



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:00 AM UTC

PDB ID : 4BQI / pdb_00004bqi
Title : ARABIDOPSIS THALIANA cytosolic alpha-1,4-glucan phosphorylase (PHS2)
in complex with maltotriose
Authors : O'Neill, E.C.; Rashid, A.M.; Stevenson, C.E.M.; Hetru, A.C.; Gunning, A.P.;
Rejzek, M.; Nepogodiev, S.A.; Bornemann, S.; Lawson, D.M.; Field, R.A.
Deposited on : 2013-05-30
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

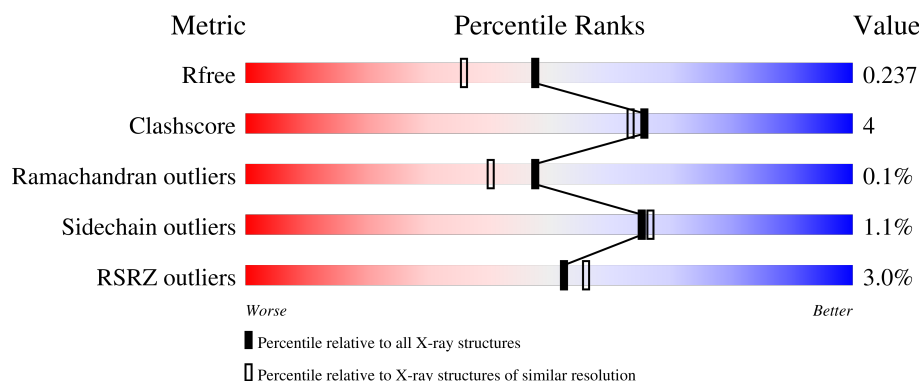
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

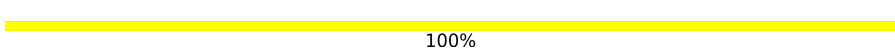
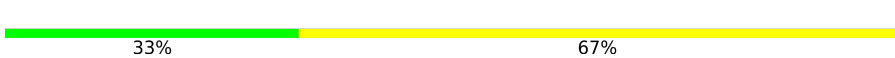
The reported resolution of this entry is 1.90 Å.

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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	874	
1	B	874	
2	C	3	
2	D	3	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PEG	A	1842	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14073 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 ALPHA-GLUCAN PHOSPHORYLASE 2, CYTOSOLIC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	824	Total	C	N	O	S	0	8	0
			6531	4169	1110	1229	23			
1	B	824	Total	C	N	O	S	0	7	0
			6512	4157	1109	1223	23			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	expression tag	UNP Q9SD76
A	-31	HIS	-	expression tag	UNP Q9SD76
A	-30	HIS	-	expression tag	UNP Q9SD76
A	-29	HIS	-	expression tag	UNP Q9SD76
A	-28	HIS	-	expression tag	UNP Q9SD76
A	-27	HIS	-	expression tag	UNP Q9SD76
A	-26	HIS	-	expression tag	UNP Q9SD76
A	-25	GLY	-	expression tag	UNP Q9SD76
A	-24	LYS	-	expression tag	UNP Q9SD76
A	-23	PRO	-	expression tag	UNP Q9SD76
A	-22	ILE	-	expression tag	UNP Q9SD76
A	-21	PRO	-	expression tag	UNP Q9SD76
A	-20	ASN	-	expression tag	UNP Q9SD76
A	-19	PRO	-	expression tag	UNP Q9SD76
A	-18	LEU	-	expression tag	UNP Q9SD76
A	-17	LEU	-	expression tag	UNP Q9SD76
A	-16	GLY	-	expression tag	UNP Q9SD76
A	-15	LEU	-	expression tag	UNP Q9SD76
A	-14	ASP	-	expression tag	UNP Q9SD76
A	-13	SER	-	expression tag	UNP Q9SD76
A	-12	THR	-	expression tag	UNP Q9SD76
A	-11	GLU	-	expression tag	UNP Q9SD76
A	-10	ASN	-	expression tag	UNP Q9SD76
A	-9	LEU	-	expression tag	UNP Q9SD76
A	-8	TYR	-	expression tag	UNP Q9SD76

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	PHE	-	expression tag	UNP Q9SD76
A	-6	GLN	-	expression tag	UNP Q9SD76
A	-5	GLY	-	expression tag	UNP Q9SD76
A	-4	ILE	-	expression tag	UNP Q9SD76
A	-3	ASP	-	expression tag	UNP Q9SD76
A	-2	PRO	-	expression tag	UNP Q9SD76
A	-1	PHE	-	expression tag	UNP Q9SD76
A	0	THR	-	expression tag	UNP Q9SD76
B	-32	MET	-	expression tag	UNP Q9SD76
B	-31	HIS	-	expression tag	UNP Q9SD76
B	-30	HIS	-	expression tag	UNP Q9SD76
B	-29	HIS	-	expression tag	UNP Q9SD76
B	-28	HIS	-	expression tag	UNP Q9SD76
B	-27	HIS	-	expression tag	UNP Q9SD76
B	-26	HIS	-	expression tag	UNP Q9SD76
B	-25	GLY	-	expression tag	UNP Q9SD76
B	-24	LYS	-	expression tag	UNP Q9SD76
B	-23	PRO	-	expression tag	UNP Q9SD76
B	-22	ILE	-	expression tag	UNP Q9SD76
B	-21	PRO	-	expression tag	UNP Q9SD76
B	-20	ASN	-	expression tag	UNP Q9SD76
B	-19	PRO	-	expression tag	UNP Q9SD76
B	-18	LEU	-	expression tag	UNP Q9SD76
B	-17	LEU	-	expression tag	UNP Q9SD76
B	-16	GLY	-	expression tag	UNP Q9SD76
B	-15	LEU	-	expression tag	UNP Q9SD76
B	-14	ASP	-	expression tag	UNP Q9SD76
B	-13	SER	-	expression tag	UNP Q9SD76
B	-12	THR	-	expression tag	UNP Q9SD76
B	-11	GLU	-	expression tag	UNP Q9SD76
B	-10	ASN	-	expression tag	UNP Q9SD76
B	-9	LEU	-	expression tag	UNP Q9SD76
B	-8	TYR	-	expression tag	UNP Q9SD76
B	-7	PHE	-	expression tag	UNP Q9SD76
B	-6	GLN	-	expression tag	UNP Q9SD76
B	-5	GLY	-	expression tag	UNP Q9SD76
B	-4	ILE	-	expression tag	UNP Q9SD76
B	-3	ASP	-	expression tag	UNP Q9SD76
B	-2	PRO	-	expression tag	UNP Q9SD76
B	-1	PHE	-	expression tag	UNP Q9SD76
B	0	THR	-	expression tag	UNP Q9SD76

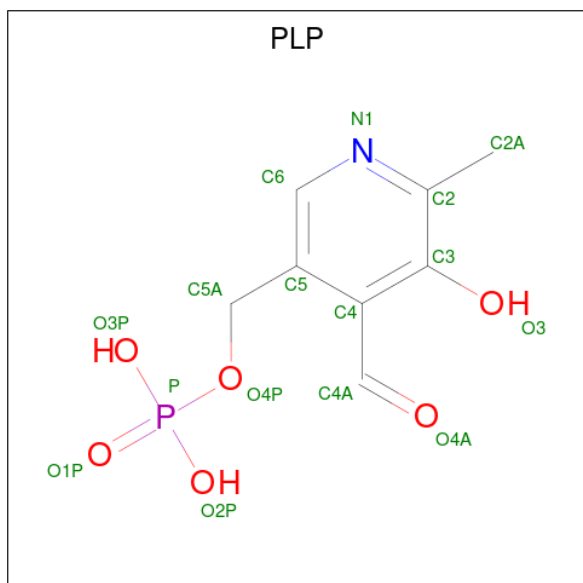
- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-

(1-4)-alpha-D-glucopyranose.



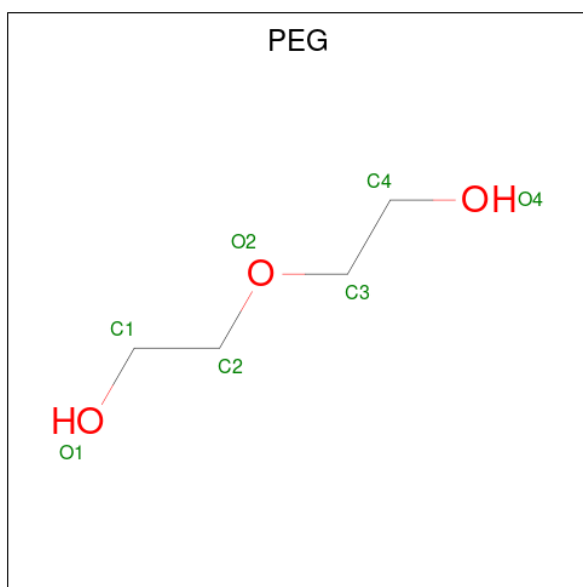
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	3	Total	C	O	0	0	0
			34	18	16			
2	D	3	Total	C	O	0	0	0
			34	18	16			

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



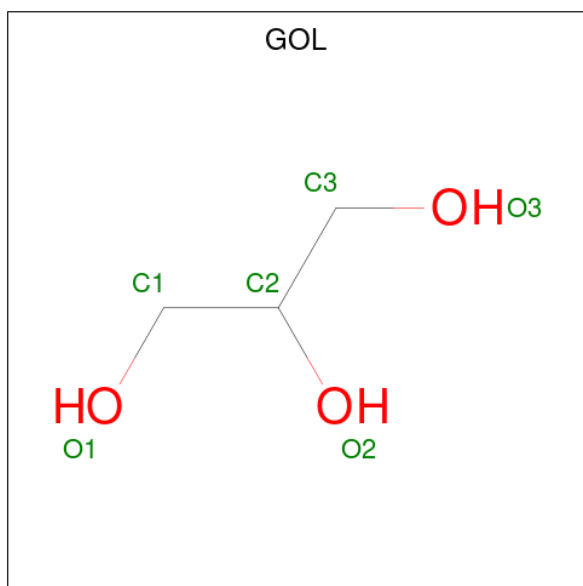
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

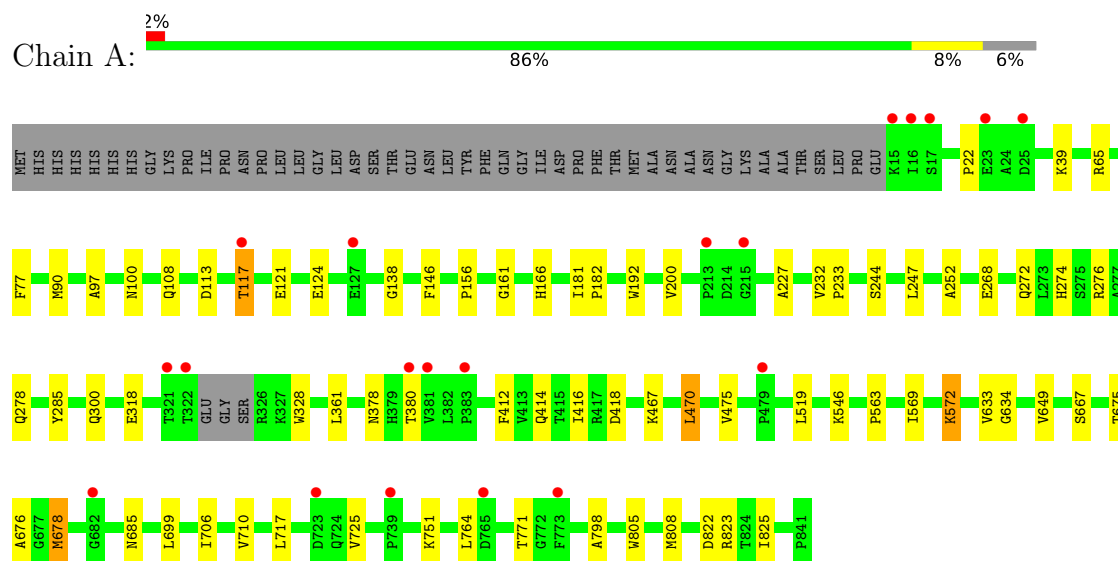
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	486	Total 486	O 486	0	0
6	B	433	Total 433	O 433	0	0

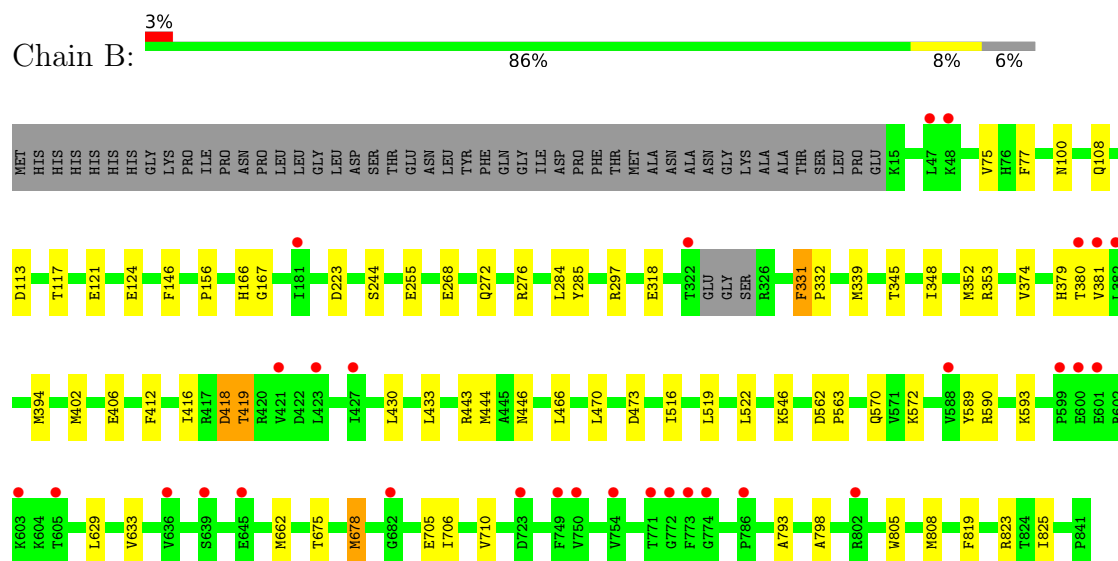
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: ALPHA-GLUCAN PHOSPHORYLASE 2, CYTOSOLIC



• Molecule 1: ALPHA-GLUCAN PHOSPHORYLASE 2, CYTOSOLIC



• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranos e

Chain C:  100%

GLC1
GLC2
GLC3

- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D:  33%  67%

GLC1
GLC2
GLC3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.71Å 116.07Å 94.34Å 90.00° 107.38° 90.00°	Depositor
Resolution (Å)	52.48 – 1.90 52.48 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.2 (52.48-1.90) 98.2 (52.48-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.196 , 0.241 (Not available) , 0.237	Depositor DCC
R_{free} test set	6646 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14073	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.70 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.6338e-03.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: PLP, PEG, GLC, GOL

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	1.06	4/6706 (0.1%)	0.97	4/9107 (0.0%)
1	B	0.99	3/6683 (0.0%)	0.95	5/9075 (0.1%)
All	All	1.02	7/13389 (0.1%)	0.96	9/18182 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	232	VAL	CA-C	7.66	1.59	1.53
1	A	725	VAL	CA-CB	7.50	1.57	1.54
1	A	285	TYR	C-O	-7.34	1.20	1.23
1	B	379	HIS	CG-ND1	-6.52	1.31	1.38
1	B	285	TYR	C-O	-5.71	1.21	1.23
1	A	676	ALA	N-CA	5.35	1.52	1.46
1	B	166	HIS	CG-ND1	-5.33	1.32	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	418	ASP	CB-CA-C	-6.02	103.49	111.74
1	B	166	HIS	N-CA-C	5.64	119.74	112.41
1	B	108	GLN	N-CA-C	5.21	117.37	111.02
1	B	331	PHE	CA-C-N	-5.19	114.43	120.04
1	B	331	PHE	C-N-CA	-5.19	114.43	120.04
1	A	233	PRO	CA-C-N	-5.18	117.55	123.25
1	A	233	PRO	C-N-CA	-5.18	117.55	123.25
1	A	108	GLN	N-CA-C	5.14	116.57	111.07
1	A	166	HIS	N-CA-C	5.11	119.05	112.41

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	6531	0	6352	48	0
1	B	6512	0	6319	51	0
2	C	34	0	30	0	0
2	D	34	0	30	0	0
3	A	15	0	7	2	0
3	B	15	0	6	0	0
4	A	7	0	10	6	0
5	B	6	0	8	2	0
6	A	486	0	0	5	0
6	B	433	0	0	9	0
All	All	14073	0	12762	98	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 4.

All (98) 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:B:418:ASP:O	1:B:419:THR:HG23	1.19	1.32
1:B:418:ASP:O	1:B:419:THR:CG2	2.02	1.07
1:A:519:LEU:H	4:A:1842:PEG:H41	1.39	0.87
1:A:822:ASP:HB2	4:A:1842:PEG:H31	1.60	0.83
1:B:705[B]:GLU:CD	1:B:819:PHE:HE1	1.87	0.81
1:B:805:TRP:HA	1:B:808:MET:HE3	1.65	0.78
1:A:798:ALA:HB1	1:A:808:MET:HE1	1.69	0.75
1:A:378:ASN:HD21	1:A:380:THR:HG22	1.50	0.74
1:A:808:MET:HE2	6:A:2468:HOH:O	1.88	0.73
1:B:705[B]:GLU:CD	1:B:819:PHE:CE1	2.67	0.72
1:A:113:ASP:O	1:A:117:THR:HG23	1.94	0.67
1:B:146:PHE:CG	1:B:825:ILE:HD11	2.31	0.65
1:A:519:LEU:H	4:A:1842:PEG:C4	2.09	0.65
1:A:519:LEU:N	4:A:1842:PEG:H41	2.10	0.64
1:A:268:GLU:OE1	1:B:268:GLU:OE1	2.17	0.63
1:A:146:PHE:CG	1:A:825:ILE:HD11	2.34	0.63
1:A:121:GLU:O	1:A:124:GLU:HG2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:805:TRP:HA	1:A:808:MET:HE3	1.81	0.61
1:A:470:LEU:HD12	1:A:470:LEU:O	2.00	0.60
1:B:412:PHE:CZ	1:B:416:ILE:HD11	2.39	0.58
1:B:798:ALA:HB1	1:B:808:MET:HE1	1.86	0.58
1:A:378:ASN:ND2	1:A:380:THR:HG22	2.20	0.56
1:A:634:GLY:HA2	1:A:649:VAL:HG13	1.87	0.56
1:B:705[B]:GLU:OE1	1:B:819:PHE:HE1	1.89	0.55
1:A:138:GLY:HA2	3:A:901:PLP:H5A2	1.87	0.54
1:A:272:GLN:O	1:A:276:ARG:HG3	2.07	0.54
1:B:272:GLN:O	1:B:276:ARG:HG3	2.07	0.54
1:A:822:ASP:CB	4:A:1842:PEG:H31	2.37	0.54
1:B:113:ASP:O	1:B:117:THR:HG23	2.07	0.54
1:B:353:ARG:HH22	5:B:1842:GOL:H2	1.72	0.54
1:A:706:ILE:O	1:A:710:VAL:HG22	2.09	0.53
1:B:808:MET:HE2	6:B:2420:HOH:O	2.09	0.53
1:A:138:GLY:CA	3:A:901:PLP:H5A2	2.39	0.53
1:B:121:GLU:O	1:B:124:GLU:HG2	2.08	0.53
1:B:430:LEU:HD21	1:B:473:ASP:HB2	1.92	0.52
1:B:443:ARG:HD3	1:B:446:ASN:ND2	2.24	0.52
1:B:706:ILE:O	1:B:710:VAL:HG22	2.09	0.52
1:B:339:MET:HE2	1:B:374:VAL:CG1	2.40	0.51
1:B:75:VAL:O	6:B:2035:HOH:O	2.19	0.51
1:B:167:GLY:C	1:B:284:LEU:HD12	2.36	0.50
1:A:274[B]:HIS:CD2	1:A:278:GLN:NE2	2.80	0.50
1:B:297:ARG:NH2	6:B:2211:HOH:O	2.44	0.50
1:B:793:ALA:HB3	6:B:2417:HOH:O	2.12	0.50
1:A:182:PRO:HA	6:A:2128:HOH:O	2.11	0.49
1:B:345:THR:HB	1:B:444:MET:HE3	1.94	0.49
1:A:634:GLY:CA	1:A:649:VAL:HG13	2.42	0.49
1:A:274[B]:HIS:NE2	1:A:278:GLN:NE2	2.61	0.49
1:B:223:ASP:OD2	1:B:276:ARG:NH2	2.40	0.49
1:A:328:TRP:CD1	1:A:361:LEU:HD11	2.49	0.48
1:A:97:ALA:HB3	1:A:192:TRP:CE2	2.49	0.47
1:B:75:VAL:HG13	6:B:2035:HOH:O	2.13	0.47
1:A:634:GLY:HA2	1:A:649:VAL:CG1	2.44	0.46
1:B:352:MET:HE3	1:B:352:MET:HB3	1.76	0.46
1:B:353:ARG:NH2	5:B:1842:GOL:H2	2.31	0.46
1:B:466:LEU:HD23	1:B:470:LEU:HD22	1.98	0.46
1:A:252:ALA:HB3	1:A:274[A]:HIS:CD2	2.51	0.46
1:A:546:LYS:HE2	1:A:563:PRO:O	2.16	0.46
1:A:569:ILE:HD12	1:A:667:SER:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:MET:HE2	1:B:374:VAL:HG12	1.97	0.45
1:B:519:LEU:HD11	1:B:522:LEU:HD11	1.98	0.45
1:B:675:THR:HB	1:B:678:MET:HG3	1.99	0.45
1:B:418:ASP:C	1:B:419:THR:HG23	2.23	0.44
1:A:751:LYS:HD2	1:A:764:LEU:HD12	1.98	0.44
1:A:675:THR:HB	1:A:678:MET:HG3	2.00	0.44
1:A:633:VAL:HG12	1:A:649:VAL:HG11	1.99	0.44
1:A:414:GLN:NE2	1:A:418:ASP:OD1	2.47	0.44
1:A:412:PHE:CZ	1:A:416:ILE:HD11	2.52	0.44
1:B:381:VAL:O	1:B:470:LEU:HD11	2.17	0.44
1:A:699:LEU:HB2	1:A:717:LEU:HD11	2.00	0.43
1:B:546:LYS:HE2	1:B:563:PRO:O	2.18	0.43
1:B:100:ASN:ND2	6:B:2080:HOH:O	2.50	0.43
1:B:590[B]:ARG:NH2	6:B:2360:HOH:O	2.35	0.43
1:B:394:MET:HG3	1:B:402:MET:HG2	2.00	0.43
1:A:100:ASN:ND2	6:A:2084:HOH:O	2.52	0.43
1:A:572:LYS:HD2	6:A:2375:HOH:O	2.19	0.42
1:A:380:THR:O	1:A:380:THR:HG23	2.18	0.42
1:B:331:PHE:HB3	1:B:332:PRO:HD3	2.01	0.42
1:B:589:TYR:CE1	1:B:593:LYS:HD3	2.54	0.42
1:B:662:MET:HE3	1:B:662:MET:HA	2.02	0.42
1:A:200:VAL:HA	1:A:227:ALA:O	2.19	0.42
1:A:39:LYS:HE3	6:A:2014:HOH:O	2.20	0.42
1:A:467:LYS:HA	1:A:475:VAL:HG21	2.01	0.42
1:A:77:PHE:CE2	1:A:156:PRO:HA	2.55	0.42
1:B:394:MET:HG2	1:B:402:MET:SD	2.60	0.42
1:B:380:THR:O	1:B:380:THR:HG23	2.20	0.41
1:B:516:ILE:HD11	6:B:2316:HOH:O	2.20	0.41
1:B:562:ASP:OD1	1:B:562:ASP:C	2.63	0.41
1:A:161:GLY:O	1:A:247:LEU:HA	2.21	0.41
1:B:339:MET:HE1	1:B:348:ILE:HD11	2.02	0.41
1:A:22:PRO:O	1:A:65:ARG:HD2	2.21	0.41
1:B:406:GLU:HG2	1:B:433:LEU:HD11	2.03	0.41
1:B:805:TRP:HA	1:B:808:MET:CE	2.45	0.41
1:A:519:LEU:HB2	4:A:1842:PEG:H42	2.02	0.41
1:B:77:PHE:CE2	1:B:156:PRO:HA	2.55	0.41
1:A:90:MET:HE1	1:A:300:GLN:HB3	2.02	0.41
1:A:181:ILE:HD13	1:A:181:ILE:HG21	1.87	0.41
1:B:570:GLN:NE2	6:B:2353:HOH:O	2.53	0.40
1:B:629:LEU:O	1:B:633:VAL:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	828/874 (95%)	807 (98%)	21 (2%)	0	100	100
1	B	827/874 (95%)	803 (97%)	23 (3%)	1 (0%)	48	40
All	All	1655/1748 (95%)	1610 (97%)	44 (3%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	419	THR

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	687/752 (91%)	678 (99%)	9 (1%)	61	61
1	B	680/752 (90%)	674 (99%)	6 (1%)	70	73
All	All	1367/1504 (91%)	1352 (99%)	15 (1%)	65	67

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

Mol	Chain	Res	Type
1	A	117	THR
1	A	244	SER
1	A	318	GLU
1	A	470	LEU
1	A	572	LYS

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Mol	Chain	Res	Type
1	A	678	MET
1	A	685	ASN
1	A	771	THR
1	A	823	ARG
1	B	244	SER
1	B	255	GLU
1	B	318	GLU
1	B	572	LYS
1	B	678	MET
1	B	823	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	A	210	GLN
1	A	226	GLN
1	A	278	GLN
1	A	300	GLN
1	A	310	GLN
1	A	484	ASN
1	A	631	ASN
1	B	78	ASN
1	B	100	ASN
1	B	210	GLN
1	B	226	GLN
1	B	278	GLN
1	B	300	GLN
1	B	310	GLN
1	B	460	GLN
1	B	484	ASN
1	B	487	ASN
1	B	748	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 ⓘ

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$
2	GLC	C	1	2	12,12,12	0.72	0	17,17,17	1.48	3 (17%)
2	GLC	C	2	2	11,11,12	0.66	0	15,15,17	1.66	2 (13%)
2	GLC	C	3	2	11,11,12	0.32	0	15,15,17	1.45	3 (20%)
2	GLC	D	1	2	12,12,12	0.73	0	17,17,17	0.95	1 (5%)
2	GLC	D	2	2	11,11,12	0.62	0	15,15,17	1.72	4 (26%)
2	GLC	D	3	2	11,11,12	0.43	0	15,15,17	1.05	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
2	GLC	C	1	2	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	1/2/19/22	0/1/1/1
2	GLC	C	3	2	-	2/2/19/22	0/1/1/1
2	GLC	D	1	2	-	0/2/22/22	0/1/1/1
2	GLC	D	2	2	-	2/2/19/22	0/1/1/1
2	GLC	D	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	GLC	C1-O5-C5	4.34	118.00	112.19
2	C	3	GLC	C1-O5-C5	4.08	117.65	112.19
2	D	2	GLC	O5-C5-C6	3.80	115.05	107.66
2	C	1	GLC	O5-C1-C2	3.16	115.85	110.30
2	C	1	GLC	C1-O5-C5	3.15	119.74	113.65
2	D	2	GLC	O3-C3-C4	-2.71	103.99	110.38
2	D	2	GLC	O3-C3-C2	2.41	114.97	110.05
2	C	1	GLC	O5-C5-C6	2.38	112.33	106.44
2	D	2	GLC	O2-C2-C3	2.20	114.70	110.15
2	C	3	GLC	C2-C3-C4	-2.13	107.11	110.86
2	C	3	GLC	C6-C5-C4	-2.11	107.83	113.02
2	C	2	GLC	C6-C5-C4	-2.08	107.92	113.02
2	D	1	GLC	C1-C2-C3	2.07	114.58	110.36

There are no chirality outliers.

All (5) torsion outliers are listed below:

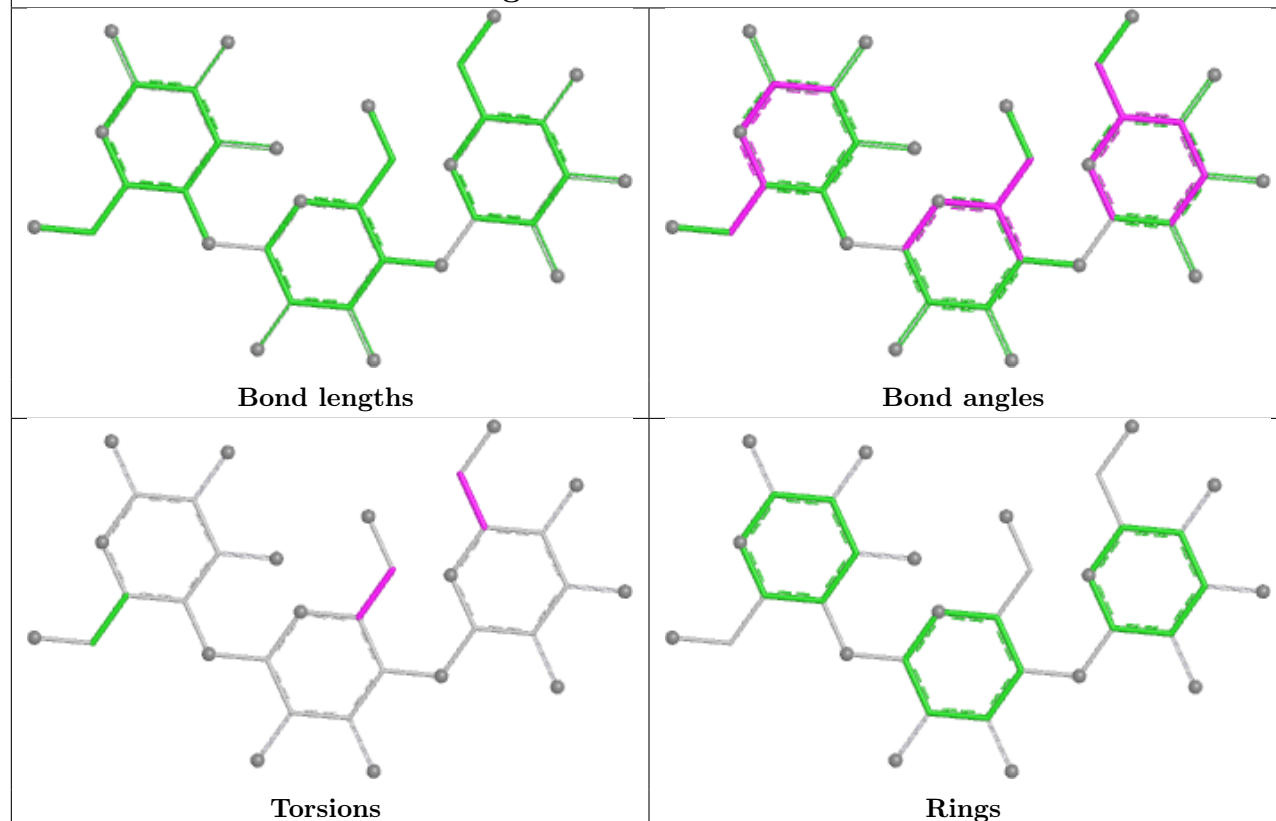
Mol	Chain	Res	Type	Atoms
2	D	2	GLC	O5-C5-C6-O6
2	D	2	GLC	C4-C5-C6-O6
2	C	3	GLC	O5-C5-C6-O6
2	C	2	GLC	O5-C5-C6-O6
2	C	3	GLC	C4-C5-C6-O6

There are no ring outliers.

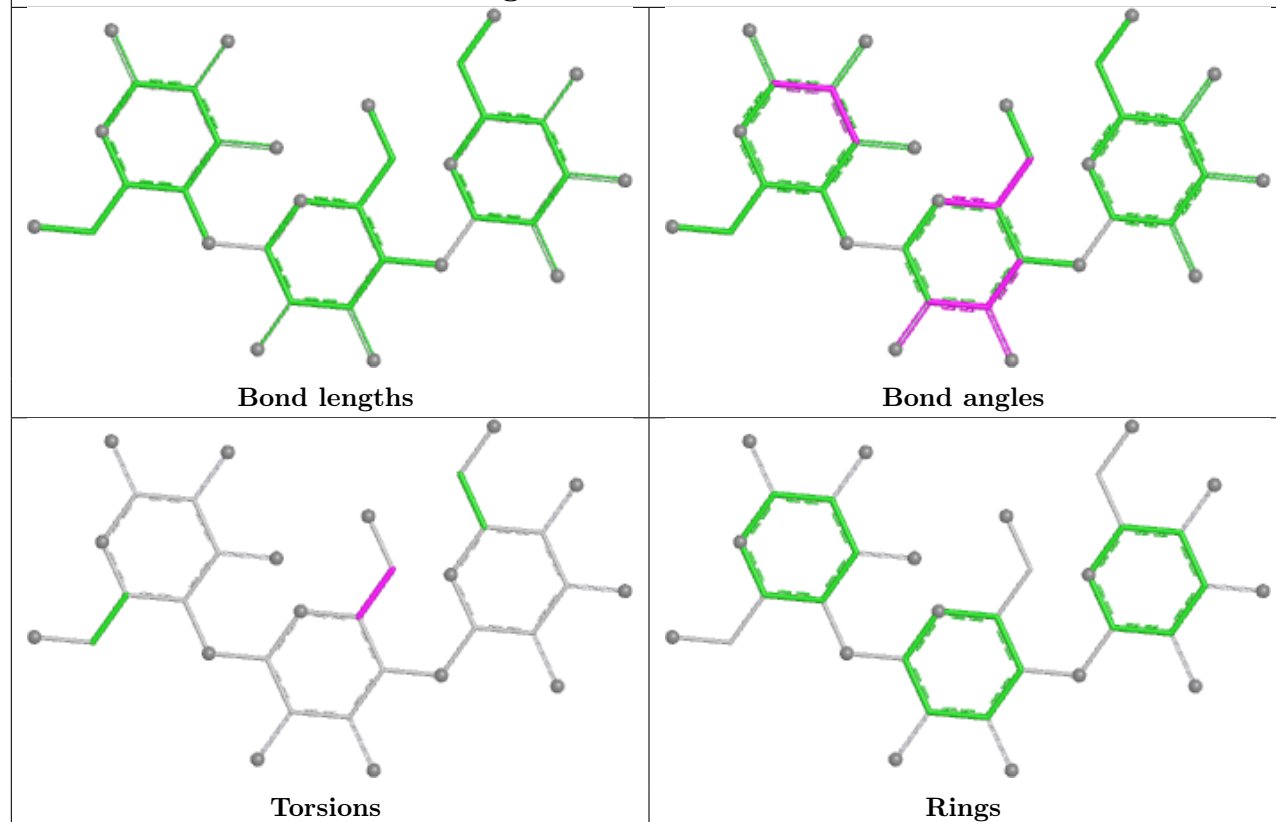
No monomer is involved in short contacts.

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 C



Oligosaccharide Chain D



5.6 Ligand geometry

4 ligands 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
5	GOL	B	1842	-	5,5,5	0.47	0	5,5,5	1.01	0
3	PLP	B	901	1	15,15,16	1.23	0	21,22,23	1.44	1 (4%)
4	PEG	A	1842	-	6,6,6	0.56	0	5,5,5	1.94	2 (40%)
3	PLP	A	901	1	15,15,16	0.90	1 (6%)	21,22,23	1.83	5 (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
5	GOL	B	1842	-	-	4/4/4/4	-
3	PLP	B	901	1	-	5/6/6/8	0/1/1/1
4	PEG	A	1842	-	-	2/4/4/4	-
3	PLP	A	901	1	-	3/6/6/8	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	901	PLP	O4P-C5A	-2.34	1.36	1.44

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	901	PLP	O3P-P-O4P	4.28	117.83	106.67
3	A	901	PLP	C4A-C4-C5	-3.70	117.12	120.94
4	A	1842	PEG	O2-C2-C1	-3.50	94.68	110.11
3	A	901	PLP	O3P-P-O4P	3.00	114.50	106.67
3	A	901	PLP	O2P-P-O4P	-2.86	99.20	106.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901	PLP	C2A-C2-C3	-2.68	117.66	120.80
4	A	1842	PEG	O2-C3-C4	-2.51	99.04	110.11
3	A	901	PLP	O4P-C5A-C5	-2.33	104.99	109.36

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	901	PLP	C5A-O4P-P-O1P
3	A	901	PLP	C5A-O4P-P-O2P
3	A	901	PLP	C5A-O4P-P-O3P
3	B	901	PLP	C5A-O4P-P-O2P
3	B	901	PLP	C5A-O4P-P-O3P
5	B	1842	GOL	O1-C1-C2-C3
5	B	1842	GOL	O1-C1-C2-O2
5	B	1842	GOL	C1-C2-C3-O3
5	B	1842	GOL	O2-C2-C3-O3
3	B	901	PLP	C5A-O4P-P-O1P
4	A	1842	PEG	C4-C3-O2-C2
3	B	901	PLP	C4-C5-C5A-O4P
4	A	1842	PEG	C1-C2-O2-C3
3	B	901	PLP	C6-C5-C5A-O4P

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1842	GOL	2	0
4	A	1842	PEG	6	0
3	A	901	PLP	2	0

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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	824/874 (94%)	0.25	20 (2%) 59 63	14, 29, 47, 74	8 (0%)
1	B	824/874 (94%)	0.52	30 (3%) 46 49	14, 33, 55, 88	7 (0%)
All	All	1648/1748 (94%)	0.38	50 (3%) 52 56	14, 31, 51, 88	15 (0%)

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	600	GLU	6.5
1	B	773	PHE	4.8
1	B	421	VAL	4.4
1	B	599	PRO	3.9
1	B	381	VAL	3.8
1	B	774	GLY	3.7
1	B	322	THR	3.3
1	B	603	LYS	3.3
1	B	723	ASP	3.1
1	B	772	GLY	3.1
1	A	215	GLY	3.0
1	A	321	THR	2.9
1	A	322	THR	2.9
1	B	771	THR	2.9
1	A	127	GLU	2.8
1	B	682	GLY	2.7
1	B	639	SER	2.7
1	A	380	THR	2.6
1	A	213	PRO	2.6
1	A	739	PRO	2.6
1	A	773	PHE	2.6
1	A	765	ASP	2.6
1	A	25	ASP	2.5
1	A	15	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	645	GLU	2.5
1	B	47	LEU	2.5
1	B	181	ILE	2.5
1	A	117	THR	2.4
1	B	786	PRO	2.4
1	B	382	LEU	2.4
1	A	16	ILE	2.3
1	A	723	ASP	2.3
1	B	750	VAL	2.3
1	B	427	ILE	2.2
1	B	749	PHE	2.2
1	B	601	GLU	2.2
1	A	479	PRO	2.2
1	A	682	GLY	2.2
1	B	48	LYS	2.2
1	A	381	VAL	2.1
1	A	17	SER	2.1
1	A	383	PRO	2.1
1	B	605	THR	2.1
1	B	802	ARG	2.1
1	A	23	GLU	2.1
1	B	636	VAL	2.1
1	B	588	VAL	2.0
1	B	423	LEU	2.0
1	B	380	THR	2.0
1	B	754	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

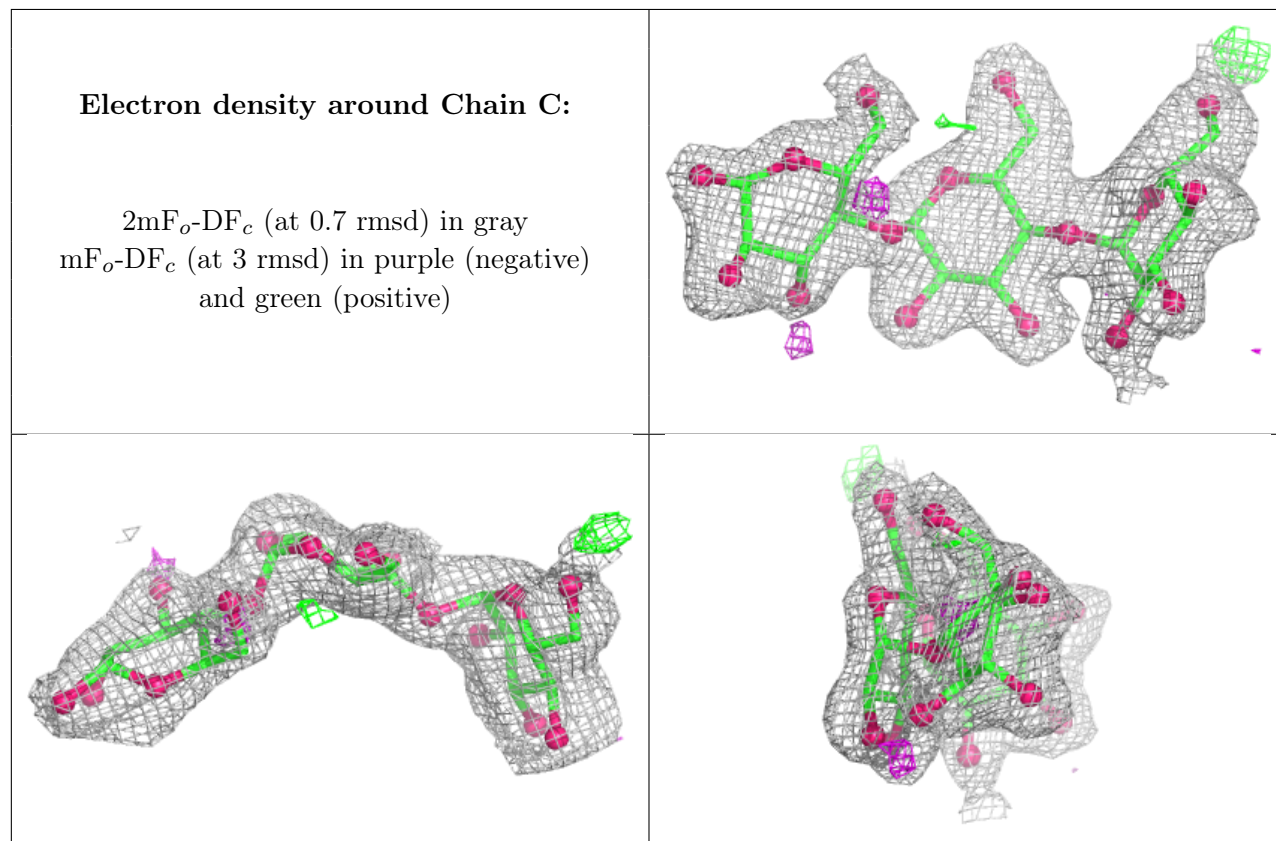
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	C	3	11/12	0.83	0.11	38,43,49,50	0
2	GLC	C	1	12/12	0.87	0.11	41,44,50,52	0

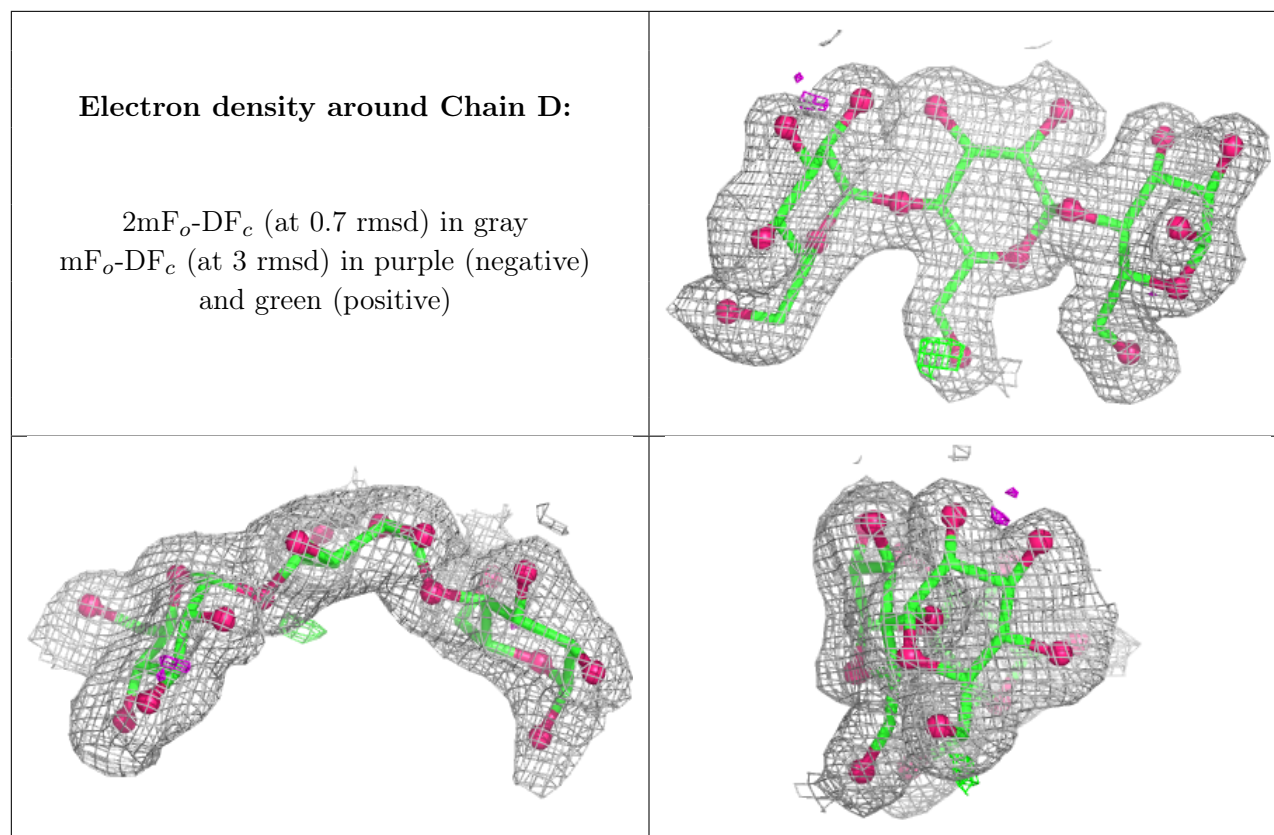
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	C	2	11/12	0.88	0.11	35,40,42,42	0
2	GLC	D	1	12/12	0.88	0.10	34,37,40,49	0
2	GLC	D	2	11/12	0.90	0.10	29,34,36,36	0
2	GLC	D	3	11/12	0.91	0.08	31,34,37,39	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	GOL	B	1842	6/6	0.88	0.12	30,36,36,37	0
4	PEG	A	1842	7/7	0.92	0.09	30,34,36,37	0
3	PLP	A	901	15/16	0.94	0.07	23,25,37,37	0
3	PLP	B	901	15/16	0.94	0.08	23,26,46,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.