

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 20, 2020 – 05:38 PM BST

PDB ID	:	4BQI
Title	:	ARABIDOPSIS THALIANA cytosolic alpha-1,4-glucan phosphorylase (PHS2)
		in complex with maltotriose
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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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
CCP4	:	7.0.044  (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

# 1 Overall quality at a glance (i)

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082(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 on 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 <=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	А	874	%	87%	7%	6%		
1	В	874	%	86%	8%	6%		
2	С	3		100%				
2	D	3	33%	67%				

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 crite-



ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PEG	А	1842	-	-	Х	-



## 2 Entry composition (i)

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	824	Total 6531	C 4169	N 1110	O 1229	S 23	0	8	0
1	В	824	Total 6512	$\begin{array}{c} \mathrm{C} \\ 4157 \end{array}$	N 1109	O 1223	S 23	0	7	0

• Molecule 1 is a protein called ALPHA-GLUCAN PHOSPHORYLASE 2, CYTOSOLIC.

Chain	Residue	Modelled	Actual	$\mathbf{Comment}$	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
А	-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

There are 66 discrepancies between the modelled and reference sequences:

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

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• 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	С	3	Total 34	C 18	O 16	0	0	0
2	D	3	Total 34	C 18	O 16	0	0	0

• Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula:  $C_8H_{10}NO_6P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	Λ	1	Total	С	Ν	Ο	Р	0	0
0	л	L	15	8	1	5	1	0	0
2	В	1	Total	С	Ν	Ο	Р	0	0
0	D	L	15	8	1	5	1	0	0

• Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	А	1	Total 7	С 4	O 3	0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	В	1	Total 6	${ m C} { m 3}$	O 3	0	0

• Molecule 6 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	486	Total O 486 486	0	0
6	В	433	Total         O           433         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 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranos e



Chain C:		100%	
6LC1 6LC2 6LC3			
• Molecule 2 e	: alpha-D-glucopy	ranose-(1-4)-alpha-D-glucopyranose-(1-4)-a	alpha-D-glucopyranos
Chain D:	33%	67%	
GLC1 GLC2 GLC3			



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	83.71Å 116.07Å 94.34Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $107.38^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution(A)	52.48 - 1.90	Depositor
Resolution (A)	52.48 - 1.90	EDS
% Data completeness	98.2 (52.48-1.90)	Depositor
(in resolution range)	98.2 (52.48-1.90)	EDS
$R_{merge}$	0.06	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.99 (at 1.90 Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
B B.	0.196 , $0.241$	Depositor
$\Pi, \Pi_{free}$	0.199 , $0.243$	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, $48.2$	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.43, < L^2>=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.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: GLC, GOL, PEG, PLP

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).

Mal Chain		Bo	nd lengths	Bond angles		
10101	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.78	1/6706~(0.0%)	0.80	2/9107~(0.0%)	
1	В	0.76	7/6683~(0.1%)	0.79	5/9075~(0.1%)	
All	All	0.77	8/13389~(0.1%)	0.79	7/18182~(0.0%)	

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
1	В	367	TRP	CD2-CE2	6.06	1.48	1.41
1	А	509	TRP	CD2-CE2	5.96	1.48	1.41
1	В	389	TRP	CD2-CE2	5.62	1.48	1.41
1	В	219	TRP	CD2-CE2	5.50	1.48	1.41
1	В	158	TRP	CD2-CE2	5.43	1.47	1.41
1	В	70	TRP	CD2-CE2	5.26	1.47	1.41
1	В	92	TYR	CZ-OH	5.07	1.46	1.37
1	В	248	TRP	CD2-CE2	5.06	1.47	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	493	ARG	NE-CZ-NH2	-6.93	116.83	120.30
1	В	96[A]	ARG	NE-CZ-NH1	-6.86	116.87	120.30
1	В	96[B]	ARG	NE-CZ-NH1	-6.86	116.87	120.30
1	В	443	ARG	NE-CZ-NH1	6.15	123.37	120.30
1	В	443	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	А	822	ASP	CB-CG-OD1	5.77	123.49	118.30
1	В	493	ARG	NE-CZ-NH2	-5.69	117.45	120.30

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	А	6531	0	6352	48	0
1	В	6512	0	6319	45	0
2	С	34	0	30	0	0
2	D	34	0	30	0	0
3	А	15	0	7	2	0
3	В	15	0	6	0	0
4	А	7	0	10	6	0
5	В	6	0	8	2	0
6	А	486	0	0	6	0
6	B	433	0	0	10	0
All	All	14073	0	12762	92	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 (92) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	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	0.76
1:A:378:ASN:HD21	1:A:380:THR:HG22	1.50	0.74
1:A:113:ASP:O	1:A:117:THR:HG23	1.94	0.67
1:B:705[B]:GLU:CD	1:B:819:PHE:CE1	2.67	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
1:A:470:LEU:O	1:A:470:LEU:HD12	2.00	0.60
1:B:412:PHE:CZ	1:B:416:ILE:HD11	2.39	0.58
1:A:378:ASN:ND2	1:A:380:THR:HG22	2.20	0.56

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		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
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: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:75:VAL:O	6:B:2035:HOH:O	2.19	0.51
1:A:274[B]:HIS:CD2	1:A:278:GLN:NE2	2.80	0.50
1:B:798:ALA:HB1	1:B:808:MET:HE1	1.93	0.50
1:B:339:MET:HE1	1:B:348:ILE:HD11	1.92	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: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:B:808:MET:HE1	6:B:2420:HOH:O	2.12	0.48
1:B:379:HIS:ND1	6:B:2255:HOH:O	2.35	0.48
1:A:808:MET:CE	6:A:2468:HOH:O	2.62	0.48
1:A:328:TRP:CD1	1:A:361:LEU:HD11	2.49	0.48
1:A:808:MET:HE1	6:A:2468:HOH:O	2.13	0.47
1:A:339:MET:HE1	1:A:348:ILE:HD11	1.95	0.47
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:B:805:TRP:HA	1:B:808:MET:CE	2.45	0.47
1:A:634:GLY:HA2	1:A:649:VAL:CG1	2.44	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:B:167:GLY:C	1:B:284:LEU:HD12	2.36	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
1:B:519:LEU:HD11	1:B:522:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:B:675:THR:HB	1:B:678:MET:HG3	1.99	0.45
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:B:805:TRP:HA	1:B:808:MET:HE2	2.01	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:A:798:ALA:HB1	1:A:808:MET:HE1	2.01	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: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:HG23	1:B:380:THR:O	2.20	0.41
1:B:516:ILE:HD11	6:B:2316:HOH:O	2.20	0.41
1:A:161:GLY:O	1:A:247:LEU:HA	2.21	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: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: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

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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 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	Perce	ntiles
1	А	828/874~(95%)	807~(98%)	21 (2%)	0	100	100
1	В	827/874~(95%)	803~(97%)	23~(3%)	1 (0%)	51	43
All	All	1655/1748~(95%)	1610 (97%)	44 (3%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	419	THR

#### 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 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	А	687/752~(91%)	679~(99%)	8 (1%)	71 70		
1	В	680/752~(90%)	673~(99%)	7 (1%)	76 76		
All	All	1367/1504~(91%)	1352~(99%)	15 (1%)	73 73		

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

Mol	Chain	Res	Type
1	А	244	SER
1	А	318	GLU
1	А	470	LEU
1	А	572	LYS
1	А	620	TYR

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Mol	Chain	Res	Type
1	А	678	MET
1	А	685	ASN
1	А	771	THR
1	В	244	SER
1	В	318	GLU
1	В	358	ASP
1	В	572	LYS
1	В	620	TYR
1	В	678	MET
1	В	685	ASN

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Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	100	ASN
1	А	278	GLN
1	А	460	GLN
1	В	100	ASN
1	В	278	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)

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).



Mal	Tune	Chain	Res	Tink	Bo	Bond lengths			Bond angles		
	туре	Chain			Counts	RMSZ	# Z  > 2	Counts	RMSZ	#  Z  > 2	
2	GLC	C	1	2	12,12,12	0.71	0	17,17,17	1.49	3 (17%)	
2	GLC	C	2	2	11, 11, 12	0.67	0	$15,\!15,\!17$	1.76	5 (33%)	
2	GLC	С	3	2	11, 11, 12	0.32	0	$15,\!15,\!17$	1.51	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	1.96	4 (26%)	
2	GLC	D	3	2	11,11,12	0.43	0	$15,\!15,\!17$	1.18	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	С	1	2	-	0/2/22/22	0/1/1/1
2	GLC	С	2	2	-	1/2/19/22	0/1/1/1
2	GLC	С	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 (16) bond angle outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	D	2	GLC	O5-C5-C6	5.00	115.05	107.20
2	С	2	GLC	C1-O5-C5	4.29	118.00	112.19
2	С	3	GLC	C1-O5-C5	4.03	117.65	112.19
2	С	1	GLC	C1-O5-C5	3.22	119.74	113.66
2	С	1	GLC	O5-C1-C2	3.12	115.85	110.28
2	D	2	GLC	O3-C3-C4	-2.75	103.99	110.35
2	D	2	GLC	O3-C3-C2	2.60	114.97	109.99
2	С	1	GLC	O5-C5-C6	2.37	112.33	106.44
2	D	2	GLC	O2-C2-C3	2.28	114.70	110.14
2	С	2	GLC	O5-C5-C6	2.27	110.76	107.20
2	С	3	GLC	C6-C5-C4	-2.21	107.83	113.00
2	С	3	GLC	C2-C3-C4	-2.19	107.11	110.89
2	С	2	GLC	C6-C5-C4	-2.17	107.92	113.00
2	С	2	GLC	O2-C2-C1	-2.06	104.93	109.15
2	D	1	GLC	C1-C2-C3	2.06	114.58	110.31
2	C	2	GLC	O3-C3-C4	-2.02	105.67	110.35



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	С	3	GLC	O5-C5-C6-O6
2	С	2	GLC	O5-C5-C6-O6
2	С	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.









## 5.6 Ligand geometry (i)

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).

Mal	True	Cype Chain	Ros	Link	Bo	ond leng	$_{\rm sths}$	Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GOL	В	1842	-	5, 5, 5	0.46	0	$5,\!5,\!5$	0.95	0
4	PEG	А	1842	-	$^{6,6,6}$	0.56	0	$5,\!5,\!5$	1.94	2 (40%)
3	PLP	А	901	1	15, 15, 16	0.88	1 (6%)	20,22,23	1.85	5 (25%)
3	PLP	В	901	1	15, 15, 16	1.19	0	20,22,23	1.40	1(5%)

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.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	В	1842	-	-	4/4/4/4	-
4	PEG	А	1842	-	-	2/4/4/4	-
3	PLP	А	901	1	-	3/6/6/8	0/1/1/1
3	PLP	В	901	1	-	5/6/6/8	0/1/1/1

'-' means no outliers of that kind were identified.

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
3	А	901	PLP	O4P-C5A	-2.34	1.36	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	901	PLP	O3P-P-O4P	4.17	117.83	106.73
3	А	901	PLP	C4A-C4-C5	-3.70	117.12	120.94
4	А	1842	PEG	O2-C2-C1	-3.50	94.68	110.07
3	А	901	PLP	O3P-P-O4P	2.92	114.50	106.73
3	А	901	PLP	O2P-P-O4P	-2.83	99.20	106.73
3	А	901	PLP	C2A-C2-C3	-2.61	117.66	120.89
4	А	1842	PEG	O2-C3-C4	-2.51	99.04	110.07
3	А	901	PLP	O4P-C5A-C5	-2.29	104.99	109.35

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms
5	В	1842	GOL	O1-C1-C2-C3
3	А	901	PLP	C5A-O4P-P-O1P
3	А	901	PLP	C5A-O4P-P-O2P
3	А	901	PLP	C5A-O4P-P-O3P
3	В	901	PLP	C5A-O4P-P-O2P
3	В	901	PLP	C5A-O4P-P-O3P
5	В	1842	GOL	O1-C1-C2-O2
5	В	1842	GOL	C1-C2-C3-O3
5	В	1842	GOL	O2-C2-C3-O3
3	В	901	PLP	C5A-O4P-P-O1P
3	В	901	PLP	C4-C5-C5A-O4P
4	А	1842	PEG	C4-C3-O2-C2
4	А	1842	PEG	C1-C2-O2-C3
3	В	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	В	1842	GOL	2	0
4	А	1842	PEG	6	0
3	А	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 (i)

## 6.1 Protein, DNA and RNA chains (i)

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,  $95^{th}$  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	А	824/874~(94%)	-0.10	8 (0%) 82 84	19, 29, 47, 74	0
1	В	824/874~(94%)	0.05	13 (1%) 72 74	17, 33, 55, 88	0
All	All	1648/1748~(94%)	-0.03	21 (1%) 77 79	17, 31, 51, 88	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	772	GLY	5.6
1	А	773	PHE	5.4
1	В	773	PHE	5.1
1	В	774	GLY	4.8
1	А	322	THR	4.0
1	А	321	THR	4.0
1	В	736	LEU	3.8
1	В	599	PRO	3.3
1	А	213	PRO	3.2
1	В	600	GLU	3.2
1	В	322	THR	2.9
1	В	381	VAL	2.9
1	В	421	VAL	2.8
1	В	734	ASP	2.5
1	В	321	THR	2.5
1	В	802	ARG	2.5
1	А	15	LYS	2.2
1	А	17	SER	2.2
1	А	739	PRO	2.2
1	В	16	ILE	2.1
1	А	134	LEU	2.1



## 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,  $95^{th}$  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	$\mathbf{B} extsf{-}\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q < 0.9
2	GLC	С	1	12/12	0.84	0.20	$41,\!44,\!50,\!52$	0
2	GLC	D	1	12/12	0.85	0.12	$34,\!37,\!40,\!49$	0
2	GLC	С	2	11/12	0.85	0.12	$35,\!40,\!42,\!42$	0
2	GLC	С	3	11/12	0.87	0.16	$38,\!43,\!49,\!50$	0
2	GLC	D	2	11/12	0.92	0.11	29,34,36,36	0
2	GLC	D	3	11/12	0.93	0.12	$31,\!34,\!37,\!39$	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,  $95^{th}$  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>B-factors</b> (Å <sup>2</sup> )	Q<0.9
5	GOL	В	1842	6/6	0.89	0.13	$30,\!36,\!36,\!37$	0
4	PEG	А	1842	7/7	0.94	0.28	$30,\!34,\!36,\!37$	0
3	PLP	В	901	15/16	0.95	0.13	23, 26, 46, 50	0
3	PLP	А	901	15/16	0.96	0.12	$23,\!25,\!37,\!37$	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

