



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 10:02 AM BST

PDB ID : 5D4Y
Title : A psychrophilic glycoside hydrolase family 10 endo-beta-1,4-xylanase
Authors : Zheng, Y.; Guo, R.T.
Deposited on : 2015-08-10
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

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 : 1.8.5 (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

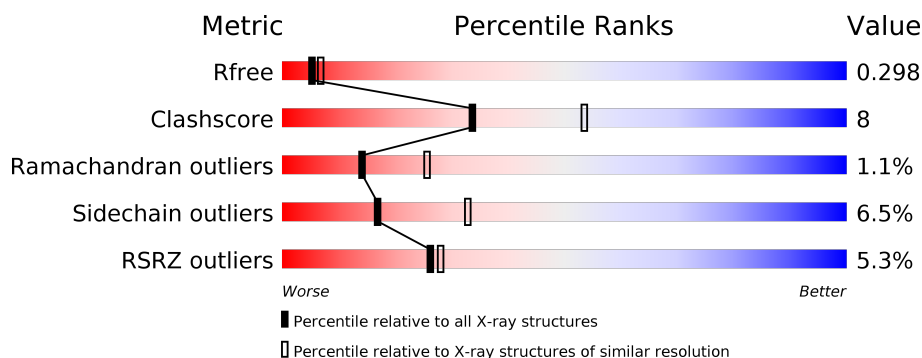
1 Overall quality at a glance

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 ≥ 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	355	<div> <div>4%</div> <div> <div></div> <div>68%</div> <div>19%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	355	<div> <div>5%</div> <div> <div></div> <div>67%</div> <div>17%</div> <div>•</div> <div>12%</div> </div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>
2	D	2	<div> <div></div> <div>100%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5300 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 xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2581	1647	439	483	12			
1	B	312	Total	C	N	O	S	0	0	0
			2564	1639	437	476	12			

- 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
			18	10	8			
2	D	2	Total	C	O	0	0	0
			18	10	8			

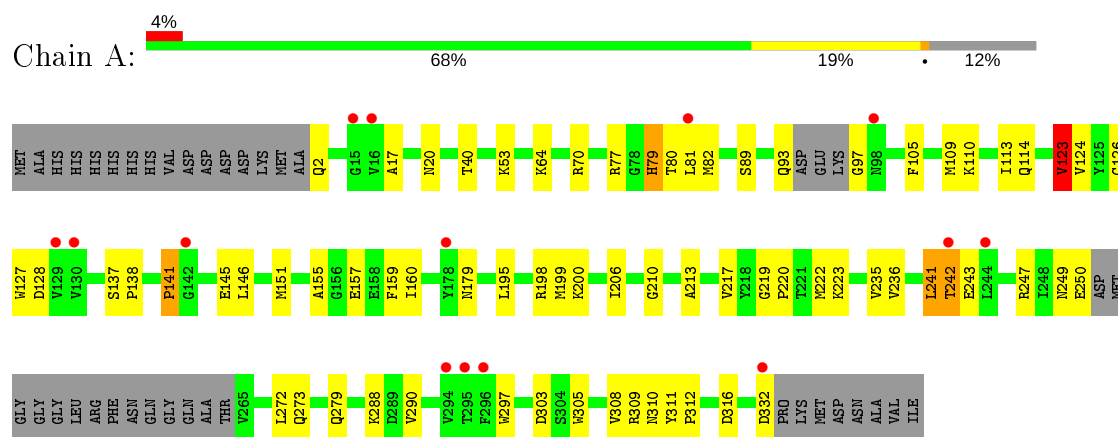
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		
3	B	43	Total	O	0	0
			43	43		

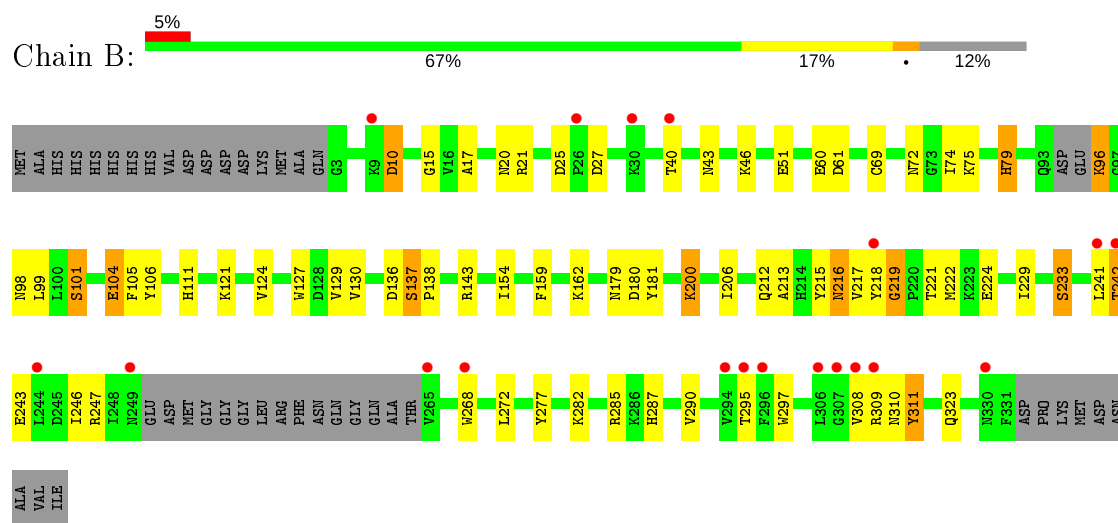
3 Residue-property plots [i](#)

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: xylanase



- Molecule 1: xylanase



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



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

Chain D:

100%

XYP1
XYP2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.39Å 78.44Å 88.72Å 90.00° 100.49° 90.00°	Depositor
Resolution (Å)	25.00 – 2.50 24.89 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (25.00-2.50) 97.1 (24.89-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	12.90 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.191 , 0.285 0.206 , 0.298	Depositor DCC
R_{free} test set	1181 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5300	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.55% 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

5.1 Standard geometry

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

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	0.64	0/2647	0.77	2/3586 (0.1%)
1	B	0.59	1/2630 (0.0%)	0.74	0/3562
All	All	0.61	1/5277 (0.0%)	0.76	2/7148 (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	3
1	B	0	3
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	219	GLY	N-CA	5.41	1.54	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	80	THR	N-CA-C	5.35	125.44	111.00
1	A	123	VAL	CB-CA-C	-5.14	101.62	111.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	SER	Peptide
1	A	219	GLY	Peptide
1	A	79	HIS	Peptide
1	B	137	SER	Peptide
1	B	311	TYR	Peptide
1	B	79	HIS	Peptide

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	2581	0	2479	44	0
1	B	2564	0	2474	42	0
2	C	18	0	0	0	0
2	D	18	0	0	3	0
3	A	76	0	0	5	0
3	B	43	0	0	2	0
All	All	5300	0	4953	86	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 8.

All (86) 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:242:THR:HG22	1:A:243:GLU:HG3	1.46	0.98
1:A:179:ASN:HD21	1:A:242:THR:HG21	1.42	0.85
1:B:179:ASN:HD21	1:B:242:THR:HG21	1.40	0.85
1:B:99:LEU:HD13	1:B:154:ILE:HG13	1.69	0.73
1:A:97:GLY:N	3:A:502:HOH:O	2.21	0.72
1:B:104:GLU:OE1	1:B:104:GLU:N	2.21	0.71
1:A:157:GLU:OE1	1:A:198:ARG:NH1	2.24	0.70
1:A:17:ALA:HB3	1:A:297:TRP:O	1.94	0.68
1:B:179:ASN:ND2	1:B:242:THR:HG21	2.12	0.63
1:A:141:PRO:O	2:D:1:XYP:O2	2.18	0.61
1:A:179:ASN:ND2	1:A:242:THR:HG21	2.14	0.61
1:B:124:VAL:HG11	1:B:127:TRP:CE2	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:ARG:NH2	3:B:502:HOH:O	2.28	0.59
1:B:243:GLU:HG2	1:B:297:TRP:CE3	2.37	0.59
1:B:104:GLU:CD	1:B:104:GLU:H	2.06	0.58
1:B:15:GLY:C	1:B:295:THR:HG23	2.24	0.58
1:A:222:MET:HG3	1:A:279:GLN:HB3	1.85	0.58
1:B:104:GLU:N	1:B:104:GLU:CD	2.58	0.56
1:B:96:LYS:N	3:B:503:HOH:O	2.39	0.55
1:A:213:ALA:HB2	1:A:241:LEU:HD13	1.89	0.55
1:B:179:ASN:HD21	1:B:242:THR:CG2	2.18	0.55
1:A:146:LEU:HD21	1:A:195:LEU:HD13	1.89	0.54
1:A:77:ARG:HG2	1:A:126:CYS:SG	2.48	0.54
1:A:20:ASN:ND2	3:A:501:HOH:O	2.13	0.54
1:A:242:THR:CG2	1:A:243:GLU:HG3	2.28	0.54
1:A:311:TYR:N	1:A:312:PRO:HD3	2.23	0.53
1:B:101:SER:OG	1:B:104:GLU:OE1	2.24	0.52
1:B:200:LYS:HE2	1:B:206:ILE:HG23	1.90	0.52
1:A:81:LEU:HD13	1:A:113:ILE:HG23	1.92	0.52
1:B:218:TYR:O	1:B:219:GLY:O	2.28	0.51
1:A:105:PHE:CZ	1:A:109:MET:CE	2.94	0.51
1:A:155:ALA:HB3	1:A:159:PHE:HB3	1.93	0.50
1:A:316:ASP:OD1	1:A:316:ASP:C	2.49	0.50
1:B:20:ASN:HD21	1:B:61:ASP:HB3	1.77	0.50
1:B:79:HIS:HE1	2:D:2:XYP:C5	2.24	0.50
1:B:221:THR:O	1:B:224:GLU:N	2.44	0.49
1:B:106:TYR:CE2	1:B:162:LYS:HG3	2.48	0.49
1:A:179:ASN:HD22	1:A:210:GLY:HA3	1.77	0.49
1:B:104:GLU:OE2	1:B:105:PHE:N	2.46	0.49
1:B:17:ALA:HA	1:B:40:THR:O	2.12	0.49
1:A:155:ALA:CB	1:A:159:PHE:HB3	2.42	0.49
1:A:273:GLN:NE2	1:A:311:TYR:O	2.47	0.48
1:A:2:GLN:HG3	3:A:535:HOH:O	2.13	0.47
1:B:181:TYR:HB3	1:B:212:GLN:NE2	2.29	0.47
1:A:249:ASN:HD22	1:A:310:ASN:ND2	2.12	0.47
1:B:69:CYS:HB3	1:B:74:ILE:O	2.14	0.47
1:A:70:ARG:HG3	1:A:123:VAL:CG1	2.45	0.47
1:A:110:LYS:O	1:A:114:GLN:HG3	2.16	0.46
1:A:105:PHE:CZ	1:A:109:MET:HE2	2.50	0.46
1:A:297:TRP:HD1	1:A:305:TRP:CD1	2.34	0.46
1:A:145:GLU:OE1	1:A:198:ARG:NH2	2.49	0.46
1:B:129:VAL:HG12	1:B:130:VAL:HG23	1.98	0.46
1:B:40:THR:HG23	1:B:79:HIS:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:MET:HE2	1:A:151:MET:HG2	1.98	0.45
1:B:213:ALA:HA	1:B:215:TYR:CE1	2.51	0.45
1:B:247:ARG:HB2	1:B:310:ASN:HB3	1.99	0.45
1:B:217:VAL:HG11	1:B:272:LEU:HD13	1.98	0.45
1:A:160:ILE:HG21	1:A:199:MET:CE	2.48	0.44
1:A:247:ARG:HD3	3:A:553:HOH:O	2.16	0.44
1:B:233:SER:OG	1:B:290:VAL:HG11	2.17	0.44
1:A:160:ILE:HG21	1:A:199:MET:HE1	1.99	0.44
1:B:10:ASP:N	1:B:10:ASP:OD1	2.49	0.44
1:B:212:GLN:HA	1:B:242:THR:HG22	1.99	0.44
1:A:124:VAL:HG11	1:A:127:TRP:CE2	2.53	0.43
1:A:77:ARG:NH2	1:A:128:ASP:OD1	2.44	0.43
1:A:17:ALA:HA	1:A:40:THR:O	2.18	0.43
1:B:216:ASN:ND2	1:B:219:GLY:CA	2.82	0.43
1:B:101:SER:O	1:B:104:GLU:OE1	2.35	0.43
1:B:180:ASP:OD1	1:B:181:TYR:N	2.51	0.43
1:A:195:LEU:HG	1:A:199:MET:HE3	2.00	0.42
1:B:229:ILE:HG21	1:B:287:HIS:CG	2.55	0.42
1:A:235:VAL:HG13	1:A:236:VAL:HG13	2.01	0.42
1:A:217:VAL:CG1	1:A:272:LEU:HD13	2.49	0.42
1:B:21:ARG:NH1	1:B:25:ASP:HB2	2.34	0.42
1:B:79:HIS:CE1	2:D:2:XYP:C5	3.02	0.42
1:A:79:HIS:HD2	1:A:128:ASP:OD2	2.02	0.42
1:B:246:ILE:HD12	1:B:277:TYR:CG	2.56	0.41
1:B:51:GLU:OE2	1:B:111:HIS:NE2	2.53	0.41
1:B:242:THR:HG23	1:B:243:GLU:HG3	2.03	0.41
1:B:43:ASN:HA	1:B:46:LYS:HD2	2.03	0.41
1:A:222:MET:CG	1:A:279:GLN:HB3	2.50	0.41
1:A:200:LYS:HE2	1:A:206:ILE:HG23	2.03	0.41
1:A:93:GLN:C	3:A:503:HOH:O	2.59	0.40
1:A:297:TRP:CE3	1:A:297:TRP:HA	2.57	0.40
1:B:136:ASP:CG	1:B:181:TYR:HH	2.25	0.40
1:A:310:ASN:O	1:A:311:TYR:C	2.58	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	308/355 (87%)	289 (94%)	16 (5%)	3 (1%)	15	28
1	B	306/355 (86%)	281 (92%)	21 (7%)	4 (1%)	12	21
All	All	614/710 (86%)	570 (93%)	37 (6%)	7 (1%)	14	26

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	PRO
1	B	138	PRO
1	A	220	PRO
1	B	222	MET
1	B	311	TYR
1	B	308	VAL
1	A	141	PRO

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	276/309 (89%)	262 (95%)	14 (5%)	24	45
1	B	274/309 (89%)	252 (92%)	22 (8%)	12	23
All	All	550/618 (89%)	514 (94%)	36 (6%)	17	33

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	LYS
1	A	64	LYS
1	A	89	SER
1	A	123	VAL
1	A	223	LYS
1	A	241	LEU
1	A	242	THR
1	A	250	GLU
1	A	288	LYS
1	A	290	VAL
1	A	303	ASP
1	A	308	VAL
1	A	309	ARG
1	A	332	ASP
1	B	10	ASP
1	B	27	ASP
1	B	60	GLU
1	B	72	ASN
1	B	75	LYS
1	B	96	LYS
1	B	98	ASN
1	B	101	SER
1	B	104	GLU
1	B	121	LYS
1	B	137	SER
1	B	143	ARG
1	B	159	PHE
1	B	200	LYS
1	B	216	ASN
1	B	233	SER
1	B	241	LEU
1	B	242	THR
1	B	268	TRP
1	B	282	LYS
1	B	309	ARG
1	B	323	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	43	ASN
1	A	72	ASN

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Mol	Chain	Res	Type
1	A	79	HIS
1	A	86	GLN
1	A	118	ASN
1	A	179	ASN
1	A	212	GLN
1	A	310	ASN
1	A	323	GLN
1	B	20	ASN
1	B	28	GLN
1	B	43	ASN
1	B	79	HIS
1	B	86	GLN
1	B	179	ASN
1	B	212	GLN
1	B	216	ASN
1	B	276	GLN
1	B	298	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	XYP	C	1	2	9,9,10	2.17	4 (44%)	10,12,14	3.04	6 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	XYP	C	2	2	9,9,10	2.38	3 (33%)	10,12,14	1.33	2 (20%)
2	XYP	D	1	2	9,9,10	2.25	3 (33%)	10,12,14	1.98	3 (30%)
2	XYP	D	2	2	9,9,10	1.94	3 (33%)	10,12,14	2.03	3 (30%)

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 (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	XYP	O5-C1	5.54	1.53	1.42
2	D	1	XYP	C2-C3	4.38	1.59	1.52
2	D	2	XYP	O2-C2	-3.56	1.35	1.43
2	D	1	XYP	O5-C5	3.53	1.49	1.42
2	C	1	XYP	C4-C3	-3.49	1.47	1.52
2	D	1	XYP	O2-C2	3.13	1.50	1.43
2	C	1	XYP	C1-C2	2.92	1.58	1.52
2	C	1	XYP	O5-C5	2.90	1.48	1.42
2	D	2	XYP	C2-C3	-2.75	1.48	1.52
2	C	2	XYP	C1-C2	2.73	1.58	1.52
2	C	1	XYP	O4-C4	-2.31	1.38	1.43
2	D	2	XYP	C5-C4	2.07	1.56	1.52
2	C	2	XYP	C2-C3	2.01	1.55	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	XYP	O4-C4-C3	-5.11	99.90	110.14
2	D	1	XYP	C5-O5-C1	4.34	118.20	111.52
2	D	2	XYP	C4-C3-C2	-4.21	105.92	110.92
2	C	1	XYP	O2-C2-C3	-4.00	102.13	110.14
2	C	1	XYP	C1-C2-C3	3.84	114.39	109.67
2	C	1	XYP	C5-C4-C3	3.61	114.11	109.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	XYP	C4-C3-C2	2.90	114.36	110.92
2	D	2	XYP	O2-C2-C3	-2.69	104.76	110.14
2	C	1	XYP	O3-C3-C4	-2.67	104.89	109.99
2	C	2	XYP	O3-C3-C2	2.58	114.93	109.99
2	D	1	XYP	O4-C4-C3	-2.54	105.05	110.14
2	D	1	XYP	C5-C4-C3	-2.37	106.76	109.67
2	C	2	XYP	C4-C3-C2	-2.16	108.36	110.92
2	D	2	XYP	O3-C3-C2	2.01	113.84	109.99

There are no chirality outliers.

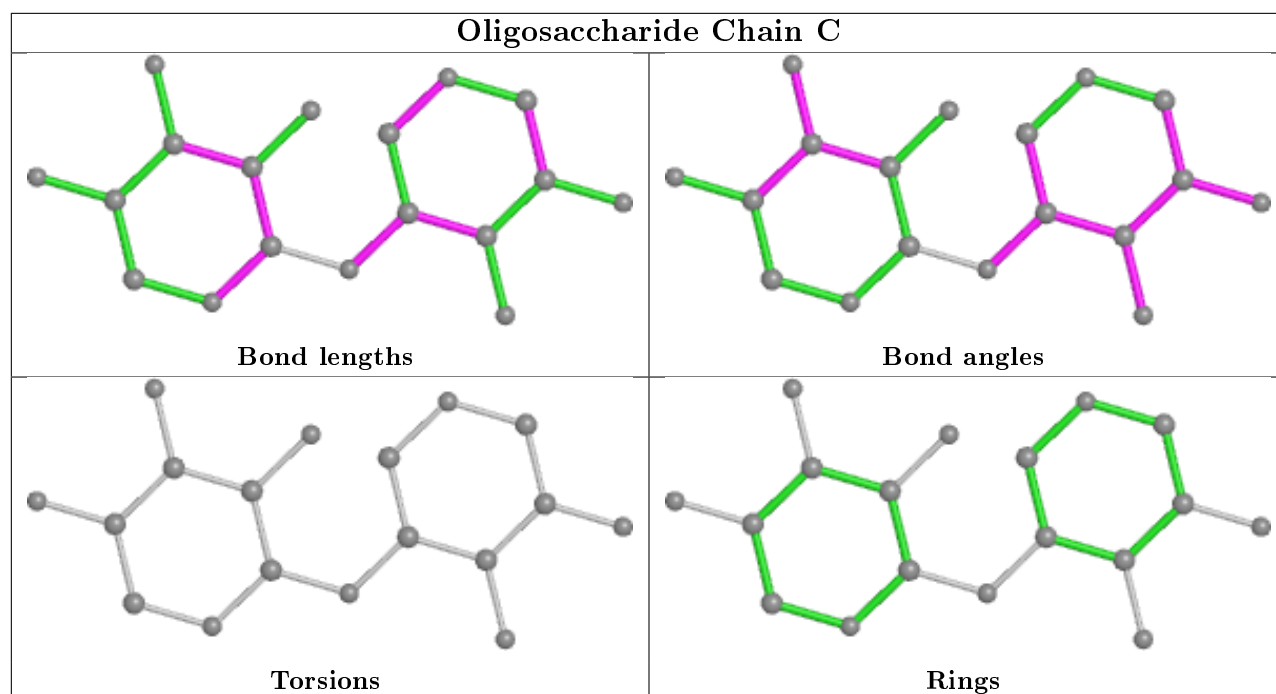
There are no torsion outliers.

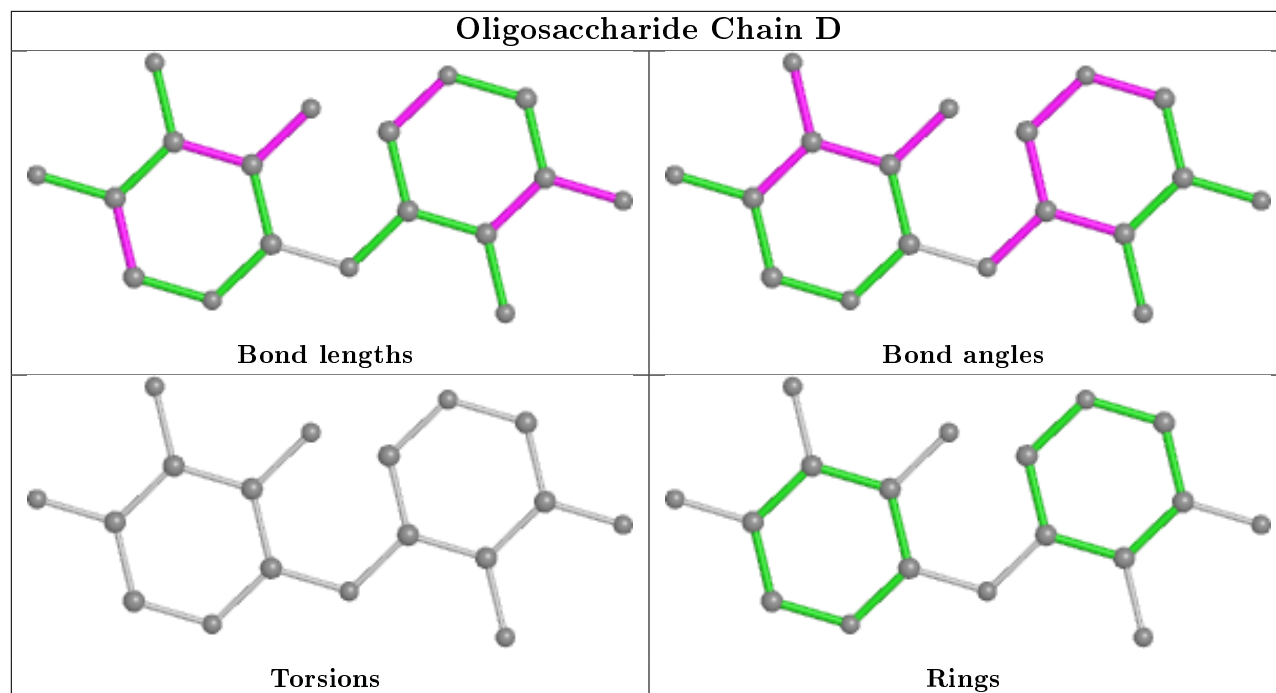
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	XYP	2	0
2	D	1	XYP	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 [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 ⓘ

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, 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	314/355 (88%)	-0.01	14 (4%) 33 36	33, 50, 70, 87	0
1	B	312/355 (87%)	0.16	19 (6%) 21 22	30, 58, 92, 112	0
All	All	626/710 (88%)	0.07	33 (5%) 26 28	30, 54, 85, 112	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	244	LEU	3.9
1	B	295	THR	3.6
1	A	129	VAL	3.3
1	A	242	THR	3.1
1	A	332	ASP	3.1
1	B	330	ASN	3.1
1	B	218	TYR	3.0
1	A	295	THR	3.0
1	B	268	TRP	3.0
1	A	296	PHE	3.0
1	A	130	VAL	2.9
1	B	307	GLY	2.8
1	B	309	ARG	2.8
1	B	241	LEU	2.8
1	B	296	PHE	2.8
1	A	244	LEU	2.7
1	B	265	VAL	2.6
1	B	308	VAL	2.5
1	B	294	VAL	2.4
1	B	40	THR	2.4
1	B	30	LYS	2.4
1	A	15	GLY	2.3
1	B	242	THR	2.3
1	B	249	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	9	LYS	2.3
1	A	294	VAL	2.3
1	A	16	VAL	2.3
1	B	26	PRO	2.2
1	A	142	GLY	2.2
1	B	306	LEU	2.1
1	A	178	TYR	2.0
1	A	98	ASN	2.0
1	A	81	LEU	2.0

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](#)

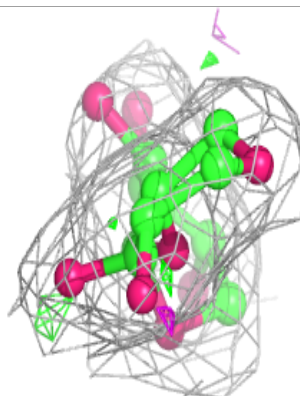
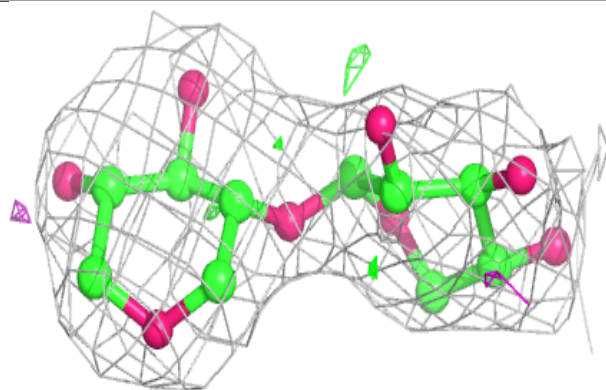
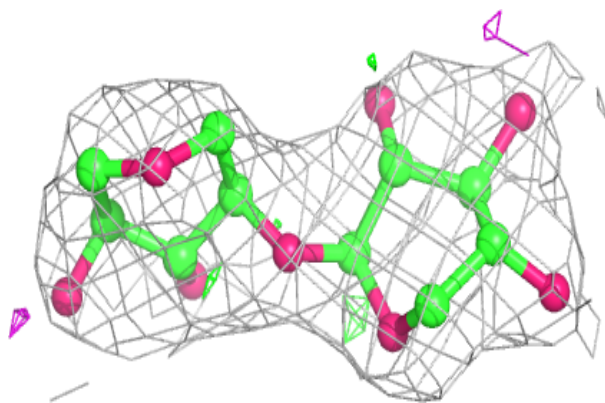
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	XYP	D	1	9/10	0.86	0.17	60,67,73,78	0
2	XYP	C	1	9/10	0.92	0.16	50,51,55,57	0
2	XYP	C	2	9/10	0.93	0.14	54,57,61,69	0
2	XYP	D	2	9/10	0.94	0.12	49,54,57,57	0

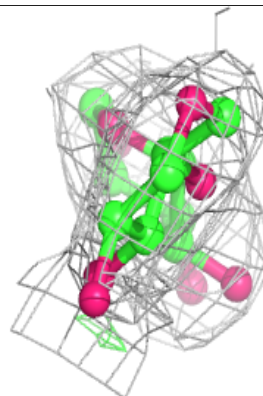
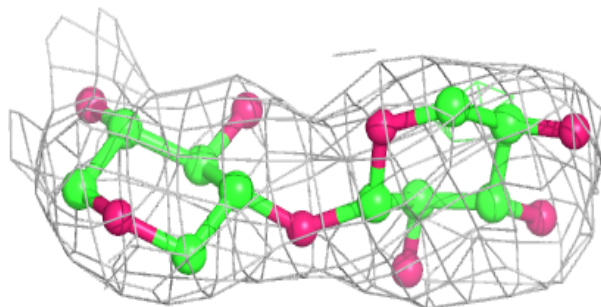
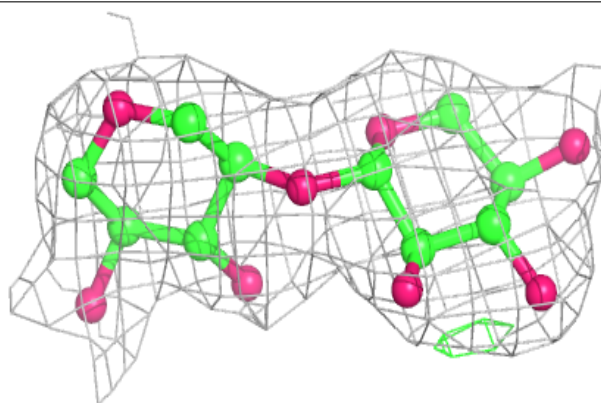
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.