Full wwPDB X-ray Structure Validation Report (i)

Nov 25, 2023 – 10:21 PM EST

PDB ID	:	3OSQ
Title	:	Maltose-bound maltose sensor engineered by insertion of circularly permuted green fluorescent protein into E. coli maltose binding protein at position 175
Authors	:	Echevarria, I.M.; Marvin, J.S.; Looger, L.L.; Schreiter, E.R.
Deposited on	:	2010-09-09
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 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:

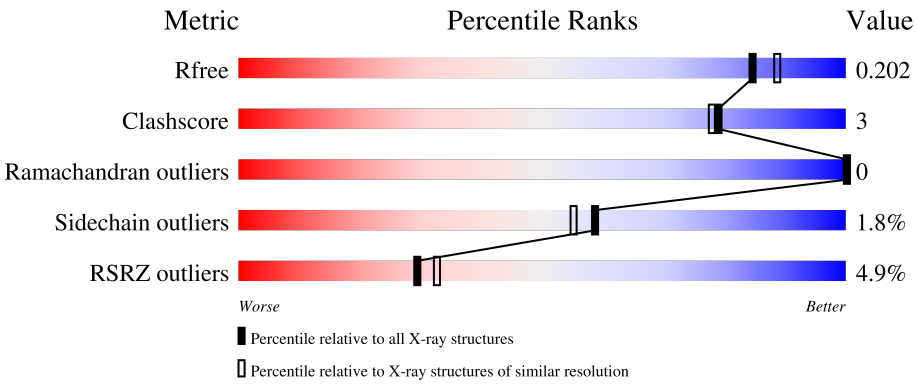
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	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 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 <=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	661	5%; 84%; 7% • 8%
2	B	2	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5130 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 Maltose-binding periplasmic protein,Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	608	4803	3082	788	920	13	0	4	0

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	expression tag	UNP P0AEY0
A	-34	ARG	-	expression tag	UNP P0AEY0
A	-33	GLY	-	expression tag	UNP P0AEY0
A	-32	SER	-	expression tag	UNP P0AEY0
A	-31	HIS	-	expression tag	UNP P0AEY0
A	-30	HIS	-	expression tag	UNP P0AEY0
A	-29	HIS	-	expression tag	UNP P0AEY0
A	-28	HIS	-	expression tag	UNP P0AEY0
A	-27	HIS	-	expression tag	UNP P0AEY0
A	-26	HIS	-	expression tag	UNP P0AEY0
A	-25	GLY	-	expression tag	UNP P0AEY0
A	-24	MET	-	expression tag	UNP P0AEY0
A	-23	ALA	-	expression tag	UNP P0AEY0
A	-22	SER	-	expression tag	UNP P0AEY0
A	-21	MET	-	expression tag	UNP P0AEY0
A	-20	THR	-	expression tag	UNP P0AEY0
A	-19	GLY	-	expression tag	UNP P0AEY0
A	-18	GLY	-	expression tag	UNP P0AEY0
A	-17	GLN	-	expression tag	UNP P0AEY0
A	-16	GLN	-	expression tag	UNP P0AEY0
A	-15	MET	-	expression tag	UNP P0AEY0
A	-14	GLY	-	expression tag	UNP P0AEY0
A	-13	ARG	-	expression tag	UNP P0AEY0
A	-12	ASP	-	expression tag	UNP P0AEY0
A	-11	LEU	-	expression tag	UNP P0AEY0
A	-10	TYR	-	expression tag	UNP P0AEY0
A	-9	ASP	-	expression tag	UNP P0AEY0

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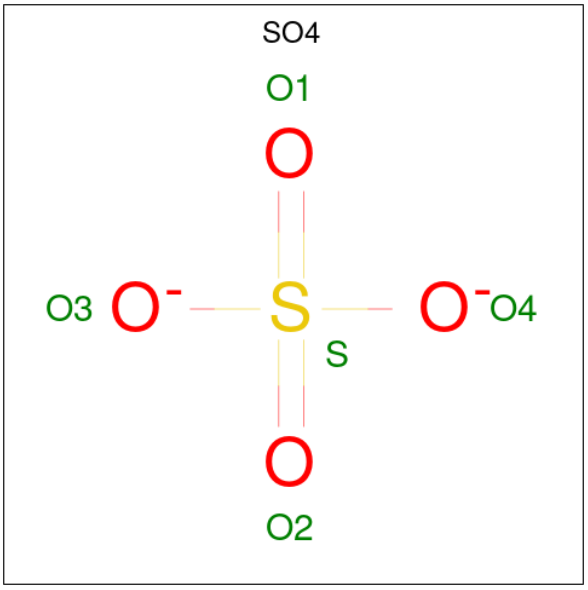
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP P0AEY0
A	-7	ASP	-	expression tag	UNP P0AEY0
A	-6	ASP	-	expression tag	UNP P0AEY0
A	-5	LYS	-	expression tag	UNP P0AEY0
A	-4	ASP	-	expression tag	UNP P0AEY0
A	-3	ARG	-	expression tag	UNP P0AEY0
A	-2	TRP	-	expression tag	UNP P0AEY0
A	-1	GLY	-	expression tag	UNP P0AEY0
A	0	SER	-	expression tag	UNP P0AEY0
A	174	HIS	-	linker	UNP P0AEY0
A	175	LEU	-	linker	UNP P0AEY0
A	192	ALA	VAL	conflict	UNP P42212
A	204	GLY	SER	conflict	UNP P42212
A	209	TYR	ASP	conflict	UNP P42212
A	235	LYS	ALA	conflict	UNP P42212
A	260	LEU	HIS	conflict	UNP P42212
A	268	GLY	-	linker	UNP P42212
A	269	GLY	-	linker	UNP P42212
A	270	THR	-	linker	UNP P42212
A	271	GLY	-	linker	UNP P42212
A	272	GLY	-	linker	UNP P42212
A	273	SER	-	linker	UNP P42212
A	274	MET	-	linker	UNP P42212
A	275	VAL	-	linker	UNP P42212
A	338	LEU	PHE	conflict	UNP P42212
A	340	C12	SER	chromophore	UNP P42212
A	340	C12	TYR	chromophore	UNP P42212
A	340	C12	GLY	chromophore	UNP P42212
A	367	ILE	VAL	conflict	UNP P42212
A	419	PHE	TYR	conflict	UNP P42212
A	421	GLY	-	linker	UNP P42212
A	560	VAL	ALA	conflict	UNP P0AEY0
A	608	ASP	ALA	conflict	UNP P0AEY0
A	619	GLY	-	expression tag	UNP P0AEY0
A	620	SER	-	expression tag	UNP P0AEY0
A	621	HIS	-	expression tag	UNP P0AEY0
A	622	HIS	-	expression tag	UNP P0AEY0
A	623	HIS	-	expression tag	UNP P0AEY0
A	624	HIS	-	expression tag	UNP P0AEY0
A	625	HIS	-	expression tag	UNP P0AEY0
A	626	HIS	-	expression tag	UNP P0AEY0
A	627	GLY	-	expression tag	UNP P0AEY0

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	B	2	23	12	11	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0
			Total	O	S		
3	A	1	5	4	1	0	0

- Molecule 4 is water.

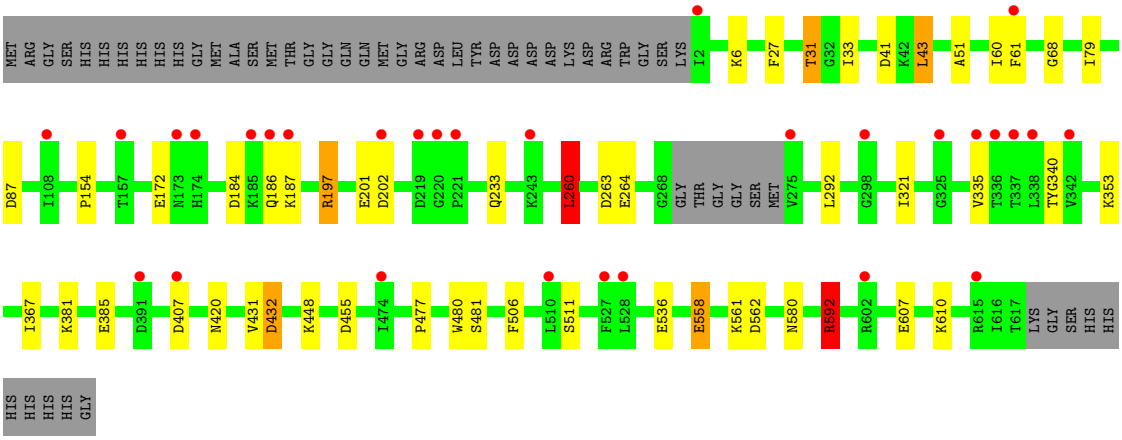
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	294	294	294	0	0

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.

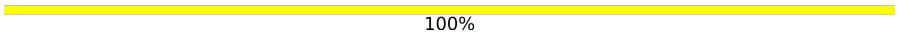
• Molecule 1: Maltose-binding periplasmic protein,Green fluorescent protein

Chain A:



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

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.26Å 88.69Å 119.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.06 – 1.90 29.06 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.06-1.90) 99.9 (29.06-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.25 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.165 , 0.199 0.174 , 0.202	Depositor DCC
R_{free} test set	3486 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	26.9	Xtriage
Anisotropy	0.454	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 40.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5130	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: C12, SO4, GLC

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	1.24	10/4905 (0.2%)	0.98	17/6644 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	607	GLU	CG-CD	7.42	1.63	1.51
1	A	536	GLU	CD-OE1	6.57	1.32	1.25
1	A	431	VAL	CB-CG2	-5.78	1.40	1.52
1	A	407	ASP	CB-CG	5.77	1.63	1.51
1	A	79	ILE	CB-CG2	5.74	1.70	1.52
1	A	51	ALA	CA-CB	5.65	1.64	1.52
1	A	481	SER	CB-OG	-5.59	1.34	1.42
1	A	172	GLU	CB-CG	5.46	1.62	1.52
1	A	558	GLU	CG-CD	5.34	1.59	1.51
1	A	335	VAL	CB-CG2	5.17	1.63	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	260	LEU	CB-CG-CD2	-8.87	95.92	111.00
1	A	197	ARG	NE-CZ-NH1	7.13	123.87	120.30
1	A	260	LEU	CA-CB-CG	6.75	130.84	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	592	ARG	CG-CD-NE	6.69	125.85	111.80
1	A	592	ARG	CD-NE-CZ	6.58	132.81	123.60
1	A	381	LYS	CD-CE-NZ	6.36	126.32	111.70
1	A	432	ASP	CB-CG-OD2	-6.35	112.58	118.30
1	A	31	THR	CA-CB-CG2	6.16	121.03	112.40
1	A	87[A]	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	A	87[B]	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	A	197	ARG	NE-CZ-NH2	-6.11	117.24	120.30
1	A	31	THR	OG1-CB-CG2	6.05	123.93	110.00
1	A	31	THR	N-CA-CB	-5.61	99.64	110.30
1	A	353	LYS	CD-CE-NZ	-5.28	99.55	111.70
1	A	455	ASP	CB-CG-OD1	5.27	123.04	118.30
1	A	562	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	A	43	LEU	N-CA-CB	5.09	120.58	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	31	THR	CB

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	4803	0	4727	27	0
2	B	23	0	20	0	0
3	A	10	0	0	0	0
4	A	294	0	0	1	0
All	All	5130	0	4747	27	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 3.

All (27) 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:43:LEU:HD13	1:A:60:ILE:HD11	1.66	0.77
1:A:31:THR:HG23	1:A:33:ILE:HG12	1.72	0.71
1:A:31:THR:CG2	1:A:33:ILE:H	2.05	0.69
1:A:43:LEU:CD1	1:A:60:ILE:HD11	2.22	0.68
1:A:263:ASP:OD1	4:A:846:HOH:O	2.12	0.67
1:A:43:LEU:HD13	1:A:60:ILE:CD1	2.26	0.65
1:A:201:GLU:O	1:A:202:ASP:HB2	1.97	0.65
1:A:292:LEU:HD23	1:A:292:LEU:C	2.21	0.61
1:A:31:THR:HG23	1:A:33:ILE:H	1.67	0.58
1:A:31:THR:HG22	1:A:33:ILE:H	1.71	0.55
1:A:154:PRO:HD2	1:A:592:ARG:NH1	2.23	0.53
1:A:367:ILE:CD1	1:A:385:GLU:HG2	2.39	0.52
1:A:31:THR:HG23	1:A:33:ILE:CG1	2.40	0.52
1:A:201:GLU:O	1:A:202:ASP:CB	2.61	0.49
1:A:592:ARG:HH11	1:A:592:ARG:HB2	1.75	0.49
1:A:558:GLU:OE2	1:A:558:GLU:HA	2.13	0.49
1:A:367:ILE:HD13	1:A:385:GLU:HG2	1.95	0.48
1:A:184:ASP:OD1	1:A:187:LYS:HG2	2.14	0.47
1:A:68:GLY:HA3	1:A:580:ASN:O	2.16	0.46
1:A:27:PHE:O	1:A:31:THR:HB	2.16	0.45
1:A:31:THR:CG2	1:A:33:ILE:HB	2.49	0.43
1:A:321:ILE:HG23	1:A:321:ILE:HD12	1.84	0.43
1:A:477:PRO:HA	1:A:480:TRP:CE2	2.54	0.42
1:A:61:PHE:HA	1:A:511:SER:O	2.21	0.41
1:A:197:ARG:O	1:A:420:ASN:HA	2.20	0.41
1:A:260:LEU:HD12	1:A:264:GLU:CD	2.41	0.41
1:A:432:ASP:OD2	1:A:610:LYS:CG	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	605/661 (92%)	597 (99%)	8 (1%)	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 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	508/545 (93%)	499 (98%)	9 (2%)	59	55

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	41	ASP
1	A	186	GLN
1	A	233	GLN
1	A	260	LEU
1	A	448	LYS
1	A	506	PHE
1	A	561	LYS
1	A	592	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	C12	A	340	1	20,23,23	2.20	6 (30%)	21,32,32	1.82	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
1	C12	A	340	1	-	3/8/15/15	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	340	C12	CA3-C3	-6.42	1.33	1.49
1	A	340	C12	CB2-CA2	-3.62	1.48	1.51
1	A	340	C12	CA3-N3	-3.60	1.42	1.49
1	A	340	C12	C1-N2	3.05	1.39	1.34
1	A	340	C12	CE2-CD2	2.51	1.43	1.38
1	A	340	C12	CE1-CD1	2.13	1.42	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	340	C12	CG2-CB2-CA2	5.36	126.15	112.40
1	A	340	C12	CB2-CG2-CD2	-3.30	111.92	120.92
1	A	340	C12	CE1-CD1-CG2	-2.36	117.78	121.03
1	A	340	C12	CB2-CA2-C2	-2.34	124.40	131.20
1	A	340	C12	CB2-CG2-CD1	2.09	126.62	120.92

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	340	C12	C2-CA2-CB2-CG2
1	A	340	C12	CA2-CB2-CG2-CD1

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Mol	Chain	Res	Type	Atoms
1	A	340	C12	N2-CA2-CB2-CG2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

2 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	B	1	2	12,12,12	1.39	2 (16%)	17,17,17	1.46	4 (23%)
2	GLC	B	2	2	11,11,12	0.92	0	15,15,17	1.50	3 (20%)

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	B	1	2	-	1/2/22/22	0/1/1/1
2	GLC	B	2	2	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	GLC	C1-C2	2.47	1.58	1.52
2	B	1	GLC	C4-C5	2.03	1.57	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	GLC	O1-C1-C2	3.21	118.08	109.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	GLC	C1-O5-C5	-2.96	108.19	112.19
2	B	1	GLC	O1-C1-O5	2.38	117.52	110.38
2	B	2	GLC	C2-C3-C4	-2.31	106.90	110.89
2	B	1	GLC	O2-C2-C3	-2.18	105.32	110.35
2	B	1	GLC	C1-C2-C3	-2.09	105.98	110.31
2	B	2	GLC	C1-C2-C3	-2.01	107.20	109.67

There are no chirality outliers.

All (1) torsion outliers are listed below:

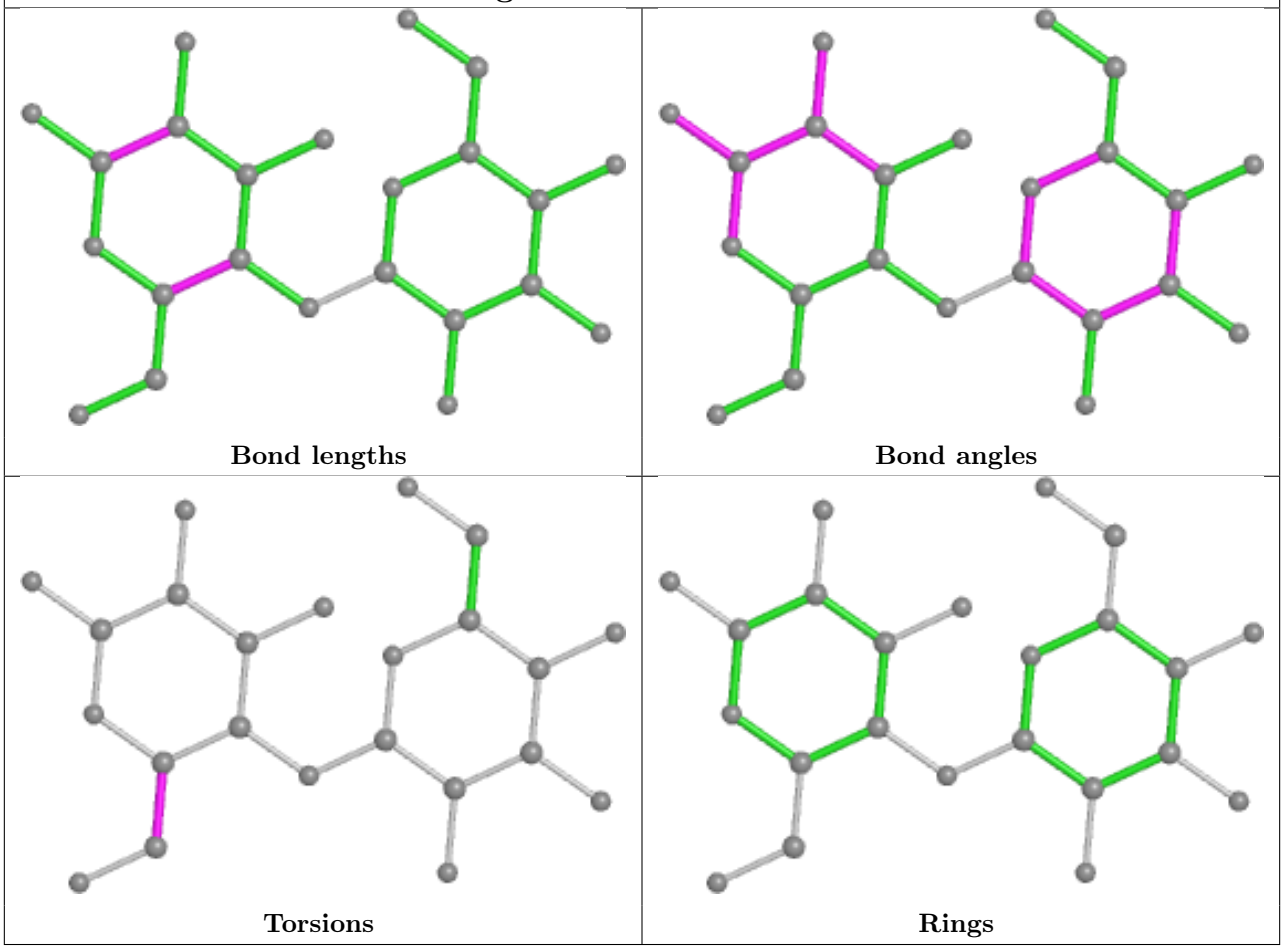
Mol	Chain	Res	Type	Atoms
2	B	1	GLC	C4-C5-C6-O6

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 B



5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
3	SO4	A	628	-	4,4,4	0.26	0	6,6,6	1.45	1 (16%)
3	SO4	A	629	-	4,4,4	0.37	0	6,6,6	0.73	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	628	SO4	O4-S-O1	-2.50	96.25	109.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	607/661 (91%)	0.07	30 (4%) 29 33	16, 28, 45, 65	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	602	ARG	5.8
1	A	186	GLN	5.4
1	A	173	ASN	3.9
1	A	2	ILE	3.9
1	A	219	ASP	3.4
1	A	157[A]	THR	3.2
1	A	275	VAL	3.2
1	A	407	ASP	3.2
1	A	108	ILE	3.0
1	A	510	LEU	2.9
1	A	174	HIS	2.8
1	A	187	LYS	2.7
1	A	220	GLY	2.6
1	A	61	PHE	2.5
1	A	337	THR	2.4
1	A	335	VAL	2.4
1	A	221	PRO	2.4
1	A	338	LEU	2.4
1	A	185	LYS	2.4
1	A	298	GLY	2.4
1	A	342	VAL	2.3
1	A	325	GLY	2.3
1	A	528	LEU	2.2
1	A	474	ILE	2.2
1	A	336	THR	2.1
1	A	243	LYS	2.1
1	A	391[A]	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	527	PHE	2.1
1	A	202	ASP	2.0
1	A	615	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	C12	A	340	22/22	0.97	0.21	19,23,28,31	0

6.3 Carbohydrates (i)

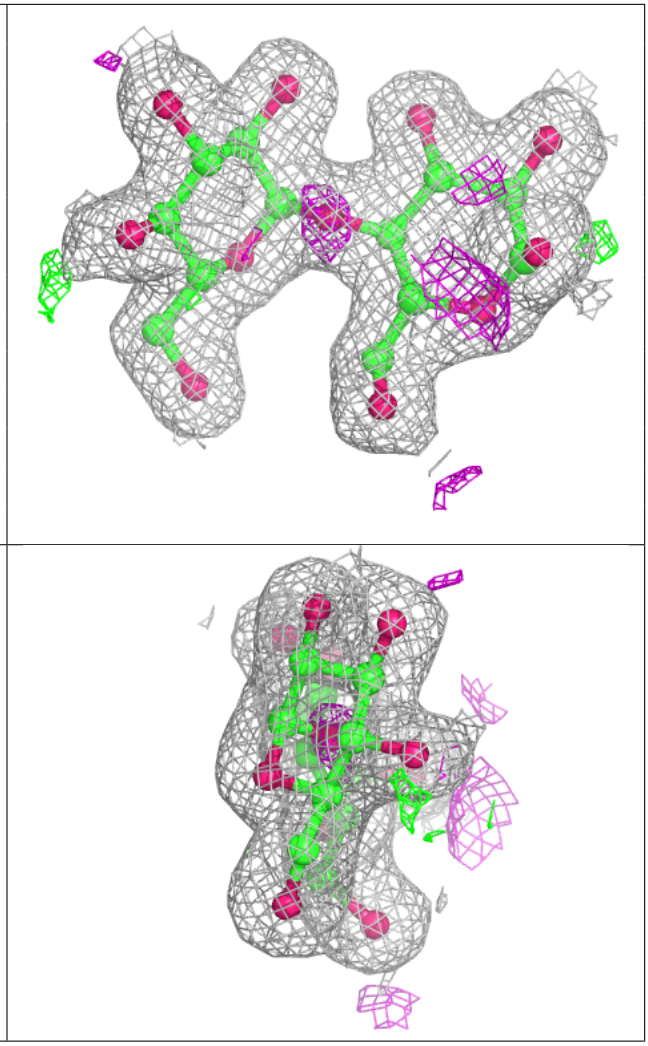
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	B	1	12/12	0.96	0.11	13,21,24,25	0
2	GLC	B	2	11/12	0.97	0.11	15,21,24,26	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.

Electron density around Chain B:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



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(Å^2)	Q<0.9
3	SO4	A	628	5/5	0.97	0.10	48,48,53,54	0
3	SO4	A	629	5/5	0.98	0.08	33,37,40,41	0

6.5 Other polymers (i)

There are no such residues in this entry.