



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 11:34 PM BST

PDB ID : 2F61  
Title : Crystal structure of partially deglycosylated acid beta-glucosidase  
Authors : Hegde, R.S.; Grabowski, G.  
Deposited on : 2005-11-28  
Resolution : 2.50 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

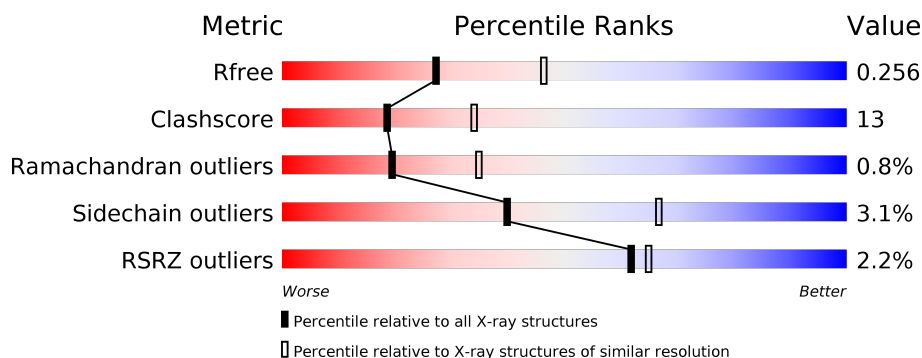
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	497	<div> <div>3%</div> <div> <div></div> <div>70%</div> <div>28%</div> <div></div> </div> </div>
1	B	497	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>25%</div> <div></div> </div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>

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
3	NAG	A	1001	X	-	-	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8338 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 Acid beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	0	0
			3930	2532	671	711	16			
1	B	497	Total	C	N	O	S	0	0	0
			3930	2532	671	711	16			

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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		

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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		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	214	Total	O	0	0
			214	214		
5	B	192	Total	O	0	0
			192	192		

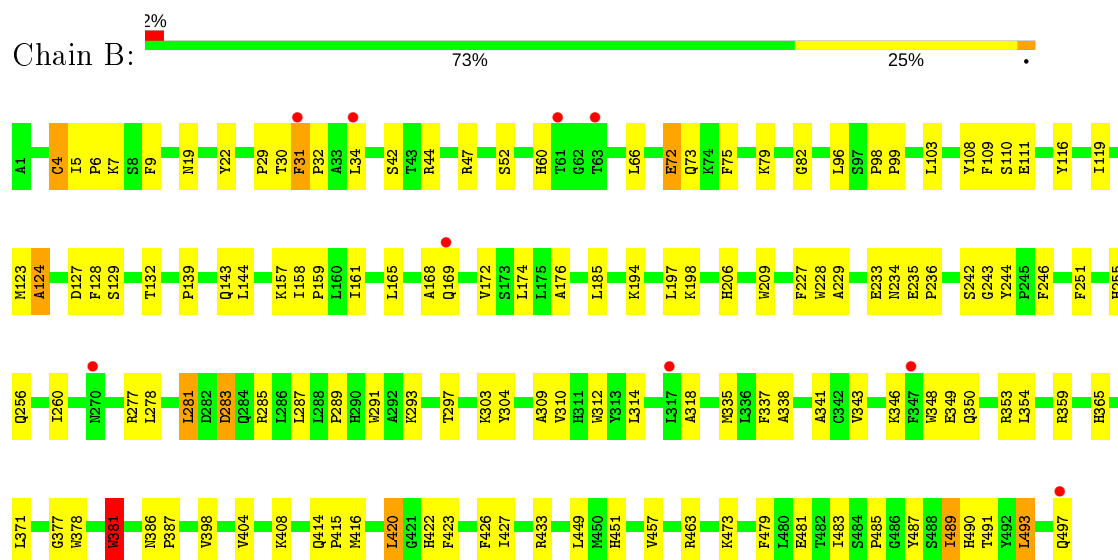
### 3 Residue-property plots [i](#)

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: Acid beta-glucosidase



#### • Molecule 1: Acid beta-glucosidase



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

100%

MAG1  
MAG2



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.64Å 284.43Å 91.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	67.98 – 2.50 101.49 – 2.49	Depositor EDS
% Data completeness (in resolution range)	84.6 (67.98-2.50) 84.3 (101.49-2.49)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.72 (at 2.48Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.196 , 0.256 0.198 , 0.256	Depositor DCC
$R_{free}$ test set	4436 reflections (10.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.7	Xtriage
Anisotropy	0.799	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8338	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, SO4

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	0.34	0/4051	0.60	0/5523
1	B	0.34	0/4051	0.59	0/5523
All	All	0.34	0/8102	0.60	0/11046

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3930	0	3843	109	0
1	B	3930	0	3843	98	0
2	C	28	0	25	0	0
3	A	14	0	13	0	0
4	A	15	0	0	0	0
4	B	15	0	0	1	0
5	A	214	0	0	11	0
5	B	192	0	0	9	0
All	All	8338	0	7724	206	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 13.

All (206) 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:285:ARG:H	1:A:312:TRP:HD1	1.14	0.94
1:A:31:PHE:HB2	1:A:495:HIS:HE1	1.41	0.82
1:A:95:ALA:HB1	1:A:406:ILE:HG12	1.63	0.80
1:A:285:ARG:HG2	1:A:312:TRP:CD1	2.17	0.79
1:B:314:LEU:HB2	1:B:343:VAL:HG12	1.64	0.78
1:A:260:ILE:HD12	1:A:278:LEU:HD21	1.67	0.77
1:A:157:LYS:O	1:A:161:ILE:HG12	1.86	0.76
1:A:31:PHE:HB2	1:A:495:HIS:CE1	2.21	0.76
1:B:109:PHE:CZ	1:B:119:ILE:HD11	2.21	0.76
1:A:285:ARG:N	1:A:312:TRP:HD1	1.85	0.75
1:A:406:ILE:HD13	1:A:406:ILE:O	1.88	0.73
1:A:194:LYS:HB2	1:A:242:SER:HA	1.70	0.73
1:B:285:ARG:HH12	1:B:318:ALA:HB3	1.53	0.72
1:A:293:LYS:HE2	1:A:330:LEU:HD13	1.72	0.72
1:A:289:PRO:HG3	1:A:326:GLU:HG2	1.72	0.72
1:B:109:PHE:CE2	1:B:119:ILE:HD11	2.25	0.71
1:B:451:HIS:HB3	5:B:1562:HOH:O	1.90	0.70
1:B:169:GLN:HB3	5:B:1677:HOH:O	1.92	0.70
1:A:358:ASP:HB3	5:A:1552:HOH:O	1.92	0.68
1:B:30:THR:HB	5:B:1670:HOH:O	1.93	0.68
1:B:285:ARG:NH1	1:B:318:ALA:HB3	2.09	0.67
1:A:89:ALA:O	1:A:93:ILE:HG13	1.96	0.66
1:B:165:LEU:HD22	1:B:172:VAL:HB	1.75	0.66
1:B:285:ARG:HD2	1:B:312:TRP:CZ2	2.31	0.65
1:A:117:ASN:O	1:A:118:ILE:HD13	1.96	0.65
1:A:312:TRP:CZ2	1:A:318:ALA:HB2	2.32	0.64
1:A:95:ALA:HB1	1:A:406:ILE:CG1	2.27	0.64
1:B:489:ILE:HD13	1:B:490:HIS:N	2.12	0.64
1:A:328:HIS:HD2	5:A:1682:HOH:O	1.79	0.63
1:B:229:ALA:HB2	1:B:277:ARG:HB2	1.81	0.63
1:A:312:TRP:CH2	1:A:318:ALA:HB2	2.33	0.62
1:B:31:PHE:HD2	1:B:32:PRO:HD2	1.64	0.61
1:A:229:ALA:HB2	1:A:277:ARG:HB2	1.80	0.61
1:B:422:HIS:CG	1:B:489:ILE:HD12	2.35	0.61
1:A:293:LYS:HE2	1:A:330:LEU:CD1	2.30	0.61
1:A:116:TYR:OH	1:A:420:LEU:HD13	2.03	0.58
1:A:483:ILE:O	1:A:485:PRO:HD3	2.02	0.58
1:B:289:PRO:O	1:B:293:LYS:HG3	2.03	0.57
1:A:33:ALA:HB2	1:B:139:PRO:O	2.04	0.57
1:B:423:PHE:O	1:B:427:ILE:HG12	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:MET:HG3	5:A:1515:HOH:O	2.05	0.56
1:A:165:LEU:HD22	1:A:172:VAL:HB	1.87	0.56
1:B:66:LEU:HD11	1:B:473:LYS:HB2	1.86	0.56
1:A:451:HIS:HB3	5:A:1623:HOH:O	2.05	0.56
1:B:123:MET:O	1:B:124:ALA:HB3	2.05	0.56
1:B:176:ALA:HB2	1:B:227:PHE:CE2	2.41	0.56
1:A:258:ASP:O	1:A:262:ARG:HB2	2.05	0.56
1:B:157:LYS:O	1:B:161:ILE:HG12	2.06	0.56
1:B:350:GLN:HE21	1:B:353:ARG:HG2	1.70	0.56
1:A:20:ALA:HB2	1:A:409:ASP:OD2	2.05	0.56
1:A:120:ARG:HB2	1:A:379:THR:HG21	1.87	0.56
1:B:127:ASP:HB3	1:B:246:PHE:CG	2.42	0.55
1:B:236:PRO:HB2	1:B:251:PHE:HB2	1.89	0.55
1:B:483:ILE:O	1:B:485:PRO:HD3	2.07	0.55
1:B:169:GLN:HA	1:B:169:GLN:NE2	2.22	0.54
1:A:123:MET:O	1:A:124:ALA:HB3	2.06	0.54
1:A:207:GLN:HB3	1:A:211:ARG:HH12	1.72	0.54
1:A:201:PRO:HG2	1:A:258:ASP:HB2	1.90	0.54
1:A:82:GLY:HA3	1:A:118:ILE:O	2.08	0.54
1:B:234:ASN:ND2	1:B:235:GLU:HG3	2.23	0.53
1:B:349:GLU:HG2	1:B:359:ARG:HH21	1.72	0.53
1:B:72:GLU:HB2	5:B:1608:HOH:O	2.08	0.53
1:A:256:GLN:O	1:A:260:ILE:HG12	2.08	0.53
1:A:423:PHE:O	1:A:427:ILE:HG12	2.07	0.53
1:B:287:LEU:HB3	1:B:291:TRP:CD1	2.42	0.53
1:B:314:LEU:HB2	1:B:343:VAL:CG1	2.35	0.53
1:A:426:PHE:CD2	1:A:493:LEU:HD11	2.42	0.53
1:B:116:TYR:OH	1:B:420:LEU:HD13	2.09	0.53
1:A:31:PHE:CB	1:A:495:HIS:HE1	2.18	0.53
1:B:34:LEU:HD13	1:B:497:GLN:O	2.07	0.53
1:B:98:PRO:HB2	1:B:99:PRO:HD3	1.90	0.53
1:A:314:LEU:HB2	1:A:343:VAL:CG2	2.39	0.52
1:A:314:LEU:HD12	1:A:343:VAL:HB	1.90	0.52
1:B:426:PHE:HB3	1:B:493:LEU:HD21	1.91	0.52
1:A:285:ARG:N	1:A:312:TRP:CD1	2.71	0.52
1:B:285:ARG:HH22	1:B:318:ALA:C	2.13	0.52
1:B:206:HIS:NE2	1:B:255:HIS:HE1	2.08	0.52
1:B:260:ILE:HD12	1:B:278:LEU:HD21	1.92	0.52
1:A:176:ALA:HB3	1:A:230:VAL:HG12	1.91	0.52
1:B:489:ILE:C	1:B:489:ILE:HD13	2.31	0.52
1:B:96:LEU:HD21	1:B:404:VAL:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:GLN:O	1:A:211:ARG:HG3	2.10	0.51
1:B:5:ILE:HG12	1:B:22:TYR:CE2	2.46	0.51
1:A:170:ARG:HD3	5:A:1677:HOH:O	2.10	0.51
1:B:312:TRP:O	1:B:341:ALA:HA	2.11	0.51
1:B:194:LYS:HB2	1:B:242:SER:HA	1.93	0.51
1:A:109:PHE:CE2	1:A:119:ILE:HD11	2.45	0.51
1:A:346:LYS:HB2	1:A:349:GLU:HB2	1.93	0.51
1:B:346:LYS:HE2	1:B:348:TRP:HE1	1.76	0.50
1:A:313:TYR:N	1:A:313:TYR:CD1	2.79	0.50
1:B:44:ARG:NH1	1:B:487:TYR:CE1	2.80	0.50
1:A:60:HIS:CD2	1:A:471:THR:HG21	2.46	0.50
1:B:353:ARG:HG3	1:B:359:ARG:NH1	2.26	0.50
1:A:408:LYS:O	1:A:410:THR:CG2	2.60	0.50
1:B:158:ILE:HB	1:B:159:PRO:HD3	1.94	0.49
1:B:29:PRO:CD	1:B:111:GLU:HG2	2.41	0.49
1:A:381:TRP:HA	1:A:381:TRP:CE3	2.47	0.49
1:B:185:LEU:O	1:B:198:LYS:HG3	2.13	0.49
1:A:176:ALA:HB2	1:A:227:PHE:CE2	2.48	0.49
1:A:313:TYR:HD1	1:A:313:TYR:H	1.60	0.49
1:B:4:CYS:O	1:B:6:PRO:HD3	2.13	0.49
1:A:350:GLN:CD	1:A:350:GLN:H	2.16	0.49
1:B:338:ALA:HB3	1:B:378:TRP:HA	1.95	0.49
1:A:343:VAL:HG22	1:A:344:GLY:N	2.27	0.48
1:A:72:GLU:HB2	5:A:1591:HOH:O	2.13	0.48
1:A:489:ILE:HD13	1:A:490:HIS:N	2.27	0.48
1:B:381:TRP:HA	1:B:381:TRP:CE3	2.48	0.48
1:B:381:TRP:HA	1:B:381:TRP:HE3	1.78	0.48
1:A:354:LEU:HA	1:A:414:GLN:OE1	2.12	0.48
1:A:165:LEU:O	1:A:168:ALA:HB3	2.13	0.48
1:B:422:HIS:ND1	1:B:489:ILE:HD12	2.29	0.48
1:B:34:LEU:HD22	1:B:497:GLN:C	2.34	0.48
1:B:426:PHE:O	1:B:427:ILE:HD13	2.14	0.48
1:B:128:PHE:HZ	1:B:398:VAL:HG22	1.79	0.47
1:A:287:LEU:HB3	1:A:291:TRP:CD1	2.50	0.47
1:A:37:PHE:CD2	1:A:480:LEU:HG	2.50	0.47
1:A:192:ASN:HB2	1:A:244:TYR:O	2.14	0.47
1:B:143:GLN:O	1:B:144:LEU:HB2	2.15	0.47
1:B:285:ARG:HD2	1:B:312:TRP:CE2	2.49	0.47
1:A:132:THR:O	1:A:133:TYR:HB3	2.14	0.47
1:A:260:ILE:CD1	1:A:278:LEU:HD21	2.42	0.47
1:B:408:LYS:HE3	5:B:1602:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:ILE:HB	1:A:336:LEU:HD23	1.97	0.47
1:A:236:PRO:O	1:A:250:GLY:HA2	2.15	0.46
1:A:381:TRP:HA	1:A:381:TRP:HE3	1.80	0.46
1:A:226:GLN:NE2	5:A:1660:HOH:O	2.47	0.46
1:B:109:PHE:O	1:B:168:ALA:HA	2.16	0.46
1:A:158:ILE:HB	1:A:159:PRO:HD3	1.98	0.46
1:A:449:LEU:HB2	1:A:457:VAL:CG1	2.46	0.46
1:A:453:ASP:OD1	1:A:453:ASP:C	2.54	0.46
1:B:386:ASN:HB2	1:B:387:PRO:CD	2.45	0.46
1:B:256:GLN:O	1:B:260:ILE:HG12	2.15	0.46
1:A:309:ALA:HA	1:A:337:PHE:O	2.15	0.45
1:B:309:ALA:HA	1:B:337:PHE:O	2.16	0.45
1:A:422:HIS:CG	1:A:489:ILE:HD12	2.52	0.45
1:A:457:VAL:O	1:A:457:VAL:HG13	2.17	0.45
1:A:66:LEU:HB3	1:A:439:SER:HB3	1.98	0.45
1:B:283:ASP:O	1:B:310:VAL:HA	2.17	0.45
1:B:7:LYS:HE3	1:B:9:PHE:CZ	2.52	0.45
1:A:98:PRO:HB2	1:A:99:PRO:HD3	1.99	0.44
1:B:29:PRO:HD3	1:B:111:GLU:HG2	1.99	0.44
1:B:293:LYS:O	1:B:297:THR:HG23	2.17	0.44
1:B:416:MET:HG3	5:B:1546:HOH:O	2.18	0.44
1:A:345:SER:O	1:A:346:LYS:C	2.54	0.44
1:A:337:PHE:CE1	1:A:377:GLY:HA3	2.52	0.44
1:A:48:ARG:HD2	1:A:418:TYR:CD1	2.52	0.44
1:B:116:TYR:HH	1:B:420:LEU:HD13	1.81	0.44
1:B:281:LEU:HG	1:B:283:ASP:H	1.83	0.44
1:B:119:ILE:HB	1:B:174:LEU:HD23	1.99	0.44
1:A:340:GLU:HG2	5:A:1678:HOH:O	2.17	0.43
1:A:75:PHE:CG	1:A:433:ARG:NH1	2.86	0.43
1:A:209:TRP:CE3	1:A:209:TRP:HA	2.53	0.43
1:A:7:LYS:HG2	1:A:9:PHE:CE1	2.53	0.43
1:B:371:LEU:O	1:B:433:ARG:HD2	2.18	0.43
1:A:209:TRP:O	1:A:212:TYR:HB3	2.19	0.43
1:A:489:ILE:O	1:A:489:ILE:HG23	2.18	0.43
1:A:408:LYS:O	1:A:410:THR:HG23	2.18	0.43
1:A:232:ALA:HB3	1:A:256:GLN:NE2	2.33	0.43
1:B:82:GLY:HA2	1:B:116:TYR:CG	2.53	0.43
1:B:365:HIS:CD2	1:B:463:ARG:CZ	3.02	0.43
1:B:109:PHE:HZ	1:B:119:ILE:HD11	1.81	0.43
1:B:426:PHE:CD1	1:B:491:THR:HG21	2.53	0.43
1:A:37:PHE:CD1	1:A:37:PHE:C	2.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:SER:OG	1:B:111:GLU:N	2.52	0.43
1:B:73:GLN:HG3	1:B:75:PHE:CE1	2.53	0.43
1:A:203:ASP:OD1	1:A:205:TYR:HB2	2.19	0.42
1:B:44:ARG:HD2	4:B:1505:SO4:O3	2.17	0.42
1:B:197:LEU:HD11	1:B:209:TRP:CD1	2.53	0.42
1:B:354:LEU:HA	1:B:414:GLN:OE1	2.20	0.42
1:A:367:ILE:HG12	1:A:378:TRP:CD2	2.54	0.42
1:A:346:LYS:HD3	1:A:348:TRP:CZ2	2.54	0.42
1:B:337:PHE:CE1	1:B:377:GLY:HA3	2.54	0.42
1:A:282:ASP:OD1	1:A:339:SER:OG	2.25	0.42
1:A:96:LEU:HB3	1:A:100:ALA:HB3	2.01	0.42
1:B:169:GLN:HA	1:B:169:GLN:HE21	1.85	0.42
1:B:19:ASN:O	1:B:103:LEU:HD12	2.19	0.42
1:A:314:LEU:HB3	1:A:362:GLN:HB3	2.02	0.42
1:A:40:TYR:HA	1:A:50:GLU:O	2.19	0.42
1:B:132:THR:HG21	5:B:1633:HOH:O	2.20	0.42
1:A:232:ALA:O	1:A:233:GLU:HB2	2.20	0.42
1:B:47:ARG:NH1	5:B:1596:HOH:O	2.52	0.42
1:A:111:GLU:HB2	1:A:169:GLN:HG3	2.00	0.41
1:A:42:SER:HB2	1:A:489:ILE:HG22	2.02	0.41
1:A:182:PRO:HD2	1:A:185:LEU:HD12	2.01	0.41
1:A:413:LYS:HE3	1:A:417:PHE:CZ	2.56	0.41
1:B:243:GLY:O	1:B:244:TYR:C	2.57	0.41
1:A:183:THR:O	1:A:189:GLY:HA2	2.20	0.41
1:A:496:ARG:HD3	5:A:1553:HOH:O	2.20	0.41
1:B:457:VAL:HG13	1:B:457:VAL:O	2.21	0.41
1:A:314:LEU:HB2	1:A:343:VAL:HG21	2.02	0.41
1:A:314:LEU:HD12	1:A:343:VAL:CB	2.51	0.41
1:A:19:ASN:HB2	5:A:1616:HOH:O	2.20	0.41
1:B:128:PHE:CZ	1:B:398:VAL:HG22	2.54	0.41
1:B:449:LEU:O	1:B:457:VAL:HG12	2.20	0.41
1:B:42:SER:HA	1:B:47:ARG:O	2.20	0.41
1:B:129:SER:HB3	5:B:1555:HOH:O	2.21	0.41
1:A:358:ASP:CB	5:A:1552:HOH:O	2.60	0.40
1:A:365:HIS:CD2	1:A:463:ARG:CZ	3.04	0.40
1:B:79:LYS:HE2	1:B:228:TRP:CE2	2.55	0.40
1:A:106:LYS:O	1:A:110:SER:HB3	2.21	0.40
1:A:408:LYS:O	1:A:410:THR:HG22	2.21	0.40
1:B:303:LYS:HE3	1:B:304:TYR:CZ	2.57	0.40
1:A:44:ARG:O	1:A:44:ARG:HG2	2.20	0.40
1:B:109:PHE:HB3	1:B:168:ALA:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:HIS:HB3	1:B:479:PHE:CD2	2.57	0.40
1:B:60:HIS:HD2	1:B:481:GLU:OE2	2.05	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	495/497 (100%)	460 (93%)	31 (6%)	4 (1%)	19	35
1	B	495/497 (100%)	457 (92%)	34 (7%)	4 (1%)	19	35
All	All	990/994 (100%)	917 (93%)	65 (7%)	8 (1%)	19	35

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	312	TRP
1	A	124	ALA
1	A	281	LEU
1	B	124	ALA
1	B	233	GLU
1	B	381	TRP
1	A	233	GLU
1	B	281	LEU

### 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	424/424 (100%)	410 (97%)	14 (3%)	38	64
1	B	424/424 (100%)	412 (97%)	12 (3%)	43	70
All	All	848/848 (100%)	822 (97%)	26 (3%)	40	67

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	PHE
1	A	55	PRO
1	A	59	ASN
1	A	313	TYR
1	A	316	PHE
1	A	335	MET
1	A	351	SER
1	A	358	ASP
1	A	370	ASN
1	A	379	THR
1	A	381	TRP
1	A	406	ILE
1	A	410	THR
1	A	489	ILE
1	B	4	CYS
1	B	31	PHE
1	B	52	SER
1	B	72	GLU
1	B	108	TYR
1	B	283	ASP
1	B	335	MET
1	B	381	TRP
1	B	415	PRO
1	B	420	LEU
1	B	489	ILE
1	B	493	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	A	92	ASN

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Mol	Chain	Res	Type
1	A	169	GLN
1	A	226	GLN
1	A	274	HIS
1	A	328	HIS
1	A	365	HIS
1	A	396	ASN
1	A	495	HIS
1	B	102	ASN
1	B	145	HIS
1	B	166	GLN
1	B	169	GLN
1	B	255	HIS
1	B	270	ASN
1	B	284	GLN
1	B	350	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 ⓘ

2 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	NAG	C	1	1,2	14,14,15	0.46	0	17,19,21	0.72	1 (5%)
2	NAG	C	2	2	14,14,15	0.51	0	17,19,21	0.76	1 (5%)

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	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C2-N2-C7	-2.28	119.66	122.90
2	C	1	NAG	C2-N2-C7	-2.00	120.05	122.90

There are no chirality outliers.

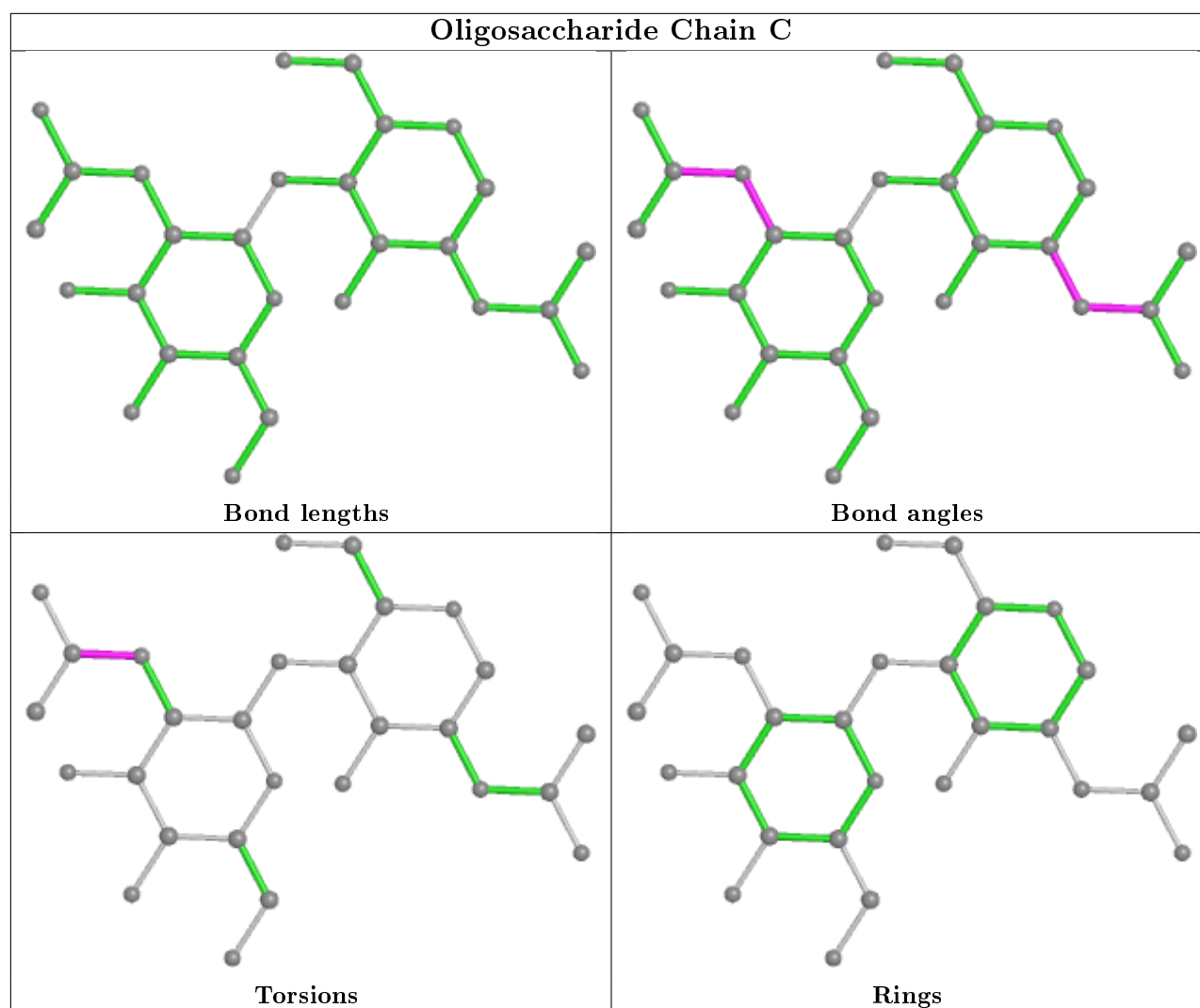
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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



## 5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	SO4	A	1500	-	4,4,4	0.24	0	6,6,6	0.12	0
4	SO4	B	1503	-	4,4,4	0.23	0	6,6,6	0.16	0
4	SO4	B	1504	-	4,4,4	0.25	0	6,6,6	0.06	0
4	SO4	A	1501	-	4,4,4	0.28	0	6,6,6	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	SO4	A	1502	-	4,4,4	0.26	0	6,6,6	0.11	0
3	NAG	A	1001	1	14,14,15	0.66	0	17,19,21	0.83	1 (5%)
4	SO4	B	1505	-	4,4,4	0.25	0	6,6,6	0.08	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	NAG	A	1001	1	1/1/5/7	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	NAG	C2-N2-C7	-2.58	119.23	122.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1001	NAG	C1

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	NAG	C4-C5-C6-O6
3	A	1001	NAG	C8-C7-N2-C2
3	A	1001	NAG	O7-C7-N2-C2
3	A	1001	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1505	SO4	1	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	497/497 (100%)	-0.02	13 (2%) 56 59	8, 24, 50, 78	5 (1%)
1	B	497/497 (100%)	0.01	9 (1%) 68 71	12, 24, 47, 76	7 (1%)
All	All	994/994 (100%)	-0.00	22 (2%) 62 65	8, 24, 49, 78	12 (1%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	316	PHE	9.2
1	B	347	PHE	5.6
1	A	314	LEU	5.2
1	A	313	TYR	4.5
1	A	312	TRP	4.4
1	B	63	THR	3.8
1	A	347	PHE	3.4
1	B	317	LEU	3.3
1	B	497	GLN	3.3
1	A	345	SER	3.1
1	A	344	GLY	3.1
1	B	31	PHE	3.0
1	A	200	GLN	2.9
1	A	318	ALA	2.6
1	A	341	ALA	2.6
1	A	315	ASP	2.6
1	B	169	GLN	2.4
1	B	34	LEU	2.3
1	A	378	TRP	2.3
1	B	61	THR	2.2
1	A	358	ASP	2.2
1	B	270	ASN	2.2

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

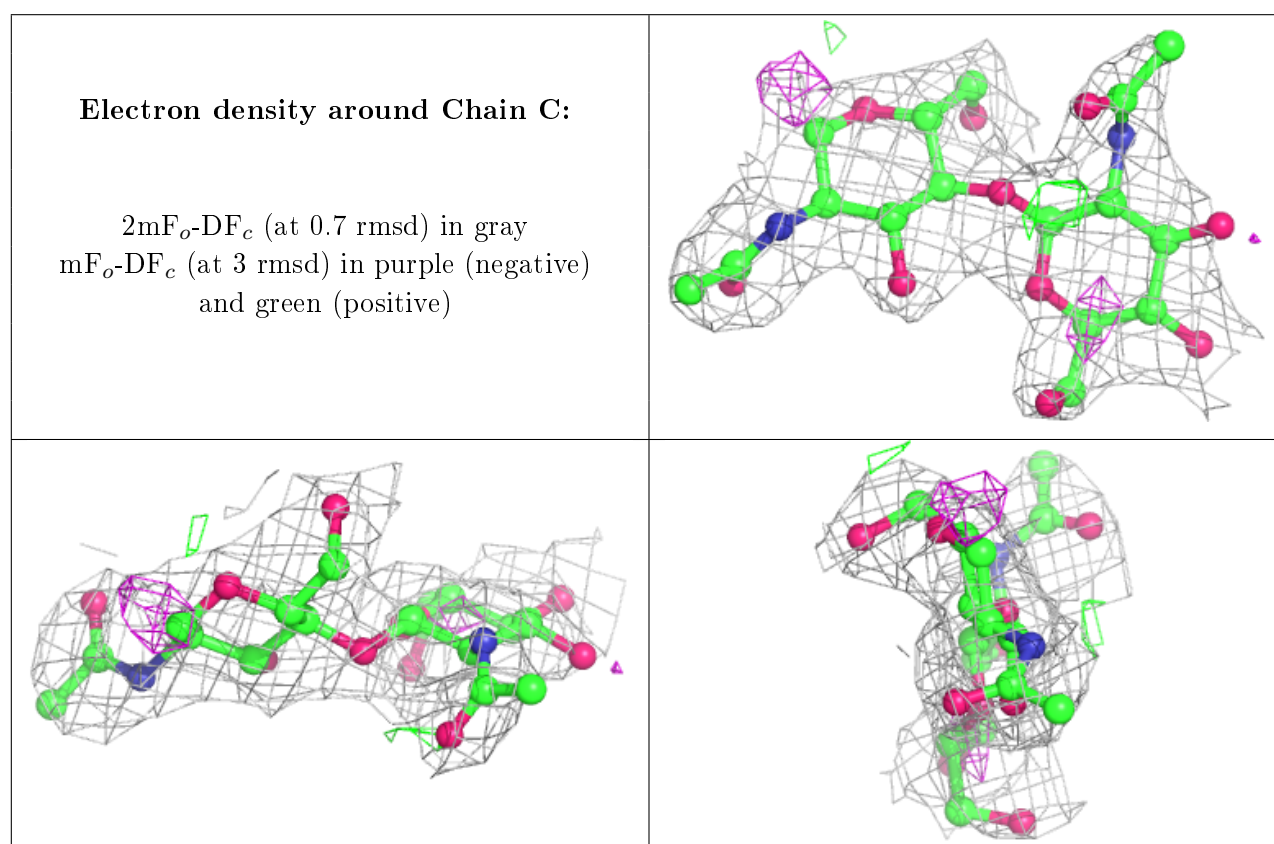
There are no non-standard protein/DNA/RNA residues in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NAG	C	2	14/15	0.83	0.30	55,58,59,60	0
2	NAG	C	1	14/15	0.92	0.18	40,42,46,51	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.



## 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, 95<sup>th</sup> 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	NAG	A	1001	14/15	0.87	0.19	35,37,45,46	0
4	SO4	B	1505	5/5	0.92	0.19	64,65,66,66	0
4	SO4	B	1504	5/5	0.96	0.17	56,56,57,58	0
4	SO4	A	1501	5/5	0.97	0.14	37,38,41,41	0
4	SO4	A	1502	5/5	0.97	0.14	38,39,42,42	0
4	SO4	B	1503	5/5	0.98	0.15	32,33,34,35	0
4	SO4	A	1500	5/5	0.99	0.15	25,26,28,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.