



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 17, 2024 – 04:12 pm BST

PDB ID : 8OPX
Title : Structure of Mycobacterium tuberculosis beta-oxidation trifunctional enzyme
in complex with Trehalose (Fragment-B-TRE)
Authors : Dalwani, S.; Wierenga, R.K.; Venkatesan, R.
Deposited on : 2023-04-10
Resolution : 2.90 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	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

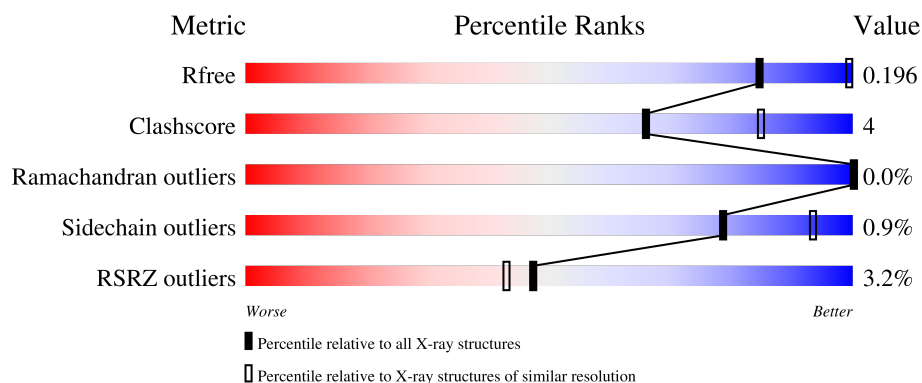
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	736	<div> <div>7%</div> <div> <div></div> <div>87%</div> <div>11%</div> <div></div> </div> </div>
1	B	736	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>11%</div> <div></div> </div> </div>
2	C	403	<div> <div></div> <div> <div></div> <div>90%</div> <div>8%</div> <div></div> </div> </div>
2	D	403	<div> <div></div> <div> <div></div> <div>89%</div> <div>10%</div> <div></div> </div> </div>
3	G	2	<div> <div></div> <div> <div></div> <div>50%</div> <div>50%</div> <div></div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	H	2	<div><div></div><div>50%</div><div>50%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16841 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 3-hydroxyacyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	724	Total	C	N	O	S	0	0	0
			5389	3411	925	1032	21			
1	A	722	Total	C	N	O	S	0	0	0
			5377	3404	923	1029	21			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	initiating methionine	UNP O53872
B	-14	GLY	-	expression tag	UNP O53872
B	-13	SER	-	expression tag	UNP O53872
B	-12	SER	-	expression tag	UNP O53872
B	-11	HIS	-	expression tag	UNP O53872
B	-10	HIS	-	expression tag	UNP O53872
B	-9	HIS	-	expression tag	UNP O53872
B	-8	HIS	-	expression tag	UNP O53872
B	-7	HIS	-	expression tag	UNP O53872
B	-6	HIS	-	expression tag	UNP O53872
B	-5	SER	-	expression tag	UNP O53872
B	-4	GLN	-	expression tag	UNP O53872
B	-3	ASP	-	expression tag	UNP O53872
B	-2	PRO	-	expression tag	UNP O53872
B	-1	ASN	-	expression tag	UNP O53872
B	0	SER	-	expression tag	UNP O53872
A	-15	MET	-	initiating methionine	UNP O53872
A	-14	GLY	-	expression tag	UNP O53872
A	-13	SER	-	expression tag	UNP O53872
A	-12	SER	-	expression tag	UNP O53872
A	-11	HIS	-	expression tag	UNP O53872
A	-10	HIS	-	expression tag	UNP O53872
A	-9	HIS	-	expression tag	UNP O53872
A	-8	HIS	-	expression tag	UNP O53872
A	-7	HIS	-	expression tag	UNP O53872

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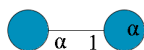
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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	HIS	-	expression tag	UNP O53872
A	-5	SER	-	expression tag	UNP O53872
A	-4	GLN	-	expression tag	UNP O53872
A	-3	ASP	-	expression tag	UNP O53872
A	-2	PRO	-	expression tag	UNP O53872
A	-1	ASN	-	expression tag	UNP O53872
A	0	SER	-	expression tag	UNP O53872

- Molecule 2 is a protein called Putative acyltransferase Rv0859.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	396	Total	C	N	O	S	0	0	0
			2921	1822	519	565	15			
2	D	399	Total	C	N	O	S	0	0	0
			2942	1836	522	568	16			

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	G	2	Total	C	O	0	0	0
			23	12	11			
3	H	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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

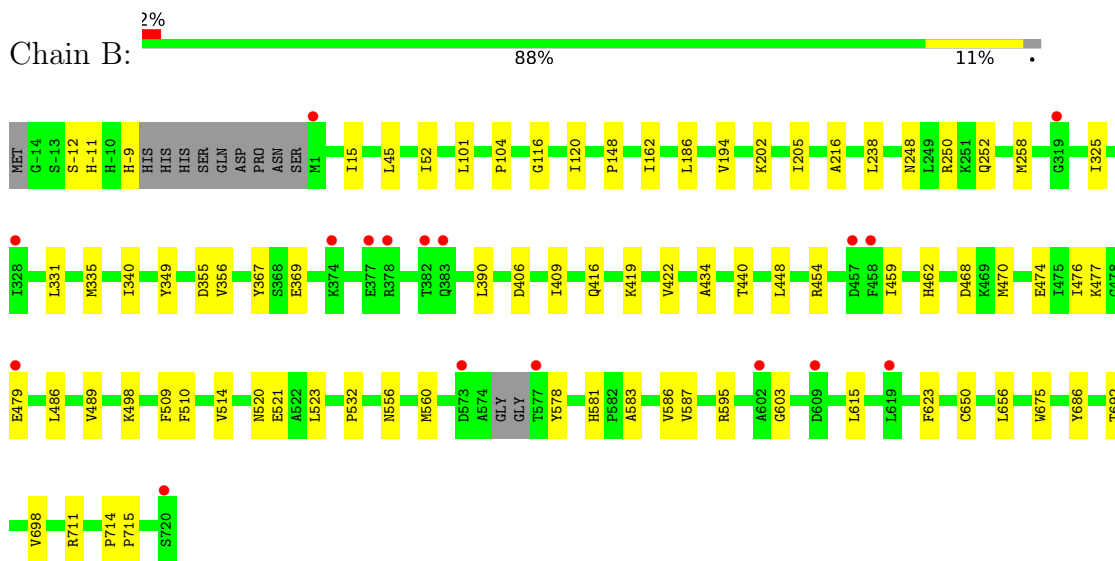
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	14	Total	O	0	0
			14	14		
5	C	9	Total	O	0	0
			9	9		
5	A	13	Total	O	0	0
			13	13		
5	D	10	Total	O	0	0
			10	10		

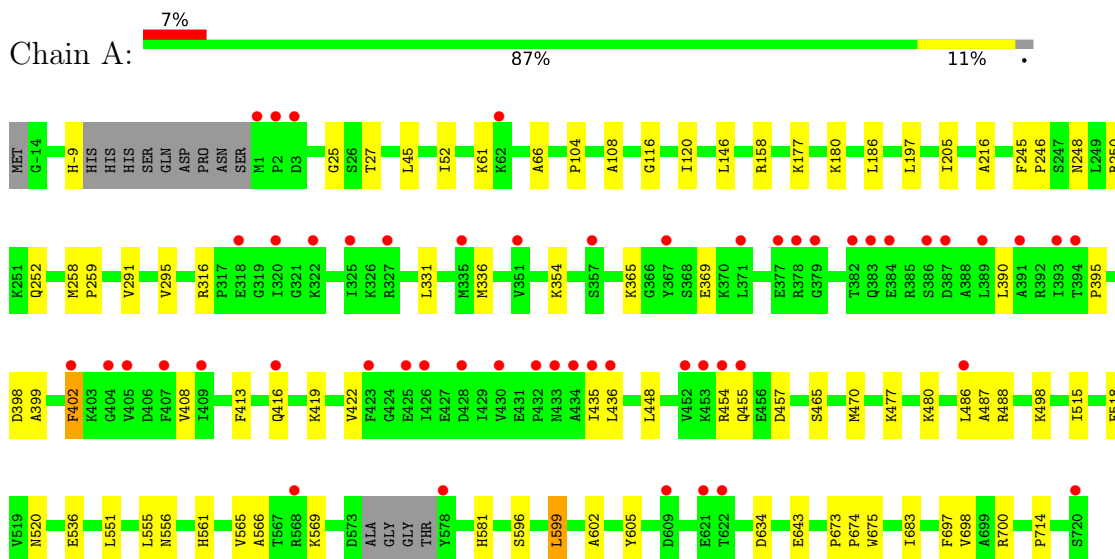
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

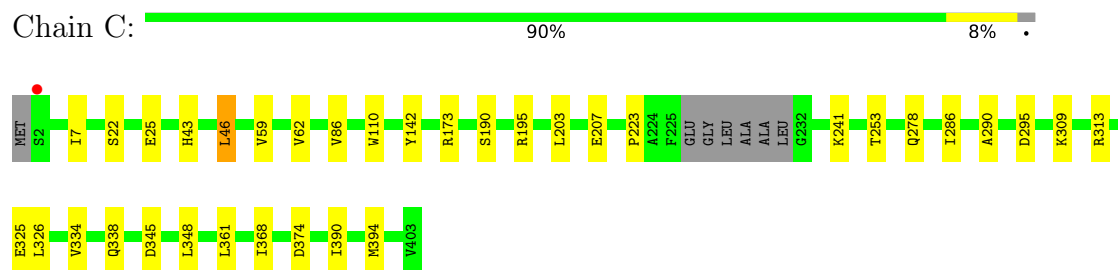
- Molecule 1: 3-hydroxyacyl-CoA dehydrogenase



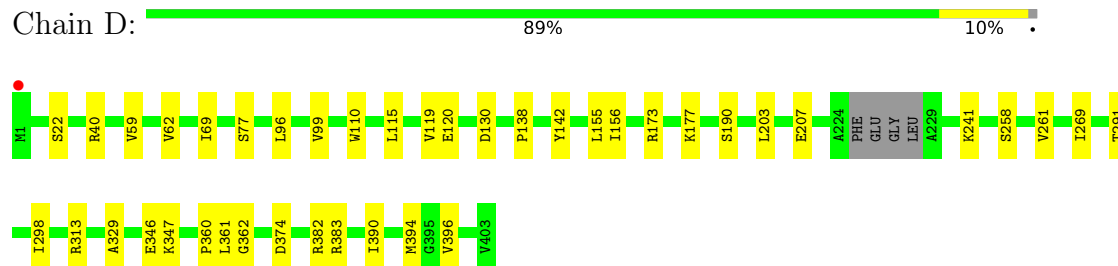
- Molecule 1: 3-hydroxyacyl-CoA dehydrogenase



- Molecule 2: Putative acyltransferase Rv0859



- Molecule 2: Putative acyltransferase Rv0859



- Molecule 3: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose



- Molecule 3: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	248.41Å 135.16Å 119.16Å 90.00° 110.56° 90.00°	Depositor
Resolution (Å)	48.37 – 2.90 48.37 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.9 (48.37-2.90) 97.9 (48.37-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.189 , 0.224 0.188 , 0.196	Depositor DCC
R_{free} test set	3904 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	59.4	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16841	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.25	0/5476	0.48	0/7408
1	B	0.25	0/5488	0.47	0/7425
2	C	0.25	0/2964	0.51	0/4012
2	D	0.25	0/2985	0.51	0/4040
All	All	0.25	0/16913	0.49	0/22885

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 [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	5377	0	5425	46	0
1	B	5389	0	5437	45	0
2	C	2921	0	2937	24	0
2	D	2942	0	2968	27	0
3	G	23	0	21	2	0
3	H	23	0	21	1	0
4	A	25	0	0	0	0
4	B	30	0	0	1	0
4	C	35	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	30	0	0	1	0
5	A	13	0	0	1	0
5	B	14	0	0	0	0
5	C	9	0	0	0	0
5	D	10	0	0	0	0
All	All	16841	0	16809	135	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 (135) 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:250:ARG:HH22	3:G:1:GLC:H62	1.53	0.72
1:A:556:ASN:HD21	1:A:599:LEU:HD22	1.56	0.71
1:B:250:ARG:NH1	2:C:142:TYR:O	2.25	0.69
1:B:-9:HIS:NE2	4:B:803:SO4:O1	2.26	0.68
1:A:365:LYS:HD2	1:A:395:PRO:HG3	1.78	0.65
1:A:369:GLU:HG2	1:A:390:LEU:HD13	1.80	0.62
1:A:158:ARG:NH1	5:A:901:HOH:O	2.31	0.62
2:C:241:LYS:NZ	3:G:1:GLC:O2	2.33	0.61
1:A:250:ARG:NH1	2:D:142:TYR:O	2.34	0.61
1:A:470:MET:O	1:A:498:LYS:NZ	2.31	0.61
2:C:173:ARG:NH2	2:C:348:LEU:O	2.31	0.60
1:B:367:TYR:OH	1:B:468:ASP:OD1	2.16	0.58
2:D:291:THR:HG22	2:D:396:VAL:HG22	1.85	0.58
1:B:477:LYS:HB2	1:B:486:LEU:HD21	1.85	0.58
1:B:419:LYS:HE2	1:B:440:THR:HB	1.86	0.57
1:B:369:GLU:HG2	1:B:390:LEU:HD13	1.87	0.57
1:A:104:PRO:HG2	1:A:205:ILE:HG23	1.87	0.56
1:B:520:ASN:HB3	1:B:581:HIS:CE1	2.42	0.55
1:A:25:GLY:O	1:A:61:LYS:NZ	2.36	0.54
2:C:22:SER:OG	2:C:207:GLU:OE2	2.25	0.54
1:B:355:ASP:OD1	1:B:356:VAL:N	2.33	0.54
2:C:62:VAL:HG12	2:D:62:VAL:HG12	1.89	0.54
1:B:459:ILE:HG21	1:B:489:VAL:HG21	1.89	0.54
1:B:510:PHE:CG	1:B:656:LEU:HD21	2.43	0.54
1:A:435:ILE:HD11	1:A:488:ARG:HB3	1.90	0.54
2:C:110:TRP:O	2:D:313:ARG:NH1	2.42	0.53
2:D:69:ILE:HD13	2:D:119:VAL:HG11	1.91	0.53
1:B:532:PRO:HB2	1:B:615:LEU:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:LEU:HD13	1:B:422:VAL:HG12	1.90	0.52
1:B:434:ALA:O	1:B:454:ARG:NH2	2.36	0.52
2:C:110:TRP:CD1	2:D:313:ARG:HD3	2.45	0.52
2:C:195:ARG:NH2	4:C:502:SO4:O3	2.31	0.52
1:B:459:ILE:HD11	1:B:486:LEU:HD23	1.91	0.52
1:B:462:HIS:HB3	1:B:474:GLU:HB3	1.91	0.51
1:A:331:LEU:HD13	1:A:422:VAL:HG12	1.92	0.51
2:C:338:GLN:NE2	2:C:345:ASP:OD1	2.42	0.51
1:A:413:PHE:O	1:A:419:LYS:NZ	2.43	0.51
1:B:258:MET:HG2	1:B:675:TRP:HB3	1.92	0.51
1:B:162:ILE:HD12	1:B:238:LEU:HD21	1.92	0.51
1:A:566:ALA:HA	1:A:569:LYS:HE3	1.92	0.51
2:D:99:VAL:HG13	2:D:269:ILE:HD11	1.93	0.50
2:C:46:LEU:HD22	2:C:278:GLN:HB3	1.92	0.50
1:B:523:LEU:HD11	1:B:560:MET:HE1	1.93	0.50
1:B:416:GLN:HG3	1:B:448:LEU:HD23	1.94	0.50
1:B:470:MET:O	1:B:498:LYS:NZ	2.37	0.50
2:C:309:LYS:HE2	2:C:313:ARG:HH22	1.77	0.49
1:A:248:ASN:O	1:A:252:GLN:HG2	2.11	0.49
1:A:246:PRO:HG3	2:D:138:PRO:HB3	1.95	0.49
2:C:390:ILE:HB	2:C:394:MET:HB2	1.94	0.49
2:C:43:HIS:HA	4:C:506:SO4:O2	2.13	0.48
1:B:477:LYS:HD2	1:B:486:LEU:HD11	1.96	0.48
1:B:595:ARG:HB3	1:B:603:GLY:HA2	1.94	0.48
1:A:177:LYS:HB2	1:A:180:LYS:HD3	1.95	0.48
2:D:203:LEU:HD11	2:D:207:GLU:HG3	1.96	0.48
1:B:248:ASN:O	1:B:252:GLN:HG2	2.14	0.48
1:A:259:PRO:HD2	1:A:295:VAL:HG11	1.95	0.48
2:C:190:SER:OG	2:C:374:ASP:OD2	2.28	0.47
1:A:477:LYS:HB2	1:A:486:LEU:HD11	1.96	0.47
1:A:408:VAL:HG11	1:A:436:LEU:HD23	1.96	0.47
2:C:59:VAL:HG21	2:C:361:LEU:HB3	1.96	0.47
1:A:398:ASP:OD1	1:A:399:ALA:N	2.47	0.47
1:B:521:GLU:OE2	1:B:711:ARG:NE	2.35	0.47
2:D:96:LEU:HD23	2:D:396:VAL:HG12	1.95	0.47
2:D:346:GLU:HG2	2:D:347:LYS:HG3	1.97	0.47
1:A:561:HIS:O	1:A:565:VAL:HG23	2.15	0.47
1:B:476:ILE:HG21	1:B:509:PHE:CE1	2.50	0.46
1:A:146:LEU:HD22	1:A:291:VAL:HG22	1.96	0.46
2:D:40:ARG:NH1	2:D:77:SER:O	2.37	0.46
1:A:116:GLY:O	1:A:120:ILE:HG12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:354:LYS:HB2	1:A:402:PHE:CE1	2.51	0.46
1:A:416:GLN:HG3	1:A:448:LEU:HD23	1.97	0.46
1:A:520:ASN:HB3	1:A:581:HIS:CE1	2.51	0.45
1:A:683:ILE:HG12	1:A:697:PHE:CZ	2.52	0.45
1:A:698:VAL:HG13	1:A:714:PRO:HG3	1.97	0.45
1:B:340:ILE:HG21	1:B:409:ILE:HG21	1.98	0.45
2:C:325:GLU:HG2	2:C:368:ILE:HB	1.98	0.45
1:B:104:PRO:HD3	1:B:216:ALA:HB1	1.99	0.45
2:D:190:SER:OG	2:D:374:ASP:OD2	2.28	0.45
2:C:241:LYS:HE2	2:C:295:ASP:OD1	2.16	0.45
1:A:316:ARG:CZ	1:A:487:ALA:HB1	2.47	0.45
1:A:454:ARG:NH2	1:A:457:ASP:OD2	2.50	0.45
2:D:173:ARG:HG2	2:D:177:LYS:HE2	1.97	0.45
1:A:336:MET:SD	1:A:465:SER:HB3	2.57	0.45
1:A:515:ILE:HD11	1:A:551:LEU:HD21	1.99	0.45
1:A:104:PRO:HD3	1:A:216:ALA:HB1	1.99	0.45
2:C:290:ALA:HB1	2:C:309:LYS:HD3	1.98	0.44
2:D:241:LYS:NZ	3:H:1:GLC:O2	2.50	0.44
2:D:59:VAL:HG21	2:D:361:LEU:HB3	1.99	0.44
2:D:258:SER:HB3	2:D:329:ALA:HA	1.99	0.44
1:B:459:ILE:HD13	1:B:489:VAL:HG21	2.00	0.44
2:D:313:ARG:NE	4:D:506:SO4:O2	2.46	0.44
1:A:108:ALA:HB1	1:A:197:LEU:HB3	2.00	0.44
1:A:536:GLU:OE2	1:A:605:TYR:OH	2.25	0.44
1:A:673:PRO:HA	1:A:674:PRO:HD3	1.93	0.44
2:D:390:ILE:HB	2:D:394:MET:HB2	2.01	0.43
2:D:156:ILE:HG12	2:D:298:ILE:HD11	2.00	0.43
1:B:15:ILE:HG21	1:B:202:LYS:HG2	1.99	0.43
1:B:698:VAL:HG13	1:B:714:PRO:HG3	2.00	0.43
2:D:155:LEU:HD23	2:D:298:ILE:HB	1.99	0.43
1:B:583:ALA:O	1:B:587:VAL:HG23	2.19	0.43
1:A:258:MET:HG2	1:A:675:TRP:HB3	2.00	0.43
1:A:556:ASN:ND2	1:A:599:LEU:HD22	2.29	0.43
2:C:223:PRO:HA	2:C:253:THR:HG22	1.99	0.42
1:A:45:LEU:HD23	1:A:52:ILE:HD13	2.00	0.42
1:A:634:ASP:OD1	1:A:700:ARG:NH2	2.38	0.42
1:A:354:LYS:HB2	1:A:402:PHE:HE1	1.83	0.42
1:B:101:LEU:HD12	1:B:101:LEU:HA	1.89	0.42
1:A:518:PHE:HB2	1:A:643:GLU:CD	2.40	0.42
2:C:309:LYS:HE2	2:C:313:ARG:NH2	2.34	0.42
2:C:7:ILE:HD11	2:C:286:ILE:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:LEU:HD23	1:B:52:ILE:HD13	2.01	0.42
1:B:325:ILE:HB	1:B:349:TYR:CE1	2.55	0.42
1:B:406:ASP:OD1	1:B:406:ASP:N	2.52	0.42
1:A:336:MET:HB3	1:A:336:MET:HE3	1.96	0.42
1:B:-12:SER:OG	1:B:-11:HIS:N	2.53	0.41
2:C:313:ARG:HD3	2:D:110:TRP:CD1	2.55	0.41
1:A:27:THR:HG21	1:A:66:ALA:HB3	2.01	0.41
1:B:104:PRO:HG2	1:B:205:ILE:HG23	2.02	0.41
1:B:650:CYS:HB3	1:B:656:LEU:HD23	2.01	0.41
2:D:130:ASP:OD1	2:D:130:ASP:N	2.53	0.41
1:B:116:GLY:O	1:B:120:ILE:HG12	2.20	0.41
1:B:523:LEU:HB2	1:B:583:ALA:HB1	2.02	0.41
1:A:245:PHE:HB2	1:A:246:PRO:HD3	2.03	0.41
1:A:455:GLN:OE1	1:A:480:LYS:HG3	2.20	0.41
1:B:686:TYR:O	1:B:692:THR:HA	2.20	0.41
2:D:22:SER:OG	2:D:207:GLU:OE2	2.22	0.41
2:D:382:ARG:HG3	2:D:383:ARG:HG3	2.02	0.41
2:D:261:VAL:HG23	2:D:360:PRO:HG3	2.02	0.41
1:A:596:SER:N	1:A:602:ALA:O	2.54	0.40
2:C:326:LEU:HD23	2:C:334:VAL:HA	2.03	0.40
1:B:714:PRO:HA	1:B:715:PRO:HD3	1.96	0.40
2:D:120:GLU:HB2	2:D:362:GLY:H	1.85	0.40
1:B:510:PHE:CE1	1:B:514:VAL:HG21	2.56	0.40
1:B:586:VAL:HG13	1:B:623:PHE:CZ	2.57	0.40
2:C:203:LEU:HD11	2:C:207:GLU:HG3	2.03	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	716/736 (97%)	683 (95%)	33 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	718/736 (98%)	693 (96%)	24 (3%)	1 (0%)	51	82
2	C	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
2	D	395/403 (98%)	378 (96%)	17 (4%)	0	100	100
All	All	2221/2278 (98%)	2135 (96%)	85 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	148	PRO

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	555/566 (98%)	550 (99%)	5 (1%)	78	93
1	B	556/566 (98%)	550 (99%)	6 (1%)	73	92
2	C	305/310 (98%)	302 (99%)	3 (1%)	76	92
2	D	307/310 (99%)	306 (100%)	1 (0%)	92	98
All	All	1723/1752 (98%)	1708 (99%)	15 (1%)	78	93

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

Mol	Chain	Res	Type
1	B	186	LEU
1	B	194	VAL
1	B	335	MET
1	B	479	GLU
1	B	556	ASN
1	B	578	TYR
2	C	25	GLU
2	C	46	LEU
2	C	86	VAL
1	A	-9	HIS

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Mol	Chain	Res	Type
1	A	186	LEU
1	A	402	PHE
1	A	555	LEU
1	A	599	LEU
2	D	115	LEU

Sometimes 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	$\# Z > 2$
3	GLC	G	1	3	11,11,12	0.37	0	15,15,17	0.31	0
3	GLC	G	2	3	12,12,12	0.24	0	17,17,17	0.38	0
3	GLC	H	1	3	11,11,12	0.36	0	15,15,17	0.30	0
3	GLC	H	2	3	12,12,12	0.22	0	17,17,17	0.23	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
3	GLC	G	1	3	-	2/2/19/22	0/1/1/1
3	GLC	G	2	3	-	0/2/22/22	0/1/1/1
3	GLC	H	1	3	-	2/2/19/22	0/1/1/1
3	GLC	H	2	3	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

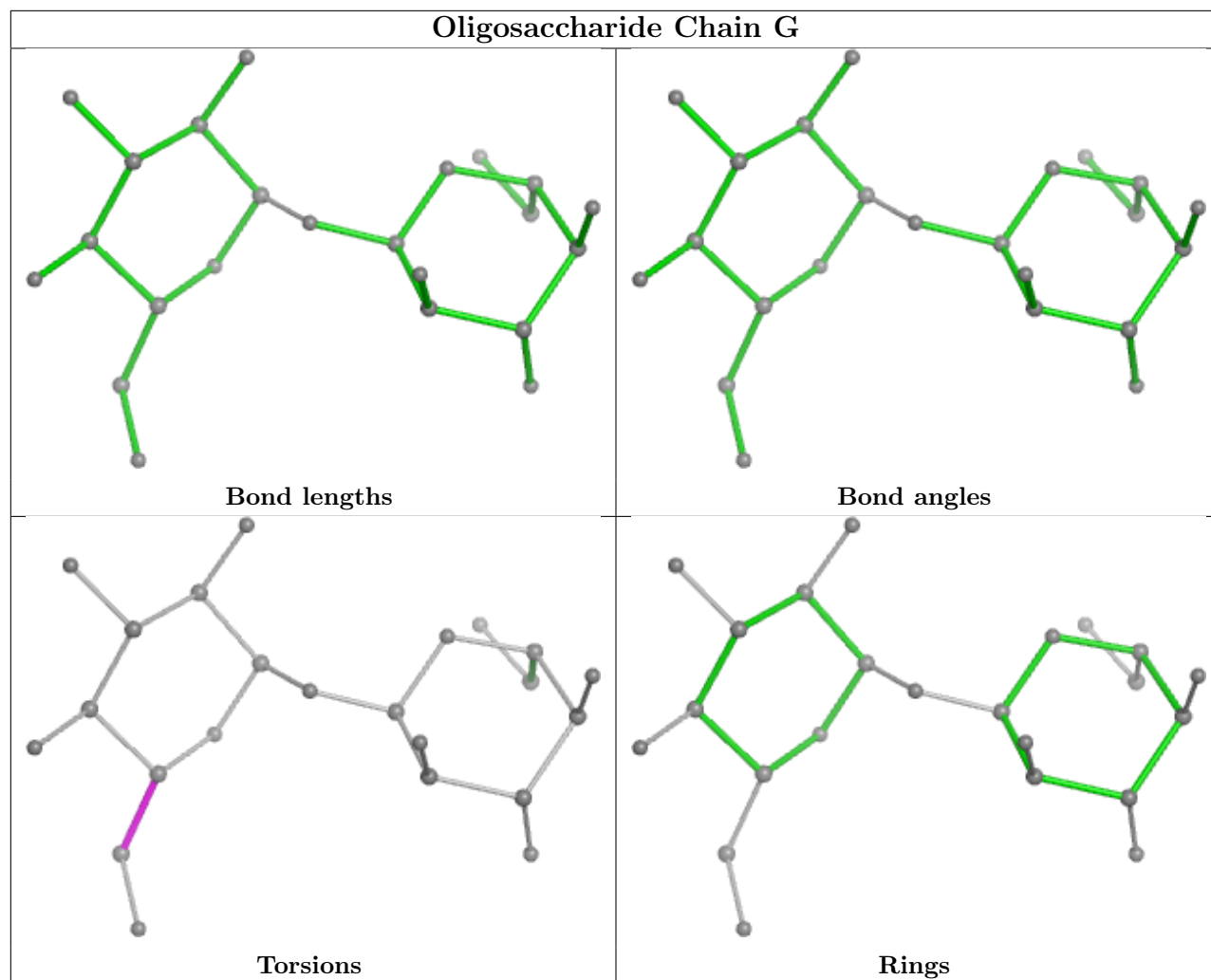
Mol	Chain	Res	Type	Atoms
3	G	1	GLC	O5-C5-C6-O6
3	G	1	GLC	C4-C5-C6-O6
3	H	1	GLC	C4-C5-C6-O6
3	H	1	GLC	O5-C5-C6-O6

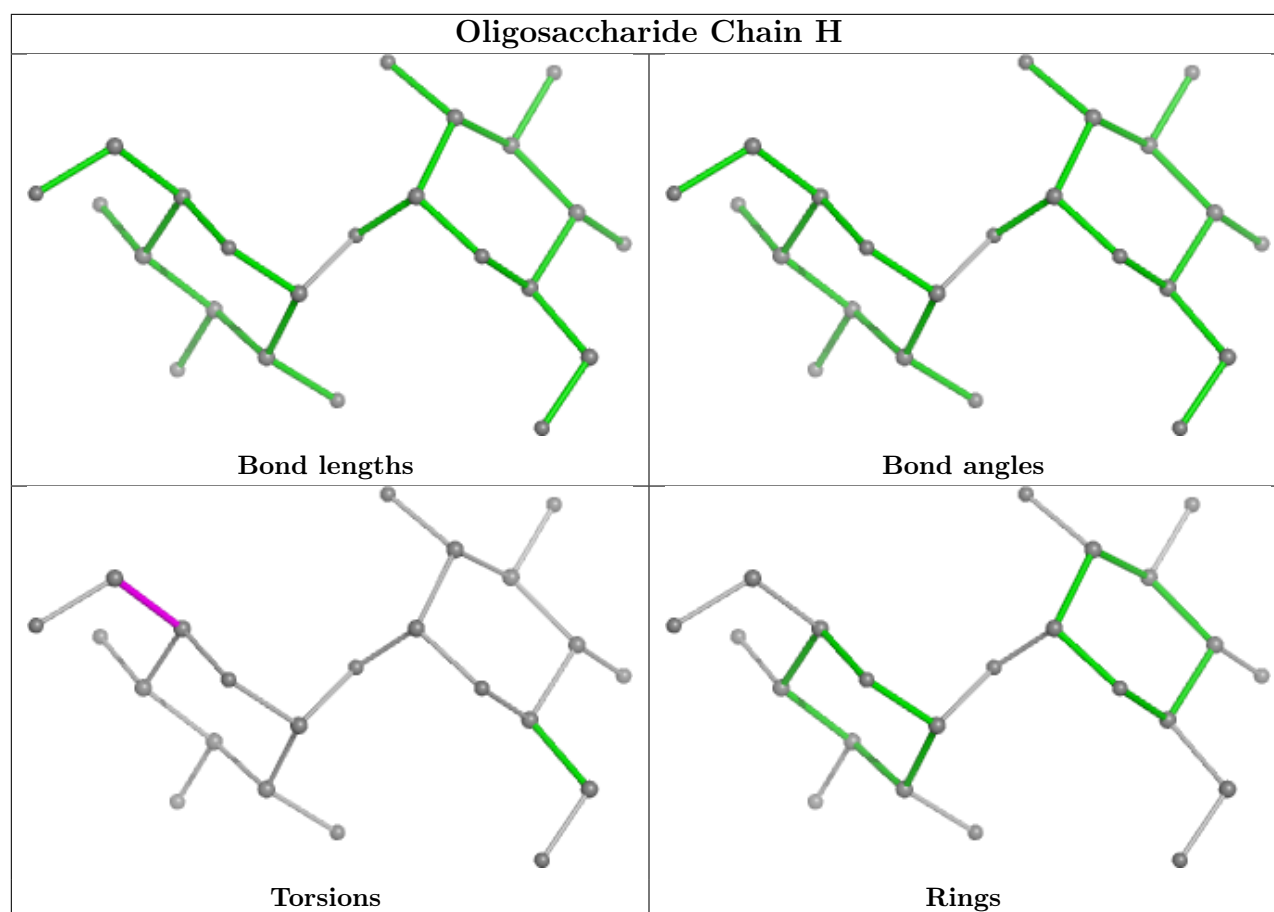
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	GLC	1	0
3	G	1	GLC	2	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](#)

24 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	SO4	B	803	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	C	507	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	D	505	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	C	504	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	D	506	-	4,4,4	0.14	0	6,6,6	0.09	0
4	SO4	B	805	-	4,4,4	0.14	0	6,6,6	0.08	0
4	SO4	C	503	-	4,4,4	0.14	0	6,6,6	0.07	0
4	SO4	D	502	-	4,4,4	0.14	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	C	501	-	4,4,4	0.13	0	6,6,6	0.09	0
4	SO4	C	505	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	D	503	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	B	801	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	B	804	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	A	801	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	C	502	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	B	806	-	4,4,4	0.15	0	6,6,6	0.06	0
4	SO4	D	501	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	A	805	-	4,4,4	0.15	0	6,6,6	0.10	0
4	SO4	A	804	-	4,4,4	0.14	0	6,6,6	0.09	0
4	SO4	D	504	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	B	802	-	4,4,4	0.14	0	6,6,6	0.04	0
4	SO4	C	506	-	4,4,4	0.13	0	6,6,6	0.09	0
4	SO4	A	802	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	A	803	-	4,4,4	0.14	0	6,6,6	0.07	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	803	SO4	1	0
4	D	506	SO4	1	0
4	C	502	SO4	1	0
4	C	506	SO4	1	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	722/736 (98%)	0.20	53 (7%) 15 11	37, 72, 144, 203	0
1	B	724/736 (98%)	-0.09	17 (2%) 60 58	35, 63, 112, 176	0
2	C	396/403 (98%)	-0.22	1 (0%) 94 94	34, 49, 73, 116	0
2	D	399/403 (99%)	-0.22	1 (0%) 94 94	34, 52, 81, 123	0
All	All	2241/2278 (98%)	-0.04	72 (3%) 47 43	34, 59, 127, 203	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	382	THR	7.0
1	A	434	ALA	5.5
1	A	383	GLN	5.4
1	A	402	PHE	4.6
1	B	377	GLU	4.6
1	A	1	MET	4.4
1	A	322	LYS	4.2
1	A	404	GLY	4.2
1	A	423	PHE	4.0
1	A	3	ASP	3.9
1	A	387	ASP	3.8
1	A	351	VAL	3.7
1	A	325	ILE	3.7
1	A	454	ARG	3.7
1	A	609	ASP	3.5
1	A	377	GLU	3.5
1	A	453	LYS	3.4
1	A	384	GLU	3.3
1	A	379	GLY	3.2
1	A	391	ALA	3.1
1	A	357	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	621	GLU	3.0
1	B	720	SER	3.0
1	B	619	LEU	2.9
1	B	378	ARG	2.9
1	A	378	ARG	2.9
1	A	452	VAL	2.9
1	B	1	MET	2.9
1	A	393	ILE	2.8
1	A	371	LEU	2.8
1	A	433	ASN	2.8
1	A	436	LEU	2.8
1	A	386	SER	2.7
1	B	577	THR	2.7
1	A	622	THR	2.7
1	B	383	GLN	2.7
1	B	609	ASP	2.7
1	A	428	ASP	2.7
1	A	578	TYR	2.6
1	A	394	THR	2.5
1	A	367	TYR	2.5
1	A	2	PRO	2.5
1	A	486	LEU	2.4
2	D	1	MET	2.4
1	B	328	ILE	2.4
1	A	389	LEU	2.4
2	C	2	SER	2.4
1	A	432	PRO	2.4
1	A	318	GLU	2.3
1	B	382	THR	2.3
1	A	327	ARG	2.3
1	A	435	ILE	2.3
1	A	416	GLN	2.3
1	A	430	VAL	2.3
1	B	374	LYS	2.2
1	A	320	ILE	2.2
1	A	425	GLU	2.2
1	A	409	ILE	2.2
1	A	720	SER	2.2
1	A	405	VAL	2.2
1	A	426	ILE	2.1
1	A	455	GLN	2.1
1	A	335	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	458	PHE	2.1
1	B	457	ASP	2.1
1	B	573	ASP	2.1
1	B	319	GLY	2.1
1	B	479	GLU	2.1
1	A	407	PHE	2.0
1	B	602	ALA	2.0
1	A	568	ARG	2.0
1	A	62	LYS	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](#)

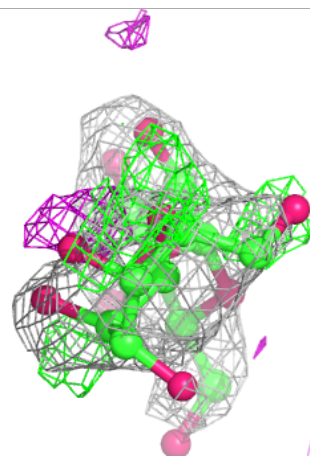
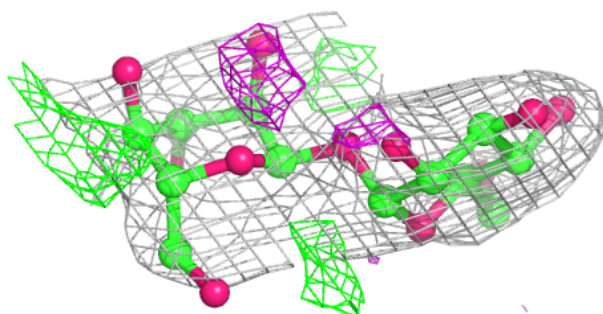
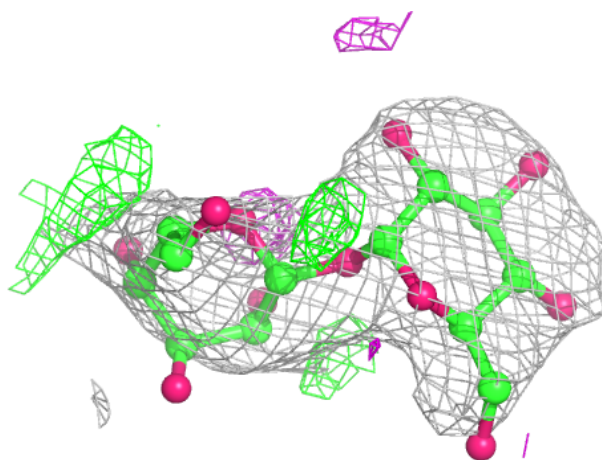
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

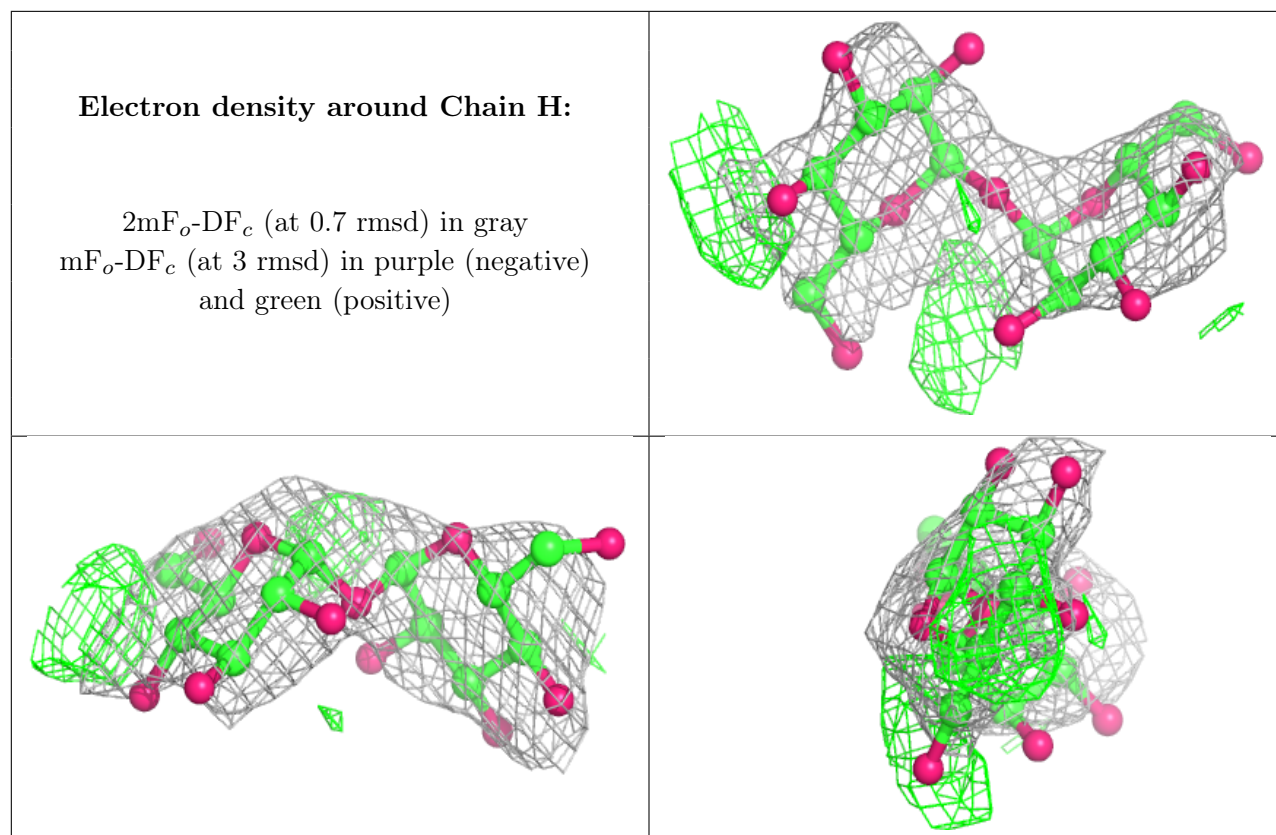
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GLC	G	2	12/12	0.83	0.31	71,88,96,113	12
3	GLC	G	1	11/12	0.85	0.23	73,87,96,104	11
3	GLC	H	1	11/12	0.86	0.30	63,71,76,79	11
3	GLC	H	2	12/12	0.86	0.34	58,63,77,78	12

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 G:

$2mF_o-DF_c$ (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	SO4	C	506	5/5	0.75	0.38	113,161,171,191	0
4	SO4	B	806	5/5	0.81	0.47	120,144,160,189	0
4	SO4	D	506	5/5	0.84	0.17	120,134,157,176	0
4	SO4	C	507	5/5	0.85	0.37	116,134,151,161	0
4	SO4	A	804	5/5	0.86	0.24	99,109,141,143	0
4	SO4	B	805	5/5	0.86	0.28	113,121,165,168	0
4	SO4	B	803	5/5	0.91	0.15	81,138,144,148	0
4	SO4	C	504	5/5	0.91	0.34	100,112,125,141	0
4	SO4	A	805	5/5	0.92	0.10	88,93,110,158	0
4	SO4	D	505	5/5	0.92	0.32	102,112,138,149	0
4	SO4	C	505	5/5	0.92	0.16	86,91,100,108	0
4	SO4	C	502	5/5	0.93	0.14	93,96,115,118	0
4	SO4	D	504	5/5	0.94	0.11	123,125,130,135	5
4	SO4	B	804	5/5	0.95	0.23	83,106,117,119	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	D	502	5/5	0.96	0.30	81,88,116,123	0
4	SO4	D	503	5/5	0.96	0.11	92,110,113,118	0
4	SO4	B	802	5/5	0.96	0.15	79,91,100,105	0
4	SO4	C	503	5/5	0.96	0.16	93,105,113,116	0
4	SO4	D	501	5/5	0.96	0.21	85,88,98,98	0
4	SO4	A	801	5/5	0.97	0.14	71,88,113,115	0
4	SO4	A	802	5/5	0.97	0.12	63,74,98,100	0
4	SO4	A	803	5/5	0.98	0.07	76,81,112,117	0
4	SO4	B	801	5/5	0.98	0.09	71,81,87,89	0
4	SO4	C	501	5/5	0.98	0.20	79,86,92,96	0

6.5 Other polymers [i](#)

There are no such residues in this entry.