



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 04:27 PM UTC

PDB ID : 6JE2 / pdb_00006je2
Title : Ligand complex structure of GH10 family xylanase XynAF1, soaking for 80 minutes
Authors : Li, G.; Miao, Y.; Zhang, R.
Deposited on : 2019-02-02
Resolution : 1.22 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

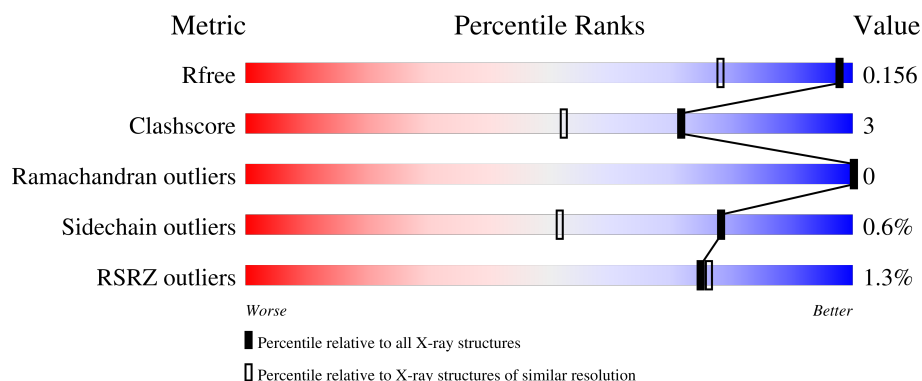
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.22 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}	180053	2002 (1.24-1.20)
Clashscore	190562	2061 (1.24-1.20)
Ramachandran outliers	187476	2009 (1.24-1.20)
Sidechain outliers	187428	2008 (1.24-1.20)
RSRZ outliers	180081	2000 (1.24-1.20)

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	319	% 91% 9%
1	B	319	2% 89% 10%
2	C	2	50% 50%
2	D	2	50% 50%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	

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
2	XYP	D	1	X	-	-	-
2	XYP	F	1	X	-	-	-
4	GOL	B	507	-	-	X	-
6	PEG	A	510	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5813 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 Beta-xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	13	0
			2505	1598	410	486	11			
1	B	319	Total	C	N	O	S	0	16	0
			2521	1608	412	490	11			

- 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
			19	10	9			
2	E	2	Total	C	O	0	0	0
			18	10	8			
2	F	2	Total	C	O	0	0	0
			19	10	9			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



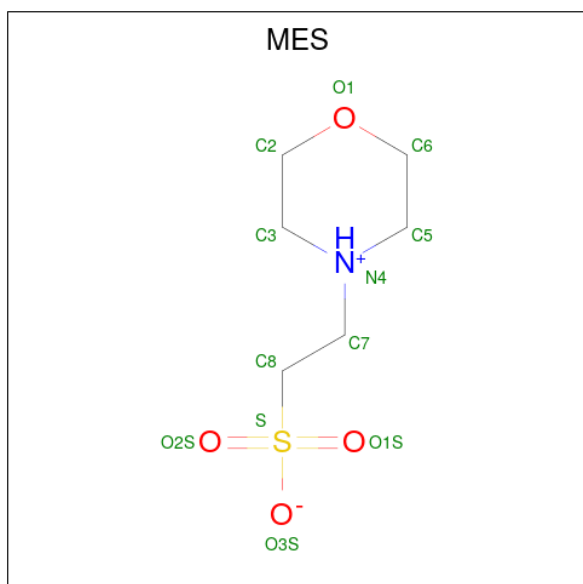
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	333	Total	O	0	0
			333	333		
7	B	297	Total	O	0	0
			297	297		

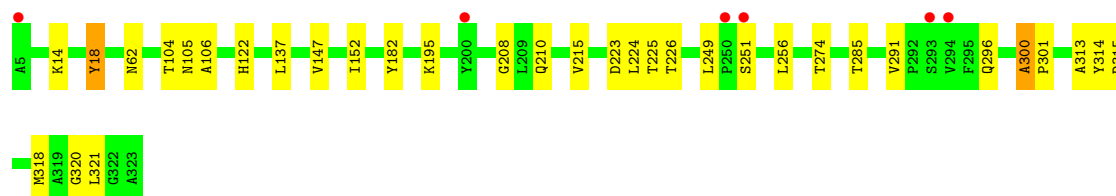
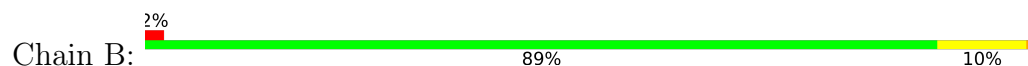
3 Residue-property plots [i](#)

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: Beta-xylanase



- Molecule 1: Beta-xylanase



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



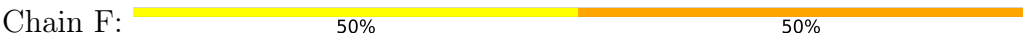
- Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	44.31Å 57.19Å 64.70Å 74.04° 80.74° 68.78°	Depositor
Resolution (Å)	62.07 – 1.22 62.06 – 1.22	Depositor EDS
% Data completeness (in resolution range)	91.7 (62.07-1.22) 91.9 (62.06-1.22)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 1.22Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.137 , 0.155 0.138 , 0.156	Depositor DCC
R_{free} test set	7747 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	8.4	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5813	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.46% 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: PEG, MES, XYP, GOL, NAG

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	1.59	14/2589 (0.5%)	1.23	4/3532 (0.1%)
1	B	1.66	18/2611 (0.7%)	1.32	10/3564 (0.3%)
All	All	1.63	32/5200 (0.6%)	1.27	14/7096 (0.2%)

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	B	0	1

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	106	ALA	N-CA	-9.40	1.35	1.46
1	A	300	ALA	N-CA	-7.62	1.41	1.46
1	B	105	ASN	C-O	6.69	1.31	1.24
1	A	14	LYS	CA-CB	-6.44	1.42	1.53
1	B	300	ALA	C-N	6.25	1.38	1.33
1	B	18	TYR	CA-C	-6.12	1.45	1.52
1	A	223	ASP	CG-OD2	-6.07	1.13	1.25
1	B	321	LEU	N-CA	-5.97	1.38	1.46
1	B	296	GLN	C-O	-5.96	1.16	1.23
1	A	169	PRO	C-N	-5.96	1.25	1.33
1	A	150	GLN	C-O	5.95	1.31	1.24
1	A	168	ASP	CA-C	-5.81	1.43	1.52
1	B	256	LEU	N-CA	-5.67	1.39	1.46
1	B	320	GLY	CA-C	-5.60	1.45	1.51
1	A	143	PHE	CA-C	-5.50	1.45	1.52
1	B	314	TYR	CA-C	5.45	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	114	ASN	CG-ND2	-5.42	1.21	1.33
1	B	147	VAL	CA-CB	5.37	1.61	1.54
1	B	223	ASP	CB-CG	5.36	1.65	1.52
1	B	251	SER	CA-C	5.26	1.59	1.52
1	A	176	ASN	N-CA	5.24	1.52	1.46
1	A	245	ILE	CA-CB	-5.20	1.48	1.53
1	A	310	LYS	C-O	5.18	1.29	1.23
1	A	103	TRP	C-O	5.14	1.30	1.23
1	B	315	ASP	C-O	5.13	1.30	1.24
1	B	137	LEU	CA-C	-5.13	1.46	1.52
1	B	274	THR	N-CA	-5.11	1.39	1.46
1	A	9	THR	CB-OG1	-5.11	1.35	1.43
1	A	288	TYR	N-CA	-5.09	1.39	1.46
1	B	122	HIS	CB-CG	-5.07	1.43	1.50
1	B	152	ILE	C-N	-5.01	1.26	1.33
1	B	300	ALA	N-CA	-5.00	1.43	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	215	VAL	O-C-N	7.03	129.84	122.67
1	B	291	VAL	O-C-N	6.86	124.81	120.42
1	B	249	LEU	CA-C-O	-6.14	114.31	120.64
1	A	291	VAL	O-C-N	6.13	124.34	120.42
1	B	208	GLY	O-C-N	5.89	127.06	123.35
1	B	318	MET	O-C-N	5.87	128.34	122.12
1	B	291	VAL	CA-C-O	-5.70	114.87	118.69
1	A	86	HIS	CA-C-N	5.50	131.59	121.70
1	A	86	HIS	C-N-CA	5.50	131.59	121.70
1	B	105	ASN	O-C-N	-5.33	116.55	122.09
1	B	300	ALA	O-C-N	-5.33	119.08	121.53
1	A	84	ARG	NE-CZ-NH1	5.24	126.74	121.50
1	B	313	ALA	N-CA-C	5.23	117.73	111.71
1	B	104	THR	CA-CB-OG1	5.20	117.40	109.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	18	TYR	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	2505	0	2425	11	0
1	B	2521	0	2444	11	0
2	C	18	0	0	1	0
2	D	19	0	0	3	0
2	E	18	0	0	3	0
2	F	19	0	0	5	0
3	A	14	0	12	0	0
3	B	14	0	13	0	0
4	A	18	0	24	2	0
4	B	18	0	24	4	0
5	A	12	0	12	1	0
6	A	7	0	10	4	0
7	A	333	0	0	5	2
7	B	297	0	0	12	1
All	All	5813	0	4964	34	2

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 3.

All (34) 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)
7:B:601:HOH:O	2:F:2:XYP:C3	1.96	1.14
7:A:601:HOH:O	2:D:2:XYP:C3	2.09	0.99
2:E:1:XYP:O5	2:F:2:XYP:O4	1.81	0.96
4:B:507:GOL:C1	7:B:603:HOH:O	2.20	0.88
1:B:225[B]:THR:CA	1:B:226:THR:N	2.43	0.82
1:B:62[B]:ASN:OD1	7:B:602:HOH:O	2.00	0.80
1:A:113:LYS:HZ2	6:A:510:PEG:H31	1.45	0.79
7:B:601:HOH:O	2:F:2:XYP:O3	1.95	0.79
1:A:64:PHE:C	1:A:65[C]:SER:CA	2.56	0.78
2:C:1:XYP:O5	2:D:2:XYP:O4	2.01	0.78
4:B:507:GOL:C2	7:B:603:HOH:O	2.33	0.77
1:B:224:LEU:C	1:B:225[B]:THR:CA	2.58	0.75
1:A:65[C]:SER:CA	1:A:66:PHE:N	2.49	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:601:HOH:O	2:D:2:XYP:O3	2.01	0.74
1:B:210:GLN:OE1	7:B:604:HOH:O	2.08	0.71
1:B:62[B]:ASN:CG	7:B:602:HOH:O	2.35	0.68
2:E:1:XYP:C1	2:F:2:XYP:O4	2.42	0.68
5:A:509:MES:H21	7:A:895:HOH:O	1.94	0.67
1:B:225[B]:THR:HG21	7:B:737:HOH:O	1.97	0.65
4:B:507:GOL:H2	7:B:603:HOH:O	1.95	0.65
1:A:113:LYS:HZ2	6:A:510:PEG:H12	1.63	0.64
1:A:113:LYS:NZ	6:A:510:PEG:H31	2.15	0.61
1:A:124:LYS:NZ	7:A:603:HOH:O	2.33	0.60
1:B:62[B]:ASN:ND2	7:B:602:HOH:O	2.32	0.60
1:A:191:GLN:HE22	4:A:507:GOL:H31	1.68	0.59
1:B:182:TYR:HB2	4:B:507:GOL:H32	1.86	0.58
2:E:1:XYP:O5	2:F:2:XYP:C4	2.57	0.52
1:B:195:LYS:NZ	7:B:606:HOH:O	2.36	0.50
1:A:100:SER:O	7:A:602:HOH:O	2.19	0.49
1:B:14:LYS:NZ	7:B:608:HOH:O	2.46	0.48
1:B:300:ALA:N	1:B:301:PRO:HD3	2.31	0.46
1:A:159:ILE:HG23	6:A:510:PEG:H32	1.97	0.45
1:A:282:TRP:CD1	4:A:506:GOL:H12	2.53	0.44
1:A:300:ALA:N	1:A:301:PRO:HD3	2.36	0.40

All (2) 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)
7:A:880:HOH:O	7:A:895:HOH:O[1_655]	1.71	0.49
7:A:820:HOH:O	7:B:688:HOH:O[1_654]	2.10	0.10

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	331/319 (104%)	327 (99%)	4 (1%)	0	100	100
1	B	334/319 (105%)	329 (98%)	5 (2%)	0	100	100
All	All	665/638 (104%)	656 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	265/251 (106%)	262 (99%)	3 (1%)	65	32
1	B	268/251 (107%)	267 (100%)	1 (0%)	84	63
All	All	533/502 (106%)	529 (99%)	4 (1%)	78	44

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75[A]	LEU
1	A	75[B]	LEU
1	A	285	THR
1	B	285	THR

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	62	ASN
1	A	118	ASN
1	A	191	GLN
1	B	96	ASN
1	B	114	ASN
1	B	118	ASN
1	B	259	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 ⓘ

8 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	1.49	1 (11%)	10,12,14	2.00	4 (40%)
2	XYP	C	2	2	9,9,10	0.96	1 (11%)	10,12,14	1.30	0
2	XYP	D	1	2	10,10,10	0.89	0	14,14,14	3.59	9 (64%)
2	XYP	D	2	2	9,9,10	2.00	3 (33%)	10,12,14	2.79	6 (60%)
2	XYP	E	1	2	9,9,10	2.29	1 (11%)	10,12,14	3.74	5 (50%)
2	XYP	E	2	2	9,9,10	1.38	0	10,12,14	2.10	5 (50%)
2	XYP	F	1	2	10,10,10	1.04	0	14,14,14	3.08	8 (57%)
2	XYP	F	2	2	9,9,10	1.21	1 (11%)	10,12,14	1.66	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	1/1/4/4	-	0/1/1/1
2	XYP	D	2	2	-	-	0/1/1/1
2	XYP	E	1	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	XYP	E	2	2	-	-	0/1/1/1
2	XYP	F	1	2	1/1/4/4	-	0/1/1/1
2	XYP	F	2	2	-	-	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	XYP	O5-C1	6.23	1.54	1.43
2	D	2	XYP	O5-C5	4.39	1.51	1.43
2	F	2	XYP	O5-C1	-3.01	1.37	1.43
2	C	1	XYP	O5-C1	2.90	1.48	1.43
2	D	2	XYP	C5-C4	2.64	1.58	1.52
2	C	2	XYP	C4-C3	-2.09	1.49	1.52
2	D	2	XYP	C2-C3	-2.02	1.49	1.52

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	XYP	C5-C4-C3	8.74	122.37	109.64
2	D	1	XYP	C5-O5-C1	-6.45	99.05	112.46
2	F	1	XYP	C5-C4-C3	6.01	118.40	109.64
2	D	1	XYP	C4-C3-C2	-5.86	100.55	110.86
2	D	1	XYP	C5-C4-C3	5.73	117.99	109.64
2	D	2	XYP	C5-C4-C3	5.44	117.57	109.64
2	F	1	XYP	C1-C2-C3	-5.09	99.97	110.36
2	F	1	XYP	O1-C1-O5	5.09	122.96	109.91
2	E	1	XYP	O4-C4-C5	5.05	120.79	109.22
2	E	1	XYP	O2-C2-C1	4.57	119.69	109.22
2	E	2	XYP	C4-C3-C2	-3.82	106.38	110.92
2	C	1	XYP	O4-C4-C5	3.69	117.68	109.22
2	D	2	XYP	C4-C3-C2	-3.62	106.62	110.92
2	D	1	XYP	O5-C1-C2	3.60	120.44	109.94
2	D	1	XYP	O2-C2-C3	-3.55	102.02	110.38
2	D	2	XYP	C1-C2-C3	-3.54	104.49	109.64
2	F	1	XYP	O5-C1-C2	3.42	119.91	109.94
2	E	2	XYP	C5-O5-C1	-3.41	105.90	111.42
2	D	1	XYP	C1-C2-C3	-3.34	103.54	110.36
2	D	1	XYP	O1-C1-C2	3.19	118.25	108.98
2	E	1	XYP	O3-C3-C4	-3.18	103.56	110.05
2	D	1	XYP	O1-C1-O5	3.07	117.78	109.91
2	D	1	XYP	O2-C2-C1	-2.84	102.69	109.25
2	F	2	XYP	C4-C3-C2	-2.84	107.55	110.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	XYP	O4-C4-C5	2.80	115.63	109.22
2	C	1	XYP	C5-C4-C3	2.67	113.54	109.64
2	F	1	XYP	O1-C1-C2	2.62	116.57	108.98
2	F	2	XYP	O2-C2-C1	-2.56	103.35	109.22
2	C	1	XYP	O3-C3-C4	-2.56	104.84	110.05
2	E	2	XYP	O3-C3-C4	2.50	115.16	110.05
2	F	1	XYP	O4-C4-C3	-2.47	105.05	110.15
2	E	2	XYP	O2-C2-C1	-2.42	103.68	109.22
2	D	2	XYP	O3-C3-C4	2.38	114.91	110.05
2	F	1	XYP	C4-C3-C2	-2.37	106.70	110.86
2	F	1	XYP	O5-C5-C4	-2.28	105.35	110.79
2	E	2	XYP	O4-C4-C3	-2.17	105.65	110.15
2	E	1	XYP	O3-C3-C2	-2.11	105.75	110.05
2	F	2	XYP	C5-O5-C1	2.07	114.76	111.42
2	D	2	XYP	O2-C2-C1	-2.01	104.63	109.22
2	C	1	XYP	O2-C2-C1	2.00	113.80	109.22

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	1	XYP	C1
2	F	1	XYP	C1

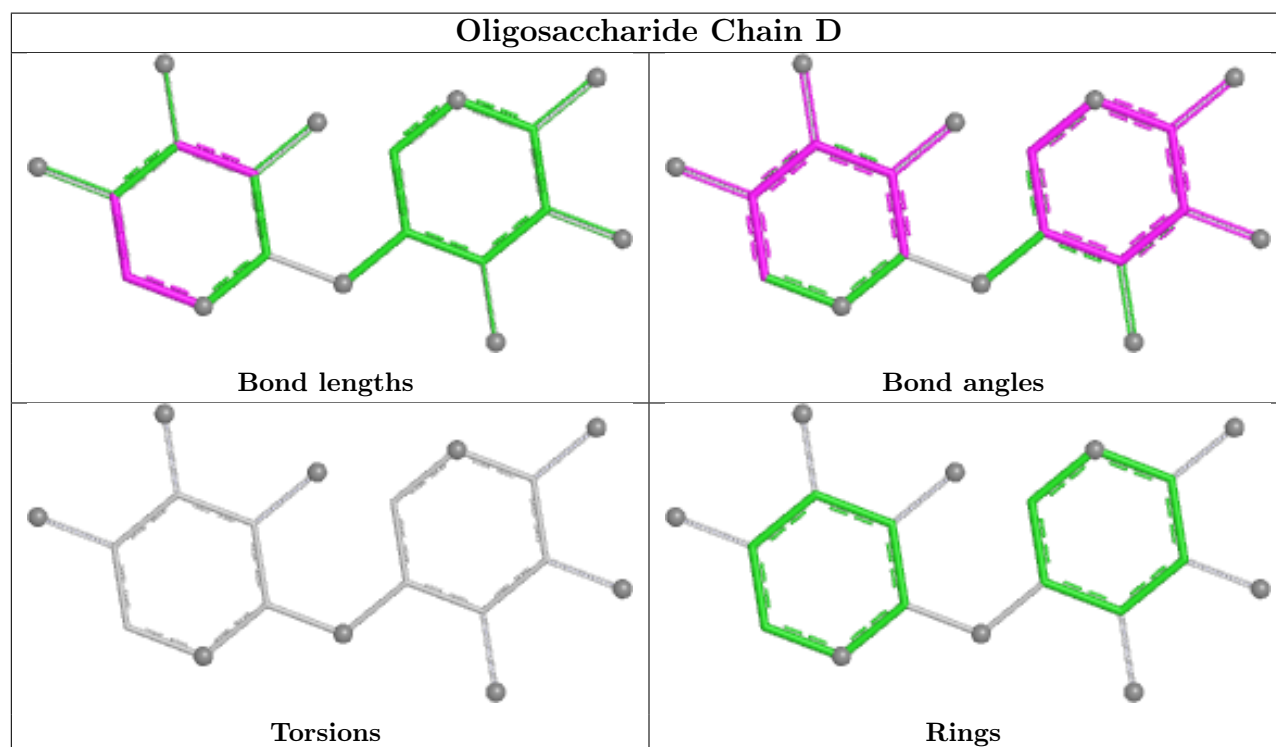
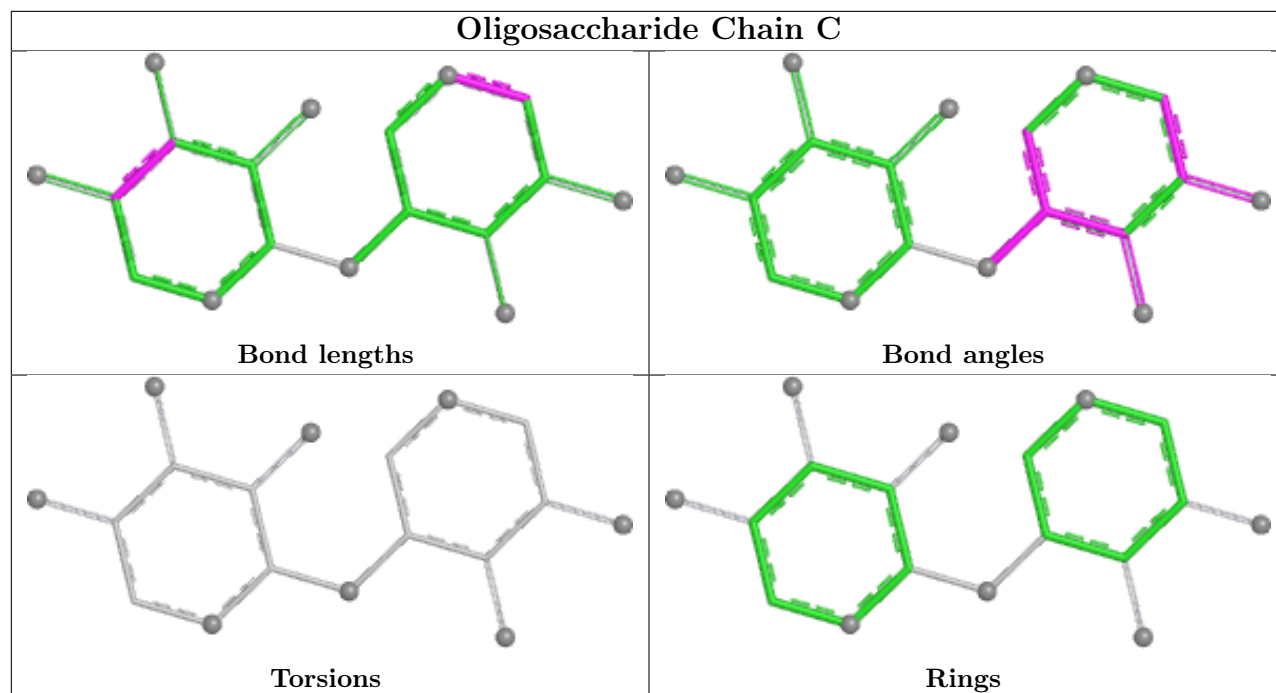
There are no torsion outliers.

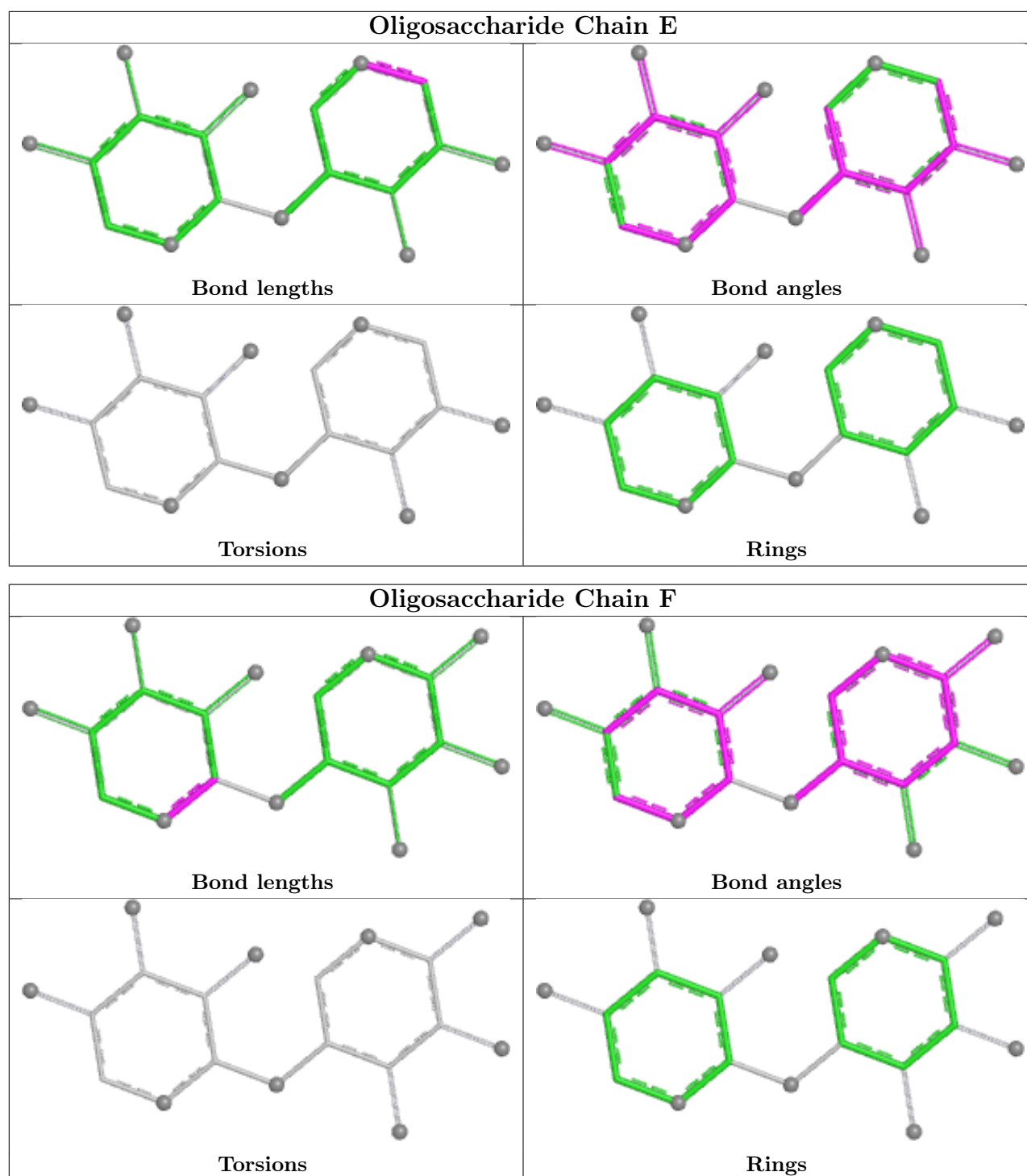
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	XYP	5	0
2	C	1	XYP	1	0
2	D	2	XYP	3	0
2	E	1	XYP	3	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](#)

10 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	GOL	B	507	-	5,5,5	1.31	1 (20%)	5,5,5	1.97	2 (40%)
4	GOL	B	508	-	5,5,5	0.29	0	5,5,5	1.03	0
4	GOL	A	508	-	5,5,5	1.08	1 (20%)	5,5,5	3.52	3 (60%)
6	PEG	A	510	-	6,6,6	0.60	0	5,5,5	1.96	1 (20%)
5	MES	A	509	-	12,12,12	1.23	2 (16%)	15,16,16	3.06	7 (46%)
3	NAG	A	505	1	14,14,15	3.02	6 (42%)	17,19,21	4.06	11 (64%)
4	GOL	A	507	-	5,5,5	0.50	0	5,5,5	0.81	0
4	GOL	B	506	-	5,5,5	0.46	0	5,5,5	2.16	3 (60%)
4	GOL	A	506	-	5,5,5	0.69	0	5,5,5	2.05	2 (40%)
3	NAG	B	505	1	14,14,15	2.42	5 (35%)	17,19,21	3.11	10 (58%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	507	-	-	0/4/4/4	-
4	GOL	B	508	-	-	4/4/4/4	-
4	GOL	A	508	-	-	0/4/4/4	-
6	PEG	A	510	-	-	3/4/4/4	-
5	MES	A	509	-	-	1/6/14/14	0/1/1/1
3	NAG	A	505	1	-	0/6/23/26	0/1/1/1
4	GOL	A	507	-	-	2/4/4/4	-
4	GOL	B	506	-	-	0/4/4/4	-
4	GOL	A	506	-	-	0/4/4/4	-
3	NAG	B	505	1	-	0/6/23/26	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	505	NAG	O5-C1	-8.18	1.30	1.43
3	B	505	NAG	O5-C1	-6.93	1.32	1.43
3	A	505	NAG	C1-C2	5.08	1.59	1.52
3	A	505	NAG	C2-N2	-3.03	1.41	1.46
4	B	507	GOL	O2-C2	2.79	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	505	NAG	O3-C3	2.79	1.49	1.43
3	B	505	NAG	C1-C2	2.78	1.56	1.52
3	A	505	NAG	O5-C5	2.59	1.48	1.43
5	A	509	MES	C8-S	-2.51	1.74	1.77
3	A	505	NAG	C7-N2	-2.44	1.26	1.34
3	B	505	NAG	O4-C4	2.24	1.48	1.43
3	B	505	NAG	O5-C5	2.14	1.47	1.43
3	A	505	NAG	C8-C7	-2.12	1.46	1.50
5	A	509	MES	O2S-S	2.05	1.50	1.45
4	A	508	GOL	O2-C2	2.04	1.49	1.43

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	505	NAG	C2-N2-C7	8.68	134.53	122.90
3	A	505	NAG	C8-C7-N2	8.33	129.94	116.12
5	A	509	MES	O3S-S-C8	6.14	118.02	106.00
3	B	505	NAG	C2-N2-C7	6.14	131.12	122.90
3	B	505	NAG	O7-C7-N2	-5.88	111.60	121.98
3	A	505	NAG	C1-O5-C5	5.58	119.67	112.19
3	A	505	NAG	O7-C7-N2	-5.57	112.14	121.98
4	A	508	GOL	O2-C2-C1	5.48	131.86	109.18
5	A	509	MES	C5-N4-C3	5.01	119.63	108.84
4	A	508	GOL	C3-C2-C1	-4.88	93.90	111.80
5	A	509	MES	O1S-S-C8	-4.63	99.73	106.73
3	A	505	NAG	C1-C2-N2	4.59	117.67	110.43
3	B	505	NAG	C1-C2-N2	4.29	117.20	110.43
5	A	509	MES	O3S-S-O1S	-4.00	101.39	111.40
3	B	505	NAG	C4-C3-C2	3.99	116.87	111.02
4	B	507	GOL	O2-C2-C3	3.89	125.30	109.18
5	A	509	MES	C7-N4-C3	3.85	121.50	111.24
6	A	510	PEG	O2-C3-C4	3.73	126.56	110.11
3	B	505	NAG	C8-C7-N2	3.60	122.08	116.12
3	A	505	NAG	C3-C4-C5	3.51	116.60	110.23
4	A	506	GOL	O2-C2-C1	-3.30	95.53	109.18
5	A	509	MES	O1-C6-C5	-3.22	104.83	111.77
3	B	505	NAG	O5-C1-C2	3.08	116.05	111.29
4	B	506	GOL	O2-C2-C3	3.06	121.86	109.18
3	A	505	NAG	O5-C5-C6	-3.01	101.80	107.66
3	B	505	NAG	O6-C6-C5	-2.81	101.78	111.33
4	A	508	GOL	O1-C1-C2	2.73	122.68	110.38
3	A	505	NAG	O6-C6-C5	-2.58	102.55	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	506	GOL	C3-C2-C1	-2.55	102.44	111.80
3	A	505	NAG	O7-C7-C8	-2.54	117.54	122.05
3	B	505	NAG	O3-C3-C4	2.43	116.10	110.38
4	B	506	GOL	O2-C2-C1	-2.42	99.15	109.18
3	B	505	NAG	O7-C7-C8	2.38	126.30	122.05
3	A	505	NAG	O5-C5-C4	-2.35	105.11	110.83
4	A	506	GOL	O1-C1-C2	2.15	120.03	110.38
3	B	505	NAG	O3-C3-C2	-2.14	104.96	109.40
3	A	505	NAG	O4-C4-C3	2.08	115.28	110.38
5	A	509	MES	O2S-S-C8	2.01	109.77	106.73
4	B	507	GOL	C3-C2-C1	-2.00	104.45	111.80

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	507	GOL	O2-C2-C3-O3
4	B	508	GOL	O1-C1-C2-C3
4	B	508	GOL	C1-C2-C3-O3
5	A	509	MES	C8-C7-N4-C3
4	B	508	GOL	O2-C2-C3-O3
4	A	507	GOL	C1-C2-C3-O3
6	A	510	PEG	O2-C3-C4-O4
4	B	508	GOL	O1-C1-C2-O2
6	A	510	PEG	O1-C1-C2-O2
6	A	510	PEG	C1-C2-O2-C3

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	507	GOL	4	0
6	A	510	PEG	4	0
5	A	509	MES	1	0
4	A	507	GOL	1	0
4	A	506	GOL	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 [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	319/319 (100%)	-0.40	2 (0%) 85 88	3, 7, 13, 31	13 (4%)
1	B	319/319 (100%)	-0.18	6 (1%) 66 67	4, 8, 15, 28	16 (5%)
All	All	638/638 (100%)	-0.29	8 (1%) 75 76	3, 8, 15, 31	29 (4%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	5	ALA	4.7
1	B	5	ALA	3.3
1	A	200[A]	TYR	2.9
1	B	251	SER	2.6
1	B	293	SER	2.5
1	B	200[A]	TYR	2.3
1	B	250	PRO	2.1
1	B	294	VAL	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 [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.

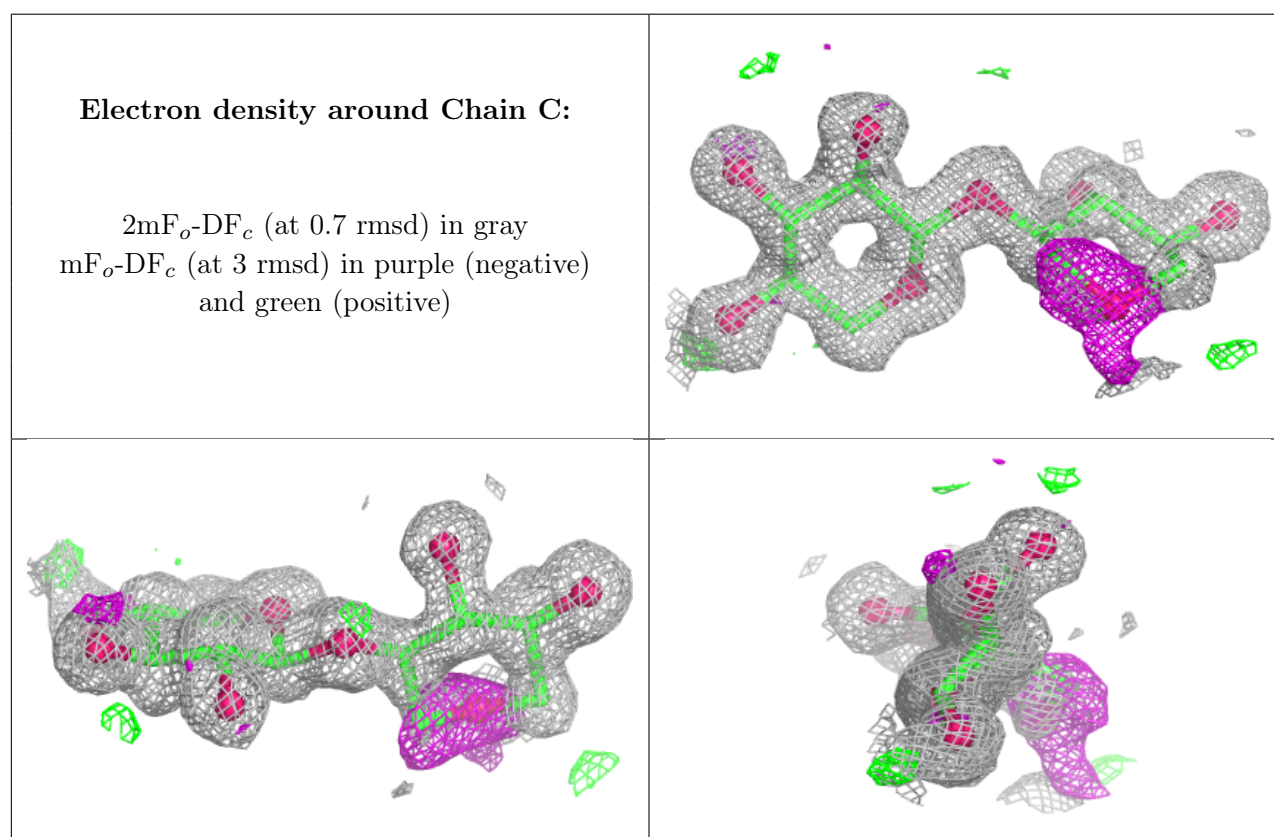
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	XYP	F	1	10/10	0.81	0.13	32,33,38,38	0

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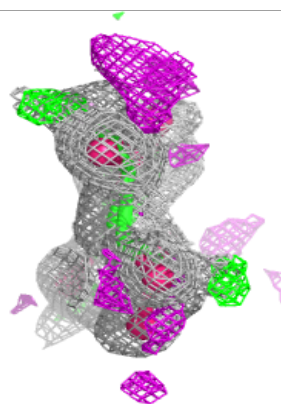
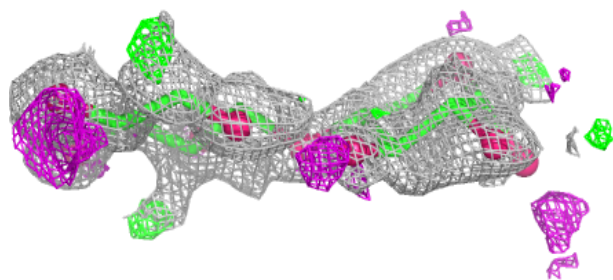
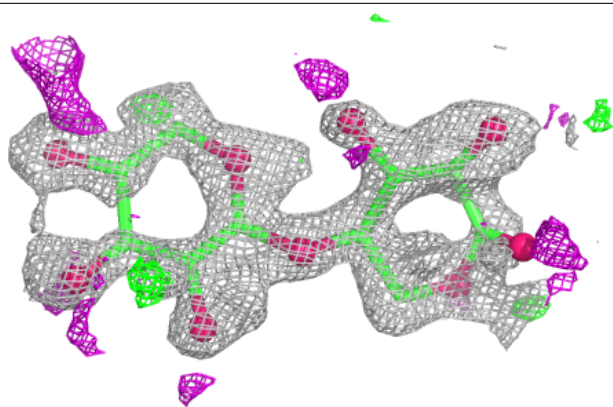
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	XYP	F	2	9/10	0.81	0.14	20,25,31,33	0
2	XYP	D	1	10/10	0.85	0.12	23,24,30,33	0
2	XYP	D	2	9/10	0.88	0.10	19,22,24,29	0
2	XYP	E	2	9/10	0.95	0.06	10,11,11,13	0
2	XYP	C	1	9/10	0.96	0.09	7,9,22,31	0
2	XYP	C	2	9/10	0.96	0.06	10,11,11,14	0
2	XYP	E	1	9/10	0.96	0.09	6,9,20,25	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.

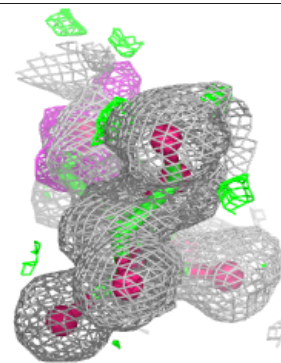
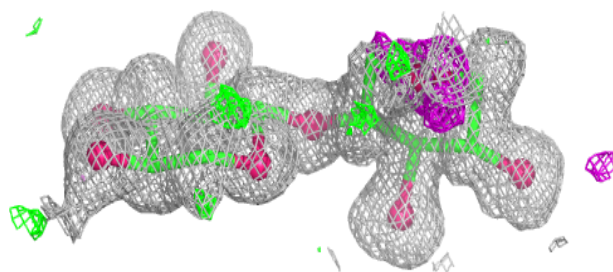
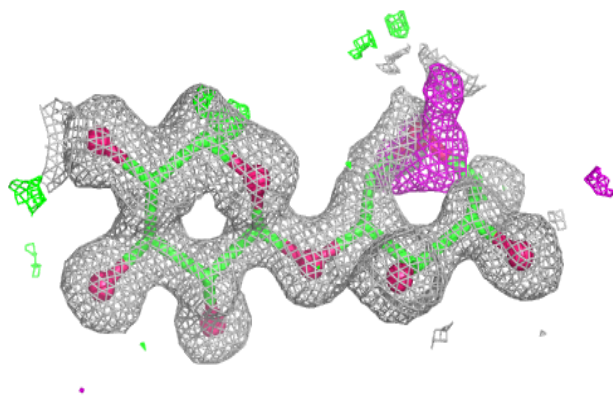


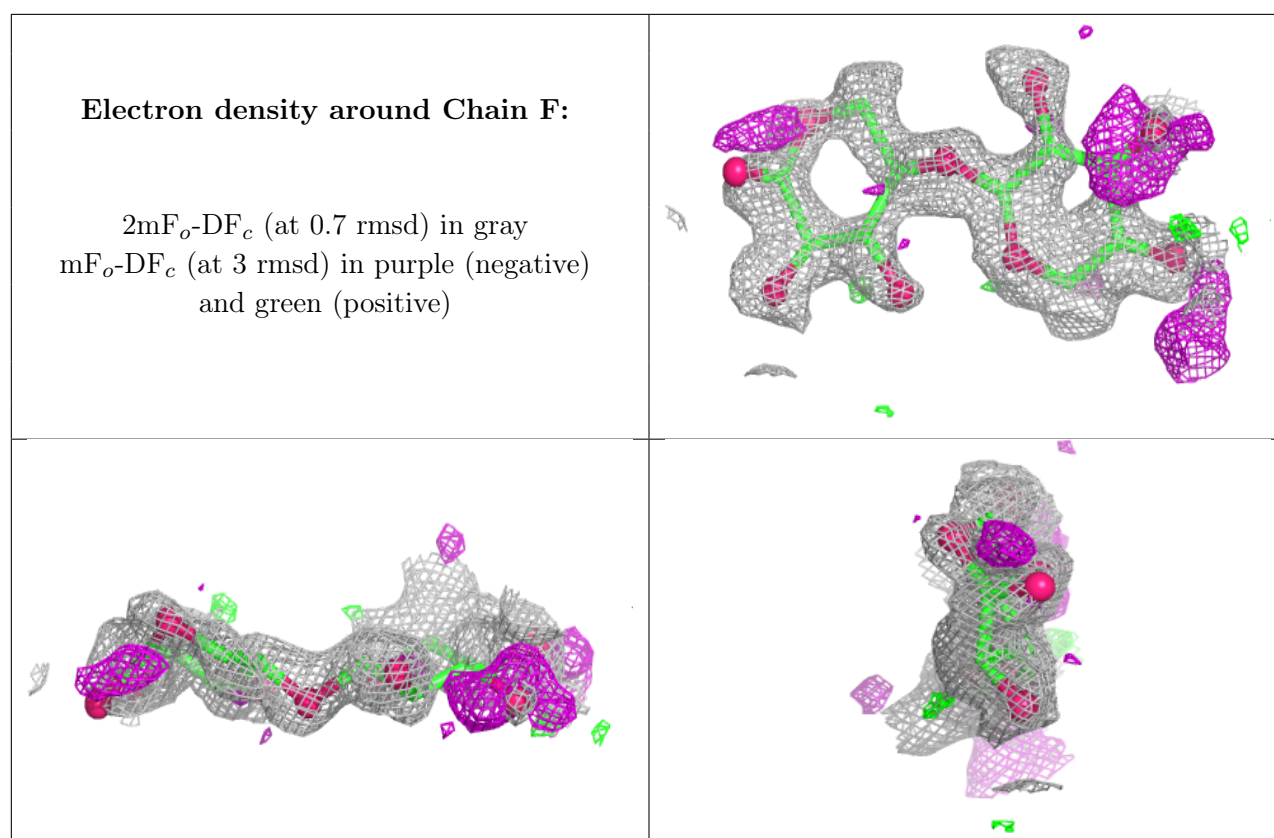
Electron density around Chain D:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Chain E:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
4	GOL	A	508	6/6	0.75	0.16	19,25,33,40	0
6	PEG	A	510	7/7	0.83	0.14	21,25,30,33	0
4	GOL	B	507	6/6	0.86	0.17	19,26,32,41	0
3	NAG	B	505	14/15	0.89	0.12	14,18,27,28	0
3	NAG	A	505	14/15	0.90	0.14	10,15,26,29	0
4	GOL	B	508	6/6	0.91	0.14	16,30,40,46	0
5	MES	A	509	12/12	0.92	0.11	14,18,20,20	0
4	GOL	B	506	6/6	0.93	0.09	13,19,20,20	0
4	GOL	A	507	6/6	0.94	0.12	9,23,27,39	0
4	GOL	A	506	6/6	0.95	0.09	11,19,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.