



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 21, 2020 – 05:10 PM BST

PDB ID : 4U31
Title : Sco GlgEI-V279S in Complex with maltose-C-phosphonate
Authors : Ronning, D.R.; Lindenberger, J.J.
Deposited on : 2014-07-18
Resolution : 1.85 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.14.6
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) : 2.14.6

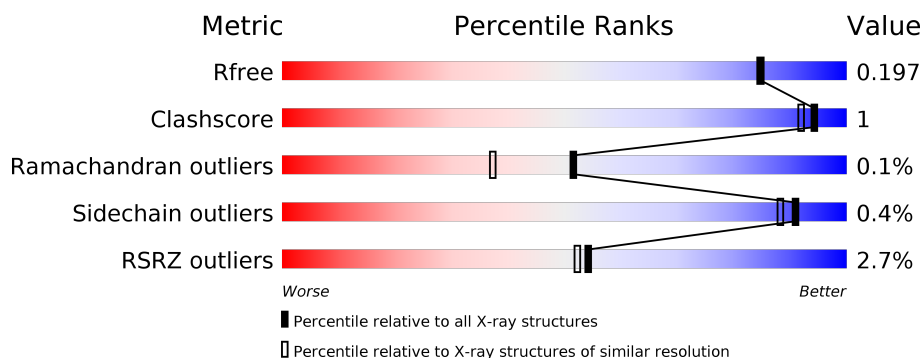
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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 $\leq 5\%$. 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	683	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>5%</div> </div> </div>
1	B	683	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>5%</div> </div> </div>
2	C	2	<div> <div>50%</div> <div>50%</div> </div>
2	D	2	<div> <div>100%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11906 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-1,4-glucan:maltose-1-phosphate maltosyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	649	Total	C	N	O	S	1	6	0
			5207	3281	959	957	10			
1	B	649	Total	C	N	O	S	0	2	0
			5152	3252	939	949	12			

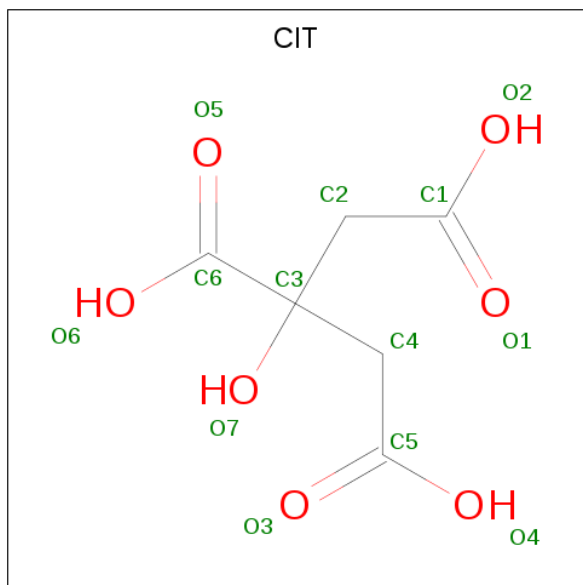
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	279	SER	VAL	engineered mutation	UNP Q9L1K2
A	676	ALA	-	expression tag	UNP Q9L1K2
A	677	LEU	-	expression tag	UNP Q9L1K2
A	678	HIS	-	expression tag	UNP Q9L1K2
A	679	HIS	-	expression tag	UNP Q9L1K2
A	680	HIS	-	expression tag	UNP Q9L1K2
A	681	HIS	-	expression tag	UNP Q9L1K2
A	682	HIS	-	expression tag	UNP Q9L1K2
A	683	HIS	-	expression tag	UNP Q9L1K2
B	279	SER	VAL	engineered mutation	UNP Q9L1K2
B	676	ALA	-	expression tag	UNP Q9L1K2
B	677	LEU	-	expression tag	UNP Q9L1K2
B	678	HIS	-	expression tag	UNP Q9L1K2
B	679	HIS	-	expression tag	UNP Q9L1K2
B	680	HIS	-	expression tag	UNP Q9L1K2
B	681	HIS	-	expression tag	UNP Q9L1K2
B	682	HIS	-	expression tag	UNP Q9L1K2
B	683	HIS	-	expression tag	UNP Q9L1K2

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-(1S)-1,5-anhydro-1-(phosphonomethyl)-D-glucitol.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	P	0	0	0
			27	13	13	1			
2	D	2	Total	C	O	P	0	0	0
			27	13	13	1			

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

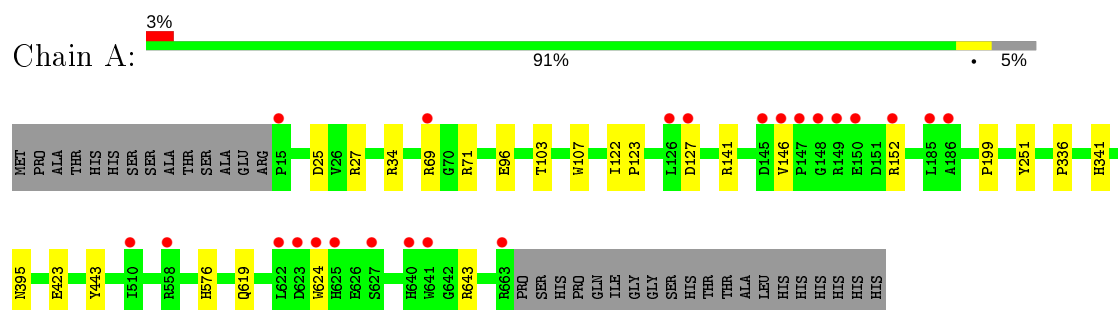
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	710	Total	O	0	0
			710	710		
5	B	737	Total	O	0	0
			737	737		

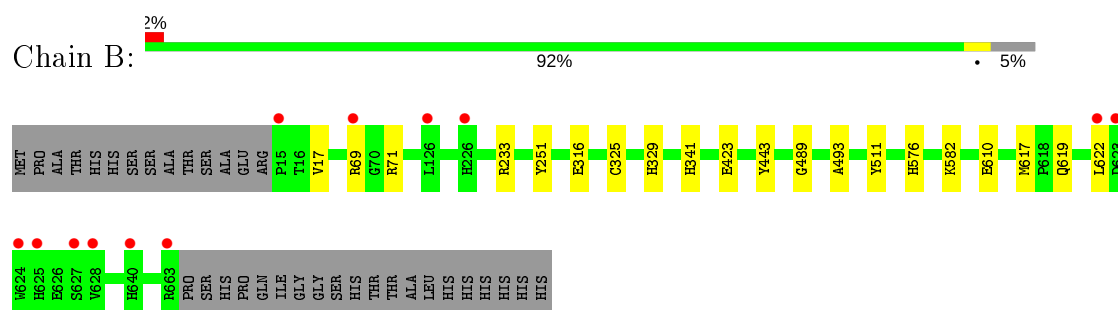
3 Residue-property plots

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-1,4-glucan:maltose-1-phosphate maltosyltransferase 1



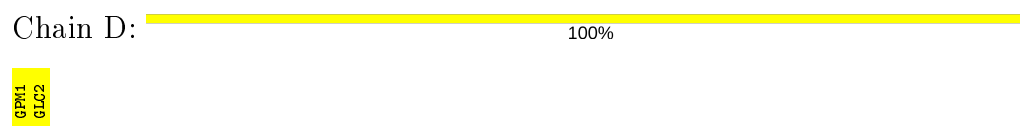
- Molecule 1: Alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase 1



- Molecule 2: alpha-D-glucopyranose-(1-4)-(1S)-1,5-anhydro-1-(phosphonomethyl)-D-glucitol



- Molecule 2: alpha-D-glucopyranose-(1-4)-(1S)-1,5-anhydro-1-(phosphonomethyl)-D-glucitol



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	113.56Å 113.56Å 315.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.69 – 1.85 42.68 – 1.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.69-1.85) 97.5 (42.68-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 1.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.164 , 0.194 0.167 , 0.197	Depositor DCC
R_{free} test set	2000 reflections (1.14%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11906	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.31% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GPM, GLC, EDO, CIT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.35	0/5359	0.51	0/7324
1	B	0.36	0/5304	0.52	0/7251
All	All	0.36	0/10663	0.51	0/14575

There are no bond length outliers.

There are no bond angle outliers.

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	5207	0	5050	13	0
1	B	5152	0	4992	11	0
2	C	27	0	22	1	0
2	D	27	0	22	0	0
3	A	13	0	2	2	0
3	B	13	0	7	2	0
4	A	16	0	24	0	0
4	B	4	0	6	0	0
5	A	710	0	0	1	2
5	B	737	0	0	3	2
All	All	11906	0	10125	27	2

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 1.

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)
3:A:702:CIT:C1	3:A:702:CIT:O1	1.66	1.42
3:B:702:CIT:C1	3:B:702:CIT:O2	1.71	1.37
1:A:25[B]:ASP:OD2	1:A:27[B]:ARG:NH1	2.16	0.79
1:A:69:ARG:NH2	1:A:96:GLU:OE2	2.16	0.78
3:A:702:CIT:O1	3:A:702:CIT:C2	2.35	0.74
1:B:316:GLU:OE1	5:B:1166:HOH:O	2.11	0.68
1:A:146:VAL:O	1:A:152:ARG:NH2	2.33	0.62
1:A:624:TRP:HB3	1:A:643:ARG:HH21	1.64	0.62
1:A:34:ARG:HE	1:B:17:VAL:HG13	1.74	0.52
1:B:576:HIS:CG	1:B:619:GLN:HG2	2.47	0.48
1:A:576:HIS:CG	1:A:619:GLN:HG2	2.49	0.48
1:A:336:PRO:O	1:A:341:HIS:HE1	1.97	0.47
1:B:489:GLY:HA3	1:B:493:ALA:HB2	1.97	0.47
1:A:141:ARG:NH1	5:A:801:HOH:O	2.43	0.45
1:B:582:LYS:HG3	1:B:610:GLU:O	2.18	0.43
1:A:423:GLU:HA	1:A:443:TYR:CD1	2.54	0.43
1:A:122:ILE:HB	1:A:123:PRO:HD3	2.01	0.42
1:A:69:ARG:HE	1:A:71:ARG:NH2	2.17	0.42
1:B:233:ARG:HG2	5:B:1066:HOH:O	2.20	0.42
1:B:341:HIS:HE1	5:B:822:HOH:O	2.03	0.42
3:B:702:CIT:HO2	3:B:702:CIT:C1	2.14	0.41
1:B:617:MET:HE3	1:B:622:LEU:HB2	2.03	0.41
1:B:69:ARG:HB2	1:B:71:ARG:HD3	2.03	0.41
1:B:325[B]:CYS:HB2	1:B:329:HIS:HB2	2.02	0.41
1:B:423:GLU:HA	1:B:443:TYR:CD1	2.56	0.41
1:A:395:ASN:OD1	2:C:1:GPM:O3P	2.39	0.40
1:A:103:THR:HG22	1:A:199:PRO:HA	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:892:HOH:O	5:B:1299:HOH:O[6_446]	2.12	0.08
5:A:892:HOH:O	5:B:863:HOH:O[6_446]	2.14	0.06

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	654/683 (96%)	640 (98%)	13 (2%)	1 (0%)	47	33
1	B	649/683 (95%)	636 (98%)	13 (2%)	0	100	100
All	All	1303/1366 (95%)	1276 (98%)	26 (2%)	1 (0%)	51	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	127	ASP

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	544/565 (96%)	542 (100%)	2 (0%)	91	88
1	B	539/565 (95%)	537 (100%)	2 (0%)	91	88
All	All	1083/1130 (96%)	1079 (100%)	4 (0%)	91	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	TRP
1	A	251	TYR
1	B	251	TYR
1	B	511	TYR

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

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 ⓘ

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GPM	C	1	2	15,16,16	1.62	2 (13%)	21,24,24	1.50	5 (23%)
2	GLC	C	2	2	11,11,12	1.31	1 (9%)	15,15,17	0.82	1 (6%)
2	GPM	D	1	2	15,16,16	1.46	2 (13%)	21,24,24	1.45	3 (14%)
2	GLC	D	2	2	11,11,12	1.45	1 (9%)	15,15,17	0.89	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GPM	C	1	2	-	0/7/27/27	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	GPM	D	1	2	-	0/7/27/27	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	GPM	P-C7	4.80	1.83	1.78
2	D	1	GPM	P-C7	3.92	1.82	1.78
2	D	2	GLC	C2-C3	-3.54	1.47	1.52
2	C	2	GLC	C2-C3	-3.43	1.47	1.52
2	D	1	GPM	C3-C2	-3.29	1.43	1.52
2	C	1	GPM	C3-C2	-3.16	1.44	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	GPM	O5-C5-C4	3.97	116.90	109.69
2	C	1	GPM	O5-C5-C4	3.63	116.28	109.69
2	C	1	GPM	O4-C4-C5	-2.87	102.18	109.30
2	D	1	GPM	O4-C4-C5	-2.55	102.97	109.30
2	D	2	GLC	C1-C2-C3	2.44	112.67	109.67
2	C	1	GPM	C3-C4-C5	2.39	114.50	110.24
2	C	2	GLC	C1-C2-C3	2.16	112.32	109.67
2	C	1	GPM	O3-C3-C2	-2.11	105.46	110.35
2	D	1	GPM	O3-C3-C2	-2.10	105.50	110.35
2	C	1	GPM	O2P-P-C7	2.05	111.75	106.74

There are no chirality outliers.

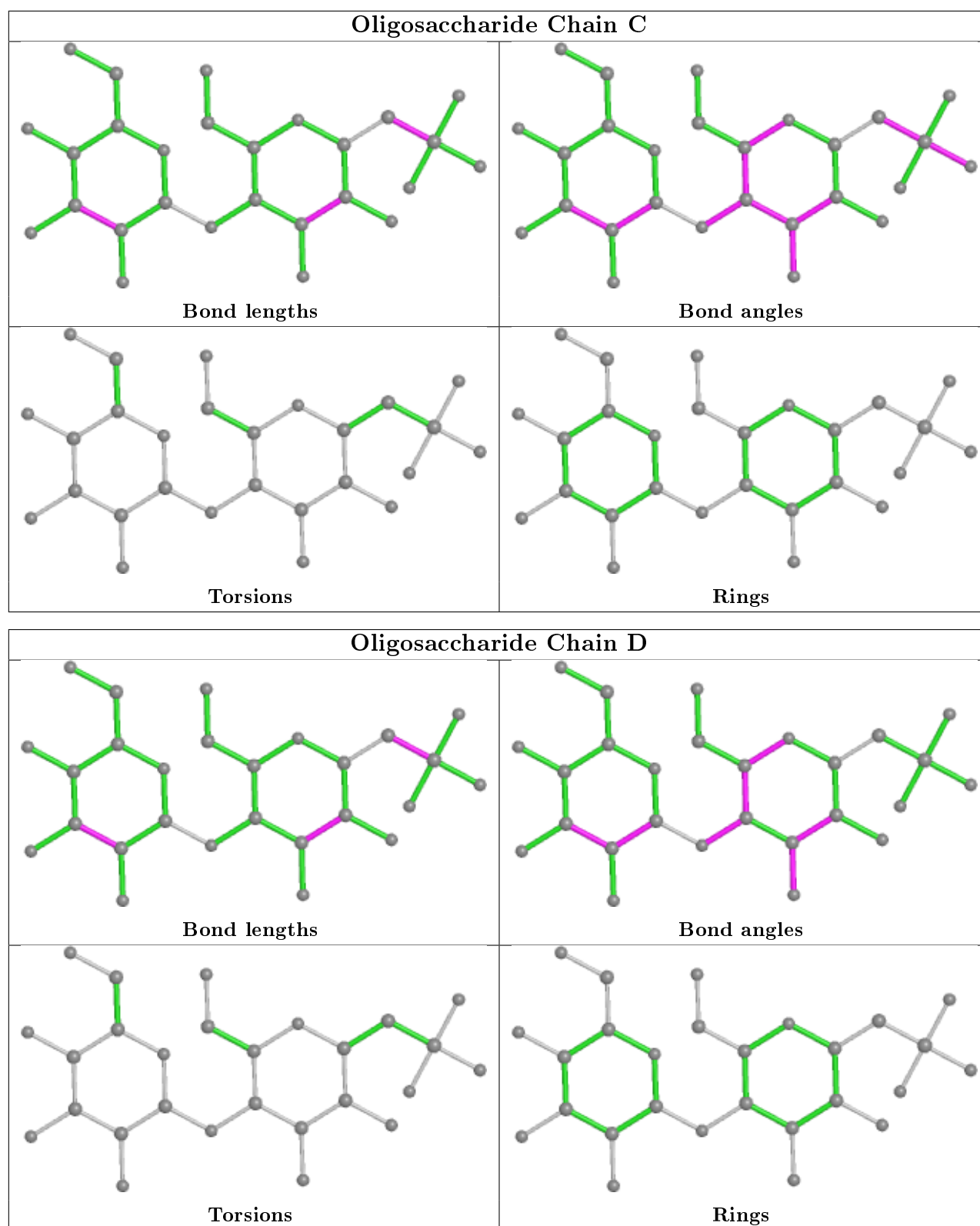
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	GPM	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](#)

7 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$
4	EDO	A	704	-	3,3,3	0.49	0	2,2,2	0.52	0
4	EDO	B	703	-	3,3,3	0.52	0	2,2,2	0.16	0
3	CIT	B	702	3	3,12,12	6.46	2 (66%)	3,17,17	11.98	2 (66%)
4	EDO	A	705	-	3,3,3	0.47	0	2,2,2	0.40	0
4	EDO	A	703	-	3,3,3	0.55	0	2,2,2	0.33	0
4	EDO	A	706	-	3,3,3	0.55	0	2,2,2	0.34	0
3	CIT	A	702	3	3,12,12	4.10	1 (33%)	3,17,17	14.06	3 (100%)

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
4	EDO	A	704	-	-	0/1/1/1	-
4	EDO	B	703	-	-	0/1/1/1	-
3	CIT	B	702	3	-	2/6/16/16	-
4	EDO	A	705	-	-	0/1/1/1	-
4	EDO	A	703	-	-	0/1/1/1	-
4	EDO	A	706	-	-	0/1/1/1	-
3	CIT	A	702	3	-	3/6/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	702	CIT	C4-C3	8.94	1.67	1.54
3	A	702	CIT	O7-C3	-6.76	1.32	1.43
3	B	702	CIT	O7-C3	6.62	1.53	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	702	CIT	C3-C4-C5	20.32	147.53	114.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	CIT	C3-C4-C5	16.92	142.07	114.98
3	A	702	CIT	C3-C2-C1	16.60	141.56	114.98
3	A	702	CIT	C4-C3-C2	5.60	124.31	109.33
3	B	702	CIT	C4-C3-C2	-3.92	98.84	109.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	702	CIT	C2-C3-C4-C5
3	A	702	CIT	O7-C3-C4-C5
3	B	702	CIT	C1-C2-C3-C6
3	B	702	CIT	C2-C3-C4-C5
3	A	702	CIT	C1-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	702	CIT	2	0
3	A	702	CIT	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	649/683 (95%)	-0.12	23 (3%)	44 40	13, 20, 44, 66	1 (0%)
1	B	649/683 (95%)	-0.17	12 (1%)	68 67	13, 21, 39, 65	5 (0%)
All	All	1298/1366 (95%)	-0.15	35 (2%)	54 52	13, 21, 42, 66	6 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	126	LEU	7.5
1	B	625	HIS	4.1
1	A	625	HIS	3.8
1	B	226	HIS	3.6
1	A	146	VAL	3.6
1	B	663	ARG	3.4
1	B	15	PRO	3.3
1	A	149	ARG	3.1
1	B	627	SER	3.1
1	A	145	ASP	3.0
1	A	623	ASP	3.0
1	A	627	SER	3.0
1	A	558[A]	ARG	3.0
1	A	663	ARG	2.9
1	A	150	GLU	2.9
1	A	624	TRP	2.7
1	A	147	PRO	2.6
1	A	152	ARG	2.6
1	A	15	PRO	2.5
1	B	624	TRP	2.5
1	A	622	LEU	2.5
1	A	640	HIS	2.5
1	B	628	VAL	2.5
1	B	622	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	69	ARG	2.4
1	B	640	HIS	2.4
1	A	69	ARG	2.3
1	A	185	LEU	2.3
1	A	127	ASP	2.2
1	A	641	TRP	2.2
1	A	186	ALA	2.2
1	B	623	ASP	2.2
1	A	510	ILE	2.2
1	B	126	LEU	2.2
1	A	148	GLY	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](#)

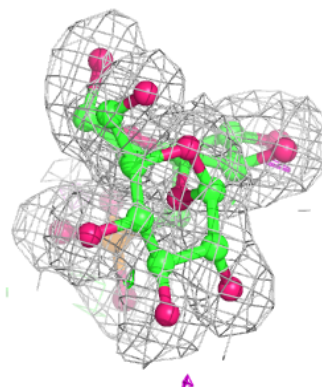
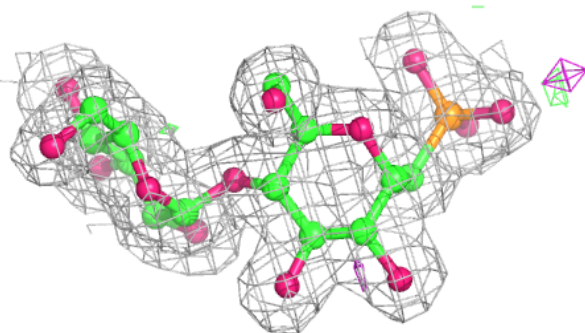
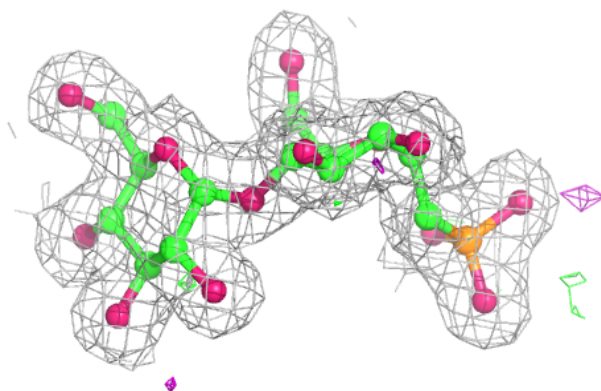
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	GLC	D	2	11/12	0.97	0.07	14,16,18,19	0
2	GPM	D	1	16/16	0.97	0.10	12,17,22,22	0
2	GLC	C	2	11/12	0.97	0.07	16,17,18,19	0
2	GPM	C	1	16/16	0.98	0.09	14,17,22,22	0

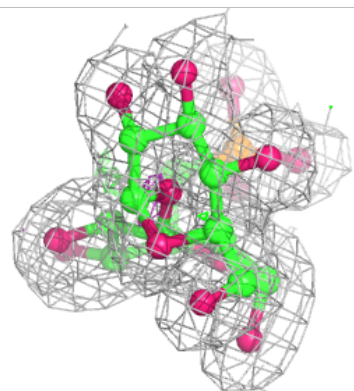
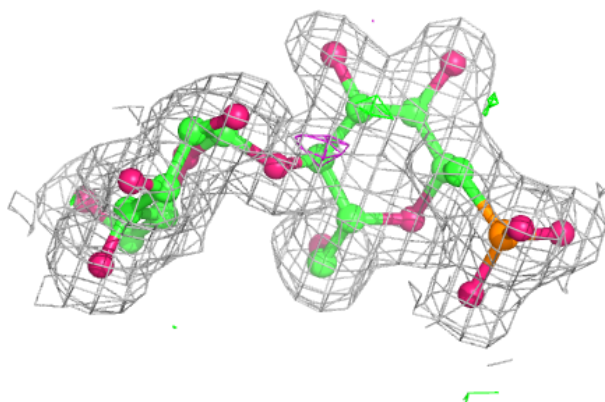
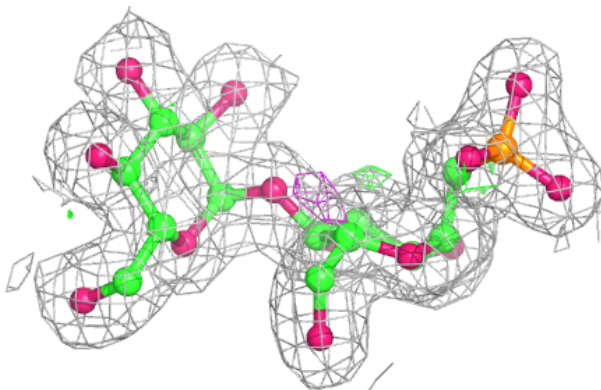
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

**Electron density around Chain D:**

$2mF_o-DF_c$ (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(\AA^2)	Q<0.9
4	EDO	A	704	4/4	0.71	0.20	31,34,34,39	4
4	EDO	A	706	4/4	0.84	0.21	25,26,28,30	4
4	EDO	B	703	4/4	0.85	0.19	25,29,33,36	0
3	CIT	B	702	13/13	0.87	0.15	28,33,37,38	13
3	CIT	A	702	13/13	0.88	0.14	28,33,36,38	13
4	EDO	A	703	4/4	0.91	0.16	22,23,24,27	4
4	EDO	A	705	4/4	0.93	0.20	32,45,46,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.