wwPDB EM Validation Summary Report (i)

Aug 27, 2026 – 09:29 am BST

PDB ID	:	6ROI / pdb_00006roi
EMDB ID	:	EMD-4973
Title	:	Cryo-EM structure of the partially activated Drs2p-Cdc50p
Authors	:	Timcenko, M.; Lyons, J.A.; Januliene, D.; Ulstrup, J.J.; Dieudonne, T.; Montigny, C.; Ash, M.R.; Karlsen, J.L.; Boesen, T.; Kuhlbrandt, W.; Lenoir, G.; Moeller, A.; Nissen, P.
Deposited on	:	2019-05-13
Resolution	:	3.70 Å(reported)

This is a wwPDB EM Validation Summary 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 (i) 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 (i)) were used in the production of this report:

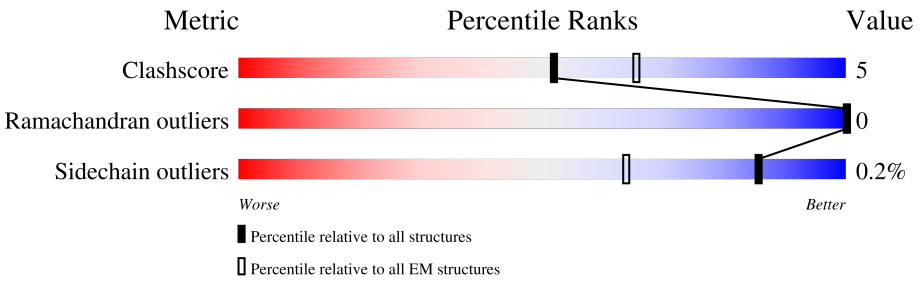
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

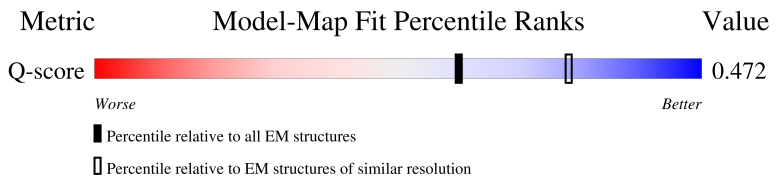
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1460	9% 63% 13% 24%
2	C	413	• 74% 8% 18%
3	B	2	50% 50% 50%
4	D	4	25% 100%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 11775 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1108	8857	5715	1448	1656	38	0	0

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1356	GLY	-	expression tag	UNP P39524
A	1357	GLY	-	expression tag	UNP P39524
A	1358	GLY	-	expression tag	UNP P39524
A	1359	GLY	-	expression tag	UNP P39524
A	1360	LEU	-	expression tag	UNP P39524
A	1361	VAL	-	expression tag	UNP P39524
A	1362	PRO	-	expression tag	UNP P39524
A	1363	ARG	-	expression tag	UNP P39524
A	1364	GLY	-	expression tag	UNP P39524
A	1365	SER	-	expression tag	UNP P39524
A	1366	GLY	-	expression tag	UNP P39524
A	1367	GLY	-	expression tag	UNP P39524
A	1368	THR	-	expression tag	UNP P39524
A	1369	ALA	-	expression tag	UNP P39524
A	1370	ALA	-	expression tag	UNP P39524
A	1371	ALA	-	expression tag	UNP P39524
A	1372	PRO	-	expression tag	UNP P39524
A	1373	GLY	-	expression tag	UNP P39524
A	1374	PRO	-	expression tag	UNP P39524
A	1375	ALA	-	expression tag	UNP P39524
A	1376	PRO	-	expression tag	UNP P39524
A	1377	ALA	-	expression tag	UNP P39524
A	1378	PRO	-	expression tag	UNP P39524
A	1379	ALA	-	expression tag	UNP P39524
A	1380	PRO	-	expression tag	UNP P39524
A	1381	ALA	-	expression tag	UNP P39524
A	1382	SER	-	expression tag	UNP P39524
A	1383	ALA	-	expression tag	UNP P39524

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1384	PRO	-	expression tag	UNP P39524
A	1385	ALA	-	expression tag	UNP P39524
A	1386	ALA	-	expression tag	UNP P39524
A	1387	ALA	-	expression tag	UNP P39524
A	1388	ALA	-	expression tag	UNP P39524
A	1389	PRO	-	expression tag	UNP P39524
A	1390	ALA	-	expression tag	UNP P39524
A	1391	GLY	-	expression tag	UNP P39524
A	1392	ALA	-	expression tag	UNP P39524
A	1393	GLY	-	expression tag	UNP P39524
A	1394	THR	-	expression tag	UNP P39524
A	1395	PRO	-	expression tag	UNP P39524
A	1396	VAL	-	expression tag	UNP P39524
A	1397	THR	-	expression tag	UNP P39524
A	1398	ALA	-	expression tag	UNP P39524
A	1399	PRO	-	expression tag	UNP P39524
A	1400	LEU	-	expression tag	UNP P39524
A	1401	ALA	-	expression tag	UNP P39524
A	1402	GLY	-	expression tag	UNP P39524
A	1403	THR	-	expression tag	UNP P39524
A	1404	ILE	-	expression tag	UNP P39524
A	1405	TRP	-	expression tag	UNP P39524
A	1406	LYS	-	expression tag	UNP P39524
A	1407	VAL	-	expression tag	UNP P39524
A	1408	LEU	-	expression tag	UNP P39524
A	1409	ALA	-	expression tag	UNP P39524
A	1410	SER	-	expression tag	UNP P39524
A	1411	GLU	-	expression tag	UNP P39524
A	1412	GLY	-	expression tag	UNP P39524
A	1413	GLN	-	expression tag	UNP P39524
A	1414	THR	-	expression tag	UNP P39524
A	1415	VAL	-	expression tag	UNP P39524
A	1416	ALA	-	expression tag	UNP P39524
A	1417	ALA	-	expression tag	UNP P39524
A	1418	GLY	-	expression tag	UNP P39524
A	1419	GLU	-	expression tag	UNP P39524
A	1420	VAL	-	expression tag	UNP P39524
A	1421	LEU	-	expression tag	UNP P39524
A	1422	LEU	-	expression tag	UNP P39524
A	1423	ILE	-	expression tag	UNP P39524
A	1424	LEU	-	expression tag	UNP P39524
A	1425	GLU	-	expression tag	UNP P39524

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	339	2754	1785	454	504	11	0	0

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

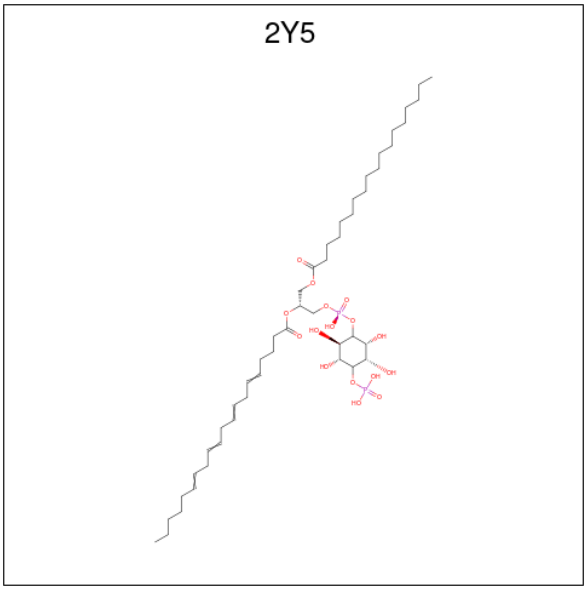
- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

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

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

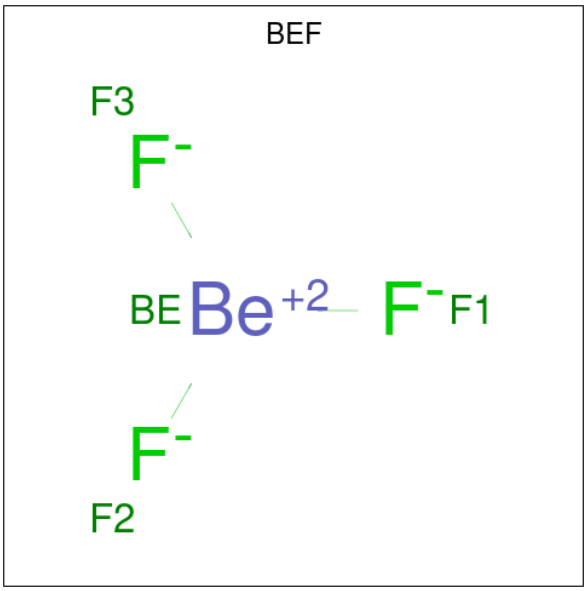
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
5	A	1	1	1	0

- Molecule 6 is (2R)-1-{[(R)-hydroxy{[(1R,2R,3R,4R,5S,6R)-2,3,5,6-tetrahydroxy-4-(phosphonooxy)cyclohexyl]oxy}phosphoryl]oxy}-3-(octadecanoyloxy)propan-2-yl (5Z,8Z,11Z,14Z)-icosa-5,8,11,14-tetraenoate (CCD ID: 2Y5) (formula: $C_{47}H_{84}O_{16}P_2$) (labeled as "Ligand of Interest" by depositor).



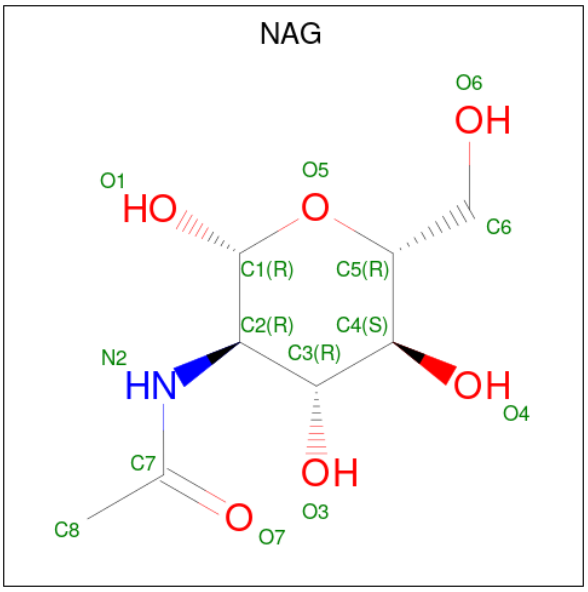
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
6	A	1	65	47	16	2	0

- Molecule 7 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	Be	F	
7	A	1	4	1	3	0

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 9 is water.

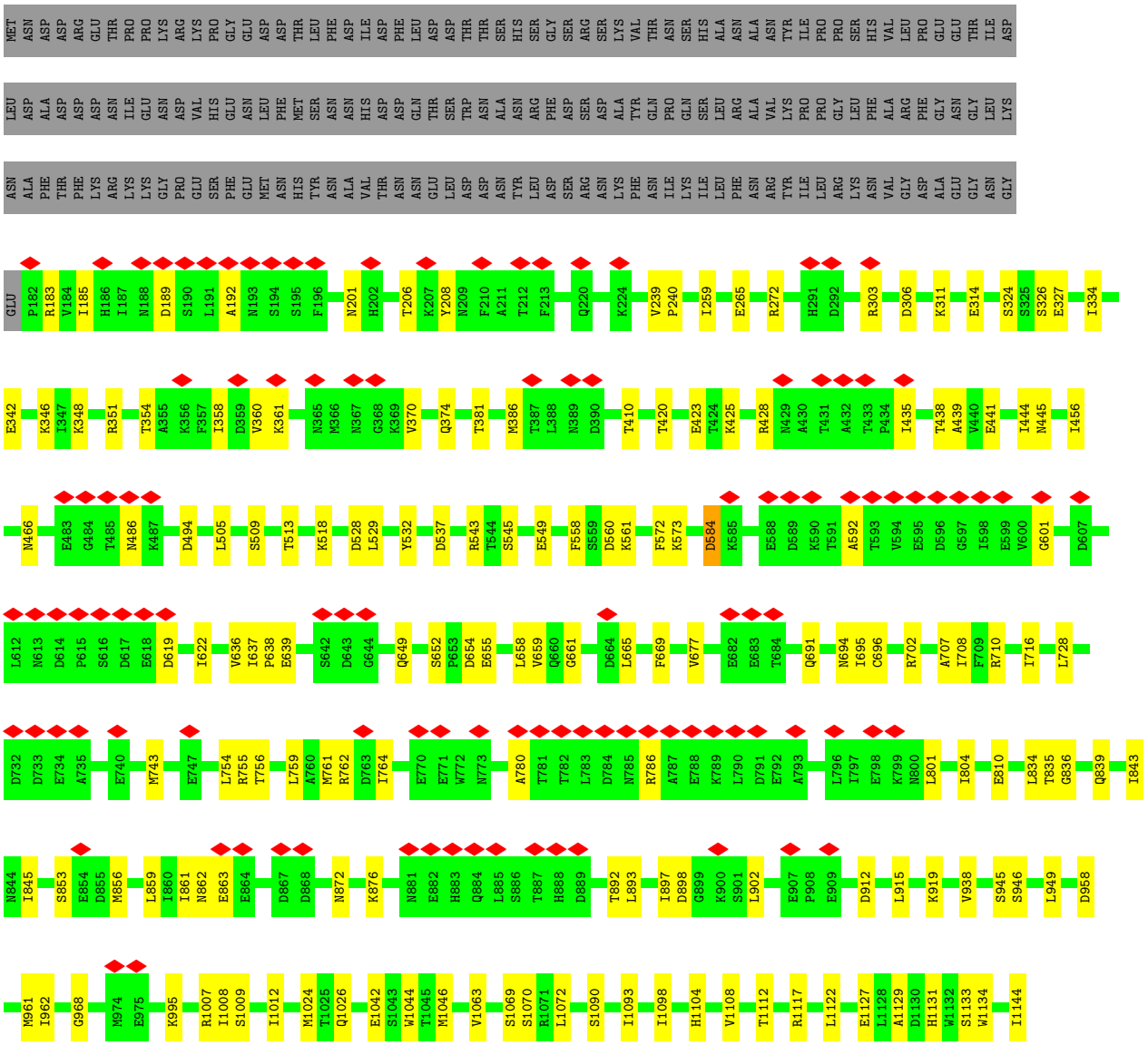
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
9	A	2	2	2	0

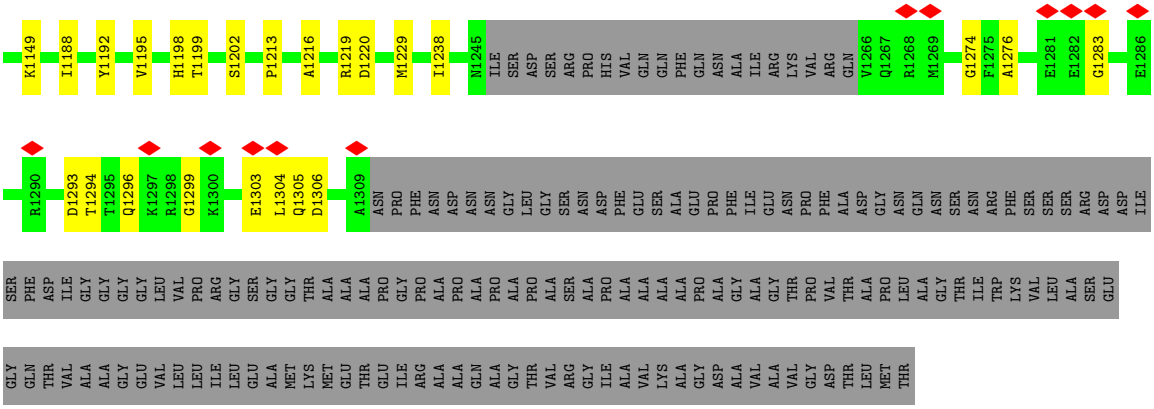
3 Residue-property plots (i)

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

- Molecule 1: Probable phospholipid-transporting ATPase DRS2

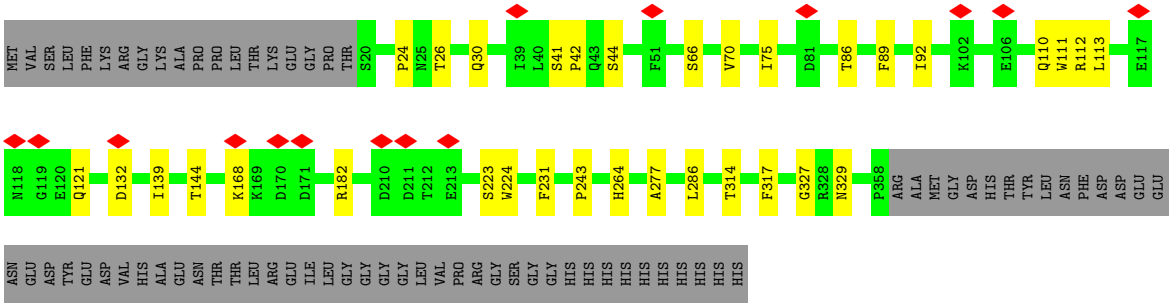
Chain A: 9% 63% 13% 24%





• Molecule 2: Cell division control protein 50

Chain C:

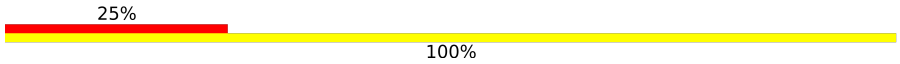


• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

• 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

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	78981	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.201	Depositor
Minimum map value	-0.128	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	275.712, 275.712, 275.712	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.077, 1.077, 1.077	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, BEF, BMA, NAG, MG

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	0.35	0/9048	0.59	3/12259 (0.0%)
2	C	0.35	0/2828	0.55	0/3835
All	All	0.35	0/11876	0.58	3/16094 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1283	GLY	N-CA-C	-5.73	105.83	115.80
1	A	560	ASP	N-CA-C	-5.29	100.40	108.76
1	A	1192	TYR	CA-CB-CG	5.19	123.25	113.90

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	8857	0	8865	111	0
2	C	2754	0	2749	20	0
3	B	28	0	25	0	0
4	D	50	0	43	0	0
5	A	1	0	0	0	0
6	A	65	0	79	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	4	0	0	0	0
8	C	14	0	13	0	0
9	A	2	0	0	0	0
All	All	11775	0	11774	128	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 128 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:183:ARG:H	1:A:374:GLN:HE22	1.45	0.63
1:A:423:GLU:HA	1:A:428:ARG:HD3	1.82	0.61
1:A:938:VAL:HG13	1:A:949:LEU:HD11	1.81	0.61
1:A:1026:GLN:NE2	1:A:1046:MET:SD	2.73	0.61
1:A:716:ILE:HG13	1:A:764:ILE:HG23	1.84	0.60

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	1104/1460 (76%)	1047 (95%)	57 (5%)	0	100	100
2	C	337/413 (82%)	321 (95%)	16 (5%)	0	100	100
All	All	1441/1873 (77%)	1368 (95%)	73 (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	970/1253 (77%)	967 (100%)	3 (0%)	86	83
2	C	309/370 (84%)	309 (100%)	0	100	100
All	All	1279/1623 (79%)	1276 (100%)	3 (0%)	85	86

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	435	ILE
1	A	584	ASP
1	A	898	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	30	GLN
2	C	299	GLN
2	C	161	GLN
1	A	814	GLN
1	A	1100	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)

6 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	3,2	14,14,15	0.38	0	17,19,21	0.73	1 (5%)
3	NAG	B	2	3	14,14,15	0.38	0	17,19,21	0.36	0
4	NAG	D	1	2,4	14,14,15	1.02	1 (7%)	17,19,21	0.75	0
4	NAG	D	2	4	14,14,15	0.22	0	17,19,21	1.16	2 (11%)
4	BMA	D	3	4	11,11,12	1.01	0	15,15,17	1.02	2 (13%)
4	BMA	D	4	4	11,11,12	0.94	1 (9%)	15,15,17	1.22	1 (6%)

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	3,2	-	4/6/23/26	0/1/1/1
3	NAG	B	2	3	-	1/6/23/26	0/1/1/1
4	NAG	D	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	3/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	BMA	D	4	4	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	NAG	O5-C1	-3.51	1.38	1.43
4	D	4	BMA	C1-C2	2.06	1.56	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	2	NAG	C2-N2-C7	3.16	127.40	122.90
4	D	4	BMA	C1-O5-C5	2.89	116.11	112.19
3	B	1	NAG	C1-O5-C5	2.38	115.42	112.19

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Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	3	BMA	C2-C3-C4	2.10	114.52	110.89
4	D	3	BMA	O2-C2-C3	-2.05	106.03	110.14

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

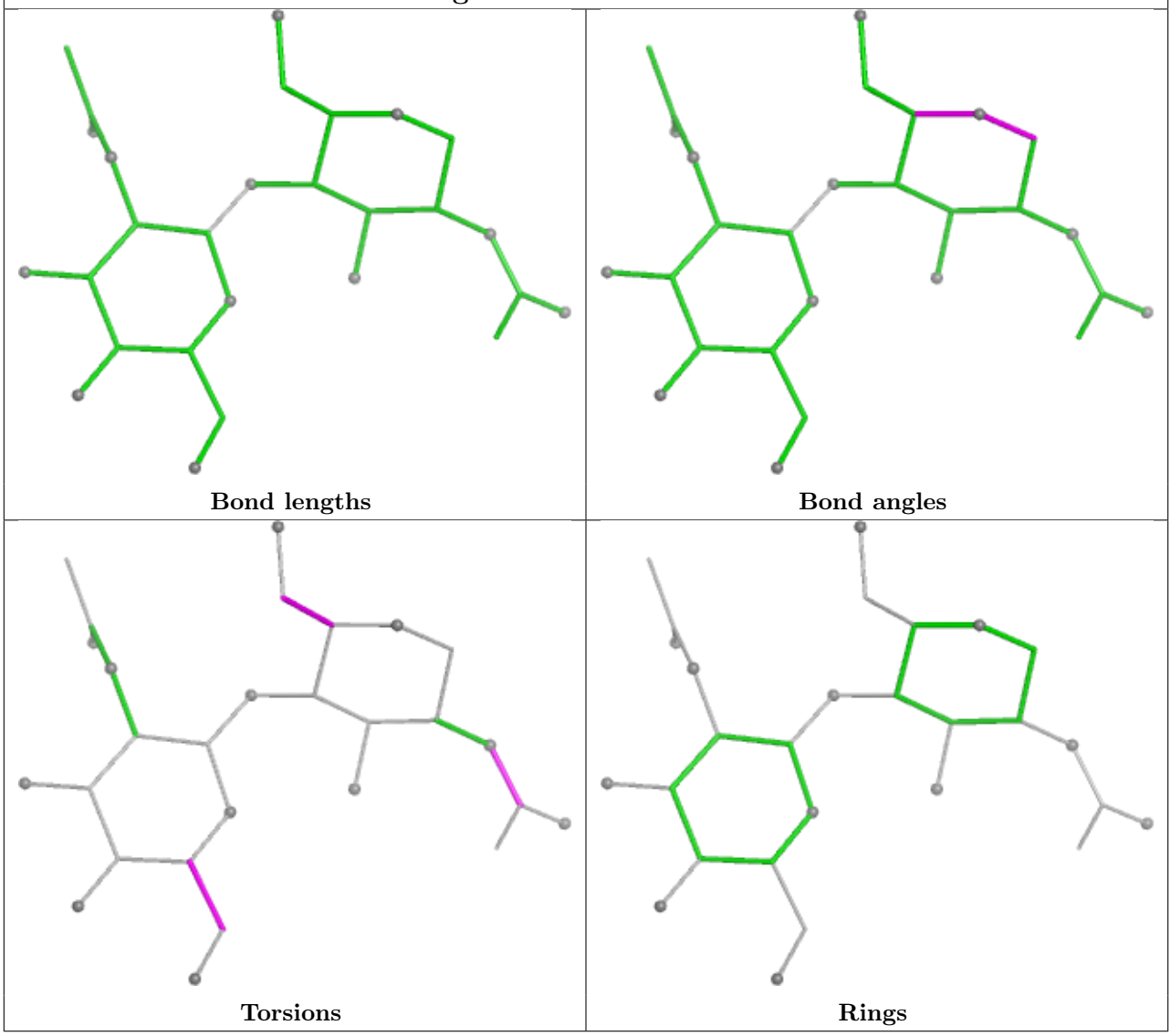
Mol	Chain	Res	Type	Atoms
4	D	4	BMA	O5-C5-C6-O6
4	D	4	BMA	C4-C5-C6-O6
3	B	1	NAG	C8-C7-N2-C2
3	B	1	NAG	O7-C7-N2-C2
4	D	1	NAG	O5-C5-C6-O6

There are no ring outliers.

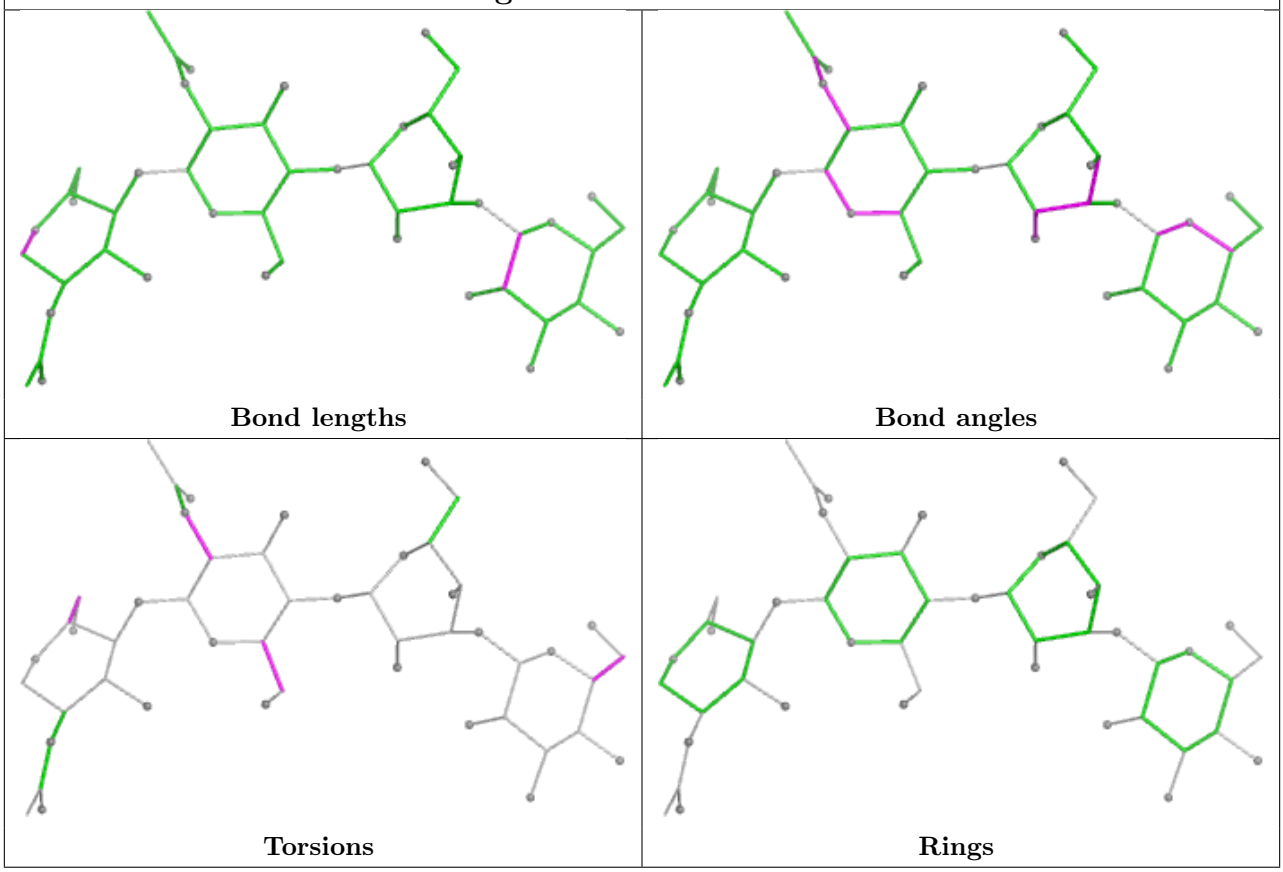
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain B



Oligosaccharide Chain D



5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	BEF	A	1503	1	0,3,3	-	-	-		
6	2Y5	A	1502	1	65,65,65	0.94	5 (7%)	77,80,80	1.14	5 (6%)
8	NAG	C	501	2	14,14,15	0.38	0	17,19,21	0.57	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
6	2Y5	A	1502	1	-	27/61/85/85	0/1/1/1
8	NAG	C	501	2	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1502	2Y5	P4-O4	3.02	1.65	1.59
6	A	1502	2Y5	O18-C11	2.54	1.40	1.33
6	A	1502	2Y5	O16-C8	-2.45	1.40	1.46
6	A	1502	2Y5	O16-C10	2.31	1.40	1.34
6	A	1502	2Y5	O18-C9	-2.13	1.40	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	1502	2Y5	C5-C4-C3	3.76	116.27	110.85
6	A	1502	2Y5	O16-C10-C12	3.75	119.58	111.50
6	A	1502	2Y5	C3-C2-C1	3.19	116.97	109.68
6	A	1502	2Y5	C2-C3-C4	3.06	116.68	109.68
6	A	1502	2Y5	O18-C11-C31	2.90	121.02	111.91

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1502	2Y5	C4-O4-P4-O43
6	A	1502	2Y5	O19-C11-O18-C9
6	A	1502	2Y5	O17-C10-O16-C8
6	A	1502	2Y5	C31-C11-O18-C9
6	A	1502	2Y5	C12-C10-O16-C8

There are no ring outliers.

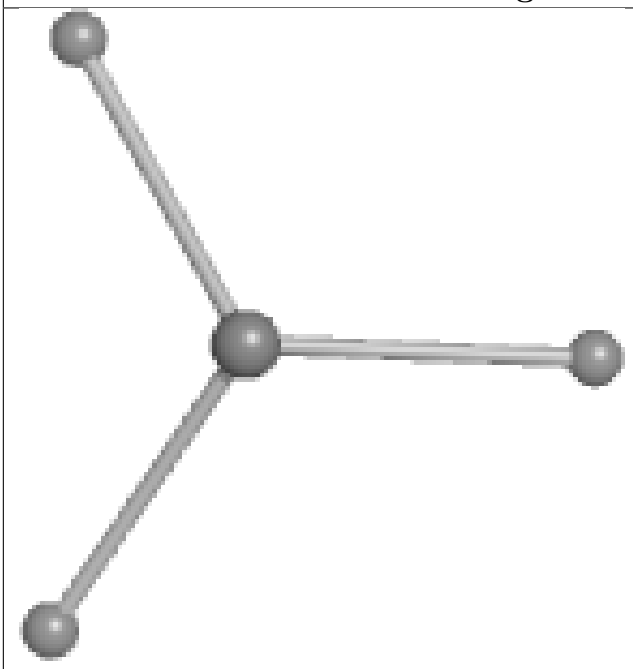
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1502	2Y5	2	0

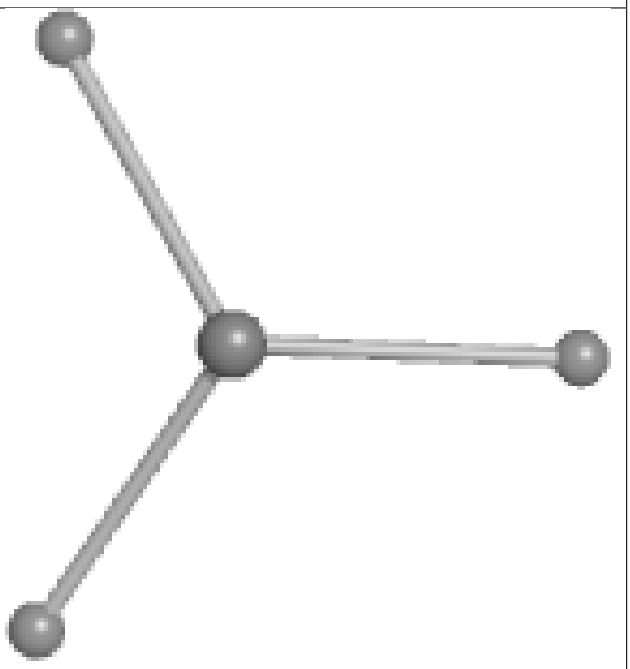
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

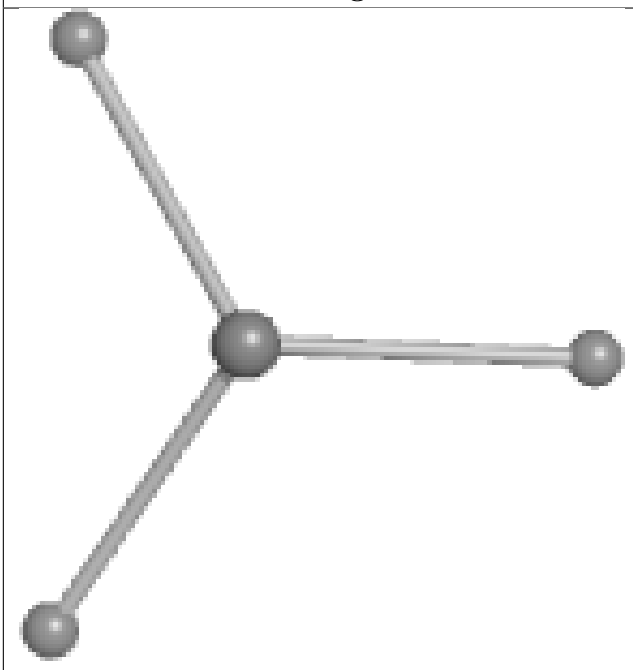
Ligand BEF A 1503



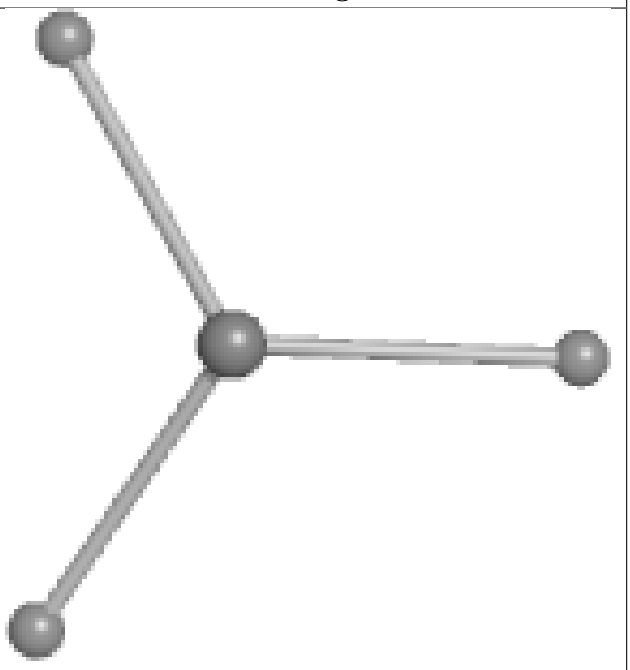
Bond lengths



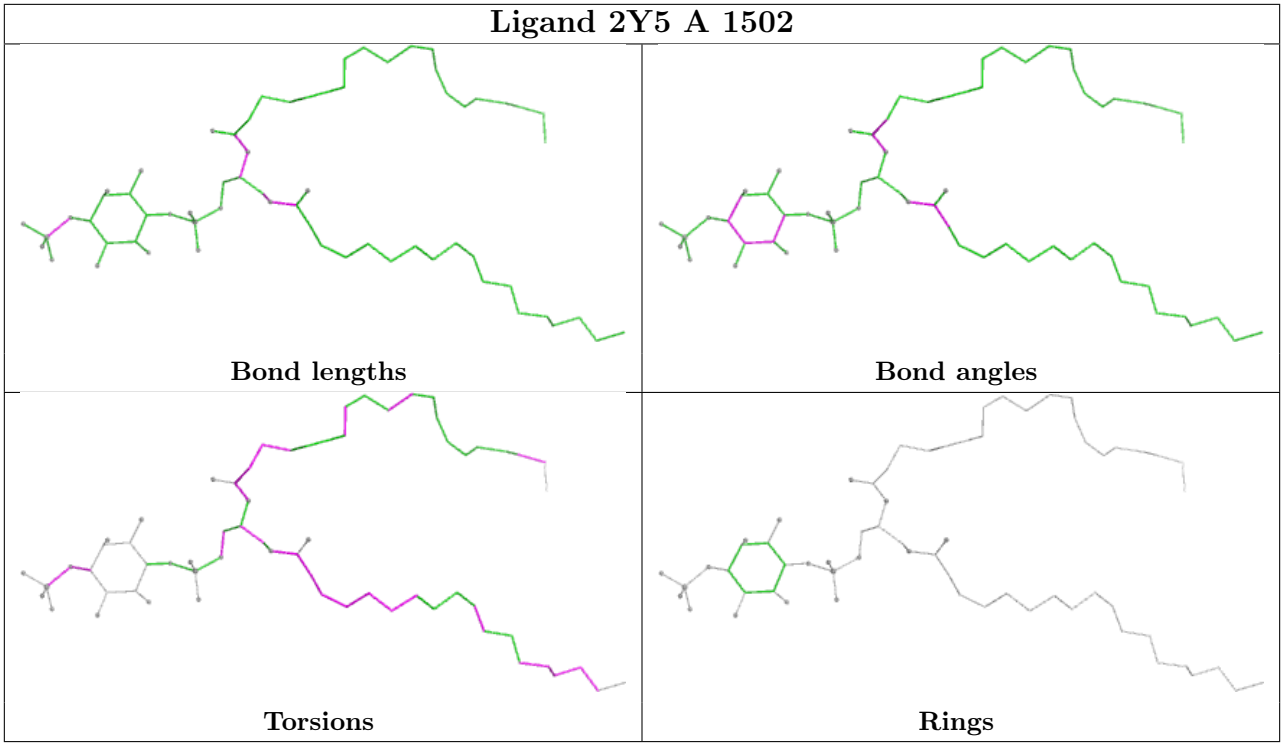
Bond angles



Torsions



Rings



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)

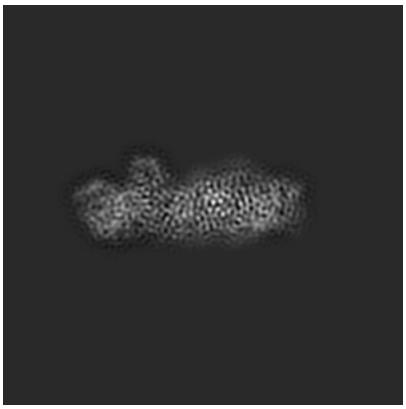
This section contains visualisations of the EMDB entry EMD-4973. These allow visual inspection of the internal detail of the map and identification of artifacts.

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.

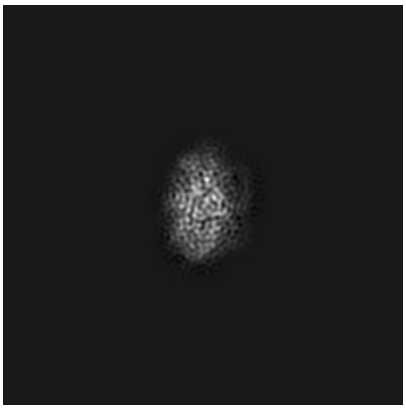
6.1 Orthogonal projections (i)

6.1.1 Primary map

X

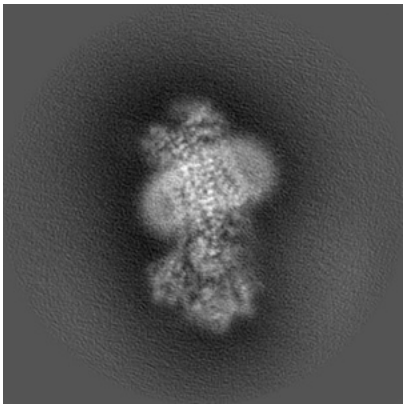


Y

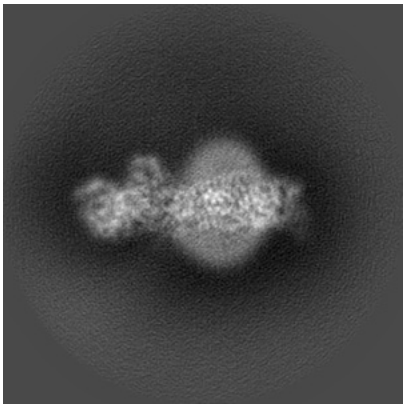


Z

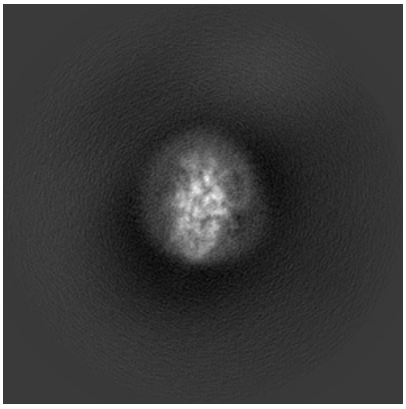
6.1.2 Raw map



X



Y



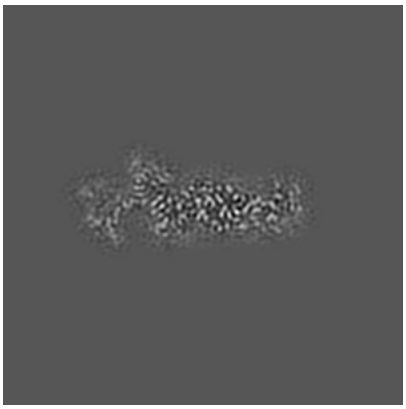
Z

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

6.2 Central slices (i)

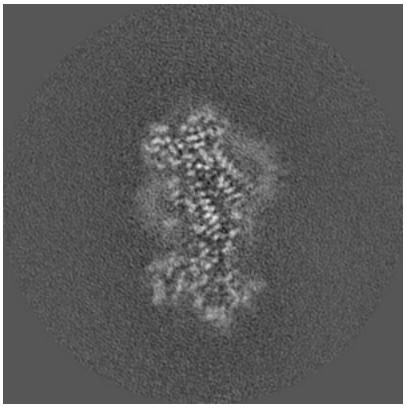
6.2.1 Primary map

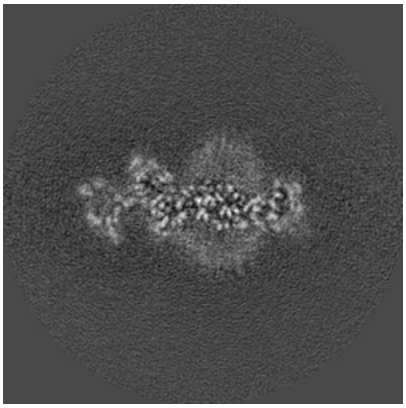
X Index: 128

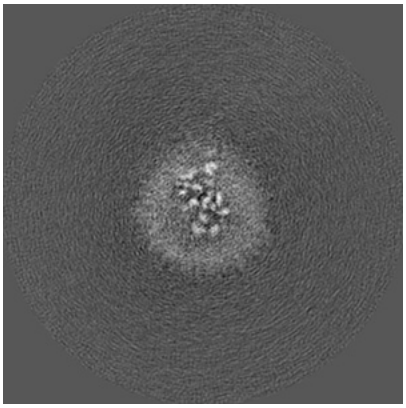

Y Index: 128

Z Index: 128

6.2.2 Raw map


X Index: 128


Y Index: 128

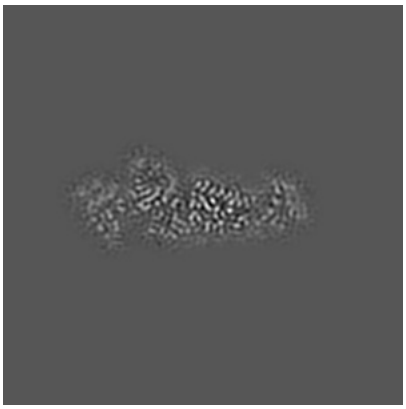

Z Index: 128

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

6.3 Largest variance slices (i)

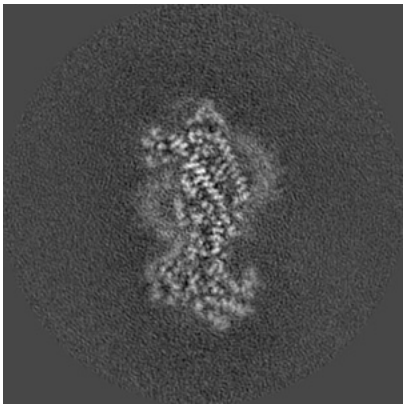
6.3.1 Primary map

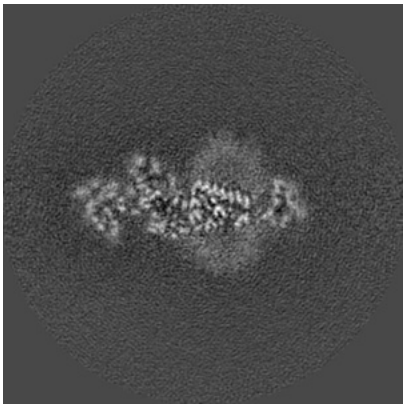
X Index: 125

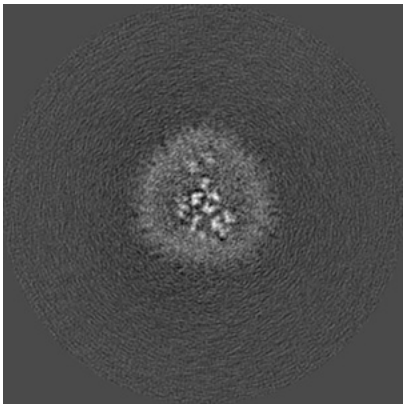

Y Index: 131

Z Index: 151

6.3.2 Raw map


X Index: 123

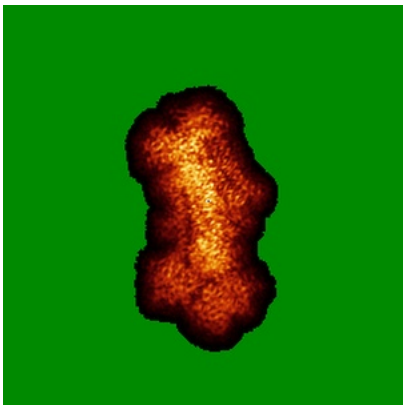

Y Index: 132

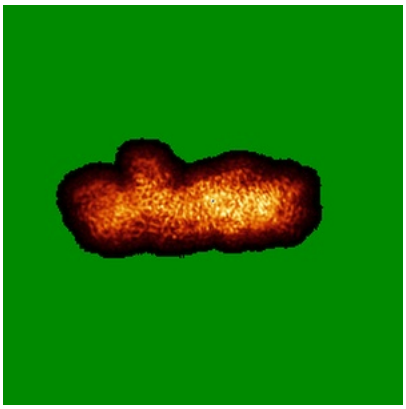

Z Index: 140

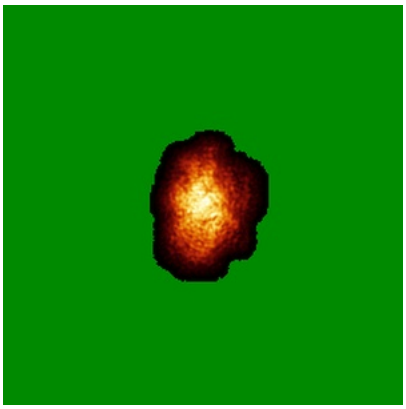
The images above show the largest variance slices of the map in three orthogonal directions.

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

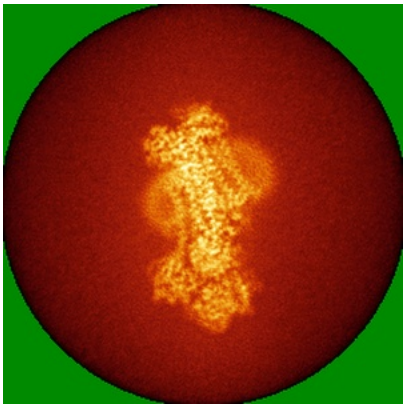
6.4.1 Primary map

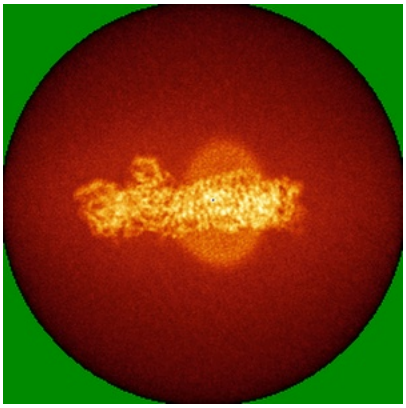

X

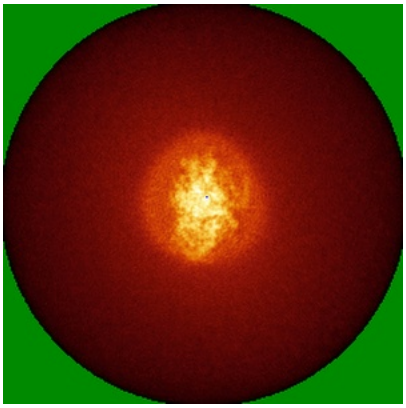

Y


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.

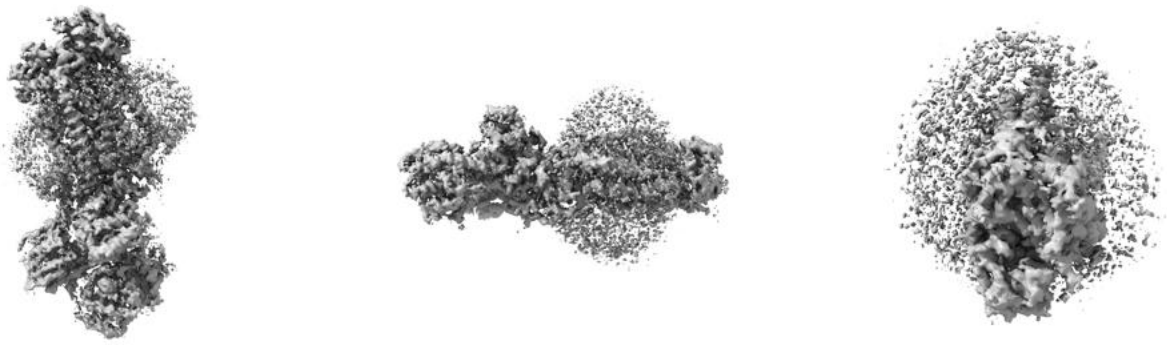
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

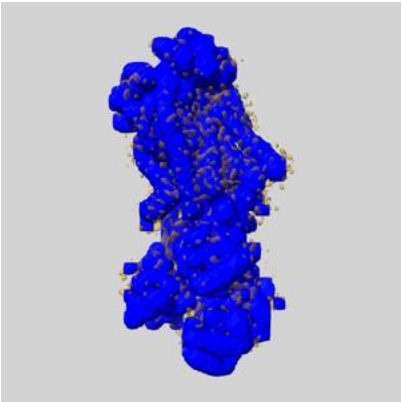
6.6 Mask visualisation (i)

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

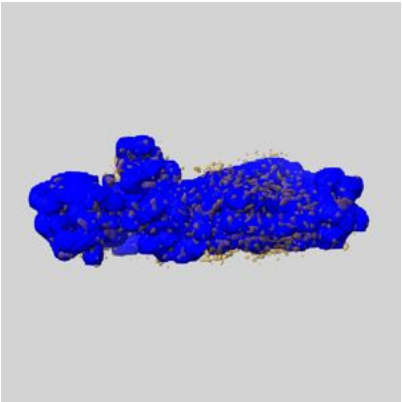
A mask typically either:

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

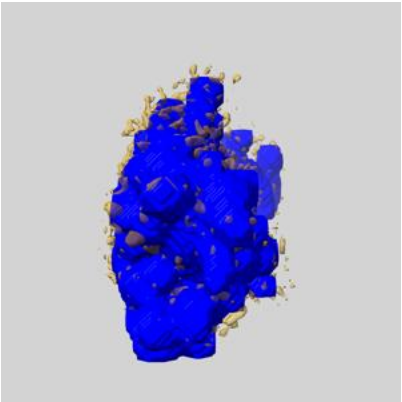
6.6.1 emd_4973_msk_1.map (i)



X



Y

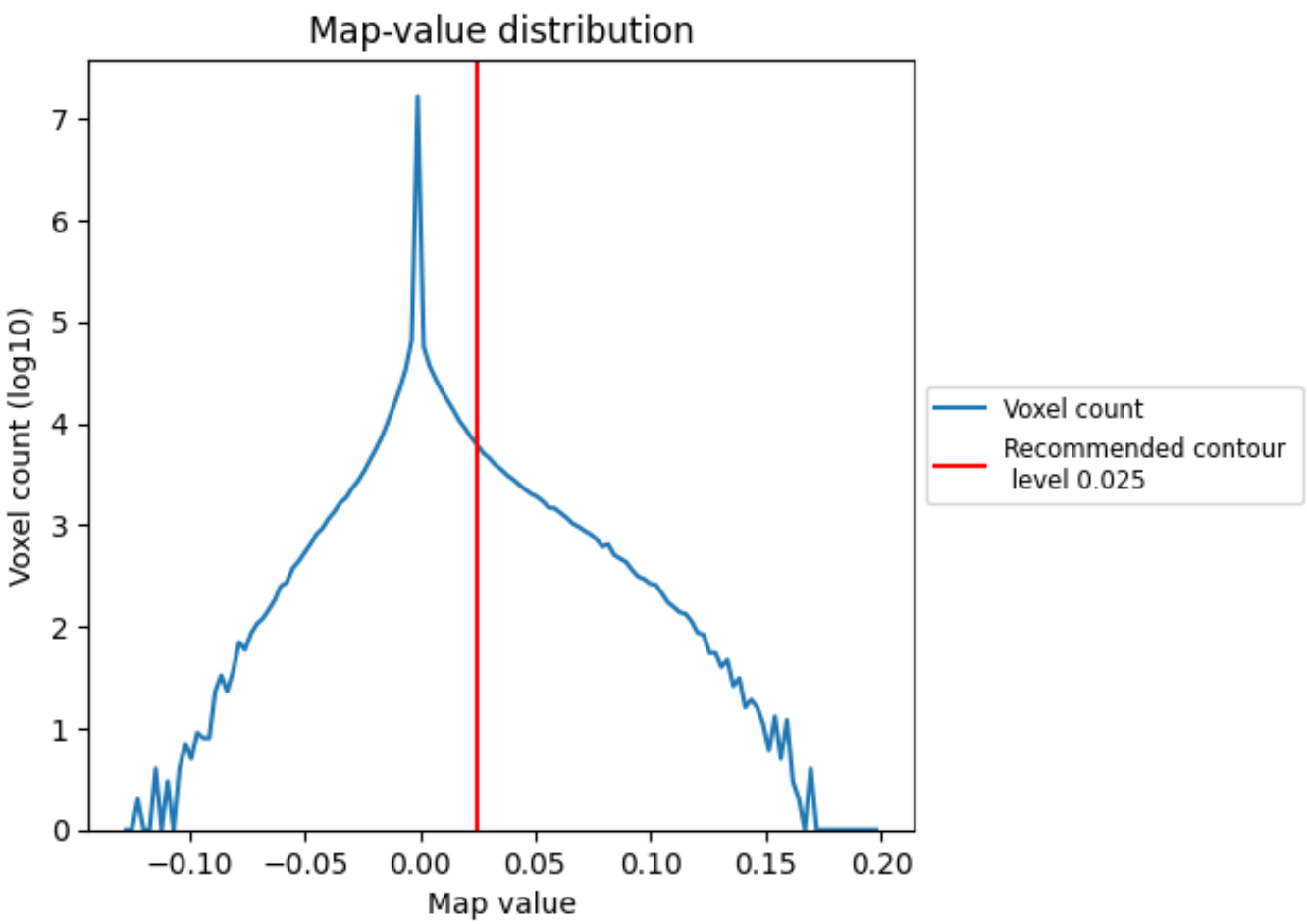


Z

7 Map analysis (i)

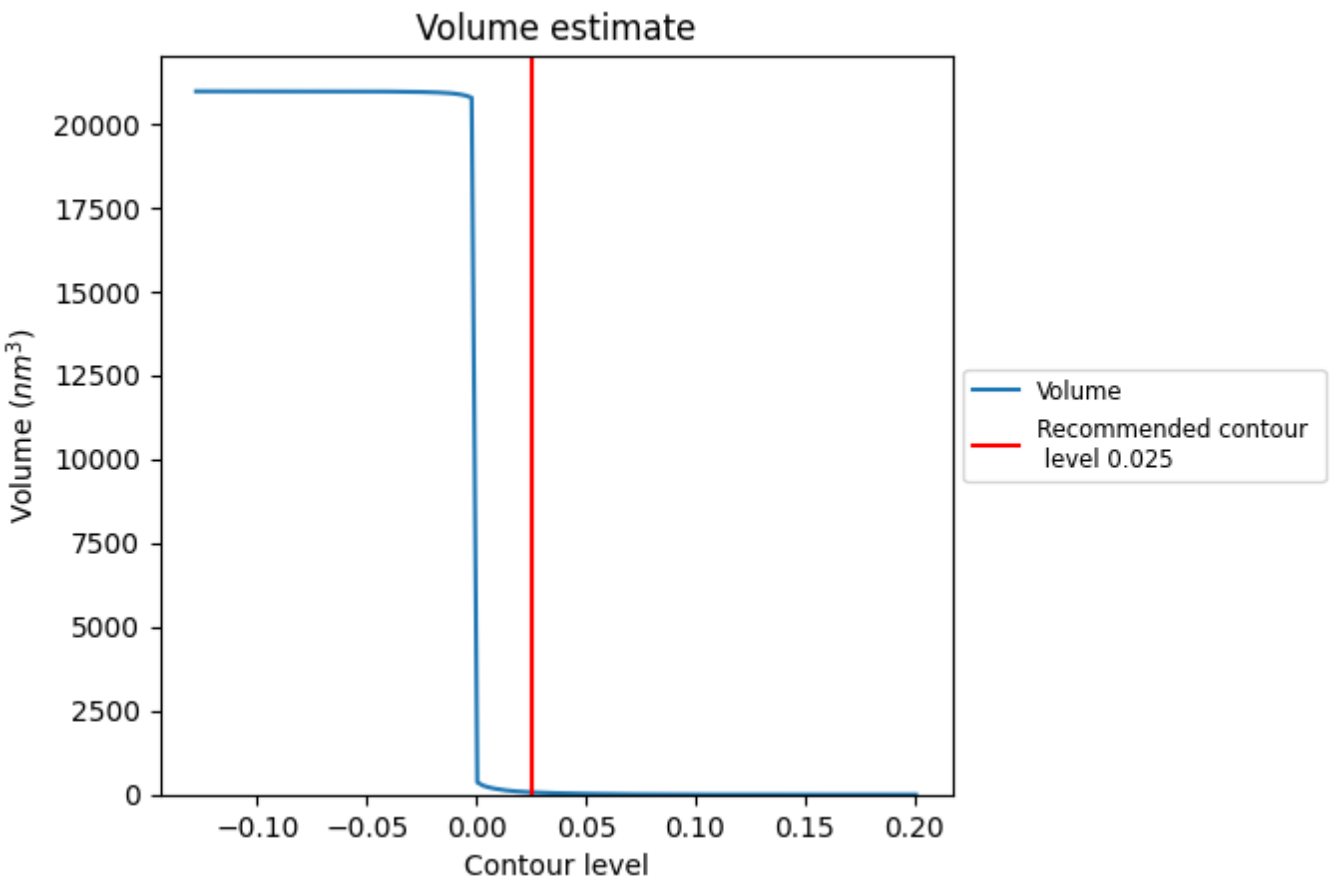
This section contains the results of statistical analysis of the map.

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.

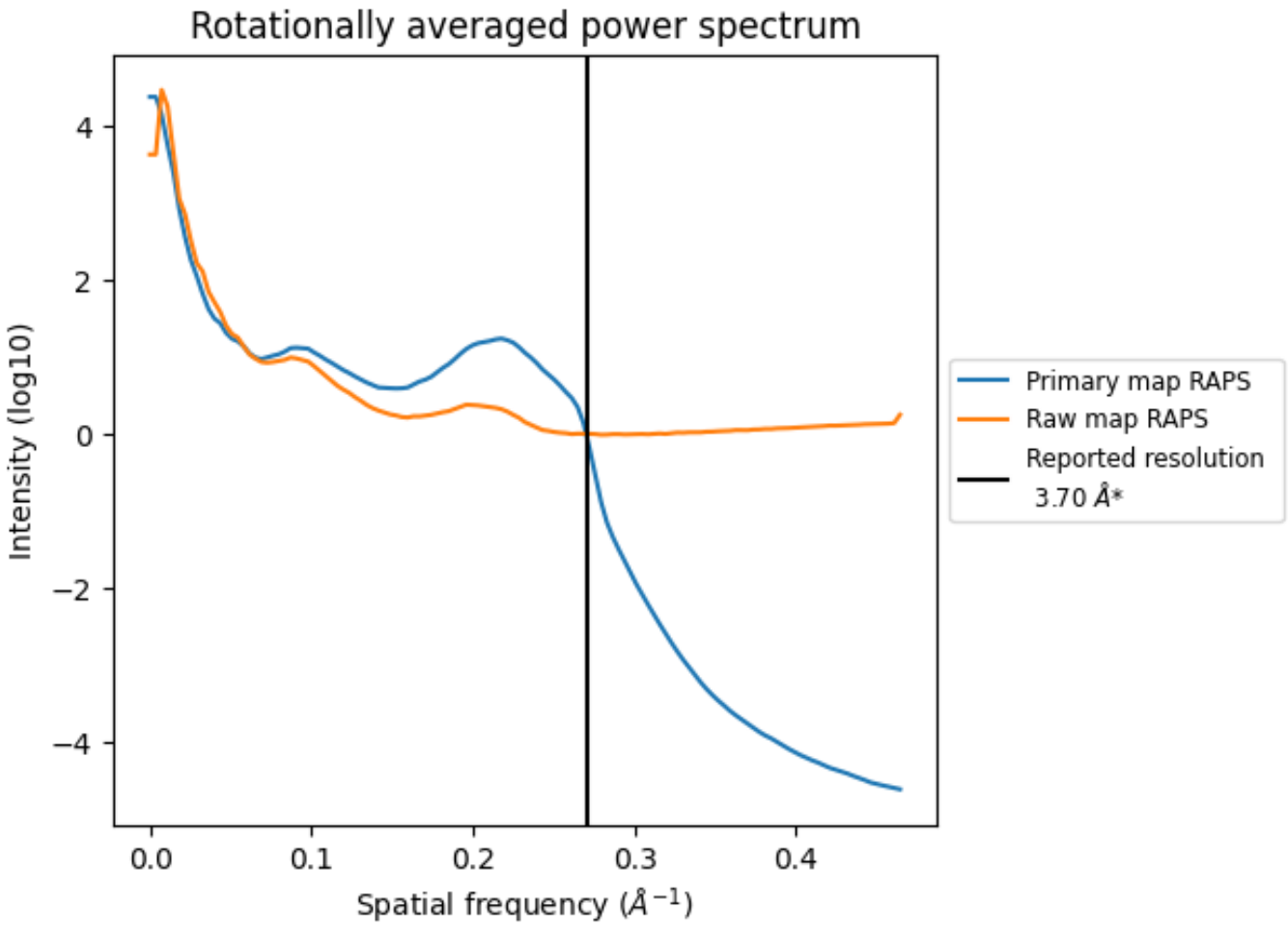
7.2 Volume estimate (i)



The volume at the recommended contour level is 68 nm^3; this corresponds to an approximate mass of 62 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)

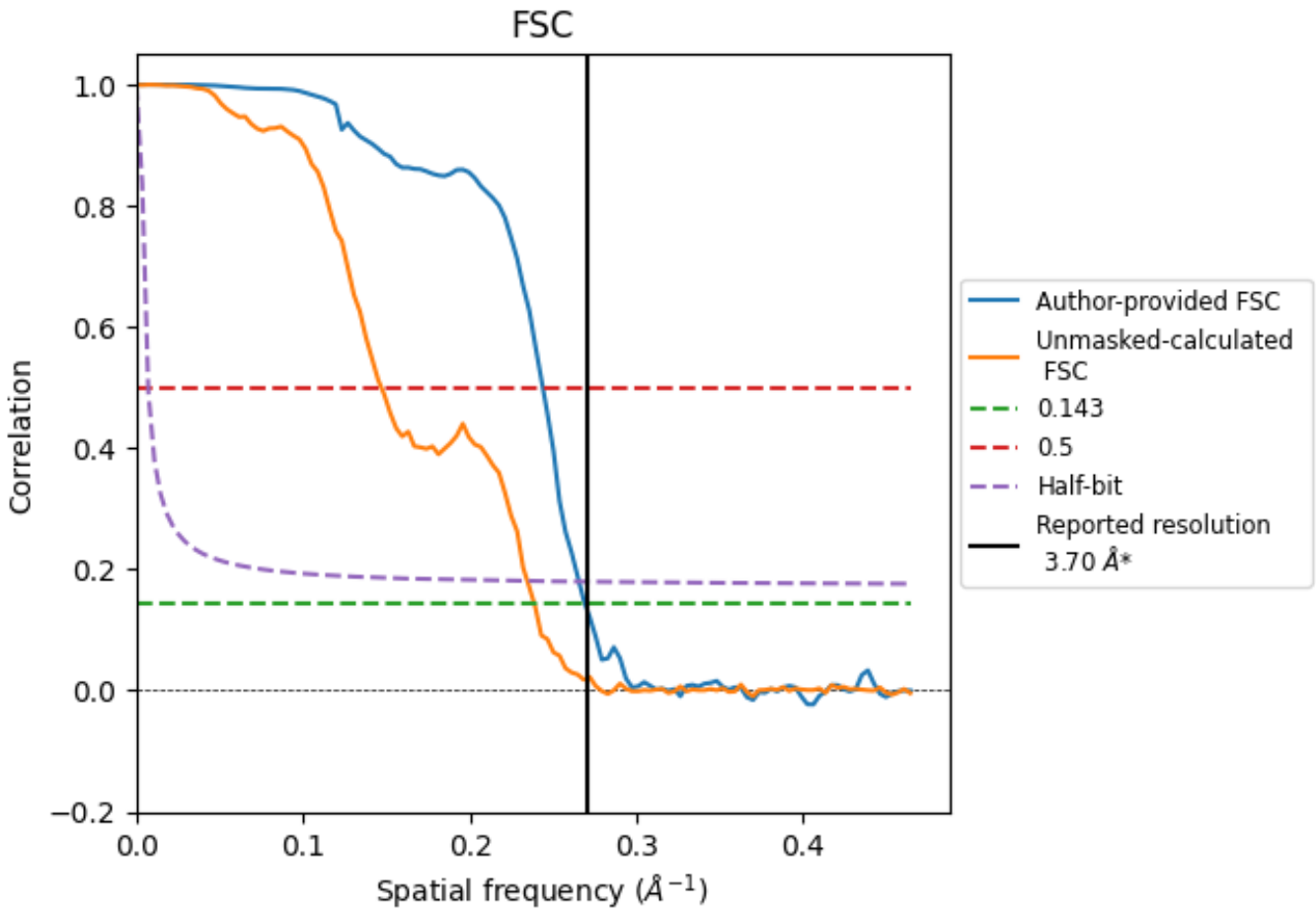


*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

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 0.270 Å^{-1}

8.2 Resolution estimates (i)

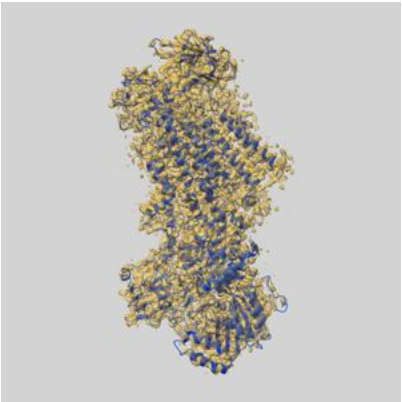
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.71	4.10	3.77
Unmasked-calculated*	4.19	6.80	4.26

*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 4.19 differs from the reported value 3.7 by more than 10 %

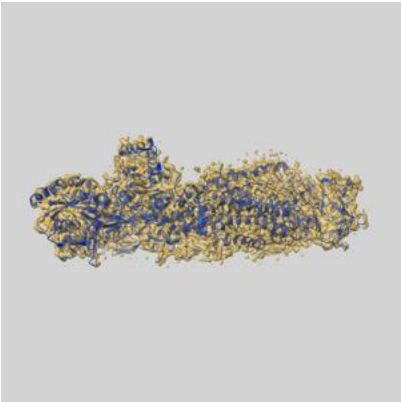
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4973 and PDB model 6ROI. Per-residue inclusion information can be found in section 3 on page 10.

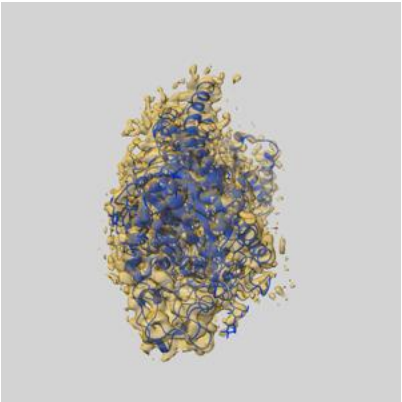
9.1 Map-model overlay (i)



X



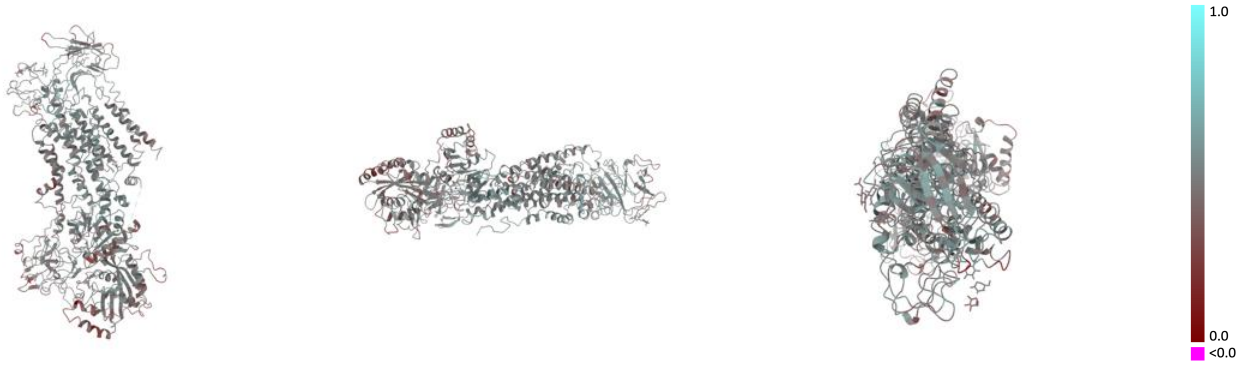
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



X Y Z

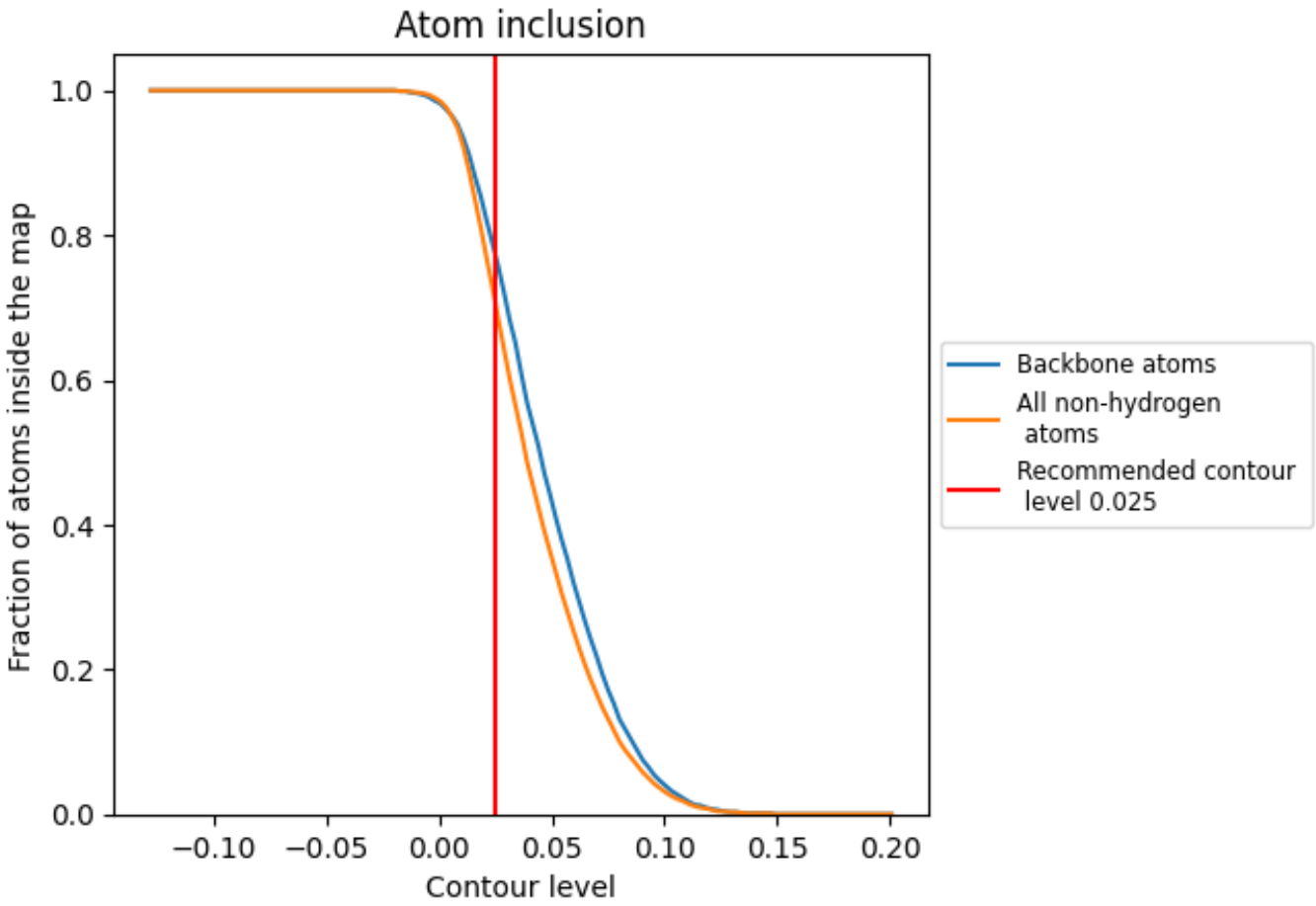
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)

X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7070	0.4720
A	0.6930	0.4670
B	0.5000	0.4220
C	0.7620	0.4860
D	0.6400	0.4800