Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2022 – 03:33 pm GMT

PDB ID	:	6R5V
Title	:	The crystal structure of Glycoside Hydrolase BglX inactive mutant D286N from P. aeruginosa in complex with xylotriose
Authors	:	Batuecas, M.T.; Hermoso, J.A.
Deposited on	:	2019-03-25
Resolution	:	1.80 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:

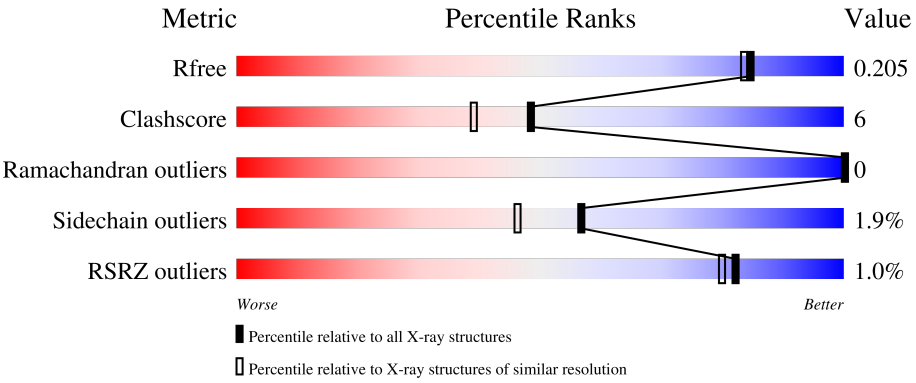
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	733	90% 9%
1	B	733	89% 9%
2	C	2	100%
2	D	2	50% 50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12464 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 Periplasmic beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	733	Total	C	N	O	S	0	16	0
			5711	3593	1022	1075	21			
1	A	730	Total	C	N	O	S	0	12	0
			5667	3569	1014	1063	21			

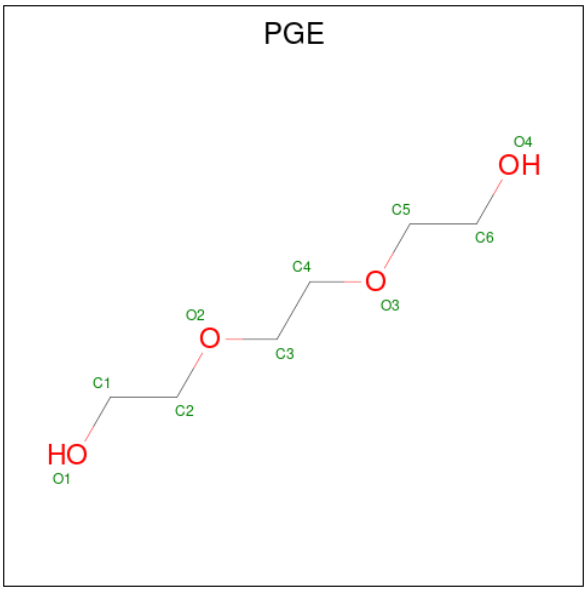
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	286	ASN	ASP	engineered mutation	UNP Q9I311
A	286	ASN	ASP	engineered mutation	UNP Q9I311

- Molecule 2 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.

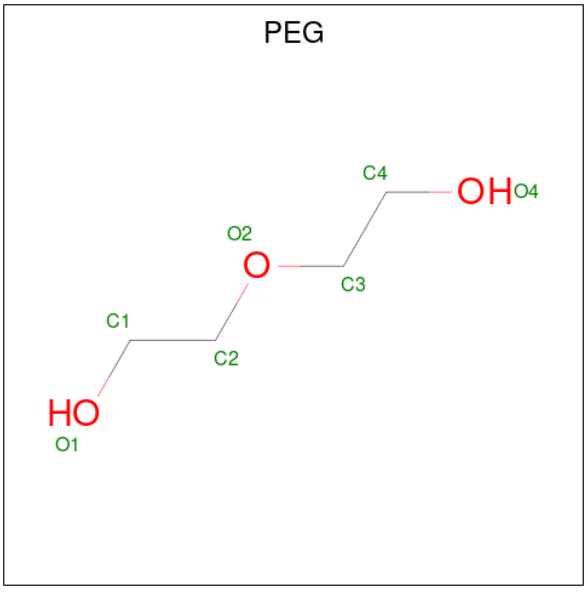
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	0	0	0
			19	10	9			
2	D	2	Total	C	O	0	0	0
			19	10	9			

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 10 6 4	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is water.

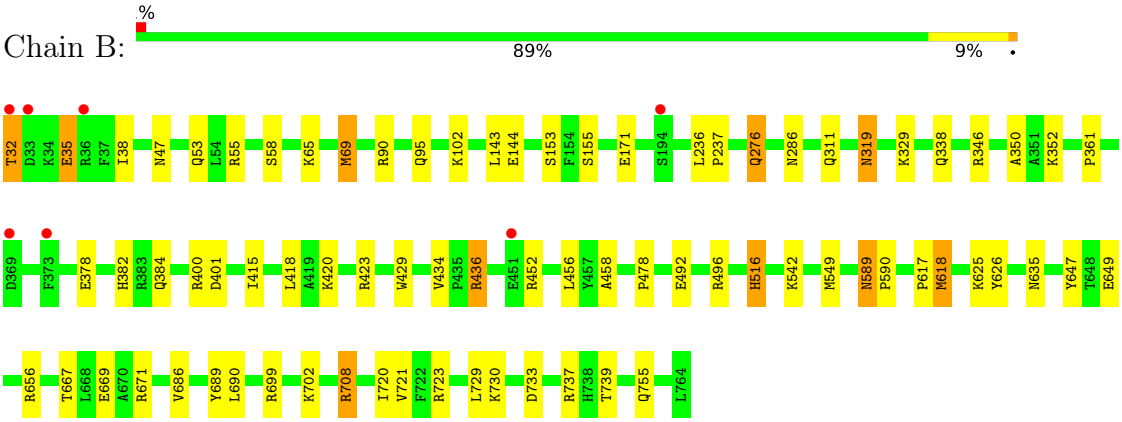
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	555	Total O 555 555	0	0
6	A	467	Total O 467 467	0	0

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.

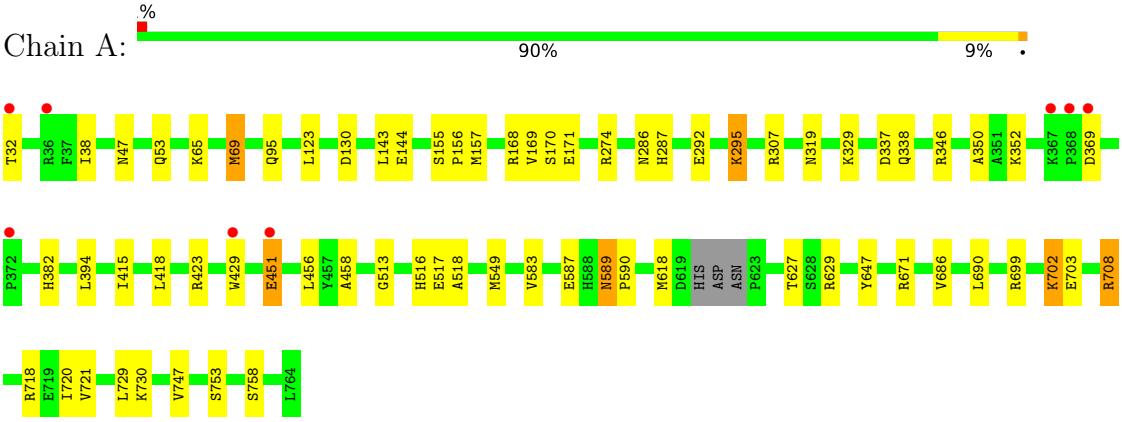
• Molecule 1: Periplasmic beta-glucosidase

Chain B:



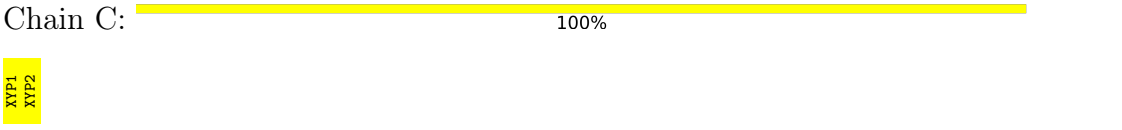
• Molecule 1: Periplasmic beta-glucosidase

Chain A:



• Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain C:



• Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain D:


XYP1
XYP2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	70.95Å 73.67Å 81.44Å 65.55° 73.46° 69.66°	Depositor
Resolution (Å)	45.27 – 1.80 45.27 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.3 (45.27-1.80) 96.3 (45.27-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.163 , 0.197 0.173 , 0.205	Depositor DCC
R_{free} test set	6198 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	17.0	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	12464	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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: MG, XYP, PEG, PGE

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	0.74	0/5815	0.88	3/7879 (0.0%)
1	B	0.75	0/5872	0.87	2/7958 (0.0%)
All	All	0.74	0/11687	0.87	5/15837 (0.0%)

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.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	274	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	B	699	ARG	NE-CZ-NH2	-6.70	116.95	120.30
1	A	423	ARG	NE-CZ-NH2	-6.29	117.16	120.30
1	A	708	ARG	CG-CD-NE	-6.17	98.84	111.80
1	B	90	ARG	CG-CD-NE	-5.89	99.43	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	369	ASP	Peptide

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	5667	0	5685	61	1
1	B	5711	0	5728	78	1
2	C	19	0	0	0	0
2	D	19	0	0	2	0
3	B	10	0	14	3	0
4	A	7	0	10	0	0
4	B	7	0	10	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	467	0	0	11	12
6	B	555	0	0	28	20
All	All	12464	0	11447	138	21

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 6.

All (138) 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:171:GLU:OE2	1:B:429[B]:TRP:CH2	1.98	1.16
1:B:496[A]:ARG:NH1	6:B:903:HOH:O	1.82	1.12
1:A:171:GLU:OE2	1:A:429[B]:TRP:CZ2	2.03	1.12
1:B:618:MET:HE1	1:B:635:ASN:CB	1.90	1.00
1:A:292:GLU:OE2	6:A:901:HOH:O	1.85	0.94
1:B:32:THR:HG23	1:B:35:GLU:HB2	1.51	0.93
1:A:130:ASP:OD2	6:A:902:HOH:O	1.87	0.92
1:B:589:ASN:HD21	1:B:647:TYR:H	1.15	0.91
1:A:589:ASN:HD21	1:A:647:TYR:H	1.18	0.90
1:B:276:GLN:OE1	6:B:904:HOH:O	1.91	0.88
1:B:478:PRO:HB2	3:B:801:PGE:H32	1.55	0.87
1:A:47:ASN:HD21	1:A:338:GLN:HE22	1.20	0.86
1:A:171:GLU:OE2	1:A:429[B]:TRP:CH2	2.30	0.85
1:A:287:HIS:HD2	1:A:319:ASN:HD22	1.25	0.84
1:B:171:GLU:OE2	1:B:429[B]:TRP:CZ2	2.31	0.84
1:B:492:GLU:HG2	6:B:1395:HOH:O	1.77	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:HIS:CD2	1:A:319:ASN:HD22	1.97	0.82
1:A:170:SER:HG	1:A:429[B]:TRP:HZ3	1.28	0.81
1:B:32:THR:CG2	1:B:35:GLU:HB2	2.11	0.81
1:B:618:MET:HE1	1:B:635:ASN:HB3	1.63	0.80
1:A:518:ALA:O	6:A:903:HOH:O	1.99	0.80
1:B:618:MET:HE1	1:B:635:ASN:HB2	1.65	0.79
6:B:1088:HOH:O	1:A:295:LYS:HE2	1.83	0.79
1:A:702:LYS:HE3	1:A:753:SER:O	1.84	0.78
1:B:690:LEU:HD21	1:B:729:LEU:HD23	1.67	0.77
1:B:378:GLU:OE2	6:B:906:HOH:O	2.03	0.75
1:A:170:SER:OG	1:A:429[B]:TRP:HZ3	1.69	0.75
1:B:32:THR:HG23	1:B:35:GLU:H	1.52	0.73
1:A:618:MET:HG2	6:A:1052:HOH:O	1.88	0.73
1:A:429[B]:TRP:HE3	6:A:1252:HOH:O	1.71	0.72
1:A:418[B]:LEU:HD23	1:A:549:MET:HB2	1.72	0.71
1:B:286:ASN:ND2	6:B:912:HOH:O	2.23	0.71
1:B:47:ASN:HD21	1:B:338:GLN:HE22	1.37	0.70
1:B:625:LYS:NZ	6:B:917:HOH:O	2.27	0.67
1:B:649:GLU:OE2	6:B:907:HOH:O	2.13	0.66
1:B:478:PRO:HB2	3:B:801:PGE:C3	2.26	0.66
1:A:171:GLU:HG3	1:A:429[B]:TRP:CZ3	2.32	0.65
1:B:144:GLU:OE2	1:B:382:HIS:HD2	1.79	0.64
1:A:144:GLU:OE2	1:A:382:HIS:HD2	1.79	0.64
1:A:286:ASN:ND2	6:A:907:HOH:O	2.30	0.64
1:B:690:LEU:HD21	1:B:729:LEU:CD2	2.27	0.64
1:A:429[B]:TRP:CE3	6:A:1252:HOH:O	2.49	0.64
1:B:171:GLU:OE2	1:B:429[B]:TRP:CZ3	2.49	0.63
1:B:53:GLN:HE22	1:B:352:LYS:NZ	1.97	0.63
1:A:418[B]:LEU:CD2	1:A:549:MET:HB2	2.28	0.62
1:B:423:ARG:NH1	6:B:916:HOH:O	2.26	0.61
1:A:53:GLN:HE22	1:A:352:LYS:NZ	1.99	0.61
1:A:53:GLN:HE22	1:A:352:LYS:HZ2	1.49	0.60
1:A:513:GLY:O	1:A:516[B]:HIS:CE1	2.55	0.59
1:A:47:ASN:ND2	1:A:338:GLN:HE22	1.98	0.58
1:B:496[A]:ARG:NH1	6:B:905:HOH:O	2.02	0.58
1:A:690:LEU:HD11	1:A:729:LEU:HD23	1.85	0.57
1:A:418[A]:LEU:HD13	1:A:549:MET:HB2	1.86	0.57
1:B:418:LEU:HD13	1:B:549:MET:HB2	1.87	0.57
1:B:755[A]:GLN:OE1	6:B:908:HOH:O	2.18	0.57
1:B:276:GLN:HG2	6:B:950:HOH:O	2.04	0.56
1:A:329:LYS:HG3	6:A:1047:HOH:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:667[B]:THR:HG21	1:B:723:ARG:NH2	2.21	0.55
1:B:329:LYS:HG3	6:B:1008:HOH:O	2.05	0.55
1:B:429[B]:TRP:CH2	1:B:516:HIS:HA	2.42	0.55
1:A:47:ASN:HD21	1:A:338:GLN:NE2	1.97	0.55
1:B:589:ASN:ND2	1:B:647:TYR:H	1.97	0.54
1:B:542:LYS:O	6:B:909:HOH:O	2.18	0.53
1:A:65:LYS:O	1:A:69:MET:HG2	2.09	0.53
1:A:171:GLU:HG3	1:A:429[B]:TRP:CE3	2.43	0.53
1:A:589:ASN:ND2	1:A:647:TYR:H	1.99	0.52
1:B:65:LYS:O	1:B:69:MET:HG2	2.09	0.52
6:B:1088:HOH:O	1:A:295:LYS:CE	2.48	0.51
1:B:47:ASN:HD21	1:B:338:GLN:NE2	2.08	0.51
1:B:58:SER:H	1:B:319:ASN:HD21	1.57	0.51
1:A:708:ARG:HG3	1:A:720:ILE:HG23	1.92	0.51
1:A:671:ARG:HG2	1:A:721:VAL:HG22	1.92	0.51
1:B:311:GLN:OE1	6:B:911:HOH:O	2.20	0.50
1:B:617:PRO:HD2	1:A:295:LYS:HE3	1.93	0.50
1:B:667[A]:THR:HG21	1:B:723:ARG:HH21	1.77	0.50
1:B:669:GLU:OE2	1:B:723:ARG:NH1	2.45	0.50
1:A:168:ARG:HH22	2:D:2:XYP:C5	2.25	0.49
1:B:384:GLN:NE2	6:B:919:HOH:O	2.32	0.49
1:B:171:GLU:HG3	1:B:429[B]:TRP:CE3	2.47	0.49
1:B:361:PRO:HG3	6:B:1203:HOH:O	2.11	0.49
1:B:400:ARG:HD3	1:B:401[B]:ASP:OD2	2.14	0.48
1:B:53:GLN:HE22	1:B:352:LYS:HZ1	1.61	0.48
1:B:589:ASN:HD22	1:B:590:PRO:HD2	1.78	0.48
1:A:53:GLN:NE2	1:A:352:LYS:HZ2	2.11	0.48
1:A:337:ASP:HB3	6:A:1075:HOH:O	2.14	0.47
1:B:47:ASN:ND2	1:B:338:GLN:HE22	2.08	0.47
6:B:917:HOH:O	1:A:516[B]:HIS:CE1	2.68	0.47
1:A:429[B]:TRP:CH2	1:A:516[B]:HIS:HA	2.50	0.46
1:A:456:LEU:N	1:A:456:LEU:HD12	2.30	0.46
1:A:143:LEU:HD12	6:A:1001:HOH:O	2.15	0.46
1:B:429[B]:TRP:HE3	6:B:1285:HOH:O	1.97	0.46
1:B:618:MET:HB3	1:B:618:MET:HE3	1.61	0.46
1:A:451:GLU:H	1:A:451:GLU:CD	2.19	0.46
1:A:516[A]:HIS:CG	1:A:517:GLU:N	2.83	0.45
1:B:400:ARG:HG3	6:B:1400:HOH:O	2.16	0.45
1:A:155[B]:SER:HB2	1:A:156:PRO:HA	1.97	0.45
1:A:38:ILE:HD11	1:A:350:ALA:HA	1.97	0.45
1:A:69:MET:HE2	1:A:95:GLN:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ARG:HH12	2:D:2:XYP:C5	2.30	0.44
1:B:456:LEU:HD12	1:B:456:LEU:N	2.32	0.44
1:B:69:MET:HE2	1:B:95:GLN:HG3	1.99	0.44
1:B:667[B]:THR:CG2	1:B:723:ARG:NH2	2.81	0.44
1:B:143:LEU:HD12	6:B:1099:HOH:O	2.16	0.44
1:B:478:PRO:CB	3:B:801:PGE:H32	2.39	0.44
1:A:699:ARG:NH2	1:A:703:GLU:OE1	2.50	0.44
1:A:730:LYS:NZ	6:A:935:HOH:O	2.50	0.44
1:B:689:TYR:HB3	1:B:702:LYS:HB2	2.00	0.44
1:A:513:GLY:O	1:A:516[B]:HIS:ND1	2.50	0.43
1:B:55:ARG:HB2	6:B:1077:HOH:O	2.18	0.43
1:B:102:LYS:HE3	6:B:1264:HOH:O	2.17	0.43
1:B:32:THR:HG23	1:B:35:GLU:N	2.28	0.43
1:B:730:LYS:HA	1:B:739:THR:O	2.18	0.43
1:A:415:ILE:HA	1:A:458:ALA:O	2.18	0.43
1:B:420:LYS:NZ	6:B:947:HOH:O	2.51	0.43
1:B:708:ARG:NH2	1:B:721:VAL:O	2.51	0.43
1:A:686:VAL:HG21	1:A:720:ILE:CD1	2.49	0.43
1:B:733:ASP:HB2	6:B:1247:HOH:O	2.20	0.42
1:B:415:ILE:HA	1:B:458:ALA:O	2.18	0.42
1:B:171:GLU:HG3	1:B:429[B]:TRP:CZ3	2.55	0.42
1:A:394:LEU:HD12	1:A:583:VAL:HG21	2.01	0.42
1:B:236:LEU:N	1:B:237:PRO:CD	2.83	0.41
1:B:153:SER:HG	1:B:155[A]:SER:HB3	1.83	0.41
1:B:434:VAL:HG12	1:B:436:ARG:HG2	2.02	0.41
1:A:123:LEU:HD22	1:A:169[B]:VAL:HG12	2.01	0.41
1:B:38:ILE:HD11	1:B:350:ALA:HA	2.01	0.41
1:B:319:ASN:HD22	1:B:319:ASN:HA	1.73	0.41
1:B:436:ARG:HD2	6:B:1338:HOH:O	2.19	0.41
1:A:589:ASN:HD22	1:A:590:PRO:HD2	1.86	0.41
1:B:53:GLN:HE22	1:B:352:LYS:HZ2	1.66	0.41
1:B:436:ARG:CZ	6:B:1061:HOH:O	2.69	0.41
1:A:170:SER:OG	1:A:429[B]:TRP:CZ3	2.60	0.41
1:B:733:ASP:OD2	1:B:737:ARG:NH1	2.54	0.41
1:B:669:GLU:OE1	1:B:671:ARG:NH2	2.53	0.41
1:B:686:VAL:HG21	1:B:720:ILE:CD1	2.51	0.41
1:A:747:VAL:O	1:A:758:SER:HA	2.21	0.41
1:B:625:LYS:HE2	1:B:626:TYR:OH	2.20	0.40
1:A:589:ASN:HD22	1:A:589:ASN:C	2.25	0.40
1:A:627:THR:OG1	1:A:629:ARG:HD2	2.21	0.40

All (21) 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)
6:B:919:HOH:O	6:A:918:HOH:O[1_546]	0.97	1.23
6:B:1179:HOH:O	6:B:1213:HOH:O[1_455]	1.09	1.11
6:B:1354:HOH:O	6:A:1322:HOH:O[1_645]	1.10	1.10
6:B:923:HOH:O	6:B:1264:HOH:O[1_455]	1.27	0.93
6:B:1314:HOH:O	6:B:1389:HOH:O[1_455]	1.29	0.91
6:B:1332:HOH:O	6:A:1196:HOH:O[1_645]	1.30	0.90
6:B:936:HOH:O	6:B:1288:HOH:O[1_655]	1.55	0.65
6:B:1343:HOH:O	6:A:1008:HOH:O[1_546]	1.55	0.65
6:B:1366:HOH:O	6:A:1249:HOH:O[1_546]	1.55	0.65
6:B:1441:HOH:O	6:A:1324:HOH:O[1_645]	1.57	0.63
6:B:1122:HOH:O	6:A:935:HOH:O[1_545]	1.59	0.61
6:B:1200:HOH:O	6:B:1261:HOH:O[1_455]	1.62	0.58
6:B:1401:HOH:O	6:A:1305:HOH:O[1_645]	1.72	0.48
1:B:452:ARG:NH2	1:A:587:GLU:OE2[1_546]	1.88	0.32
6:B:1342:HOH:O	6:A:1132:HOH:O[1_545]	1.88	0.32
6:B:1399:HOH:O	6:B:1420:HOH:O[1_655]	1.96	0.24
6:B:1452:HOH:O	6:A:1348:HOH:O[1_655]	2.00	0.20
6:B:1351:HOH:O	6:B:1440:HOH:O[1_565]	2.05	0.15
6:B:1245:HOH:O	6:A:1270:HOH:O[1_545]	2.07	0.13
6:B:901:HOH:O	6:B:1213:HOH:O[1_455]	2.14	0.06
6:B:966:HOH:O	6:A:1132:HOH:O[1_545]	2.18	0.02

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	738/733 (101%)	717 (97%)	21 (3%)	0	100	100
1	B	747/733 (102%)	725 (97%)	22 (3%)	0	100	100
All	All	1485/1466 (101%)	1442 (97%)	43 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	595/586 (102%)	585 (98%)	10 (2%)	60 51
1	B	602/586 (103%)	590 (98%)	12 (2%)	55 44
All	All	1197/1172 (102%)	1175 (98%)	22 (2%)	57 48

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	32	THR
1	B	35	GLU
1	B	69	MET
1	B	276	GLN
1	B	319	ASN
1	B	346	ARG
1	B	436	ARG
1	B	516	HIS
1	B	589	ASN
1	B	618	MET
1	B	656	ARG
1	B	708	ARG
1	A	32	THR
1	A	69	MET
1	A	157	MET
1	A	295	LYS
1	A	307	ARG
1	A	346	ARG
1	A	451	GLU
1	A	589	ASN
1	A	702	LYS
1	A	718	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	47	ASN
1	B	53	GLN
1	B	276	GLN
1	B	287	HIS
1	B	311	GLN
1	B	319	ASN
1	B	382	HIS
1	B	589	ASN
1	A	47	ASN
1	A	53	GLN
1	A	287	HIS
1	A	382	HIS
1	A	589	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

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	XYP	C	1	2	10,10,10	0.83	0	14,14,14	1.54	4 (28%)
2	XYP	C	2	2	9,9,10	0.76	0	10,12,14	2.23	6 (60%)
2	XYP	D	1	2	10,10,10	0.93	0	14,14,14	2.18	5 (35%)
2	XYP	D	2	2	9,9,10	1.12	1 (11%)	10,12,14	1.66	2 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	XYP	C	1	2	-	-	0/1/1/1
2	XYP	C	2	2	-	-	0/1/1/1
2	XYP	D	1	2	-	-	0/1/1/1
2	XYP	D	2	2	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	XYP	C2-C3	2.15	1.55	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1	XYP	O2-C2-C3	4.13	119.89	110.35
2	D	2	XYP	O3-C3-C4	-4.12	102.10	109.99
2	D	1	XYP	O3-C3-C2	3.98	119.56	110.35
2	C	2	XYP	O3-C3-C2	3.74	117.16	109.99
2	D	1	XYP	O2-C2-C1	-3.69	100.61	109.16
2	C	2	XYP	C5-O5-C1	2.88	115.95	111.52
2	C	2	XYP	C4-C3-C2	-2.86	107.52	110.92
2	C	1	XYP	O3-C3-C2	2.82	116.86	110.35
2	C	2	XYP	O2-C2-C3	2.76	115.66	110.14
2	C	1	XYP	O2-C2-C1	-2.60	103.13	109.16
2	D	1	XYP	O1-C1-O5	2.48	116.19	109.72
2	D	2	XYP	O3-C3-C2	2.42	114.63	109.99
2	D	1	XYP	C1-C2-C3	-2.28	105.57	110.31
2	C	1	XYP	O2-C2-C3	2.24	115.52	110.35
2	C	2	XYP	C5-C4-C3	2.23	112.41	109.67
2	C	2	XYP	O3-C3-C4	-2.19	105.81	109.99
2	C	1	XYP	C4-C3-C2	-2.07	107.32	110.89

There are no chirality outliers.

There are no torsion outliers.

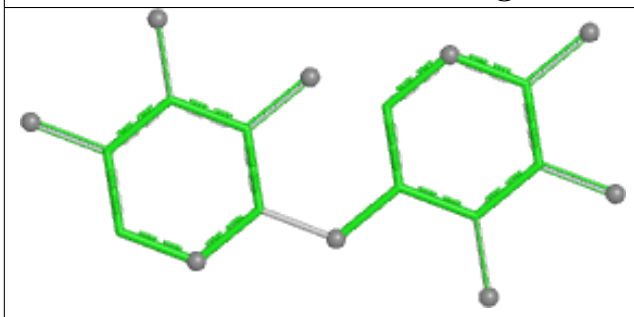
There are no ring outliers.

1 monomer is involved in 2 short contacts:

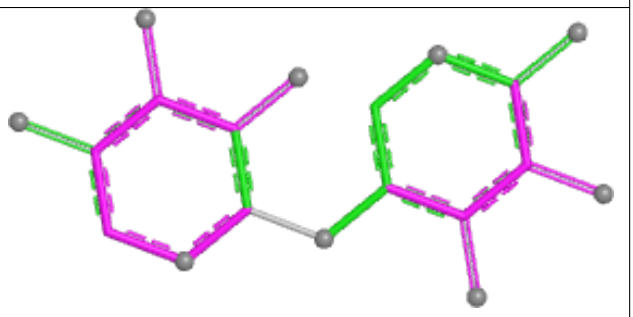
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	XYP	2	0

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

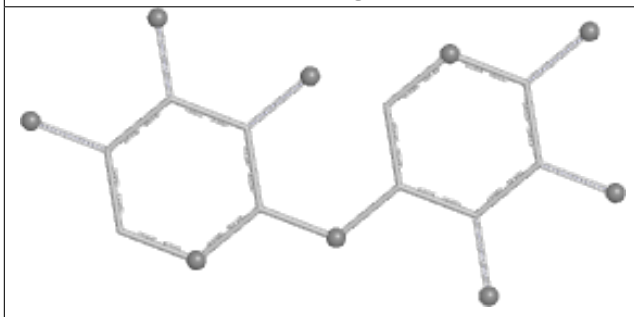
Oligosaccharide Chain C



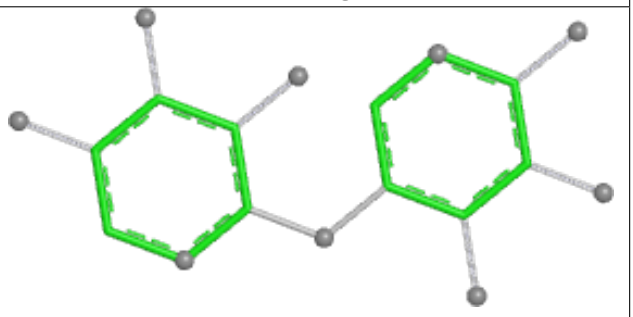
Bond lengths



Bond angles

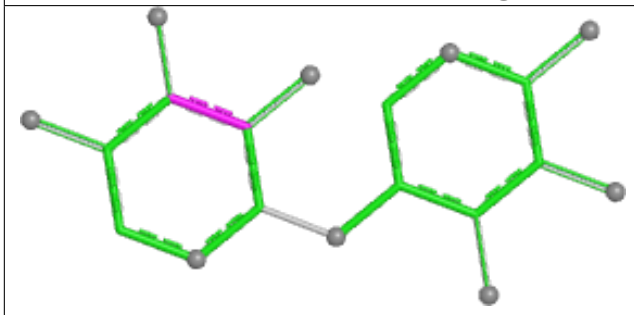


Torsions

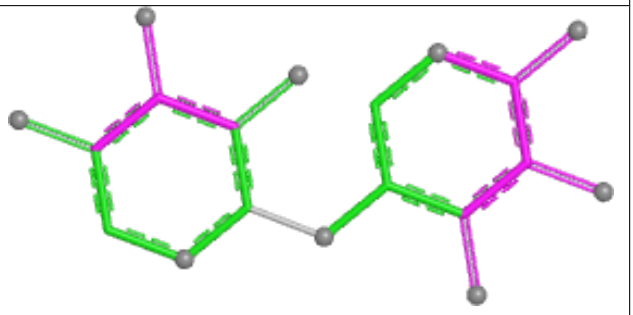


Rings

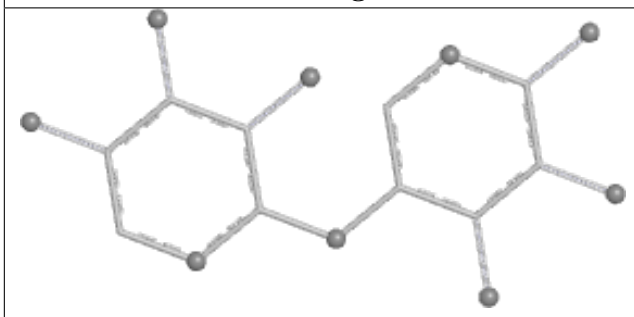
Oligosaccharide Chain D



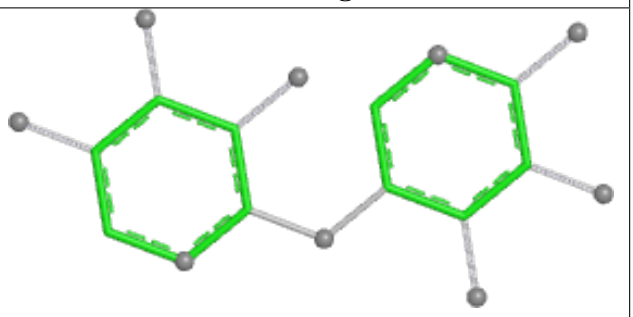
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
4	PEG	A	801	-	6,6,6	0.20	0	5,5,5	0.37	0
3	PGE	B	801	-	9,9,9	0.54	0	8,8,8	0.35	0
4	PEG	B	802	-	6,6,6	0.23	0	5,5,5	0.22	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
4	PEG	A	801	-	-	1/4/4/4	-
3	PGE	B	801	-	-	4/7/7/7	-
4	PEG	B	802	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	801	PGE	O3-C5-C6-O4
4	B	802	PEG	O2-C3-C4-O4
4	A	801	PEG	O2-C3-C4-O4
4	B	802	PEG	O1-C1-C2-O2
3	B	801	PGE	C6-C5-O3-C4
3	B	801	PGE	C1-C2-O2-C3
3	B	801	PGE	O2-C3-C4-O3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	801	PGE	3	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, 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	730/733 (99%)	-0.26	8 (1%)	80	78	9, 18, 37, 63	0
1	B	733/733 (100%)	-0.37	7 (0%)	82	80	9, 17, 32, 67	0
All	All	1463/1466 (99%)	-0.32	15 (1%)	82	80	9, 17, 35, 67	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	369	ASP	6.6
1	A	372	PRO	3.2
1	A	368	PRO	3.0
1	A	367	LYS	2.8
1	B	33	ASP	2.6
1	A	429[A]	TRP	2.5
1	B	36	ARG	2.3
1	B	32	THR	2.1
1	B	451	GLU	2.1
1	B	194	SER	2.1
1	B	373	PHE	2.1
1	A	451	GLU	2.1
1	A	36	ARG	2.0
1	B	369	ASP	2.0
1	A	32	THR	2.0

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 (i)

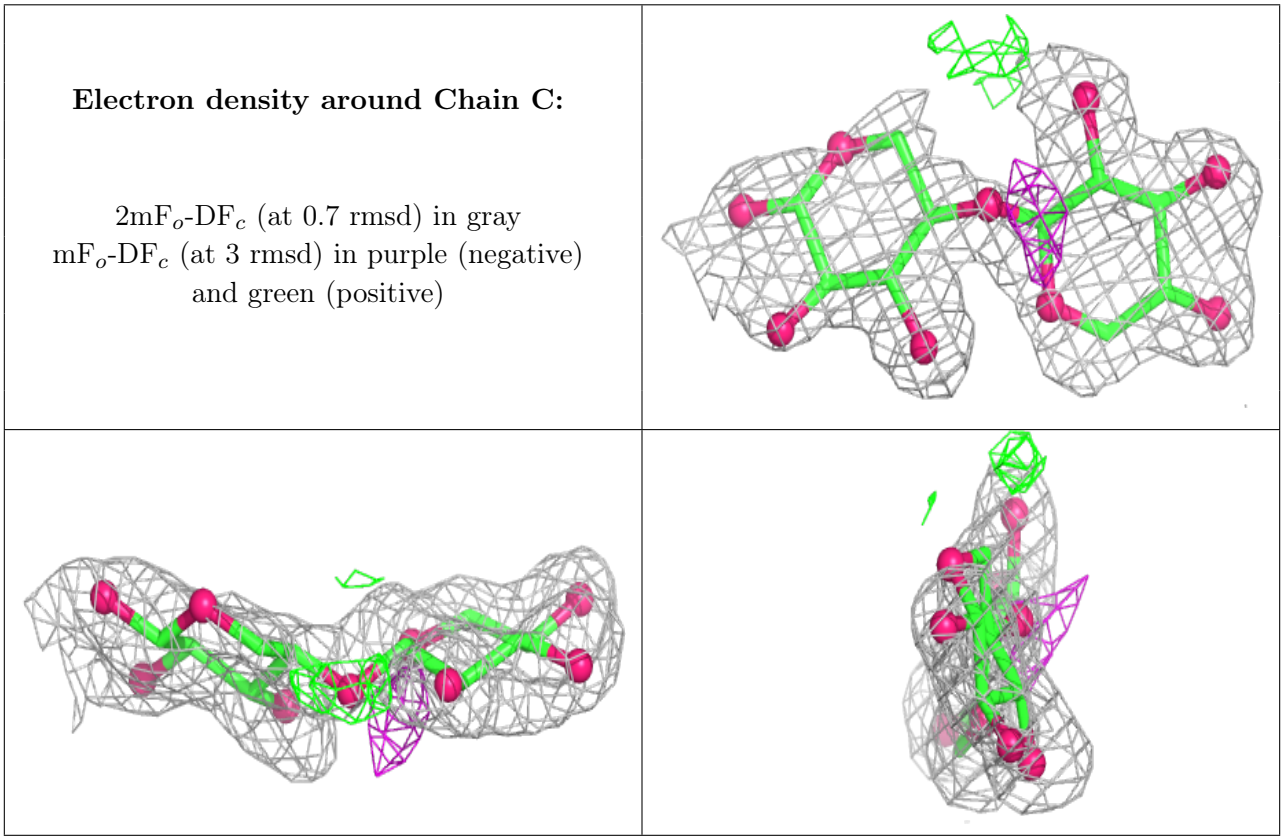
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	XYP	D	1	10/10	0.78	0.19	25,32,37,39	10
2	XYP	D	2	9/10	0.79	0.21	25,30,31,32	9
2	XYP	C	1	10/10	0.80	0.17	33,48,50,54	0
2	XYP	C	2	9/10	0.82	0.18	29,38,46,46	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.

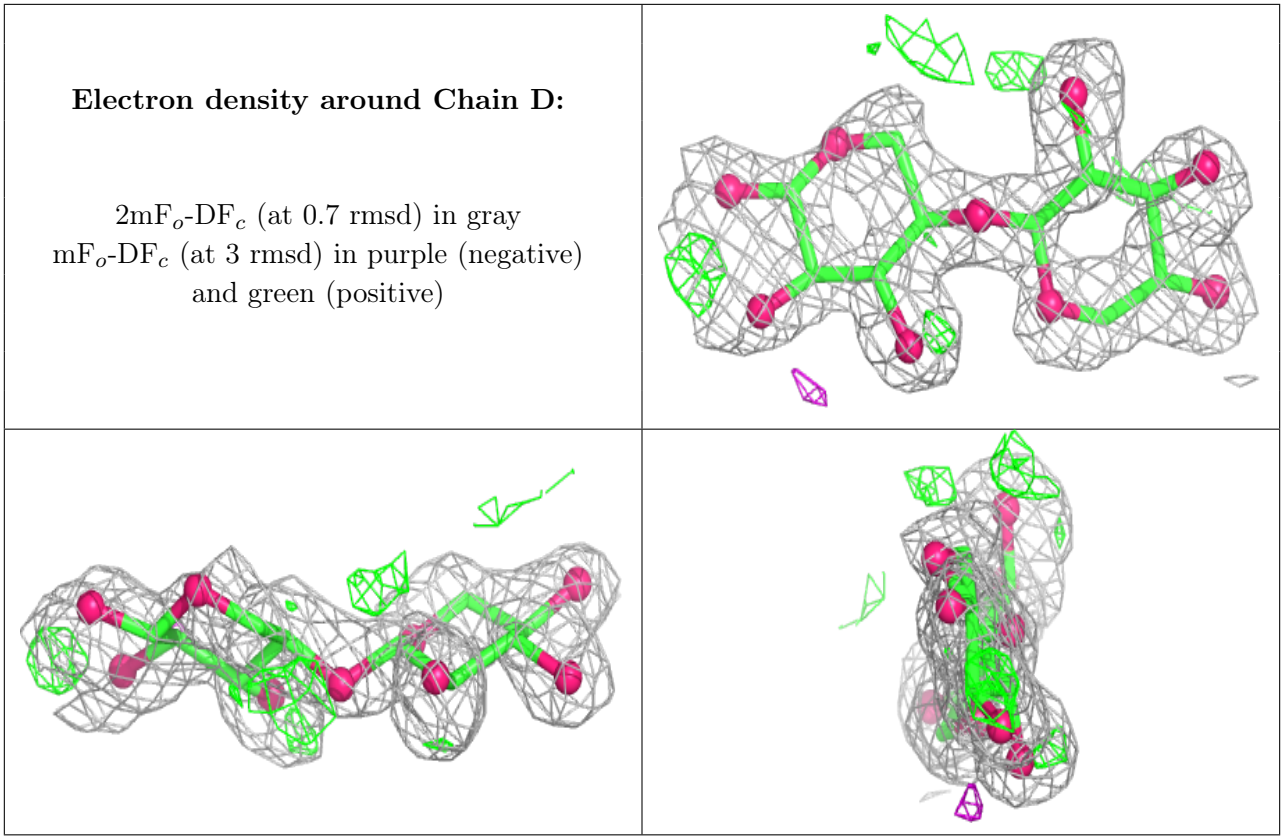
Electron density around Chain C:

$2mF_o$-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

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
4	PEG	B	802	7/7	0.82	0.15	32,35,37,40	0
3	PGE	B	801	10/10	0.86	0.14	28,32,38,39	0
4	PEG	A	801	7/7	0.89	0.17	33,33,35,38	0
5	MG	A	802	1/1	0.98	0.06	18,18,18,18	0
5	MG	B	803	1/1	0.99	0.06	17,17,17,17	0

6.5 Other polymers

There are no such residues in this entry.