



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 4, 2024 – 12:32 AM JST

PDB ID : 6KJ0
Title : Bifunctional xylosidase/glucosidase LXYL mutant E529Q C2221
Authors : Gong, W.M.; Yang, L.Y.
Deposited on : 2019-07-20
Resolution : 2.27 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>.

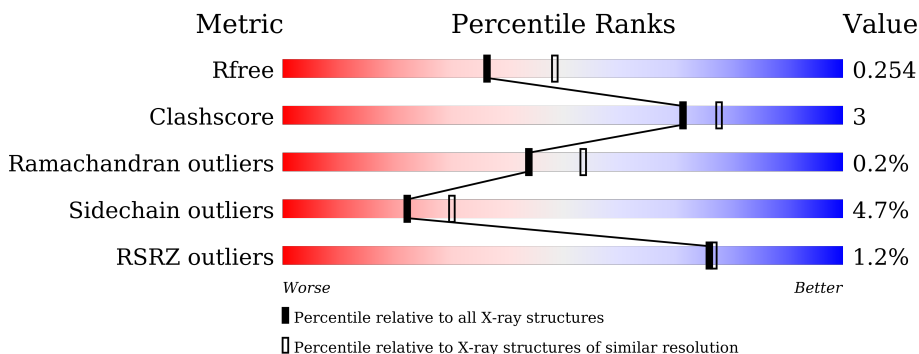
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
buster-report : 1.1.7 (2018)
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

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X-RAY DIFFRACTION

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.



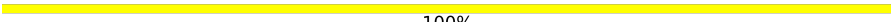
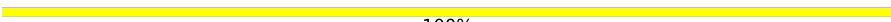
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	164625	8487 (2.30-2.26)
Clashscore	180529	9437 (2.30-2.26)
Ramachandran outliers	177936	9341 (2.30-2.26)
Sidechain outliers	177891	9342 (2.30-2.26)
RSRZ outliers	164620	8487 (2.30-2.26)

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	809	<div> <div></div> <div>82%</div> <div>9%</div> <div>7%</div> </div>
1	B	809	<div> <div></div> <div>84%</div> <div>8%</div> <div>7%</div> </div>
2	C	3	<div> <div></div> <div>100%</div> </div>
2	F	3	<div> <div></div> <div>67%</div> <div>33%</div> </div>
3	D	7	<div> <div></div> <div>100%</div> </div>
3	G	7	<div> <div></div> <div>86%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
4	E	4	 100%
4	H	4	 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12707 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-D-xylosidase/beta-D-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	756	Total	C	N	O	S	0	0	0
			5713	3618	957	1121	17			
1	B	756	Total	C	N	O	S	0	2	0
			5720	3622	959	1122	17			

There are 14 discrepancies between the modelled and reference sequences:

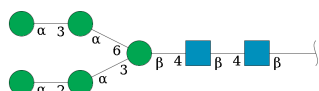
Chain	Residue	Modelled	Actual	Comment	Reference
A	529	GLN	GLU	engineered mutation	UNP G8GLP2
A	804	HIS	-	expression tag	UNP G8GLP2
A	805	HIS	-	expression tag	UNP G8GLP2
A	806	HIS	-	expression tag	UNP G8GLP2
A	807	HIS	-	expression tag	UNP G8GLP2
A	808	HIS	-	expression tag	UNP G8GLP2
A	809	HIS	-	expression tag	UNP G8GLP2
B	529	GLN	GLU	engineered mutation	UNP G8GLP2
B	804	HIS	-	expression tag	UNP G8GLP2
B	805	HIS	-	expression tag	UNP G8GLP2
B	806	HIS	-	expression tag	UNP G8GLP2
B	807	HIS	-	expression tag	UNP G8GLP2
B	808	HIS	-	expression tag	UNP G8GLP2
B	809	HIS	-	expression tag	UNP G8GLP2

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	7	Total	C	N	O	0	0	0
			83	46	2	35			
3	G	7	Total	C	N	O	0	0	0
			83	46	2	35			

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



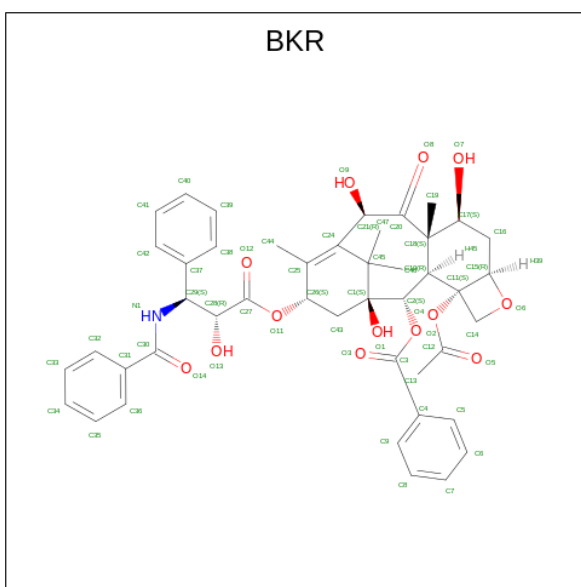
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	4	Total	C	N	O	0	0	0
			50	28	2	20			
4	H	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



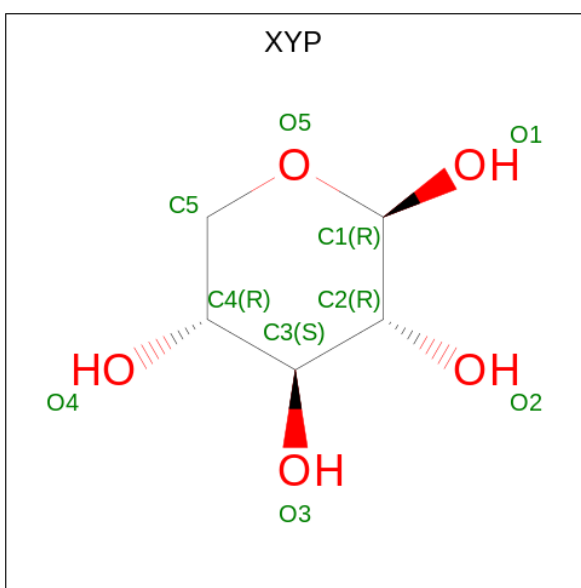
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is Deacetyltaxol (three-letter code: BKR) (formula: $C_{45}H_{49}NO_{13}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total 59	C 45	N 1	O 13	0	0
6	B	1	Total 59	C 45	N 1	O 13	0	0

- Molecule 7 is beta-D-xylopyranose (three-letter code: XYP) (formula: $C_5H_{10}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 10	C 5	O 5	0	0
7	B	1	Total 10	C 5	O 5	0	0

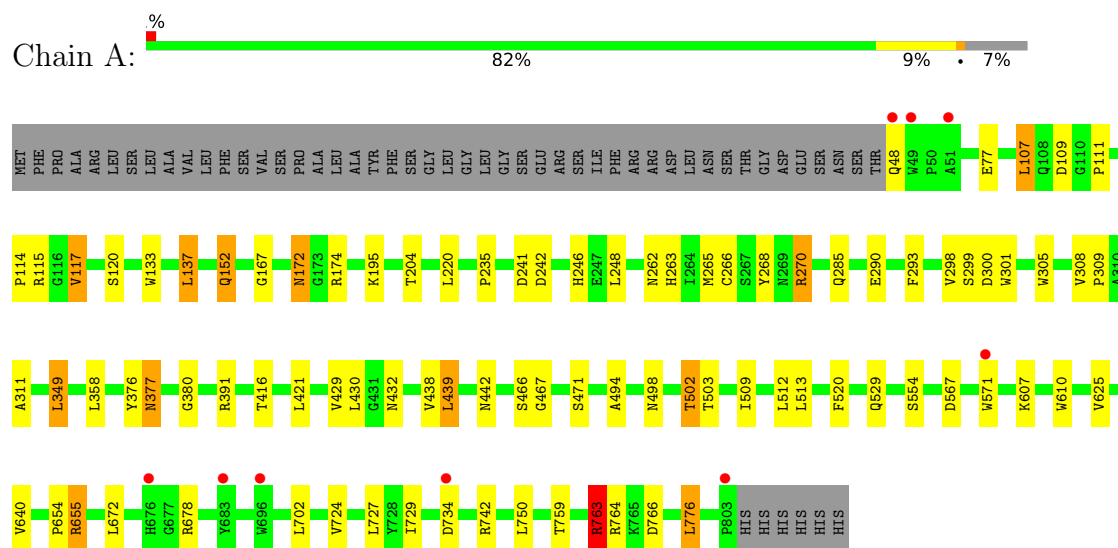
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	343	Total 343	O 343	0	0
8	B	337	Total 337	O 337	0	0

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-D-xylosidase/beta-D-glucosidase



Chain C:  100%

MAG1
MAG2
MAN3

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

Chain F:  67% 33%


MAG1
MAG2
MAN3

- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7

- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  86% 14%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7

- Molecule 4: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1
MAG2
BMA3
MAN4

- Molecule 4: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%

MAG1
MAG2
BMA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	80.00Å 182.23Å 241.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	120.76 – 2.27 120.76 – 2.27	Depositor EDS
% Data completeness (in resolution range)	93.1 (120.76-2.27) 93.2 (120.76-2.27)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.91 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.192 , 0.252 0.203 , 0.254	Depositor DCC
R_{free} test set	4078 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 23.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12707	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.33 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0776e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MAN, BMA, NAG, XYP, BKR

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	0.86	1/5854 (0.0%)	0.95	17/8009 (0.2%)
1	B	0.89	2/5860 (0.0%)	0.94	17/8018 (0.2%)
All	All	0.88	3/11714 (0.0%)	0.94	34/16027 (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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	133	TRP	CE3-CZ3	5.67	1.48	1.38
1	B	400	GLU	CG-CD	5.62	1.60	1.51
1	B	777	TRP	CB-CG	5.36	1.59	1.50

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	763	ARG	NE-CZ-NH1	9.42	125.01	120.30
1	A	270	ARG	NE-CZ-NH1	8.96	124.78	120.30
1	A	391	ARG	NE-CZ-NH1	8.89	124.75	120.30
1	B	270	ARG	NE-CZ-NH1	8.38	124.49	120.30
1	B	391	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	B	135	ARG	NE-CZ-NH1	8.20	124.40	120.30
1	A	655	ARG	NE-CZ-NH2	-8.12	116.24	120.30
1	B	391	ARG	NE-CZ-NH2	-8.11	116.24	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	763	ARG	NE-CZ-NH2	-7.53	116.54	120.30
1	B	742	ARG	NE-CZ-NH2	-7.48	116.56	120.30
1	B	763	ARG	NE-CZ-NH1	7.39	124.00	120.30
1	A	270	ARG	NE-CZ-NH2	-7.31	116.65	120.30
1	B	270	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	A	655	ARG	NE-CZ-NH1	6.87	123.74	120.30
1	B	742	ARG	NE-CZ-NH1	6.87	123.74	120.30
1	B	763	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	A	391	ARG	NE-CZ-NH2	-6.39	117.10	120.30
1	B	602	VAL	CB-CA-C	-6.11	99.79	111.40
1	A	115	ARG	NE-CZ-NH1	6.01	123.31	120.30
1	B	704	ASP	CB-CG-OD1	5.93	123.63	118.30
1	A	115	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	B	129	VAL	CB-CA-C	-5.73	100.52	111.40
1	A	567	ASP	CB-CG-OD2	-5.52	113.34	118.30
1	A	776	LEU	CA-CB-CG	5.49	127.93	115.30
1	B	107	LEU	CA-CB-CG	5.38	127.68	115.30
1	A	567	ASP	CB-CG-OD1	5.26	123.03	118.30
1	A	764	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	B	776	LEU	CA-CB-CG	5.21	127.28	115.30
1	A	241	ASP	CB-CG-OD1	5.15	122.93	118.30
1	B	484	ARG	NE-CZ-NH1	-5.13	117.73	120.30
1	A	137	LEU	CB-CG-CD1	5.07	119.61	111.00
1	B	134	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	B	138	MET	CG-SD-CE	5.05	108.28	100.20
1	A	655	ARG	CG-CD-NE	-5.01	101.28	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	699	THR	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	5713	0	5506	39	0
1	B	5720	0	5515	36	0
2	C	39	0	34	0	0
2	F	39	0	34	1	0
3	D	83	0	70	0	0
3	G	83	0	70	1	0
4	E	50	0	43	0	0
4	H	50	0	43	0	0
5	A	56	0	52	0	0
5	B	56	0	52	0	0
6	A	59	0	0	0	0
6	B	59	0	0	0	0
7	A	10	0	0	1	0
7	B	10	0	0	0	0
8	A	343	0	0	5	0
8	B	337	0	0	2	0
All	All	12707	0	11419	76	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 3.

All (76) 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:502:THR:HG21	8:A:1260:HOH:O	1.80	0.81
1:B:246:HIS:HE1	1:B:290:GLU:OE2	1.68	0.77
1:A:421:LEU:HD11	1:A:520:PHE:HZ	1.53	0.72
1:B:421:LEU:HD11	1:B:520:PHE:HZ	1.54	0.72
1:B:55:ASN:H	1:B:294:GLN:HE22	1.38	0.72
1:B:438:VAL:HG23	1:B:439:LEU:HD13	1.72	0.69
1:B:55:ASN:H	1:B:294:GLN:NE2	1.95	0.65
1:B:442:ASN:HD21	1:B:471:SER:H	1.46	0.63
1:A:117:VAL:HG22	1:A:376:TYR:CD2	2.35	0.61
1:A:763:ARG:HD3	1:A:766:ASP:OD2	2.01	0.61
1:A:466:SER:OG	1:A:529:GLN:NE2	2.34	0.59
1:A:377:ASN:HD22	1:A:377:ASN:C	2.07	0.58
1:B:172:ASN:HD22	1:B:174:ARG:H	1.52	0.58
1:A:246:HIS:HE1	1:A:290:GLU:OE2	1.87	0.57
1:B:134:ASP:OD1	1:B:136:THR:OG1	2.18	0.57
1:A:172:ASN:HD22	1:A:174:ARG:H	1.53	0.57
1:A:513:LEU:HD13	8:A:1287:HOH:O	2.05	0.56
1:B:98:THR:CG2	2:F:1:NAG:O3	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:235:PRO:O	1:B:270:ARG:HD3	2.06	0.55
1:B:763:ARG:HD3	1:B:766:ASP:OD2	2.05	0.55
1:A:442:ASN:HD21	1:A:471:SER:H	1.56	0.53
1:A:242:ASP:O	1:A:246:HIS:HD2	1.92	0.53
1:B:724:VAL:HG22	1:B:746:LYS:HG3	1.91	0.53
1:A:498:ASN:O	1:A:502:THR:HG23	2.09	0.52
1:A:377:ASN:HD21	1:A:380:GLY:H	1.57	0.52
1:A:509:ILE:HA	8:A:1287:HOH:O	2.09	0.52
1:A:220:LEU:HB3	1:A:268:TYR:CE1	2.44	0.52
1:A:654:PRO:HA	8:A:1130:HOH:O	2.11	0.51
1:B:74:MET:HE1	1:B:358:LEU:HD11	1.91	0.51
1:B:391:ARG:HD3	8:B:1308:HOH:O	2.10	0.51
1:A:607:LYS:HD2	1:A:724:VAL:HB	1.94	0.50
1:B:197:LEU:O	1:B:202[A]:VAL:HG12	2.12	0.49
1:B:375:VAL:HG22	8:B:1176:HOH:O	2.11	0.49
1:A:466:SER:CB	1:A:529:GLN:HE22	2.26	0.48
1:A:311:ALA:O	1:A:349:LEU:HD11	2.13	0.48
1:A:727:LEU:C	1:A:727:LEU:HD23	2.34	0.48
1:A:265:MET:HA	1:A:298:VAL:O	2.13	0.48
1:B:354:ALA:HA	1:B:357:ILE:HD12	1.96	0.47
1:A:204:THR:H	1:A:262:ASN:HD22	1.62	0.47
1:B:701:SER:O	1:B:764:ARG:NH1	2.47	0.47
1:B:152:GLN:HE21	1:B:152:GLN:HA	1.80	0.47
1:B:246:HIS:CE1	1:B:290:GLU:OE2	2.59	0.46
1:A:172:ASN:HD22	1:A:174:ARG:N	2.14	0.46
1:A:172:ASN:ND2	1:A:174:ARG:H	2.12	0.46
1:B:725:ALA:O	1:B:744:PHE:HA	2.16	0.46
1:A:248:LEU:HD22	1:A:640:VAL:HA	1.98	0.45
1:A:152:GLN:HE21	1:A:152:GLN:HA	1.82	0.44
1:B:442:ASN:ND2	1:B:471:SER:H	2.15	0.44
1:B:204:THR:H	1:B:262:ASN:HD22	1.65	0.44
1:B:242:ASP:O	1:B:246:HIS:HD2	2.01	0.43
1:A:429:VAL:O	1:A:494:ALA:HA	2.18	0.43
1:B:524:ASN:C	1:B:524:ASN:HD22	2.22	0.43
1:A:235:PRO:O	1:A:270:ARG:HD3	2.18	0.43
3:G:1:NAG:H61	3:G:2:NAG:C7	2.48	0.43
1:A:300:ASP:OD1	7:A:920:XYP:C1	2.67	0.43
1:B:253:PHE:O	1:B:257:VAL:HG23	2.18	0.43
1:A:512:LEU:HB3	8:A:1287:HOH:O	2.19	0.42
1:B:202[A]:VAL:O	1:B:202[A]:VAL:HG13	2.18	0.42
1:A:109:ASP:O	1:A:114:PRO:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:HIS:HA	1:A:293:PHE:HZ	1.84	0.42
1:B:442:ASN:HD21	1:B:471:SER:N	2.14	0.41
1:A:438:VAL:HG23	1:A:439:LEU:HD13	2.02	0.41
1:B:112:ILE:HG22	1:B:125:ALA:HA	2.02	0.41
1:B:776:LEU:C	1:B:776:LEU:HD23	2.40	0.41
1:A:107:LEU:HD23	1:A:107:LEU:N	2.36	0.41
1:B:203:ALA:HB2	1:B:364:LEU:HD12	2.03	0.41
1:B:340:ILE:HD11	1:B:350:VAL:HG21	2.03	0.41
1:B:592:ASN:OD1	1:B:592:ASN:N	2.53	0.41
1:A:235:PRO:HD3	1:A:305:TRP:CZ2	2.55	0.41
1:A:111:PRO:HD2	1:A:467:GLY:HA2	2.03	0.41
1:A:266:CYS:SG	1:A:299:SER:HA	2.61	0.41
1:A:308:VAL:HB	1:A:309:PRO:HD3	2.03	0.41
1:A:729:ILE:HD12	1:A:742:ARG:HG3	2.03	0.41
1:B:111:PRO:HD2	1:B:467:GLY:HA2	2.03	0.41
1:B:377:ASN:C	1:B:377:ASN:HD22	2.24	0.41
1:B:715:ASN:HB2	1:B:750:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

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	754/809 (93%)	718 (95%)	35 (5%)	1 (0%)	48	59
1	B	756/809 (93%)	719 (95%)	35 (5%)	2 (0%)	37	45
All	All	1510/1618 (93%)	1437 (95%)	70 (5%)	3 (0%)	44	53

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	386	ALA

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Mol	Chain	Res	Type
1	B	167	GLY
1	A	167	GLY

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	609/654 (93%)	576 (95%)	33 (5%)	18	24
1	B	610/654 (93%)	586 (96%)	24 (4%)	27	39
All	All	1219/1308 (93%)	1162 (95%)	57 (5%)	22	30

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	77	GLU
1	A	107	LEU
1	A	117	VAL
1	A	120	SER
1	A	137	LEU
1	A	152	GLN
1	A	172	ASN
1	A	195	LYS
1	A	285	GLN
1	A	301	TRP
1	A	349	LEU
1	A	358	LEU
1	A	377	ASN
1	A	416	THR
1	A	430	LEU
1	A	432	ASN
1	A	439	LEU
1	A	502	THR
1	A	503	THR
1	A	554	SER

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Mol	Chain	Res	Type
1	A	571	TRP
1	A	610	TRP
1	A	625	VAL
1	A	655	ARG
1	A	672	LEU
1	A	678	ARG
1	A	702	LEU
1	A	734	ASP
1	A	750	LEU
1	A	759	THR
1	A	763	ARG
1	A	776	LEU
1	B	68	LYS
1	B	98	THR
1	B	107	LEU
1	B	128	THR
1	B	129	VAL
1	B	137	LEU
1	B	152	GLN
1	B	172	ASN
1	B	195	LYS
1	B	264	ILE
1	B	301	TRP
1	B	377	ASN
1	B	432	ASN
1	B	439	LEU
1	B	524	ASN
1	B	581	LEU
1	B	602	VAL
1	B	610	TRP
1	B	672	LEU
1	B	709	VAL
1	B	750	LEU
1	B	759	THR
1	B	763	ARG
1	B	776	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	A	172	ASN

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Mol	Chain	Res	Type
1	A	229	GLN
1	A	246	HIS
1	A	262	ASN
1	A	263	HIS
1	A	377	ASN
1	A	442	ASN
1	A	529	GLN
1	A	740	GLN
1	B	152	GLN
1	B	172	ASN
1	B	229	GLN
1	B	246	HIS
1	B	262	ASN
1	B	263	HIS
1	B	294	GLN
1	B	377	ASN
1	B	442	ASN
1	B	524	ASN
1	B	529	GLN
1	B	740	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 ⓘ

28 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	2,1	14,14,15	1.26	2 (14%)	17,19,21	1.95	5 (29%)
2	NAG	C	2	2	14,14,15	1.16	0	17,19,21	1.61	4 (23%)
2	MAN	C	3	2	11,11,12	0.98	0	15,15,17	3.18	5 (33%)
3	NAG	D	1	3,1	14,14,15	1.63	3 (21%)	17,19,21	2.98	7 (41%)
3	NAG	D	2	3	14,14,15	0.84	0	17,19,21	1.29	2 (11%)
3	BMA	D	3	3	11,11,12	0.86	0	15,15,17	2.35	3 (20%)
3	MAN	D	4	3	11,11,12	1.22	1 (9%)	15,15,17	2.30	4 (26%)
3	MAN	D	5	3	11,11,12	0.90	0	15,15,17	2.31	3 (20%)
3	MAN	D	6	3	11,11,12	0.78	0	15,15,17	1.28	1 (6%)
3	MAN	D	7	3	11,11,12	0.76	0	15,15,17	1.19	2 (13%)
4	NAG	E	1	1,4	14,14,15	0.60	0	17,19,21	1.91	4 (23%)
4	NAG	E	2	4	14,14,15	0.61	0	17,19,21	2.05	5 (29%)
4	BMA	E	3	4	11,11,12	0.98	0	15,15,17	2.44	6 (40%)
4	MAN	E	4	4	11,11,12	1.09	0	15,15,17	1.76	4 (26%)
2	NAG	F	1	2,1	14,14,15	1.34	2 (14%)	17,19,21	1.10	1 (5%)
2	NAG	F	2	2	14,14,15	0.98	0	17,19,21	1.53	3 (17%)
2	MAN	F	3	2	11,11,12	1.09	0	15,15,17	1.66	3 (20%)
3	NAG	G	1	3,1	14,14,15	1.28	2 (14%)	17,19,21	1.64	2 (11%)
3	NAG	G	2	3	14,14,15	0.63	0	17,19,21	1.10	0
3	BMA	G	3	3	11,11,12	0.54	0	15,15,17	0.94	1 (6%)
3	MAN	G	4	3	11,11,12	0.83	0	15,15,17	2.60	2 (13%)
3	MAN	G	5	3	11,11,12	1.31	1 (9%)	15,15,17	1.34	2 (13%)
3	MAN	G	6	3	11,11,12	0.91	1 (9%)	15,15,17	2.57	4 (26%)
3	MAN	G	7	3	11,11,12	0.65	0	15,15,17	0.94	1 (6%)
4	NAG	H	1	1,4	14,14,15	0.82	1 (7%)	17,19,21	1.24	3 (17%)
4	NAG	H	2	4	14,14,15	0.78	0	17,19,21	1.50	2 (11%)
4	BMA	H	3	4	11,11,12	1.03	1 (9%)	15,15,17	1.93	4 (26%)
4	MAN	H	4	4	11,11,12	0.84	0	15,15,17	2.12	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	MAN	C	3	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	1/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	-	2/2/19/22	0/1/1/1
3	MAN	D	5	3	-	0/2/19/22	0/1/1/1
3	MAN	D	6	3	-	0/2/19/22	0/1/1/1
3	MAN	D	7	3	-	0/2/19/22	0/1/1/1
4	NAG	E	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	BMA	E	3	4	-	2/2/19/22	0/1/1/1
4	MAN	E	4	4	-	2/2/19/22	0/1/1/1
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	1/6/23/26	0/1/1/1
2	MAN	F	3	2	-	2/2/19/22	0/1/1/1
3	NAG	G	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	MAN	G	4	3	-	0/2/19/22	0/1/1/1
3	MAN	G	5	3	-	0/2/19/22	0/1/1/1
3	MAN	G	6	3	-	2/2/19/22	0/1/1/1
3	MAN	G	7	3	-	0/2/19/22	0/1/1/1
4	NAG	H	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	0/2/19/22	0/1/1/1
4	MAN	H	4	4	-	0/2/19/22	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	5	MAN	C2-C3	2.89	1.56	1.52
3	D	1	NAG	O5-C1	-2.89	1.39	1.43
3	D	1	NAG	C2-N2	-2.83	1.41	1.46
3	D	1	NAG	O7-C7	-2.76	1.17	1.23
3	D	4	MAN	O5-C1	-2.69	1.39	1.43
3	G	1	NAG	C2-N2	-2.61	1.41	1.46
2	F	1	NAG	O7-C7	-2.59	1.17	1.23
2	F	1	NAG	C2-N2	-2.49	1.42	1.46
2	C	1	NAG	O7-C7	-2.45	1.17	1.23
4	H	1	NAG	O5-C1	-2.41	1.39	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	NAG	O5-C1	-2.33	1.40	1.43
3	G	1	NAG	O7-C7	-2.25	1.18	1.23
4	H	3	BMA	C2-C3	2.09	1.55	1.52
3	G	6	MAN	C6-C5	2.06	1.58	1.51

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	4	MAN	C1-O5-C5	8.58	123.81	112.19
2	C	3	MAN	C1-C2-C3	7.75	119.19	109.67
3	D	1	NAG	O5-C5-C6	-7.62	95.26	107.20
3	G	6	MAN	C1-O5-C5	7.45	122.29	112.19
2	C	3	MAN	C1-O5-C5	7.30	122.08	112.19
3	D	5	MAN	C1-O5-C5	6.59	121.11	112.19
3	D	4	MAN	C1-O5-C5	6.48	120.97	112.19
3	D	1	NAG	C1-O5-C5	5.97	120.28	112.19
4	E	2	NAG	C1-O5-C5	5.91	120.20	112.19
3	D	3	BMA	O3-C3-C2	5.88	121.25	109.99
4	H	4	MAN	C1-O5-C5	5.54	119.70	112.19
3	D	3	BMA	O3-C3-C4	-5.53	97.57	110.35
4	E	3	BMA	C1-O5-C5	5.24	119.30	112.19
3	D	1	NAG	O5-C1-C2	-5.07	103.29	111.29
4	H	4	MAN	C1-C2-C3	4.85	115.62	109.67
4	E	3	BMA	C3-C4-C5	4.83	118.85	110.24
4	H	3	BMA	C3-C4-C5	4.72	118.66	110.24
2	C	1	NAG	C1-O5-C5	4.68	118.54	112.19
2	F	3	MAN	C1-O5-C5	4.65	118.50	112.19
4	H	2	NAG	C1-O5-C5	4.60	118.42	112.19
4	E	1	NAG	O5-C5-C6	4.38	114.06	107.20
3	G	1	NAG	C3-C4-C5	-4.32	102.54	110.24
4	E	4	MAN	C1-O5-C5	4.30	118.02	112.19
4	E	1	NAG	O5-C1-C2	-4.02	104.94	111.29
3	G	4	MAN	O2-C2-C1	-3.95	101.07	109.15
3	D	4	MAN	C6-C5-C4	-3.78	104.15	113.00
2	C	1	NAG	C3-C4-C5	-3.59	103.84	110.24
2	C	2	NAG	C4-C3-C2	3.58	116.26	111.02
3	D	6	MAN	C1-O5-C5	3.57	117.03	112.19
3	G	5	MAN	C1-O5-C5	3.56	117.02	112.19
3	D	2	NAG	C4-C3-C2	-3.54	105.84	111.02
3	G	1	NAG	C1-O5-C5	3.52	116.96	112.19
3	G	6	MAN	O6-C6-C5	3.49	123.28	111.29
3	D	5	MAN	O2-C2-C3	3.46	117.06	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	5	MAN	O5-C1-C2	3.22	115.75	110.77
2	C	3	MAN	O5-C5-C6	3.19	112.21	107.20
4	E	1	NAG	C2-N2-C7	-3.09	118.51	122.90
2	F	2	NAG	C2-N2-C7	3.07	127.27	122.90
2	F	2	NAG	C4-C3-C2	3.04	115.47	111.02
4	E	4	MAN	C3-C4-C5	3.01	115.61	110.24
3	G	6	MAN	O5-C5-C6	2.97	111.86	107.20
2	C	3	MAN	O5-C1-C2	2.88	115.21	110.77
3	D	1	NAG	O4-C4-C5	2.86	116.39	109.30
4	E	2	NAG	C8-C7-N2	-2.82	111.32	116.10
4	E	3	BMA	O3-C3-C2	2.79	115.34	109.99
2	C	1	NAG	O5-C1-C2	-2.77	106.92	111.29
2	C	1	NAG	O4-C4-C3	2.72	116.64	110.35
4	E	3	BMA	O2-C2-C3	2.68	115.51	110.14
4	E	3	BMA	O5-C1-C2	2.63	114.83	110.77
4	H	1	NAG	O5-C5-C6	2.56	111.22	107.20
3	D	1	NAG	C3-C4-C5	-2.55	105.69	110.24
3	G	5	MAN	O2-C2-C3	2.48	115.12	110.14
2	F	3	MAN	O5-C5-C6	2.48	111.09	107.20
4	H	1	NAG	O5-C1-C2	-2.48	107.38	111.29
4	H	3	BMA	O3-C3-C2	2.47	114.73	109.99
2	C	3	MAN	C6-C5-C4	-2.45	107.27	113.00
3	D	7	MAN	O5-C5-C6	2.43	111.01	107.20
2	C	1	NAG	O4-C4-C5	2.43	115.33	109.30
3	D	4	MAN	O3-C3-C4	-2.39	104.81	110.35
2	C	2	NAG	C2-N2-C7	2.39	126.31	122.90
3	D	1	NAG	C2-N2-C7	2.38	126.28	122.90
2	C	2	NAG	O7-C7-C8	-2.35	117.69	122.06
4	H	1	NAG	O4-C4-C3	-2.31	105.00	110.35
4	E	2	NAG	O7-C7-C8	2.29	126.31	122.06
4	E	2	NAG	O5-C5-C6	2.29	110.79	107.20
3	D	7	MAN	O3-C3-C2	2.27	114.34	109.99
3	D	4	MAN	O2-C2-C1	-2.26	104.52	109.15
4	E	3	BMA	O5-C5-C6	2.26	110.75	107.20
3	G	6	MAN	C3-C4-C5	2.26	114.27	110.24
3	G	3	BMA	C1-C2-C3	2.25	112.44	109.67
4	E	2	NAG	C6-C5-C4	-2.25	107.73	113.00
4	E	4	MAN	O5-C1-C2	2.25	114.24	110.77
3	D	1	NAG	C1-C2-N2	2.23	114.30	110.49
3	D	3	BMA	O4-C4-C3	-2.20	105.25	110.35
2	F	2	NAG	C1-C2-N2	-2.20	106.73	110.49
4	E	1	NAG	O5-C5-C4	-2.19	105.50	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	3	BMA	C1-C2-C3	2.15	112.30	109.67
2	F	3	MAN	C1-C2-C3	2.14	112.30	109.67
4	E	4	MAN	C1-C2-C3	2.10	112.25	109.67
3	G	7	MAN	C1-O5-C5	2.10	115.03	112.19
2	F	1	NAG	O4-C4-C5	2.09	114.48	109.30
4	H	2	NAG	C6-C5-C4	-2.08	108.14	113.00
3	D	2	NAG	C8-C7-N2	-2.03	112.66	116.10
2	C	2	NAG	C6-C5-C4	2.02	117.73	113.00
4	H	3	BMA	O4-C4-C3	-2.01	105.70	110.35

There are no chirality outliers.

All (13) torsion outliers are listed below:

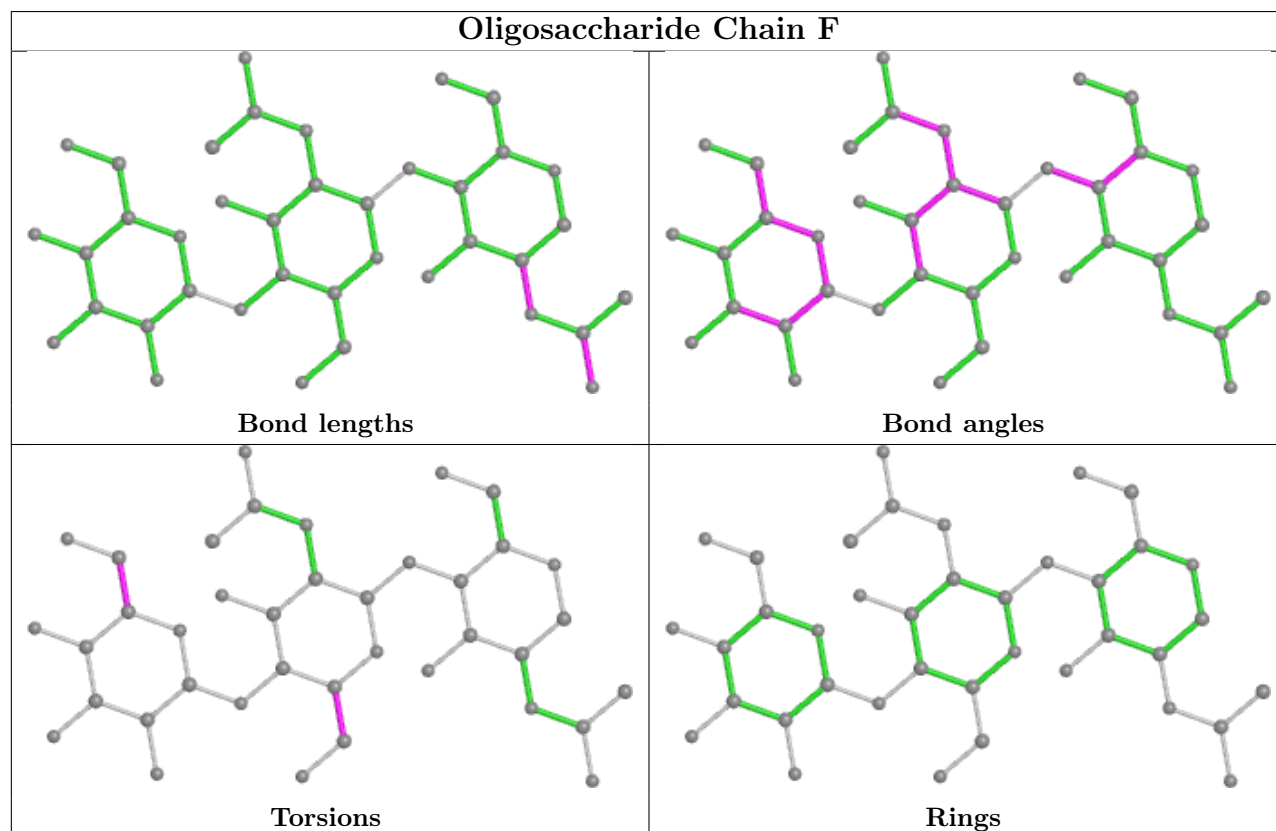
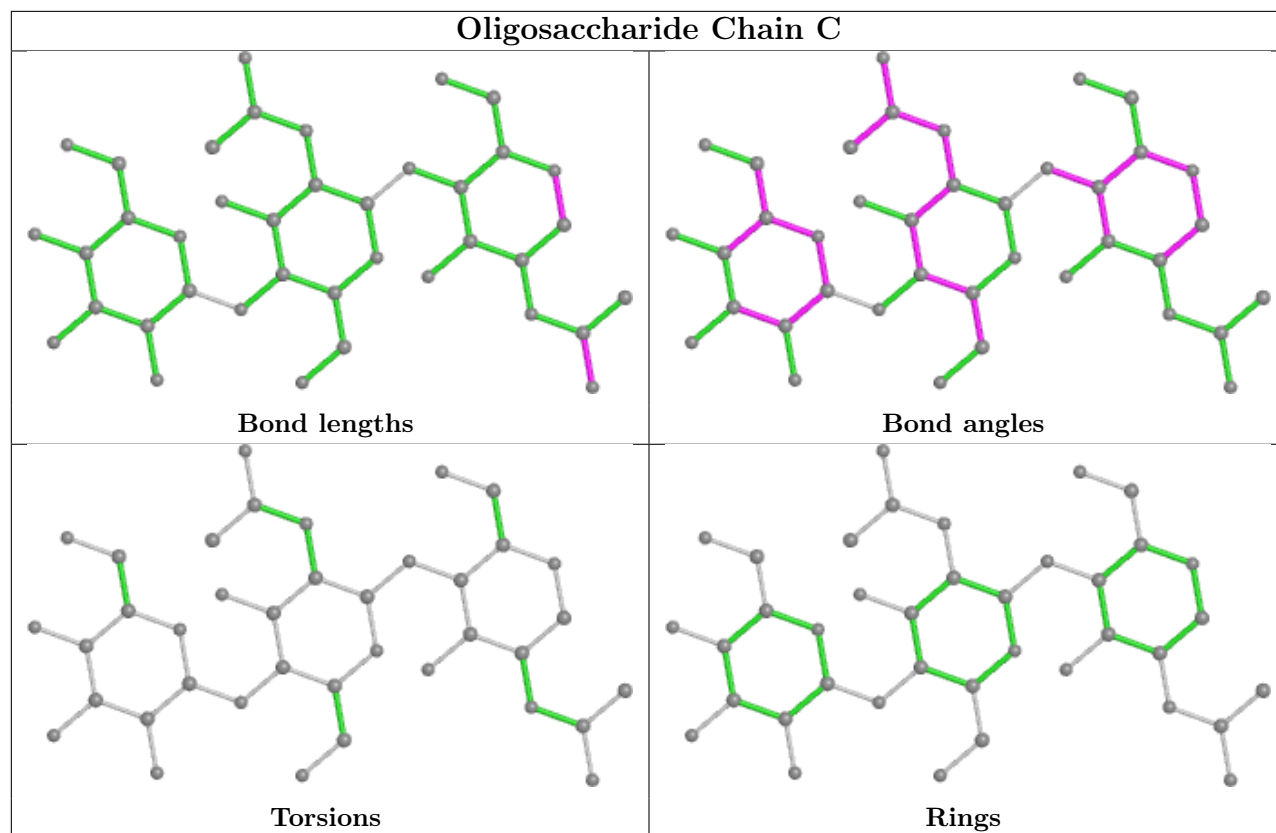
Mol	Chain	Res	Type	Atoms
4	E	4	MAN	O5-C5-C6-O6
2	F	3	MAN	O5-C5-C6-O6
4	E	4	MAN	C4-C5-C6-O6
3	D	4	MAN	C4-C5-C6-O6
4	E	3	BMA	C4-C5-C6-O6
3	D	4	MAN	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
2	F	3	MAN	C4-C5-C6-O6
3	G	6	MAN	C4-C5-C6-O6
4	E	3	BMA	O5-C5-C6-O6
3	G	6	MAN	O5-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6

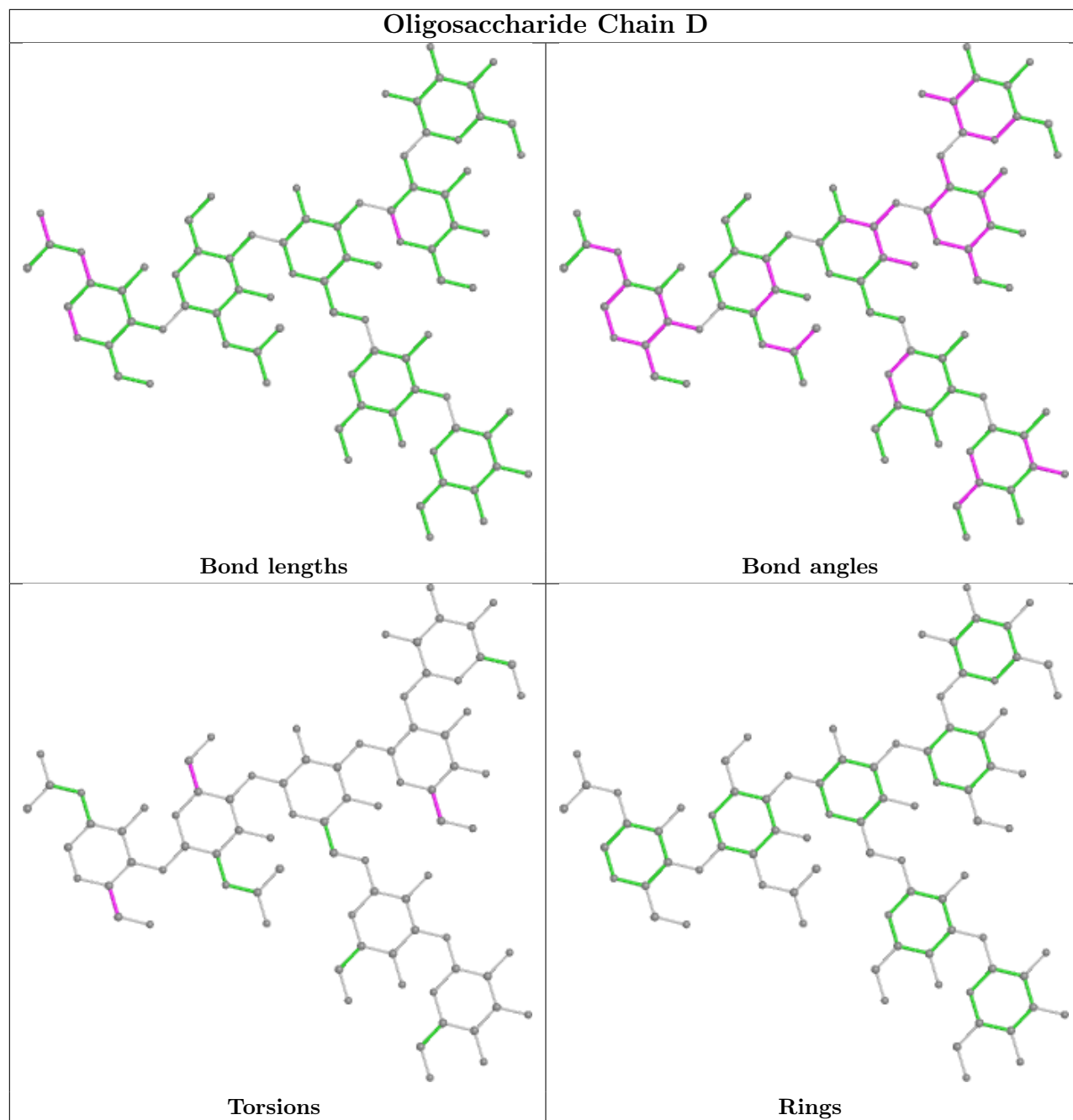
There are no ring outliers.

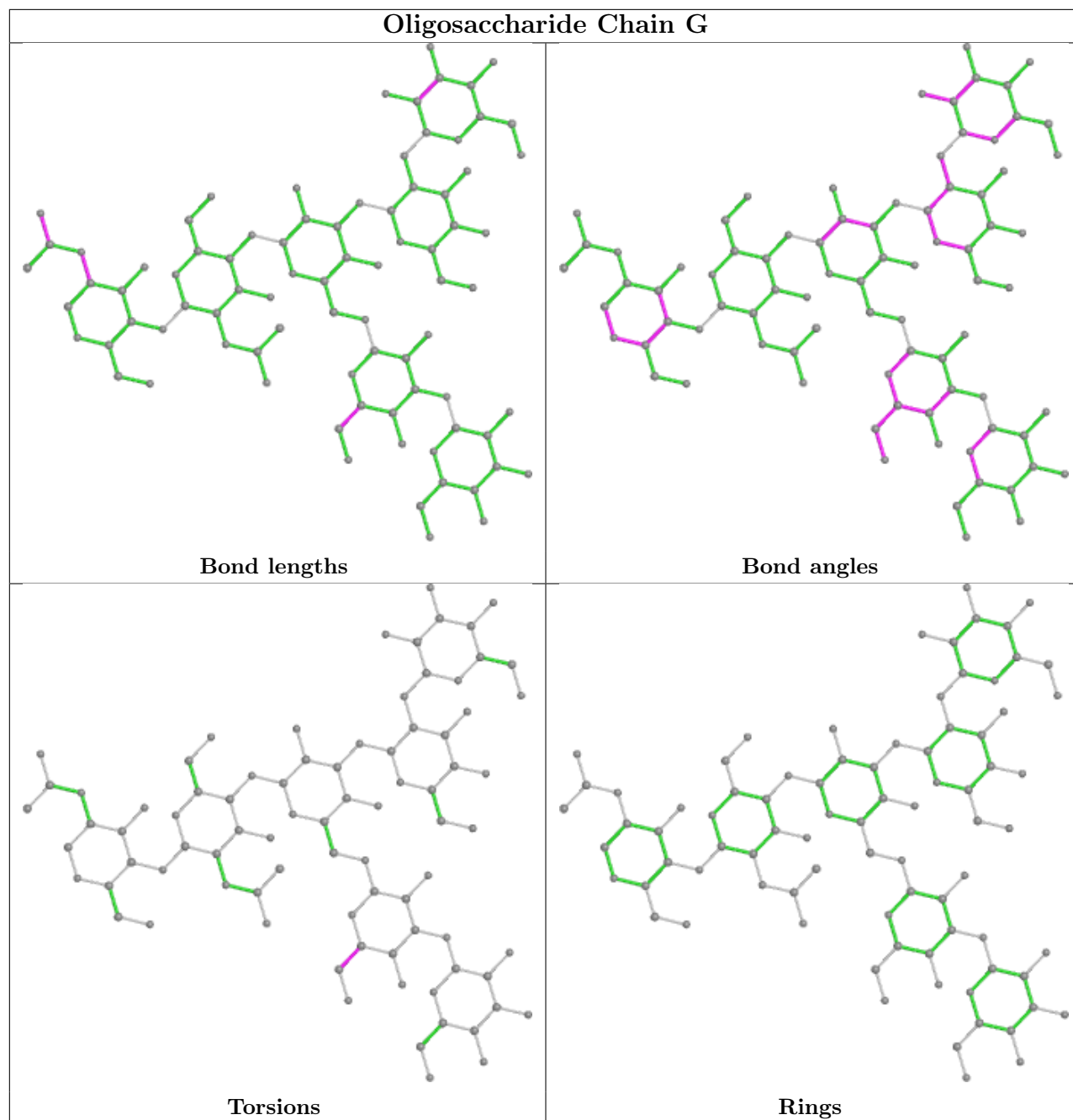
3 monomers are involved in 2 short contacts:

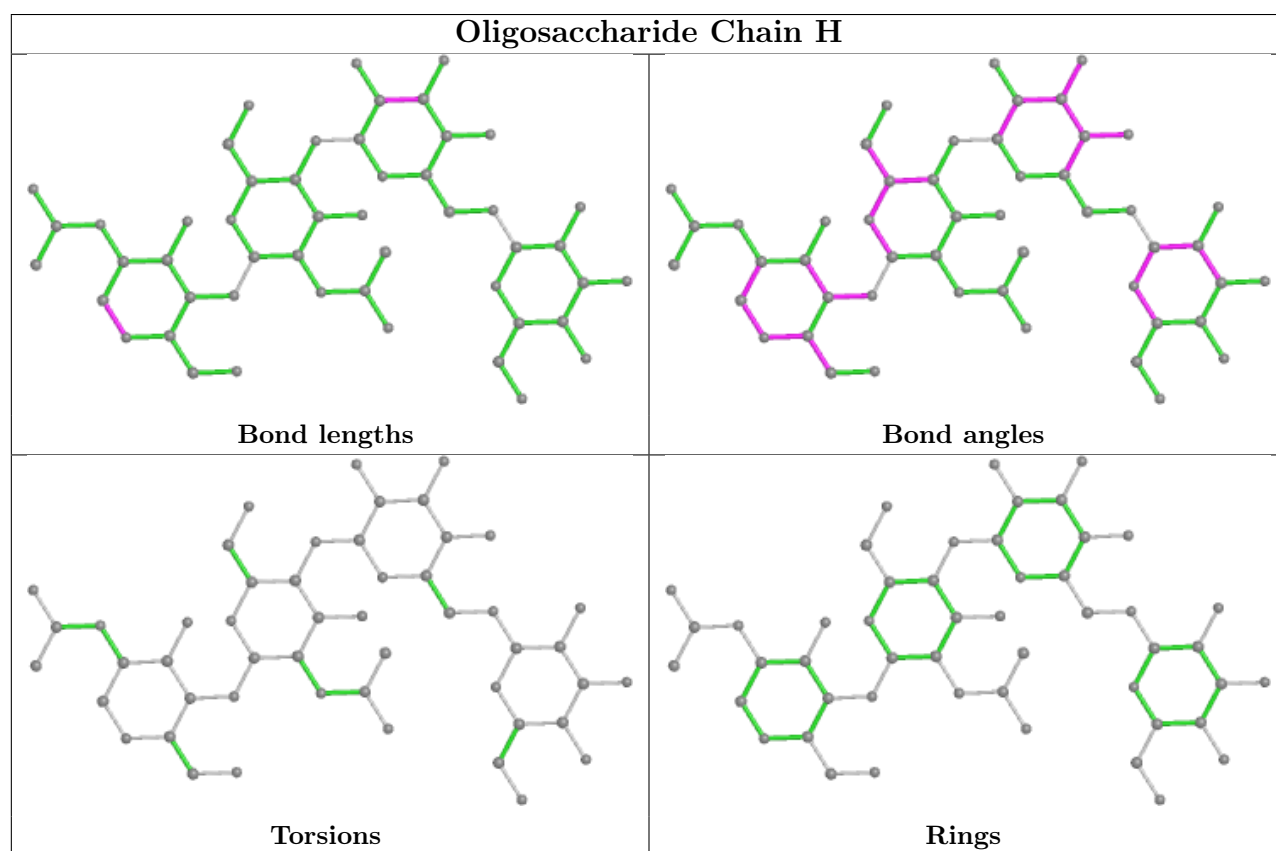
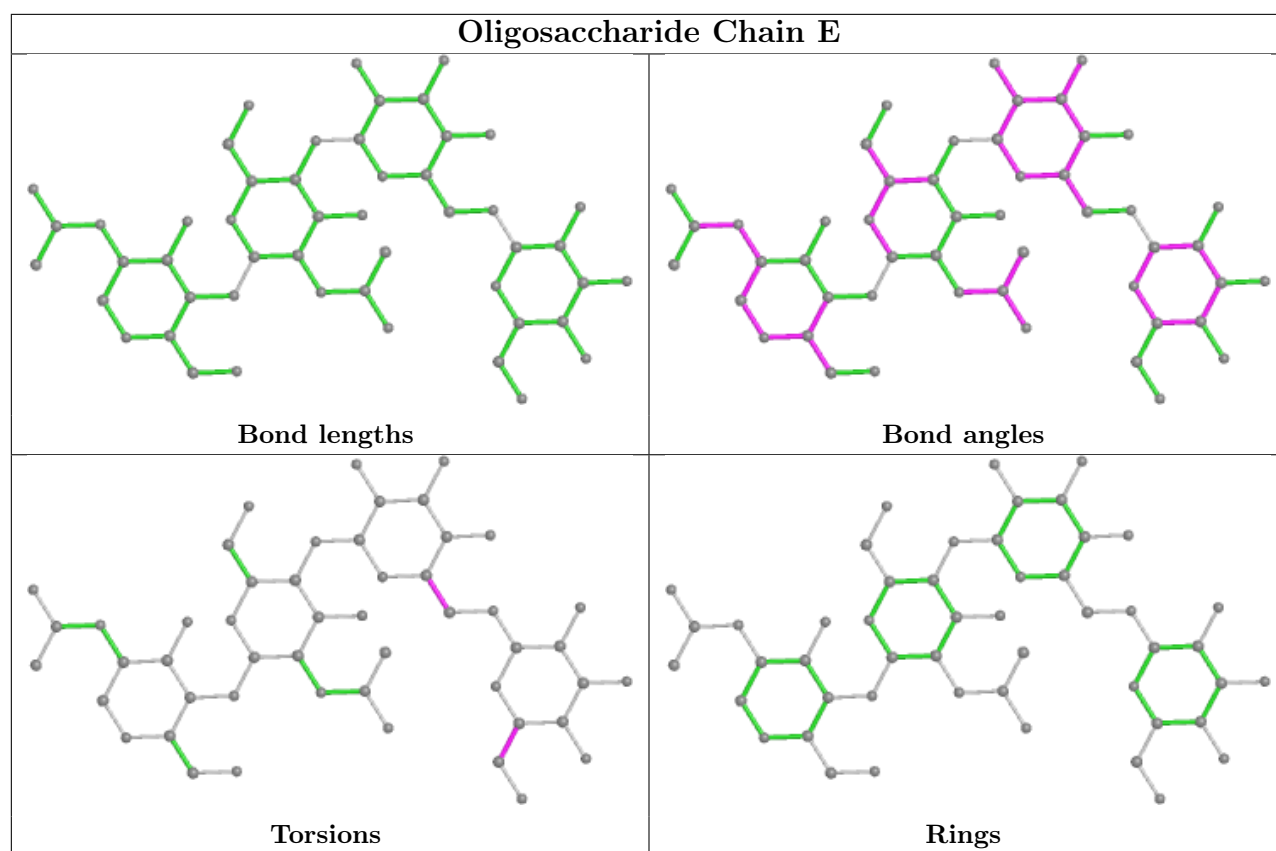
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2	NAG	1	0
3	G	1	NAG	1	0
2	F	1	NAG	1	0

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

12 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	$\# Z > 2$
5	NAG	B	911	1	14,14,15	0.40	0	17,19,21	1.79	2 (11%)
5	NAG	B	918	1	14,14,15	0.91	1 (7%)	17,19,21	1.31	2 (11%)
6	BKR	A	919	-	65,65,65	1.33	4 (6%)	101,101,101	1.37	13 (12%)
5	NAG	A	911	1	14,14,15	0.65	0	17,19,21	1.54	2 (11%)
5	NAG	B	917	1	14,14,15	0.49	0	17,19,21	1.47	1 (5%)
5	NAG	B	912	1	14,14,15	0.72	0	17,19,21	1.17	1 (5%)
5	NAG	A	918	1	14,14,15	0.49	0	17,19,21	1.50	2 (11%)
7	XYP	B	920	-	10,10,10	2.09	4 (40%)	14,14,14	3.74	8 (57%)
7	XYP	A	920	-	10,10,10	1.32	1 (10%)	14,14,14	3.21	7 (50%)
6	BKR	B	919	-	65,65,65	1.34	3 (4%)	101,101,101	1.23	9 (8%)
5	NAG	A	917	1	14,14,15	0.61	0	17,19,21	1.13	1 (5%)
5	NAG	A	912	1	14,14,15	0.62	0	17,19,21	1.31	2 (11%)

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
5	NAG	B	911	1	-	1/6/23/26	0/1/1/1
5	NAG	B	918	1	-	0/6/23/26	0/1/1/1
6	BKR	A	919	-	-	14/37/123/123	0/7/7/7
5	NAG	A	911	1	-	0/6/23/26	0/1/1/1
5	NAG	B	917	1	-	0/6/23/26	0/1/1/1
5	NAG	B	912	1	-	0/6/23/26	0/1/1/1
5	NAG	A	918	1	-	2/6/23/26	0/1/1/1
7	XYP	B	920	-	-	-	0/1/1/1
7	XYP	A	920	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BKR	B	919	-	-	3/37/123/123	0/7/7/7
5	NAG	A	917	1	-	0/6/23/26	0/1/1/1
5	NAG	A	912	1	-	1/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	919	BKR	O2-C3	5.64	1.46	1.34
6	B	919	BKR	O2-C3	5.46	1.45	1.34
6	B	919	BKR	O11-C27	5.10	1.46	1.34
6	A	919	BKR	O11-C27	4.67	1.45	1.34
6	A	919	BKR	O4-C12	3.92	1.44	1.35
7	B	920	XYP	O5-C1	3.32	1.47	1.43
7	B	920	XYP	O5-C5	3.18	1.48	1.43
6	B	919	BKR	O4-C12	3.03	1.42	1.35
7	A	920	XYP	O5-C1	-2.73	1.39	1.43
7	B	920	XYP	O1-C1	2.73	1.48	1.39
7	B	920	XYP	O4-C4	2.57	1.48	1.43
6	A	919	BKR	O4-C11	-2.43	1.41	1.46
5	B	918	NAG	C1-C2	2.32	1.55	1.52

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	920	XYP	C5-C4-C3	-8.66	99.02	109.67
7	B	920	XYP	O4-C4-C3	6.97	124.10	110.14
7	A	920	XYP	C5-C4-C3	-6.37	101.84	109.67
5	B	911	NAG	C1-O5-C5	5.52	119.67	112.19
7	A	920	XYP	O4-C4-C3	5.46	121.07	110.14
6	A	919	BKR	O2-C3-C4	5.25	120.40	111.92
5	B	917	NAG	C1-O5-C5	4.98	118.94	112.19
6	B	919	BKR	C45-C24-C21	4.52	124.25	119.52
7	A	920	XYP	O5-C5-C4	-4.52	103.80	110.77
5	A	911	NAG	C1-O5-C5	4.50	118.28	112.19
7	B	920	XYP	O4-C4-C5	4.49	118.34	109.15
7	A	920	XYP	C4-C3-C2	-4.39	103.29	110.89
7	B	920	XYP	C5-O5-C1	-4.04	105.92	112.71
6	A	919	BKR	O11-C27-C28	3.98	117.68	111.15
6	A	919	BKR	C45-C24-C21	3.88	123.58	119.52
5	A	918	NAG	O5-C5-C6	3.72	113.03	107.20
6	A	919	BKR	C45-C1-C2	3.50	115.75	111.91
7	B	920	XYP	O1-C1-C2	3.29	118.31	109.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	919	BKR	C45-C1-C2	3.23	115.44	111.91
5	A	911	NAG	O5-C5-C6	3.14	112.13	107.20
5	A	912	NAG	O5-C1-C2	-3.14	106.33	111.29
6	A	919	BKR	O2-C3-O3	-3.10	118.47	123.53
7	A	920	XYP	C5-O5-C1	-3.05	107.58	112.71
6	B	919	BKR	O2-C3-C4	3.04	116.83	111.92
7	B	920	XYP	C4-C3-C2	-3.02	105.67	110.89
5	B	918	NAG	C1-O5-C5	2.98	116.23	112.19
5	B	918	NAG	O5-C1-C2	2.90	115.87	111.29
6	B	919	BKR	C45-C24-C25	-2.90	115.59	119.61
6	B	919	BKR	O2-C3-O3	-2.85	118.87	123.53
6	B	919	BKR	O4-C12-O5	-2.80	118.46	123.61
6	A	919	BKR	C18-C10-C2	2.80	121.94	115.69
6	A	919	BKR	O8-C20-C21	2.63	120.38	117.37
7	A	920	XYP	C1-C2-C3	-2.57	104.97	110.31
5	A	918	NAG	C1-C2-N2	2.56	114.86	110.49
7	B	920	XYP	O1-C1-O5	2.56	116.38	109.72
6	A	919	BKR	C46-C45-C47	-2.53	98.82	106.26
6	A	919	BKR	O4-C11-C14	2.43	113.41	108.09
6	B	919	BKR	O6-C15-C11	2.31	93.17	90.58
6	B	919	BKR	C2-O2-C3	2.30	122.15	117.79
6	B	919	BKR	C44-C25-C24	-2.23	122.59	125.30
7	B	920	XYP	O3-C3-C4	2.21	114.22	109.99
6	A	919	BKR	C2-O2-C3	2.20	121.96	117.79
5	A	912	NAG	C4-C3-C2	2.19	114.22	111.02
5	B	911	NAG	C4-C3-C2	2.17	114.20	111.02
6	A	919	BKR	O2-C2-C1	-2.13	100.25	104.76
6	A	919	BKR	C14-O6-C15	2.11	93.81	91.39
5	A	917	NAG	O4-C4-C5	2.05	114.40	109.30
6	A	919	BKR	C44-C25-C24	-2.05	122.81	125.30
5	B	912	NAG	O7-C7-N2	2.01	125.65	121.95
7	A	920	XYP	O1-C1-C2	2.00	114.67	109.03

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	918	NAG	O5-C5-C6-O6
5	A	918	NAG	C4-C5-C6-O6
6	B	919	BKR	O12-C27-C28-O13
6	A	919	BKR	O11-C27-C28-O13
6	A	919	BKR	O12-C27-C28-O13

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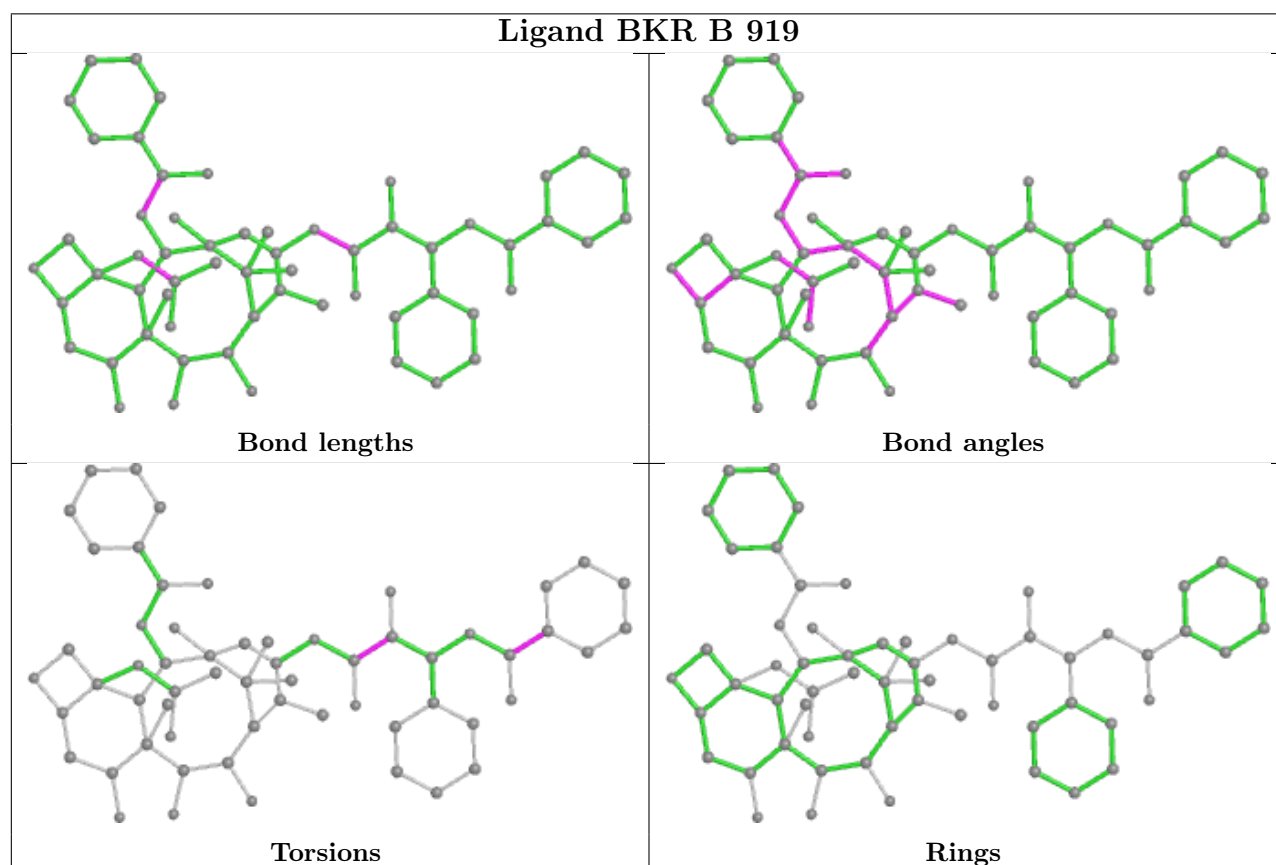
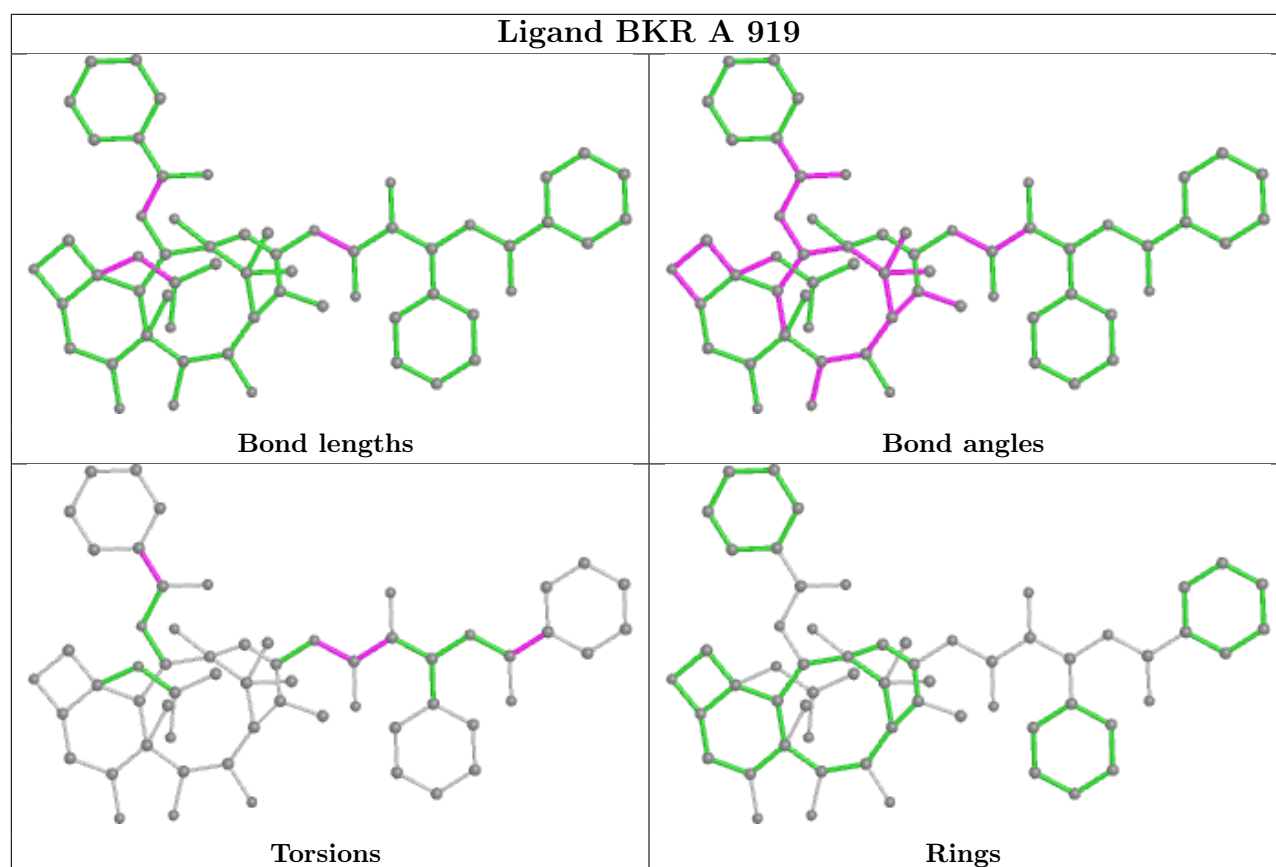
Mol	Chain	Res	Type	Atoms
6	B	919	BKR	O11-C27-C28-O13
6	A	919	BKR	O12-C27-O11-C26
5	B	911	NAG	C4-C5-C6-O6
5	A	912	NAG	C4-C5-C6-O6
6	A	919	BKR	C28-C27-O11-C26
6	A	919	BKR	O12-C27-C28-C29
6	A	919	BKR	O11-C27-C28-C29
6	A	919	BKR	N1-C30-C31-C32
6	A	919	BKR	O14-C30-C31-C32
6	A	919	BKR	O2-C3-C4-C9
6	A	919	BKR	N1-C30-C31-C36
6	A	919	BKR	O2-C3-C4-C5
6	A	919	BKR	O14-C30-C31-C36
6	B	919	BKR	N1-C30-C31-C32
6	A	919	BKR	O3-C3-C4-C9
6	A	919	BKR	O3-C3-C4-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	920	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	756/809 (93%)	-0.13	9 (1%) 76 77	19, 31, 49, 104	0
1	B	756/809 (93%)	-0.12	9 (1%) 76 77	12, 32, 48, 91	2 (0%)
All	All	1512/1618 (93%)	-0.13	18 (1%) 76 77	12, 31, 49, 104	2 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	696	TRP	4.7
1	A	683	TYR	3.9
1	A	48	GLN	3.9
1	B	696	TRP	3.8
1	B	803	PRO	3.7
1	B	676	HIS	3.3
1	A	734	ASP	3.0
1	B	679	TRP	3.0
1	B	683	TYR	3.0
1	A	571	TRP	2.7
1	A	49	TRP	2.6
1	B	48	GLN	2.5
1	A	803	PRO	2.3
1	A	676	HIS	2.3
1	B	49	TRP	2.3
1	B	699	THR	2.2
1	A	51	ALA	2.1
1	B	695	GLU	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 ⓘ

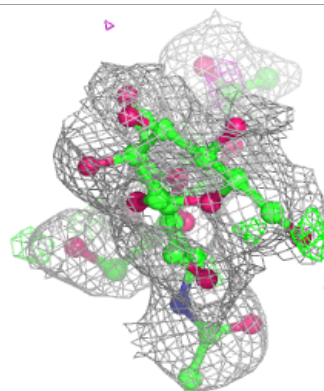
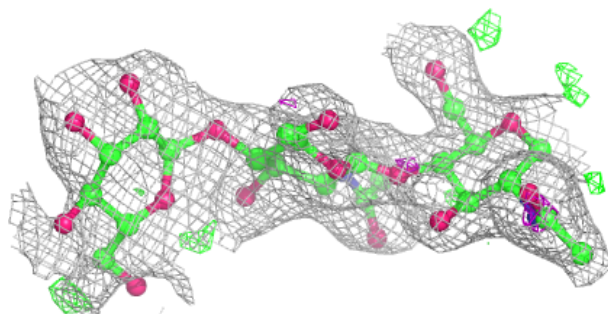
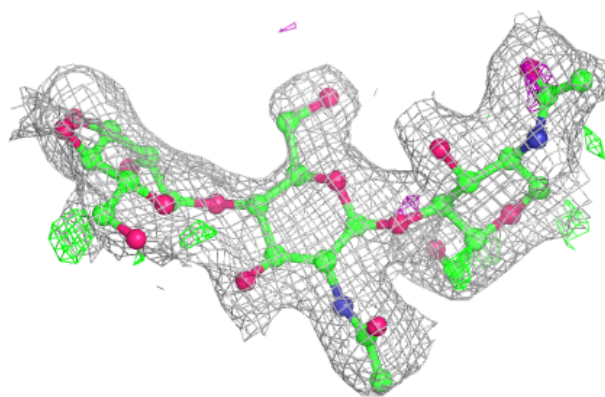
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	E	3	11/12	0.53	0.17	62,80,85,87	0
2	MAN	C	3	11/12	0.60	0.16	69,78,83,89	0
4	MAN	E	4	11/12	0.60	0.17	72,89,91,94	0
4	BMA	H	3	11/12	0.61	0.15	75,85,98,99	0
2	MAN	F	3	11/12	0.63	0.14	60,76,80,83	0
4	MAN	H	4	11/12	0.65	0.14	83,95,103,107	0
3	MAN	D	4	11/12	0.72	0.17	20,20,20,20	0
3	MAN	G	5	11/12	0.77	0.14	59,69,74,75	0
3	MAN	D	6	11/12	0.78	0.11	40,43,55,60	0
3	MAN	D	5	11/12	0.78	0.12	46,53,56,57	0
3	MAN	G	4	11/12	0.81	0.11	51,60,64,66	0
3	MAN	G	6	11/12	0.84	0.10	42,45,48,50	0
4	NAG	E	2	14/15	0.85	0.14	41,48,58,72	0
3	NAG	D	1	14/15	0.86	0.11	20,20,20,20	0
2	NAG	F	2	14/15	0.87	0.12	45,50,66,79	0
3	NAG	G	1	14/15	0.88	0.12	20,20,20,20	0
3	NAG	D	2	14/15	0.88	0.10	31,37,39,40	0
2	NAG	C	2	14/15	0.88	0.11	46,50,58,66	0
3	MAN	G	7	11/12	0.90	0.09	52,55,58,64	0
3	MAN	D	7	11/12	0.91	0.09	46,49,52,53	0
3	NAG	G	2	14/15	0.92	0.08	34,41,44,46	0
2	NAG	F	1	14/15	0.93	0.10	20,20,20,20	0
4	NAG	H	2	14/15	0.93	0.10	39,46,62,67	0
3	BMA	D	3	11/12	0.93	0.07	35,40,42,44	0
3	BMA	G	3	11/12	0.93	0.07	41,45,49,50	0
2	NAG	C	1	14/15	0.94	0.10	20,20,20,20	0
4	NAG	H	1	14/15	0.96	0.05	25,27,31,38	0
4	NAG	E	1	14/15	0.96	0.05	23,26,28,36	0

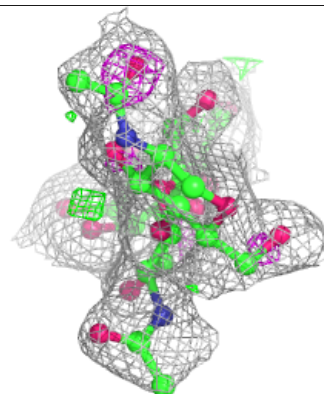
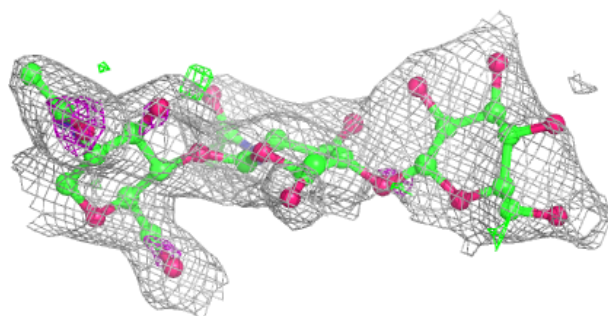
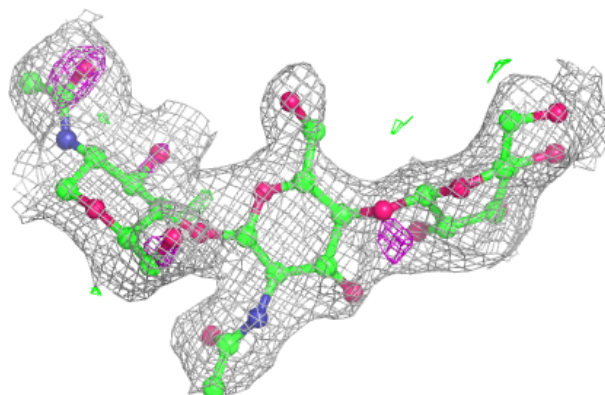
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

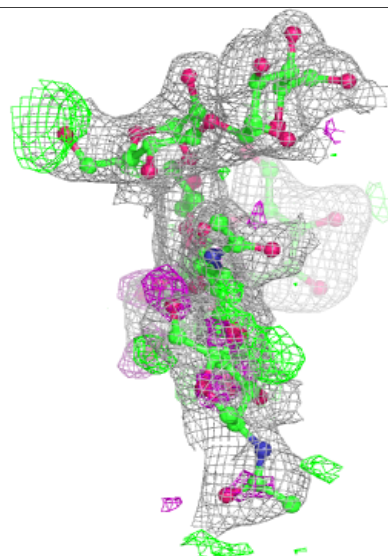
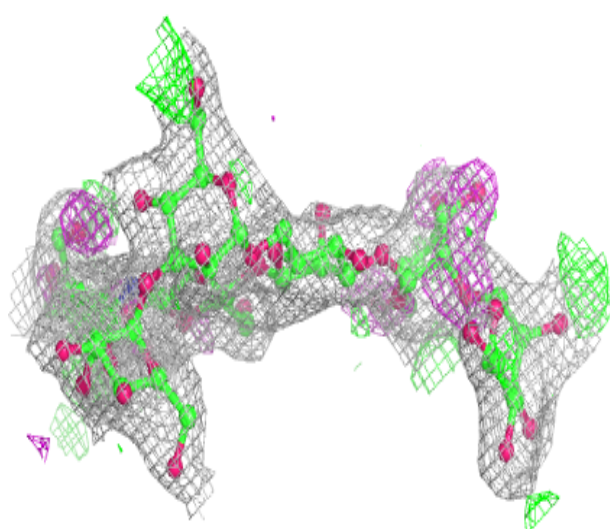
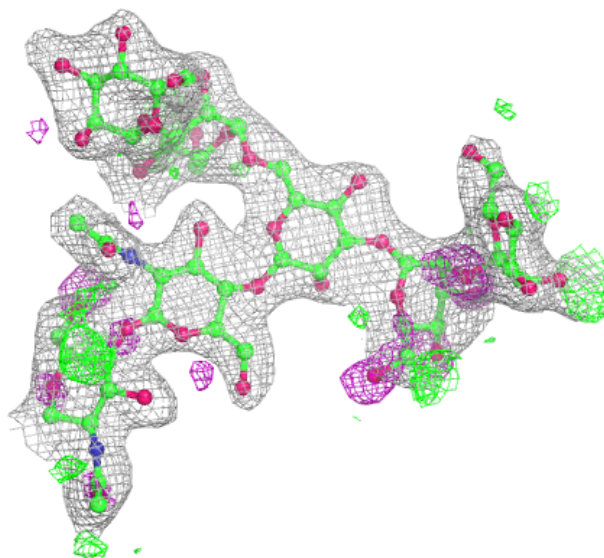
**Electron density around Chain F:**

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



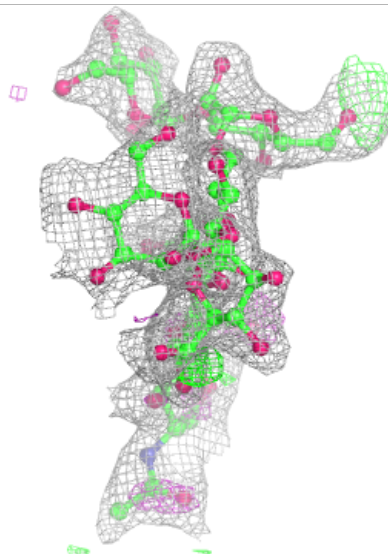
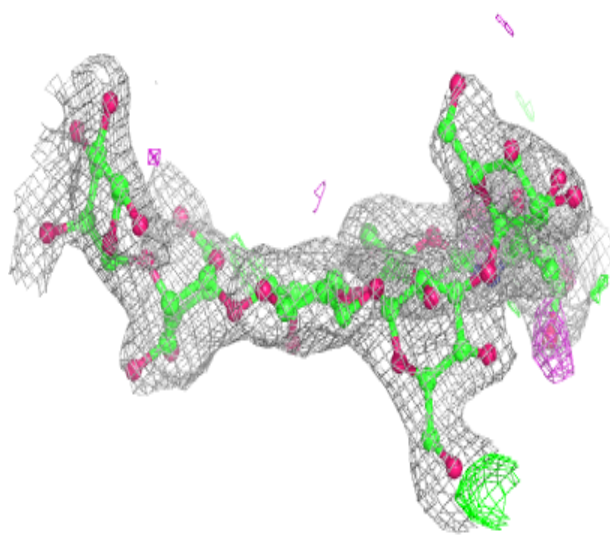
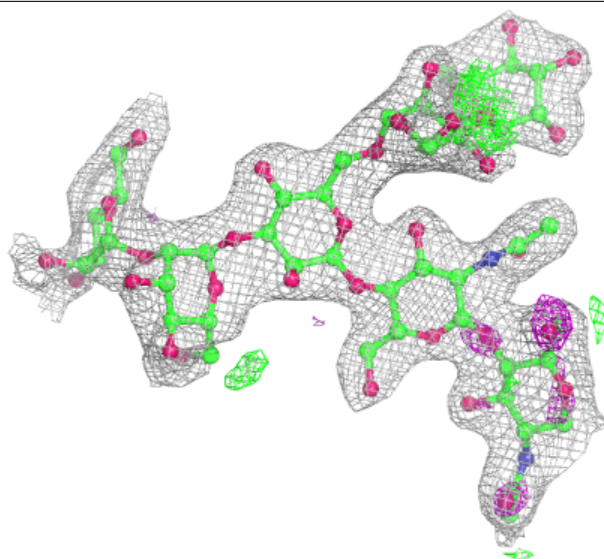
Electron density around Chain D:

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



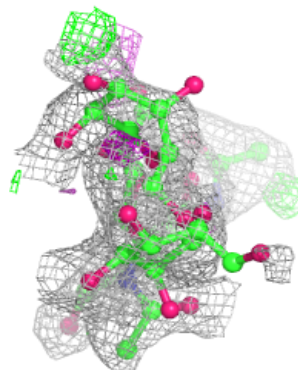
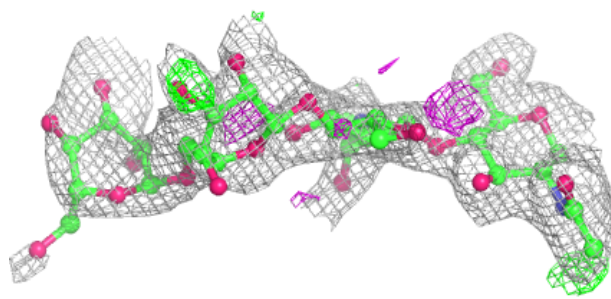
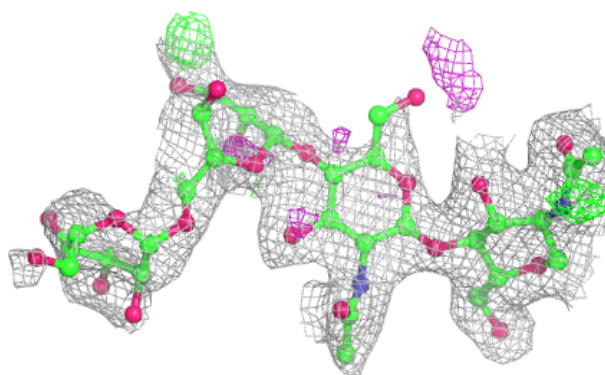
Electron density around Chain G:

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

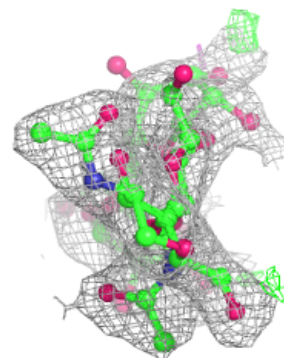
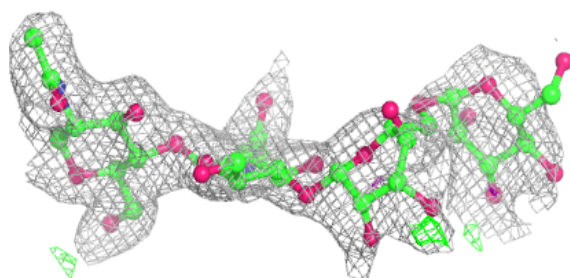
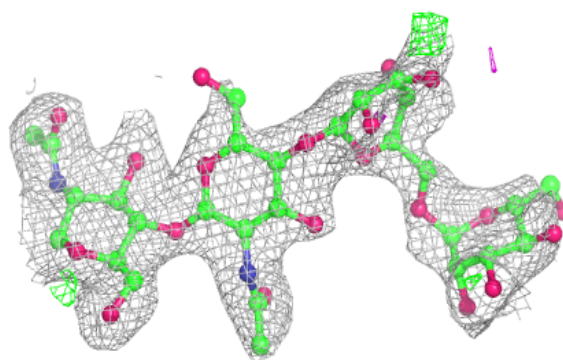


Electron density around Chain E:

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

**Electron density around Chain H:**

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



6.4 Ligands

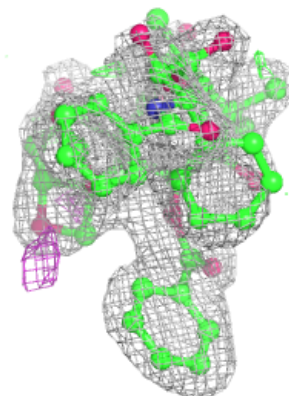
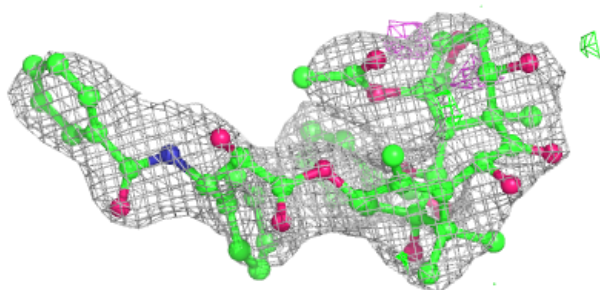
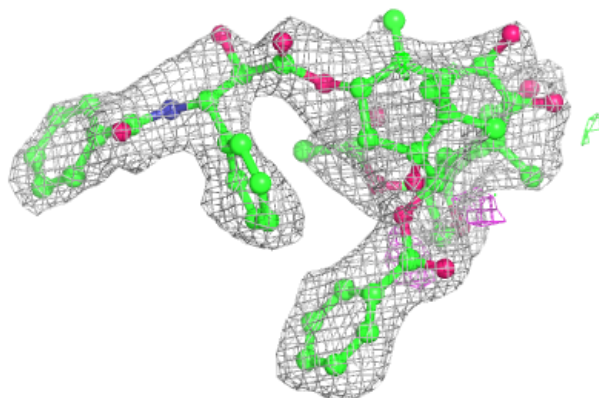
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	B	918	14/15	0.67	0.17	78,89,96,99	0
5	NAG	A	918	14/15	0.69	0.16	62,77,84,85	0
5	NAG	A	911	14/15	0.78	0.14	61,69,76,78	0
7	XYP	A	920	10/10	0.81	0.12	31,34,36,39	0
5	NAG	B	911	14/15	0.84	0.12	61,65,70,73	0
6	BKR	B	919	59/59	0.86	0.12	42,53,68,70	0
6	BKR	A	919	59/59	0.86	0.13	38,53,68,74	0
7	XYP	B	920	10/10	0.87	0.11	32,37,39,40	0
5	NAG	B	912	14/15	0.89	0.09	41,48,51,51	0
5	NAG	A	912	14/15	0.91	0.09	42,47,49,50	0
5	NAG	A	917	14/15	0.94	0.07	34,38,40,46	0
5	NAG	B	917	14/15	0.95	0.06	35,38,41,44	0

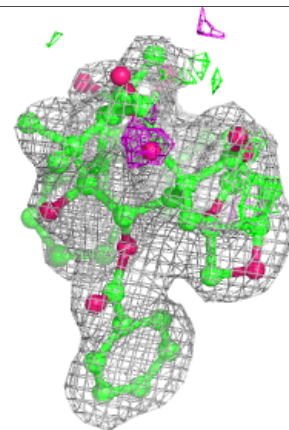
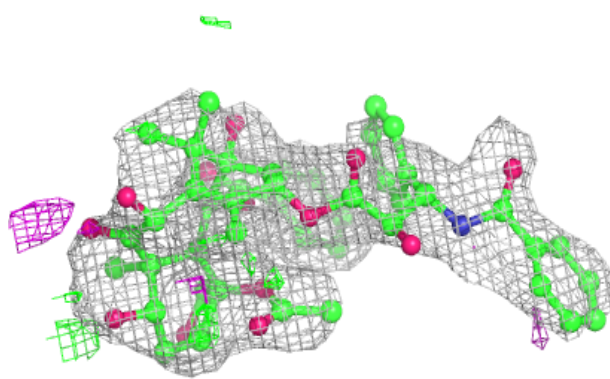
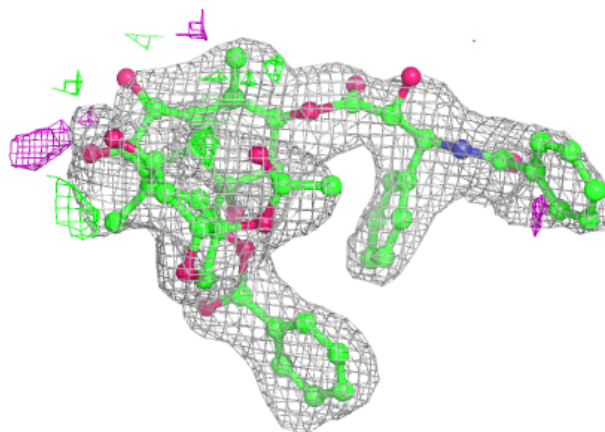
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around BKR B 919:

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

**Electron density around BKR A 919:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.