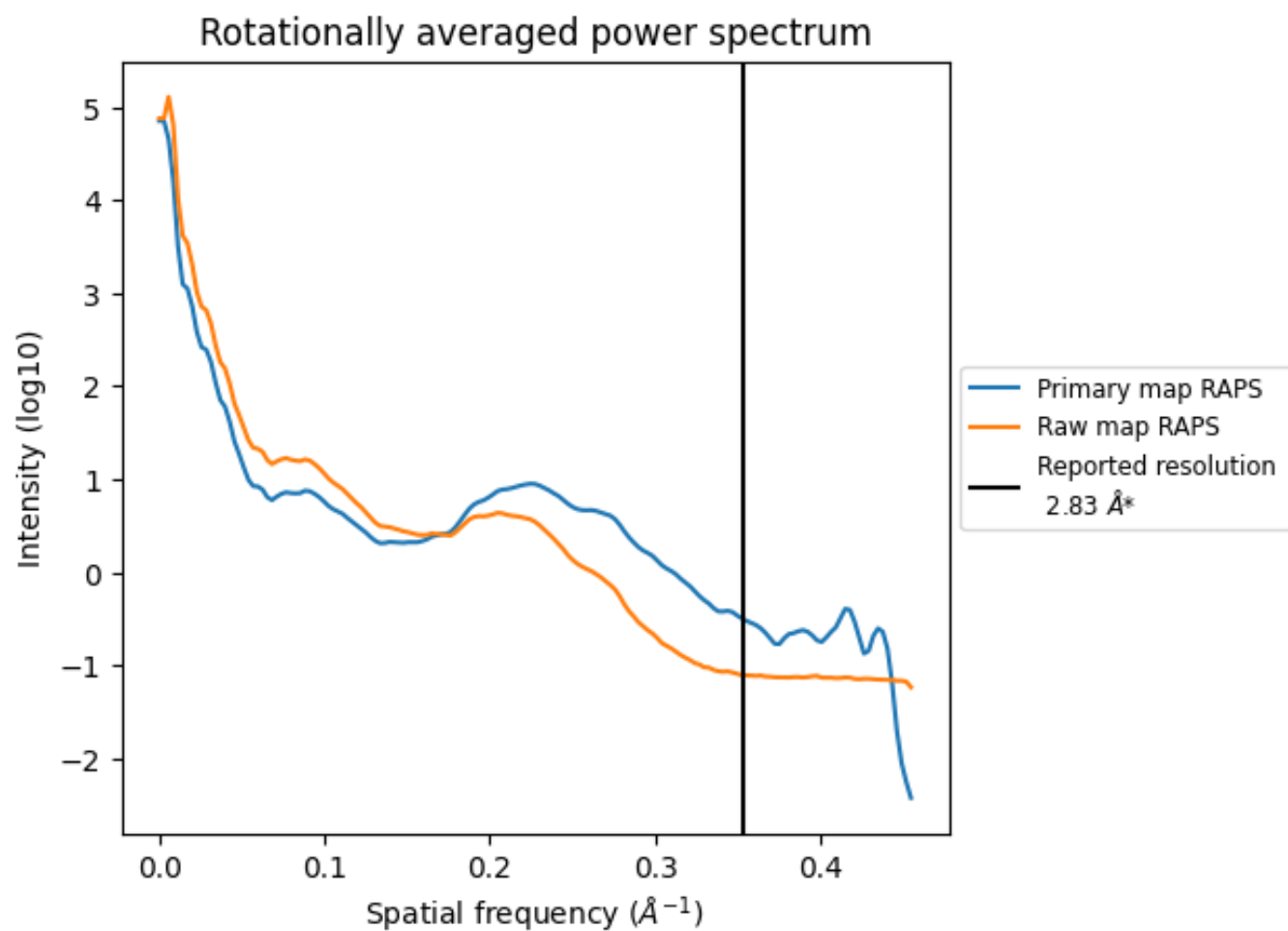
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm^3 ; this corresponds to an approximate mass of 106 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

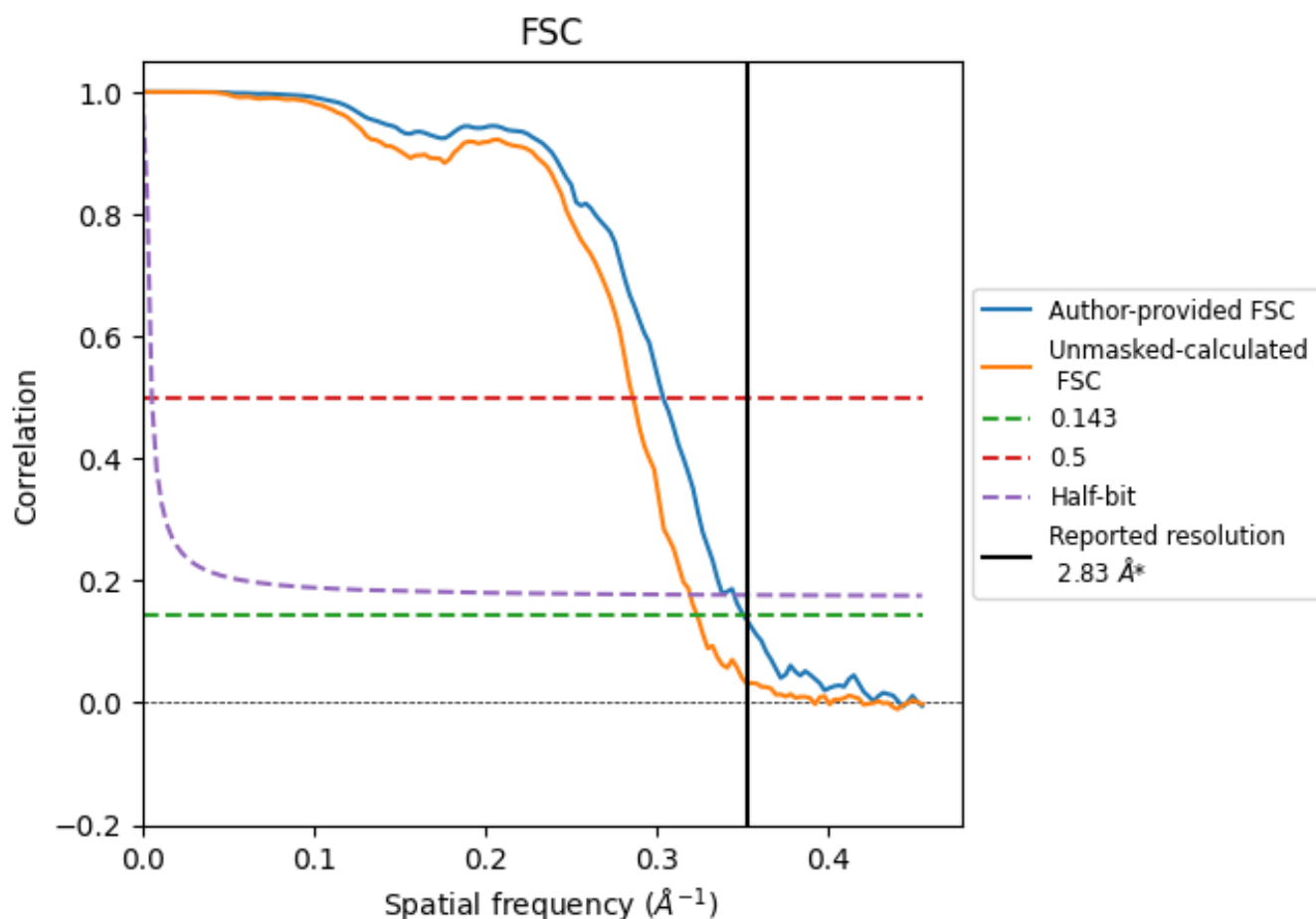


*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

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 0.353 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.85	3.29	2.90
Unmasked-calculated*	3.09	3.49	3.13

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

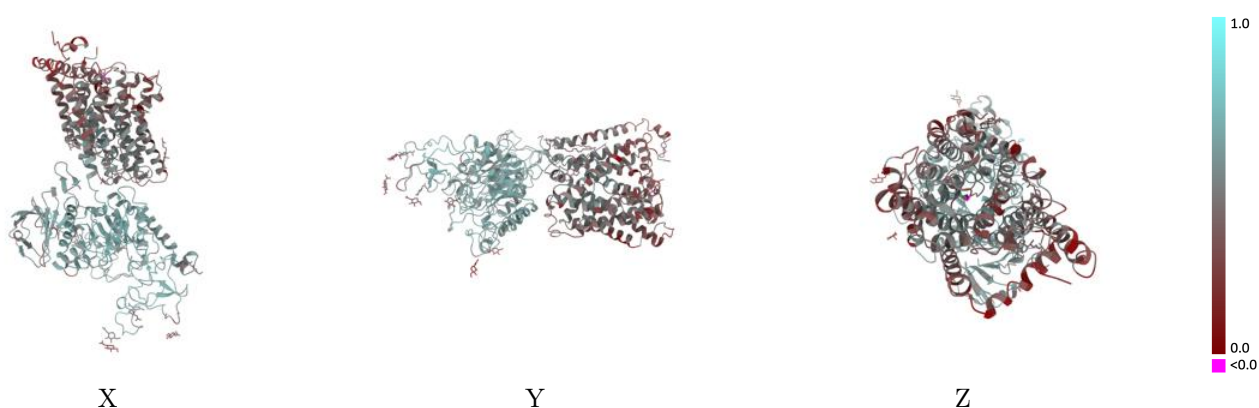
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-12298 and PDB model 7NF8. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

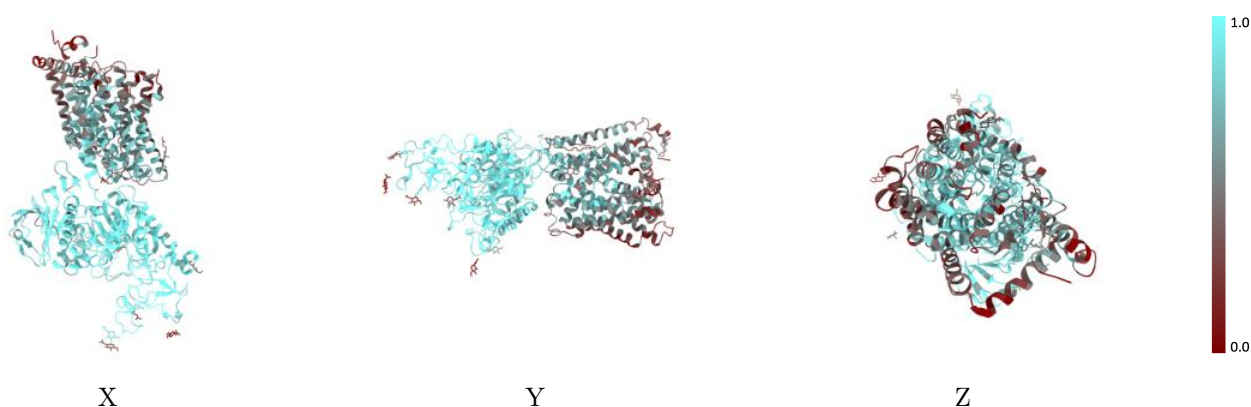
This section was not generated.

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



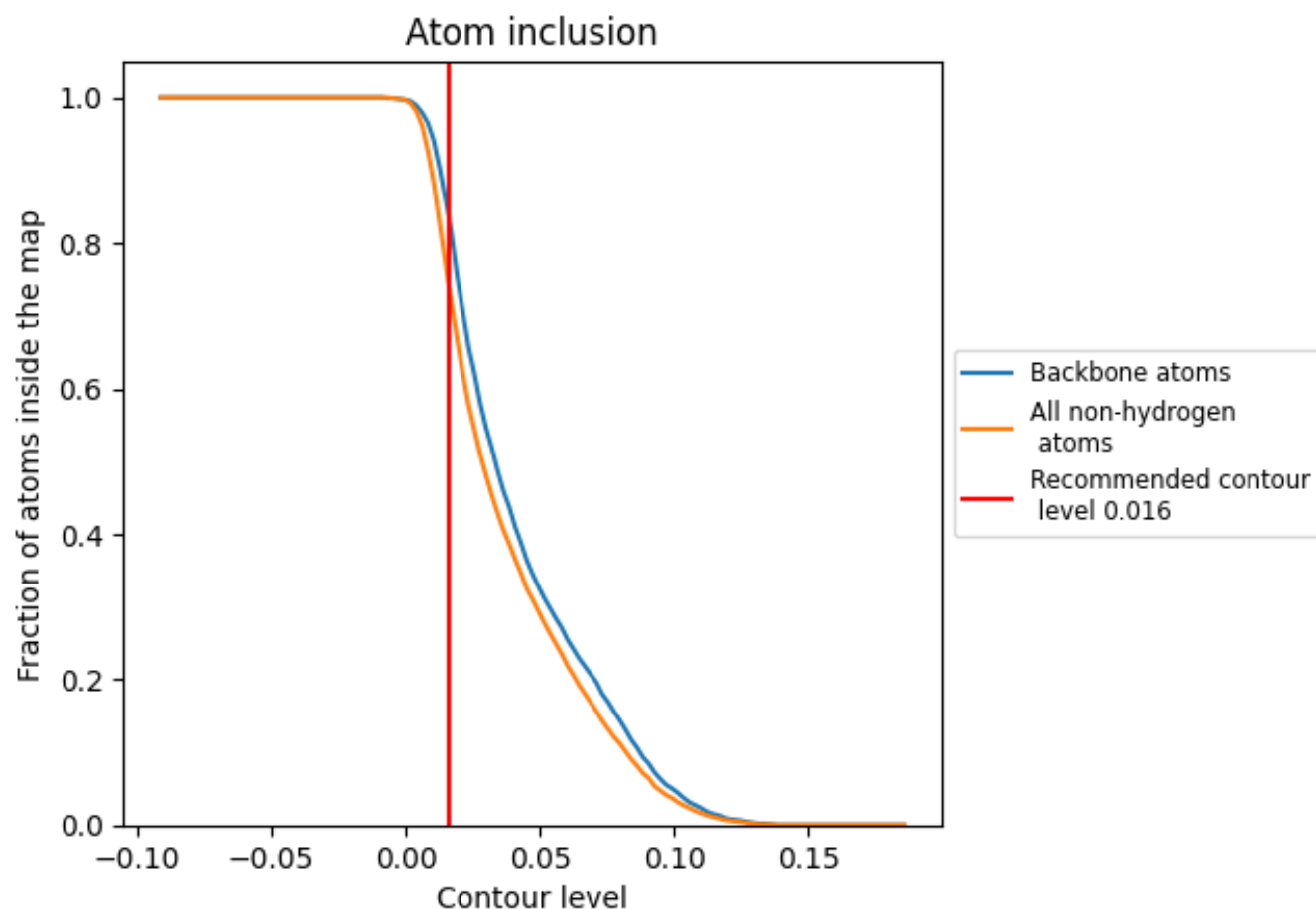
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7440	0.4960
A	0.8810	0.5640
B	0.5490	0.3990
C	0.5360	0.3410
D	0.5000	0.4250

