Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2025 – 12:22 AM JST

PDB ID	:	8ZYI / pdb_00008zyi
Title	:	crystal structure of GH57 family amylopullulanase mutant D352N from Aquifex aeolicus in complex wih 6-alpha-D-maltotriosyl-maltotriose
Authors	:	Zhu, Z.M.; Wang, W.W.; Yu, F.
Deposited on	:	2024-06-17
Resolution	:	1.66 Å(reported)

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

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

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

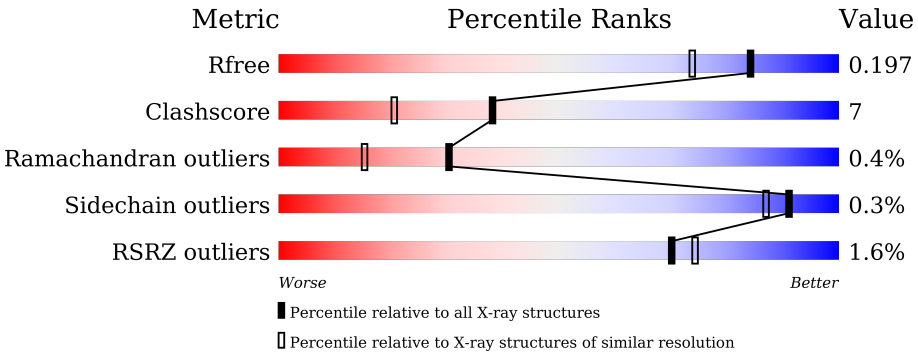
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

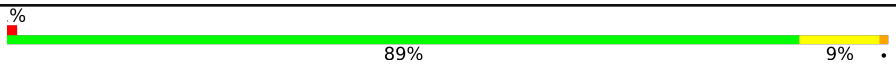
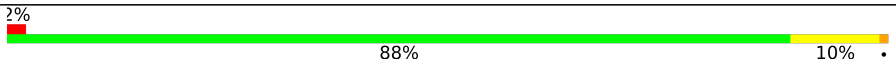
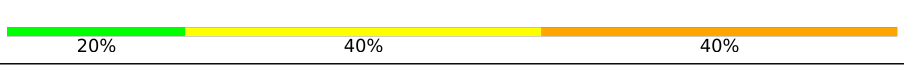
The reported resolution of this entry is 1.66 Å.

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	2328 (1.66-1.66)
Clashscore	180529	2515 (1.66-1.66)
Ramachandran outliers	177936	2475 (1.66-1.66)
Sidechain outliers	177891	2475 (1.66-1.66)
RSRZ outliers	164620	2328 (1.66-1.66)

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	477	
1	B	477	
2	C	5	
2	D	5	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8869 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.

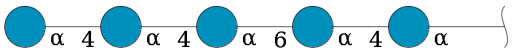
- Molecule 1 is a protein called Glycoside hydrolase family 57 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			4044	2646	648	741	9			
1	B	476	Total	C	N	O	S	0	0	0
			4044	2646	648	741	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	352	ASN	ASP	engineered mutation	UNP O66934
B	352	ASN	ASP	engineered mutation	UNP O66934

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	O		0	0	0
			56	30	26				
2	D	5	Total	C	O		0	0	0
			56	30	26				

- Molecule 3 is water.

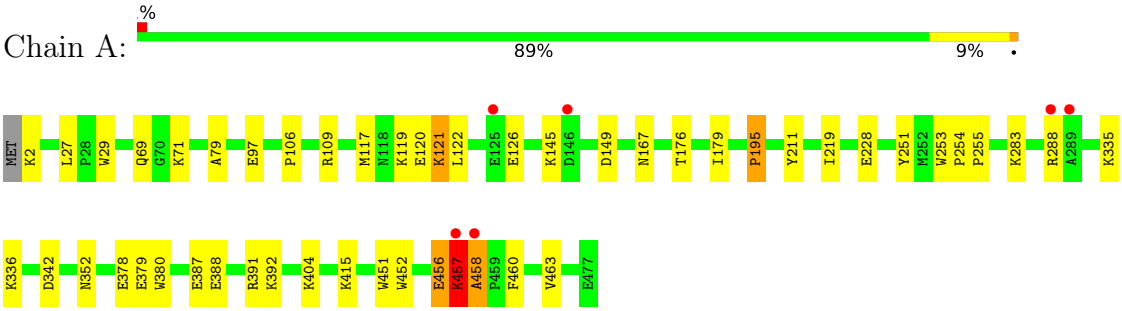
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	429	Total	O		0	0
			429	429			
3	B	240	Total	O		0	0
			240	240			

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.

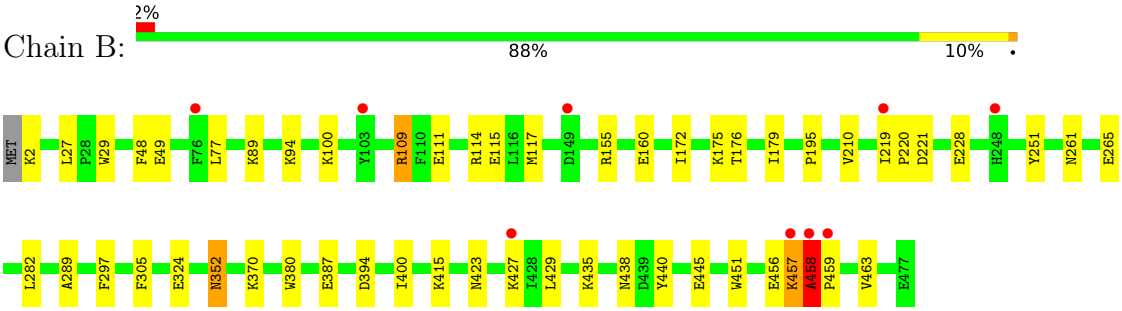
• Molecule 1: Glycoside hydrolase family 57 N-terminal domain-containing protein

Chain A:



• Molecule 1: Glycoside hydrolase family 57 N-terminal domain-containing protein

Chain B:

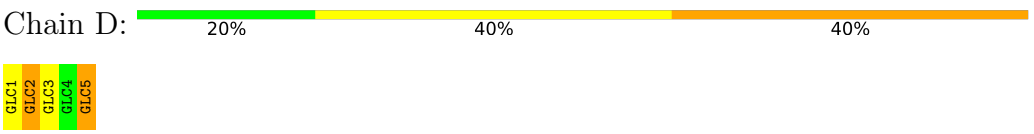


• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain C:

• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	61.79Å 41.52Å 194.51Å 90.00° 96.08° 90.00°	Depositor
Resolution (Å)	40.12 – 1.66 40.12 – 1.66	Depositor EDS
% Data completeness (in resolution range)	98.9 (40.12-1.66) 98.8 (40.12-1.66)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 1.66Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.170 , 0.201 0.167 , 0.197	Depositor DCC
R_{free} test set	5959 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	18.5	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	8869	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.53% 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: GLC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.46	0/4157	0.57	3/5623 (0.1%)
1	B	0.47	2/4157 (0.0%)	0.55	2/5623 (0.0%)
All	All	0.46	2/8314 (0.0%)	0.56	5/11246 (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
1	B	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	352	ASN	C-O	-6.32	1.16	1.23
1	B	458	ALA	C-N	5.78	1.40	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	456	GLU	N-CA-C	-6.38	102.29	110.53
1	B	458	ALA	CA-C-N	-5.69	113.92	119.90
1	B	458	ALA	C-N-CA	-5.69	113.92	119.90
1	A	458	ALA	CA-C-N	-5.40	114.00	119.83
1	A	458	ALA	C-N-CA	-5.40	114.00	119.83

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	195	PRO	Peptide
1	B	195	PRO	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	4044	0	3977	53	0
1	B	4044	0	3977	56	0
2	C	56	0	48	3	0
2	D	56	0	48	4	0
3	A	429	0	0	16	5
3	B	240	0	0	9	0
All	All	8869	0	8050	110	5

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 (110) 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:451:TRP:HZ3	1:A:452:TRP:CZ3	1.50	1.30
1:A:451:TRP:CZ3	1:A:452:TRP:CZ3	2.35	1.12
1:A:2:LYS:N	3:A:501:HOH:O	1.88	1.04
1:B:109:ARG:HD2	3:B:512:HOH:O	1.67	0.92
1:B:111:GLU:HG2	1:B:114:ARG:NH2	1.86	0.90
1:B:100:LYS:HZ1	1:B:117:MET:HG3	1.35	0.88
1:A:451:TRP:CZ3	1:A:452:TRP:CH2	2.65	0.83
1:A:451:TRP:HZ3	1:A:452:TRP:CE3	1.96	0.82
1:B:456:GLU:HG3	1:B:457:LYS:HG2	1.62	0.79
1:A:451:TRP:CZ3	1:A:452:TRP:CE3	2.70	0.79
1:B:456:GLU:HG3	1:B:457:LYS:N	1.98	0.77
1:B:109:ARG:CD	3:B:512:HOH:O	2.30	0.76
1:A:378:GLU:OE2	3:A:502:HOH:O	2.05	0.75
1:A:288:ARG:NH2	3:A:505:HOH:O	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:GLU:HA	1:B:114:ARG:NH2	2.03	0.74
1:B:48:PHE:O	3:B:501:HOH:O	2.05	0.73
1:B:220:PRO:HB2	1:B:427:LYS:HD3	1.72	0.72
1:A:388:GLU:HA	1:A:391:ARG:HD2	1.71	0.71
1:B:100:LYS:NZ	1:B:117:MET:HG3	2.06	0.71
1:A:457:LYS:O	3:A:503:HOH:O	2.10	0.70
1:B:220:PRO:CB	1:B:427:LYS:HD3	2.21	0.70
1:B:111:GLU:HG2	1:B:114:ARG:HH21	1.55	0.70
1:A:106:PRO:HA	1:A:109:ARG:HG3	1.74	0.70
1:B:100:LYS:CE	1:B:117:MET:SD	2.83	0.66
1:B:457:LYS:HG3	1:B:458:ALA:H	1.64	0.63
1:B:89:LYS:NZ	3:B:504:HOH:O	2.32	0.62
1:A:109:ARG:HG2	3:A:539:HOH:O	2.00	0.61
1:B:324:GLU:OE1	1:B:370:LYS:HE2	2.00	0.60
1:B:456:GLU:HG3	1:B:457:LYS:H	1.66	0.58
1:A:120:GLU:H	1:A:120:GLU:CD	2.12	0.58
1:B:457:LYS:CG	1:B:458:ALA:H	2.15	0.58
1:B:100:LYS:HE3	1:B:117:MET:SD	2.44	0.58
1:A:119:LYS:HE2	1:A:126:GLU:OE2	2.03	0.57
1:A:97:GLU:OE2	1:A:460:PHE:HE1	1.87	0.57
1:A:404:LYS:NZ	3:A:507:HOH:O	2.20	0.56
1:A:391:ARG:HD3	1:A:392:LYS:N	2.20	0.56
1:A:119:LYS:HE2	1:A:126:GLU:CD	2.30	0.56
1:B:415:LYS:HG2	1:B:451:TRP:CZ3	2.41	0.56
1:B:210:VAL:HG21	1:B:219:ILE:HG13	1.86	0.56
1:B:94:LYS:NZ	3:B:508:HOH:O	2.37	0.56
1:A:117:MET:HA	1:A:117:MET:HE2	1.88	0.55
1:A:228:GLU:HG2	3:A:733:HOH:O	2.06	0.54
1:A:228:GLU:OE1	1:A:228:GLU:N	2.38	0.54
1:B:394:ASP:OD1	1:B:394:ASP:N	2.40	0.53
1:B:220:PRO:HB3	1:B:427:LYS:HD3	1.91	0.53
1:B:457:LYS:HG3	1:B:458:ALA:N	2.24	0.52
1:A:121:LYS:HG3	1:A:122:LEU:N	2.22	0.52
1:B:100:LYS:NZ	1:B:117:MET:CG	2.72	0.52
1:B:160:GLU:OE2	3:B:503:HOH:O	2.19	0.51
1:B:176:THR:O	1:B:179:ILE:HG22	2.11	0.51
1:A:145:LYS:NZ	3:A:515:HOH:O	2.39	0.51
1:B:228:GLU:CD	1:B:228:GLU:H	2.18	0.51
1:B:49:GLU:HA	3:B:501:HOH:O	2.11	0.50
1:B:282:LEU:HB2	1:B:305:PHE:CD2	2.46	0.50
1:B:456:GLU:CG	1:B:457:LYS:HG2	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:LYS:CE	3:A:537:HOH:O	2.59	0.50
1:B:29:TRP:CD2	2:D:5:GLC:H2	2.47	0.50
1:A:451:TRP:CE3	1:A:452:TRP:CE3	2.99	0.49
1:B:2:LYS:HD2	3:B:608:HOH:O	2.12	0.49
1:A:167:ASN:ND2	3:A:512:HOH:O	2.37	0.49
1:A:342:ASP:OD1	1:A:342:ASP:N	2.41	0.48
1:A:456:GLU:C	1:A:457:LYS:HG2	2.38	0.48
1:A:352:ASN:ND2	2:C:2:GLC:H4	2.29	0.48
1:B:172:ILE:HD13	1:B:175:LYS:NZ	2.29	0.48
1:A:120:GLU:CD	1:A:120:GLU:N	2.72	0.47
1:A:176:THR:O	1:A:179:ILE:HG22	2.14	0.47
1:B:100:LYS:HE2	1:B:117:MET:SD	2.53	0.47
1:A:149:ASP:OD2	3:A:506:HOH:O	2.20	0.47
1:B:111:GLU:HG2	1:B:114:ARG:HH22	1.75	0.47
1:B:282:LEU:HG	1:B:289:ALA:HB1	1.95	0.47
1:B:352:ASN:ND2	2:D:2:GLC:H4	2.29	0.47
1:A:378:GLU:OE1	1:A:380:TRP:NE1	2.47	0.46
1:A:451:TRP:CE3	1:A:452:TRP:CD2	3.03	0.46
1:A:336:LYS:HB3	1:A:336:LYS:HE3	1.66	0.46
1:B:27:LEU:HG	1:B:463:VAL:HG11	1.97	0.46
1:A:283:LYS:HE2	3:A:543:HOH:O	2.14	0.46
1:B:221:ASP:H	1:B:427:LYS:NZ	2.14	0.45
1:B:429:LEU:HD21	1:B:445:GLU:HG2	1.97	0.45
1:A:109:ARG:HG2	1:A:109:ARG:HH11	1.82	0.45
1:B:427:LYS:HD2	1:B:427:LYS:HA	1.53	0.45
1:A:29:TRP:CD2	2:C:5:GLC:H2	2.53	0.44
1:A:391:ARG:HD3	1:A:391:ARG:C	2.41	0.44
1:A:27:LEU:HG	1:A:463:VAL:HG11	2.00	0.44
1:A:195:PRO:HD2	1:A:255:PRO:HD3	1.98	0.44
1:A:253:TRP:CE3	1:A:254:PRO:HD2	2.53	0.43
1:B:261:ASN:O	1:B:265:GLU:HG3	2.18	0.43
1:A:228:GLU:H	1:A:228:GLU:CD	2.25	0.43
1:A:391:ARG:NH1	3:A:535:HOH:O	2.52	0.43
1:B:251:TYR:OH	1:B:387:GLU:HA	2.19	0.43
1:B:77:LEU:HD12	1:B:77:LEU:HA	1.87	0.43
1:A:335:LYS:HB2	1:A:335:LYS:HE3	1.77	0.43
1:A:79:ALA:HB3	3:A:627:HOH:O	2.17	0.42
1:A:451:TRP:HE3	1:A:452:TRP:CD2	2.37	0.42
1:B:115:GLU:CD	1:B:155:ARG:HH22	2.27	0.42
1:B:220:PRO:HD3	1:B:423:ASN:CG	2.45	0.42
1:B:100:LYS:HZ2	1:B:117:MET:HB3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1:GLC:H62	2:C:2:GLC:O5	2.20	0.41
1:A:109:ARG:NH1	3:A:539:HOH:O	2.54	0.41
1:A:211:TYR:OH	1:A:219:ILE:HG12	2.19	0.41
1:A:251:TYR:OH	1:A:387:GLU:HA	2.20	0.41
1:A:415:LYS:HE2	3:A:537:HOH:O	2.19	0.41
1:B:380:TRP:CD1	1:B:380:TRP:H	2.37	0.41
1:B:352:ASN:HD22	2:D:2:GLC:H4	1.85	0.41
1:A:379:GLU:H	1:A:379:GLU:CD	2.29	0.41
1:B:297:PHE:HA	1:B:400:ILE:HG23	2.02	0.41
1:B:438:ASN:OD1	1:B:440:TYR:HB2	2.21	0.40
1:A:69:GLN:HB3	1:A:71:LYS:HE3	2.03	0.40
1:B:456:GLU:HG3	1:B:457:LYS:CG	2.44	0.40
1:B:435:LYS:HE3	3:B:617:HOH:O	2.21	0.40
1:B:459:PRO:HG2	2:D:5:GLC:H61	2.04	0.40

All (5) 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)
3:A:513:HOH:O	3:A:658:HOH:O[1_565]	2.08	0.12
3:A:510:HOH:O	3:A:726:HOH:O[2_556]	2.10	0.10
3:A:867:HOH:O	3:A:877:HOH:O[1_455]	2.11	0.09
3:A:574:HOH:O	3:A:623:HOH:O[1_655]	2.14	0.06
3:A:819:HOH:O	3:A:836:HOH:O[1_545]	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	474/477 (99%)	466 (98%)	6 (1%)	2 (0%)	30 15
1	B	474/477 (99%)	465 (98%)	7 (2%)	2 (0%)	30 15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	948/954 (99%)	931 (98%)	13 (1%)	4 (0%)	30 15

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	457	LYS
1	A	457	LYS
1	B	458	ALA
1	A	458	ALA

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	436/437 (100%)	434 (100%)	2 (0%)	86 80
1	B	436/437 (100%)	435 (100%)	1 (0%)	92 88
All	All	872/874 (100%)	869 (100%)	3 (0%)	91 87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	LYS
1	A	457	LYS
1	B	109	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	319	HIS
1	A	352	ASN
1	A	476	GLN
1	B	134	ASN
1	B	156	ASN
1	B	352	ASN

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Mol	Chain	Res	Type
1	B	476	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

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GLC	C	1	2	12,12,12	1.24	1 (8%)	17,17,17	1.63	3 (17%)
2	GLC	C	2	2	11,11,12	1.12	1 (9%)	15,15,17	1.23	1 (6%)
2	GLC	C	3	2	11,11,12	0.67	0	15,15,17	1.51	2 (13%)
2	GLC	C	4	2	11,11,12	0.66	0	15,15,17	0.72	0
2	GLC	C	5	2	11,11,12	0.86	1 (9%)	15,15,17	2.72	7 (46%)
2	GLC	D	1	2	12,12,12	0.92	0	17,17,17	1.69	4 (23%)
2	GLC	D	2	2	11,11,12	1.11	0	15,15,17	1.20	2 (13%)
2	GLC	D	3	2	11,11,12	1.02	1 (9%)	15,15,17	1.39	1 (6%)
2	GLC	D	4	2	11,11,12	1.13	0	15,15,17	1.03	0
2	GLC	D	5	2	11,11,12	1.08	0	15,15,17	2.43	6 (40%)

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

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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	GLC	O5-C1	-2.63	1.39	1.43
2	C	1	GLC	O3-C3	-2.50	1.37	1.43
2	D	3	GLC	O5-C1	-2.26	1.40	1.43
2	C	5	GLC	C2-C3	2.10	1.55	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	5	GLC	O2-C2-C3	6.45	123.06	110.14
2	D	5	GLC	O2-C2-C3	5.76	121.67	110.14
2	C	5	GLC	C1-C2-C3	-4.75	103.83	109.67
2	D	5	GLC	C1-C2-C3	-4.58	104.03	109.67
2	D	1	GLC	C1-O5-C5	4.18	121.55	113.66
2	C	5	GLC	O2-C2-C1	-3.77	101.44	109.15
2	C	3	GLC	O5-C1-C2	-3.73	105.02	110.77
2	D	1	GLC	O5-C5-C4	3.51	116.08	109.69
2	C	3	GLC	C1-O5-C5	3.46	116.87	112.19
2	C	5	GLC	C1-O5-C5	3.34	116.71	112.19
2	C	1	GLC	O2-C2-C1	-3.22	101.68	109.16
2	C	1	GLC	C6-C5-C4	-3.10	105.73	113.00
2	D	3	GLC	C1-C2-C3	-3.06	105.91	109.67
2	D	2	GLC	C1-O5-C5	3.04	116.32	112.19
2	D	5	GLC	C1-O5-C5	2.86	116.07	112.19
2	D	1	GLC	C6-C5-C4	-2.81	106.42	113.00
2	C	1	GLC	C1-O5-C5	2.74	118.84	113.66
2	D	5	GLC	O2-C2-C1	-2.68	103.67	109.15
2	C	2	GLC	O2-C2-C3	-2.60	104.93	110.14
2	D	2	GLC	O5-C5-C6	2.40	110.97	107.20
2	C	5	GLC	O3-C3-C2	2.37	114.53	109.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	5	GLC	C2-C3-C4	-2.26	106.99	110.89
2	C	5	GLC	O4-C4-C3	2.17	115.37	110.35
2	D	1	GLC	O3-C3-C4	-2.09	105.52	110.35
2	D	5	GLC	O5-C5-C6	2.03	110.39	107.20
2	D	5	GLC	O5-C1-C2	-2.01	107.67	110.77

There are no chirality outliers.

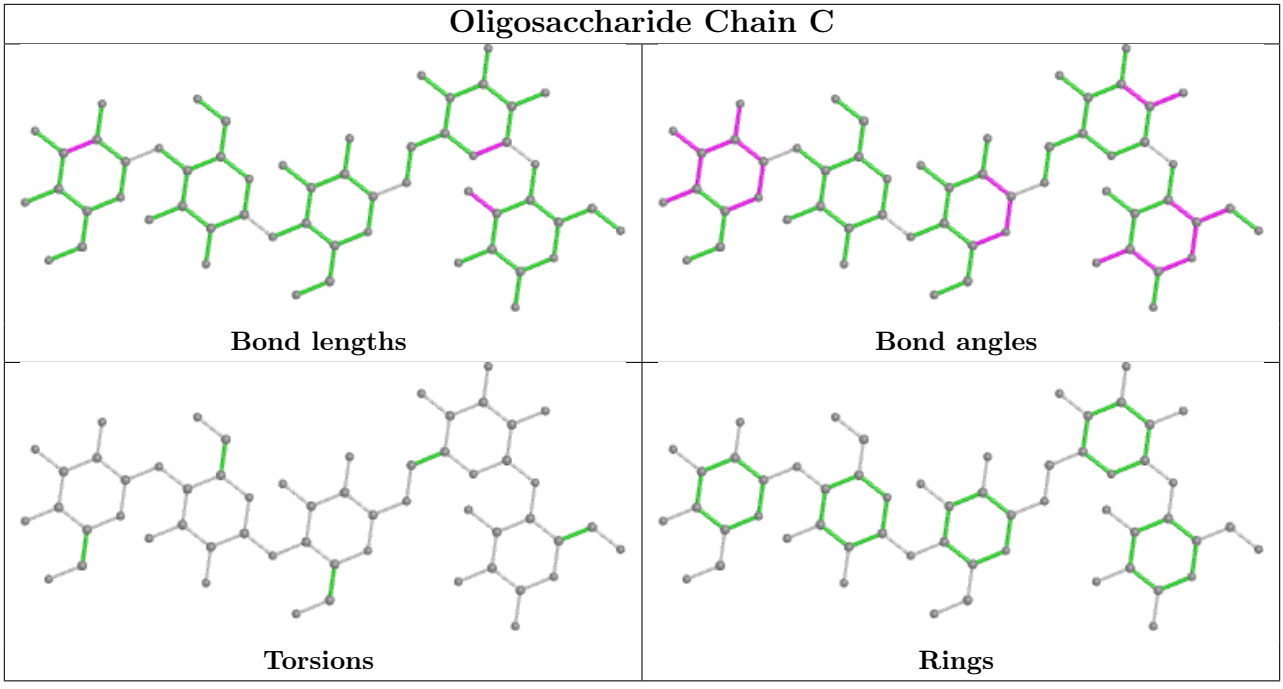
There are no torsion outliers.

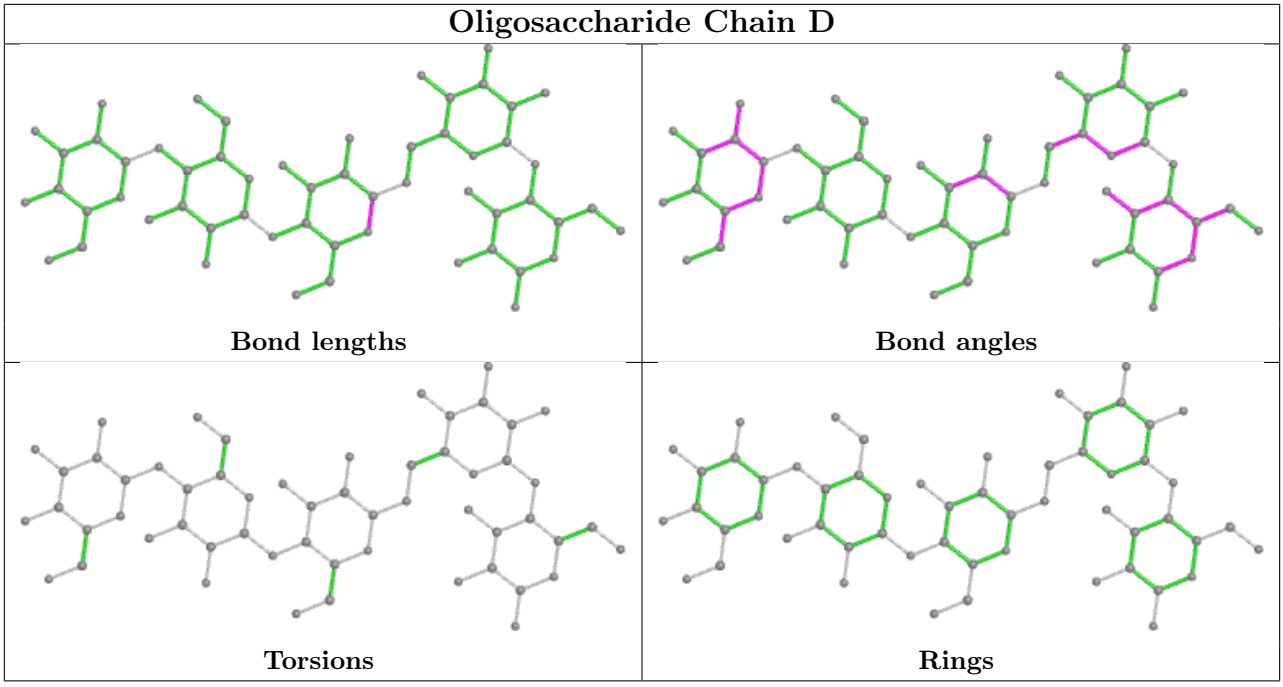
There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	GLC	2	0
2	D	5	GLC	2	0
2	C	1	GLC	1	0
2	D	2	GLC	2	0
2	C	5	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.





5.6 Ligand geometry

There are no ligands in this entry.

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	476/477 (99%)	-0.42	6 (1%)	74 79	7, 17, 42, 72	0
1	B	476/477 (99%)	-0.00	9 (1%)	66 70	13, 30, 56, 86	0
All	All	952/954 (99%)	-0.21	15 (1%)	70 74	7, 23, 51, 86	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	458	ALA	5.7
1	B	458	ALA	5.4
1	A	289	ALA	3.4
1	B	459	PRO	3.3
1	A	288	ARG	3.1
1	B	149	ASP	2.9
1	B	457	LYS	2.8
1	B	219	ILE	2.7
1	B	248	HIS	2.5
1	B	103	TYR	2.4
1	B	76	PHE	2.3
1	A	146	ASP	2.2
1	B	427	LYS	2.2
1	A	457	LYS	2.1
1	A	125	GLU	2.1

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)

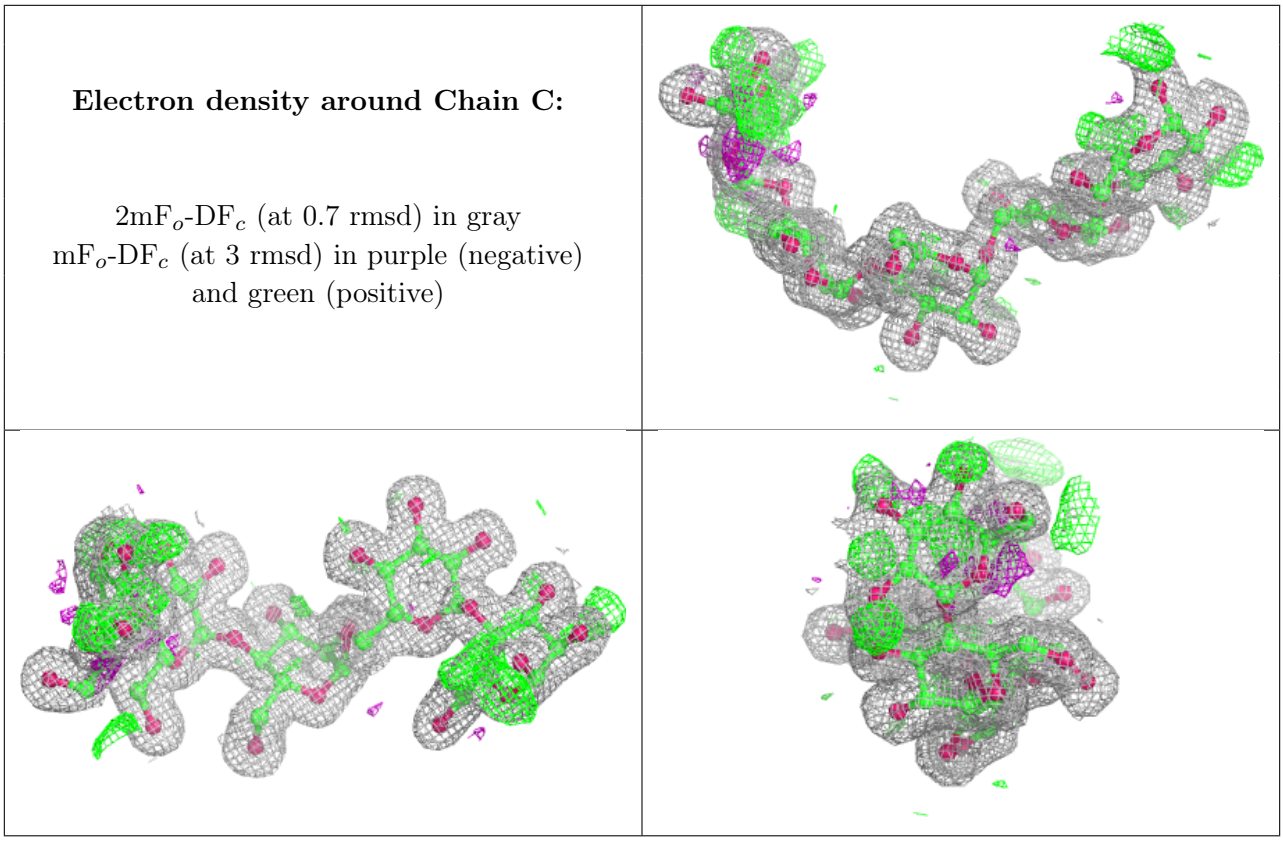
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	GLC	C	5	11/12	0.90	0.12	10,19,32,33	0
2	GLC	D	1	12/12	0.90	0.10	18,29,36,52	0
2	GLC	D	5	11/12	0.90	0.11	22,28,38,43	0
2	GLC	C	1	12/12	0.92	0.09	11,23,32,49	0
2	GLC	D	4	11/12	0.96	0.06	11,13,17,18	0
2	GLC	D	2	11/12	0.96	0.06	13,15,18,23	0
2	GLC	D	3	11/12	0.97	0.04	13,15,16,16	0
2	GLC	C	2	11/12	0.98	0.04	8,11,15,16	0
2	GLC	C	3	11/12	0.98	0.04	5,7,10,11	0
2	GLC	C	4	11/12	0.98	0.04	5,8,9,10	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.

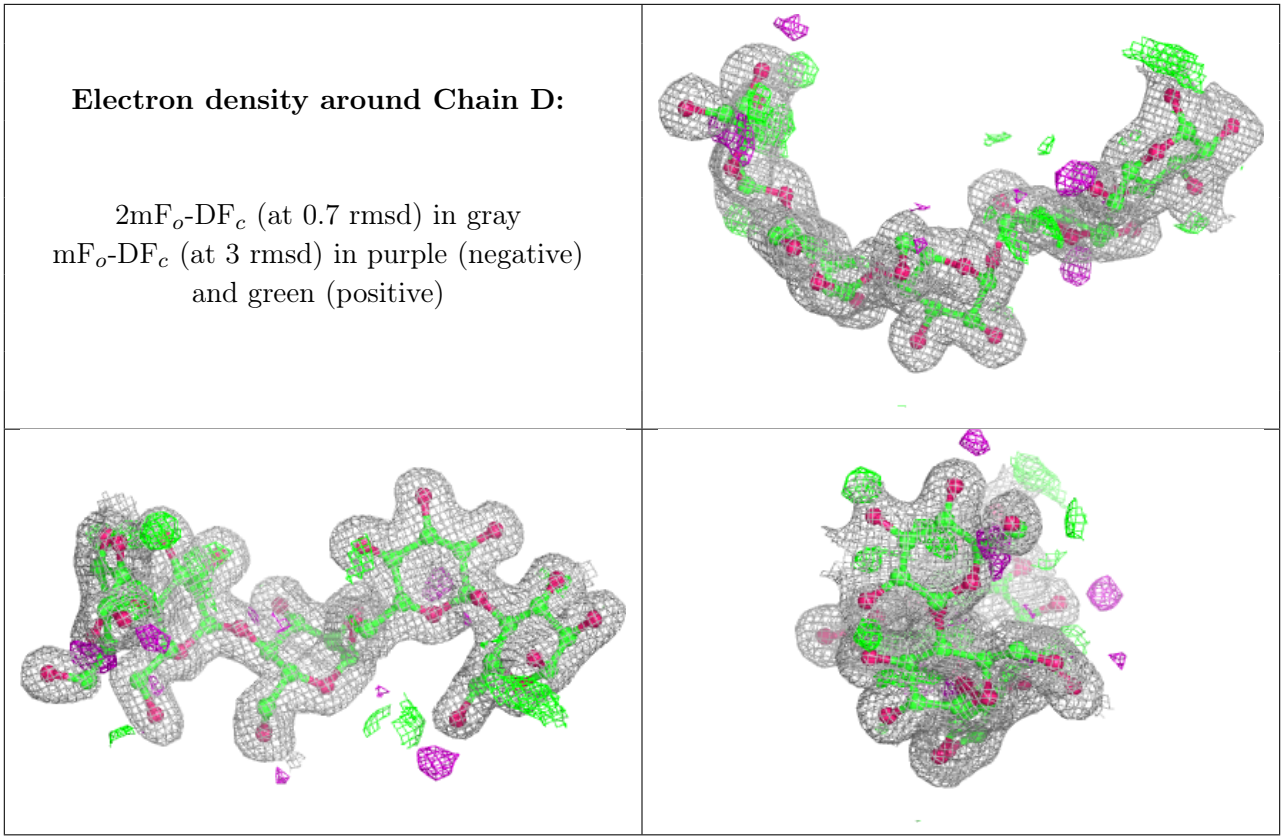
Electron density around Chain C:

$2mF_o$-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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.