

wwPDB EM Validation Summary Report (i)

Jan 28, 2024 – 12:12 AM JST

PDB ID : 8WO7

EMDB ID : EMD-37681

Title : Apo state of Arabidopsis AZG1 T440Y

Authors : Xu, L.; Guo, J. Deposited on : 2023-10-06

Resolution : 2.90 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.dev70

Mogul : 1.8.5 (274361), CSD as541be (2020)

MolProbity: 4.02b-467

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)

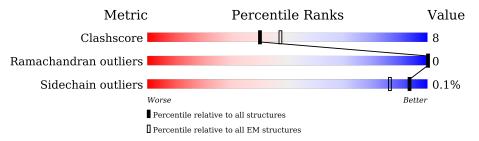
 $\begin{tabular}{lll} Validation Pipeline (wwPDB-VP) & : & 2.36 \end{tabular}$

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 2.90 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 $(\# \mathrm{Entries})$	${ m EM\ structures} \ (\#{ m Entries})$
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 <=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	615	72%	16% 12%				
1	В	615	73%	14% 12%				
2	С	2	50% 50%	50%				
2	D	2	50% 50%	50%				



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8118 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 Adenine/guanine permease AZG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	540	Total 4031	C 2629		O 725	S 26	0	0
1	В	540	Total 4031	C 2629	N 651	O 725	S 26	0	0

There are 74 discrepancies between the modelled and reference sequences:

Chain Residue Modelled Actual Comment Reference A 440 TYR THR engineered mutation UNP Q9SRK7 A 580 SER - expression tag UNP Q9SRK7 A 581 GLY - expression tag UNP Q9SRK7 A 582 ARG - expression tag UNP Q9SRK7 A 583 ASP - expression tag UNP Q9SRK7 A 584 TYR - expression tag UNP Q9SRK7 A 585 LYS - expression tag UNP Q9SRK7 A 586 ASP - expression tag UNP Q9SRK7 A 588 ASP - expression tag UNP Q9SRK7 A 589 ASP - expression tag UNP Q9SRK7 A 590 LYS - expression tag UNP Q9SRK7 A 591 TRP - expression tag <th></th> <th>-</th> <th></th> <th></th> <th>~</th> <th></th>		-			~	
A 580 SER - expression tag UNP Q9SRK7 A 581 GLY - expression tag UNP Q9SRK7 A 582 ARG - expression tag UNP Q9SRK7 A 583 ASP - expression tag UNP Q9SRK7 A 584 TYR - expression tag UNP Q9SRK7 A 585 LYS - expression tag UNP Q9SRK7 A 586 ASP - expression tag UNP Q9SRK7 A 588 ASP - expression tag UNP Q9SRK7 A 589 ASP - expression tag UNP Q9SRK7 A 590 LYS - expression tag UNP Q9SRK7 A 591 TRP - expression tag UNP Q9SRK7 A 592 SER - expression tag UNP Q9SRK7 A 593 HIS - expression tag UNP	Chain	Residue	Modelled	Actual	Comment	Reference
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A 582 ARG - expression tag UNP Q9SRK7 A 583 ASP - expression tag UNP Q9SRK7 A 584 TYR - expression tag UNP Q9SRK7 A 585 LYS - expression tag UNP Q9SRK7 A 586 ASP - expression tag UNP Q9SRK7 A 587 ASP - expression tag UNP Q9SRK7 A 588 ASP - expression tag UNP Q9SRK7 A 589 ASP - expression tag UNP Q9SRK7 A 590 LYS - expression tag UNP Q9SRK7 A 591 TRP - expression tag UNP Q9SRK7 A 592 SER - expression tag UNP Q9SRK7 A 593 HIS - expression tag UNP Q9SRK7 A 594 PRO - expression tag UNP	A	580	SER	-	expression tag	UNP Q9SRK7
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A 587 ASP - expression tag UNP Q9SRK7 A 588 ASP - expression tag UNP Q9SRK7 A 589 ASP - expression tag UNP Q9SRK7 A 590 LYS - expression tag UNP Q9SRK7 A 591 TRP - expression tag UNP Q9SRK7 A 592 SER - expression tag UNP Q9SRK7 A 593 HIS - expression tag UNP Q9SRK7 A 594 PRO - expression tag UNP Q9SRK7 A 595 GLN - expression tag UNP Q9SRK7 A 596 PHE - expression tag UNP Q9SRK7 A 597 GLU - expression tag UNP Q9SRK7 A 599 GLY - expression tag UNP Q9SRK7 A 600 GLY - expression tag UNP	A	585	LYS	-	expression tag	UNP Q9SRK7
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A 594 PRO - expression tag UNP Q9SRK7 A 595 GLN - expression tag UNP Q9SRK7 A 596 PHE - expression tag UNP Q9SRK7 A 597 GLU - expression tag UNP Q9SRK7 A 598 LYS - expression tag UNP Q9SRK7 A 599 GLY - expression tag UNP Q9SRK7 A 600 GLY - expression tag UNP Q9SRK7 A 601 GLY - expression tag UNP Q9SRK7 A 602 GLY - expression tag UNP Q9SRK7 A 603 SER - expression tag UNP Q9SRK7	A	592	SER	-	expression tag	UNP Q9SRK7
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A 597 GLU - expression tag UNP Q9SRK7 A 598 LYS - expression tag UNP Q9SRK7 A 599 GLY - expression tag UNP Q9SRK7 A 600 GLY - expression tag UNP Q9SRK7 A 601 GLY - expression tag UNP Q9SRK7 A 602 GLY - expression tag UNP Q9SRK7 A 603 SER - expression tag UNP Q9SRK7	A	595	GLN	-	expression tag	UNP Q9SRK7
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A 602 GLY - expression tag UNP Q9SRK7 A 603 SER - expression tag UNP Q9SRK7	A	600	GLY	-	expression tag	UNP Q9SRK7
A 603 SER - expression tag UNP Q9SRK7	A	601	GLY	-	expression tag	UNP Q9SRK7
	A	602	GLY	-	expression tag	UNP Q9SRK7
A 604 GLY - expression tag UNP Q9SRK7	A	603	SER	-	expression tag	UNP Q9SRK7
	A	604	GLY	-	expression tag	UNP Q9SRK7

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Chain	Residue	Modelled Modelled	Actual	Comment	Reference
A	605	GLY	-	expression tag	UNP Q9SRK7
A	606	SER	-	expression tag	UNP Q9SRK7
A	607	ALA	-	expression tag	UNP Q9SRK7
A	608	TRP	-	expression tag	UNP Q9SRK7
A	609	SER	-	expression tag	UNP Q9SRK7
A	610	HIS	-	expression tag	UNP Q9SRK7
A	611	PRO	-	expression tag	UNP Q9SRK7
A	612	GLN	-	expression tag	UNP Q9SRK7
A	613	PHE	-	expression tag	UNP Q9SRK7
A	614	GLU	-	expression tag	UNP Q9SRK7
A	615	LYS	-	expression tag	UNP Q9SRK7
В	440	TYR	THR	engineered mutation	UNP Q9SRK7
В	580	SER	-	expression tag	UNP Q9SRK7
В	581	GLY	-	expression tag	UNP Q9SRK7
В	582	ARG	-	expression tag	UNP Q9SRK7
В	583	ASP	-	expression tag	UNP Q9SRK7
В	584	TYR	-	expression tag	UNP Q9SRK7
В	585	LYS	-	expression tag	UNP Q9SRK7
В	586	ASP	-	expression tag	UNP Q9SRK7
В	587	ASP	-	expression tag	UNP Q9SRK7
В	588	ASP	-	expression tag	UNP Q9SRK7
В	589	ASP	_	expression tag	UNP Q9SRK7
В	590	LYS	-	expression tag	UNP Q9SRK7
В	591	TRP	-	expression tag	UNP Q9SRK7
В	592	SER	-	expression tag	UNP Q9SRK7
В	593	HIS	-	expression tag	UNP Q9SRK7
В	594	PRO	-	expression tag	UNP Q9SRK7
В	595	GLN	-	expression tag	UNP Q9SRK7
В	596	PHE	-	expression tag	UNP Q9SRK7
В	597	GLU	-	expression tag	UNP Q9SRK7
В	598	LYS	-	expression tag	UNP Q9SRK7
В	599	GLY	-	expression tag	UNP Q9SRK7
В	600	GLY	-	expression tag	UNP Q9SRK7
В	601	GLY	-	expression tag	UNP Q9SRK7
В	602	GLY	-	expression tag	UNP Q9SRK7
В	603	SER	-	expression tag	UNP Q9SRK7
В	604	GLY	-	expression tag	UNP Q9SRK7
В	605	GLY	-	expression tag	UNP Q9SRK7
В	606	SER	-	expression tag	UNP Q9SRK7
В	607	ALA	-	expression tag	UNP Q9SRK7
В	608	TRP	-	expression tag	UNP Q9SRK7
В	609	SER	-	expression tag	UNP Q9SRK7

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Chain	Residue	Modelled	Actual	Comment	Reference
В	610	HIS	-	expression tag	UNP Q9SRK7
В	611	PRO	-	expression tag	UNP Q9SRK7
В	612	GLN	-	expression tag	UNP Q9SRK7
В	613	PHE	-	expression tag	UNP Q9SRK7
В	614	GLU	-	expression tag	UNP Q9SRK7
В	615	LYS	-	expression tag	UNP Q9SRK7

 \bullet Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



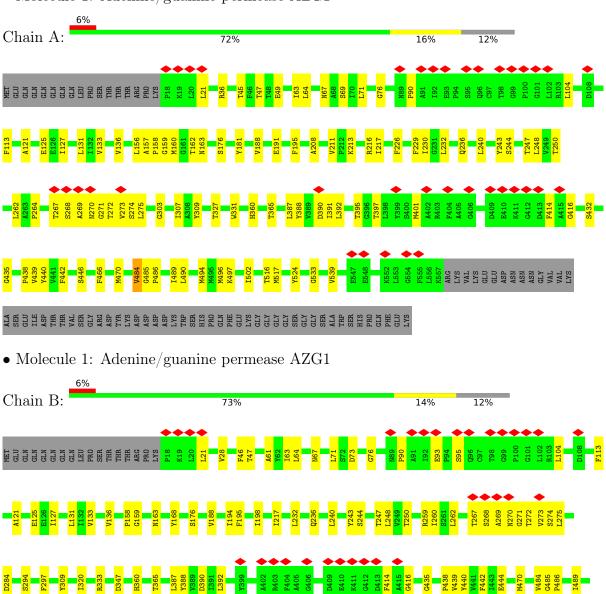
Mol	Chain	Residues	Atoms	AltConf	Trace
2	С	2	Total C N O	0	0
			28 16 2 10		
9	D	9	Total C N O	0	0
2	D	2	28 16 2 10		



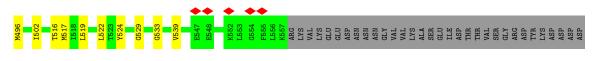
3 Residue-property plots (i)

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: Adenine/guanine permease AZG1







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

Chain C: 50% 50%



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

Chain D: 50% 50%





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1097561	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	52	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.083	Depositor
Minimum map value	-0.050	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	204.24, 204.24, 204.24	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.851, 0.851, 0.851	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: 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	Clasica	Bond	lengths	Bond angles		
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.30	0/4125	0.48	0/5615	
1	В	0.30	0/4125	0.47	0/5615	
All	All	0.30	0/8250	0.48	0/11230	

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 maintain group or atoms of a sidechain that are expected to be planar.

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	484	VAL	Peptide
1	В	484	VAL	Peptide

5.2 Too-close contacts (i)

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4031	0	4106	75	0
1	В	4031	0	4106	60	0
2	С	28	0	25	1	0
2	D	28	0	25	1	0
All	All	8118	0	8262	124	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.

The worst 5 of 124 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:269:ALA:HB3	1:B:90:PRO:HB3	1.65	0.78
1:A:90:PRO:HB3	1:B:269:ALA:HB3	1.67	0.77
1:B:244:SER:HB2	1:B:250:THR:HG23	1.68	0.74
1:B:67:ASN:OD1	1:B:163:ASN:ND2	2.23	0.71
1:A:211:VAL:HG21	1:A:392:LEU:HD21	1.72	0.71

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	Percentil	es
1	A	538/615~(88%)	524 (97%)	14 (3%)	0	100 100	0
1	В	538/615~(88%)	523 (97%)	15 (3%)	0	100 100	0
All	All	1076/1230~(88%)	1047 (97%)	29 (3%)	0	100 100	0

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	429/494 (87%)	428 (100%)	1 (0%)	93 98
1	В	429/494 (87%)	429 (100%)	0	100 100
All	All	858/988 (87%)	857 (100%)	1 (0%)	93 98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	163	ASN
1	A	236	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

4 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond



length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Tuno	Chain	Res	Res Link Bond lengths			Bond angles			
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	С	1	2,1	14,14,15	2.60	7 (50%)	17,19,21	1.42	2 (11%)
2	NAG	С	2	2	14,14,15	2.65	7 (50%)	17,19,21	1.18	2 (11%)
2	NAG	D	1	2,1	14,14,15	2.55	7 (50%)	17,19,21	2.05	6 (35%)
2	NAG	D	2	2	14,14,15	2.72	7 (50%)	17,19,21	1.52	4 (23%)

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
2	NAG	С	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	С	2	2	-	1/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	D	2	NAG	O5-C5	5.46	1.54	1.43
2	С	2	NAG	O5-C5	5.09	1.53	1.43
2	С	1	NAG	O5-C5	4.86	1.53	1.43
2	D	1	NAG	O5-C5	4.73	1.53	1.43
2	С	2	NAG	C2-N2	4.10	1.53	1.46

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
2	D	1	NAG	C4-C3-C2	4.77	118.00	111.02
2	D	1	NAG	C3-C4-C5	3.71	116.86	110.24
2	D	2	NAG	C1-O5-C5	3.37	116.75	112.19
2	D	2	NAG	O5-C5-C6	2.78	111.56	107.20
2	D	2	NAG	C2-N2-C7	-2.51	119.34	122.90

There are no chirality outliers.

All (5) torsion outliers are listed below:



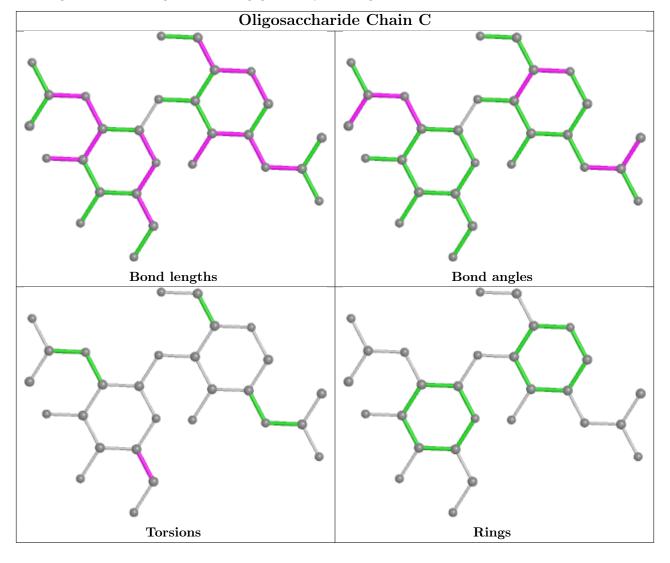
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C4-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	С	2	NAG	O5-C5-C6-O6

There are no ring outliers.

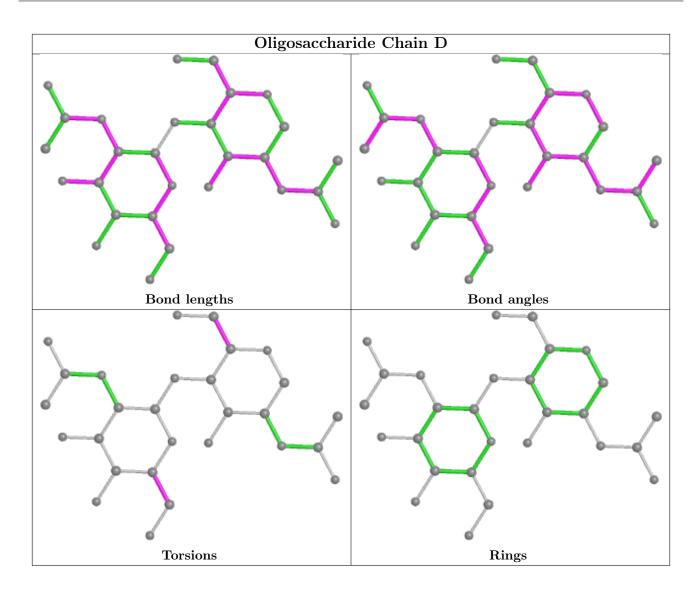
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	NAG	1	0
2	С	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)

There are no ligands in this entry.

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.



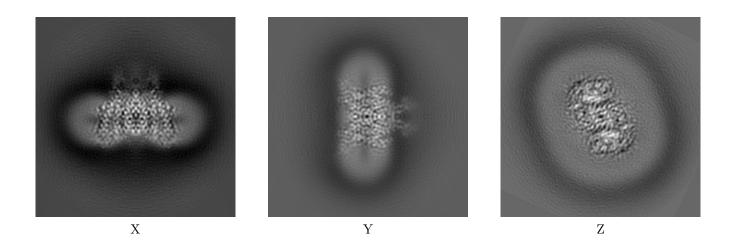
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-37681. These allow visual inspection of the internal detail of the map and identification of artifacts.

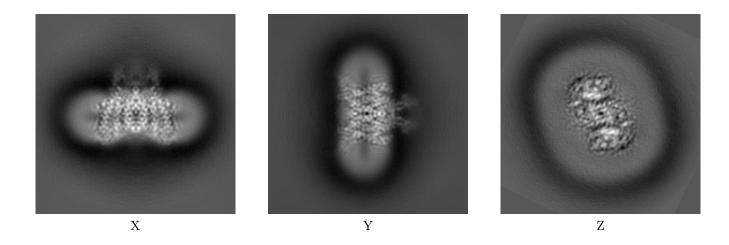
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map

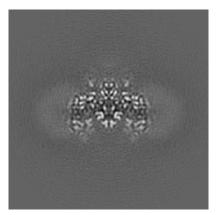


The images above show the map projected in three orthogonal directions.

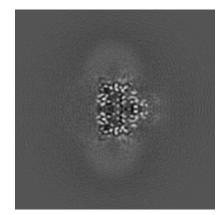


6.2 Central slices (i)

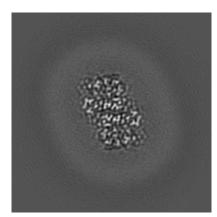
6.2.1 Primary map





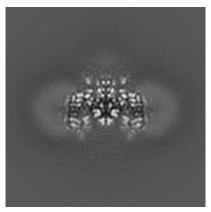


Y Index: 120

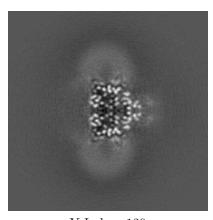


Z Index: 120

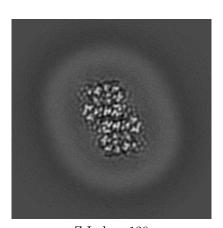
6.2.2 Raw map



X Index: 120



Y Index: 120



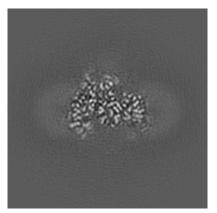
Z Index: 120

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

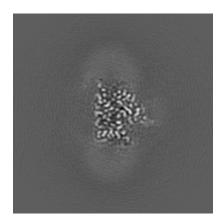


6.3 Largest variance slices (i)

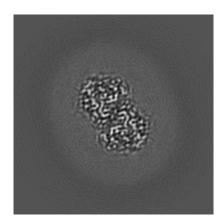
6.3.1 Primary map





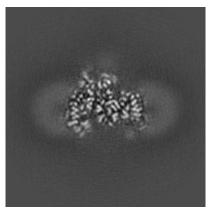


Y Index: 123

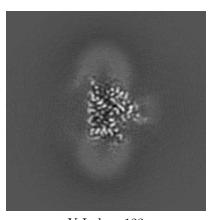


Z Index: 129

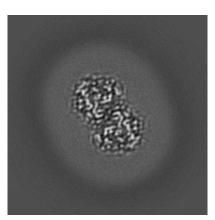
6.3.2 Raw map



X Index: 124



Y Index: 123



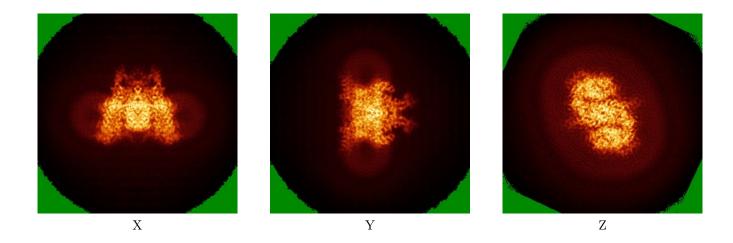
Z Index: 129

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

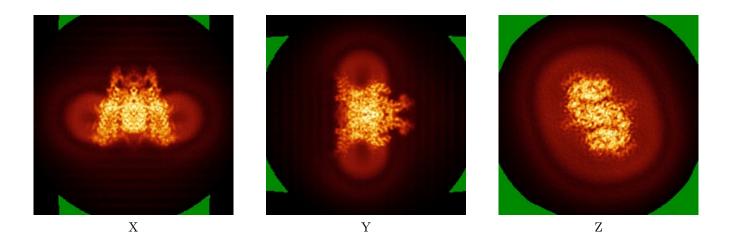


6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



6.4.2 Raw map

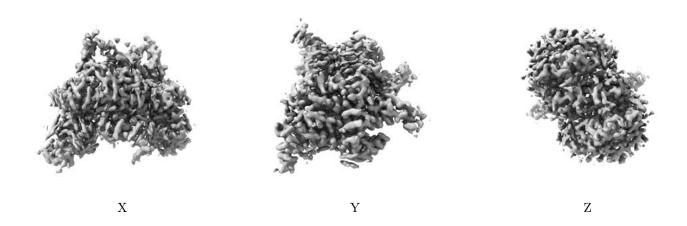


The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

6.6 Mask visualisation (i)

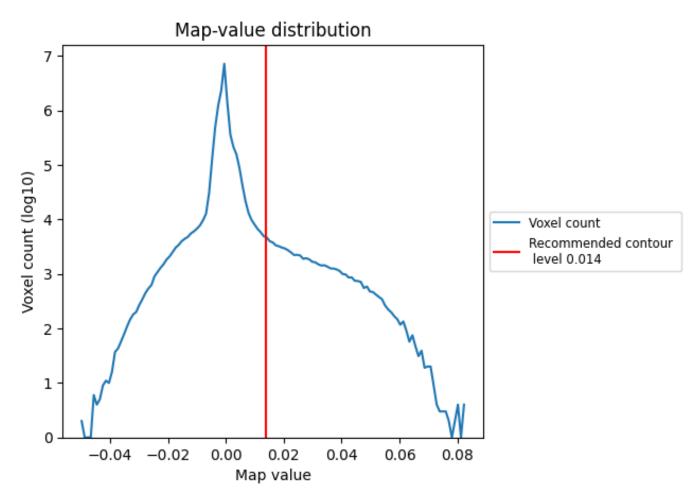
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

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

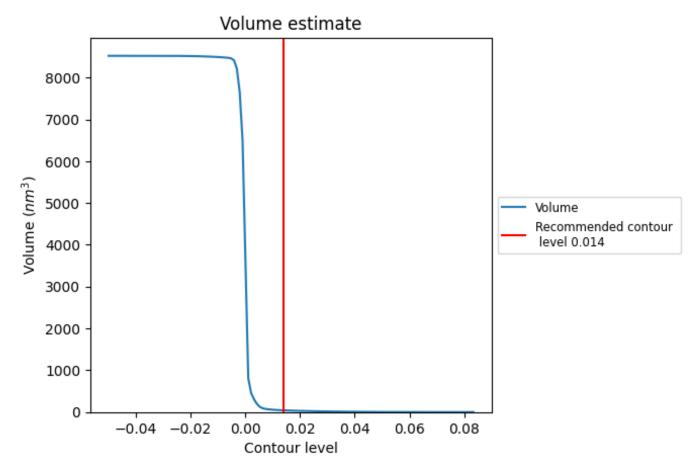
7.1 Map-value distribution (i)



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)

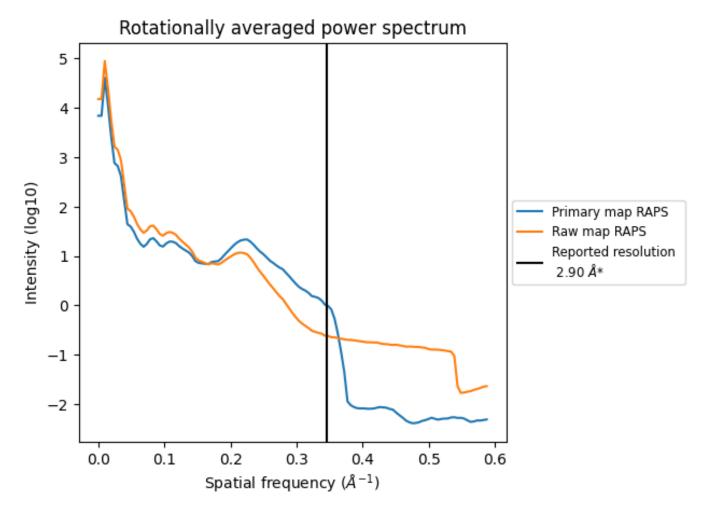


The volume at the recommended contour level is 42 nm^3 ; this corresponds to an approximate mass of 38 kDa.

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)



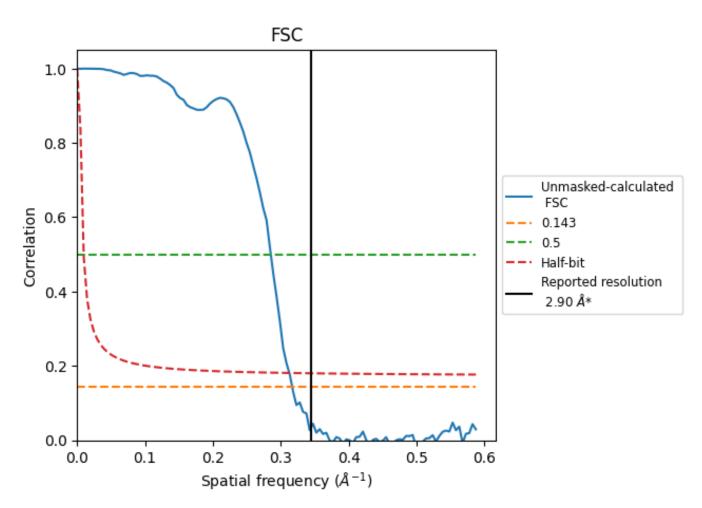
^{*}Reported resolution corresponds to spatial frequency of 0.345 $\rm \mathring{A}^{-1}$



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 0.345 $\rm \mathring{A}^{-1}$



8.2 Resolution estimates (i)

Resolution estimate (Å)	Estim	ation	criterion (FSC cut-off)
rtesolution estimate (A)	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	3.51	3.20

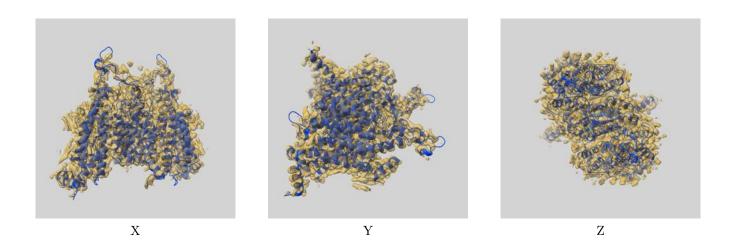
^{*}Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-37681 and PDB model 8WO7. Per-residue inclusion information can be found in section 3 on page 6.

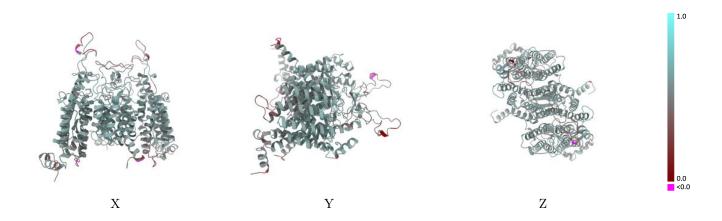
9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

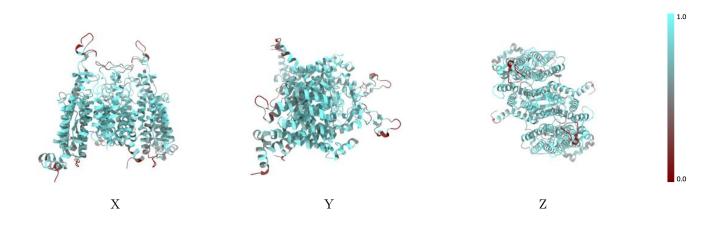


9.2 Q-score mapped to coordinate model (i)



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

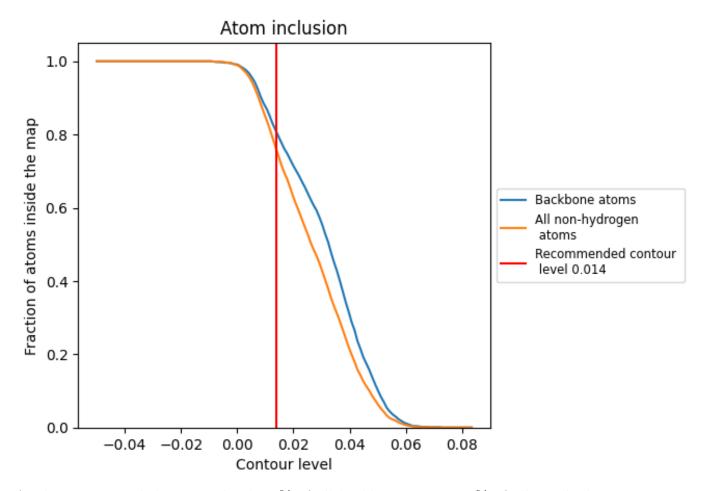
9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.014).



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 (i)

The table lists the average atom inclusion at the recommended contour level (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7580	0.5410
A	0.7610	0.5430
В	0.7610	0.5410
С	0.3210	0.3820
D	0.3570	0.2720



