



Full wwPDB EM Validation Report ⓘ

Nov 29, 2022 – 01:34 PM JST

PDB ID : 7WHW
EMDB ID : EMD-32513
Title : Cryo-EM structure of Dnf1 from *Saccharomyces cerevisiae* in detergent with AMPPCP (E1-ATP state)
Authors : Xu, J.; He, Y.; Wu, X.; Li, L.
Deposited on : 2021-12-31
Resolution : 3.10 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.dev43
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) : 2.31.3

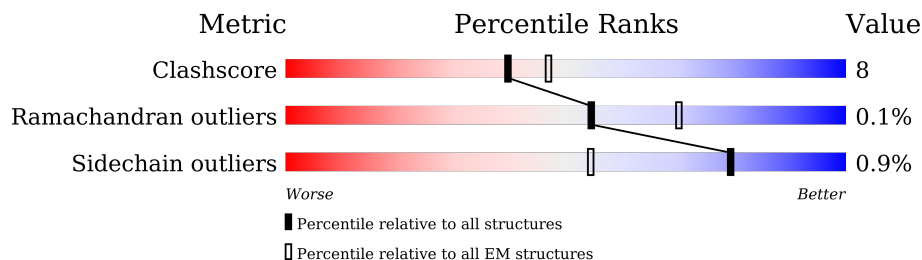
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	1571	
2	B	414	
3	C	3	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11978 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 Phospholipid-transporting ATPase DNF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1126	8973	5789	1486	1654	44	0	0

- Molecule 2 is a protein called Alkylphosphocholine resistance protein LEM3.

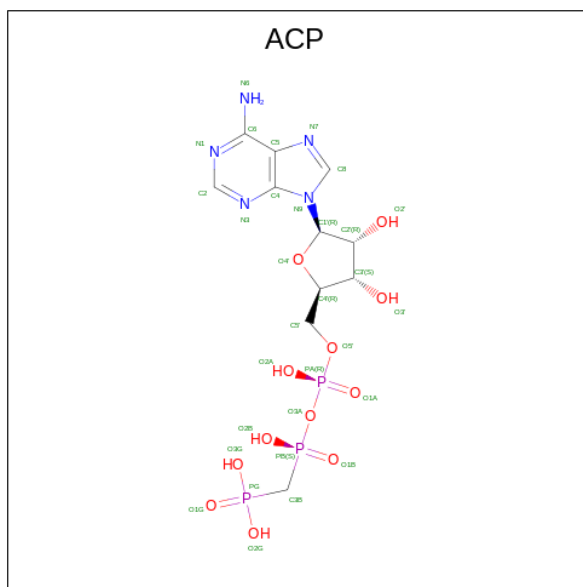
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	362	2934	1884	494	543	13	0	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-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	3	39	22	2	15	0	0

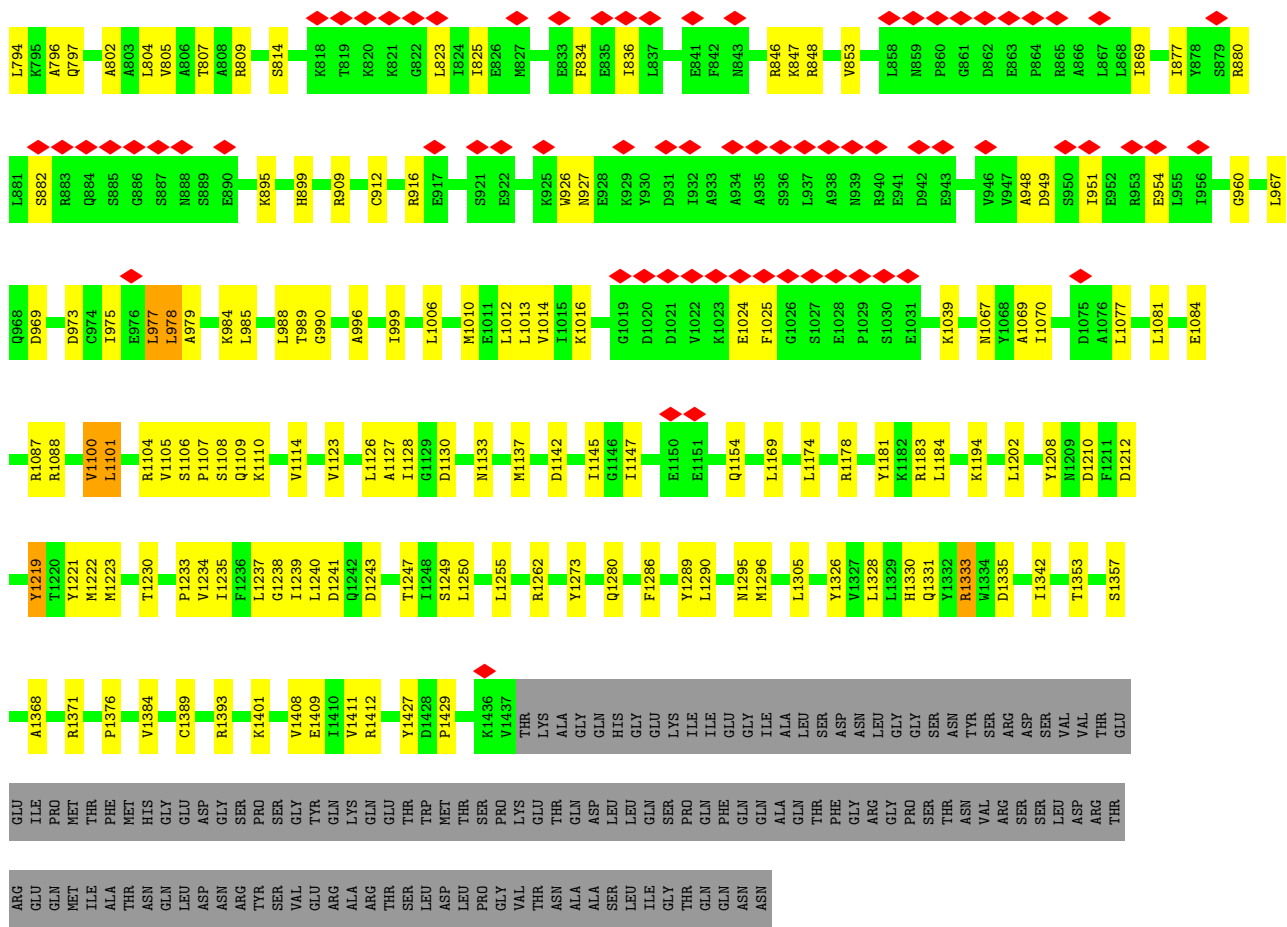
- Molecule 4 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



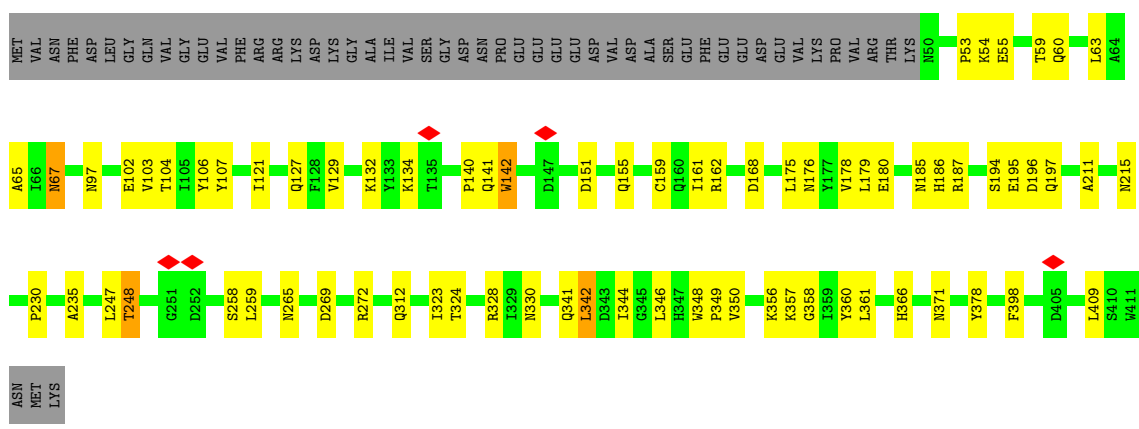
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	A	1	31	11	5	12	3	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
5	A	1	1	1	0



• Molecule 2: Alkylphosphocholine resistance protein LEM3



• Molecule 3: beta-D-mannopyranose-(1-4)-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, Not provided	
Number of particles used	295853	Depositor
Resolution determination method	FSC 0.33 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.169	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	342.40002, 342.40002, 342.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: MG, ACP, BMA, 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	A	0.44	0/9169	0.63	5/12425 (0.0%)
2	B	0.50	0/3017	0.66	3/4104 (0.1%)
All	All	0.45	0/12186	0.64	8/16529 (0.0%)

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
1	A	0	4
2	B	0	2
All	All	0	6

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	151	ASP	CB-CG-OD1	9.41	126.77	118.30
1	A	978	LEU	CA-CB-CG	6.96	131.30	115.30
2	B	342	LEU	CA-CB-CG	6.05	129.21	115.30
2	B	409	LEU	CA-CB-CG	5.90	128.87	115.30
1	A	969	ASP	CB-CG-OD1	5.67	123.41	118.30
1	A	1202	LEU	CA-CB-CG	5.27	127.42	115.30
1	A	1333	ARG	CA-CB-CG	5.11	124.64	113.40
1	A	1013	LEU	CA-CB-CG	5.01	126.83	115.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1100	VAL	Peptide
1	A	1101	LEU	Peptide
1	A	1219	TYR	Peptide
1	A	977	LEU	Peptide
2	B	398	PHE	Peptide,Mainchain

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	8973	0	8978	146	0
2	B	2934	0	2842	48	0
3	C	39	0	34	2	0
4	A	31	0	14	3	0
5	A	1	0	0	0	0
All	All	11978	0	11868	183	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 (183) 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:B:176:ASN:HB2	2:B:360:TYR:HB3	1.71	0.72
1:A:1130:ASP:HB3	1:A:1147:ILE:HB	1.80	0.64
2:B:248:THR:HG23	2:B:341:GLN:HB3	1.80	0.64
1:A:661:VAL:HG21	1:A:1126:LEU:HB2	1.82	0.62
1:A:1357:SER:HB2	1:A:1368:ALA:H	1.66	0.61
1:A:880:ARG:NH2	1:A:949:ASP:OD1	2.34	0.60
1:A:916:ARG:NH1	1:A:951:ILE:O	2.35	0.60
2:B:132:LYS:HB3	2:B:134:LYS:HE3	1.83	0.60
2:B:265:ASN:ND2	2:B:269:ASP:OD2	2.34	0.60
1:A:424:THR:HG23	1:A:426:ASP:H	1.67	0.59
1:A:1208:TYR:O	2:B:185:ASN:ND2	2.36	0.59
1:A:979:ALA:HB2	1:A:985:LEU:HD13	1.84	0.58
1:A:734:SER:H	1:A:737:SER:HB2	1.68	0.58
1:A:909:ARG:NH1	4:A:1601:ACP:O1B	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ASP:HB2	1:A:523:MET:HB3	1.85	0.57
2:B:103:VAL:HB	2:B:361:LEU:HB3	1.86	0.57
1:A:775:ALA:O	1:A:778:HIS:ND1	2.37	0.57
1:A:1178:ARG:NH2	1:A:1243:ASP:OD2	2.37	0.57
2:B:176:ASN:HD22	2:B:360:TYR:HD2	1.52	0.57
1:A:399:LYS:HB2	1:A:416:PRO:HG3	1.87	0.56
1:A:1296:MET:HB2	2:B:324:THR:HB	1.87	0.56
1:A:669:THR:O	1:A:673:THR:OG1	2.22	0.56
1:A:673:THR:HG22	1:A:967:LEU:HD23	1.86	0.56
1:A:710:THR:HA	1:A:713:ARG:HE	1.71	0.56
1:A:582:ARG:HA	1:A:586:GLU:HB3	1.87	0.56
1:A:447:ARG:NH2	1:A:502:ILE:O	2.39	0.56
1:A:977:LEU:HD11	1:A:1429:PRO:HG2	1.88	0.56
1:A:1247:THR:HG22	1:A:1427:TYR:H	1.70	0.56
1:A:1333:ARG:HA	2:B:67:ASN:HA	1.88	0.56
1:A:975:ILE:HG22	1:A:979:ALA:HB3	1.88	0.56
1:A:773:ALA:HB1	1:A:869:ILE:HG12	1.87	0.55
1:A:780:VAL:HG22	1:A:796:ALA:HB2	1.86	0.55
2:B:180:GLU:HB2	2:B:356:LYS:HB2	1.89	0.55
1:A:409:ILE:HB	1:A:518:ALA:HB3	1.89	0.55
1:A:1243:ASP:HB2	1:A:1408:VAL:HG11	1.89	0.54
1:A:1255:LEU:HD22	1:A:1408:VAL:HG22	1.89	0.54
1:A:1194:LYS:HD2	1:A:1234:VAL:HG21	1.90	0.54
1:A:988:LEU:HD22	1:A:1104:ARG:HG2	1.89	0.54
1:A:1286:PHE:HA	1:A:1289:TYR:HB3	1.89	0.54
1:A:592:GLY:HA3	1:A:596:THR:HG23	1.90	0.54
1:A:431:CYS:HB3	1:A:447:ARG:HB2	1.90	0.54
1:A:1243:ASP:O	1:A:1412:ARG:NH1	2.38	0.53
2:B:97:ASN:ND2	2:B:371:ASN:O	2.37	0.53
1:A:1077:LEU:HD22	1:A:1104:ARG:HE	1.74	0.53
1:A:437:ASN:OD1	1:A:1154:GLN:NE2	2.41	0.53
1:A:624:ILE:HD11	1:A:1235:ILE:HA	1.91	0.53
1:A:530:LYS:O	1:A:534:ASN:ND2	2.42	0.53
2:B:348:TRP:HE1	3:C:1:NAG:H83	1.74	0.53
2:B:265:ASN:HD22	2:B:312:GLN:HB3	1.74	0.53
1:A:1070:ILE:HB	1:A:1100:VAL:HG22	1.89	0.52
1:A:1401:LYS:HG2	1:A:1409:GLU:HG3	1.92	0.52
1:A:1412:ARG:HH12	2:B:67:ASN:HD21	1.56	0.52
1:A:1174:LEU:O	1:A:1249:SER:OG	2.28	0.52
1:A:412:ASN:OD1	1:A:513:ARG:NH1	2.40	0.52
2:B:141:GLN:HG2	2:B:162:ARG:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:LYS:HD3	1:A:999:ILE:HD13	1.92	0.52
1:A:671:THR:HG23	1:A:1147:ILE:HG13	1.90	0.52
1:A:500:ILE:HA	1:A:504:ASN:HD22	1.75	0.52
1:A:989:THR:OG1	1:A:990:GLY:N	2.43	0.51
1:A:1010:MET:HG3	1:A:1067:ASN:HB3	1.91	0.51
1:A:847:LYS:HE3	1:A:1105:VAL:HG21	1.92	0.51
1:A:1084:GLU:OE2	1:A:1088:ARG:NH1	2.44	0.51
1:A:1212:ASP:O	2:B:187:ARG:NH2	2.43	0.51
2:B:211:ALA:HB3	2:B:215:ASN:HB3	1.93	0.51
1:A:1106:SER:OG	1:A:1109:GLN:OE1	2.27	0.51
1:A:1333:ARG:HH22	2:B:63:LEU:HB2	1.76	0.51
1:A:778:HIS:HE1	1:A:823:LEU:HD11	1.76	0.51
1:A:1012:LEU:HD23	1:A:1069:ALA:HB3	1.93	0.51
1:A:261:GLU:HG2	1:A:264:ARG:HH11	1.75	0.51
1:A:424:THR:HG22	1:A:429:GLY:HA2	1.93	0.51
2:B:175:LEU:HB3	2:B:328:ARG:HB2	1.92	0.50
1:A:1006:LEU:HD23	1:A:1101:LEU:HD21	1.92	0.50
2:B:54:LYS:O	2:B:59:THR:OG1	2.30	0.50
1:A:1106:SER:O	1:A:1108:SER:N	2.45	0.50
1:A:1123:VAL:HA	1:A:1262:ARG:HH22	1.76	0.50
1:A:747:VAL:HG22	1:A:764:GLN:HE21	1.76	0.50
4:A:1601:ACP:O2B	4:A:1601:ACP:O2A	2.30	0.50
1:A:636:VAL:HG12	2:B:53:PRO:HG2	1.94	0.50
1:A:680:LYS:HB2	1:A:807:THR:HG21	1.93	0.49
1:A:1128:ILE:HD11	1:A:1147:ILE:HD11	1.94	0.49
1:A:774:LEU:HD21	1:A:804:LEU:HD12	1.94	0.49
1:A:794:LEU:HD13	1:A:805:VAL:HG12	1.92	0.49
2:B:102:GLU:HG2	2:B:129:VAL:HB	1.93	0.49
1:A:978:LEU:HD13	1:A:985:LEU:HD11	1.95	0.49
1:A:656:ASP:N	1:A:656:ASP:OD1	2.42	0.49
1:A:618:TYR:HA	1:A:621:VAL:HG22	1.93	0.49
1:A:1335:ASP:HA	2:B:65:ALA:HA	1.94	0.49
1:A:658:LEU:HD21	1:A:1145:ILE:HD11	1.95	0.48
1:A:246:PRO:HD3	1:A:1223:MET:HG3	1.95	0.48
1:A:778:HIS:HD2	1:A:780:VAL:H	1.60	0.48
1:A:624:ILE:HD13	1:A:1238:GLY:HA3	1.95	0.48
1:A:1127:ALA:HB1	1:A:1137:MET:HG2	1.96	0.48
1:A:1128:ILE:HD12	1:A:1169:LEU:HD13	1.96	0.48
2:B:155:GLN:HE21	2:B:346:LEU:HB3	1.77	0.48
1:A:912:CYS:HA	1:A:960:GLY:HA2	1.96	0.47
1:A:988:LEU:HB3	1:A:1110:LYS:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1210:ASP:HB2	2:B:186:HIS:HE1	1.78	0.47
2:B:230:PRO:HB2	2:B:235:ALA:HB1	1.96	0.47
1:A:847:LYS:HG2	4:A:1601:ACP:H5'1	1.95	0.47
1:A:1110:LYS:NZ	1:A:1133:ASN:O	2.47	0.47
1:A:825:ILE:HG21	1:A:834:PHE:HD2	1.80	0.47
1:A:1219:TYR:HD1	1:A:1222:MET:HB2	1.78	0.47
1:A:1233:PRO:HB3	1:A:1342:ILE:HG12	1.96	0.47
2:B:159:CYS:HB2	2:B:346:LEU:HD11	1.96	0.47
1:A:836:ILE:HA	1:A:853:VAL:HA	1.96	0.47
1:A:549:LEU:HD11	1:A:617:LEU:HD21	1.96	0.47
1:A:673:THR:HA	1:A:967:LEU:HA	1.98	0.46
1:A:523:MET:SD	1:A:529:THR:OG1	2.73	0.46
1:A:778:HIS:CE1	1:A:823:LEU:HD11	2.50	0.46
2:B:107:TYR:HB3	2:B:161:ILE:HD11	1.97	0.46
2:B:178:VAL:O	2:B:358:GLY:N	2.44	0.46
1:A:895:LYS:O	1:A:899:HIS:ND1	2.47	0.46
1:A:429:GLY:HA3	1:A:449:SER:HB3	1.98	0.46
1:A:779:SER:OG	1:A:797:GLN:NE2	2.44	0.46
1:A:1243:ASP:N	1:A:1243:ASP:OD1	2.49	0.46
1:A:1255:LEU:HD21	1:A:1411:VAL:HG21	1.98	0.46
1:A:882:SER:HB3	1:A:954:GLU:HB2	1.98	0.46
1:A:1024:GLU:HG3	1:A:1025:PHE:HD1	1.80	0.46
1:A:846:ARG:HG2	1:A:848:ARG:HB2	1.98	0.45
1:A:230:GLY:HA2	1:A:237:VAL:HG11	1.98	0.45
1:A:665:PHE:CG	1:A:1114:VAL:HG12	2.52	0.45
1:A:1280:GLN:NE2	1:A:1389:CYS:O	2.50	0.45
2:B:196:ASP:N	2:B:196:ASP:OD1	2.49	0.45
1:A:239:ASN:HB3	1:A:242:LEU:HB2	1.98	0.45
1:A:449:SER:OG	1:A:450:LEU:N	2.50	0.45
1:A:1239:ILE:HG22	1:A:1240:LEU:HG	1.98	0.45
1:A:1014:VAL:HG22	1:A:1016:LYS:HB2	1.97	0.45
1:A:662:GLU:OE2	1:A:984:LYS:NZ	2.42	0.45
1:A:877:ILE:HA	1:A:880:ARG:HB2	1.98	0.45
1:A:1326:TYR:O	1:A:1330:HIS:ND1	2.34	0.45
2:B:104:THR:HB	2:B:127:GLN:HB2	1.97	0.45
2:B:342:LEU:HG	2:B:344:ILE:HD11	1.98	0.45
1:A:1289:TYR:HD2	1:A:1290:LEU:HD12	1.81	0.44
1:A:809:ARG:HA	1:A:814:SER:HB2	2.00	0.44
1:A:1221:TYR:OH	1:A:1353:THR:HB	2.17	0.44
1:A:659:GLY:HA3	1:A:1181:TYR:HB2	1.99	0.44
1:A:796:ALA:HB3	1:A:802:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:996:ALA:HA	1:A:999:ILE:HG22	1.99	0.44
2:B:121:ILE:HD11	2:B:142:TRP:HB3	2.00	0.44
1:A:1295:ASN:ND2	2:B:360:TYR:OH	2.46	0.43
2:B:55:GLU:HG2	2:B:60:GLN:HG3	2.00	0.43
1:A:778:HIS:CD2	1:A:780:VAL:H	2.36	0.43
1:A:1335:ASP:N	1:A:1335:ASP:OD1	2.51	0.43
2:B:195:GLU:OE1	2:B:272:ARG:NH2	2.43	0.43
1:A:1081:LEU:HA	1:A:1087:ARG:HG2	2.00	0.43
1:A:1328:LEU:HB2	1:A:1342:ILE:HD13	2.00	0.43
1:A:1194:LYS:HE2	1:A:1230:THR:HG23	1.99	0.43
1:A:560:LEU:HD12	1:A:612:LEU:HB3	2.01	0.43
2:B:258:SER:O	2:B:330:ASN:ND2	2.52	0.43
3:C:1:NAG:O3	3:C:2:NAG:N2	2.52	0.43
1:A:1273:TYR:OH	1:A:1393:ARG:NH1	2.52	0.42
1:A:253:ILE:HA	1:A:256:ILE:HG12	2.01	0.42
1:A:1353:THR:O	1:A:1357:SER:OG	2.25	0.42
2:B:168:ASP:N	2:B:168:ASP:OD1	2.46	0.42
2:B:259:LEU:HB3	2:B:328:ARG:HB3	2.02	0.42
1:A:585:TYR:OH	2:B:349:PRO:O	2.29	0.42
1:A:628:GLN:NE2	1:A:1238:GLY:O	2.50	0.42
1:A:977:LEU:HD13	1:A:1250:LEU:HD22	2.02	0.42
2:B:121:ILE:HD13	2:B:140:PRO:HG2	2.01	0.42
1:A:250:ILE:HG21	1:A:615:ILE:HG13	2.02	0.42
1:A:210:ASN:HD21	1:A:255:ALA:HA	1.85	0.41
1:A:435:THR:HG22	1:A:438:LEU:HB2	2.00	0.41
1:A:223:PHE:HA	1:A:226:LEU:HG	2.02	0.41
1:A:846:ARG:HH11	1:A:848:ARG:CZ	2.33	0.41
1:A:575:TYR:O	1:A:582:ARG:NH2	2.54	0.41
1:A:1183:ARG:HG2	1:A:1241:ASP:HB3	2.03	0.41
1:A:1384:VAL:HB	2:B:378:TYR:CZ	2.56	0.41
2:B:179:LEU:HB2	2:B:323:ILE:HB	2.03	0.41
1:A:679:PHE:HE1	1:A:741:PRO:HD2	1.86	0.41
1:A:1184:LEU:HA	1:A:1184:LEU:HD12	1.89	0.41
1:A:664:ILE:HG12	1:A:1126:LEU:HB3	2.03	0.41
2:B:106:TYR:HA	2:B:358:GLY:HA2	2.02	0.41
1:A:1376:PRO:HG2	2:B:366:HIS:HB3	2.03	0.41
2:B:194:SER:HB2	2:B:197:GLN:HB2	2.01	0.41
1:A:1305:LEU:HD21	1:A:1371:ARG:HB3	2.03	0.40
1:A:458:THR:HB	1:A:460:LYS:HG2	2.04	0.40
1:A:973:ASP:O	1:A:978:LEU:N	2.46	0.40
1:A:680:LYS:HB3	1:A:740:TYR:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:926:TRP:HZ2	1:A:948:ALA:HA	1.87	0.40
2:B:350:VAL:HG11	2:B:357:LYS:HB2	2.03	0.40
1:A:541:LYS:NZ	1:A:1142:ASP:O	2.45	0.40
1:A:1237:LEU:HD13	1:A:1331:GLN:HB3	2.03	0.40
2:B:247:LEU:HG	2:B:259:LEU:HD11	2.02	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	1120/1571 (71%)	1023 (91%)	96 (9%)	1 (0%)	51	83
2	B	360/414 (87%)	332 (92%)	28 (8%)	0	100	100
All	All	1480/1985 (75%)	1355 (92%)	124 (8%)	1 (0%)	54	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1107	PRO

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	974/1367 (71%)	965 (99%)	9 (1%)	78	91
2	B	318/364 (87%)	315 (99%)	3 (1%)	78	91
All	All	1292/1731 (75%)	1280 (99%)	12 (1%)	79	91

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	193	ARG
1	A	224	LEU
1	A	264	ARG
1	A	451	LYS
1	A	597	ASN
1	A	701	ARG
1	A	736	ASN
1	A	927	ASN
1	A	1039	LYS
2	B	67	ASN
2	B	142	TRP
2	B	248	THR

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	216	HIS
1	A	597	ASN
1	A	736	ASN
1	A	927	ASN
1	A	939	ASN
1	A	1139	GLN
1	A	1176	HIS
2	B	67	ASN
2	B	155	GLN
2	B	172	ASN
2	B	256	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](#)

3 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	0.94	1 (7%)	17,19,21	1.51	3 (17%)
3	NAG	C	2	3	14,14,15	0.86	1 (7%)	17,19,21	0.99	1 (5%)
3	BMA	C	3	3	11,11,12	0.95	0	15,15,17	0.70	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	-	4/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	NAG	O5-C1	-2.66	1.39	1.43
3	C	1	NAG	C8-C7	-2.25	1.45	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C1-O5-C5	3.66	117.16	112.19
3	C	2	NAG	C1-O5-C5	3.35	116.73	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C2-N2-C7	2.47	126.42	122.90
3	C	1	NAG	C1-C2-N2	2.05	113.99	110.49

There are no chirality outliers.

All (6) torsion outliers are listed below:

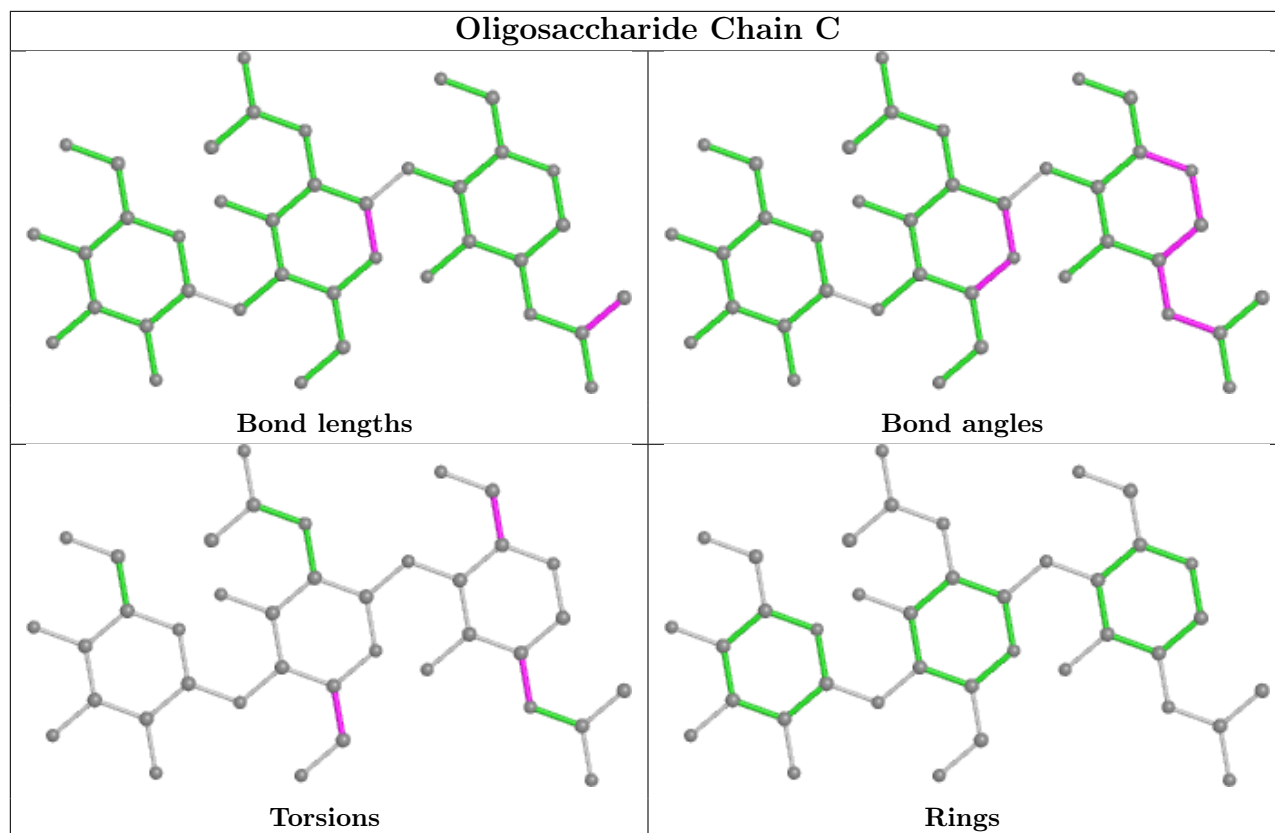
Mol	Chain	Res	Type	Atoms
3	C	1	NAG	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	1	NAG	C1-C2-N2-C7
3	C	1	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

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



5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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$
4	ACP	A	1601	5	27,33,33	1.30	4 (14%)	32,52,52	1.48	4 (12%)

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
4	ACP	A	1601	5	-	6/15/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1601	ACP	PG-O3G	2.78	1.61	1.54
4	A	1601	ACP	PG-O2G	2.75	1.61	1.54
4	A	1601	ACP	C5-C4	2.29	1.47	1.40
4	A	1601	ACP	PB-O3A	2.10	1.60	1.58

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1601	ACP	PB-O3A-PA	-3.97	119.97	132.56
4	A	1601	ACP	C3'-C2'-C1'	3.18	105.77	100.98
4	A	1601	ACP	N3-C2-N1	-3.08	123.86	128.68
4	A	1601	ACP	C4-C5-N7	-2.79	106.49	109.40

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1601	ACP	C5'-O5'-PA-O1A
4	A	1601	ACP	C5'-O5'-PA-O2A
4	A	1601	ACP	PB-O3A-PA-O1A
4	A	1601	ACP	PB-O3A-PA-O2A
4	A	1601	ACP	PG-C3B-PB-O1B
4	A	1601	ACP	C5'-O5'-PA-O3A

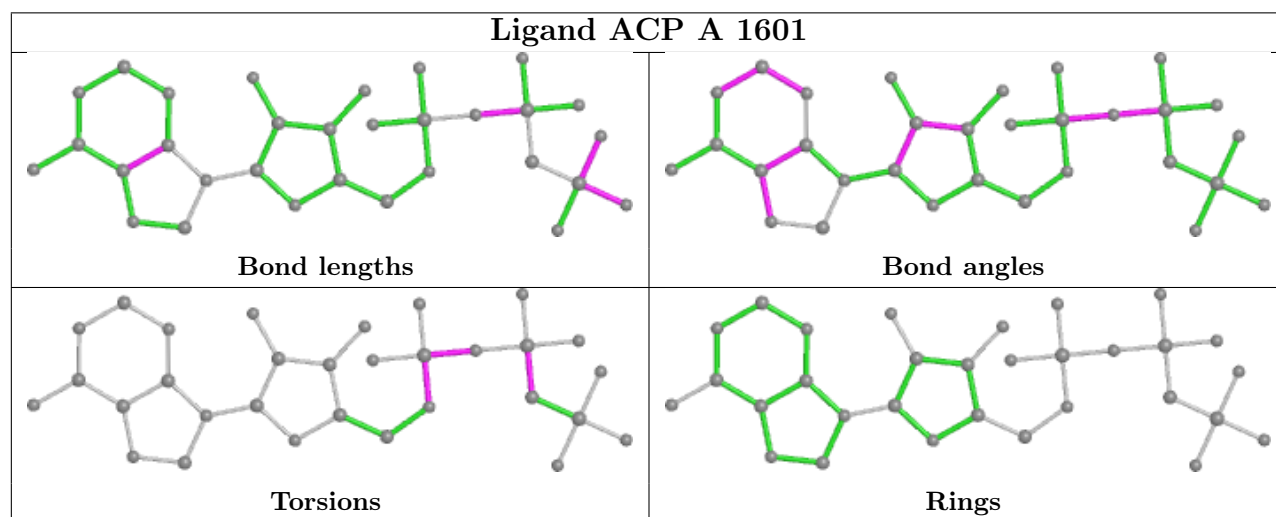
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1601	ACP	3	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.

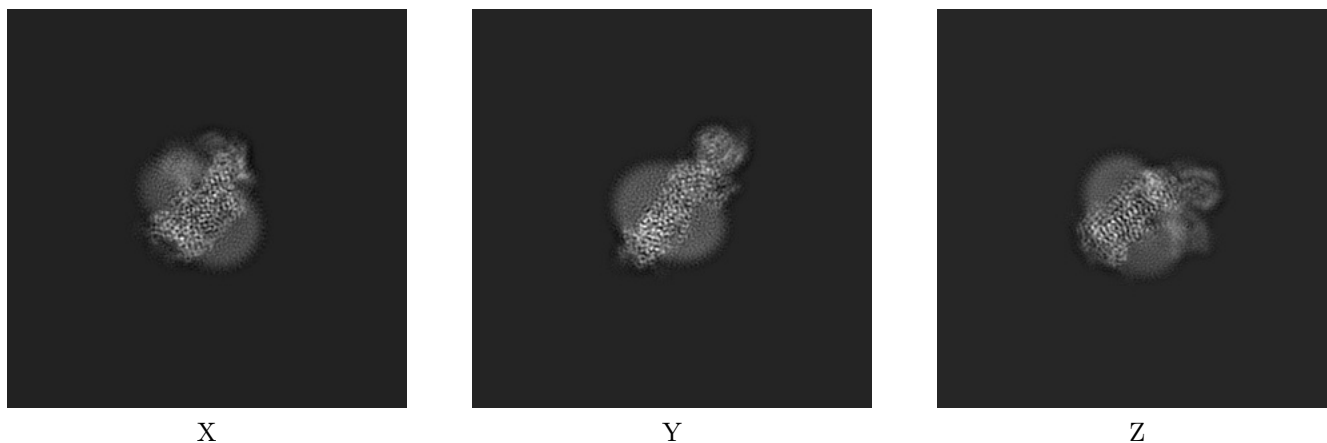
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32513. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

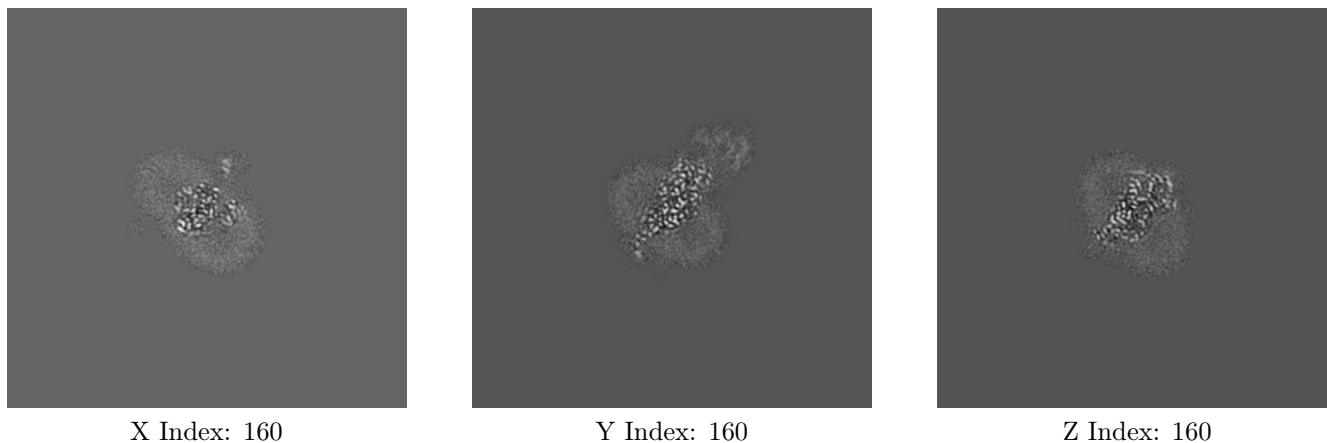
6.1.1 Primary map



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

6.2 Central slices [i](#)

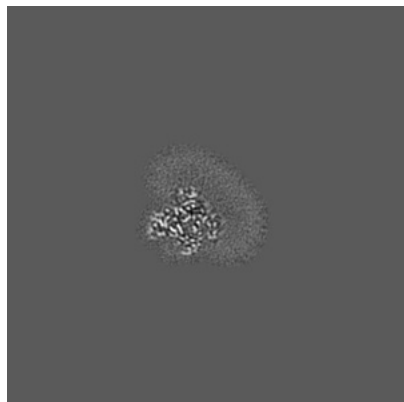
6.2.1 Primary map



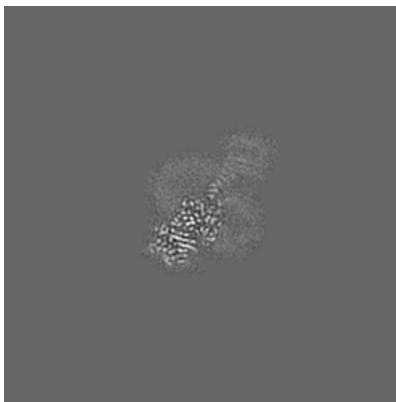
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

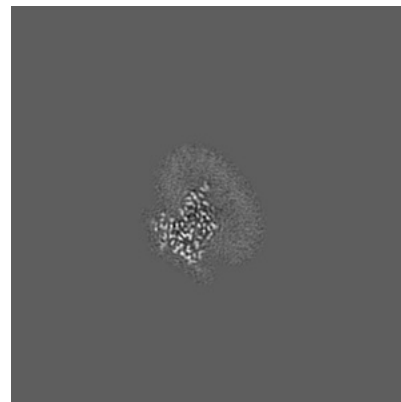
6.3.1 Primary map



X Index: 141



Y Index: 144



Z Index: 144

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

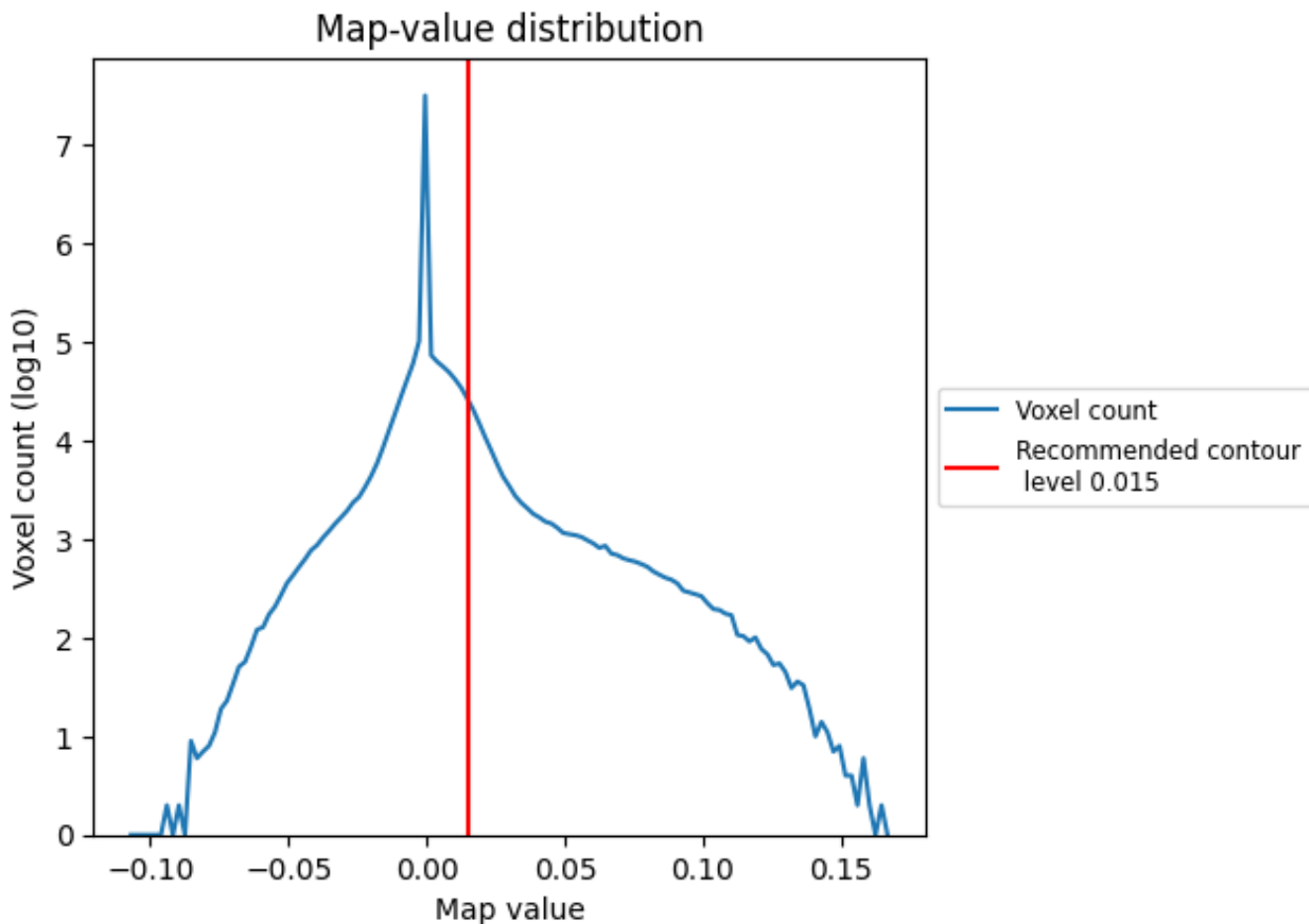
6.5 Mask visualisation

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

7 Map analysis [i](#)

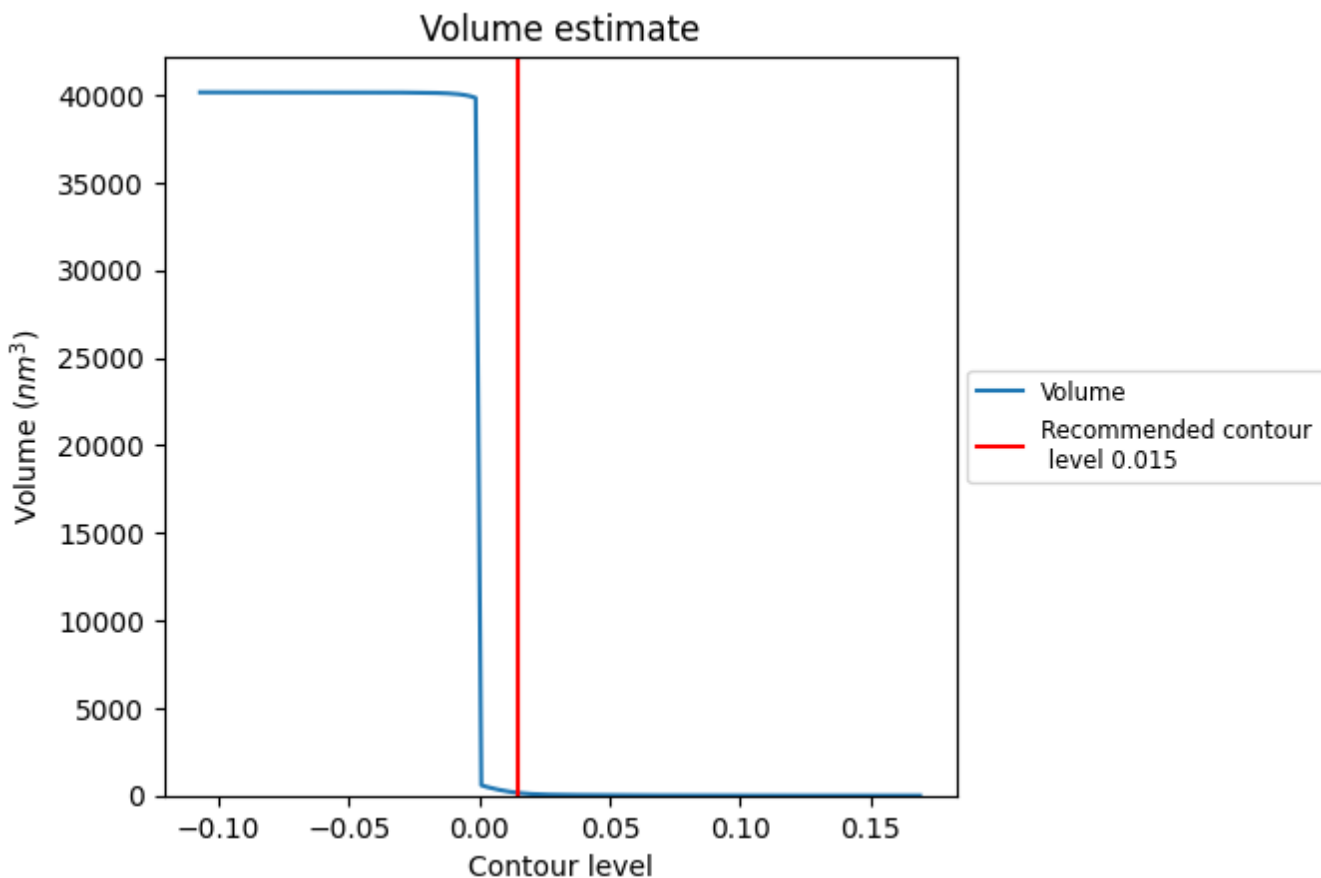
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

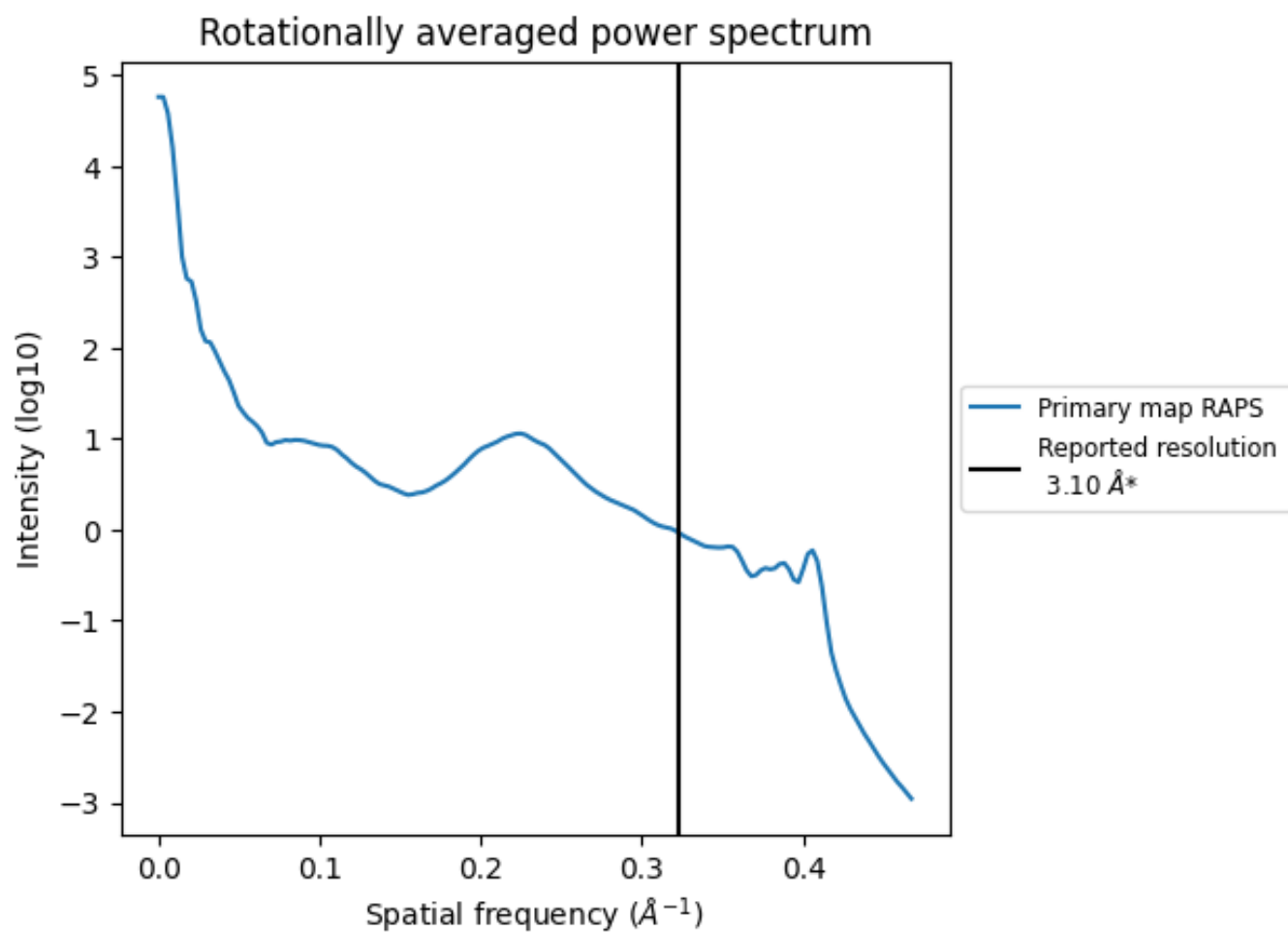
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 138 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 0.323 Å⁻¹

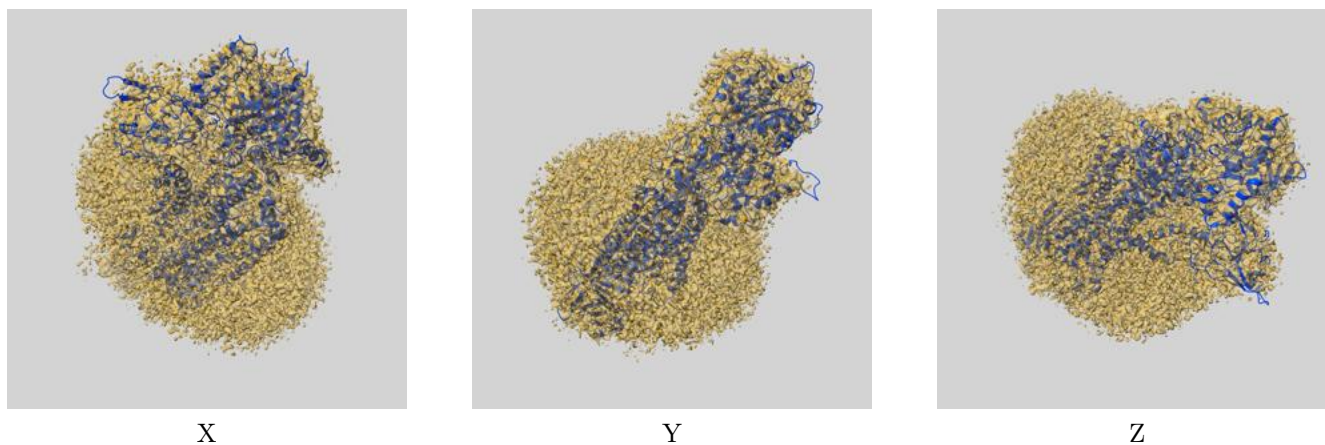
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

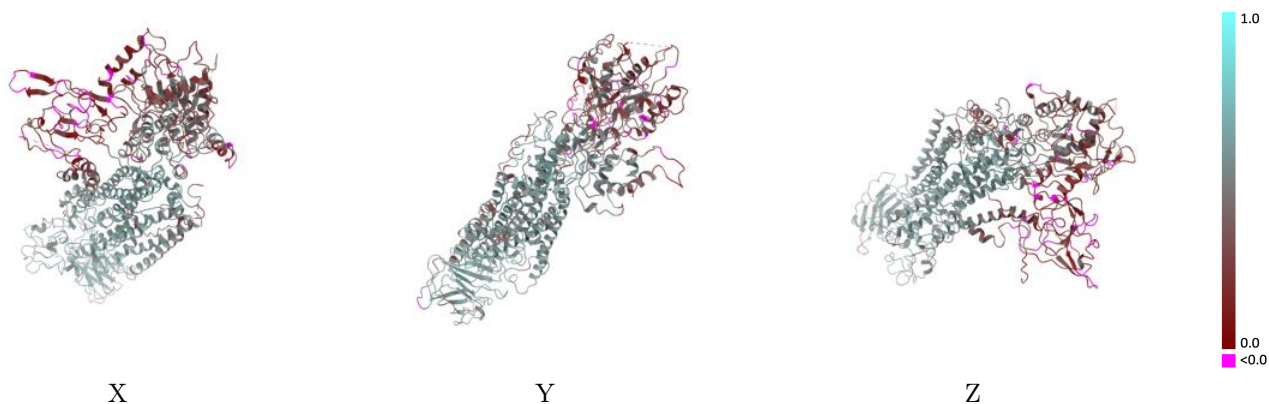
This section contains information regarding the fit between EMDB map EMD-32513 and PDB model 7WHW. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



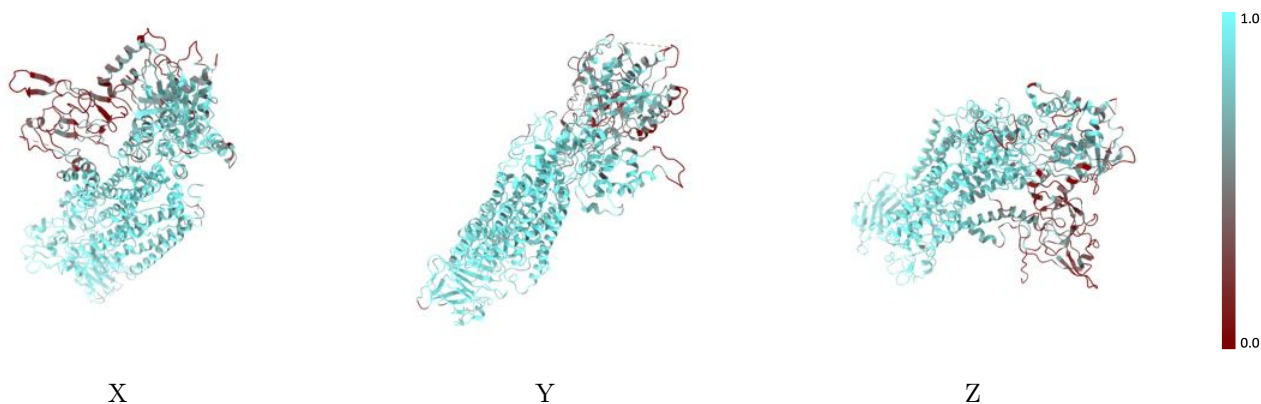
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



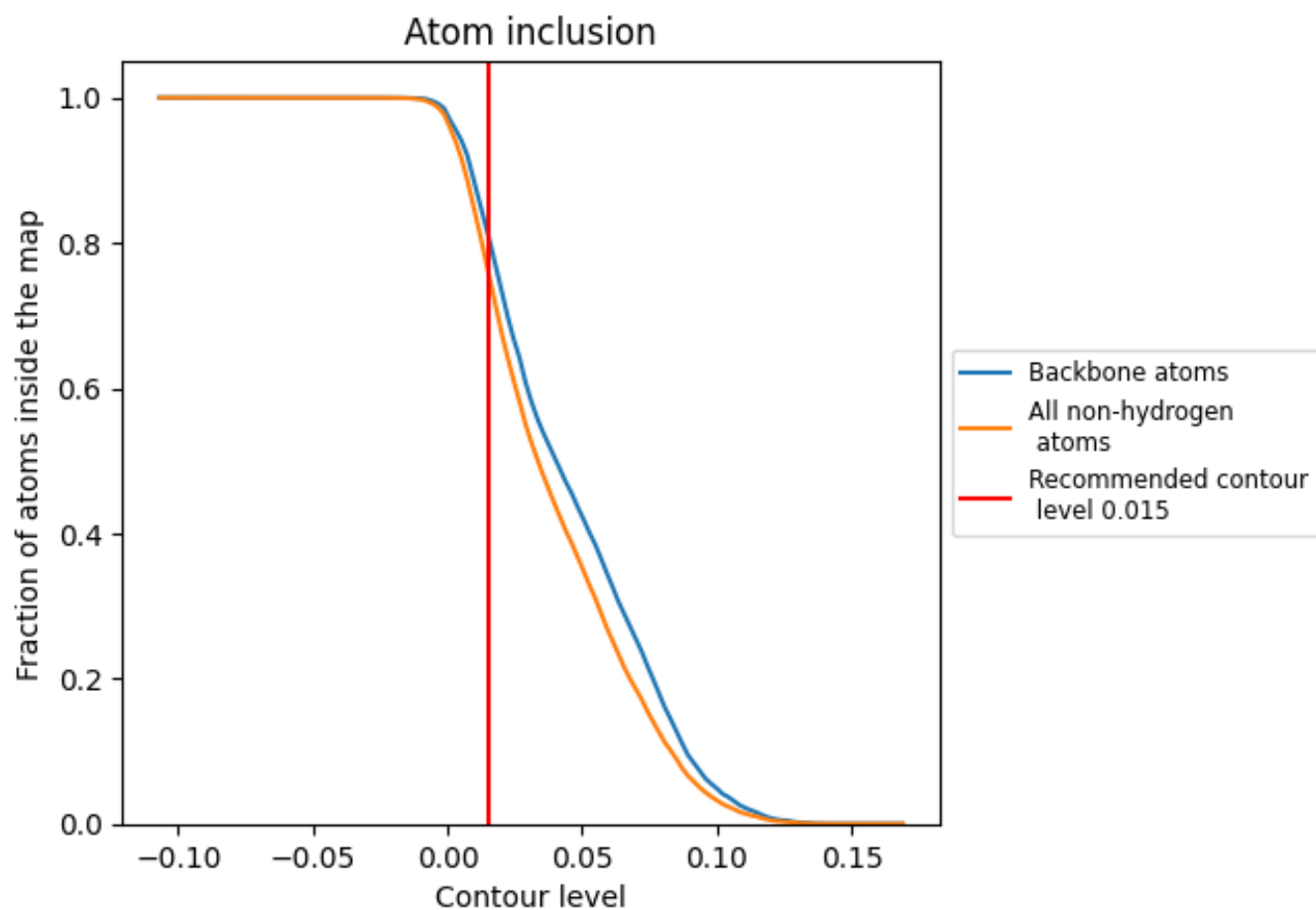
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).









9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 76% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7619	 0.4370
A	 0.7167	 0.4060
B	 0.8998	 0.5340
C	 0.8462	 0.4450

