



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 08:14 PM BST

PDB ID : 3OLU
Title : X-ray crystal structure of 1-arachidonoyl glycerol bound to the cyclooxygenase channel of R513H murine COX-2
Authors : Vecchio, A.J.; Malkowski, M.G.
Deposited on : 2010-08-26
Resolution : 2.35 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
buster-report : 1.1.7 (2018)
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

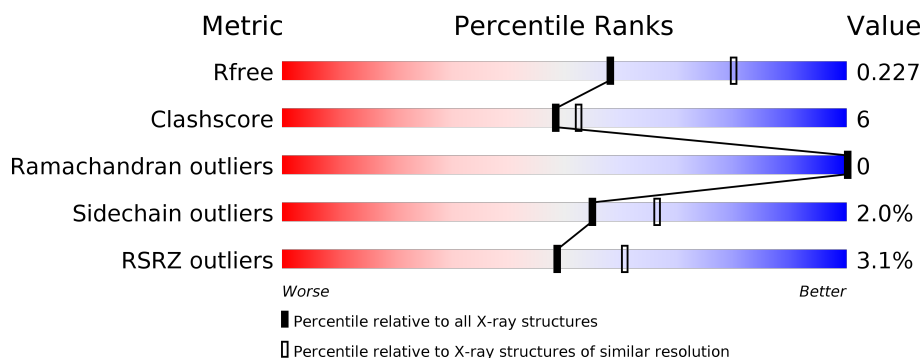
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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	592	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>7%</div> </div> </div>
1	B	592	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>8%</div> <div>7%</div> </div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>
2	E	2	<div> <div></div> <div>100%</div> </div>
3	D	3	<div> <div></div> <div>67%</div> <div>33%</div> </div>
3	F	3	<div> <div></div> <div>33%</div> <div>67%</div> </div>

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	NAG	C	1	X	-	-	-
2	NAG	C	2	-	-	-	X
2	NAG	E	2	X	-	-	-
3	MAN	F	3	-	-	-	X
4	EDO	A	1	-	-	-	X
4	EDO	B	7	-	-	X	-

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 9951 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 Prostaglandin G/H synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	551	Total	C	N	O	S	0	4	0
			4462	2882	745	810	25			
1	B	551	Total	C	N	O	S	0	5	0
			4445	2872	742	806	25			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ALA	-	expression tag	UNP Q05769
A	29	HIS	-	expression tag	UNP Q05769
A	30	HIS	-	expression tag	UNP Q05769
A	31	HIS	-	expression tag	UNP Q05769
A	32	HIS	-	expression tag	UNP Q05769
A	33	HIS	-	expression tag	UNP Q05769
A	34	HIS	-	expression tag	UNP Q05769
A	513	HIS	ARG	engineered mutation	UNP Q05769
B	28	ALA	-	expression tag	UNP Q05769
B	29	HIS	-	expression tag	UNP Q05769
B	30	HIS	-	expression tag	UNP Q05769
B	31	HIS	-	expression tag	UNP Q05769
B	32	HIS	-	expression tag	UNP Q05769
B	33	HIS	-	expression tag	UNP Q05769
B	34	HIS	-	expression tag	UNP Q05769
B	513	HIS	ARG	engineered mutation	UNP Q05769

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



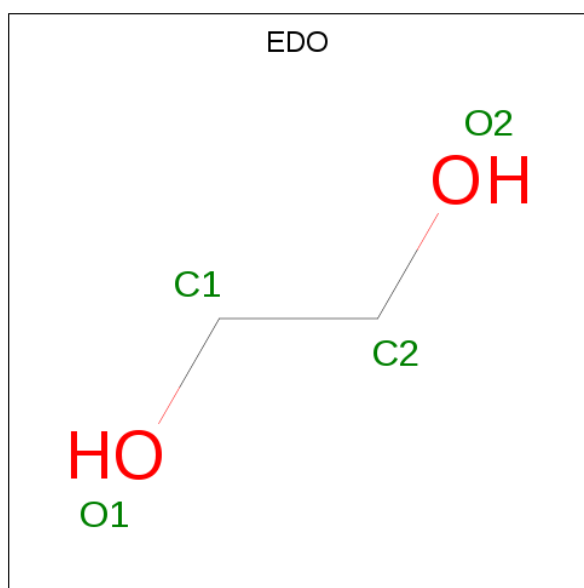
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 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
3	D	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



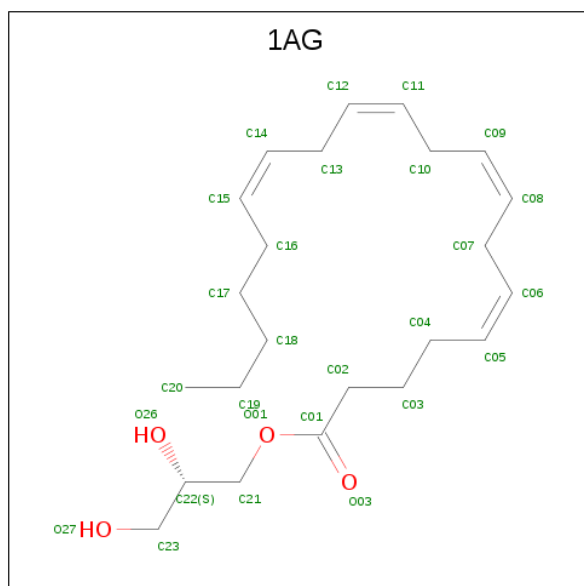
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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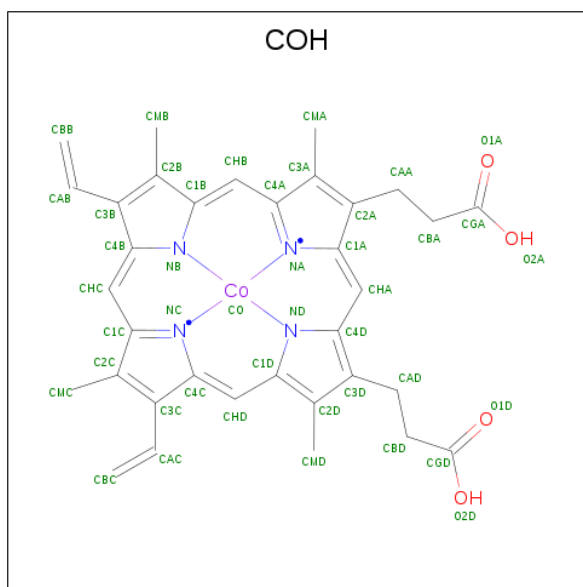
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is (2S)-2,3-dihydroxypropyl (5Z,8Z,11Z,14Z)-icosa-5,8,11,14-tetraenoate (three-letter code: 1AG) (formula: C₂₃H₃₈O₄).



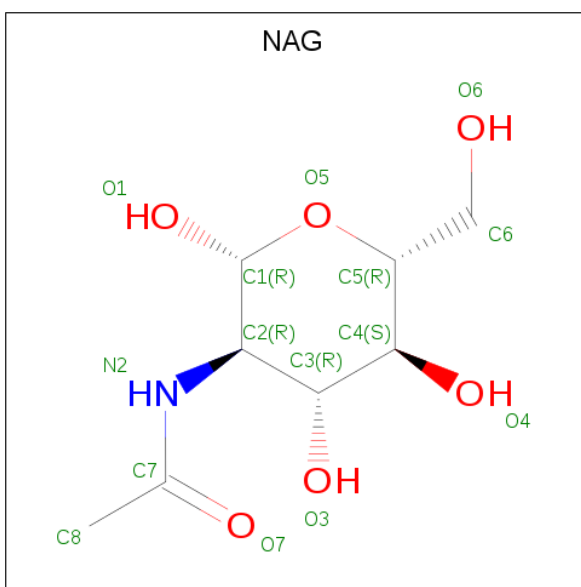
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			27	23	4		
5	B	1	Total	C	O	0	0
			27	23	4		

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING CO (three-letter code: COH) (formula: $C_{34}H_{32}CoN_4O_4$).



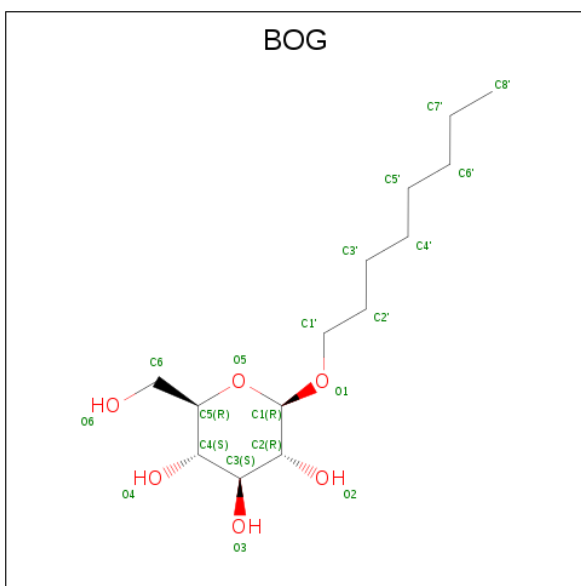
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		
6	B	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 8 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			20	14	6		

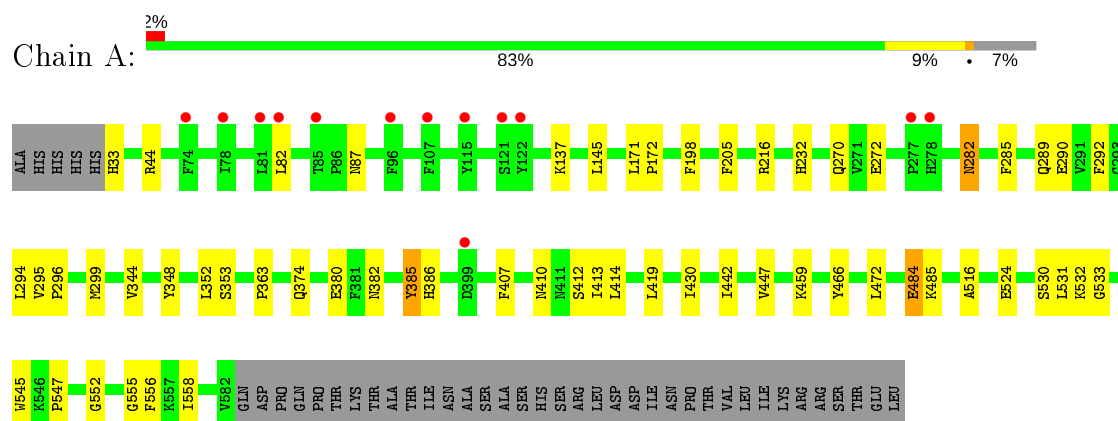
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	335	Total 335	O 335	0	0
9	B	331	Total 331	O 331	0	0

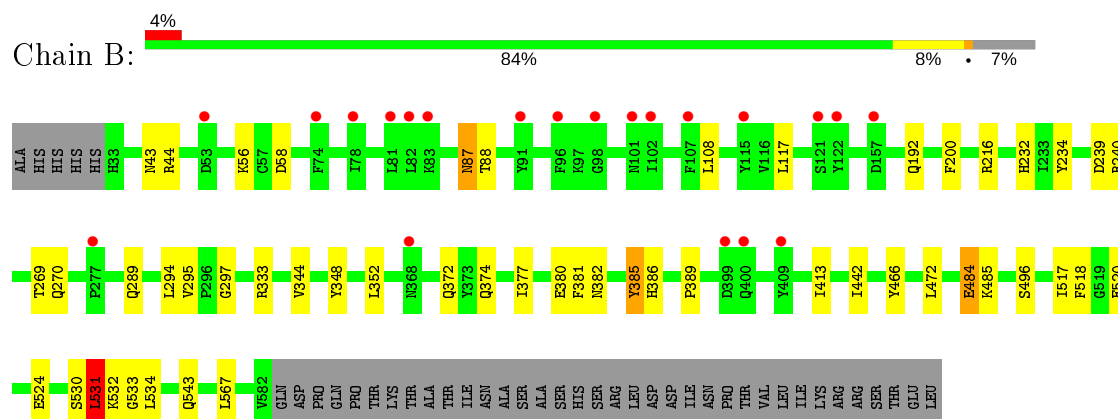
3 Residue-property plots [i](#)

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.

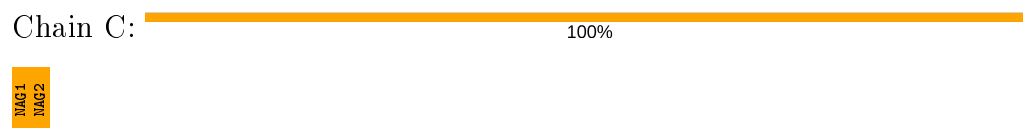
• Molecule 1: Prostaglandin G/H synthase 2



• Molecule 1: Prostaglandin G/H synthase 2



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




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

Chain E:  100%

MAG1
MAG2

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

Chain D:  67% 33%

MAG1
MAG2
MAG3

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

Chain F:  33% 67%

MAG1
MAG2
MAG3

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.31Å 131.75Å 180.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.35 19.99 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.99-2.35) 99.5 (19.99-2.35)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.35Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.162 , 0.214 0.181 , 0.227	Depositor DCC
R_{free} test set	3024 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9951	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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: NAG, EDO, 1AG, COH, MAN, BOG

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	0/4601	0.65	0/6245
1	B	0.60	0/4588	0.66	1/6233 (0.0%)
All	All	0.62	0/9189	0.65	1/12478 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	531	LEU	CA-CB-CG	6.81	130.96	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4462	0	4314	54	0
1	B	4445	0	4267	43	0
2	C	28	0	25	1	0
2	E	28	0	25	0	0
3	D	39	0	34	4	0
3	F	39	0	34	5	0
4	A	28	0	42	4	0
4	B	28	0	42	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	27	0	36	16	0
5	B	27	0	36	10	0
6	A	43	0	30	4	0
6	B	43	0	30	0	0
7	A	14	0	13	2	0
7	B	14	0	13	1	0
8	A	20	0	28	0	0
9	A	335	0	0	6	0
9	B	331	0	0	1	0
All	All	9951	0	8969	109	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 6.

All (109) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:ARG:HG2	3:F:2:NAG:H81	1.35	1.07
1:A:290:GLU:HG3	9:A:22:HOH:O	1.67	0.94
1:B:216:ARG:HH11	3:F:2:NAG:H83	1.32	0.94
1:B:87:ASN:C	1:B:87:ASN:HD22	1.71	0.93
1:A:282:ASN:HB3	9:A:827:HOH:O	1.71	0.90
1:B:216:ARG:NH1	3:F:2:NAG:H83	1.90	0.86
1:A:530[B]:SER:OG	5:A:619:1AG:H10	1.75	0.84
1:B:240:ARG:HH11	4:B:11:EDO:H21	1.41	0.82
1:B:87:ASN:C	1:B:87:ASN:ND2	2.30	0.81
1:A:216:ARG:NH1	3:D:2:NAG:H83	1.96	0.80
1:A:216:ARG:HH11	3:D:2:NAG:H83	1.45	0.79
1:A:385:TYR:OH	5:A:619:1AG:H13	1.86	0.75
1:A:294:LEU:HG	1:A:295:VAL:CG2	2.19	0.73
1:A:530[B]:SER:OG	5:A:619:1AG:H13A	1.89	0.72
5:A:619:1AG:C06	5:A:619:1AG:H10A	2.18	0.72
9:A:667:HOH:O	2:C:2:NAG:H2	1.90	0.71
1:B:56:LYS:HD3	4:B:7:EDO:H22	1.72	0.71
1:A:413:ILE:HG12	7:A:681:NAG:H61	1.73	0.71
1:A:272:GLU:HG3	4:A:14:EDO:H21	1.74	0.70
1:A:531:LEU:HD11	5:A:619:1AG:O27	1.92	0.69
5:B:1:1AG:H11	5:B:1:1AG:H06	1.75	0.69
5:A:619:1AG:O03	5:A:619:1AG:H04	1.94	0.67
1:B:472:LEU:HD22	1:B:520:GLU:OE2	1.95	0.67
1:A:216:ARG:HG2	3:D:2:NAG:H81	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:LEU:HG	1:A:295:VAL:HG22	1.78	0.65
6:A:620:COH:HHB	6:A:620:COH:HBA2	1.78	0.65
1:B:87:ASN:ND2	1:B:87:ASN:O	2.30	0.65
1:A:33:HIS:N	9:A:945:HOH:O	2.29	0.65
1:A:216:ARG:HH11	3:D:2:NAG:C8	2.10	0.64
1:A:353:SER:HA	5:A:619:1AG:H02	1.80	0.61
1:B:87:ASN:HD22	1:B:88:THR:N	1.98	0.61
5:A:619:1AG:O03	5:A:619:1AG:C04	2.48	0.60
1:B:216:ARG:HG2	3:F:2:NAG:C8	2.22	0.60
1:A:530[A]:SER:HB2	5:A:619:1AG:H10	1.84	0.58
1:A:289:GLN:HG2	1:A:292:PHE:CE1	2.38	0.58
1:A:413:ILE:CG1	7:A:681:NAG:H61	2.34	0.58
1:B:413:ILE:HG12	7:B:681:NAG:H61	1.85	0.58
1:B:472:LEU:HD21	1:B:524:GLU:HG3	1.85	0.57
1:B:385:TYR:OH	5:B:1:1AG:H13	2.05	0.57
1:B:240:ARG:NH1	4:B:11:EDO:H21	2.14	0.55
1:A:552:GLY:HA2	4:B:7:EDO:H11	1.89	0.54
1:B:534:LEU:HG	5:B:1:1AG:H17	1.89	0.54
1:A:472:LEU:HD21	1:A:524:GLU:HG3	1.89	0.54
1:A:294:LEU:HG	1:A:295:VAL:HG23	1.90	0.54
1:B:530[B]:SER:OG	5:B:1:1AG:H13A	2.07	0.54
1:B:234:TYR:CE2	1:B:333:ARG:HG3	2.43	0.54
1:A:198:PHE:CZ	1:A:352:LEU:HD21	2.44	0.53
1:B:374:GLN:O	1:B:532:LYS:HE3	2.09	0.53
1:A:374:GLN:O	1:A:532:LYS:HE3	2.10	0.51
5:A:619:1AG:C05	5:A:619:1AG:H10A	2.39	0.51
1:B:58:ASP:HB2	4:B:7:EDO:H21	1.92	0.50
9:B:657:HOH:O	3:F:3:MAN:H4	2.11	0.50
1:B:567:LEU:HA	4:B:8:EDO:H21	1.92	0.50
1:A:447:VAL:HG22	6:A:620:COH:HMA2	1.94	0.49
1:A:171:LEU:HB3	1:A:172:PRO:HD2	1.93	0.49
1:A:198:PHE:HZ	1:A:352:LEU:HD21	1.79	0.48
6:A:620:COH:HBB1	6:A:620:COH:HMB1	1.96	0.48
1:A:484:GLU:HG2	1:A:485:LYS:H	1.78	0.48
1:B:382:ASN:O	1:B:386:HIS:CD2	2.67	0.48
1:A:484:GLU:HG2	1:A:485:LYS:N	2.29	0.47
1:B:372:GLN:HB2	1:B:532:LYS:HZ1	1.80	0.47
1:B:380:GLU:HG2	1:B:466:TYR:CE2	2.50	0.47
1:A:533:GLY:HA3	5:A:619:1AG:H19	1.97	0.47
5:B:1:1AG:H11	5:B:1:1AG:C06	2.45	0.46
1:B:377:ILE:HD11	5:B:1:1AG:H20	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:GLU:HG2	1:A:466:TYR:CE1	2.51	0.46
1:A:410:ASN:OD1	1:A:412:SER:HB2	2.15	0.46
1:A:516:ALA:HB1	4:A:15:EDO:H22	1.98	0.45
1:A:205:PHE:HE2	5:A:619:1AG:C15	2.29	0.45
1:B:192:GLN:OE1	1:B:517:ILE:HG22	2.17	0.45
1:A:530[A]:SER:HA	5:A:619:1AG:H16A	1.98	0.45
1:A:363:PRO:HG2	1:A:545:TRP:CD2	2.52	0.45
1:A:414:LEU:HD11	1:A:419:LEU:HD12	1.98	0.45
5:A:619:1AG:C06	5:A:619:1AG:C10	2.89	0.45
1:A:459[B]:LYS:HE3	4:A:1:EDO:H12	1.98	0.45
1:B:269:THR:O	1:B:270:GLN:HB2	2.17	0.45
1:A:382:ASN:O	1:A:386:HIS:CD2	2.71	0.44
1:B:382:ASN:O	1:B:386:HIS:HD2	2.02	0.43
1:B:117:LEU:HD22	1:B:531:LEU:HD23	2.00	0.43
1:B:43:ASN:O	1:B:44:ARG:HB2	2.18	0.43
1:B:533:GLY:HA3	5:B:1:1AG:H18A	2.01	0.43
1:A:382:ASN:O	1:A:386:HIS:HD2	2.01	0.43
1:B:294:LEU:HG	1:B:295:VAL:HG23	2.01	0.42
1:B:533:GLY:HA3	5:B:1:1AG:C19	2.49	0.42
6:A:620:COH:HMB1	6:A:620:COH:CBB	2.49	0.42
1:A:547:PRO:HB2	4:B:7:EDO:H12	2.02	0.42
1:A:290:GLU:CD	1:A:290:GLU:H	2.22	0.41
1:A:137:LYS:HE2	1:B:543:GLN:O	2.20	0.41
1:B:377:ILE:CD1	5:B:1:1AG:H20	2.51	0.41
1:A:270:GLN:HG2	9:A:874:HOH:O	2.20	0.41
1:A:385:TYR:CZ	5:A:619:1AG:H13	2.55	0.41
1:B:352:LEU:HA	1:B:352:LEU:HD23	1.89	0.41
1:A:555:GLY:HA2	1:A:558:ILE:HD12	2.03	0.41
5:A:619:1AG:O03	5:A:619:1AG:C05	2.68	0.41
1:B:381:PHE:HE2	5:B:1:1AG:H20A	1.85	0.41
1:B:200:PHE:HE1	1:B:295:VAL:HG11	1.85	0.41
1:A:344:VAL:HA	1:A:348:TYR:HB3	2.02	0.41
1:A:459[B]:LYS:NZ	4:A:4:EDO:O1	2.54	0.41
1:B:295:VAL:HG12	1:B:297:GLY:H	1.86	0.41
1:A:484:GLU:HG3	9:A:771:HOH:O	2.20	0.41
1:A:296:PRO:HD2	1:A:407:PHE:CE2	2.56	0.41
1:B:352:LEU:HD22	1:B:518:PHE:CE2	2.56	0.41
1:A:145:LEU:HD12	4:B:9:EDO:H12	2.02	0.40
1:B:344:VAL:HA	1:B:348:TYR:HB3	2.02	0.40
1:A:285:PHE:HD2	1:A:299:MET:HG2	1.87	0.40
1:B:484:GLU:HG2	1:B:485:LYS:H	1.87	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	553/592 (93%)	533 (96%)	20 (4%)	0	100	100
1	B	554/592 (94%)	533 (96%)	21 (4%)	0	100	100
All	All	1107/1184 (94%)	1066 (96%)	41 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	485/530 (92%)	476 (98%)	9 (2%)	57	68
1	B	478/530 (90%)	468 (98%)	10 (2%)	53	65
All	All	963/1060 (91%)	944 (98%)	19 (2%)	55	66

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	82	LEU
1	A	232	HIS
1	A	282	ASN
1	A	385	TYR

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Mol	Chain	Res	Type
1	A	430	ILE
1	A	442	ILE
1	A	484	GLU
1	A	556	PHE
1	B	87	ASN
1	B	108	LEU
1	B	232	HIS
1	B	239	ASP
1	B	289	GLN
1	B	385	TYR
1	B	442	ILE
1	B	484	GLU
1	B	496	SER
1	B	531	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	87	ASN
1	B	581	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 ⓘ

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	1,2	14,14,15	0.98	2 (14%)	17,19,21	2.49	2 (11%)
2	NAG	C	2	2	14,14,15	0.68	0	17,19,21	1.41	2 (11%)
3	NAG	D	1	1,3	14,14,15	1.91	1 (7%)	17,19,21	2.07	3 (17%)
3	NAG	D	2	3	14,14,15	0.68	0	17,19,21	1.43	3 (17%)
3	MAN	D	3	3	11,11,12	0.60	0	15,15,17	1.61	2 (13%)
2	NAG	E	1	1,2	14,14,15	1.71	1 (7%)	17,19,21	1.42	2 (11%)
2	NAG	E	2	2	14,14,15	0.64	0	17,19,21	1.50	2 (11%)
3	NAG	F	1	1,3	14,14,15	0.71	0	17,19,21	0.97	1 (5%)
3	NAG	F	2	3	14,14,15	0.71	0	17,19,21	1.16	1 (5%)
3	MAN	F	3	3	11,11,12	0.86	0	15,15,17	1.12	1 (6%)

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	1,2	2/2/5/7	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	4/6/23/26	0/1/1/1
3	MAN	D	3	3	-	2/2/19/22	1/1/1/1
2	NAG	E	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	E	2	2	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	4/6/23/26	0/1/1/1
3	MAN	F	3	3	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	NAG	O5-C1	-6.59	1.33	1.43
2	E	1	NAG	O5-C1	-6.03	1.34	1.43
2	C	1	NAG	O5-C1	-2.55	1.39	1.43
2	C	1	NAG	C1-C2	2.18	1.55	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C1-O5-C5	9.23	124.70	112.19
3	D	1	NAG	C1-O5-C5	-5.46	104.79	112.19
3	D	1	NAG	O5-C5-C6	5.27	115.46	107.20
2	C	2	NAG	C4-C3-C2	4.78	118.02	111.02
3	D	3	MAN	C1-O5-C5	4.65	118.49	112.19
2	E	2	NAG	C1-O5-C5	4.06	117.69	112.19
2	E	2	NAG	O5-C5-C6	3.39	112.51	107.20
3	D	3	MAN	O5-C5-C6	3.17	112.18	107.20
3	D	2	NAG	O5-C1-C2	-3.15	106.31	111.29
3	F	2	NAG	C4-C3-C2	2.98	115.38	111.02
2	E	1	NAG	C3-C4-C5	2.94	115.49	110.24
2	C	1	NAG	C2-N2-C7	-2.58	119.23	122.90
3	D	2	NAG	C4-C3-C2	2.45	114.61	111.02
3	D	1	NAG	C1-C2-N2	-2.37	106.44	110.49
2	C	2	NAG	C3-C4-C5	2.34	114.42	110.24
3	D	2	NAG	O5-C5-C6	2.26	110.75	107.20
2	E	1	NAG	C1-O5-C5	-2.07	109.39	112.19
3	F	3	MAN	O5-C5-C6	2.04	110.41	107.20
3	F	1	NAG	C2-N2-C7	-2.04	119.99	122.90

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	2	NAG	C1
2	C	1	NAG	C5
2	C	1	NAG	C1

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	2	NAG	C8-C7-N2-C2
3	D	3	MAN	O5-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
3	F	3	MAN	O5-C5-C6-O6
2	E	1	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
2	C	1	NAG	O5-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
3	D	3	MAN	C4-C5-C6-O6
2	E	1	NAG	O7-C7-N2-C2
3	F	2	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	F	2	NAG	O7-C7-N2-C2
3	F	3	MAN	C4-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6

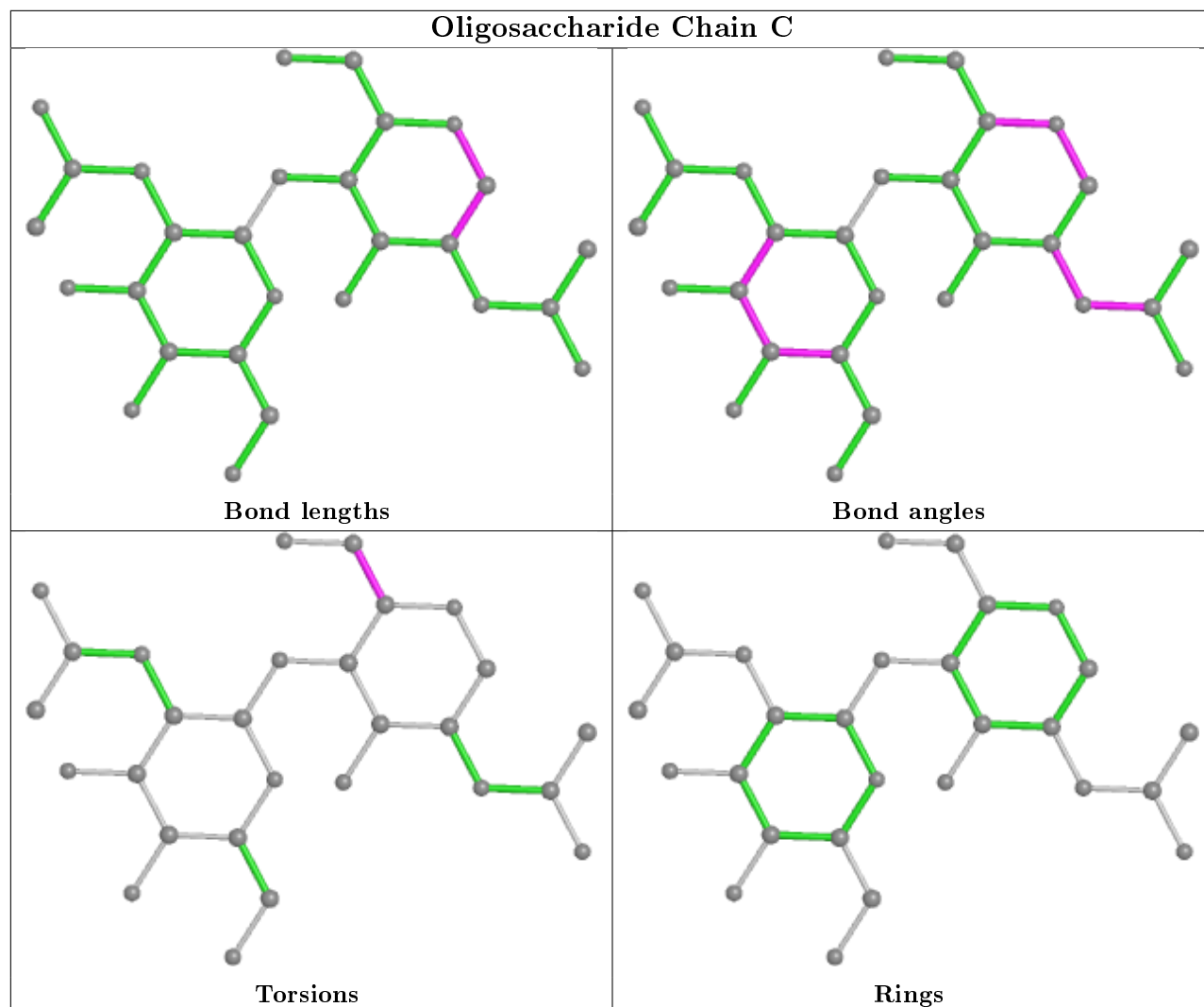
All (1) ring outliers are listed below:

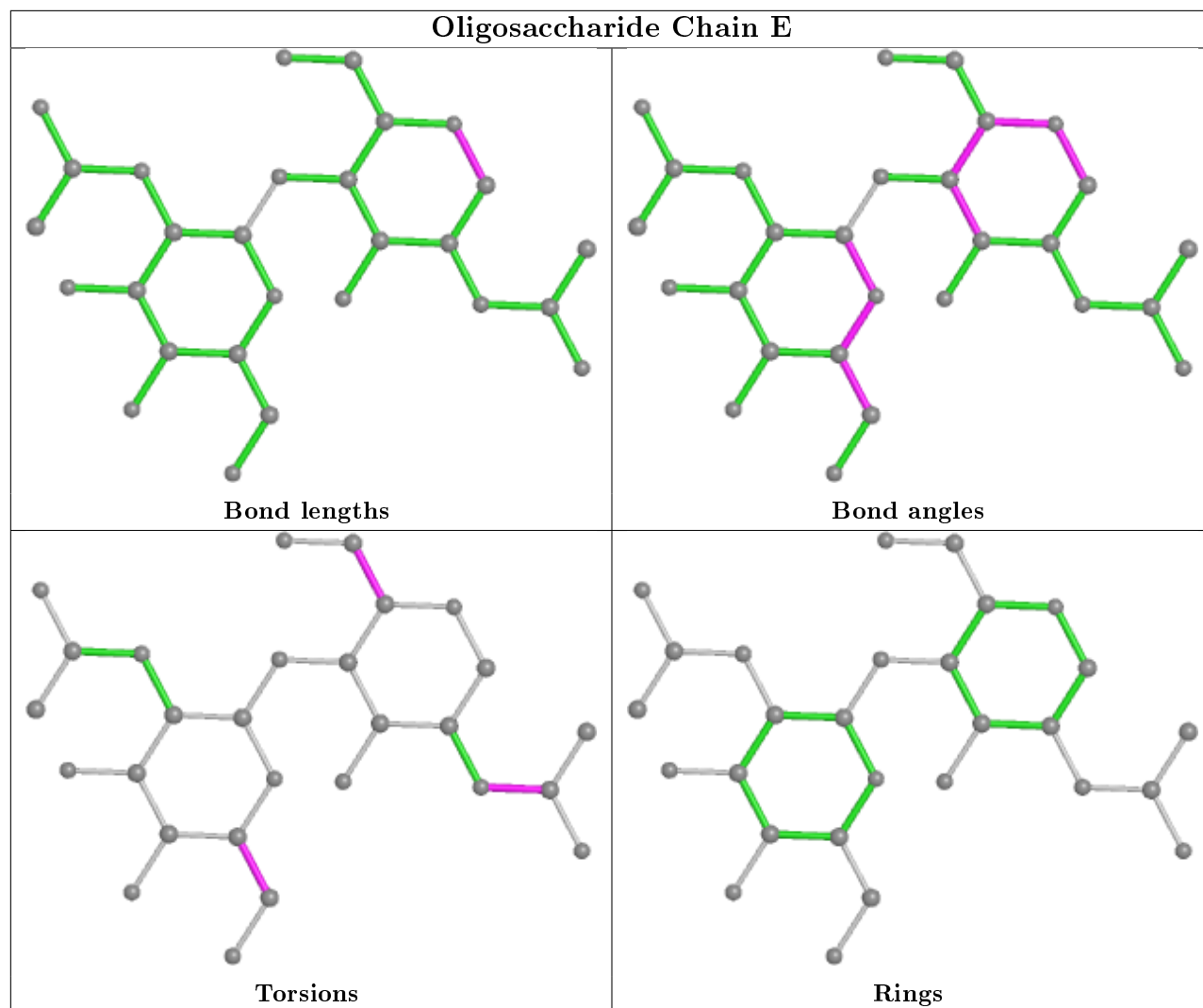
Mol	Chain	Res	Type	Atoms
3	D	3	MAN	C1-C2-C3-C4-C5-O5

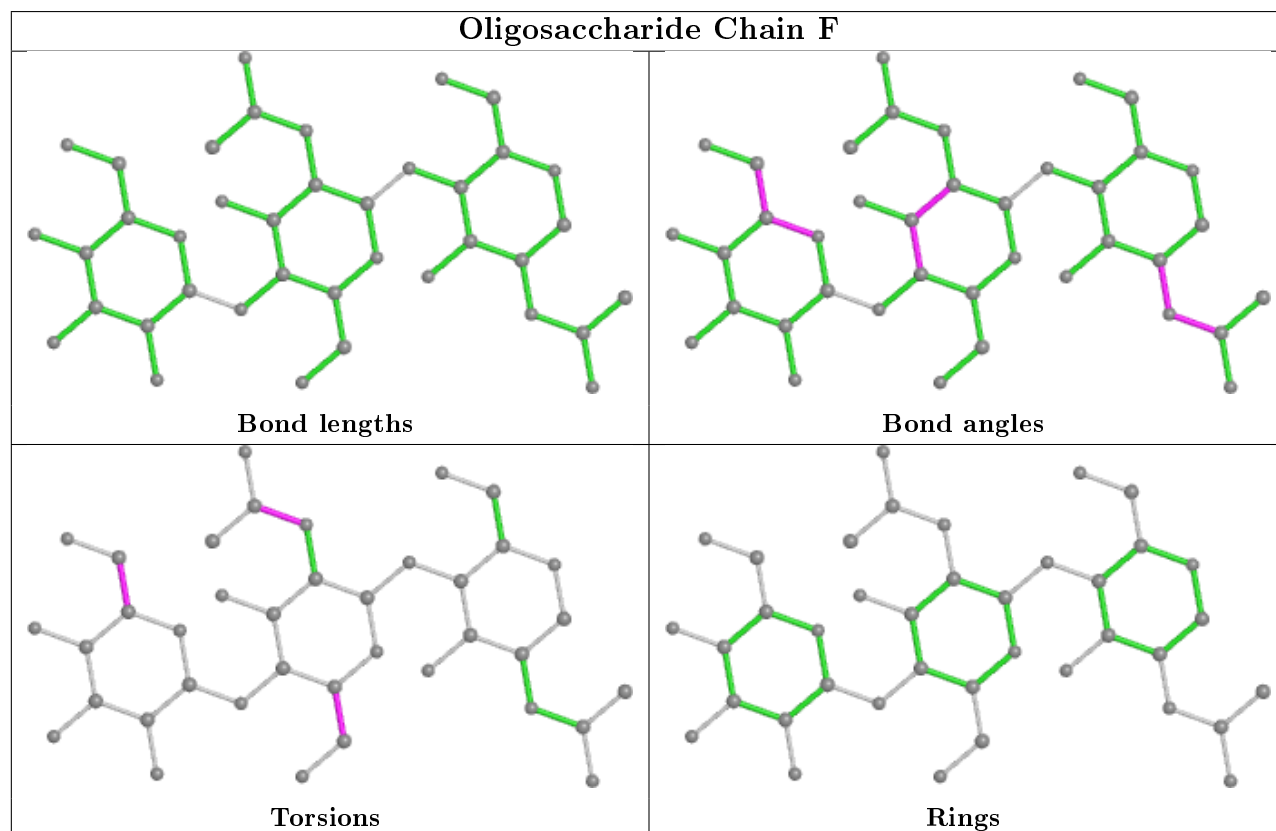
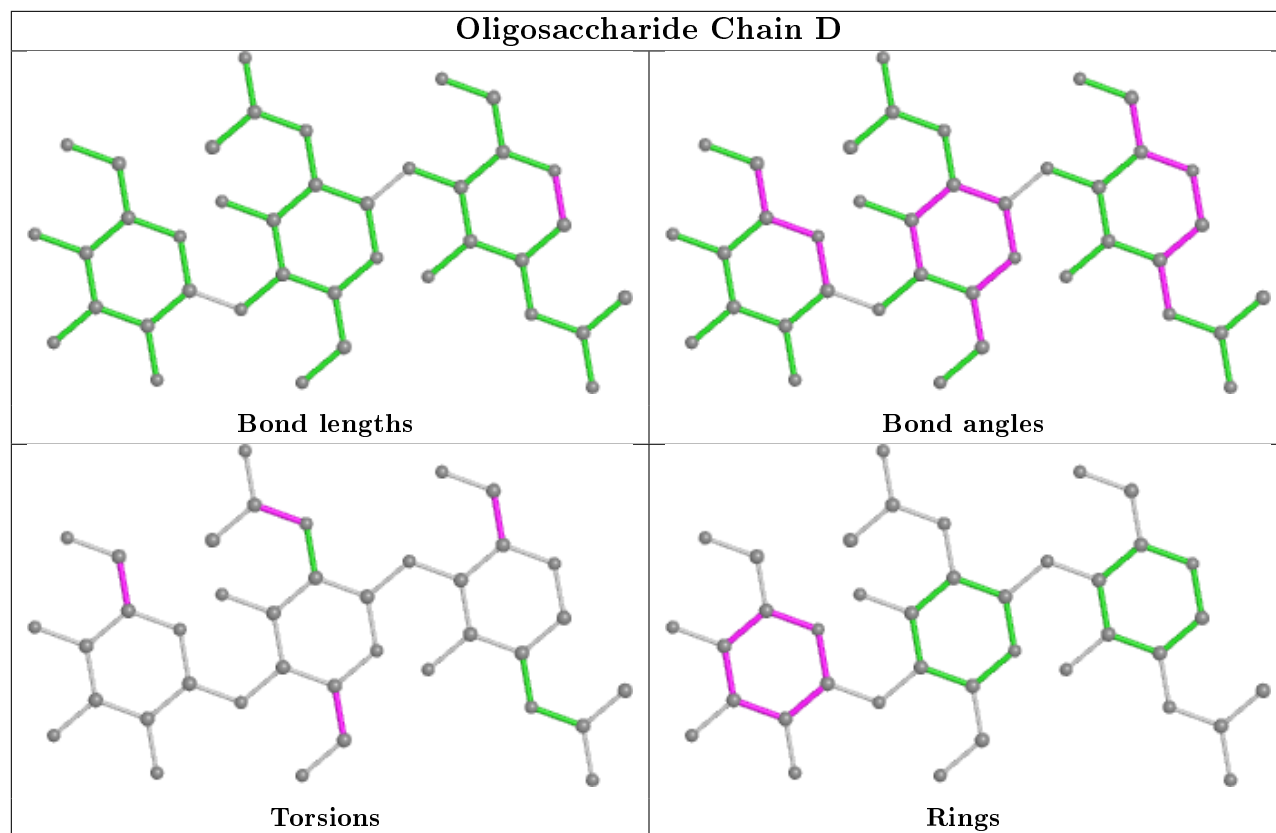
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
3	F	3	MAN	1	0
3	D	2	NAG	4	0
3	F	2	NAG	4	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

21 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	EDO	A	12	-	3,3,3	0.35	0	2,2,2	0.78	0
4	EDO	B	8	-	3,3,3	0.51	0	2,2,2	0.20	0
4	EDO	B	6	-	3,3,3	0.51	0	2,2,2	0.59	0
7	NAG	A	681	1	14,14,15	1.86	1 (7%)	17,19,21	1.99	5 (29%)
5	1AG	B	1	-	26,26,26	2.20	4 (15%)	27,27,27	0.73	0
4	EDO	A	15	-	3,3,3	0.47	0	2,2,2	0.31	0
7	NAG	B	681	1	14,14,15	1.50	1 (7%)	17,19,21	2.20	2 (11%)
4	EDO	A	14	-	3,3,3	0.33	0	2,2,2	1.04	0
4	EDO	B	2	-	3,3,3	0.60	0	2,2,2	0.41	0
4	EDO	B	9	-	3,3,3	0.75	0	2,2,2	0.30	0
5	1AG	A	619	-	26,26,26	2.32	4 (15%)	27,27,27	0.69	0
4	EDO	B	3	-	3,3,3	0.39	0	2,2,2	0.29	0
6	COH	B	619	1	31,50,50	5.45	24 (77%)	23,82,82	4.72	10 (43%)
6	COH	A	620	1	31,50,50	5.08	23 (74%)	23,82,82	4.65	7 (30%)
4	EDO	A	13	-	3,3,3	0.78	0	2,2,2	0.11	0
4	EDO	B	7	-	3,3,3	0.48	0	2,2,2	0.31	0
4	EDO	A	1	-	3,3,3	0.65	0	2,2,2	0.21	0
4	EDO	B	11	-	3,3,3	0.27	0	2,2,2	0.58	0
8	BOG	A	703	-	20,20,20	0.48	0	25,25,25	0.63	0
4	EDO	A	5	-	3,3,3	0.55	0	2,2,2	0.31	0
4	EDO	A	4	-	3,3,3	0.48	0	2,2,2	0.33	0

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	EDO	A	12	-	-	0/1/1/1	-
4	EDO	B	8	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	6	-	-	0/1/1/1	-
7	NAG	A	681	1	-	2/6/23/26	0/1/1/1
5	1AG	B	1	-	-	14/26/26/26	-
4	EDO	A	15	-	-	1/1/1/1	-
7	NAG	B	681	1	-	2/6/23/26	0/1/1/1
4	EDO	A	14	-	-	0/1/1/1	-
4	EDO	B	2	-	-	1/1/1/1	-
4	EDO	B	9	-	-	1/1/1/1	-
5	1AG	A	619	-	-	10/26/26/26	-
4	EDO	B	3	-	-	0/1/1/1	-
6	COH	B	619	1	-	0/8/94/94	-
6	COH	A	620	1	-	0/8/94/94	-
4	EDO	A	13	-	-	0/1/1/1	-
4	EDO	B	7	-	-	1/1/1/1	-
4	EDO	A	1	-	-	1/1/1/1	-
4	EDO	B	11	-	-	1/1/1/1	-
8	BOG	A	703	-	-	2/11/31/31	0/1/1/1
4	EDO	A	5	-	-	1/1/1/1	-
4	EDO	A	4	-	-	1/1/1/1	-

All (57) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	619	COH	C4D-ND	10.08	1.39	1.34
6	B	619	COH	CHD-C4C	-9.09	1.37	1.53
6	B	619	COH	CHA-C1A	-9.06	1.37	1.53
6	A	620	COH	CHC-C1C	-9.01	1.37	1.53
6	B	619	COH	CHB-C4A	-8.99	1.37	1.53
6	A	620	COH	C1D-ND	8.91	1.39	1.34
5	A	619	1AG	O01-C21	-8.74	1.25	1.45
6	B	619	COH	C1D-ND	8.65	1.38	1.34
6	A	620	COH	CHD-C4C	-8.40	1.38	1.53
6	A	620	COH	CHB-C4A	-8.37	1.38	1.53
6	B	619	COH	C4B-NB	8.23	1.38	1.34
6	B	619	COH	C1B-NB	8.10	1.38	1.34
5	B	1	1AG	O01-C21	-8.02	1.26	1.45
6	B	619	COH	CHC-C1C	-7.87	1.39	1.53
6	A	620	COH	CHA-C1A	-7.62	1.40	1.53
6	A	620	COH	C4B-NB	6.97	1.38	1.34
6	A	620	COH	C1B-NB	6.71	1.37	1.34
7	A	681	NAG	O5-C1	-6.46	1.33	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	620	COH	C1B-C2B	6.06	1.46	1.38
6	A	620	COH	C4D-ND	5.91	1.37	1.34
6	A	620	COH	C4D-C3D	5.91	1.46	1.38
5	A	619	1AG	O26-C22	-5.91	1.25	1.43
5	B	1	1AG	O26-C22	-5.88	1.25	1.43
6	B	619	COH	C4D-C3D	5.51	1.45	1.38
6	B	619	COH	C1B-C2B	5.51	1.45	1.38
6	B	619	COH	CHD-C1D	-5.45	1.37	1.51
6	B	619	COH	C3D-C2D	5.40	1.53	1.37
6	A	620	COH	C3D-C2D	5.38	1.53	1.37
6	B	619	COH	CHB-C1B	-5.33	1.38	1.51
6	A	620	COH	CHB-C1B	-5.33	1.38	1.51
7	B	681	NAG	O5-C1	-5.24	1.35	1.43
6	A	620	COH	CHC-C4B	-5.20	1.38	1.51
6	A	620	COH	CHD-C1D	-5.12	1.38	1.51
6	B	619	COH	CHC-C4B	-5.05	1.38	1.51
6	B	619	COH	CHA-C4D	-5.05	1.38	1.51
6	A	620	COH	C1D-C2D	4.89	1.44	1.38
6	A	620	COH	C3B-C2B	-4.88	1.33	1.40
6	A	620	COH	CHA-C4D	-4.84	1.39	1.51
6	B	619	COH	C1D-C2D	4.53	1.44	1.38
6	B	619	COH	C3B-C2B	-4.47	1.34	1.40
5	A	619	1AG	O27-C23	-4.06	1.25	1.42
5	B	1	1AG	O27-C23	-3.94	1.25	1.42
6	B	619	COH	C4C-C3C	-3.87	1.45	1.51
6	B	619	COH	CMA-C3A	3.78	1.56	1.50
6	A	620	COH	C3B-CAB	3.56	1.55	1.47
6	A	620	COH	CMA-C3A	3.23	1.55	1.50
6	A	620	COH	CAA-C2A	3.13	1.55	1.51
6	B	619	COH	C3B-CAB	3.06	1.54	1.47
6	B	619	COH	CMC-C2C	2.87	1.55	1.50
6	B	619	COH	CAA-C2A	2.81	1.55	1.51
6	A	620	COH	C4C-C3C	-2.74	1.46	1.51
6	A	620	COH	CMC-C2C	2.48	1.54	1.50
5	A	619	1AG	O01-C01	-2.46	1.26	1.33
5	B	1	1AG	O01-C01	-2.19	1.26	1.33
6	B	619	COH	CMB-C2B	2.03	1.55	1.51
6	B	619	COH	CAD-C3D	2.01	1.55	1.52
6	A	620	COH	CAD-C3D	2.00	1.55	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	620	COH	CHB-C4A-NA	11.49	127.04	110.12
6	A	620	COH	CHC-C1C-NC	11.12	126.48	110.12
6	B	619	COH	CHC-C1C-NC	10.30	125.28	110.12
6	B	619	COH	CHD-C4C-NC	10.24	125.19	110.12
6	A	620	COH	CHA-C1A-NA	9.93	124.74	110.12
6	B	619	COH	CHB-C4A-NA	9.90	124.69	110.12
6	A	620	COH	CHD-C4C-NC	9.78	124.52	110.12
6	B	619	COH	CHA-C1A-NA	9.58	124.22	110.12
6	B	619	COH	CBA-CAA-C2A	-7.50	101.07	114.35
7	B	681	NAG	O5-C5-C6	6.54	117.45	107.20
7	B	681	NAG	C1-O5-C5	-5.63	104.57	112.19
7	A	681	NAG	C1-O5-C5	-5.27	105.06	112.19
6	B	619	COH	CBD-CAD-C3D	-3.96	105.18	112.49
6	A	620	COH	CHC-C4B-C3B	-3.51	124.83	129.55
7	A	681	NAG	O5-C5-C6	3.50	112.69	107.20
6	A	620	COH	CBD-CAD-C3D	-2.92	107.10	112.49
6	B	619	COH	C4B-C3B-C2B	2.83	108.75	104.41
7	A	681	NAG	C1-C2-N2	-2.76	105.77	110.49
6	B	619	COH	CHD-C1D-C2D	-2.36	125.36	129.45
6	B	619	COH	CHB-C1B-C2B	-2.19	125.66	129.45
6	B	619	COH	CMC-C2C-C3C	-2.15	126.07	129.73
6	A	620	COH	C4B-C3B-C2B	2.13	107.68	104.41
7	A	681	NAG	O4-C4-C5	2.08	114.46	109.30
7	A	681	NAG	C2-N2-C7	-2.02	120.03	122.90

There are no chirality outliers.

All (39) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1	1AG	O01-C21-C22-C23
5	A	619	1AG	C06-C07-C08-C09
5	B	1	1AG	O03-C01-O01-C21
5	B	1	1AG	C02-C01-O01-C21
5	A	619	1AG	C02-C01-O01-C21
5	B	1	1AG	O01-C21-C22-O26
7	A	681	NAG	O5-C5-C6-O6
7	B	681	NAG	C4-C5-C6-O6
5	A	619	1AG	C01-C02-C03-C04
5	A	619	1AG	O03-C01-O01-C21
7	A	681	NAG	C4-C5-C6-O6
7	B	681	NAG	O5-C5-C6-O6
4	A	4	EDO	O1-C1-C2-O2
5	B	1	1AG	C02-C03-C04-C05

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Mol	Chain	Res	Type	Atoms
5	B	1	1AG	C16-C17-C18-C19
4	A	15	EDO	O1-C1-C2-O2
4	B	2	EDO	O1-C1-C2-O2
4	B	7	EDO	O1-C1-C2-O2
4	B	11	EDO	O1-C1-C2-O2
8	A	703	BOG	C4'-C5'-C6'-C7'
5	A	619	1AG	C16-C17-C18-C19
5	A	619	1AG	C17-C18-C19-C20
5	B	1	1AG	C09-C10-C11-C12
5	B	1	1AG	C11-C12-C13-C14
5	B	1	1AG	C12-C13-C14-C15
5	A	619	1AG	C11-C12-C13-C14
5	A	619	1AG	C12-C13-C14-C15
4	B	9	EDO	O1-C1-C2-O2
4	A	5	EDO	O1-C1-C2-O2
5	B	1	1AG	C17-C18-C19-C20
5	A	619	1AG	C21-C22-C23-O27
5	A	619	1AG	C14-C15-C16-C17
5	B	1	1AG	C08-C09-C10-C11
4	A	1	EDO	O1-C1-C2-O2
5	B	1	1AG	C15-C16-C17-C18
5	B	1	1AG	C01-C02-C03-C04
5	B	1	1AG	C14-C15-C16-C17
8	A	703	BOG	C3'-C4'-C5'-C6'
4	B	8	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 45 short contacts:

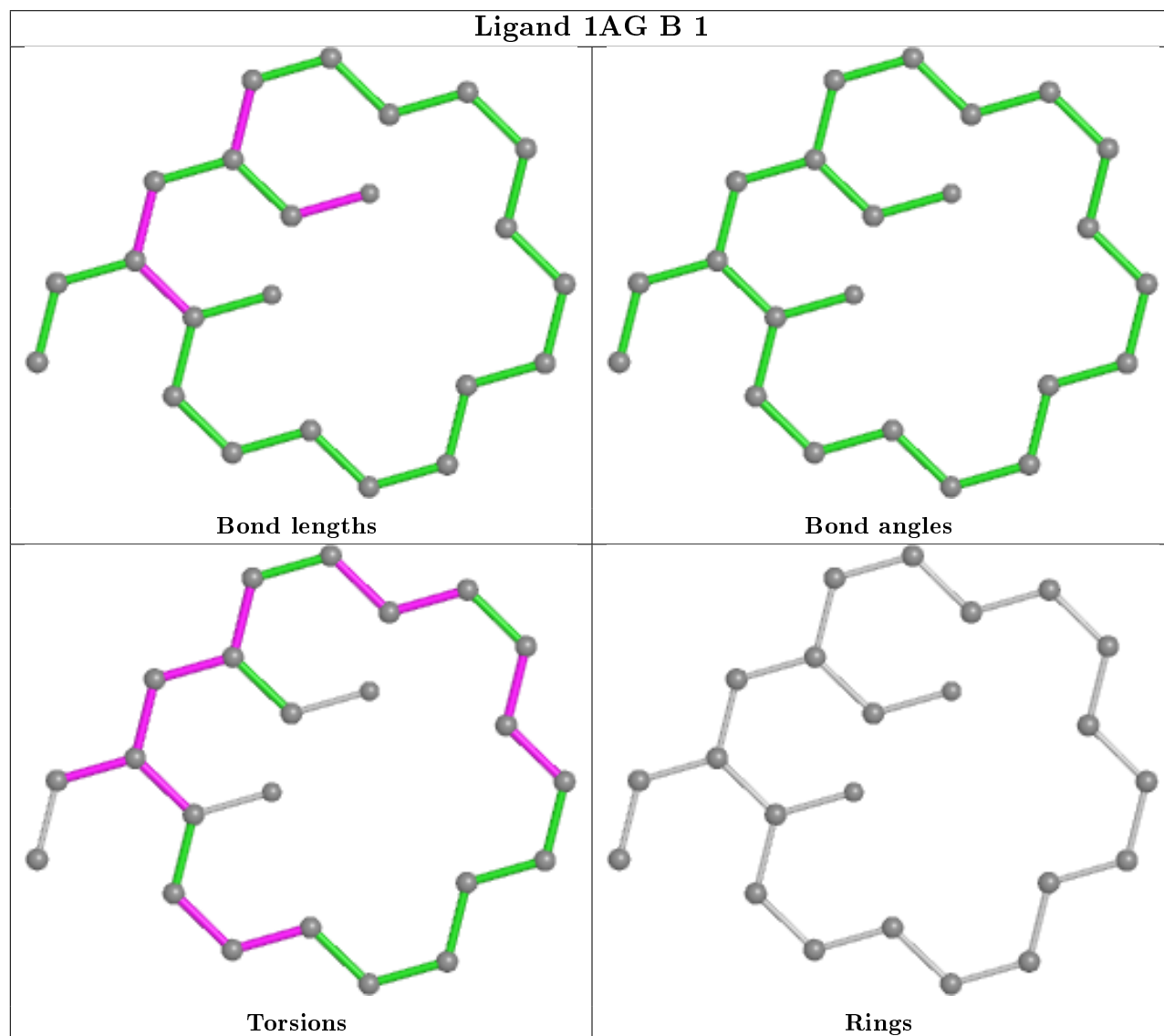
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	8	EDO	1	0
7	A	681	NAG	2	0
5	B	1	1AG	10	0
4	A	15	EDO	1	0
7	B	681	NAG	1	0
4	A	14	EDO	1	0
4	B	9	EDO	1	0
5	A	619	1AG	16	0
6	A	620	COH	4	0
4	B	7	EDO	4	0
4	A	1	EDO	1	0
4	B	11	EDO	2	0

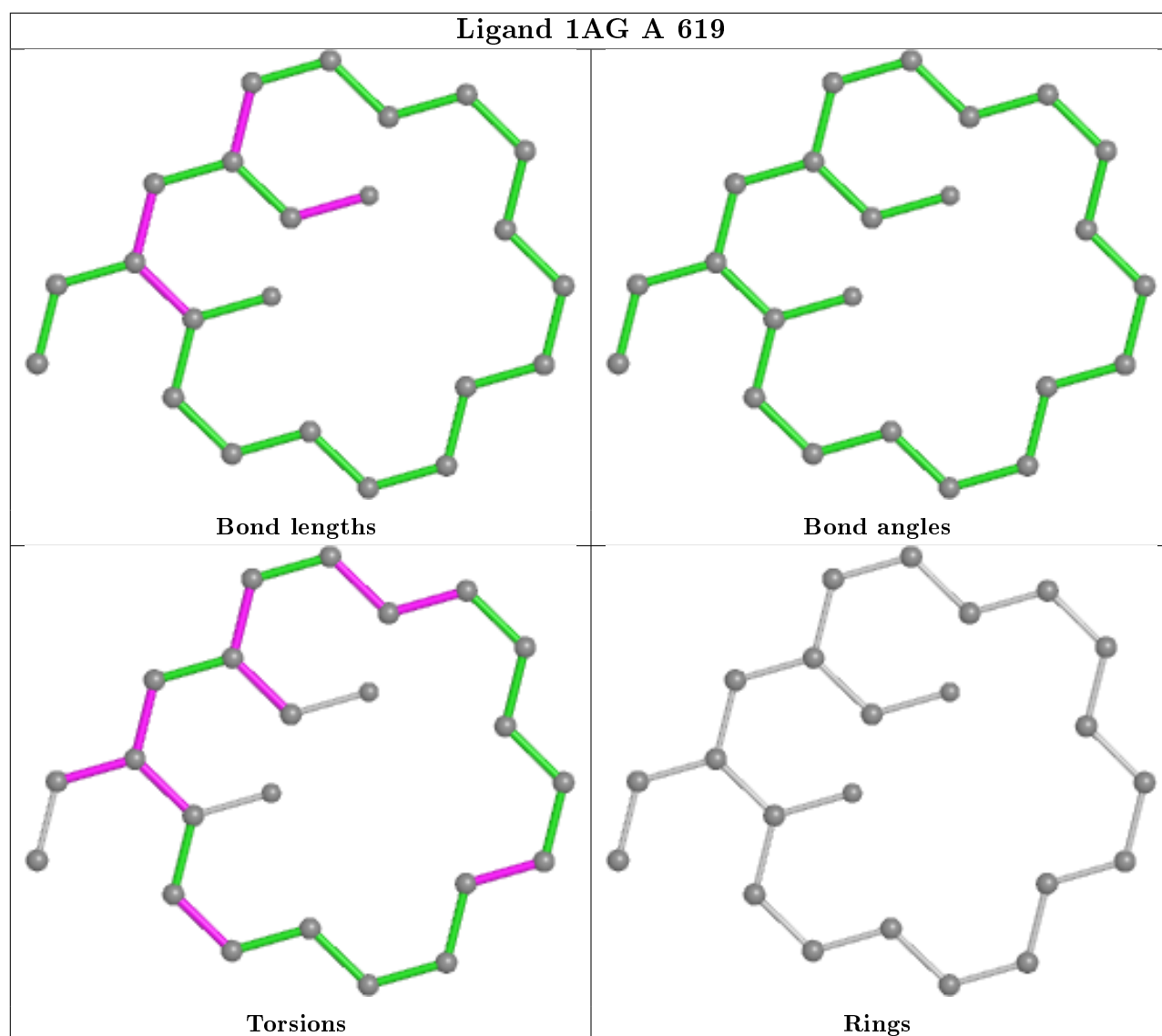
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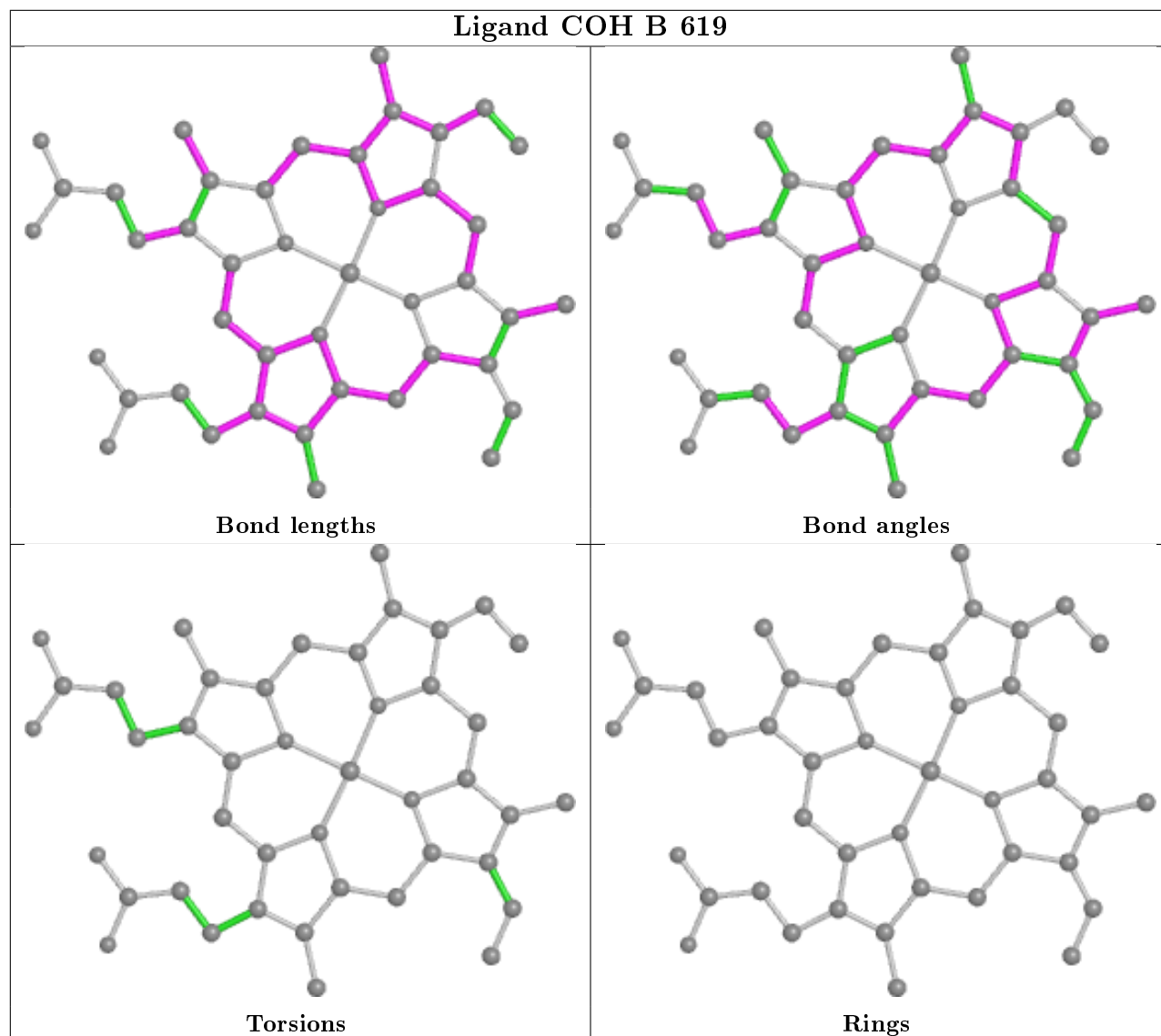
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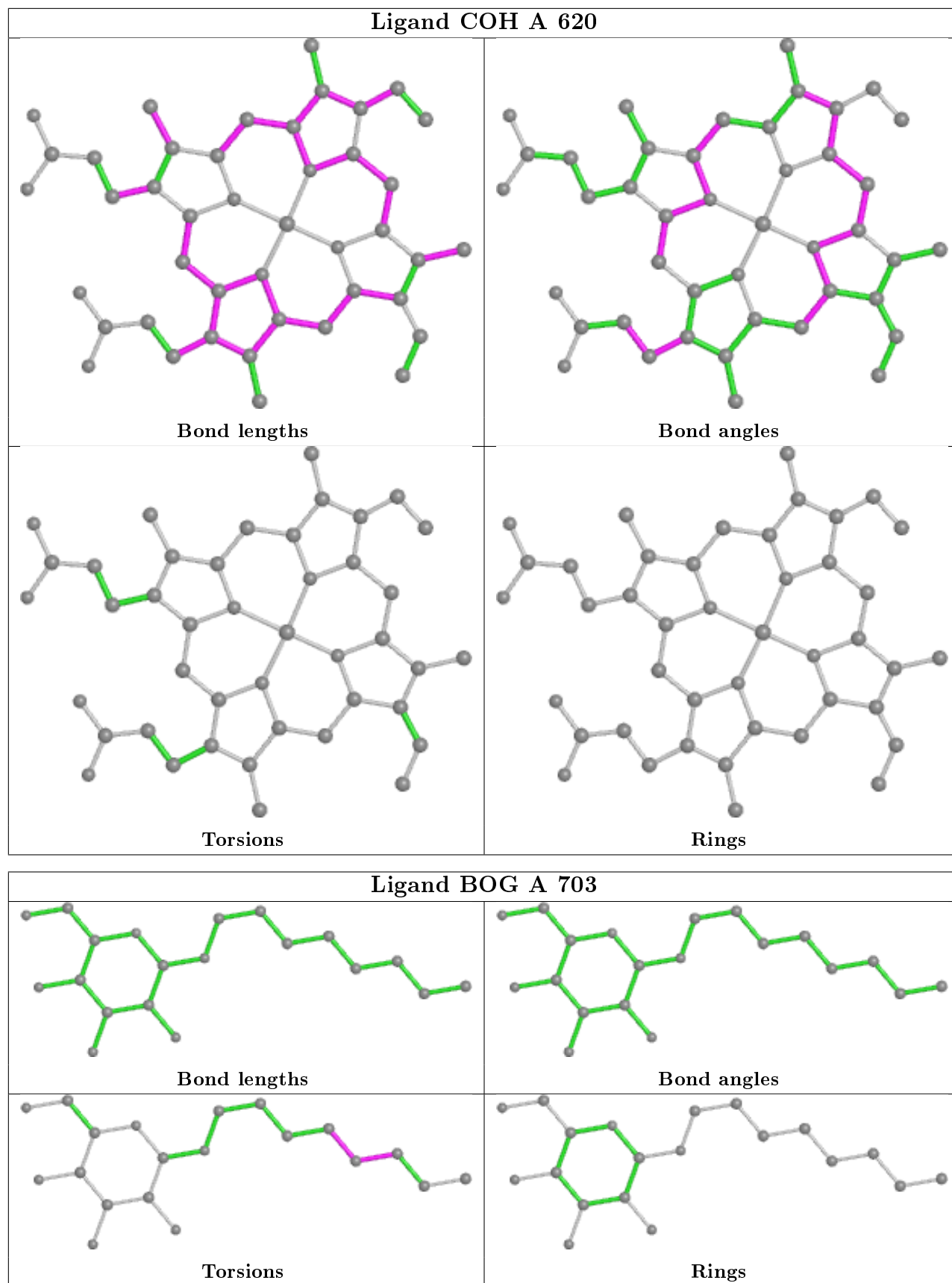
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	4	EDO	1	0

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 [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	551/592 (93%)	-0.21	13 (2%) 59 68	8, 20, 33, 48	0
1	B	551/592 (93%)	-0.12	21 (3%) 40 53	3, 22, 34, 47	0
All	All	1102/1184 (93%)	-0.16	34 (3%) 49 61	3, 21, 34, 48	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	74	PHE	4.7
1	A	81	LEU	4.5
1	B	81[A]	LEU	4.4
1	B	121	SER	4.1
1	B	78	ILE	3.8
1	A	85	THR	3.4
1	B	96	PHE	3.4
1	A	399	ASP	3.4
1	B	101	ASN	3.4
1	A	122	TYR	3.2
1	B	399	ASP	3.1
1	A	82	LEU	3.0
1	B	91	TYR	3.0
1	A	277	PRO	2.9
1	B	277	PRO	2.9
1	B	122	TYR	2.8
1	A	121	SER	2.8
1	B	107	PHE	2.7
1	B	102	ILE	2.7
1	A	107	PHE	2.6
1	A	278	HIS	2.5
1	B	82	LEU	2.5
1	A	96	PHE	2.5
1	B	115	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	157	ASP	2.2
1	A	115	TYR	2.2
1	A	74	PHE	2.2
1	B	409	TYR	2.1
1	B	53	ASP	2.1
1	B	368	ASN	2.1
1	B	83	LYS	2.1
1	B	400	GLN	2.0
1	B	98	GLY	2.0
1	A	78	ILE	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](#)

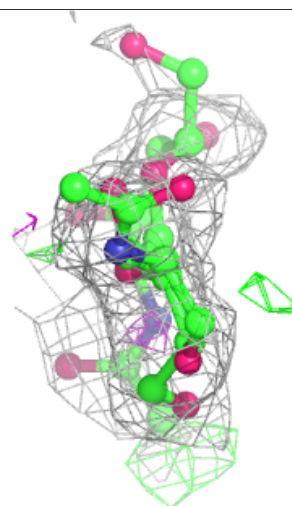
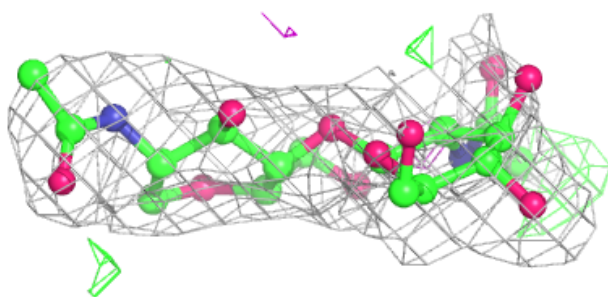
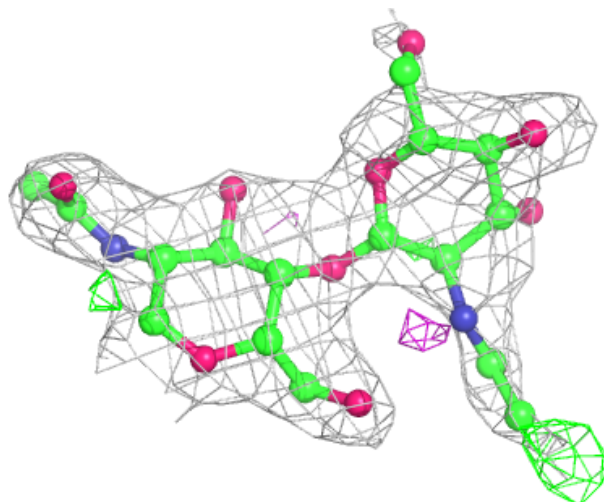
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	F	3	11/12	0.50	0.45	65,70,71,73	0
2	NAG	C	2	14/15	0.70	0.44	64,67,69,69	0
2	NAG	E	2	14/15	0.80	0.36	66,69,69,69	0
2	NAG	E	1	14/15	0.84	0.27	45,53,56,61	0
3	MAN	D	3	11/12	0.85	0.34	58,62,63,64	0
3	NAG	F	2	14/15	0.86	0.22	40,47,53,59	0
2	NAG	C	1	14/15	0.88	0.24	43,49,54,59	0
3	NAG	D	2	14/15	0.91	0.14	34,40,45,53	0
3	NAG	D	1	14/15	0.94	0.12	24,28,30,34	0
3	NAG	F	1	14/15	0.97	0.10	20,24,28,36	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.

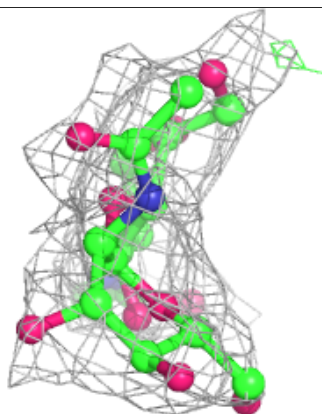
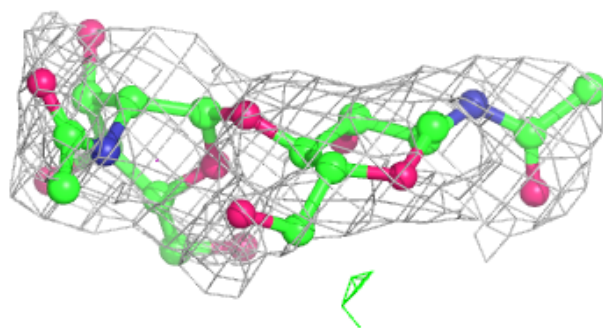
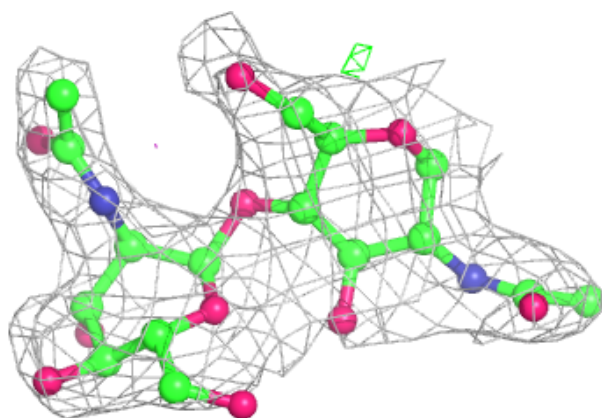
Electron density around Chain C:

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

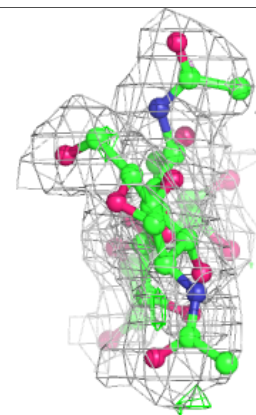
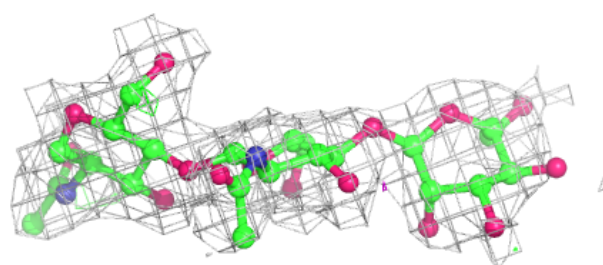
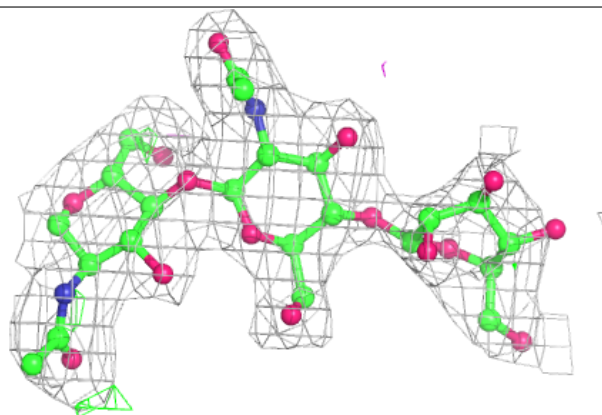


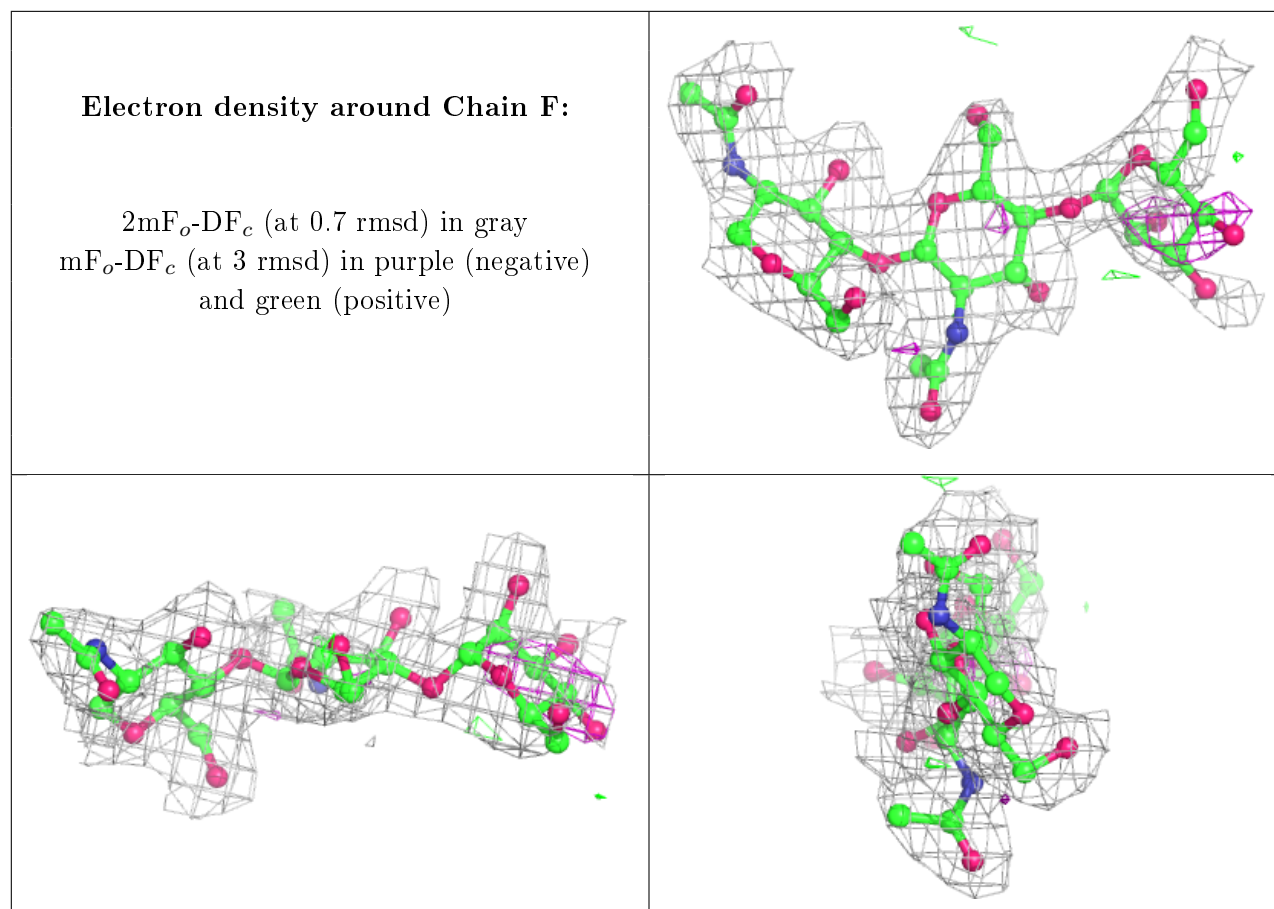
Electron density around Chain E:

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

**Electron density around Chain 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 ⓘ

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.

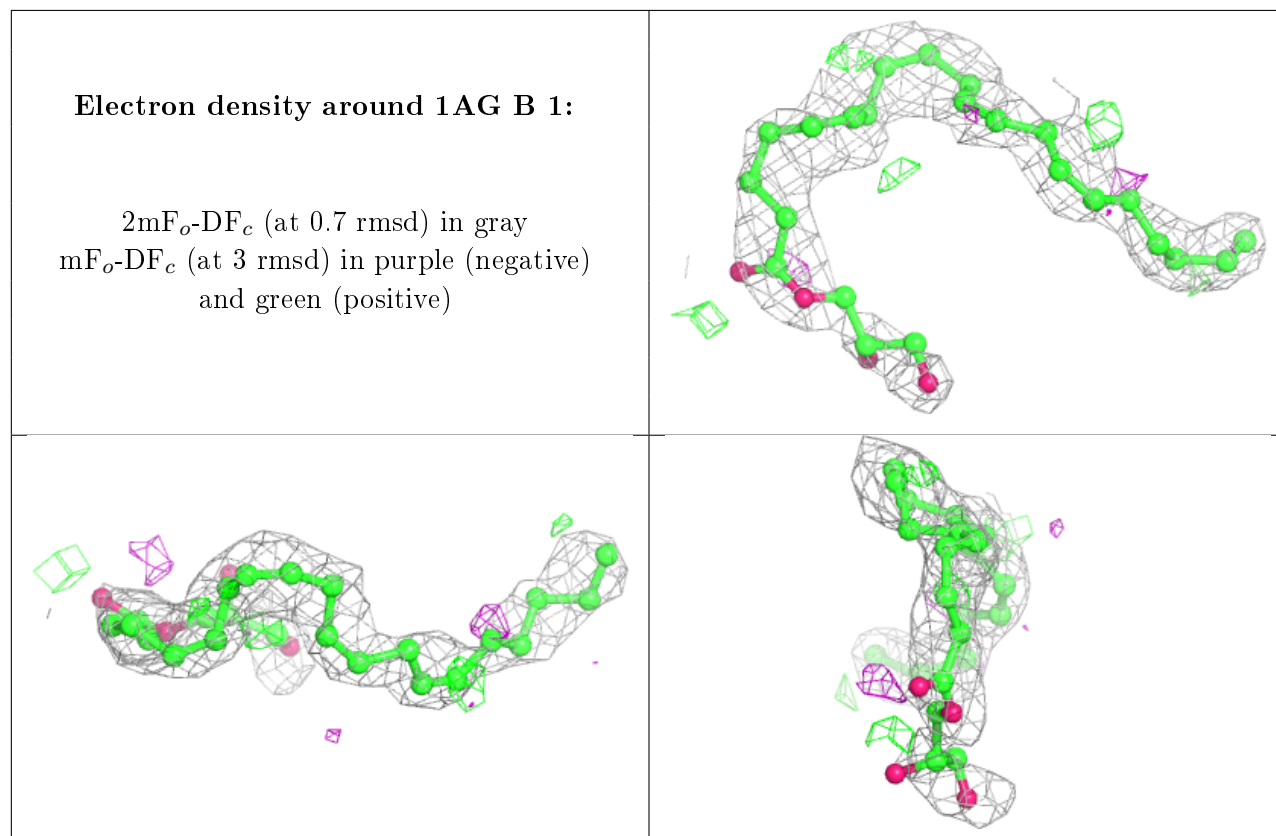
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	A	1	4/4	0.34	0.42	55,57,59,59	0
4	EDO	A	5	4/4	0.61	0.38	77,77,77,77	0
4	EDO	B	9	4/4	0.72	0.27	42,44,46,47	0
5	1AG	B	1	27/27	0.81	0.28	34,51,76,77	0
7	NAG	B	681	14/15	0.82	0.21	44,50,54,55	0
4	EDO	A	14	4/4	0.86	0.21	37,39,41,41	0
7	NAG	A	681	14/15	0.87	0.23	39,44,45,46	0
5	1AG	A	619	27/27	0.88	0.26	42,53,63,65	0
4	EDO	B	2	4/4	0.90	0.27	47,47,47,48	0
4	EDO	A	15	4/4	0.90	0.28	57,58,59,60	0
4	EDO	B	7	4/4	0.92	0.20	59,59,60,61	0
4	EDO	B	11	4/4	0.93	0.22	46,46,46,47	0

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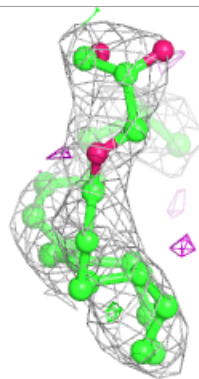
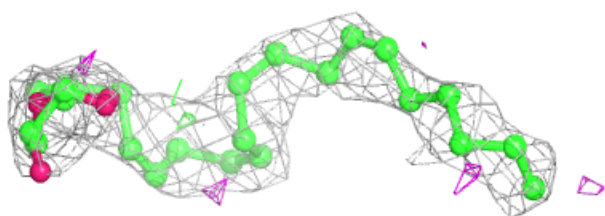
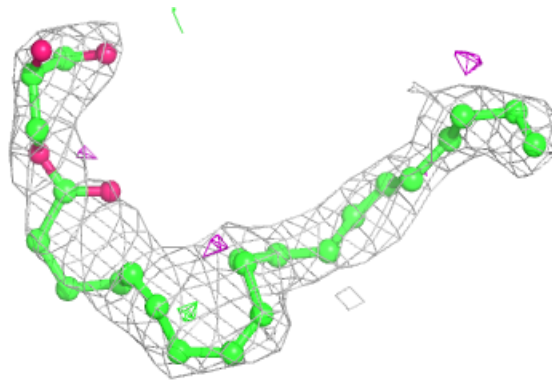
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	COH	B	619	43/43	0.94	0.15	28,34,50,57	0
8	BOG	A	703	20/20	0.95	0.16	26,29,36,36	0
4	EDO	B	3	4/4	0.96	0.13	19,20,21,21	0
4	EDO	B	6	4/4	0.96	0.13	27,29,29,32	0
6	COH	A	620	43/43	0.96	0.13	24,28,50,58	0
4	EDO	B	8	4/4	0.97	0.13	26,27,28,28	0
4	EDO	A	13	4/4	0.97	0.11	19,23,24,25	0
4	EDO	A	4	4/4	0.97	0.14	21,24,25,28	0
4	EDO	A	12	4/4	0.99	0.11	22,23,24,24	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.



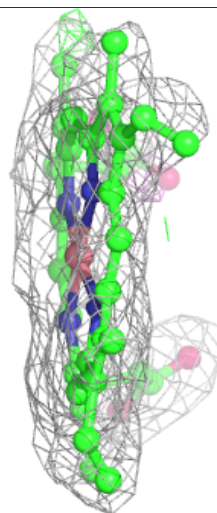
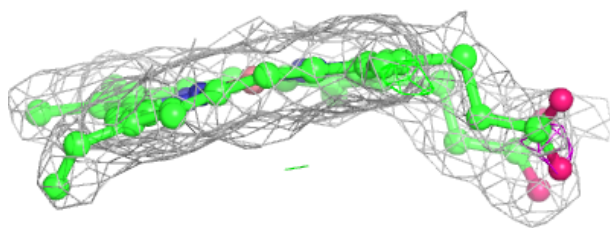
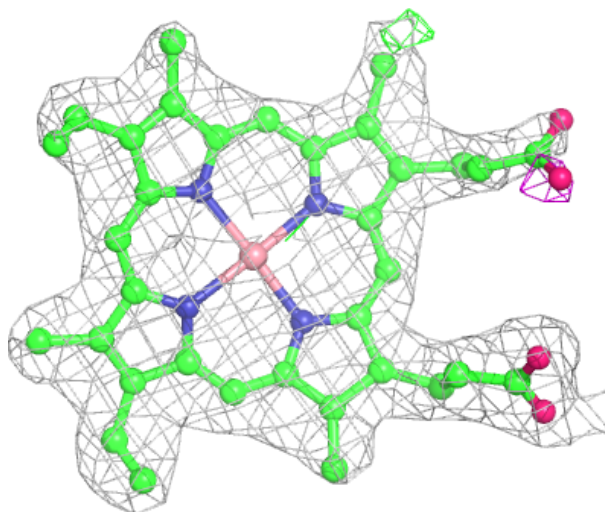
Electron density around 1AG A 619:

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



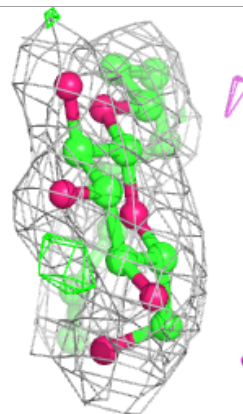
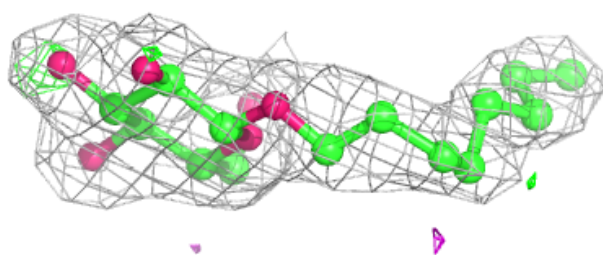
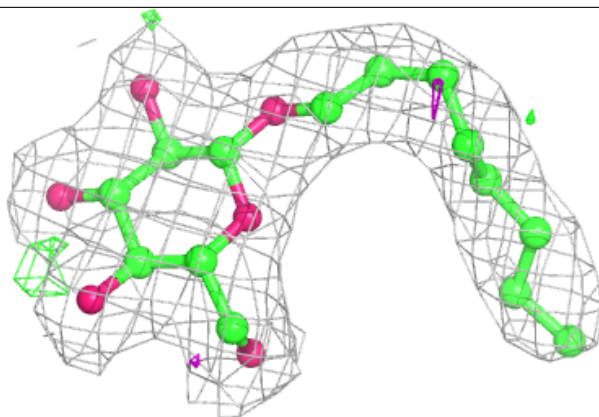
Electron density around COH B 619:

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



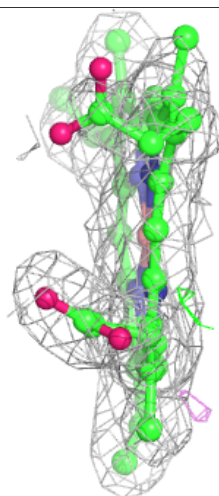
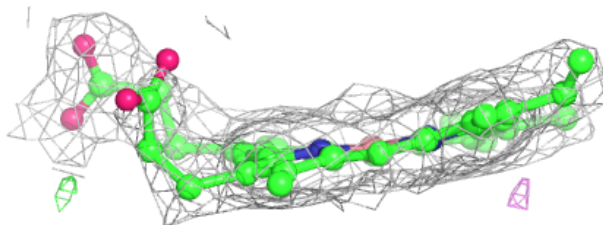
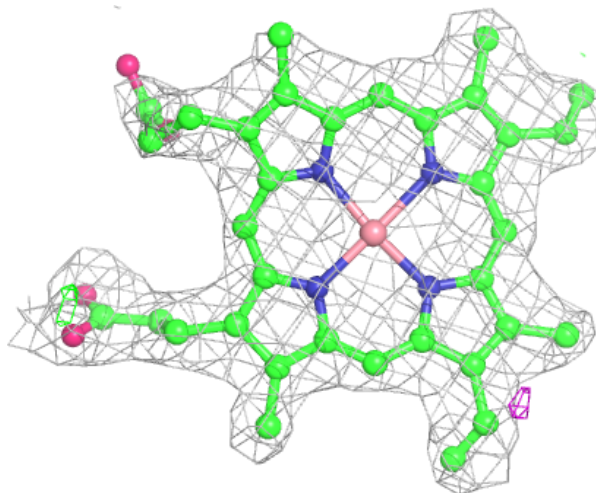
Electron density around BOG A 703:

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



Electron density around COH A 620:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.