



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2024 – 06:27 am GMT

PDB ID : 2VZV
Title : Substrate Complex of Amycolatopsis orientalis exo-chitosanase CsxA E541A with chitosan
Authors : Lammerts van Bueren, A.; Ghinet, M.G.; Gregg, K.; Fleury, A.; Brzezinski, R.; Boraston, A.B.
Deposited on : 2008-08-05
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

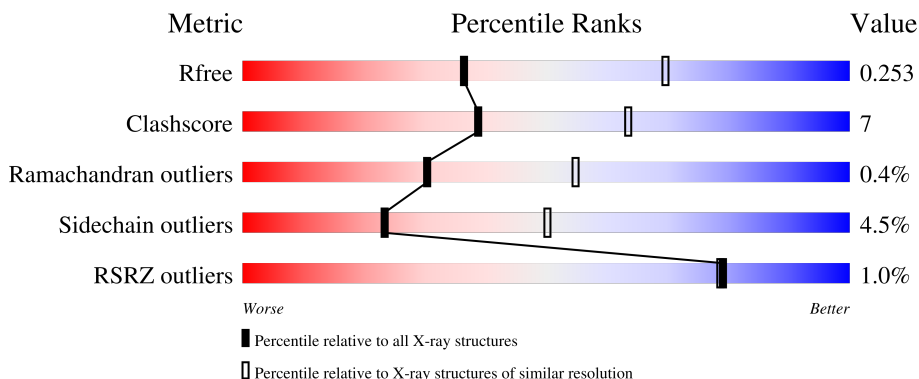
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

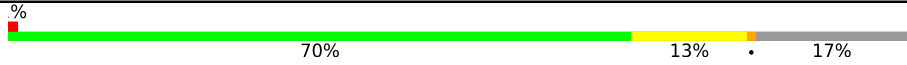

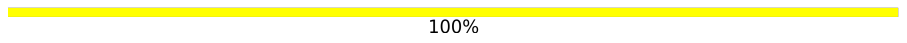

The reported resolution of this entry is 2.70 Å.

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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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	1032	
1	B	1032	
2	C	2	
2	D	2	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13565 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 EXO-BETA-D-GLUCOSAMINIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	858	Total	C	N	O	S	4	0	1
			6548	4113	1133	1285	17			
1	B	858	Total	C	N	O	S	4	0	1
			6548	4113	1133	1285	17			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	541	ALA	GLU	engineered mutation	UNP Q56F26
A	750	ASN	TRP	conflict	UNP Q56F26
B	541	ALA	GLU	engineered mutation	UNP Q56F26
B	750	ASN	TRP	conflict	UNP Q56F26

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			23	12	2	9			
2	D	2	Total	C	N	O	0	0	0
			23	12	2	9			

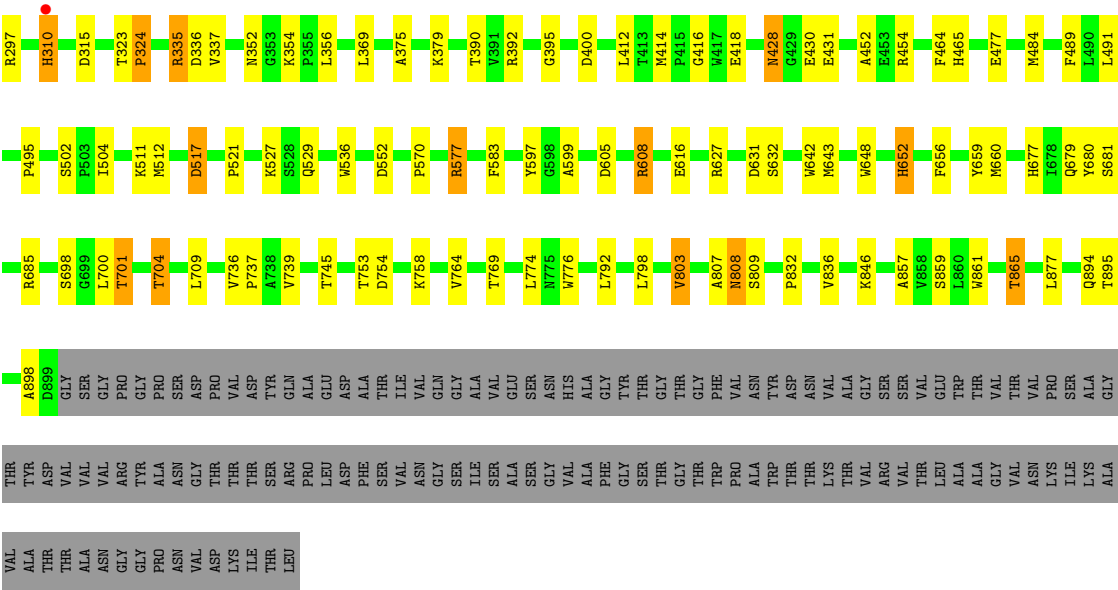
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	212	Total	O	0	0
			212	212		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	211	Total	O	0	0
			211	211		



● Molecule 2: 2-amino-2-deoxy-beta-D-glucopyranose-(1-4)-2-amino-2-deoxy-beta-D-glucopyranos e



● Molecule 2: 2-amino-2-deoxy-beta-D-glucopyranose-(1-4)-2-amino-2-deoxy-beta-D-glucopyranos e



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.86Å 121.41Å 184.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	185.70 – 2.70 101.46 – 2.70	Depositor EDS
% Data completeness (in resolution range)	91.3 (185.70-2.70) 91.3 (101.46-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.33 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.182 , 0.255 0.184 , 0.253	Depositor DCC
R_{free} test set	2545 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 24.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13565	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.86% 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: GCS

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	0.54	3/6711 (0.0%)	0.66	5/9158 (0.1%)
1	B	0.52	3/6711 (0.0%)	0.66	8/9158 (0.1%)
All	All	0.53	6/13422 (0.0%)	0.66	13/18316 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	430	GLU	CB-CG	16.66	1.83	1.52
1	B	430	GLU	CB-CG	10.96	1.73	1.52
1	B	246	ASP	CB-CG	7.18	1.66	1.51
1	B	296	ASP	CB-CG	6.59	1.65	1.51
1	A	246	ASP	CB-CG	6.17	1.64	1.51
1	A	296	ASP	CB-CG	5.84	1.64	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	ASP	CB-CG-OD1	15.77	132.49	118.30
1	B	246	ASP	CB-CG-OD1	15.13	131.92	118.30
1	B	296	ASP	CB-CG-OD1	14.89	131.71	118.30
1	A	296	ASP	CB-CG-OD2	11.98	129.08	118.30
1	A	430	GLU	CA-CB-CG	-11.08	89.02	113.40
1	A	246	ASP	OD1-CG-OD2	-8.26	107.60	123.30
1	B	246	ASP	OD1-CG-OD2	-7.67	108.73	123.30
1	B	430	GLU	CA-CB-CG	-6.06	100.07	113.40
1	B	247	LEU	CA-CB-CG	5.81	128.67	115.30
1	B	296	ASP	OD1-CG-OD2	-5.59	112.67	123.30
1	B	238	LEU	CA-CB-CG	5.54	128.04	115.30
1	A	296	ASP	OD1-CG-OD2	-5.43	112.97	123.30
1	B	144	LEU	CA-CB-CG	5.31	127.51	115.30

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	6548	0	6327	81	9
1	B	6548	0	6327	92	9
2	C	23	0	23	0	0
2	D	23	0	23	2	0
3	A	212	0	0	9	0
3	B	211	0	0	17	0
All	All	13565	0	12700	173	9

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 7.

All (173) 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:201:TRP:HE1	1:B:212:ASN:HD21	1.00	0.93
1:B:310:HIS:CE1	3:B:2079:HOH:O	2.23	0.90
1:B:577:ARG:HG2	1:B:583:PHE:O	1.75	0.85
1:B:244:HIS:HE2	1:B:246:ASP:CG	1.82	0.80
1:B:115:ALA:O	1:B:118:SER:HB2	1.82	0.79
1:A:144:LEU:HD22	1:A:165:ALA:HB2	1.64	0.79
1:B:336:ASP:H	1:B:352:ASN:ND2	1.80	0.78
1:B:310:HIS:CG	3:B:2079:HOH:O	2.39	0.76
1:B:700:LEU:HD23	1:B:754:ASP:HA	1.67	0.75
1:B:310:HIS:HB3	3:B:2082:HOH:O	1.87	0.74
1:B:310:HIS:CD2	3:B:2079:HOH:O	2.40	0.74
1:B:244:HIS:NE2	1:B:246:ASP:OD1	2.15	0.73
1:A:246:ASP:HB3	1:A:292:LEU:HD21	1.72	0.71
1:A:161:GLN:HB2	3:A:2026:HOH:O	1.89	0.71
1:B:178:HIS:HE1	3:B:2043:HOH:O	1.73	0.70
1:A:577:ARG:HG2	1:A:583:PHE:O	1.91	0.70
1:A:400:ASP:OD1	1:A:454:ARG:HD2	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:685:ARG:NH1	1:B:736:VAL:O	2.29	0.65
1:B:808:ASN:ND2	1:B:809:SER:H	1.94	0.65
1:B:127:LEU:HD11	1:B:221:VAL:HG21	1.78	0.65
1:B:335:ARG:HH22	1:B:491:LEU:HD21	1.61	0.65
1:B:161:GLN:HB2	3:B:2028:HOH:O	1.95	0.65
1:A:701:THR:HG23	1:A:753:THR:OG1	1.97	0.63
1:B:894:GLN:HB3	3:B:2208:HOH:O	1.98	0.63
1:B:310:HIS:ND1	3:B:2079:HOH:O	2.27	0.63
1:A:178:HIS:HE1	3:A:2033:HOH:O	1.80	0.62
1:A:170:ASP:OD2	1:A:230:ARG:HD2	2.00	0.62
1:A:764:VAL:HG21	1:A:859:SER:HB2	1.81	0.62
1:A:48:ALA:HB1	1:A:325:SER:O	1.99	0.62
1:A:144:LEU:CD2	1:A:165:ALA:HB2	2.29	0.61
1:A:704:THR:HG23	1:A:717:ASN:HB3	1.83	0.60
1:A:489:PHE:CE2	1:A:491:LEU:HB2	2.38	0.59
1:B:400:ASP:OD1	1:B:454:ARG:HD2	2.03	0.59
1:A:201:TRP:HE1	1:A:212:ASN:HD21	1.49	0.59
1:B:529:GLN:HG3	1:B:776:TRP:CE3	2.38	0.58
1:B:310:HIS:NE2	3:B:2079:HOH:O	2.31	0.58
1:B:709:LEU:HD11	1:B:745:THR:HB	1.85	0.58
1:A:709:LEU:HD11	1:A:745:THR:HB	1.86	0.58
1:B:216:VAL:HG11	1:B:369:LEU:HD12	1.86	0.57
1:B:677:HIS:HD2	1:B:679:GLN:HE21	1.52	0.57
1:B:354:LYS:HE3	3:B:2093:HOH:O	2.05	0.56
1:A:577:ARG:NH1	1:A:652:HIS:ND1	2.53	0.56
1:B:511:LYS:HE2	1:B:536:TRP:O	2.05	0.56
1:A:246:ASP:HB3	1:A:292:LEU:CD2	2.34	0.56
1:A:336:ASP:H	1:A:352:ASN:ND2	2.03	0.56
1:A:139:ASP:HA	1:A:169:HIS:O	2.05	0.56
1:A:244:HIS:ND1	1:A:296:ASP:OD1	2.38	0.56
1:A:515:PRO:HD2	1:A:542:THR:OG1	2.06	0.56
1:B:704:THR:HG22	3:B:2180:HOH:O	2.06	0.55
1:A:72:SER:O	1:A:183:SER:HB2	2.07	0.55
1:A:899:ASP:N	3:A:2210:HOH:O	2.40	0.54
1:A:753:THR:HB	1:A:757:GLY:O	2.07	0.54
1:A:706:LEU:HB2	1:A:715:TYR:HB3	1.89	0.54
1:B:244:HIS:NE2	1:B:246:ASP:CG	2.59	0.54
1:B:336:ASP:H	1:B:352:ASN:HD22	1.52	0.54
1:A:836:VAL:O	1:A:857:ALA:HA	2.08	0.54
1:B:495:PRO:HB3	1:B:502:SER:HB3	1.90	0.54
1:B:517:ASP:OD1	1:B:577:ARG:NH2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:HIS:NE2	1:A:246:ASP:CG	2.62	0.54
1:B:246:ASP:HB3	1:B:292:LEU:HD21	1.89	0.54
1:A:244:HIS:NE2	1:A:246:ASP:OD2	2.42	0.53
1:A:577:ARG:HD2	1:A:652:HIS:HB3	1.90	0.53
1:B:201:TRP:HE1	1:B:212:ASN:ND2	1.85	0.53
1:B:680:TYR:OH	1:B:685:ARG:HG2	2.09	0.53
1:A:677:HIS:HD2	1:A:679:GLN:HE21	1.55	0.53
1:B:512:MET:HG2	2:D:1:GCS:H61	1.90	0.53
1:B:808:ASN:HD22	1:B:809:SER:H	1.55	0.53
1:B:803:VAL:O	1:B:894:GLN:NE2	2.36	0.53
1:B:764:VAL:HG21	1:B:859:SER:HB2	1.90	0.52
1:B:375:ALA:O	1:B:379:LYS:HG3	2.10	0.52
1:B:808:ASN:HB3	3:B:2191:HOH:O	2.10	0.51
1:A:155:LYS:HD3	1:A:158:THR:HG22	1.93	0.51
1:A:297:ARG:NH2	3:A:2066:HOH:O	2.43	0.51
1:A:137:TYR:HB2	1:A:222:ARG:HB2	1.92	0.51
1:A:609:LYS:CE	1:A:796:ASN:HD21	2.24	0.50
1:A:244:HIS:NE2	1:A:246:ASP:OD1	2.44	0.50
1:A:465:HIS:HD2	3:A:2120:HOH:O	1.93	0.50
1:A:335:ARG:HA	1:A:352:ASN:HD21	1.76	0.50
1:A:701:THR:HG23	1:A:753:THR:HG1	1.74	0.50
1:A:297:ARG:HD2	3:A:2067:HOH:O	2.12	0.49
1:B:737:PRO:O	1:B:739:VAL:HG23	2.12	0.49
1:A:416:GLY:HA3	1:A:465:HIS:HB2	1.95	0.49
1:A:597:TYR:OH	1:A:616:GLU:OE2	2.21	0.49
1:A:715:TYR:HA	3:A:2173:HOH:O	2.11	0.48
1:A:677:HIS:CD2	1:A:679:GLN:HE21	2.31	0.48
1:A:85:SER:HB3	1:A:96:GLN:HE22	1.78	0.48
1:B:72:SER:O	1:B:183:SER:HB2	2.14	0.48
1:B:465:HIS:HD2	3:B:2124:HOH:O	1.96	0.48
1:B:836:VAL:O	1:B:857:ALA:HA	2.14	0.48
1:A:554:LEU:HA	1:A:557:MET:HG2	1.96	0.48
1:B:521:PRO:HG3	1:B:616:GLU:HG2	1.96	0.48
1:A:392:ARG:HA	1:A:414:MET:HB2	1.96	0.47
1:B:677:HIS:CD2	1:B:679:GLN:HE21	2.30	0.47
1:B:659:TYR:O	1:B:660:MET:HB2	2.14	0.47
1:B:597:TYR:OH	1:B:616:GLU:OE2	2.26	0.47
1:B:161:GLN:CB	3:B:2028:HOH:O	2.58	0.47
1:B:745:THR:HG23	1:B:792:LEU:HA	1.97	0.47
1:B:336:ASP:H	1:B:352:ASN:HD21	1.60	0.47
1:A:193:PRO:O	1:A:421:ASP:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:774:LEU:HD13	1:B:776:TRP:CZ2	2.51	0.46
1:B:267:GLY:HA3	1:B:315:ASP:O	2.16	0.46
1:B:416:GLY:HA3	1:B:465:HIS:HB2	1.97	0.46
1:A:144:LEU:HA	1:A:145:SER:HA	1.69	0.46
1:B:807:ALA:O	1:B:898:ALA:HA	2.16	0.46
1:A:832:PRO:HB3	1:A:861:TRP:CD2	2.51	0.46
1:B:577:ARG:HD2	1:B:652:HIS:HB3	1.97	0.46
1:A:42:LEU:HD21	1:A:54:ILE:HG12	1.98	0.45
1:B:254:ARG:HG3	1:B:285:ARG:HB2	1.99	0.45
1:B:392:ARG:HA	1:B:414:MET:HB2	1.99	0.45
1:B:129:VAL:HG13	1:B:223:ARG:HH12	1.82	0.45
1:A:159:LYS:HD3	1:A:189:TYR:CZ	2.51	0.45
1:A:255:ASN:ND2	1:A:261:VAL:HG22	2.32	0.45
1:A:529:GLN:HG3	1:A:776:TRP:CE3	2.51	0.45
1:B:477:GLU:HG2	1:B:504:ILE:HD12	1.99	0.45
1:B:709:LEU:HD22	1:B:798:LEU:HD13	1.99	0.45
1:A:472:PRO:HG2	1:A:477:GLU:HB2	1.99	0.45
1:A:517:ASP:OD1	1:A:577:ARG:NH2	2.50	0.45
1:B:395:GLY:HA3	1:B:418:GLU:OE1	2.17	0.45
1:B:46:ALA:HB2	1:B:131:ASP:HB3	1.98	0.44
1:B:570:PRO:HD2	3:B:2145:HOH:O	2.17	0.44
1:A:701:THR:HG22	3:A:2177:HOH:O	2.16	0.44
1:A:336:ASP:OD1	1:A:338:LYS:NZ	2.50	0.44
1:A:642:TRP:CD2	1:A:643:MET:HG2	2.53	0.44
1:A:201:TRP:O	1:A:202:ILE:C	2.56	0.44
1:A:547:ASP:H	1:A:652:HIS:HA	1.82	0.43
1:A:192:ASP:HA	1:A:193:PRO:HD3	1.83	0.43
1:B:310:HIS:CD2	3:B:2082:HOH:O	2.71	0.43
1:B:656:PHE:CE1	1:B:660:MET:HE1	2.53	0.43
1:A:689:VAL:O	1:A:730:LYS:HA	2.19	0.43
1:B:512:MET:HG2	2:D:1:GCS:C6	2.47	0.43
1:A:625:HIS:O	1:A:636:SER:OG	2.35	0.43
1:B:753:THR:HA	1:B:758:LYS:O	2.18	0.43
1:B:627:ARG:NH1	1:B:681:SER:HB3	2.33	0.43
1:A:144:LEU:CD2	1:A:165:ALA:CB	2.95	0.43
1:B:44:VAL:HG21	1:B:221:VAL:HG11	2.00	0.43
1:B:233:HIS:CE1	1:B:250:LYS:HB2	2.54	0.43
1:A:748:ALA:HB3	1:A:765:TYR:HB2	2.00	0.43
1:A:462:ILE:O	1:A:463:SER:HB3	2.19	0.42
1:A:642:TRP:HA	1:A:643:MET:HA	1.66	0.42
1:B:139:ASP:OD2	1:B:222:ARG:NH1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:ARG:NH2	1:B:491:LEU:HD21	2.31	0.42
1:A:208:PRO:HD3	1:A:367:LEU:HD11	2.00	0.42
1:B:390:THR:HA	1:B:412:LEU:O	2.20	0.42
1:A:50:ASN:OD1	1:A:50:ASN:C	2.57	0.42
1:B:527:LYS:NZ	1:B:631:ASP:OD2	2.47	0.42
1:A:517:ASP:HA	1:A:545:GLY:HA3	2.01	0.42
1:A:671:LYS:HB2	1:A:671:LYS:HE2	1.95	0.42
1:A:267:GLY:HA3	1:A:315:ASP:O	2.20	0.42
1:B:335:ARG:HA	1:B:352:ASN:HD21	1.85	0.42
1:B:464:PHE:HB3	1:B:484:MET:HE1	2.01	0.42
1:A:832:PRO:HB3	1:A:861:TRP:CE2	2.55	0.42
1:B:201:TRP:O	1:B:202:ILE:C	2.57	0.42
1:B:701:THR:HG23	1:B:753:THR:OG1	2.21	0.41
1:A:323:THR:HG22	1:A:324:PRO:O	2.21	0.41
1:B:129:VAL:HG13	1:B:223:ARG:NH1	2.35	0.41
1:B:428:ASN:HB2	1:B:431:GLU:HB3	2.03	0.41
1:B:452:ALA:HB1	1:B:489:PHE:HB2	2.02	0.41
1:B:642:TRP:HA	1:B:643:MET:HA	1.77	0.41
1:B:865:THR:HG22	3:B:2201:HOH:O	2.20	0.41
1:A:377:ALA:HA	1:A:405:ILE:HG21	2.02	0.41
1:A:807:ALA:HA	1:A:820:THR:O	2.21	0.41
1:B:144:LEU:HD23	1:B:144:LEU:N	2.35	0.41
1:B:605:ASP:HA	1:B:608:ARG:HD3	2.03	0.41
1:A:604:ASN:HB3	3:A:2148:HOH:O	2.19	0.41
1:A:744:THR:O	1:A:768:SER:HA	2.21	0.41
1:B:191:ASN:O	1:B:211:GLN:HG2	2.20	0.41
1:A:510:MET:HA	1:A:538:PHE:HB3	2.03	0.41
1:A:532:ARG:HA	1:A:532:ARG:HD3	1.97	0.41
1:B:144:LEU:HA	1:B:145:SER:HA	1.69	0.41
1:B:323:THR:HA	1:B:324:PRO:HD2	1.94	0.40
1:B:495:PRO:CB	1:B:502:SER:HB3	2.51	0.40
1:B:832:PRO:HB3	1:B:861:TRP:CE2	2.57	0.40
1:A:138:LEU:HG	1:A:173:ILE:HD13	2.04	0.40

All (9) 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)
1:A:246:ASP:OD2	1:B:296:ASP:OD1[3_554]	1.58	0.62
1:A:296:ASP:OD2	1:B:246:ASP:OD1[3_554]	1.61	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ASP:OD2	1:B:246:ASP:OD2[3_554]	1.61	0.59
1:A:246:ASP:OD1	1:B:296:ASP:OD1[3_554]	1.75	0.45
1:A:246:ASP:OD2	1:B:296:ASP:CG[3_554]	1.82	0.38
1:A:296:ASP:OD2	1:B:246:ASP:CG[3_554]	1.85	0.35
1:A:296:ASP:CG	1:B:246:ASP:OD2[3_554]	2.02	0.18
1:A:246:ASP:CG	1:B:296:ASP:OD1[3_554]	2.06	0.14
1:A:246:ASP:OD2	1:B:296:ASP:OD2[3_554]	2.14	0.06

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	856/1032 (83%)	811 (95%)	42 (5%)	3 (0%)	30	55
1	B	856/1032 (83%)	810 (95%)	42 (5%)	4 (0%)	25	49
All	All	1712/2064 (83%)	1621 (95%)	84 (5%)	7 (0%)	30	55

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	758	LYS
1	B	202	ILE
1	A	202	ILE
1	A	205	ALA
1	B	205	ALA
1	B	599	ALA
1	B	49	GLY

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	701/833 (84%)	672 (96%)	29 (4%)	26	54
1	B	701/833 (84%)	667 (95%)	34 (5%)	21	47
All	All	1402/1666 (84%)	1339 (96%)	63 (4%)	23	50

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	SER
1	A	88	SER
1	A	211	GLN
1	A	237	LYS
1	A	272	LYS
1	A	279	SER
1	A	283	LYS
1	A	292	LEU
1	A	335	ARG
1	A	356	LEU
1	A	428	ASN
1	A	530	LYS
1	A	577	ARG
1	A	586	LEU
1	A	608	ARG
1	A	626	SER
1	A	630	THR
1	A	644	LEU
1	A	648	TRP
1	A	652	HIS
1	A	676	LEU
1	A	701	THR
1	A	704	THR
1	A	783	TYR
1	A	803	VAL
1	A	806	THR
1	A	846	LYS
1	A	877	LEU
1	A	895	THR
1	B	118	SER
1	B	133	SER
1	B	144	LEU
1	B	198	SER

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Mol	Chain	Res	Type
1	B	211	GLN
1	B	231	SER
1	B	237	LYS
1	B	240	SER
1	B	283	LYS
1	B	292	LEU
1	B	297	ARG
1	B	310	HIS
1	B	324	PRO
1	B	335	ARG
1	B	337	VAL
1	B	356	LEU
1	B	428	ASN
1	B	517	ASP
1	B	552	ASP
1	B	577	ARG
1	B	608	ARG
1	B	632	SER
1	B	648	TRP
1	B	652	HIS
1	B	698	SER
1	B	701	THR
1	B	704	THR
1	B	769	THR
1	B	803	VAL
1	B	808	ASN
1	B	846	LYS
1	B	865	THR
1	B	877	LEU
1	B	895	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	178	HIS
1	A	194	ASN
1	A	212	ASN
1	A	352	ASN
1	A	428	ASN
1	A	465	HIS
1	A	478	GLN

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Mol	Chain	Res	Type
1	A	679	GLN
1	A	750	ASN
1	A	796	ASN
1	B	128	ASN
1	B	169	HIS
1	B	178	HIS
1	B	194	ASN
1	B	212	ASN
1	B	310	HIS
1	B	352	ASN
1	B	428	ASN
1	B	465	HIS
1	B	679	GLN
1	B	750	ASN
1	B	796	ASN
1	B	808	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	GCS	C	1	2	12,12,12	1.69	4 (33%)	16,17,17	1.39	3 (18%)
2	GCS	C	2	2	11,11,12	0.61	0	12,15,17	1.60	2 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GCS	D	1	2	12,12,12	1.39	1 (8%)	16,17,17	1.54	2 (12%)
2	GCS	D	2	2	11,11,12	0.82	0	12,15,17	1.85	1 (8%)

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	GCS	C	1	2	-	1/2/22/22	0/1/1/1
2	GCS	C	2	2	-	0/2/19/22	0/1/1/1
2	GCS	D	1	2	-	2/2/22/22	0/1/1/1
2	GCS	D	2	2	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	GCS	O4-C4	2.76	1.49	1.43
2	D	1	GCS	O4-C4	2.75	1.49	1.43
2	C	1	GCS	O5-C5	2.32	1.50	1.44
2	C	1	GCS	C6-C5	2.24	1.59	1.51
2	C	1	GCS	C4-C5	2.16	1.57	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	GCS	C1-O5-C5	5.90	120.19	112.19
2	D	1	GCS	O5-C5-C4	4.53	117.92	109.69
2	C	2	GCS	C1-O5-C5	3.62	117.09	112.19
2	C	2	GCS	O5-C5-C6	-3.61	101.55	107.20
2	C	1	GCS	O1-C1-C2	2.71	114.55	108.96
2	C	1	GCS	O4-C4-C3	2.52	116.17	110.35
2	C	1	GCS	O5-C5-C4	2.28	113.83	109.69
2	D	1	GCS	C6-C5-C4	-2.16	107.95	113.00

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	GCS	C4-C5-C6-O6

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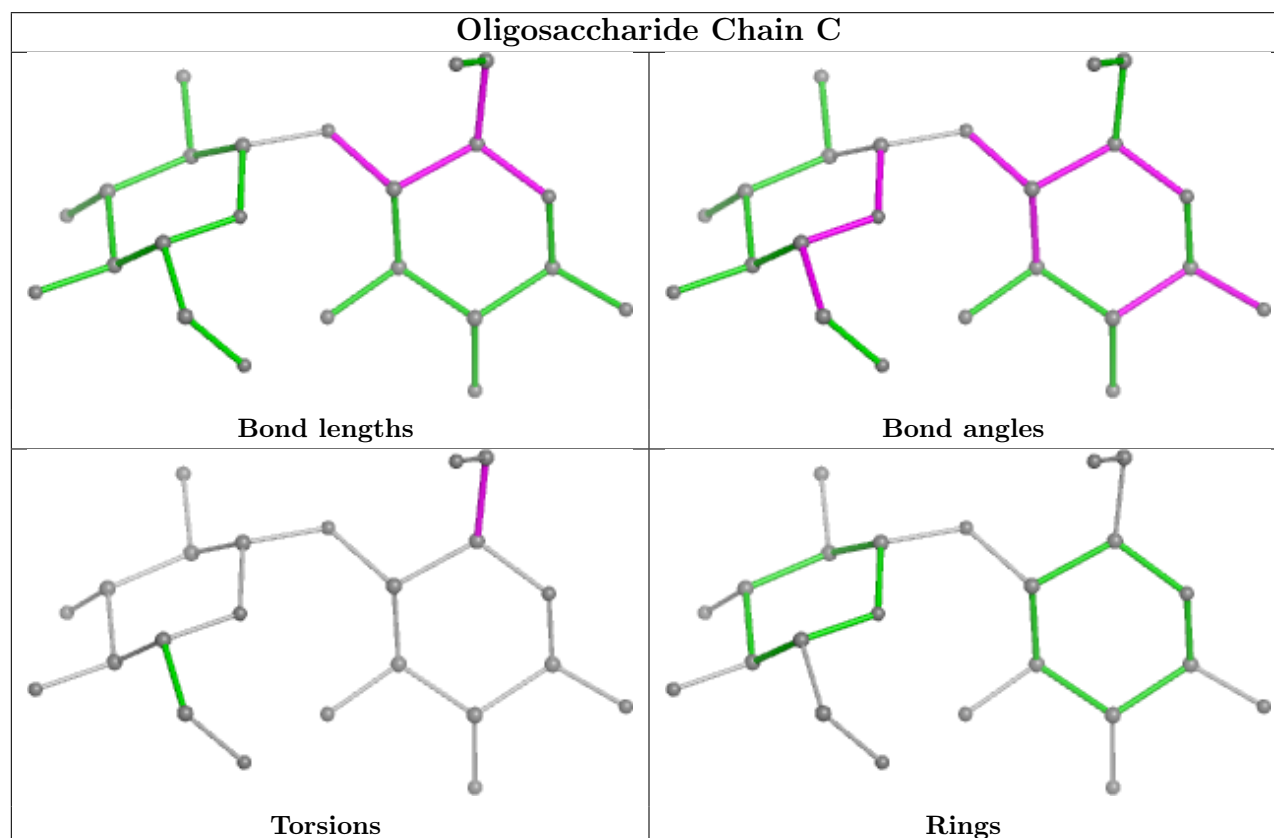
Mol	Chain	Res	Type	Atoms
2	C	1	GCS	O5-C5-C6-O6
2	D	1	GCS	O5-C5-C6-O6

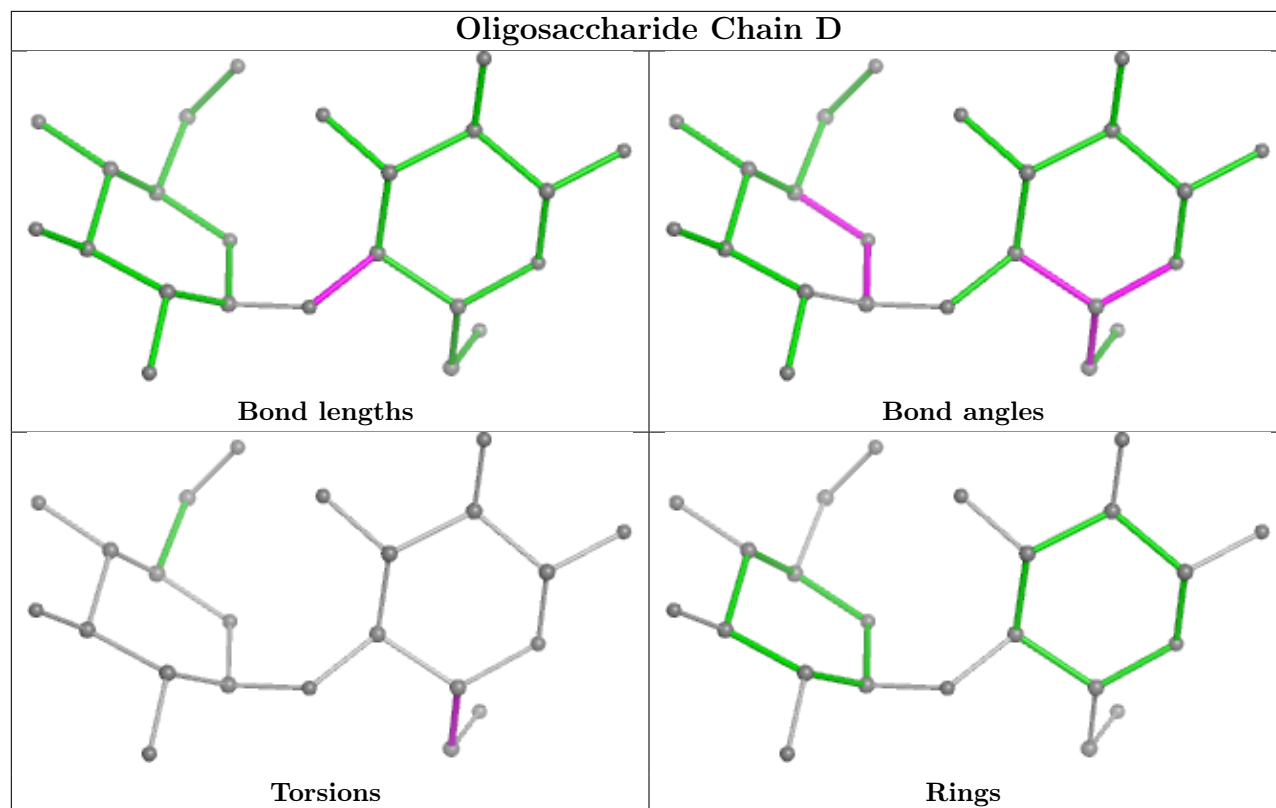
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	GCS	2	0

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





5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	858/1032 (83%)	-0.64	8 (0%) 81 80	3, 15, 27, 66	1 (0%)
1	B	858/1032 (83%)	-0.64	10 (1%) 76 76	3, 15, 25, 68	1 (0%)
All	All	1716/2064 (83%)	-0.64	18 (1%) 79 79	3, 15, 26, 68	2 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	47	ALA	6.8
1	B	46	ALA	5.8
1	A	43	SER	5.0
1	A	44	VAL	4.9
1	B	44	VAL	4.8
1	A	42	LEU	4.1
1	A	45	GLY	4.0
1	A	246	ASP	3.8
1	B	42	LEU	3.8
1	B	43	SER	3.7
1	B	47	ALA	3.5
1	B	310	HIS	3.0
1	A	296	ASP	3.0
1	B	246	ASP	3.0
1	B	45	GLY	2.9
1	B	296	ASP	2.8
1	B	48	ALA	2.5
1	A	46	ALA	2.1

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

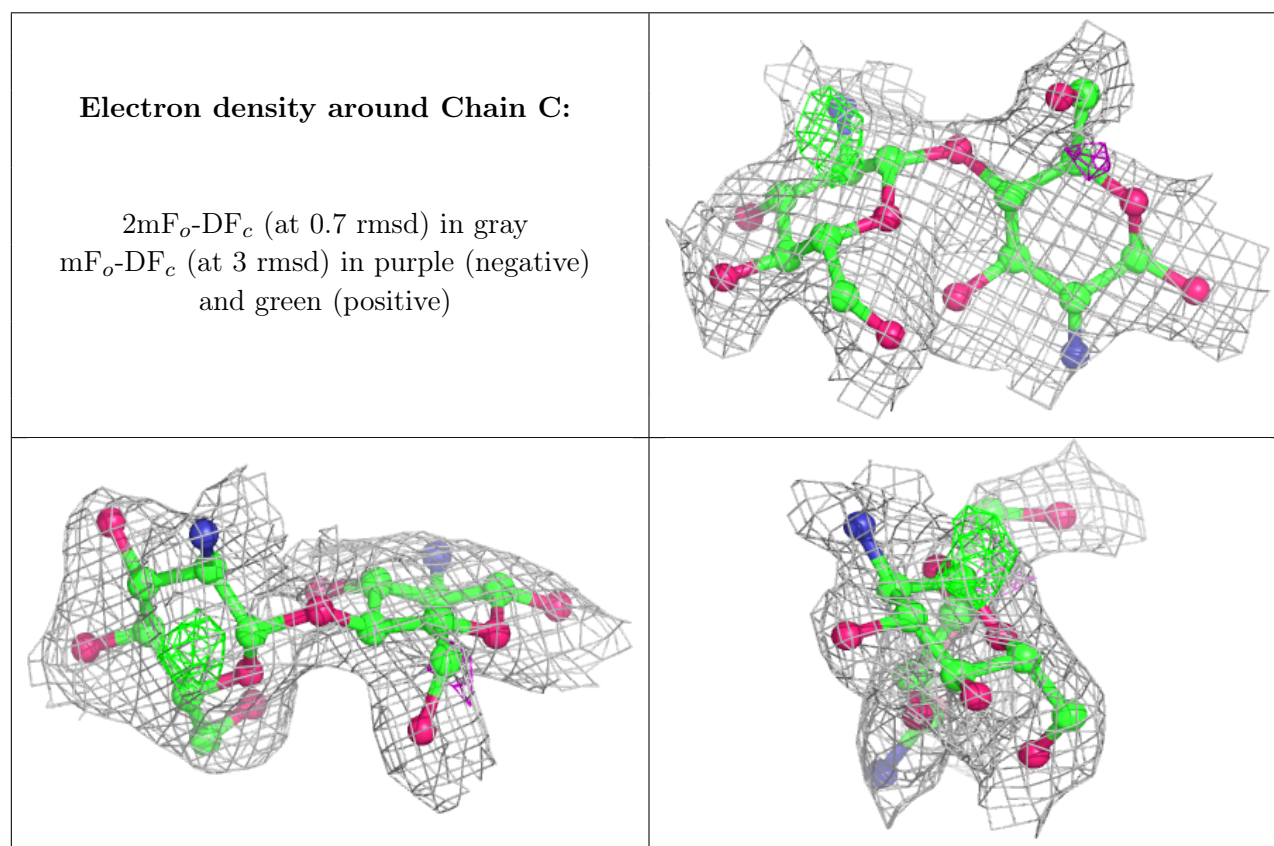
There are no non-standard protein/DNA/RNA residues in this entry.

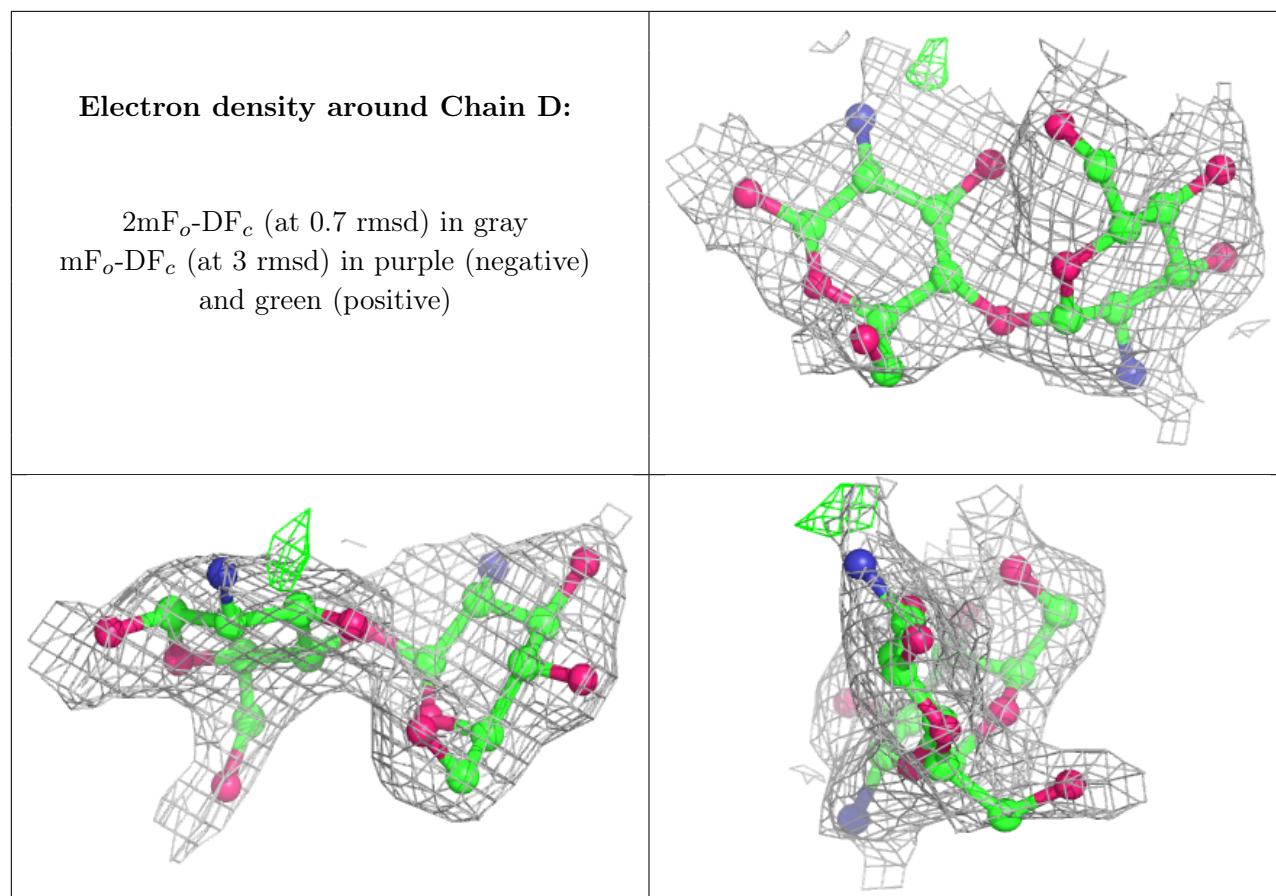
6.3 Carbohydrates ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GCS	C	1	12/12	0.87	0.13	26,28,28,29	0
2	GCS	D	1	12/12	0.90	0.11	28,33,34,35	0
2	GCS	C	2	11/12	0.93	0.09	15,19,21,22	0
2	GCS	D	2	11/12	0.94	0.09	19,22,23,24	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.