



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 05:09 PM EDT

PDB ID : 6T18 / pdb_00006t18
Title : ASR Alternansucrase in complex with oligoalternan
Authors : Cioci, G.; Molina, M.; Moulis, C.; Remaud-Simeon, M.
Deposited on : 2019-10-03
Resolution : 3.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

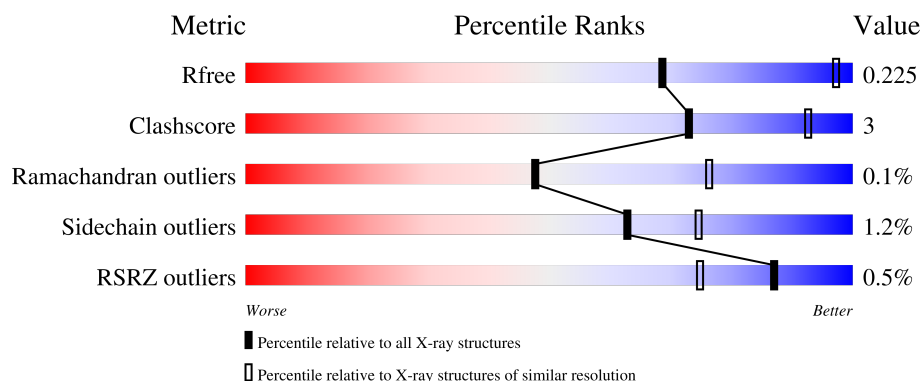
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

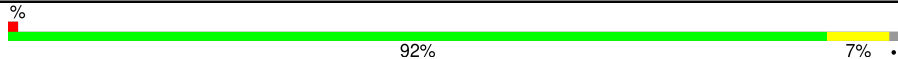
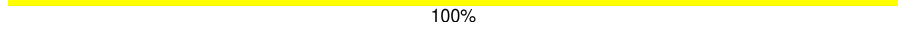
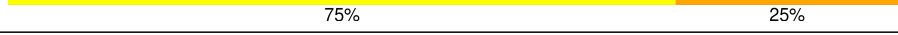
The reported resolution of this entry is 3.15 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	1278	 92% 7%
1	B	1278	 86% 6% 7%
2	C	6	 50% 50%
3	D	3	 100%
4	E	4	 75% 25%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 19369 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 Alternansucrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1266	Total	C	N	O	S	0	0	0
			9921	6199	1691	2005	26			
1	B	1185	Total	C	N	O	S	0	0	0
			9300	5814	1580	1880	26			

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	6	Total	C	O	0	0	0
			67	36	31			

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose.



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

- Molecule 4 is an oligosaccharide called alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	E	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

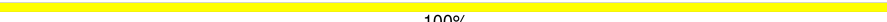
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	B	1	Total	Ca	0	0
			1	1		

- Molecule 2: alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose

Chain C:  50% 50%

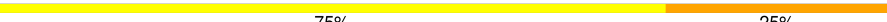
GLC1
GLC2
GLC3
GLC4
GLC5
GLC6

- Molecule 3: alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose

Chain D:  100%

GLC1
GLC2
GLC3

- Molecule 4: alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-3)-alpha-D-glucopyranose

Chain E:  75% 25%

GLC1
GLC2
GLC3
GLC4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	100.88Å 135.65Å 239.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.15 50.00 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-3.15) 99.9 (50.00-3.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.200 , 0.226 0.198 , 0.225	Depositor DCC
R_{free} test set	2769 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	78.5	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19369	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.01% 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: CA, 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	0.61	0/10130	0.80	3/13734 (0.0%)
1	B	0.59	0/9497	0.79	3/12880 (0.0%)
All	All	0.60	0/19627	0.80	6/26614 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1000	THR	N-CA-C	5.79	117.06	108.60
1	B	902	LYS	N-CA-C	5.21	116.64	111.07
1	B	1014	ILE	N-CA-C	5.19	115.05	107.88
1	A	294	ALA	CA-C-N	5.10	124.55	119.24
1	A	294	ALA	C-N-CA	5.10	124.55	119.24
1	A	900	PHE	N-CA-C	5.05	119.52	112.90

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	9921	0	9337	62	0
1	B	9300	0	8769	64	0
2	C	67	0	57	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	34	0	30	0	0
4	E	45	0	39	6	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	19369	0	18232	121	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 (121) 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:700:GLN:OE1	4:E:3:GLC:H62	0.99	1.17
1:B:700:GLN:OE1	4:E:3:GLC:C6	1.94	1.15
1:A:700:GLN:OE1	2:C:4:GLC:O6	1.84	0.93
1:A:241:TYR:OH	1:A:270:GLN:OE1	1.97	0.83
1:A:892:THR:HG23	1:A:934:LEU:HD21	1.61	0.82
1:A:342:MET:HE1	1:A:359:GLN:O	1.80	0.81
1:B:296:ASN:ND2	1:B:297:THR:HG23	1.98	0.78
1:B:271:TYR:CD1	1:B:286:VAL:HG21	2.20	0.76
1:B:358:GLU:OE1	1:B:358:GLU:N	2.13	0.76
1:A:944:LEU:HB3	1:A:946:MET:HE3	1.70	0.74
1:B:296:ASN:ND2	1:B:297:THR:N	2.37	0.73
1:B:944:LEU:HB3	1:B:946:MET:HE3	1.71	0.73
1:A:271:TYR:CD1	1:A:286:VAL:HG21	2.25	0.71
1:B:892:THR:HG23	1:B:934:LEU:HD11	1.72	0.70
1:B:271:TYR:CE1	1:B:286:VAL:CG2	2.75	0.69
1:B:713:SER:OG	4:E:2:GLC:O3	2.06	0.68
1:A:290:ARG:O	1:A:318:GLY:HA2	1.93	0.68
1:A:717:TYR:O	2:C:4:GLC:H62	1.94	0.67
1:B:290:ARG:O	1:B:318:GLY:HA2	1.95	0.67
1:B:296:ASN:HD21	1:B:297:THR:HG23	1.59	0.67
1:B:973:ASP:OD1	1:B:974:LYS:HG3	1.95	0.66
1:A:163:GLY:O	1:B:352:LYS:CE	2.44	0.66
1:B:271:TYR:CE1	1:B:286:VAL:HG22	2.31	0.65
1:A:417:PHE:HB2	1:A:1287:ILE:HD13	1.79	0.65
1:B:973:ASP:OD1	1:B:974:LYS:N	2.30	0.64
1:A:271:TYR:CE1	1:A:286:VAL:CG2	2.82	0.62
1:B:417:PHE:HB2	1:B:1287:ILE:HD13	1.79	0.62
1:B:717:TYR:O	4:E:3:GLC:O4	2.16	0.61
1:B:296:ASN:HD22	1:B:297:THR:N	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:934:LEU:C	1:A:934:LEU:HD13	2.27	0.59
1:A:271:TYR:CE1	1:A:286:VAL:HG22	2.38	0.59
1:B:296:ASN:HD22	1:B:297:THR:H	1.49	0.59
1:A:934:LEU:HD11	1:A:936:LEU:HD12	1.85	0.59
1:A:786:ASN:O	1:A:789:ASP:HB2	2.04	0.58
1:B:851:MET:HE1	1:B:1088:PHE:HZ	1.70	0.57
1:B:850:TYR:CE2	1:B:851:MET:HE3	2.40	0.56
1:B:786:ASN:O	1:B:789:ASP:HB2	2.05	0.56
1:A:851:MET:HE1	1:A:1088:PHE:HZ	1.70	0.56
1:B:995:VAL:HG12	1:B:1001:ILE:HG12	1.88	0.56
1:B:874:GLY:HA3	1:B:901:GLY:O	2.06	0.55
1:B:296:ASN:HD21	1:B:297:THR:CG2	2.19	0.55
1:A:850:TYR:CE2	1:A:851:MET:HE3	2.40	0.55
1:B:472:SER:HB3	1:B:479:THR:HA	1.89	0.55
1:B:358:GLU:H	1:B:358:GLU:CD	2.08	0.55
1:B:713:SER:CB	4:E:2:GLC:O3	2.56	0.54
1:B:284:GLN:HG3	1:B:286:VAL:HG23	1.89	0.54
1:A:472:SER:HB3	1:A:479:THR:HA	1.88	0.54
1:A:874:GLY:HA3	1:A:901:GLY:O	2.08	0.54
1:A:1222:GLY:O	1:A:1255:LYS:HE2	2.08	0.54
1:A:284:GLN:HG3	1:A:286:VAL:HG23	1.90	0.53
1:B:271:TYR:CD1	1:B:286:VAL:CG2	2.91	0.53
1:B:1222:GLY:O	1:B:1255:LYS:HE2	2.09	0.53
1:B:522:PHE:O	1:B:525:THR:HB	2.10	0.52
1:B:296:ASN:ND2	1:B:297:THR:CG2	2.72	0.52
1:A:163:GLY:O	1:B:352:LYS:HD2	2.10	0.51
1:A:325:PHE:CE1	1:A:349:ILE:HD11	2.45	0.51
1:A:522:PHE:O	1:A:525:THR:HB	2.09	0.51
1:A:885:LYS:HG3	2:C:6:GLC:H2	1.93	0.51
1:A:296:ASN:ND2	1:B:295:PRO:HB2	2.26	0.51
1:B:1097:GLU:HA	1:B:1167:ILE:HB	1.93	0.51
1:B:894:LEU:HD23	1:B:942:ILE:HD13	1.94	0.49
1:A:357:ASP:OD1	1:A:361:HIS:N	2.46	0.49
1:B:717:TYR:O	4:E:3:GLC:H61	2.11	0.49
1:A:195:VAL:HG21	1:A:200:ARG:NH2	2.27	0.49
1:A:271:TYR:CD1	1:A:286:VAL:CG2	2.96	0.49
1:A:894:LEU:HD23	1:A:942:ILE:HD13	1.94	0.49
1:A:238:LYS:HG2	1:A:254:GLY:O	2.12	0.49
1:A:1097:GLU:HA	1:A:1167:ILE:HB	1.94	0.49
1:B:325:PHE:CE1	1:B:349:ILE:HD11	2.48	0.48
1:A:163:GLY:O	1:B:352:LYS:CD	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ALA:O	1:A:1410:ALA:HA	2.13	0.48
1:B:330:ALA:O	1:B:1410:ALA:HA	2.14	0.48
1:B:271:TYR:CE1	1:B:286:VAL:HG21	2.43	0.48
1:A:271:TYR:CE1	1:A:286:VAL:HG21	2.49	0.48
1:B:470:PHE:CD2	1:B:471:MET:HE2	2.49	0.47
1:A:205:LYS:HE3	1:A:235:ASN:OD1	2.15	0.47
1:A:885:LYS:HG3	2:C:6:GLC:C2	2.45	0.47
1:A:470:PHE:CD2	1:A:471:MET:HE2	2.50	0.46
1:B:1373:MET:HB3	1:B:1374:PRO:CD	2.46	0.46
1:B:1001:ILE:CG2	1:B:1002:ILE:N	2.78	0.46
1:A:1373:MET:HB3	1:A:1374:PRO:CD	2.46	0.46
1:B:268:ASN:HD22	1:B:268:ASN:N	2.13	0.45
1:A:885:LYS:HG3	2:C:6:GLC:O2	2.17	0.45
1:A:812:GLY:HA3	1:A:1010:LEU:HD23	1.99	0.45
1:A:419:ASN:HB2	1:A:423:TYR:O	2.18	0.44
1:A:726:ASN:O	1:A:727:GLY:C	2.59	0.44
1:B:812:GLY:HA3	1:B:1010:LEU:HD23	2.00	0.44
1:A:1063:PHE:CG	1:A:1099:ALA:HB2	2.53	0.44
1:A:717:TYR:OH	1:A:885:LYS:HG2	2.18	0.43
1:B:470:PHE:HD2	1:B:471:MET:HE2	1.82	0.43
1:A:163:GLY:O	1:B:352:LYS:HE3	2.18	0.43
1:A:219:ASN:OD1	1:A:244:ASP:HA	2.17	0.43
1:B:558:THR:HG21	1:B:1185:THR:OG1	2.18	0.43
1:A:470:PHE:HD2	1:A:471:MET:HE2	1.83	0.43
1:B:717:TYR:OH	1:B:885:LYS:HG2	2.18	0.43
1:A:558:THR:HG21	1:A:1185:THR:OG1	2.18	0.43
1:B:296:ASN:ND2	1:B:296:ASN:C	2.77	0.42
1:B:1063:PHE:CG	1:B:1099:ALA:HB2	2.54	0.42
1:B:264:THR:HA	1:B:268:ASN:O	2.19	0.42
1:A:737:ASN:O	1:A:737:ASN:ND2	2.39	0.42
1:B:1298:GLN:NE2	1:B:1320:ILE:O	2.53	0.42
1:B:1136:LYS:HG3	1:B:1142:ASN:HB2	2.02	0.42
1:B:419:ASN:HB2	1:B:423:TYR:O	2.19	0.42
1:B:706:THR:HG23	1:B:818:ASP:HB3	2.00	0.42
1:A:470:PHE:CE2	1:A:522:PHE:HB2	2.54	0.42
1:B:470:PHE:CE2	1:B:522:PHE:HB2	2.55	0.42
1:A:461:LYS:HE2	1:A:484:ALA:O	2.20	0.41
1:B:1116:LEU:HA	1:B:1119:PHE:CE2	2.55	0.41
1:A:706:THR:HG23	1:A:818:ASP:HB3	2.02	0.41
1:A:973:ASP:OD1	1:A:973:ASP:N	2.45	0.41
1:A:196:LYS:HG2	1:A:214:GLY:CA	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:VAL:HG11	1:A:179:GLN:HG3	2.02	0.41
1:B:1373:MET:HB3	1:B:1374:PRO:HD2	2.03	0.41
1:A:1373:MET:HB3	1:A:1374:PRO:HD2	2.02	0.41
1:B:821:LEU:HD23	1:B:821:LEU:HA	1.93	0.41
1:B:289:LYS:HD3	1:B:317:ASN:O	2.21	0.41
1:A:572:GLN:HB2	1:A:573:PRO:HD2	2.04	0.40
1:A:1136:LYS:HG3	1:A:1142:ASN:HB2	2.03	0.40
1:A:188:PHE:HA	1:A:193:TYR:O	2.21	0.40
1:A:561:THR:O	1:A:561:THR:CG2	2.69	0.40
1:A:892:THR:HG21	1:A:894:LEU:HD22	2.04	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	1264/1278 (99%)	1212 (96%)	51 (4%)	1 (0%)	48	76
1	B	1183/1278 (93%)	1132 (96%)	50 (4%)	1 (0%)	48	76
All	All	2447/2556 (96%)	2344 (96%)	101 (4%)	2 (0%)	48	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	PHE
1	B	374	PHE

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	1057/1079 (98%)	1046 (99%)	11 (1%)	68	76
1	B	994/1079 (92%)	980 (99%)	14 (1%)	59	73
All	All	2051/2158 (95%)	2026 (99%)	25 (1%)	63	74

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	238	LYS
1	A	287	ASN
1	A	346	LEU
1	A	660	LYS
1	A	737	ASN
1	A	774	ILE
1	A	851	MET
1	A	928	VAL
1	A	934	LEU
1	A	959	VAL
1	A	1406	ILE
1	B	268	ASN
1	B	296	ASN
1	B	346	LEU
1	B	460	ASP
1	B	660	LYS
1	B	737	ASN
1	B	743	THR
1	B	771	GLN
1	B	774	ILE
1	B	792	THR
1	B	851	MET
1	B	928	VAL
1	B	959	VAL
1	B	1406	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	332	ASN
1	A	339	ASN

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Mol	Chain	Res	Type
1	A	359	GLN
1	A	688	ASN
1	A	849	GLN
1	A	938	ASN
1	A	1162	ASN
1	A	1263	ASN
1	B	270	GLN
1	B	296	ASN
1	B	299	ASN
1	B	688	ASN
1	B	771	GLN
1	B	938	ASN
1	B	1162	ASN

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 ⓘ

13 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GLC	C	1	2	12,12,12	0.48	0	17,17,17	0.60	0
2	GLC	C	2	2	11,11,12	0.64	0	15,15,17	0.75	0
2	GLC	C	3	2	11,11,12	0.58	0	15,15,17	0.67	0
2	GLC	C	4	2	11,11,12	0.67	0	15,15,17	0.86	0
2	GLC	C	5	2	11,11,12	0.54	0	15,15,17	0.99	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	C	6	2	11,11,12	0.66	0	15,15,17	0.76	0
3	GLC	D	1	3	12,12,12	0.55	0	17,17,17	1.59	2 (11%)
3	GLC	D	2	3	11,11,12	0.55	0	15,15,17	1.86	1 (6%)
3	GLC	D	3	3	11,11,12	0.56	0	15,15,17	1.20	2 (13%)
4	GLC	E	1	4	12,12,12	0.50	0	17,17,17	1.94	7 (41%)
4	GLC	E	2	4	11,11,12	0.64	0	15,15,17	0.57	0
4	GLC	E	3	4	11,11,12	0.60	0	15,15,17	0.90	1 (6%)
4	GLC	E	4	4	11,11,12	0.52	0	15,15,17	1.10	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	GLC	C	1	2	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	GLC	C	3	2	-	2/2/19/22	0/1/1/1
2	GLC	C	4	2	-	0/2/19/22	0/1/1/1
2	GLC	C	5	2	-	0/2/19/22	0/1/1/1
2	GLC	C	6	2	-	0/2/19/22	0/1/1/1
3	GLC	D	1	3	-	0/2/22/22	0/1/1/1
3	GLC	D	2	3	-	2/2/19/22	0/1/1/1
3	GLC	D	3	3	-	1/2/19/22	0/1/1/1
4	GLC	E	1	4	-	0/2/22/22	0/1/1/1
4	GLC	E	2	4	-	2/2/19/22	0/1/1/1
4	GLC	E	3	4	-	2/2/19/22	0/1/1/1
4	GLC	E	4	4	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	GLC	C1-O5-C5	5.78	119.93	112.19
3	D	1	GLC	C1-O5-C5	3.91	121.22	113.65
4	E	1	GLC	O1-C1-C2	3.88	120.25	108.98
3	D	1	GLC	O5-C1-C2	3.52	116.49	110.30
4	E	1	GLC	C1-O5-C5	-3.46	106.96	113.65
4	E	1	GLC	O5-C1-C2	2.69	115.02	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	4	GLC	C1-O5-C5	2.68	115.77	112.19
4	E	1	GLC	O1-C1-O5	2.57	118.04	110.41
3	D	3	GLC	C1-O5-C5	2.48	115.52	112.19
4	E	1	GLC	C6-C5-C4	-2.48	106.92	113.02
2	C	5	GLC	C1-O5-C5	2.42	115.43	112.19
4	E	3	GLC	C1-C2-C3	2.25	112.92	109.64
3	D	3	GLC	C2-C3-C4	-2.11	107.15	110.86
4	E	1	GLC	C3-C4-C5	2.11	114.05	110.23
4	E	1	GLC	C1-C2-C3	-2.10	106.08	110.36

There are no chirality outliers.

All (11) torsion outliers are listed below:

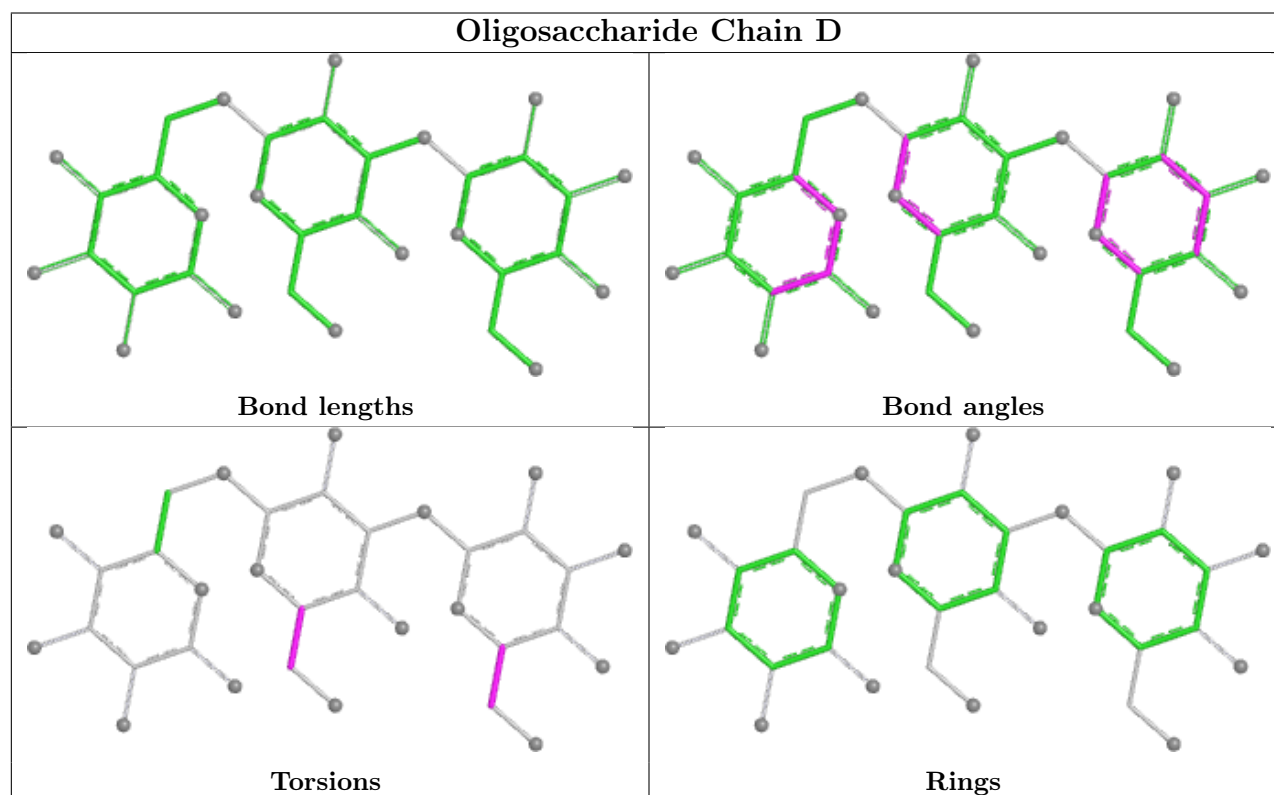
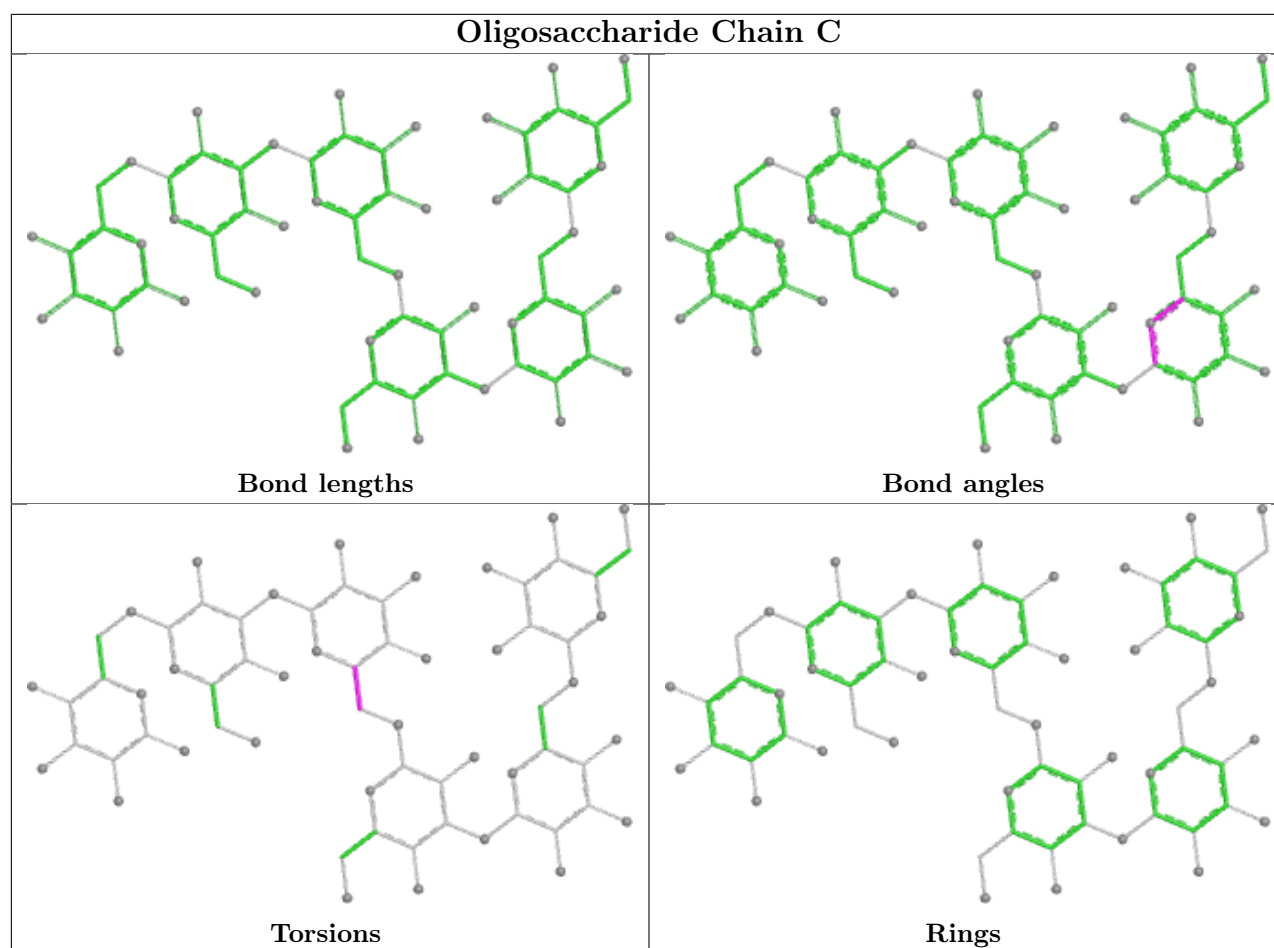
Mol	Chain	Res	Type	Atoms
3	D	2	GLC	O5-C5-C6-O6
3	D	2	GLC	C4-C5-C6-O6
4	E	3	GLC	O5-C5-C6-O6
4	E	3	GLC	C4-C5-C6-O6
2	C	3	GLC	C4-C5-C6-O6
4	E	4	GLC	C4-C5-C6-O6
2	C	3	GLC	O5-C5-C6-O6
4	E	4	GLC	O5-C5-C6-O6
4	E	2	GLC	C4-C5-C6-O6
3	D	3	GLC	O5-C5-C6-O6
4	E	2	GLC	O5-C5-C6-O6

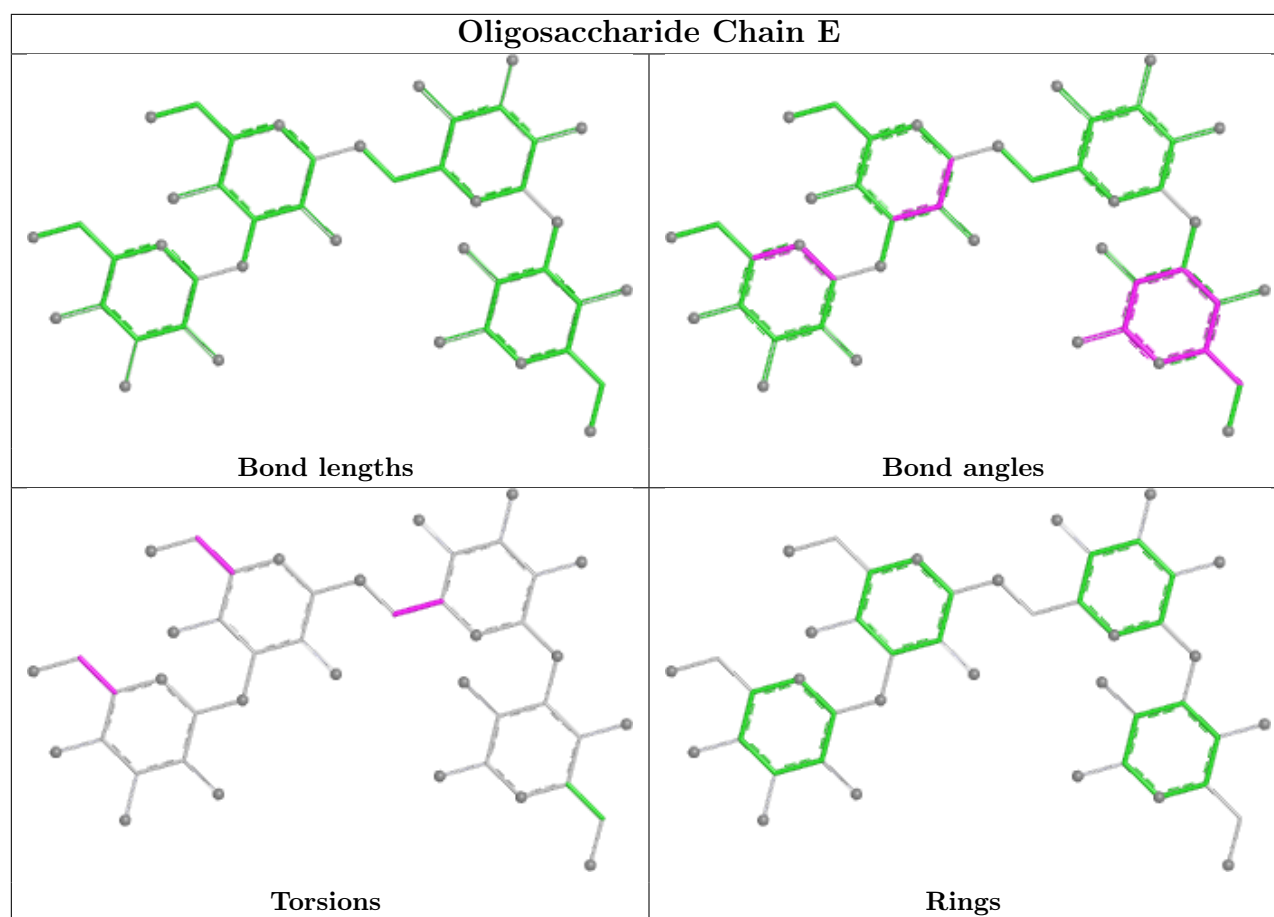
There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	4	GLC	2	0
4	E	3	GLC	4	0
4	E	2	GLC	2	0
2	C	6	GLC	3	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

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	1266/1278 (99%)	-0.35	9 (0%) 84 69	49, 76, 163, 202	0
1	B	1185/1278 (92%)	-0.31	3 (0%) 90 81	49, 89, 155, 230	0
All	All	2451/2556 (95%)	-0.33	12 (0%) 87 75	49, 83, 160, 230	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	237	LEU	3.2
1	A	181	ILE	2.9
1	B	371	ASN	2.6
1	B	740	ASN	2.5
1	A	167	TYR	2.4
1	A	998	ASP	2.3
1	A	225	GLY	2.3
1	A	224	ASN	2.3
1	B	370	PHE	2.2
1	A	217	SER	2.2
1	A	185	LEU	2.2
1	A	256	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](#)

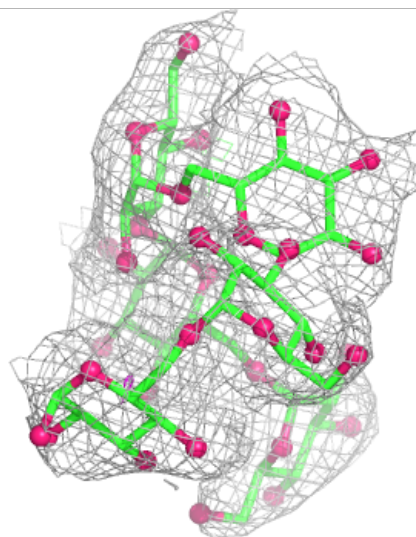
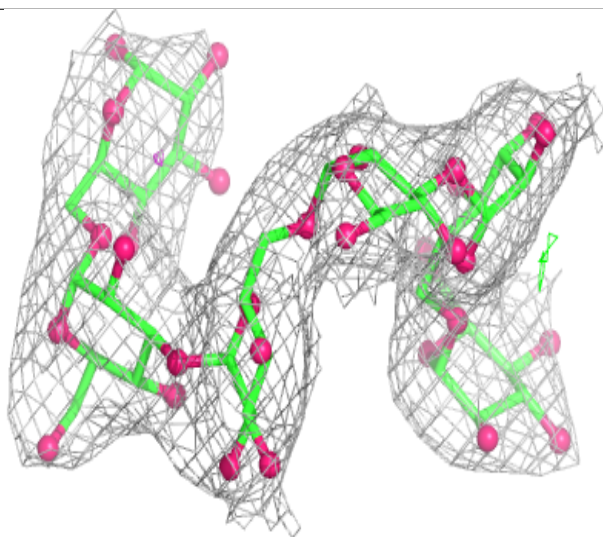
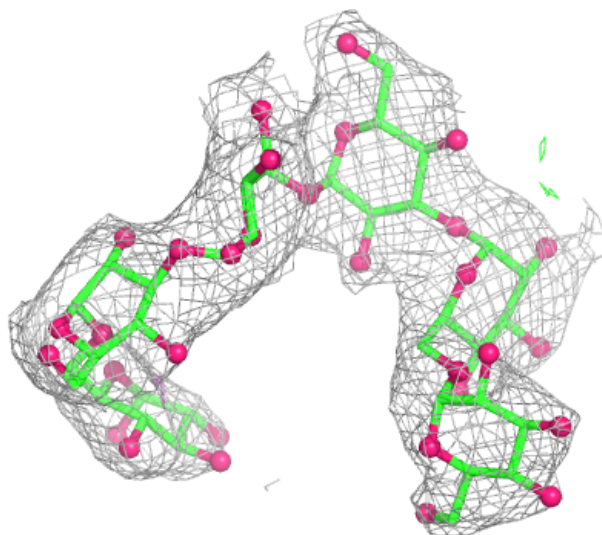
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GLC	D	2	11/12	0.54	0.12	152,160,169,172	0
2	GLC	C	1	12/12	0.55	0.09	133,139,143,149	0
4	GLC	E	1	12/12	0.65	0.10	121,129,134,134	0
4	GLC	E	4	11/12	0.68	0.11	121,124,127,131	0
3	GLC	D	3	11/12	0.75	0.09	131,139,146,146	0
2	GLC	C	6	11/12	0.77	0.09	108,116,120,121	0
3	GLC	D	1	12/12	0.79	0.10	127,139,151,160	0
2	GLC	C	2	11/12	0.82	0.07	110,117,124,126	0
4	GLC	E	3	11/12	0.88	0.09	94,104,107,114	0
2	GLC	C	5	11/12	0.89	0.07	98,101,108,111	0
2	GLC	C	3	11/12	0.91	0.07	82,93,100,104	0
4	GLC	E	2	11/12	0.93	0.07	99,106,119,120	0
2	GLC	C	4	11/12	0.95	0.06	84,91,94,104	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.

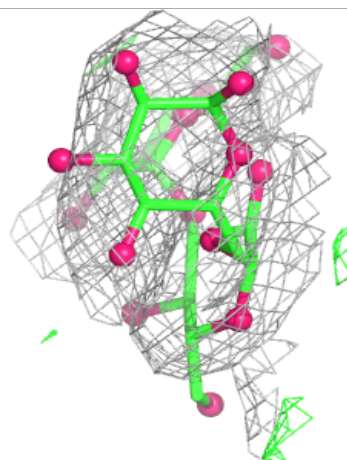
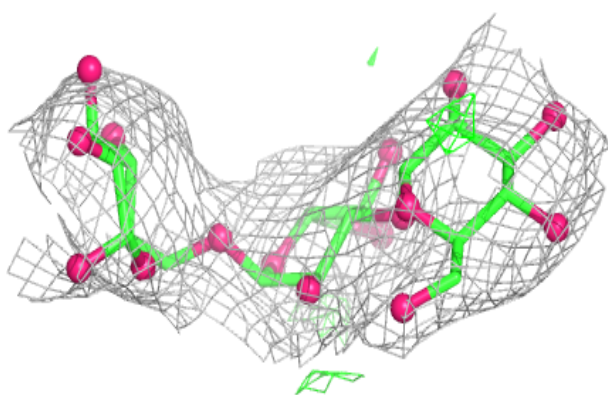
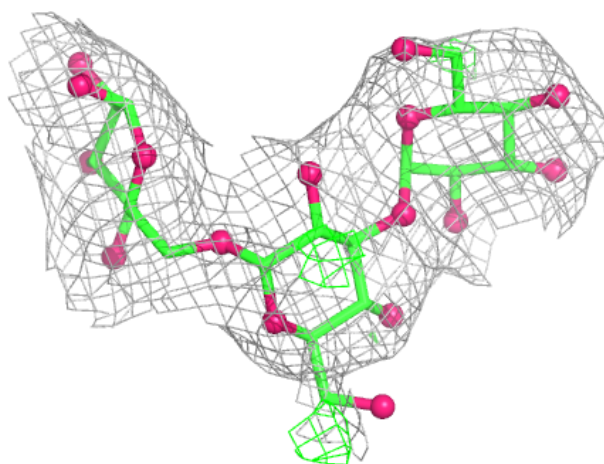
Electron density around Chain C:

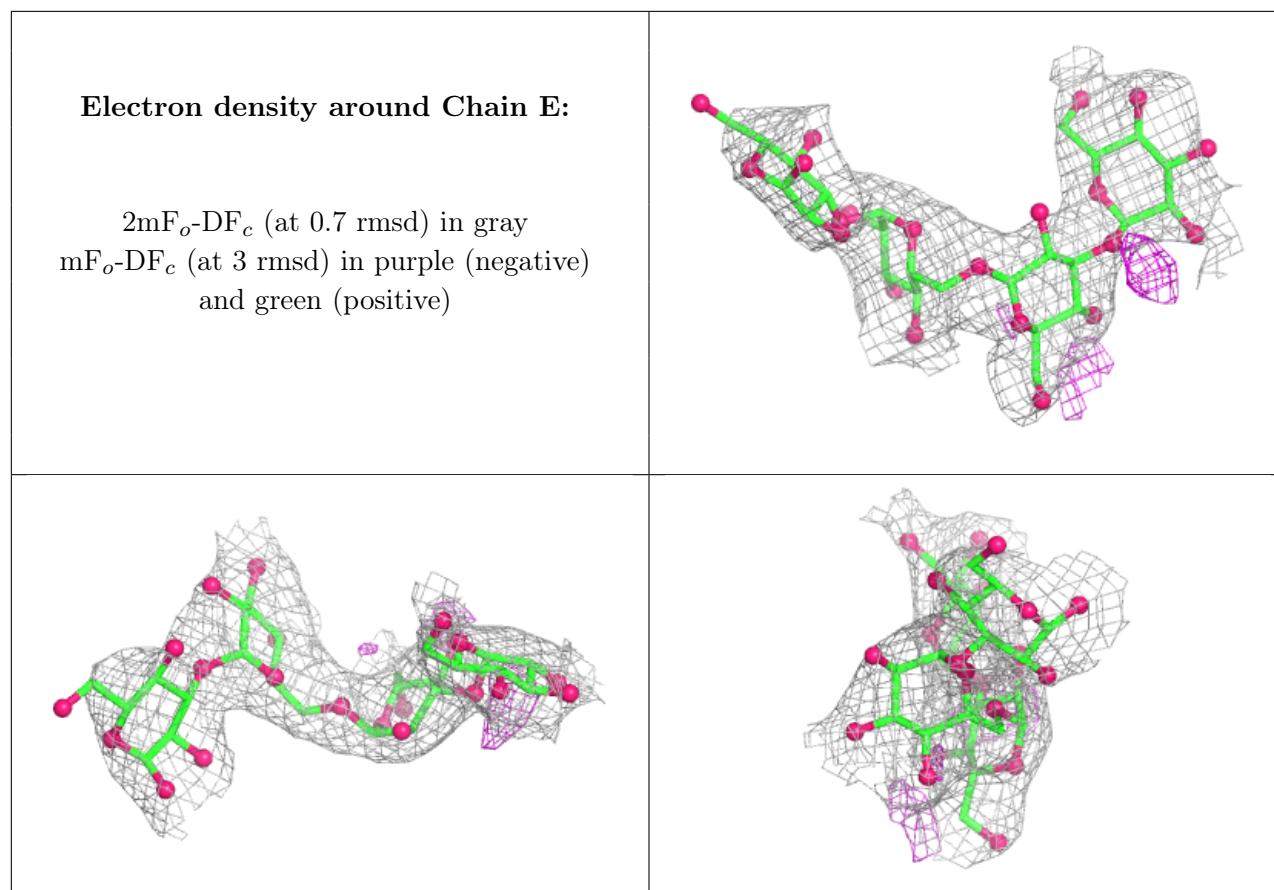
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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($\text{\AA}^2$)	Q<0.9
5	CA	B	1501	1/1	0.98	0.05	70,70,70,70	0
5	CA	A	1501	1/1	0.99	0.03	69,69,69,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.