



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 10:53 AM UTC

PDB ID : 7OH7 / pdb_00007oh7
EMDB ID : EMD-12896
Title : Cryo-EM structure of Drs2p-Cdc50p in the E1-AMPPCP state with PI4P bound
Authors : Timcenko, M.; Dieudonne, T.; Montigny, C.; Boesen, T.; Lyons, J.A.; Lenoir, G.; Nissen, P.
Deposited on : 2021-05-09
Resolution : 3.80 Å(reported)
Based on initial model : 6ROJ

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:

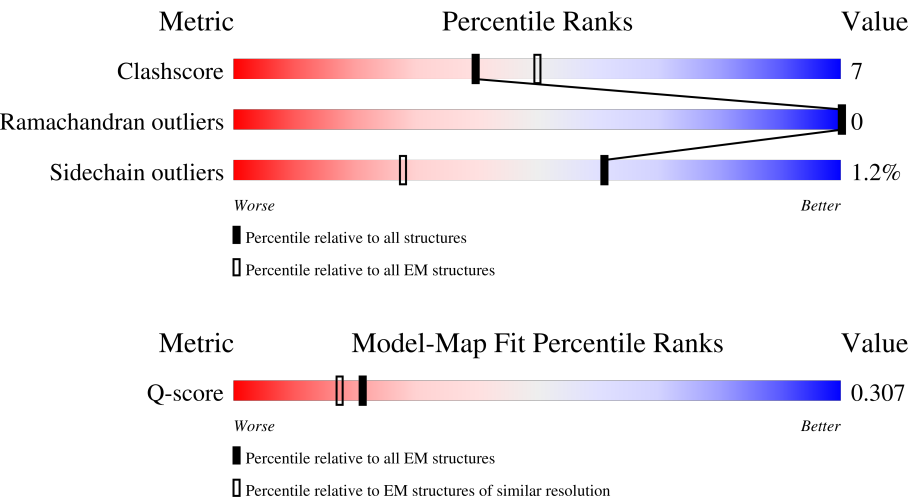
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	1465	
2	C	413	
3	B	2	

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Mol	Chain	Length	Quality of chain
3	D	2	100%
			100%
4	E	4	50%
			50%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11552 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 Probable phospholipid-transporting ATPase DRS2, Probable phospholipid-transporting ATPase DRS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1064	Total	C	N	O	S	0	0
			8504	5499	1381	1588	36		

There are 110 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1247	SER	-	linker	UNP P39524
A	1248	LEU	-	linker	UNP P39524
A	1249	VAL	-	linker	UNP P39524
A	1250	PRO	-	linker	UNP P39524
A	1251	ARG	-	linker	UNP P39524
A	1252	GLY	-	linker	UNP P39524
A	1362	GLY	-	expression tag	UNP P39524
A	1363	GLY	-	expression tag	UNP P39524
A	1364	GLY	-	expression tag	UNP P39524
A	1365	GLY	-	expression tag	UNP P39524
A	1366	LEU	-	expression tag	UNP P39524
A	1367	VAL	-	expression tag	UNP P39524
A	1368	PRO	-	expression tag	UNP P39524
A	1369	ARG	-	expression tag	UNP P39524
A	1370	GLY	-	expression tag	UNP P39524
A	1371	SER	-	expression tag	UNP P39524
A	1372	GLY	-	expression tag	UNP P39524
A	1373	GLY	-	expression tag	UNP P39524
A	1374	THR	-	expression tag	UNP P39524
A	1375	ALA	-	expression tag	UNP P39524
A	1376	ALA	-	expression tag	UNP P39524
A	1377	ALA	-	expression tag	UNP P39524
A	1378	PRO	-	expression tag	UNP P39524
A	1379	GLY	-	expression tag	UNP P39524
A	1380	PRO	-	expression tag	UNP P39524
A	1381	ALA	-	expression tag	UNP P39524
A	1382	PRO	-	expression tag	UNP P39524

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1383	ALA	-	expression tag	UNP P39524
A	1384	PRO	-	expression tag	UNP P39524
A	1385	ALA	-	expression tag	UNP P39524
A	1386	PRO	-	expression tag	UNP P39524
A	1387	ALA	-	expression tag	UNP P39524
A	1388	SER	-	expression tag	UNP P39524
A	1389	ALA	-	expression tag	UNP P39524
A	1390	PRO	-	expression tag	UNP P39524
A	1391	ALA	-	expression tag	UNP P39524
A	1392	ALA	-	expression tag	UNP P39524
A	1393	ALA	-	expression tag	UNP P39524
A	1394	ALA	-	expression tag	UNP P39524
A	1395	PRO	-	expression tag	UNP P39524
A	1396	ALA	-	expression tag	UNP P39524
A	1397	GLY	-	expression tag	UNP P39524
A	1398	ALA	-	expression tag	UNP P39524
A	1399	GLY	-	expression tag	UNP P39524
A	1400	THR	-	expression tag	UNP P39524
A	1401	PRO	-	expression tag	UNP P39524
A	1402	VAL	-	expression tag	UNP P39524
A	1403	THR	-	expression tag	UNP P39524
A	1404	ALA	-	expression tag	UNP P39524
A	1405	PRO	-	expression tag	UNP P39524
A	1406	LEU	-	expression tag	UNP P39524
A	1407	ALA	-	expression tag	UNP P39524
A	1408	GLY	-	expression tag	UNP P39524
A	1409	THR	-	expression tag	UNP P39524
A	1410	ILE	-	expression tag	UNP P39524
A	1411	TRP	-	expression tag	UNP P39524
A	1412	LYS	-	expression tag	UNP P39524
A	1413	VAL	-	expression tag	UNP P39524
A	1414	LEU	-	expression tag	UNP P39524
A	1415	ALA	-	expression tag	UNP P39524
A	1416	SER	-	expression tag	UNP P39524
A	1417	GLU	-	expression tag	UNP P39524
A	1418	GLY	-	expression tag	UNP P39524
A	1419	GLN	-	expression tag	UNP P39524
A	1420	THR	-	expression tag	UNP P39524
A	1421	VAL	-	expression tag	UNP P39524
A	1422	ALA	-	expression tag	UNP P39524
A	1423	ALA	-	expression tag	UNP P39524
A	1424	GLY	-	expression tag	UNP P39524

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1425	GLU	-	expression tag	UNP P39524
A	1426	VAL	-	expression tag	UNP P39524
A	1427	LEU	-	expression tag	UNP P39524
A	1428	LEU	-	expression tag	UNP P39524
A	1429	ILE	-	expression tag	UNP P39524
A	1430	LEU	-	expression tag	UNP P39524
A	1431	GLU	-	expression tag	UNP P39524
A	1432	ALA	-	expression tag	UNP P39524
A	1433	MET	-	expression tag	UNP P39524
A	1434	LYS	-	expression tag	UNP P39524
A	1435	MET	-	expression tag	UNP P39524
A	1436	GLU	-	expression tag	UNP P39524
A	1437	THR	-	expression tag	UNP P39524
A	1438	GLU	-	expression tag	UNP P39524
A	1439	ILE	-	expression tag	UNP P39524
A	1440	ARG	-	expression tag	UNP P39524
A	1441	ALA	-	expression tag	UNP P39524
A	1442	ALA	-	expression tag	UNP P39524
A	1443	GLN	-	expression tag	UNP P39524
A	1444	ALA	-	expression tag	UNP P39524
A	1445	GLY	-	expression tag	UNP P39524
A	1446	THR	-	expression tag	UNP P39524
A	1447	VAL	-	expression tag	UNP P39524
A	1448	ARG	-	expression tag	UNP P39524
A	1449	GLY	-	expression tag	UNP P39524
A	1450	ILE	-	expression tag	UNP P39524
A	1451	ALA	-	expression tag	UNP P39524
A	1452	VAL	-	expression tag	UNP P39524
A	1453	LYS	-	expression tag	UNP P39524
A	1454	ALA	-	expression tag	UNP P39524
A	1455	GLY	-	expression tag	UNP P39524
A	1456	ASP	-	expression tag	UNP P39524
A	1457	ALA	-	expression tag	UNP P39524
A	1458	VAL	-	expression tag	UNP P39524
A	1459	ALA	-	expression tag	UNP P39524
A	1460	VAL	-	expression tag	UNP P39524
A	1461	GLY	-	expression tag	UNP P39524
A	1462	ASP	-	expression tag	UNP P39524
A	1463	THR	-	expression tag	UNP P39524
A	1464	LEU	-	expression tag	UNP P39524
A	1465	MET	-	expression tag	UNP P39524

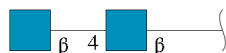
- Molecule 2 is a protein called Cell division control protein 50.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	350	Total	C	N	O	S	0	0
			2842	1838	471	521	12		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	392	GLY	-	expression tag	UNP P25656
C	393	GLY	-	expression tag	UNP P25656
C	394	GLY	-	expression tag	UNP P25656
C	395	GLY	-	expression tag	UNP P25656
C	396	LEU	-	expression tag	UNP P25656
C	397	VAL	-	expression tag	UNP P25656
C	398	PRO	-	expression tag	UNP P25656
C	399	ARG	-	expression tag	UNP P25656
C	400	GLY	-	expression tag	UNP P25656
C	401	SER	-	expression tag	UNP P25656
C	402	GLY	-	expression tag	UNP P25656
C	403	GLY	-	expression tag	UNP P25656
C	404	HIS	-	expression tag	UNP P25656
C	405	HIS	-	expression tag	UNP P25656
C	406	HIS	-	expression tag	UNP P25656
C	407	HIS	-	expression tag	UNP P25656
C	408	HIS	-	expression tag	UNP P25656
C	409	HIS	-	expression tag	UNP P25656
C	410	HIS	-	expression tag	UNP P25656
C	411	HIS	-	expression tag	UNP P25656
C	412	HIS	-	expression tag	UNP P25656
C	413	HIS	-	expression tag	UNP P25656

- 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
3	B	2	Total	C	N	O	0	0
			28	16	2	10		
3	D	2	Total	C	N	O	0	0
			28	16	2	10		

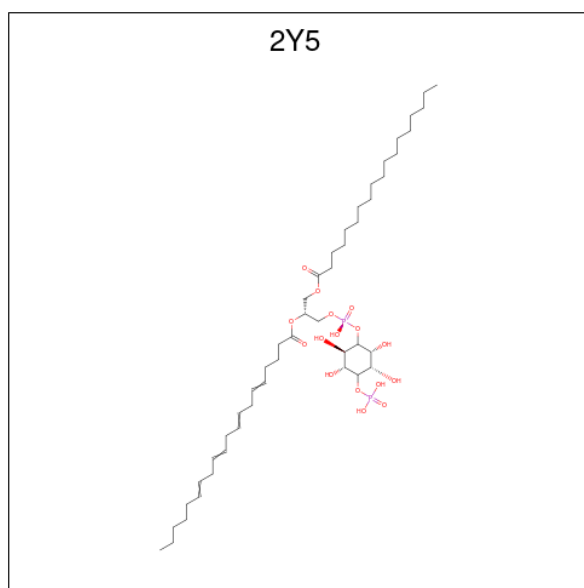
- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-3)-beta-D-mannopyranose

-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



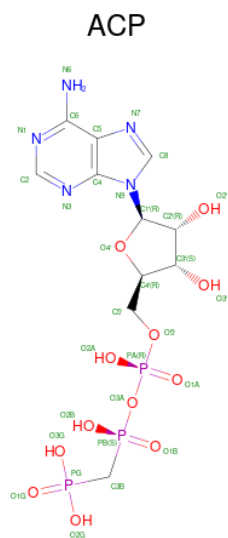
Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 5 is (2R)-1-[[[(R)-hydroxy{[(1R,2R,3R,4R,5S,6R)-2,3,5,6-tetrahydroxy-4-(phosphonoxy)cyclohexyl]oxy}phosphoryl]oxy}-3-(octadecanoyloxy)propan-2-yl (5Z,8Z,11Z,14Z)-icosa-5,8,11,14-tetraenoate (CCD ID: 2Y5) (formula: C₄₇H₈₄O₁₆P₂).



Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	O	P	0
			65	47	16	2	

- Molecule 6 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



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

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

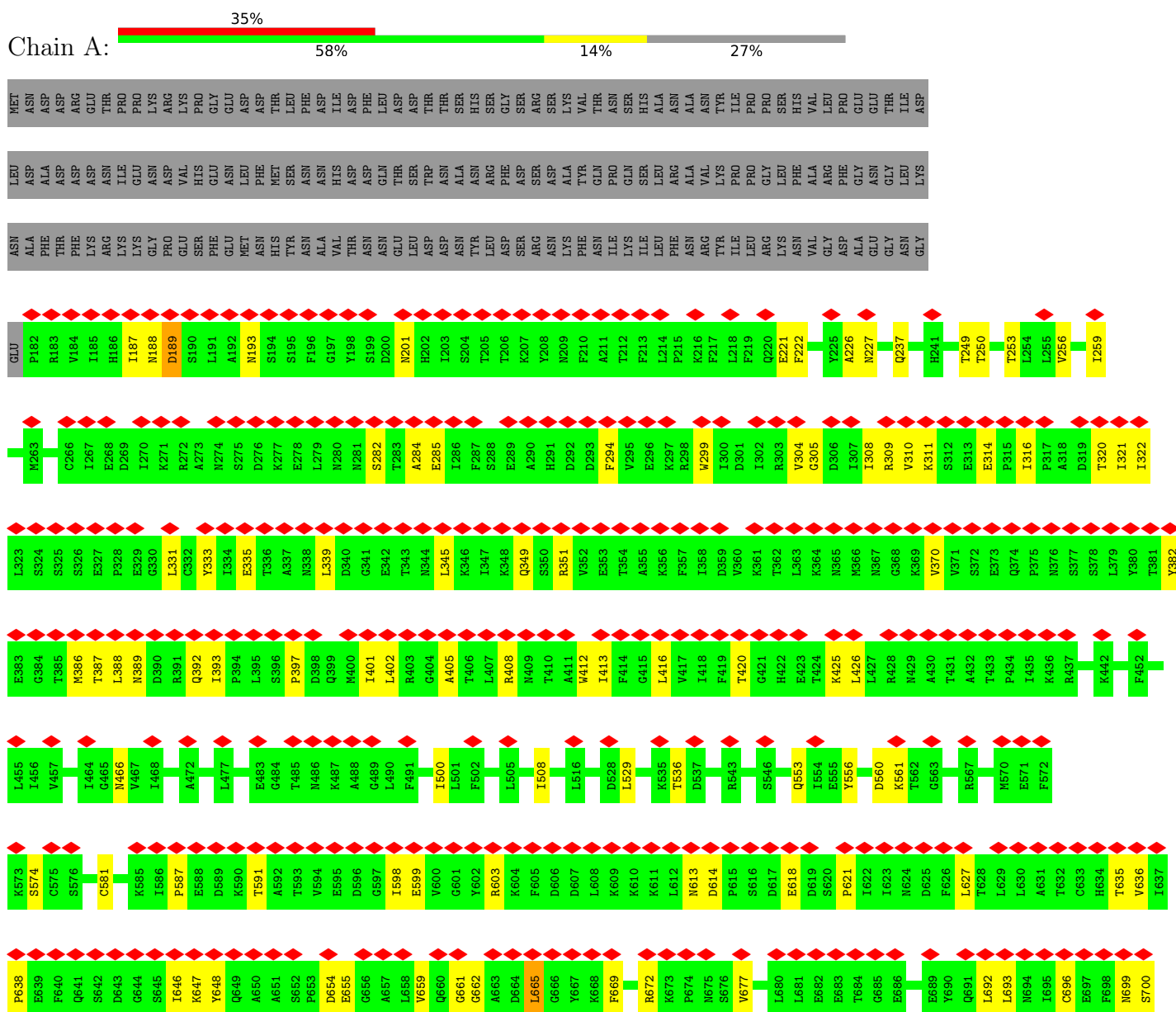
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	AltConf
8	A	3	Total O 3 3	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: Probable phospholipid-transporting ATPase DRS2, Probable phospholipid-transporting ATPase DRS2



VAL	HIS	ALA	GLU	ASN	THR	THR	LEU	ARG	GLU	ILE	LEU	GLY	GLY	GLY	LEU	VAL	PRO	ARG	GLY	SER	GLY	GLY	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

● 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



● Molecule 4: beta-D-mannopyranose-(1-3)-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, C1	Depositor
Number of particles used	32184	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.790	Depositor
Minimum map value	-0.452	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.17	Depositor
Map size ($\text{\AA}$)	263.9872, 263.9872, 263.9872	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0312, 1.0312, 1.0312	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: 2Y5, ACP, MG, NAG, BMA

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	0.10	0/8692	0.33	0/11790
2	C	0.09	0/2918	0.26	0/3957
All	All	0.10	0/11610	0.31	0/15747

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	8504	0	8516	125	0
2	C	2842	0	2830	41	0
3	B	28	0	25	1	0
3	D	28	0	25	0	0
4	E	50	0	43	2	0
5	A	65	0	81	0	0
6	A	31	0	13	1	0
7	A	1	0	0	0	0
8	A	3	0	0	0	0
All	All	11552	0	11533	164	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 7.

All (164) 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:A:696:CYS:SG	1:A:702:ARG:NH1	2.57	0.77
1:A:285:GLU:HG2	1:A:294:PHE:HB3	1.66	0.77
1:A:827:ALA:HB2	1:A:1077:PRO:HB2	1.76	0.68
1:A:322:ILE:HD11	1:A:401:ILE:HD11	1.76	0.66
1:A:638:PRO:HB2	1:A:646:ILE:HD11	1.78	0.66
1:A:943:ARG:HG3	1:A:944:LYS:HG3	1.77	0.65
1:A:1141:THR:HG21	1:A:1212:LEU:HD23	1.79	0.64
1:A:321:ILE:HD11	1:A:416:LEU:HD23	1.79	0.64
1:A:1193:TYR:HB3	2:C:226:ILE:HG12	1.79	0.64
2:C:274:ARG:O	2:C:283:LYS:NZ	2.31	0.64
1:A:1112:THR:HB	1:A:1134:TRP:HE1	1.64	0.62
1:A:840:GLU:O	1:A:844:ASN:ND2	2.32	0.61
1:A:310:VAL:HG12	1:A:314:GLU:HG3	1.82	0.61
1:A:189:ASP:N	1:A:189:ASP:OD1	2.32	0.61
1:A:699:ASN:ND2	1:A:791:ASP:OD2	2.33	0.61
1:A:635:THR:HG23	1:A:672:ARG:HH22	1.67	0.60
1:A:1117:ARG:NH1	2:C:328:ARG:O	2.35	0.60
1:A:627:LEU:HD21	1:A:665:LEU:HD21	1.84	0.59
1:A:731:LEU:HD21	1:A:803:LEU:HB2	1.85	0.59
2:C:161:GLN:NE2	2:C:188:TYR:O	2.34	0.59
2:C:159:THR:OG1	2:C:230:ARG:NH2	2.35	0.59
1:A:661:GLY:O	1:A:665:LEU:HB3	2.03	0.59
1:A:1208:THR:HA	1:A:1211:VAL:HG12	1.85	0.59
1:A:351:ARG:HG3	1:A:393:ILE:HD12	1.83	0.59
1:A:1108:VAL:HA	1:A:1212:LEU:HD21	1.83	0.59
1:A:282:SER:HG	1:A:299:TRP:CD1	2.21	0.58
2:C:285:THR:HG22	2:C:286:LEU:HG	1.85	0.58
1:A:382:TYR:H	1:A:397:PRO:HD3	1.68	0.58
1:A:285:GLU:OE1	1:A:311:LYS:NZ	2.32	0.58
2:C:91:ASP:HB3	2:C:108:LYS:HD2	1.84	0.58
1:A:839:GLN:OE1	1:A:862:ASN:ND2	2.37	0.57
1:A:226:ALA:HB1	1:A:508:ILE:HG22	1.86	0.57
2:C:359:ARG:HB2	2:C:361:MET:HG2	1.86	0.57
2:C:172:LEU:HB2	2:C:180:ARG:HE	1.70	0.55
1:A:1144:ILE:HD12	1:A:1209:LEU:HD22	1.88	0.55
2:C:222:ILE:N	2:C:267:GLU:OE2	2.38	0.55
1:A:387:THR:HA	1:A:392:GLN:HA	1.88	0.55
1:A:732:ASP:OD1	1:A:732:ASP:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:310:LEU:HD13	4:E:2:NAG:H81	1.89	0.55
1:A:820:THR:HG22	1:A:994:LYS:HE3	1.89	0.54
2:C:260:LEU:HD12	2:C:261:PRO:HD2	1.90	0.54
1:A:974:MET:N	1:A:974:MET:SD	2.80	0.54
1:A:333:TYR:HB3	1:A:345:LEU:HD23	1.91	0.53
1:A:872:ASN:OD1	1:A:876:LYS:NZ	2.37	0.53
2:C:363:ASP:OD1	2:C:365:THR:OG1	2.25	0.53
1:A:316:ILE:HG13	1:A:401:ILE:HG21	1.89	0.53
1:A:1040:ILE:HD11	1:A:1138:VAL:HG21	1.91	0.53
1:A:1165:ILE:HB	1:A:1166:PRO:HD3	1.89	0.53
1:A:466:ASN:ND2	1:A:1035:PHE:O	2.37	0.52
1:A:335:GLU:O	1:A:405:ALA:HA	2.09	0.52
1:A:705:MET:HG2	1:A:721:LYS:HE2	1.91	0.52
1:A:692:LEU:HA	1:A:709:PHE:HD1	1.75	0.52
1:A:193:ASN:ND2	1:A:304:VAL:O	2.43	0.52
1:A:339:LEU:HD22	1:A:402:LEU:HD12	1.92	0.51
1:A:1233:GLU:H	1:A:1236:HIS:HB2	1.75	0.51
1:A:762:ARG:NH1	1:A:797:ILE:O	2.43	0.51
1:A:636:VAL:HG11	1:A:648:TYR:HB3	1.93	0.51
1:A:1029:TYR:O	1:A:1033:ASN:ND2	2.44	0.50
1:A:1107:ILE:HD12	1:A:1215:PHE:HE2	1.75	0.50
1:A:599:GLU:OE2	1:A:603:ARG:NE	2.43	0.50
2:C:70:VAL:HG21	2:C:328:ARG:H	1.76	0.50
2:C:71:GLN:HA	2:C:100:HIS:O	2.11	0.50
1:A:1100:ASN:OD1	1:A:1219:ARG:NH1	2.43	0.49
1:A:1104:HIS:NE2	1:A:1216:ALA:O	2.42	0.49
1:A:553:GLN:HG3	1:A:948:LEU:HD12	1.93	0.49
1:A:370:VAL:HG22	1:A:386:MET:HG3	1.94	0.49
1:A:868:ASP:OD1	1:A:871:ARG:NH1	2.45	0.48
1:A:717:LYS:NZ	1:A:763:ASP:OD1	2.28	0.48
1:A:718:LEU:O	1:A:761:MET:HA	2.13	0.48
1:A:655:GLU:O	1:A:659:VAL:HG23	2.13	0.48
1:A:627:LEU:HD11	1:A:665:LEU:HD11	1.95	0.48
1:A:654:ASP:OD1	1:A:654:ASP:N	2.41	0.47
2:C:78:SER:HB2	2:C:308:ILE:HD13	1.96	0.47
1:A:256:VAL:O	1:A:259:ILE:HG13	2.14	0.47
1:A:1049:TYR:HE1	1:A:1143:VAL:HG12	1.79	0.47
1:A:1110:ILE:HA	1:A:1113:ILE:HG12	1.95	0.47
1:A:581:CYS:HB2	1:A:745:HIS:NE2	2.29	0.47
1:A:737:GLN:N	1:A:737:GLN:OE1	2.48	0.47
1:A:1061:ILE:HG22	1:A:1154:THR:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:THR:HG23	1:A:1051:LEU:HD11	1.96	0.47
1:A:309:ARG:HA	1:A:413:ILE:O	2.14	0.47
1:A:388:LEU:HG	1:A:389:ASN:H	1.79	0.47
1:A:760:ALA:HB1	1:A:801:LEU:HB3	1.96	0.47
2:C:58:PRO:O	2:C:61:ILE:HG13	2.15	0.47
1:A:529:LEU:HD11	2:C:25:ASN:HB2	1.97	0.47
1:A:932:LEU:H	1:A:932:LEU:HD23	1.80	0.47
2:C:246:ASN:ND2	4:E:1:NAG:O6	2.37	0.47
1:A:753:GLY:HA2	1:A:841:THR:HG23	1.97	0.46
2:C:164:GLY:O	2:C:235:LYS:NZ	2.48	0.46
1:A:700:SER:HA	1:A:703:LYS:HE2	1.98	0.46
1:A:760:ALA:HB3	1:A:801:LEU:HD13	1.98	0.46
1:A:187:ILE:HG23	1:A:188:ASN:HB2	1.98	0.46
1:A:1122:LEU:HD11	1:A:1129:ALA:HB2	1.98	0.46
2:C:169:LYS:O	2:C:180:ARG:NH2	2.49	0.46
1:A:613:ASN:OD1	1:A:614:ASP:N	2.44	0.46
1:A:863:GLU:HB2	1:A:869:THR:HG22	1.97	0.45
2:C:176:CYS:O	2:C:180:ARG:HB2	2.16	0.45
1:A:1145:ILE:HG12	1:A:1213:PRO:HA	1.98	0.45
2:C:61:ILE:O	2:C:64:ILE:HG13	2.15	0.45
1:A:308:ILE:HD11	1:A:320:THR:HG21	1.98	0.45
2:C:262:ASP:OD1	2:C:262:ASP:N	2.46	0.45
2:C:133:ILE:O	2:C:292:SER:OG	2.28	0.45
1:A:939:LYS:HA	1:A:942:LYS:HG2	1.99	0.45
1:A:310:VAL:O	1:A:412:TRP:HA	2.16	0.45
1:A:662:GLY:HA2	1:A:665:LEU:HD22	1.98	0.45
1:A:556:TYR:HE1	1:A:830:LYS:HD2	1.82	0.45
1:A:771:GLU:O	1:A:775:ILE:HG12	2.16	0.45
2:C:218:THR:OG1	3:B:1:NAG:O7	2.35	0.45
2:C:26:THR:OG1	2:C:27:ALA:N	2.49	0.45
1:A:740:GLU:HB3	1:A:744:ARG:NH1	2.32	0.44
2:C:149:ASN:ND2	2:C:277:ALA:O	2.39	0.44
1:A:339:LEU:HD22	1:A:402:LEU:HB2	2.00	0.44
1:A:729:GLU:OE1	1:A:729:GLU:N	2.44	0.44
1:A:693:LEU:HD11	1:A:710:ARG:HB2	1.98	0.44
1:A:1049:TYR:CE1	1:A:1143:VAL:HG12	2.53	0.44
1:A:402:LEU:HD22	1:A:425:LYS:HB2	1.98	0.44
1:A:740:GLU:HB3	1:A:744:ARG:HH12	1.82	0.44
1:A:237:GLN:HG3	1:A:500:ILE:HD13	1.99	0.44
1:A:627:LEU:HD12	1:A:627:LEU:HA	1.82	0.44
2:C:71:GLN:NE2	2:C:102:LYS:HB2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:73:LEU:HD21	2:C:75:ILE:HG13	2.00	0.44
1:A:222:PHE:HD1	1:A:227:ASN:HB3	1.82	0.43
2:C:188:TYR:HB2	2:C:241:ILE:HB	1.99	0.43
1:A:618:GLU:O	1:A:621:PRO:HD2	2.18	0.43
2:C:321:THR:OG1	2:C:322:ASN:N	2.51	0.43
1:A:249:THR:HG23	1:A:250:THR:HG23	2.00	0.43
1:A:820:THR:HG21	1:A:991:LYS:HA	2.00	0.43
2:C:269:PHE:O	2:C:273:MET:HG2	2.18	0.43
2:C:145:ASN:O	2:C:145:ASN:ND2	2.51	0.43
2:C:202:PHE:HB3	2:C:300:MET:HE3	2.01	0.43
1:A:730:ARG:NH2	1:A:795:ASN:OD1	2.51	0.43
1:A:201:ASN:OD1	1:A:420:THR:OG1	2.36	0.43
1:A:193:ASN:HD22	1:A:305:GLY:HA3	1.84	0.43
1:A:331:LEU:HA	1:A:349:GLN:HA	2.00	0.43
1:A:759:LEU:HD21	1:A:807:THR:HG23	2.00	0.43
1:A:587:PRO:O	1:A:591:THR:OG1	2.33	0.43
1:A:879:ALA:O	1:A:883:HIS:NE2	2.52	0.43
1:A:320:THR:HA	1:A:416:LEU:O	2.19	0.42
1:A:560:ASP:OD1	1:A:561:LYS:N	2.52	0.42
2:C:123:CYS:HB2	2:C:304:LEU:HD11	2.00	0.42
2:C:74:THR:HG23	2:C:318:VAL:HG22	2.01	0.42
1:A:221:GLU:O	1:A:227:ASN:ND2	2.40	0.42
1:A:669:PHE:HE1	1:A:677:VAL:HG13	1.84	0.42
1:A:874:LEU:O	1:A:878:ASN:ND2	2.52	0.42
1:A:614:ASP:N	1:A:614:ASP:OD1	2.53	0.42
2:C:198:PHE:CE2	2:C:200:ASP:HB2	2.54	0.42
1:A:574:SER:HG	1:A:749:TYR:HH	1.62	0.42
1:A:345:LEU:HD21	1:A:408:ARG:HE	1.85	0.41
1:A:950:LEU:HD13	1:A:997:LEU:HD11	2.02	0.41
6:A:1502:ACP:H8	6:A:1502:ACP:H2'	1.90	0.41
1:A:761:MET:HB3	1:A:804:ILE:HD11	2.01	0.41
1:A:1079:LEU:HD21	1:A:1238:ILE:HD12	2.01	0.41
2:C:39:ILE:HG13	2:C:41:SER:H	1.84	0.41
1:A:745:HIS:HA	1:A:748:ASP:OD1	2.21	0.41
2:C:166:PRO:HA	2:C:236:TYR:CZ	2.56	0.41
1:A:840:GLU:HG3	1:A:844:ASN:HD21	1.85	0.41
1:A:906:LEU:HD11	1:A:937:VAL:HG22	2.02	0.41
2:C:47:PRO:O	2:C:50:ILE:HG13	2.21	0.41
1:A:339:LEU:HB3	1:A:426:LEU:HD22	2.02	0.40
1:A:581:CYS:SG	1:A:749:TYR:OH	2.73	0.40
1:A:704:ARG:CZ	1:A:730:ARG:HH22	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:842:ALA:O	1:A:845:ILE:HG13	2.21	0.40
1:A:284:ALA:HB2	1:A:299:TRP:CD1	2.57	0.40
1:A:331:LEU:HD23	1:A:331:LEU:H	1.87	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	1062/1465 (72%)	1017 (96%)	45 (4%)	0	100	100
2	C	348/413 (84%)	327 (94%)	21 (6%)	0	100	100
All	All	1410/1878 (75%)	1344 (95%)	66 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	935/1257 (74%)	923 (99%)	12 (1%)	61	71
2	C	318/370 (86%)	315 (99%)	3 (1%)	70	74
All	All	1253/1627 (77%)	1238 (99%)	15 (1%)	61	72

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	189	ASP
1	A	536	THR
1	A	598	ILE
1	A	647	LYS
1	A	665	LEU
1	A	703	LYS
1	A	759	LEU
1	A	803	LEU
1	A	809	ILE
1	A	812	LYS
1	A	1163	ILE
1	A	1188	ILE
2	C	57	THR
2	C	94	LYS
2	C	365	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	237	GLN
1	A	280	ASN
1	A	376	ASN
1	A	389	ASN
1	A	777	ASN
1	A	825	GLN
1	A	888	HIS
2	C	30	GLN
2	C	71	GLN
2	C	161	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

8 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	B	1	2,3	14,14,15	0.23	0	17,19,21	0.47	0
3	NAG	B	2	3	14,14,15	0.23	0	17,19,21	0.44	0
3	NAG	D	1	2,3	14,14,15	0.29	0	17,19,21	0.49	0
3	NAG	D	2	3	14,14,15	0.24	0	17,19,21	0.42	0
4	NAG	E	1	2,4	14,14,15	0.27	0	17,19,21	0.40	0
4	NAG	E	2	4	14,14,15	0.20	0	17,19,21	0.56	0
4	BMA	E	3	4	11,11,12	0.59	0	15,15,17	0.76	0
4	BMA	E	4	4	11,11,12	0.56	0	15,15,17	0.74	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	B	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	B	2	3	-	1/6/23/26	0/1/1/1
3	NAG	D	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
4	NAG	E	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	3/6/23/26	0/1/1/1
4	BMA	E	3	4	-	0/2/19/22	0/1/1/1
4	BMA	E	4	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

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

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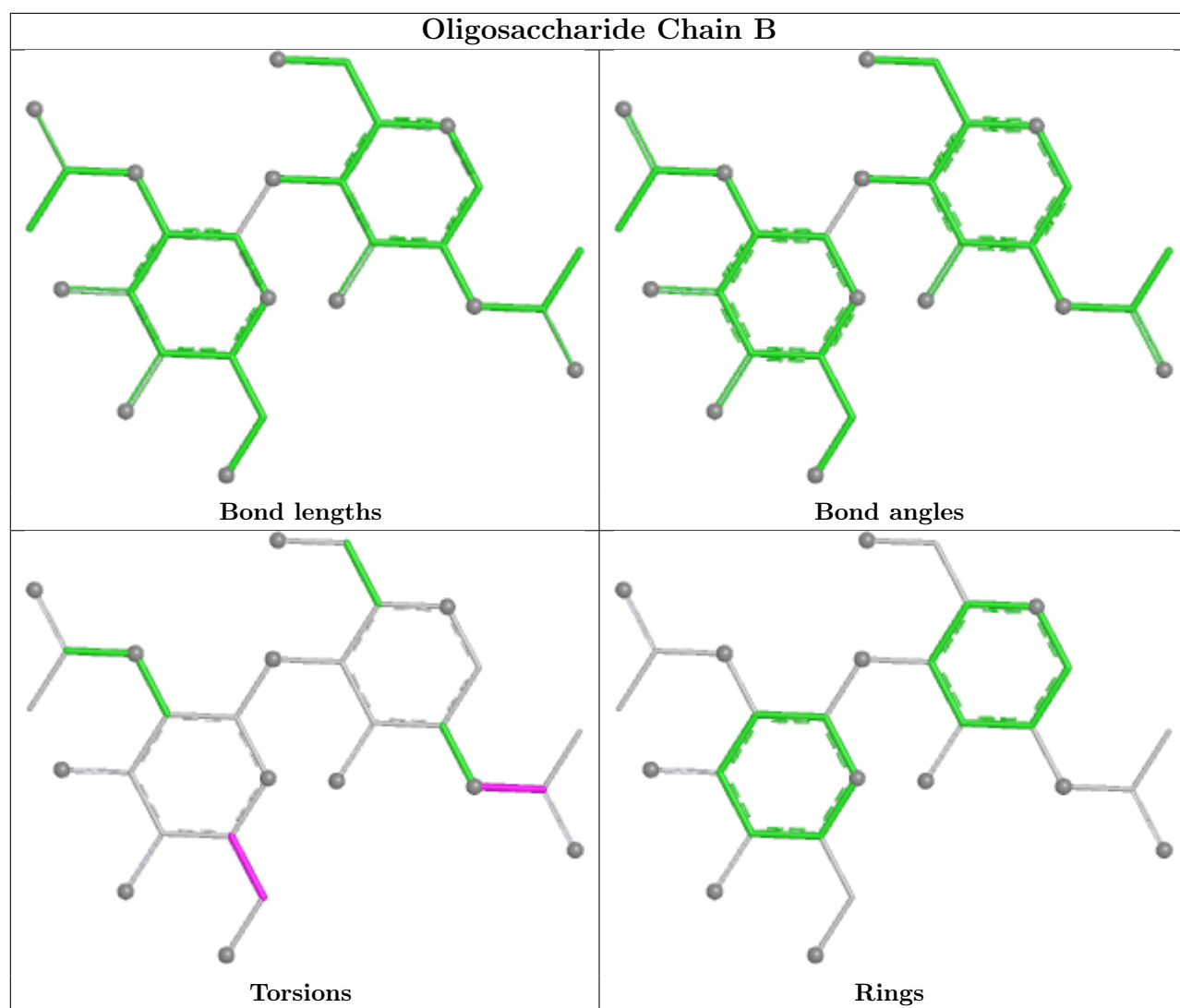
Mol	Chain	Res	Type	Atoms
3	B	1	NAG	O7-C7-N2-C2
3	D	1	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	B	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C1-C2-N2-C7
3	D	1	NAG	C4-C5-C6-O6
4	E	2	NAG	C3-C2-N2-C7
4	E	2	NAG	C4-C5-C6-O6

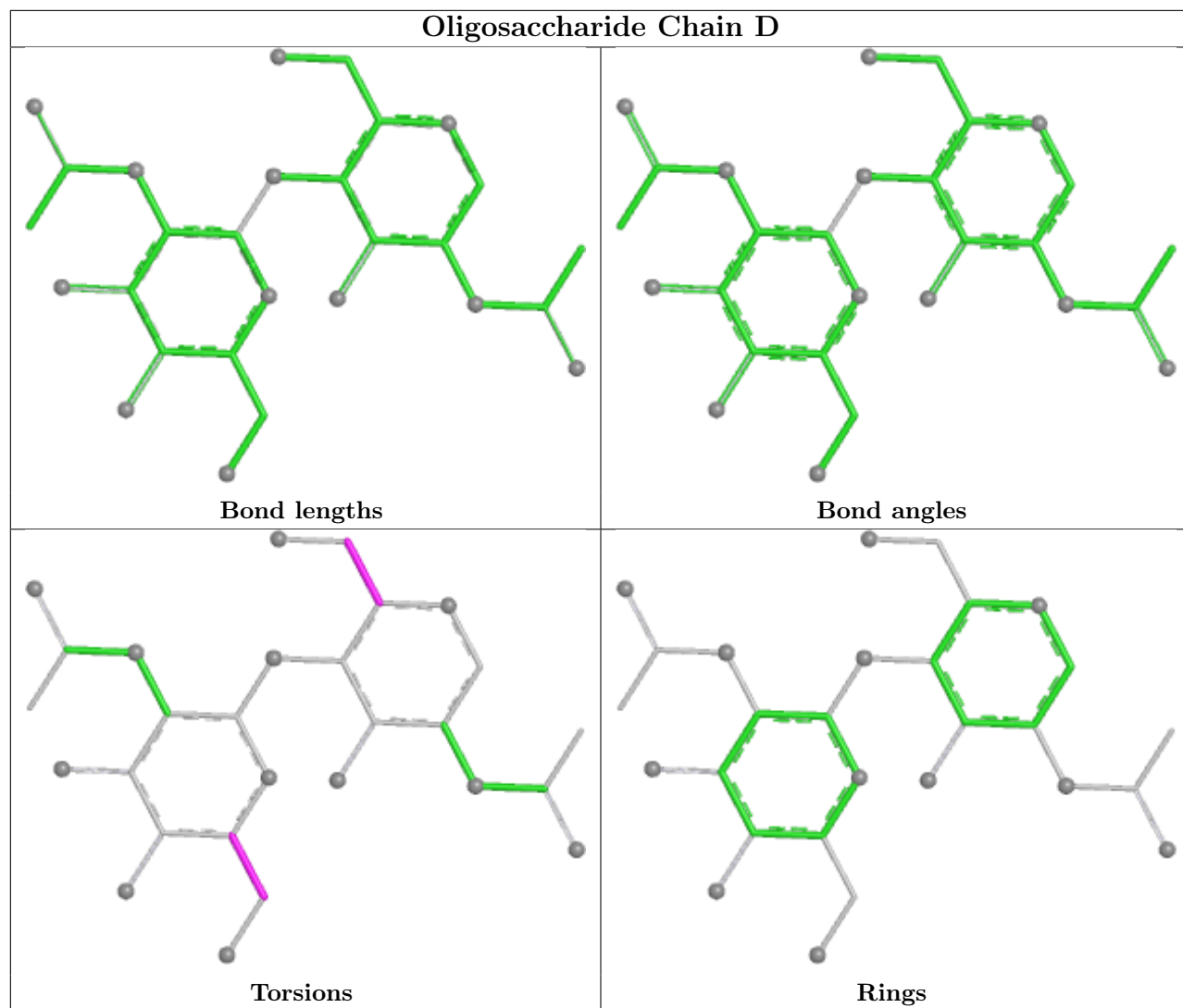
There are no ring outliers.

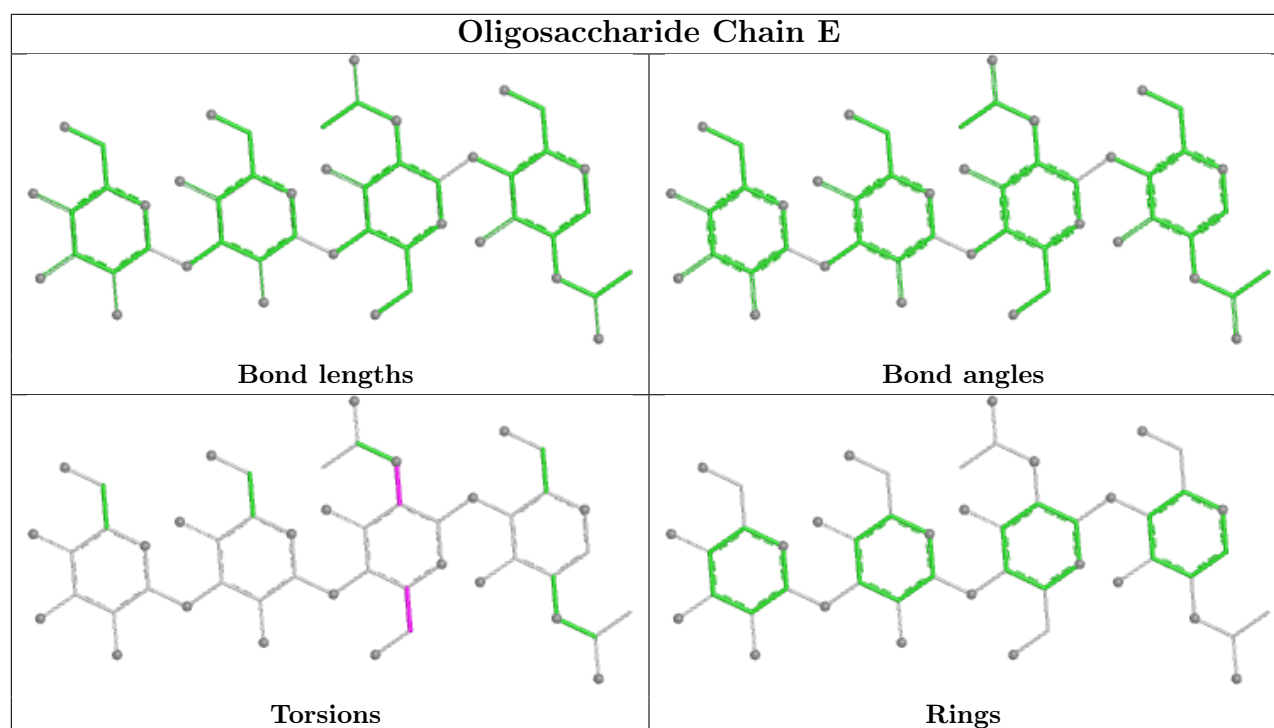
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1	NAG	1	0
3	B	1	NAG	1	0
4	E	2	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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
5	2Y5	A	1501	-	65,65,65	0.95	5 (7%)	77,80,80	1.10	5 (6%)
6	ACP	A	1502	-	31,33,33	3.20	12 (38%)	47,52,52	2.16	12 (25%)

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
5	2Y5	A	1501	-	-	24/61/85/85	0/1/1/1
6	ACP	A	1502	-	-	11/19/38/38	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1502	ACP	O4'-C1'	8.77	1.62	1.42
6	A	1502	ACP	C2'-C1'	-7.05	1.31	1.53
6	A	1502	ACP	O4'-C4'	-6.43	1.30	1.45
6	A	1502	ACP	PB-O3A	6.31	1.65	1.58
6	A	1502	ACP	PA-O3A	5.47	1.65	1.59
6	A	1502	ACP	C6-N6	4.46	1.45	1.34
5	A	1501	2Y5	P4-O4	3.25	1.65	1.59
6	A	1502	ACP	C5-C4	-2.91	1.33	1.39
6	A	1502	ACP	O2'-C2'	2.79	1.49	1.43
6	A	1502	ACP	O3'-C3'	-2.74	1.36	1.43
5	A	1501	2Y5	O16-C8	-2.68	1.40	1.46
6	A	1502	ACP	C5-N7	-2.48	1.34	1.39
5	A	1501	2Y5	O18-C11	2.37	1.40	1.33
5	A	1501	2Y5	O18-C9	-2.19	1.40	1.45
5	A	1501	2Y5	O16-C10	2.16	1.40	1.34
6	A	1502	ACP	C8-N9	-2.13	1.33	1.37
6	A	1502	ACP	PB-O2B	-2.02	1.51	1.56

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1502	ACP	N6-C6-N1	-6.26	104.44	118.38
6	A	1502	ACP	N3-C2-N1	-5.73	119.90	128.58
6	A	1502	ACP	C5-C6-N6	4.95	135.54	123.29
6	A	1502	ACP	C5-C4-N3	-4.83	120.07	126.72
6	A	1502	ACP	N9-C8-N7	-4.19	107.99	113.94
5	A	1501	2Y5	O16-C10-C12	3.98	120.09	111.48
6	A	1502	ACP	C2-N3-C4	3.39	120.10	111.83
6	A	1502	ACP	C5-N7-C8	2.89	107.99	103.45
6	A	1502	ACP	N3-C4-N9	2.85	132.02	127.17
5	A	1501	2Y5	C6-C1-C2	2.84	114.80	110.86
5	A	1501	2Y5	O18-C11-C31	2.70	120.08	111.83
6	A	1502	ACP	C3'-C2'-C1'	2.65	106.47	101.46
5	A	1501	2Y5	C5-C4-C3	2.37	114.15	110.86
6	A	1502	ACP	C4-N9-C8	2.29	108.14	105.74
6	A	1502	ACP	C4-C5-N7	-2.29	107.97	110.58
6	A	1502	ACP	PB-O3A-PA	-2.24	125.07	132.37
5	A	1501	2Y5	C2-C3-C4	2.20	114.67	109.68

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1501	2Y5	C1-O1-P1-O12
5	A	1501	2Y5	C1-O1-P1-O13
5	A	1501	2Y5	C12-C10-O16-C8
5	A	1501	2Y5	O17-C10-O16-C8
6	A	1502	ACP	PG-C3B-PB-O1B
6	A	1502	ACP	PG-C3B-PB-O2B
6	A	1502	ACP	PG-C3B-PB-O3A
6	A	1502	ACP	O4'-C4'-C5'-O5'
6	A	1502	ACP	C3'-C4'-C5'-O5'
5	A	1501	2Y5	C11-C31-C32-C33
5	A	1501	2Y5	C7-C8-C9-O18
6	A	1502	ACP	C4'-C5'-O5'-PA
5	A	1501	2Y5	C8-C7-O13-P1
5	A	1501	2Y5	C18-C19-C20-C21
5	A	1501	2Y5	C21-C22-C23-C24
5	A	1501	2Y5	C22-C23-C24-C25
5	A	1501	2Y5	C42-C43-C44-C45
5	A	1501	2Y5	C1-O1-P1-O11
5	A	1501	2Y5	O16-C8-C9-O18
6	A	1502	ACP	C5'-O5'-PA-O1A
6	A	1502	ACP	C5'-O5'-PA-O2A
6	A	1502	ACP	C5'-O5'-PA-O3A
5	A	1501	2Y5	C39-C40-C41-C42
5	A	1501	2Y5	C16-C17-C18-C19
5	A	1501	2Y5	O19-C11-O18-C9
5	A	1501	2Y5	C12-C13-C14-C15
5	A	1501	2Y5	C31-C11-O18-C9
6	A	1502	ACP	PB-C3B-PG-O1G
6	A	1502	ACP	C2'-C1'-N9-C8
5	A	1501	2Y5	C41-C42-C43-C44
5	A	1501	2Y5	O18-C11-C31-C32
5	A	1501	2Y5	C2-C1-O1-P1
5	A	1501	2Y5	C37-C38-C39-C40
5	A	1501	2Y5	O19-C11-C31-C32
5	A	1501	2Y5	C35-C36-C37-C38

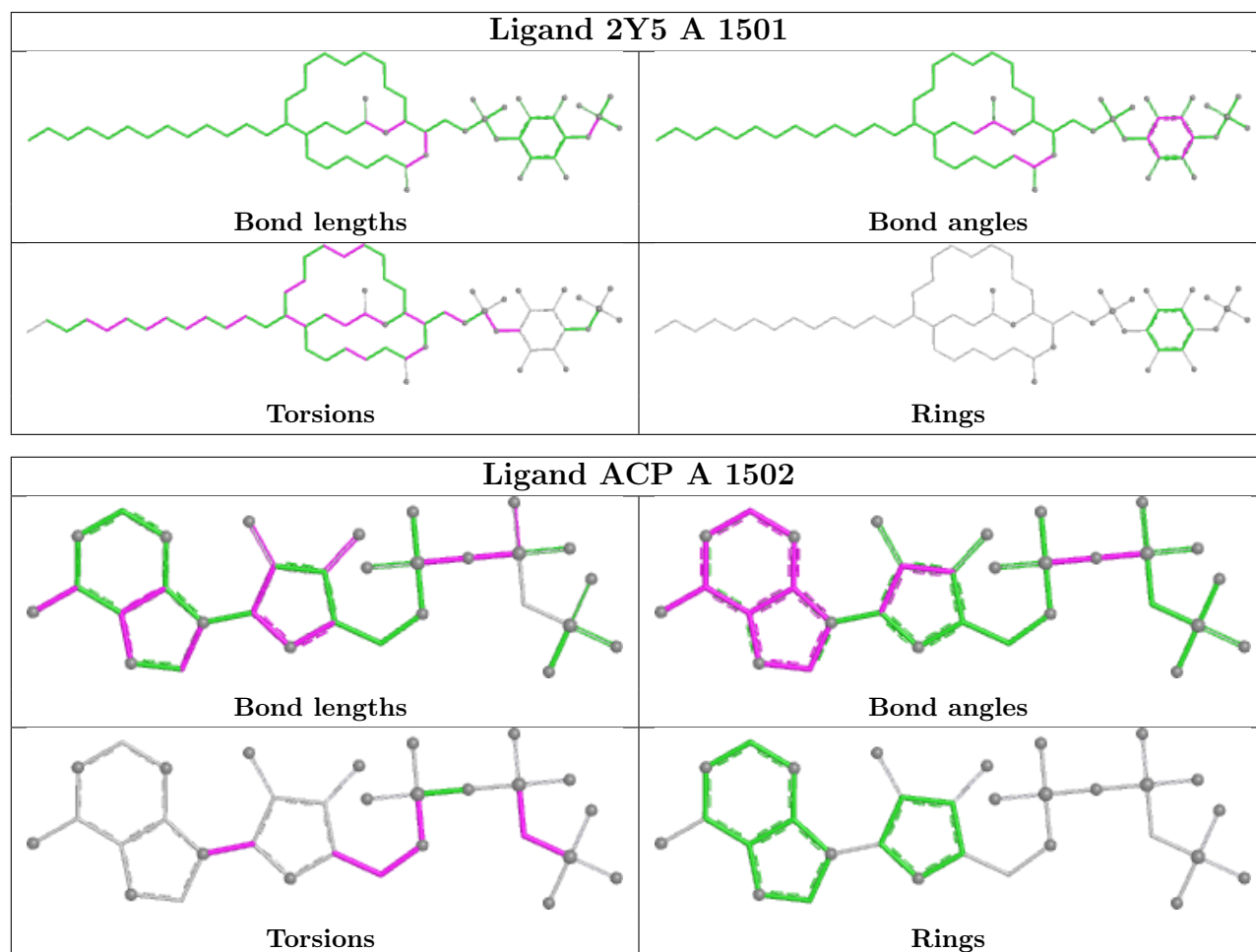
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1502	ACP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

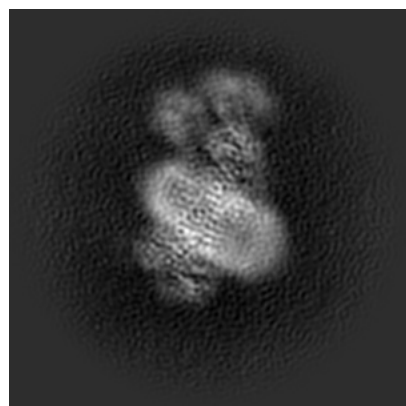
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12896. These allow visual inspection of the internal detail of the map and identification of artifacts.

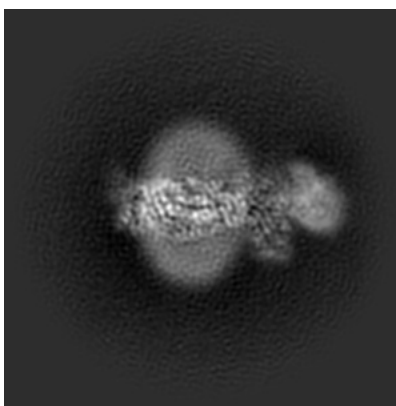
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

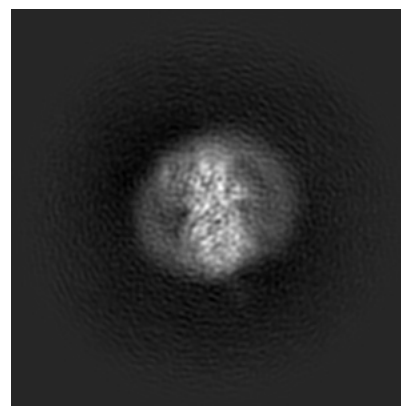
6.1.1 Primary map



X

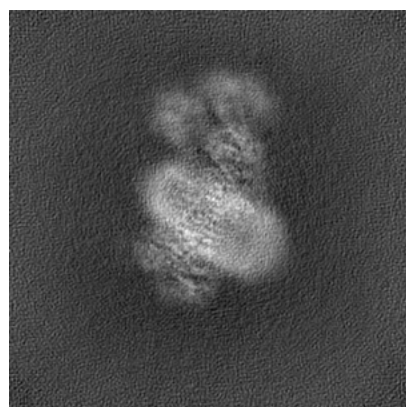


Y

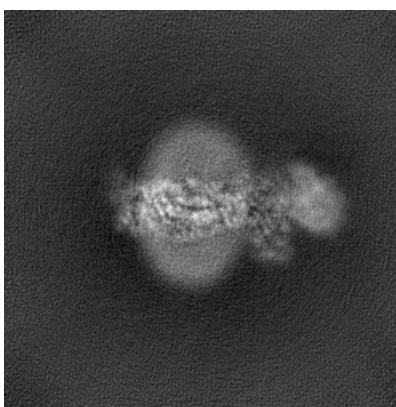


Z

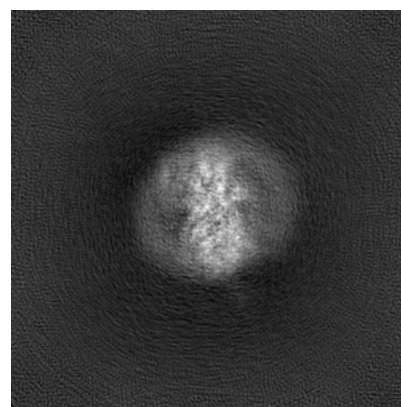
6.1.2 Raw map



X



Y

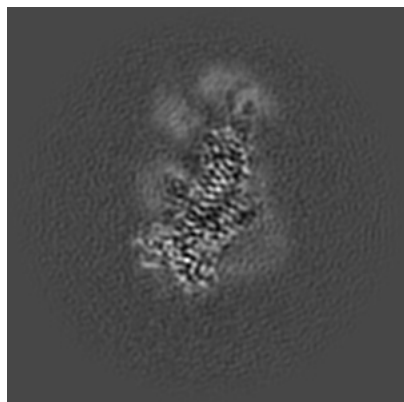


Z

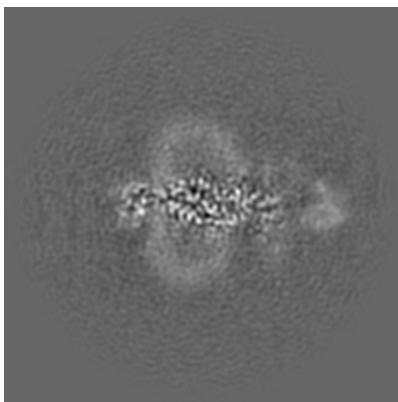
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

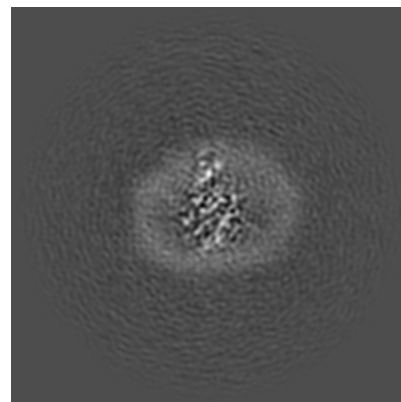
6.2.1 Primary map



X Index: 128

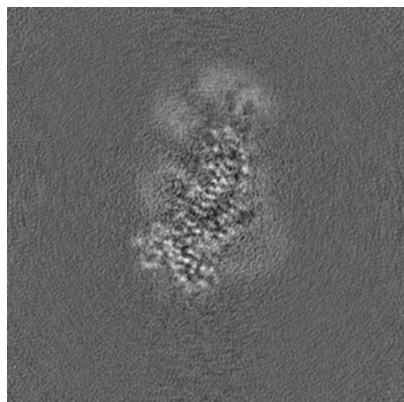


Y Index: 128

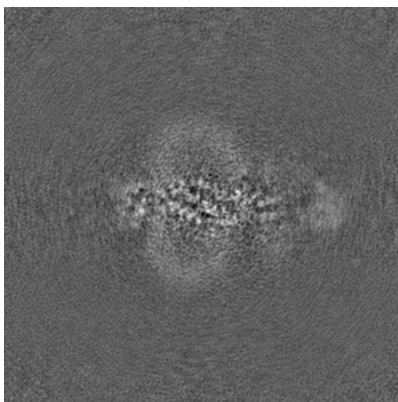


Z Index: 128

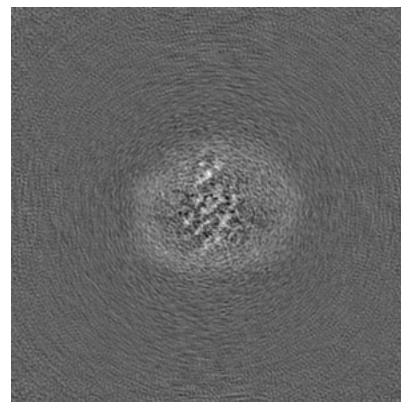
6.2.2 Raw map



X Index: 128



Y Index: 128

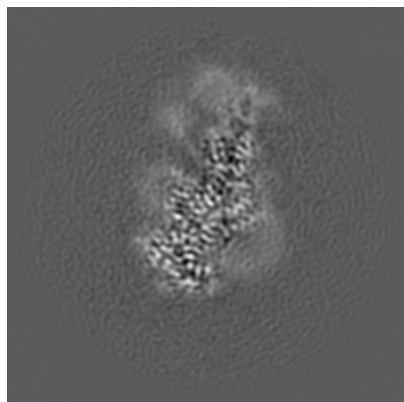


Z Index: 128

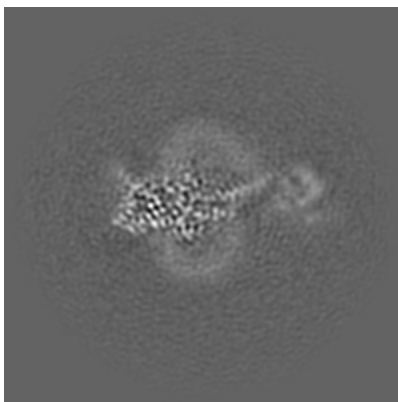
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

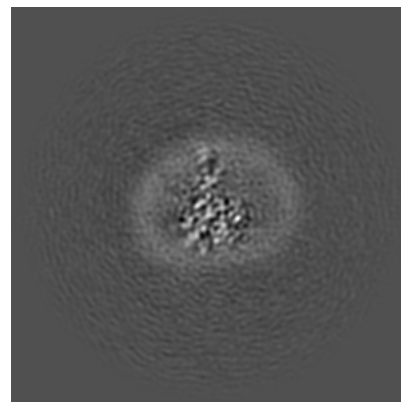
6.3.1 Primary map



X Index: 125

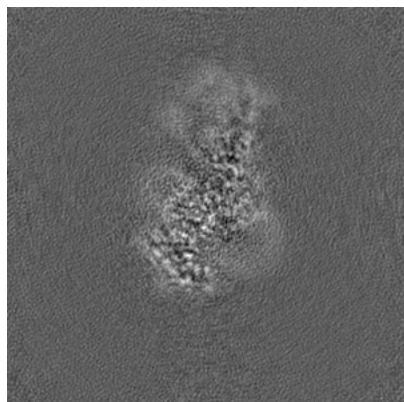


Y Index: 114

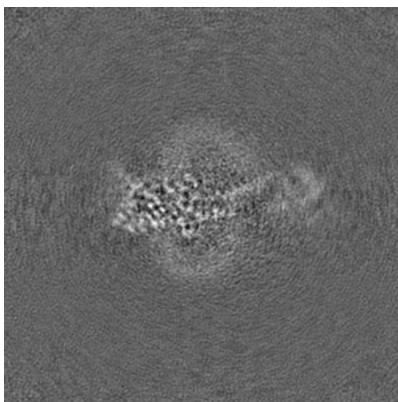


Z Index: 124

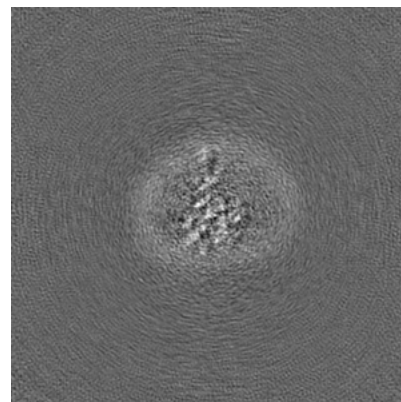
6.3.2 Raw map



X Index: 124



Y Index: 114

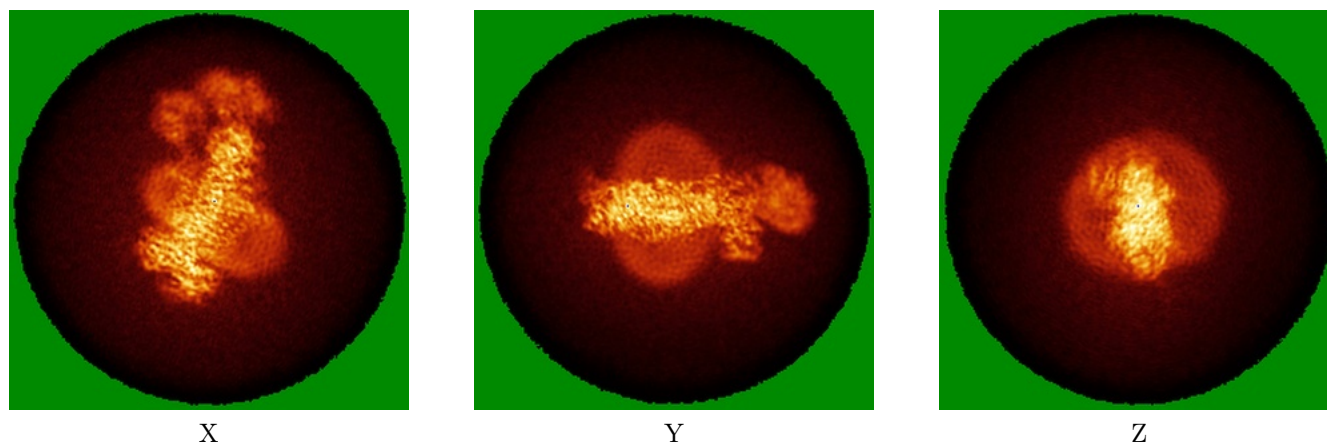


Z Index: 124

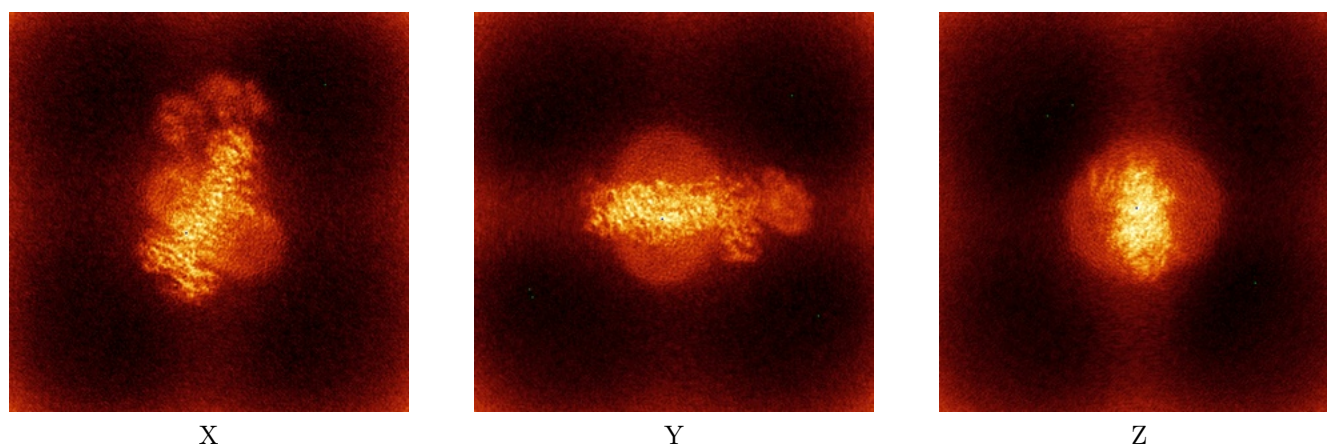
The images above show the largest variance slices of the map in three orthogonal directions.

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](#)

This section was not generated.

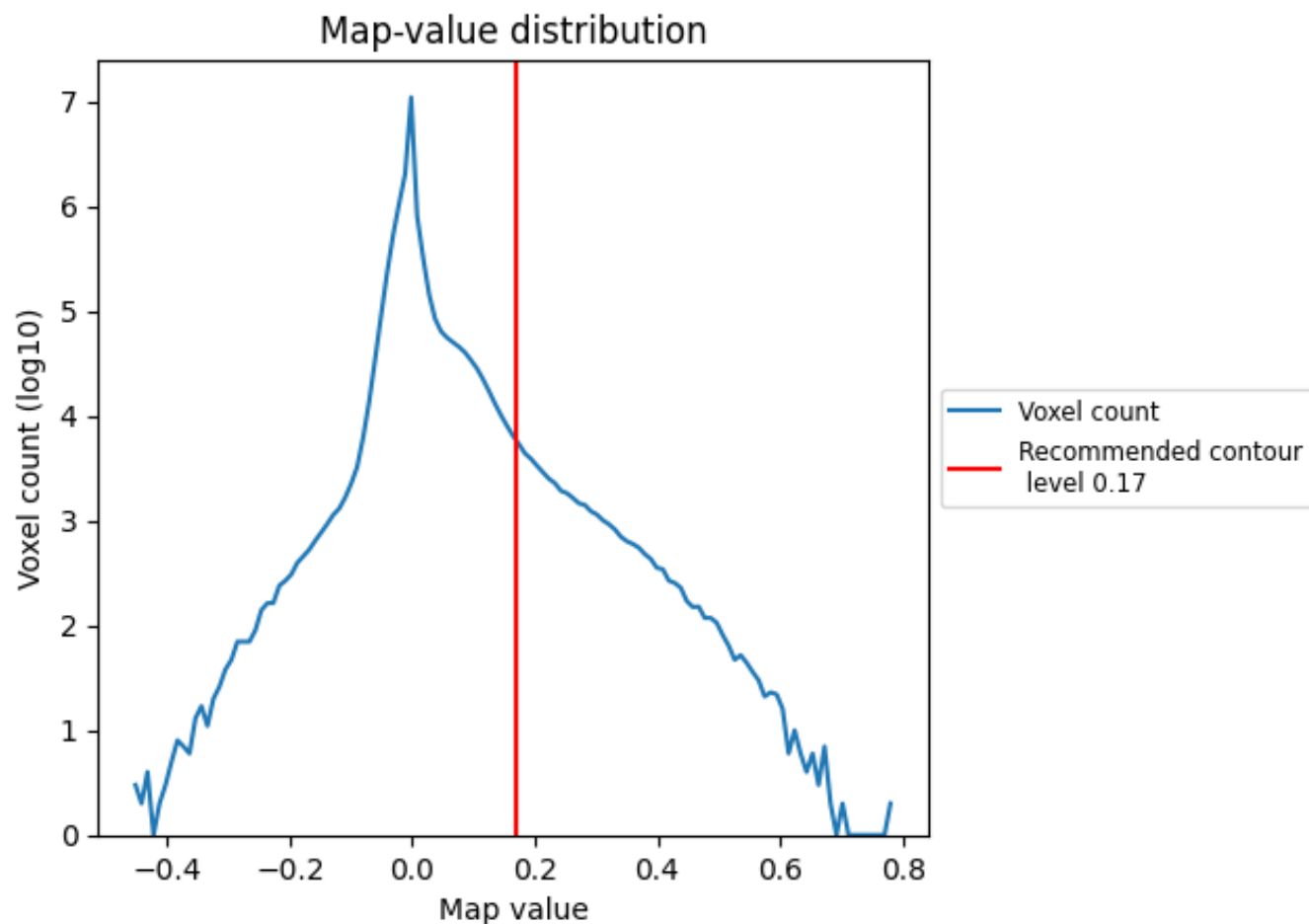
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

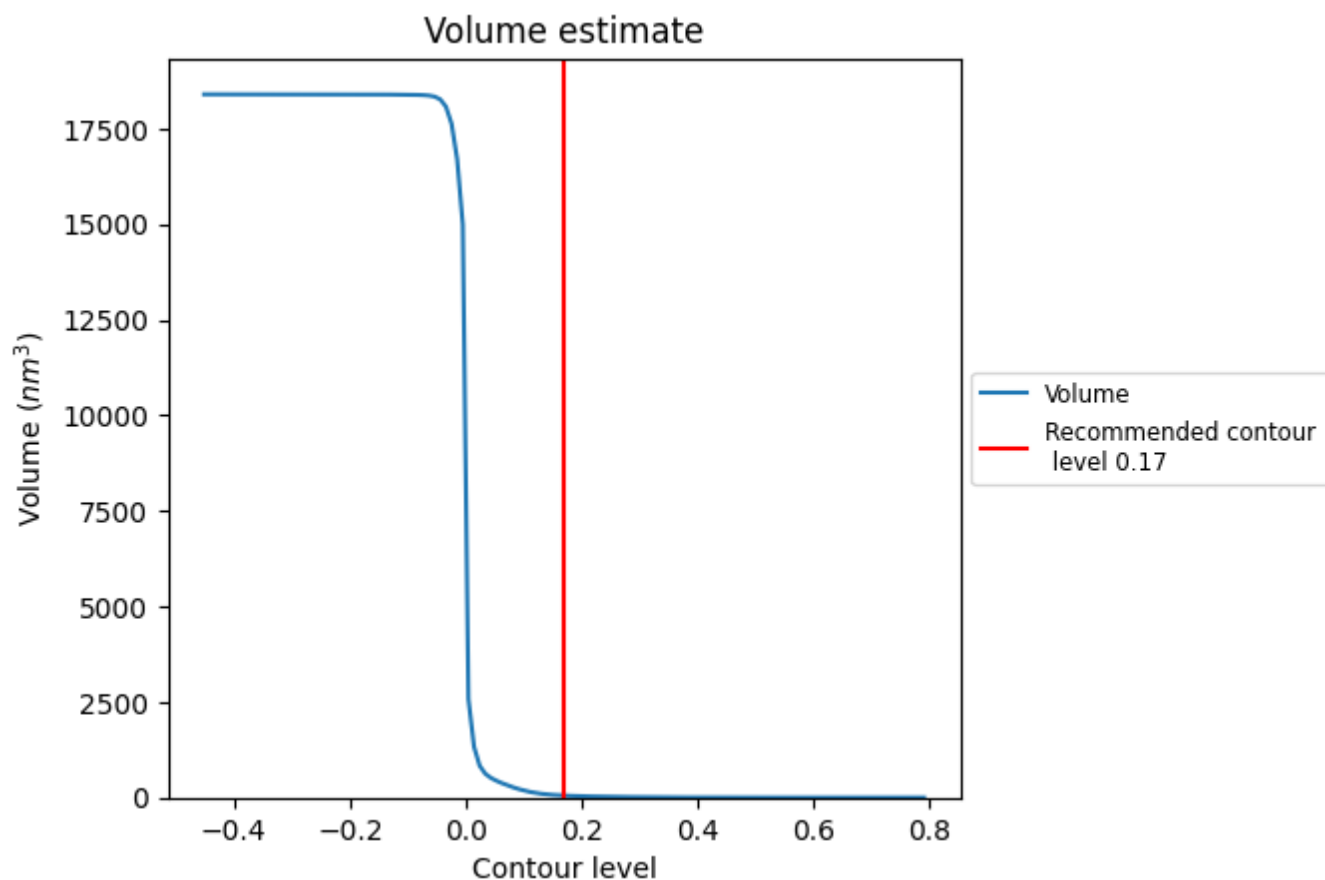
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

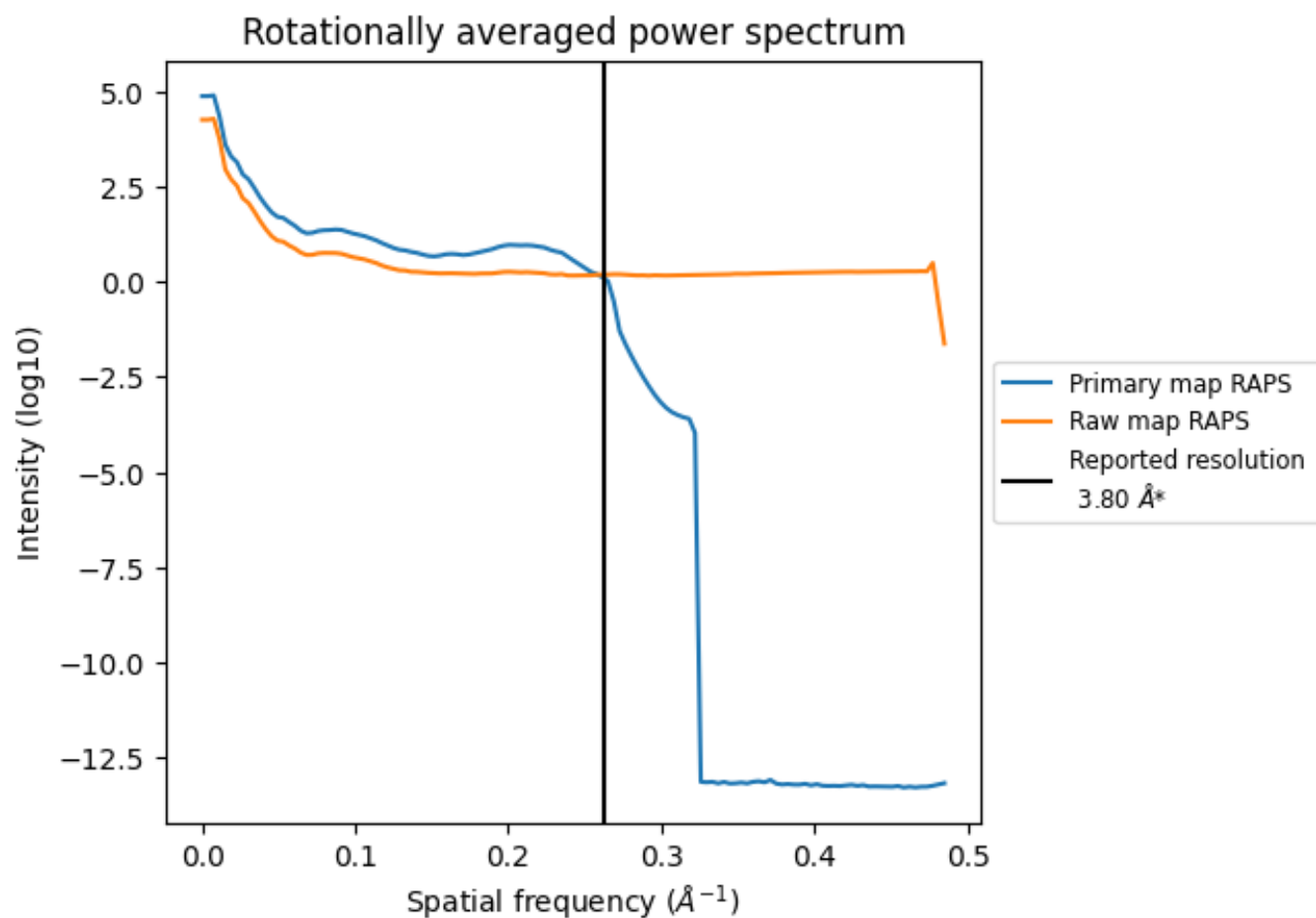
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 51 nm³; this corresponds to an approximate mass of 46 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 ⓘ

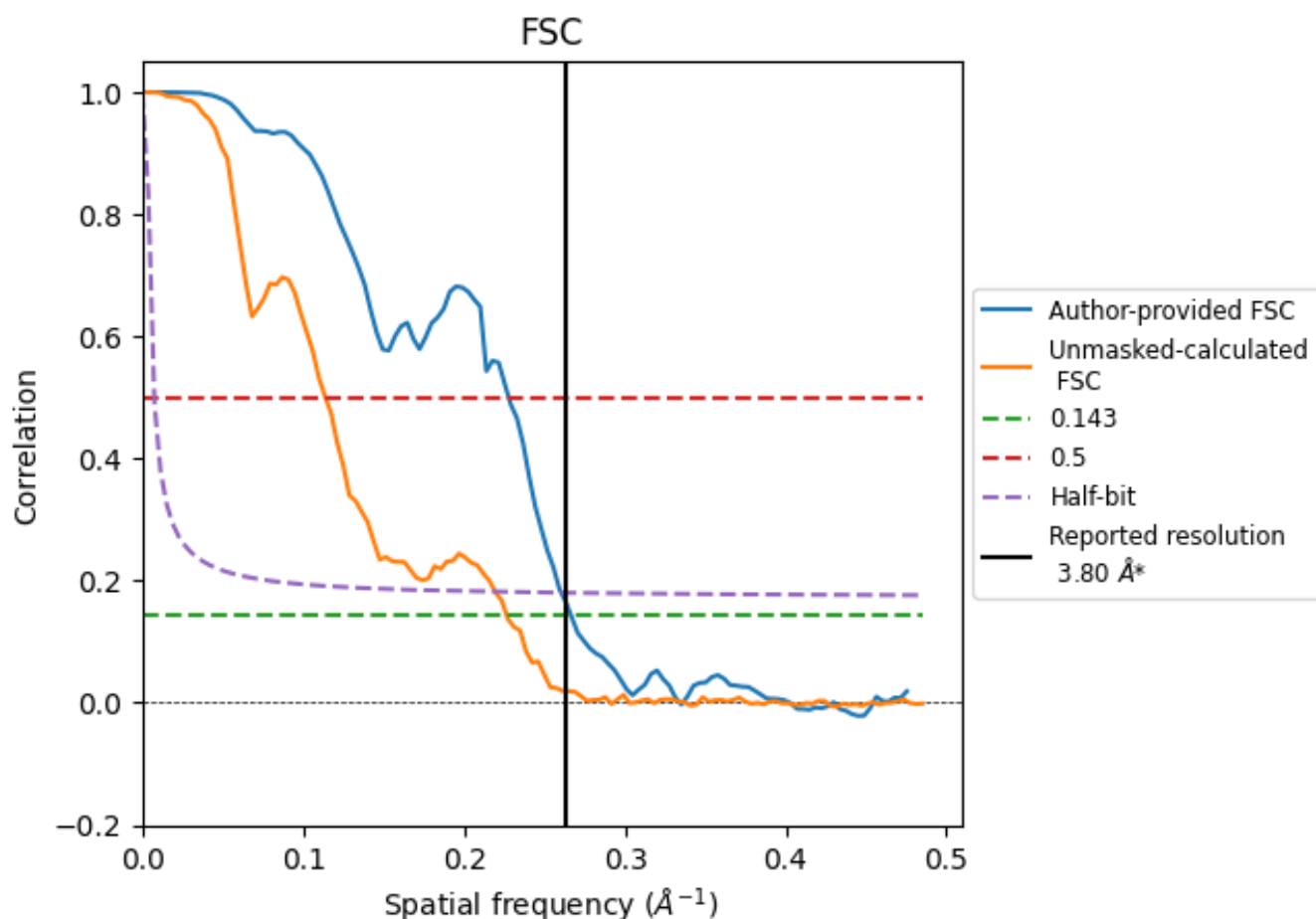


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

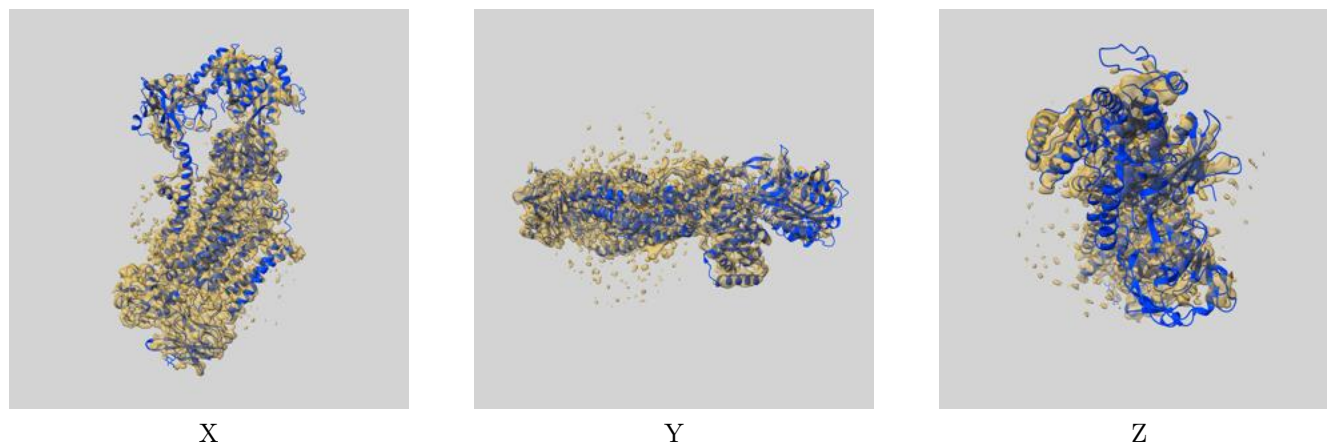
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.75	4.39	3.84
Unmasked-calculated*	4.41	8.77	4.56

*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 4.41 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

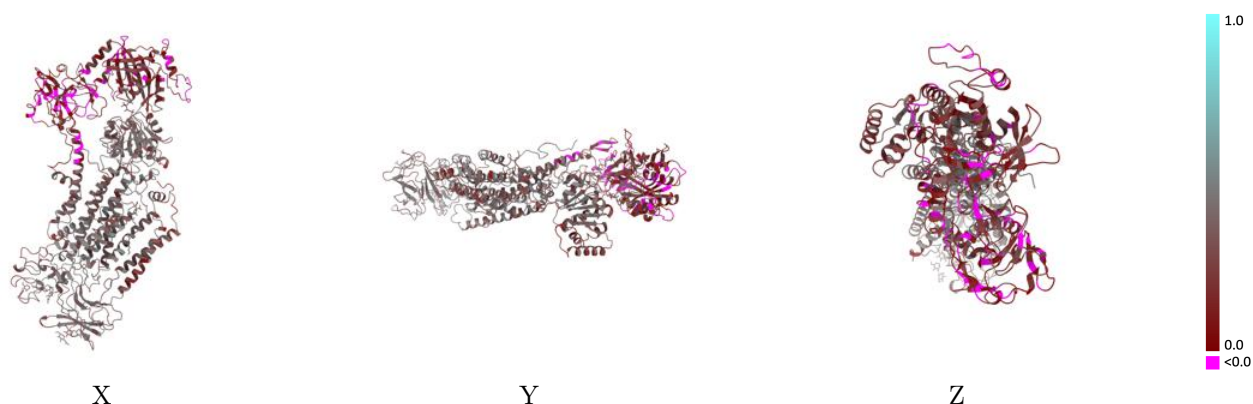
This section contains information regarding the fit between EMDB map EMD-12896 and PDB model 7OH7. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



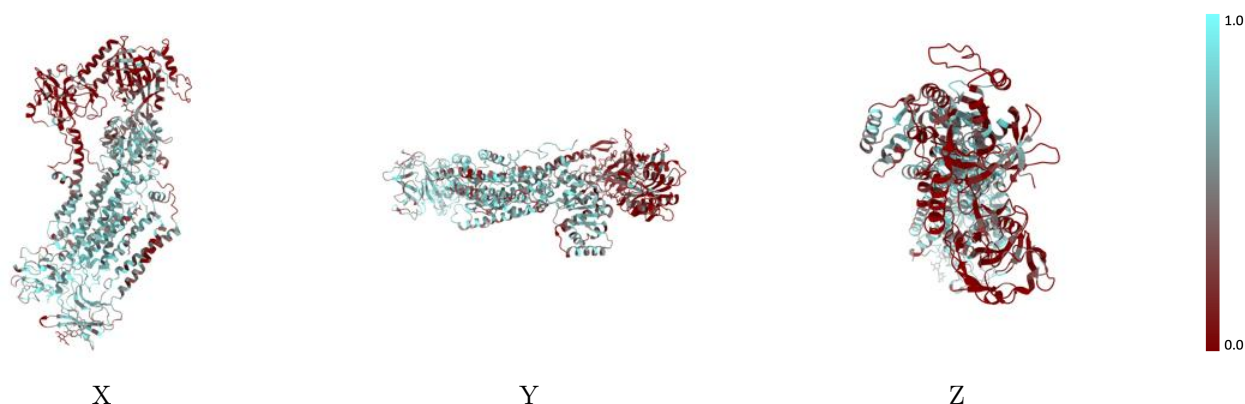
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



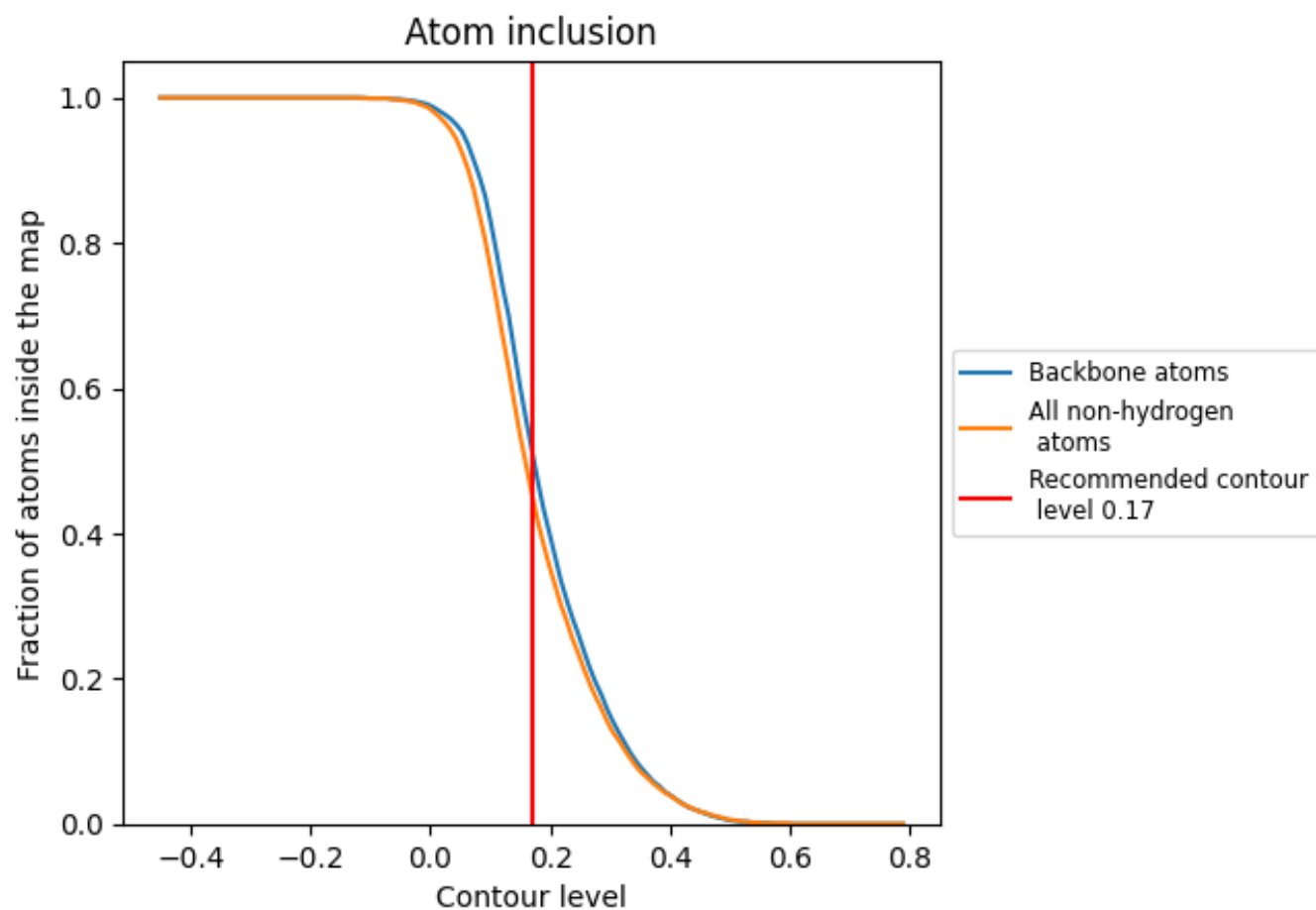
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 51% of all backbone atoms, 45% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4530	0.3070
A	0.4070	0.2830
B	0.4290	0.3670
C	0.6010	0.3780
D	0.2140	0.3400
E	0.6600	0.3730

