Full wwPDB X-ray Structure Validation Report (i)

Oct 23, 2021 – 09:05 AM EDT

PDB ID	:	6CGT
Title	:	HOXA COMPLEX OF CYCLODEXTRIN GLYCOSYLTRANSFERASE MUTANT
Authors	:	Parsiegla, G.; Schulz, G.E.
Deposited on	:	1998-06-06
Resolution	:	2.60 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

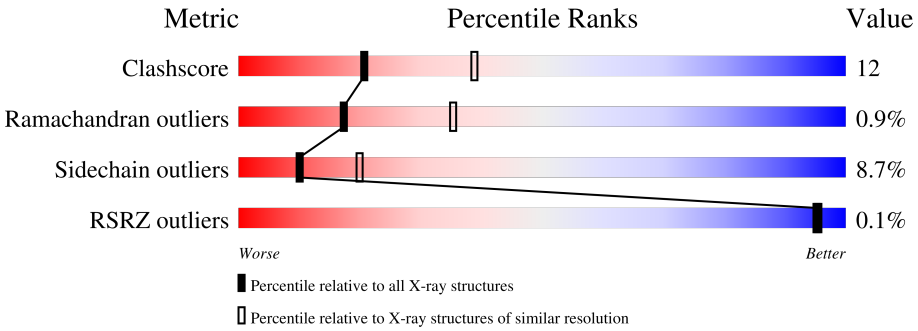
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.60 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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	684	71% 26% .
2	B	2	100%
2	C	2	50% 50%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DAG	B	2	X	-	-	-
2	DAG	C	2	X	-	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5536 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.

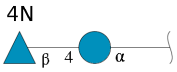
- Molecule 1 is a protein called CYCLODEXTRIN GLYCOSYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	684	Total	C	N	O	S	0	0	0
			5266	3321	891	1041	13			

There is a discrepancy between the modelled and reference sequences:

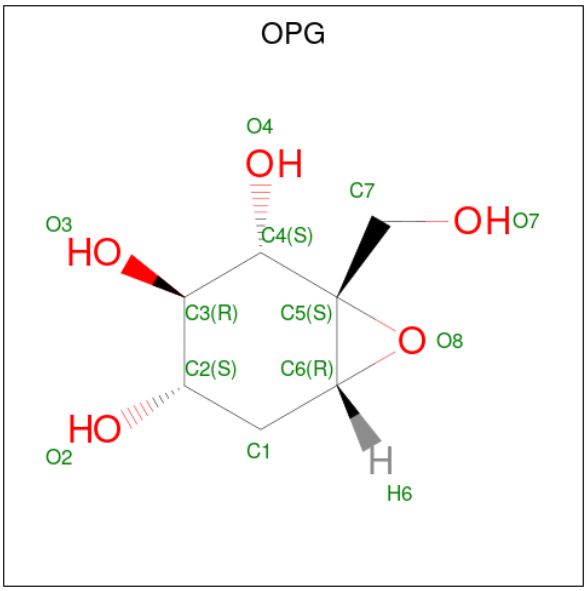
Chain	Residue	Modelled	Actual	Comment	Reference
A	194	THR	LEU	engineered mutation	UNP P30920

- Molecule 2 is an oligosaccharide called 4-amino-4,6-dideoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			22	12	1	9			
2	C	2	Total	C	N	O	0	0	0
			21	12	1	8			

- Molecule 3 is OXIRANPSEUDOGLUCOSE (three-letter code: OPG) (formula: $C_7H_{12}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 12 7 5	0	0
3	A	1	Total C O 12 7 5	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Ca 2 2	0	0

- Molecule 5 is water.

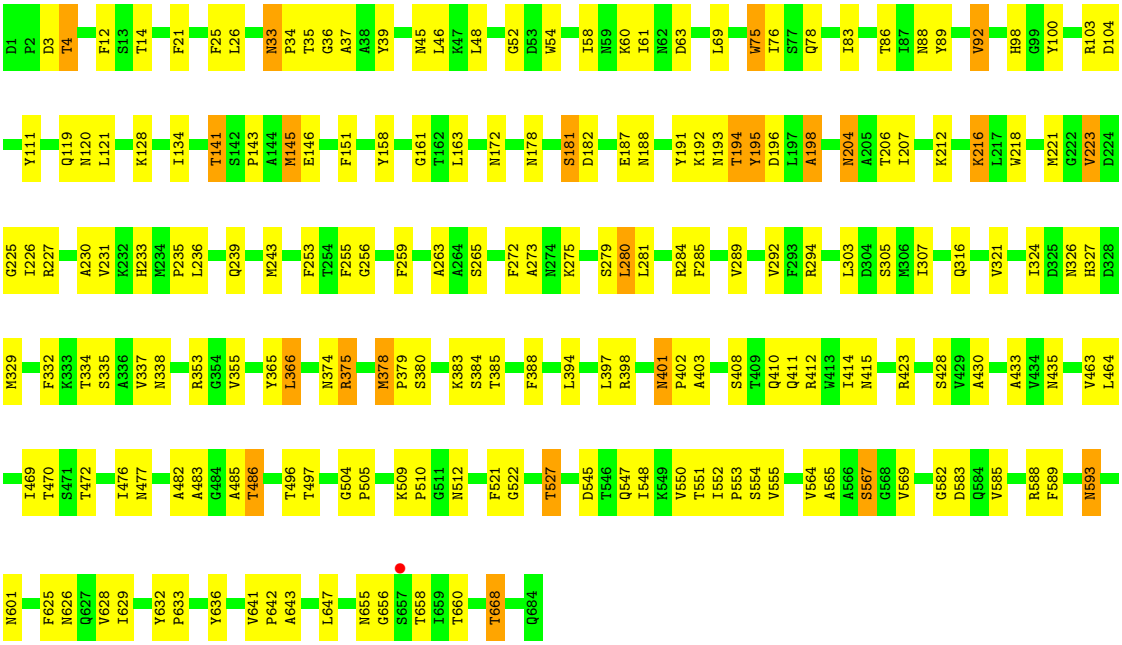
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	201	Total O 201 201	0	0

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.

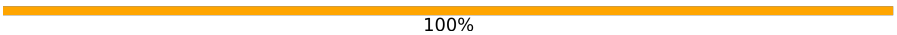
• Molecule 1: CYCLODEXTRIN GLYCOSYLTRANSFERASE

Chain A:



• Molecule 2: 4-amino-4,6-dideoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain B:



• Molecule 2: 4-amino-4,6-dideoxy-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain C:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	93.00Å 104.90Å 113.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.00 – 2.60 27.18 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (27.00-2.60) 87.1 (27.18-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	4.06 (at 2.61Å)	Xtriage
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.167 , 0.246 0.175 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	19.9	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 35.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5536	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DAG, GLC, OPG, CA

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	0.57	0/5397	0.79	0/7365

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	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	195	TYR	Sidechain

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	5266	0	5004	127	0
2	B	22	0	20	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	21	0	19	1	0
3	A	24	0	19	2	0
4	A	2	0	0	0	0
5	A	201	0	0	13	0
All	All	5536	0	5062	128	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 12.

All (128) 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:292:VAL:HG21	1:A:303:LEU:HD13	1.56	0.88
1:A:641:VAL:HG11	1:A:647:LEU:HD11	1.67	0.77
1:A:401:ASN:HD21	1:A:428:SER:HB3	1.56	0.69
1:A:482:ALA:HB3	1:A:485:ALA:HB2	1.74	0.69
1:A:273:ALA:HB2	1:A:280:LEU:HD22	1.75	0.68
1:A:338:ASN:HB3	5:A:732:HOH:O	1.93	0.68
1:A:98:HIS:HD2	1:A:100:TYR:H	1.41	0.67
1:A:527:THR:HG23	1:A:565:ALA:HB3	1.78	0.65
1:A:230:ALA:HB1	1:A:233:HIS:HD2	1.63	0.64
1:A:178:ASN:O	1:A:192:LYS:HE2	1.98	0.63
1:A:218:TRP:O	1:A:223:VAL:HG13	1.99	0.62
1:A:470:THR:HB	1:A:477:ASN:OD1	2.00	0.62
1:A:182:ASP:H	1:A:188:ASN:HD21	1.48	0.60
1:A:75:TRP:CE2	1:A:227:ARG:HG3	2.37	0.60
1:A:89:TYR:HB2	5:A:822:HOH:O	2.01	0.60
1:A:103:ARG:HA	5:A:748:HOH:O	2.02	0.59
1:A:272:PHE:CD1	1:A:280:LEU:HD11	2.37	0.59
1:A:75:TRP:CZ2	1:A:227:ARG:HG3	2.38	0.58
1:A:433:ALA:O	1:A:486:THR:HA	2.02	0.58
1:A:275:LYS:HB3	5:A:839:HOH:O	2.02	0.57
1:A:375:ARG:NH2	2:C:1:GLC:O2	2.39	0.56
1:A:334:THR:HG22	1:A:335:SER:N	2.20	0.56
1:A:14:THR:O	1:A:398:ARG:HB2	2.05	0.55
1:A:401:ASN:ND2	1:A:428:SER:HB3	2.21	0.55
1:A:641:VAL:HG13	1:A:642:PRO:HD2	1.87	0.55
1:A:510:PRO:HB3	1:A:553:PRO:O	2.07	0.54
1:A:212:LYS:O	1:A:216:LYS:HD3	2.09	0.53
1:A:45:ASN:OD1	1:A:48:LEU:HG	2.07	0.53
1:A:33:ASN:N	1:A:33:ASN:OD1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ASP:HB2	1:A:158:TYR:HB2	1.92	0.52
1:A:588:ARG:HH12	1:A:629:ILE:HD13	1.75	0.52
1:A:236:LEU:HD12	1:A:272:PHE:CD2	2.45	0.52
1:A:588:ARG:NH1	1:A:629:ILE:HD13	2.25	0.52
1:A:60:LYS:HD3	1:A:63:ASP:OD1	2.09	0.51
1:A:289:VAL:HG11	1:A:324:ILE:HG22	1.92	0.51
1:A:3:ASP:HA	1:A:547:GLN:HE21	1.76	0.50
1:A:76:ILE:HD11	1:A:134:ILE:HG22	1.92	0.50
1:A:326:ASN:OD1	1:A:329:MET:HG2	2.11	0.50
1:A:187:GLU:HB3	1:A:625:PHE:CE1	2.46	0.50
1:A:294:ARG:HG3	1:A:337:VAL:HG21	1.94	0.50
1:A:92:VAL:HG13	5:A:822:HOH:O	2.12	0.50
1:A:182:ASP:N	1:A:188:ASN:HD21	2.10	0.50
1:A:374:ASN:OD1	1:A:375:ARG:HD2	2.12	0.50
1:A:255:PHE:HA	1:A:279:SER:O	2.12	0.50
1:A:522:GLY:H	1:A:545:ASP:HA	1.75	0.50
1:A:231:VAL:HG11	1:A:256:GLY:HA3	1.94	0.50
1:A:191:TYR:CD1	1:A:629:ILE:HD11	2.48	0.49
1:A:512:ASN:HB2	1:A:552:ILE:HD12	1.95	0.49
1:A:4:THR:HG23	5:A:859:HOH:O	2.13	0.48
1:A:655:ASN:CG	1:A:656:GLY:H	2.17	0.48
1:A:463:VAL:HG23	1:A:464:LEU:HG	1.95	0.48
1:A:504:GLY:HA2	1:A:505:PRO:C	2.32	0.48
1:A:239:GLN:O	1:A:243:MET:HB2	2.13	0.48
1:A:414:ILE:HG12	1:A:415:ASN:N	2.29	0.48
1:A:235:PRO:O	1:A:239:GLN:HG3	2.14	0.48
1:A:12:PHE:CE1	1:A:253:PHE:HB3	2.48	0.48
1:A:69:LEU:HD13	1:A:388:PHE:CE2	2.48	0.48
1:A:227:ARG:HG2	1:A:255:PHE:CE2	2.49	0.48
1:A:469:ILE:HD12	1:A:476:ILE:HD12	1.95	0.48
1:A:83:ILE:HG13	1:A:83:ILE:O	2.13	0.47
1:A:60:LYS:HD3	1:A:60:LYS:HA	1.68	0.47
1:A:60:LYS:HA	1:A:63:ASP:OD1	2.15	0.47
1:A:181:SER:HB2	1:A:192:LYS:HB2	1.96	0.47
1:A:294:ARG:HB2	1:A:332:PHE:CZ	2.50	0.47
1:A:423:ARG:HB2	1:A:430:ALA:HB3	1.97	0.47
1:A:593:ASN:HA	1:A:633:PRO:HB2	1.97	0.46
1:A:14:THR:HG23	5:A:741:HOH:O	2.15	0.46
1:A:641:VAL:CG1	1:A:647:LEU:HD11	2.42	0.46
1:A:83:ILE:HA	1:A:103:ARG:HD3	1.95	0.46
1:A:550:VAL:HG22	1:A:551:THR:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:SER:HB2	5:A:862:HOH:O	2.14	0.46
1:A:158:TYR:HD2	1:A:161:GLY:O	1.98	0.46
1:A:403:ALA:HB2	1:A:428:SER:O	2.16	0.46
1:A:34:PRO:HG2	1:A:39:TYR:HB2	1.98	0.46
1:A:316:GLN:HG2	5:A:720:HOH:O	2.16	0.46
1:A:281:LEU:HD23	1:A:321:VAL:HB	1.97	0.45
1:A:583:ASP:HA	5:A:729:HOH:O	2.15	0.45
1:A:401:ASN:HD22	1:A:402:PRO:CD	2.29	0.45
1:A:145:MET:HB2	1:A:151:PHE:CD2	2.52	0.45
1:A:394:LEU:O	1:A:397:LEU:HB2	2.17	0.45
1:A:365:TYR:HE2	1:A:385:THR:HB	1.82	0.45
1:A:285:PHE:CE1	1:A:289:VAL:HG21	2.51	0.45
1:A:181:SER:HB3	1:A:193:ASN:O	2.17	0.44
1:A:98:HIS:HD2	1:A:100:TYR:N	2.13	0.44
1:A:34:PRO:HD3	1:A:111:TYR:CD1	2.53	0.44
1:A:143:PRO:HB3	1:A:196:ASP:OD2	2.16	0.44
1:A:464:LEU:HD13	1:A:486:THR:HG23	1.99	0.43
1:A:589:PHE:O	1:A:636:TYR:HA	2.17	0.43
1:A:272:PHE:HD1	1:A:280:LEU:HD11	1.80	0.43
1:A:204:ASN:HD22	1:A:206:THR:H	1.67	0.43
1:A:321:VAL:HA	1:A:355:VAL:O	2.18	0.43
1:A:25:PHE:CD1	1:A:378:MET:HG3	2.54	0.43
1:A:327:HIS:O	1:A:375:ARG:NH1	2.51	0.43
1:A:88:ASN:HB2	5:A:876:HOH:O	2.18	0.43
1:A:230:ALA:HB1	1:A:233:HIS:CD2	2.49	0.43
1:A:141:THR:OG1	1:A:198:ALA:HB3	2.19	0.43
1:A:204:ASN:ND2	1:A:206:THR:HB	2.33	0.43
1:A:259:PHE:CD1	2:B:1:GLC:H5	2.54	0.43
3:A:703:OPG:O8	2:B:2:DAG:H4	2.19	0.42
1:A:435:ASN:ND2	1:A:483:ALA:HA	2.33	0.42
1:A:58:ILE:HA	1:A:61:ILE:HD12	2.02	0.42
1:A:509:LYS:HB2	1:A:582:GLY:HA2	2.01	0.42
1:A:194:THR:O	1:A:195:TYR:HB2	2.19	0.42
1:A:408:SER:O	1:A:423:ARG:HA	2.19	0.42
1:A:548:ILE:HD12	1:A:564:VAL:HG21	2.00	0.42
1:A:204:ASN:HB3	1:A:207:ILE:HG12	2.01	0.42
1:A:383:LYS:HA	1:A:388:PHE:CD2	2.54	0.42
1:A:54:TRP:O	1:A:58:ILE:HG13	2.19	0.42
1:A:307:ILE:HD13	1:A:307:ILE:HA	1.82	0.42
1:A:263:ALA:O	1:A:284:ARG:HD2	2.19	0.42
1:A:401:ASN:HD22	1:A:402:PRO:HD2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:PRO:CB	1:A:554:SER:HA	2.50	0.41
1:A:641:VAL:HG13	1:A:642:PRO:CD	2.49	0.41
1:A:75:TRP:CD1	1:A:75:TRP:C	2.94	0.41
1:A:464:LEU:CD1	1:A:486:THR:HG23	2.50	0.41
1:A:550:VAL:CG2	1:A:551:THR:N	2.84	0.41
1:A:588:ARG:HD2	5:A:749:HOH:O	2.20	0.41
1:A:366:LEU:HD11	1:A:379:PRO:HD3	2.03	0.41
1:A:100:TYR:HB3	3:A:703:OPG:O7	2.21	0.41
1:A:196:ASP:HA	5:A:849:HOH:O	2.19	0.41
1:A:647:LEU:O	1:A:668:THR:HA	2.21	0.41
1:A:334:THR:CG2	1:A:335:SER:N	2.84	0.41
1:A:510:PRO:HA	1:A:552:ILE:HG22	2.03	0.41
1:A:567:SER:O	1:A:569:VAL:HG23	2.21	0.41
1:A:626:ASN:HB2	1:A:632:TYR:HB2	2.03	0.41
1:A:292:VAL:HG21	1:A:303:LEU:CD1	2.40	0.40
1:A:585:VAL:HG13	1:A:643:ALA:HB2	2.03	0.40
1:A:225:GLY:C	1:A:226:ILE:HG13	2.40	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	682/684 (100%)	614 (90%)	62 (9%)	6 (1%)	17 35

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	GLY
1	A	36	GLY
1	A	521	PHE
1	A	37	ALA

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Mol	Chain	Res	Type
1	A	198	ALA
1	A	628	VAL

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	566/566 (100%)	517 (91%)	49 (9%)	10 20

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	21	PHE
1	A	26	LEU
1	A	33	ASN
1	A	35	THR
1	A	46	LEU
1	A	75	TRP
1	A	78	GLN
1	A	86	THR
1	A	92	VAL
1	A	119	GLN
1	A	120	ASN
1	A	121	LEU
1	A	128	LYS
1	A	141	THR
1	A	145	MET
1	A	146	GLU
1	A	163	LEU
1	A	172	ASN
1	A	181	SER
1	A	194	THR
1	A	204	ASN
1	A	216	LYS
1	A	221	MET

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Mol	Chain	Res	Type
1	A	223	VAL
1	A	265	SER
1	A	280	LEU
1	A	305	SER
1	A	353	ARG
1	A	366	LEU
1	A	375	ARG
1	A	378	MET
1	A	384	SER
1	A	401	ASN
1	A	410	GLN
1	A	411	GLN
1	A	412	ARG
1	A	472	THR
1	A	486	THR
1	A	496	THR
1	A	497	THR
1	A	527	THR
1	A	555	VAL
1	A	567	SER
1	A	593	ASN
1	A	601	ASN
1	A	658	THR
1	A	660	THR
1	A	668	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	HIS
1	A	119	GLN
1	A	172	ASN
1	A	188	ASN
1	A	204	ASN
1	A	249	HIS
1	A	269	ASN
1	A	286	ASN
1	A	369	ASN
1	A	401	ASN
1	A	411	GLN
1	A	435	ASN
1	A	465	ASN

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Mol	Chain	Res	Type
1	A	547	GLN
1	A	575	ASN
1	A	627	GLN
1	A	631	GLN
1	A	646	GLN

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	GLC	B	1	2	12,12,12	1.27	1 (8%)	17,17,17	0.93	0
2	DAG	B	2	2,3	9,10,11	1.54	2 (22%)	14,14,16	1.06	1 (7%)
2	GLC	C	1	2,3	11,11,12	1.11	0	15,15,17	0.48	0
2	DAG	C	2	2,3	9,10,11	1.03	0	14,14,16	0.54	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	B	1	2	-	0/2/22/22	0/1/1/1
2	DAG	B	2	2,3	1/1/4/5	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	C	1	2,3	-	0/2/19/22	0/1/1/1
2	DAG	C	2	2,3	1/1/4/5	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	GLC	C1-C2	3.38	1.60	1.52
2	B	2	DAG	C3-C4	-2.69	1.50	1.53
2	B	2	DAG	O5-C1	2.57	1.47	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	DAG	C1-C2-C3	2.95	113.30	109.67

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	2	DAG	C1
2	C	2	DAG	C1

There are no torsion outliers.

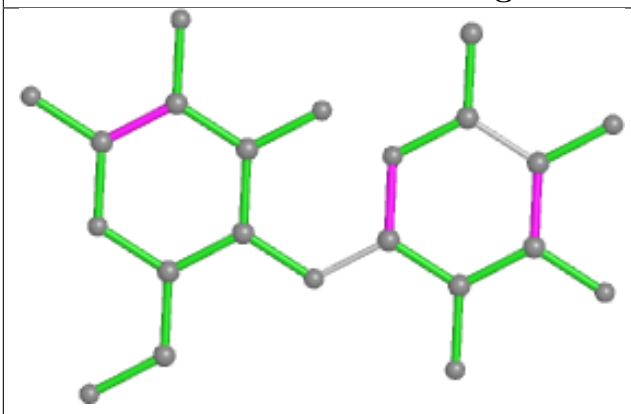
There are no ring outliers.

3 monomers are involved in 3 short contacts:

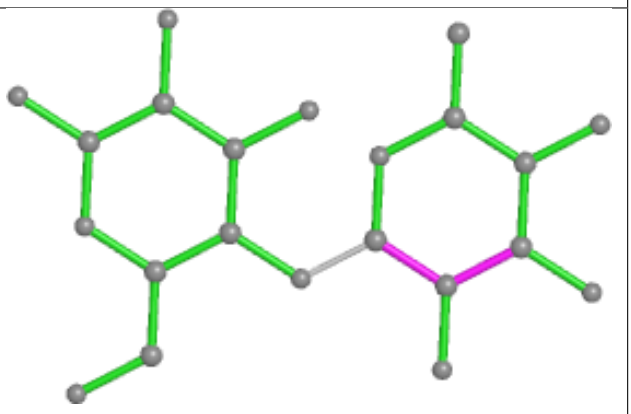
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	GLC	1	0
2	B	2	DAG	1	0
2	C	1	GLC	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

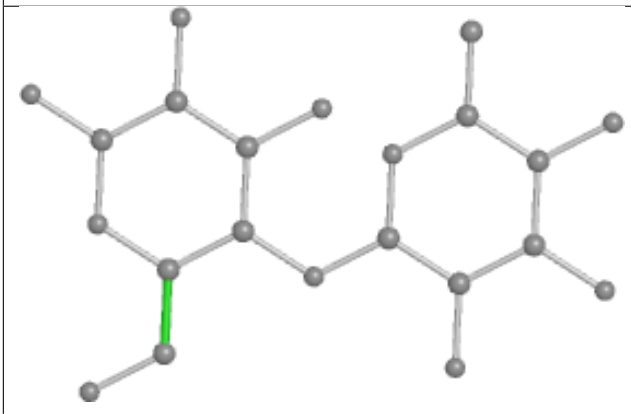
Oligosaccharide Chain B



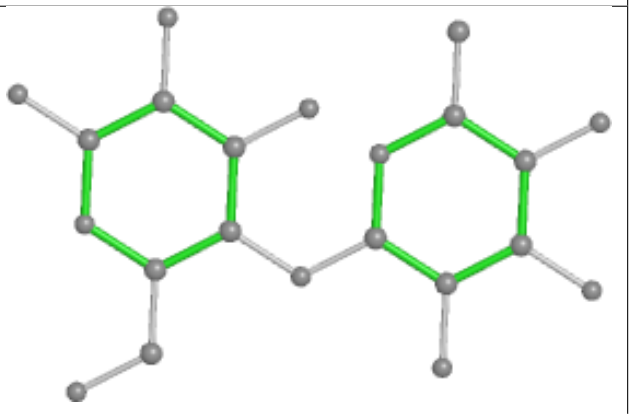
Bond lengths



Bond angles

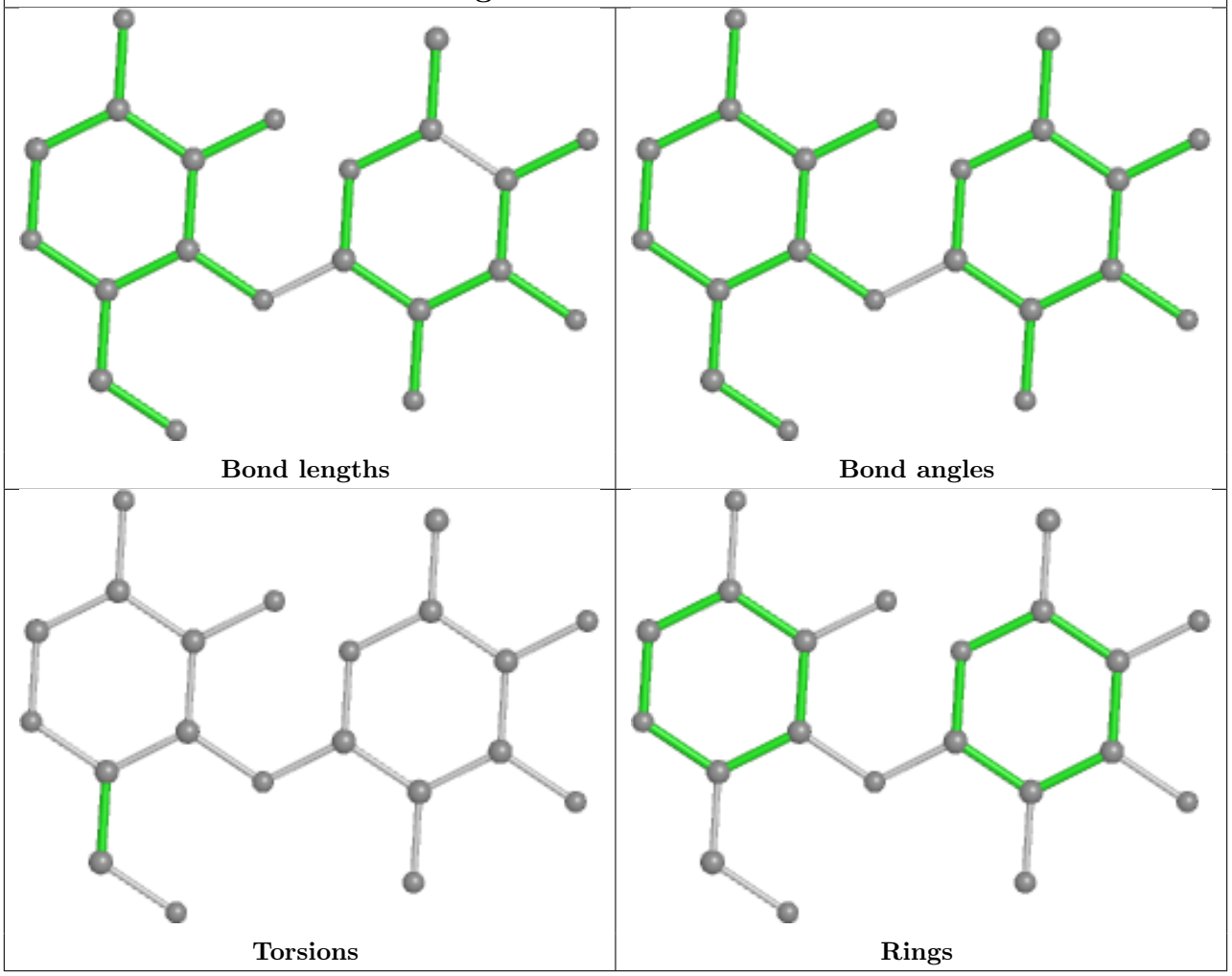


Torsions



Rings

Oligosaccharide Chain C



5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	OPG	A	706	2	13,13,13	2.37	5 (38%)	17,21,21	2.43	7 (41%)
3	OPG	A	703	2	13,13,13	1.68	4 (30%)	17,21,21	2.62	5 (29%)

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	OPG	A	706	2	-	1/3/29/29	0/2/2/2
3	OPG	A	703	2	-	1/3/29/29	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	706	OPG	C5-C6	5.37	1.54	1.46
3	A	706	OPG	C3-C4	4.34	1.61	1.53
3	A	703	OPG	C5-C6	4.12	1.52	1.46
3	A	706	OPG	C5-C4	2.79	1.59	1.53
3	A	703	OPG	O8-C5	-2.31	1.42	1.45
3	A	703	OPG	C5-C4	2.12	1.58	1.53
3	A	706	OPG	C2-C3	2.11	1.55	1.52
3	A	703	OPG	C3-C4	2.10	1.57	1.53
3	A	706	OPG	C7-C5	2.08	1.55	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	703	OPG	C5-O8-C6	6.90	64.18	60.36
3	A	706	OPG	C5-O8-C6	5.05	63.16	60.36
3	A	703	OPG	O8-C6-C5	-4.77	57.09	59.94
3	A	706	OPG	O8-C5-C4	4.37	122.82	115.37
3	A	703	OPG	O8-C6-C1	4.27	123.68	115.98
3	A	706	OPG	O8-C6-C1	4.07	123.33	115.98
3	A	706	OPG	O8-C5-C7	4.04	122.24	114.89
3	A	703	OPG	O8-C5-C4	3.35	121.08	115.37
3	A	703	OPG	O8-C5-C7	3.14	120.59	114.89
3	A	706	OPG	O8-C6-C5	-2.84	58.24	59.94
3	A	706	OPG	C6-C5-C4	-2.13	114.82	117.67
3	A	706	OPG	C1-C2-C3	-2.09	107.65	110.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	706	OPG	O8-C5-C7-O7
3	A	703	OPG	C6-C5-C7-O7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	703	OPG	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	684/684 (100%)	-0.93	1 (0%)	95	95	6, 16, 25, 39	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	657	SER	3.0

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

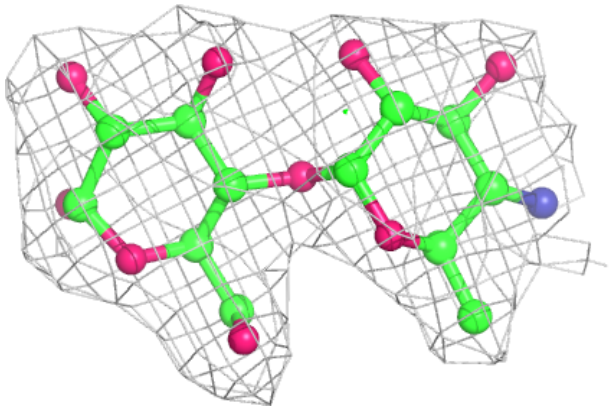
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

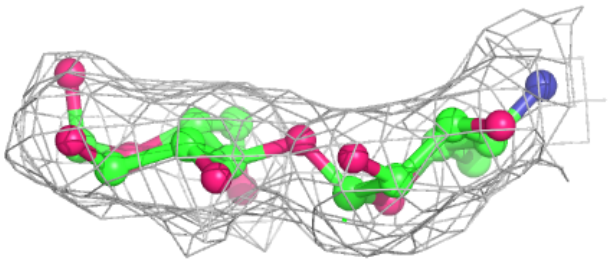
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	DAG	C	2	10/11	0.95	0.12	20,26,29,37	0
2	GLC	C	1	11/12	0.96	0.11	10,14,20,22	0
2	DAG	B	2	10/11	0.96	0.10	8,13,15,17	0
2	GLC	B	1	12/12	0.97	0.10	17,20,24,28	0

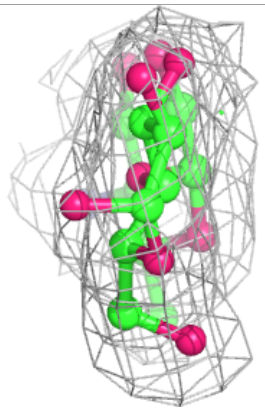
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

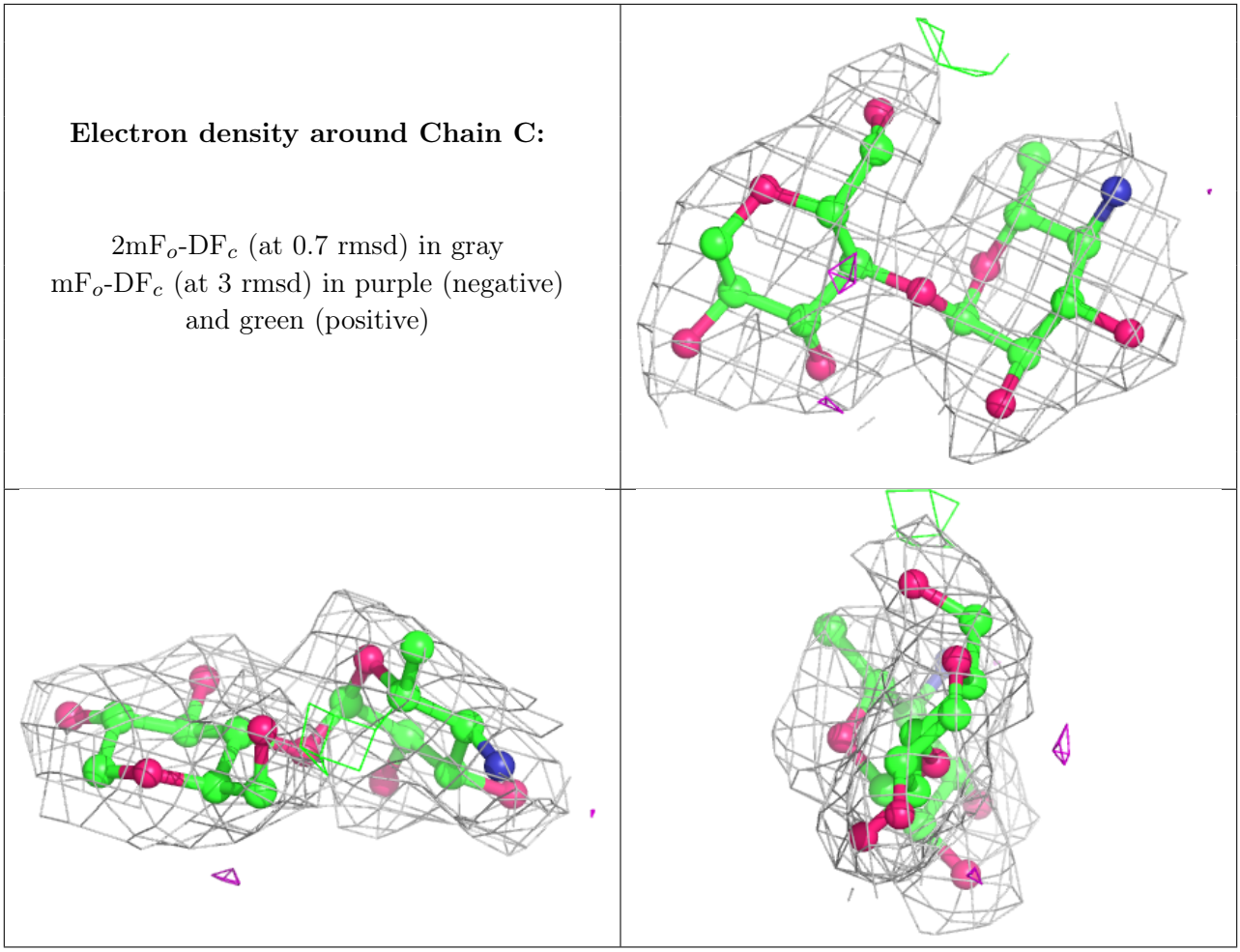






Electron density around Chain C:

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



6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	OPG	A	706	12/12	0.84	0.32	44,49,51,53	0
4	CA	A	686	1/1	0.97	0.09	18,18,18,18	0
4	CA	A	685	1/1	0.98	0.14	12,12,12,12	0
3	OPG	A	703	12/12	0.98	0.12	9,11,14,15	0

6.5 Other polymers

There are no such residues in this entry.