



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:30 PM UTC

PDB ID : 3TZI / pdb_00003tzi
Title : X-ray crystal structure of arachidonic acid bound in the cyclooxygenase channel of G533V murine COX-2
Authors : Vecchio, A.J.; Malkowski, M.G.
Deposited on : 2011-09-27
Resolution : 2.15 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

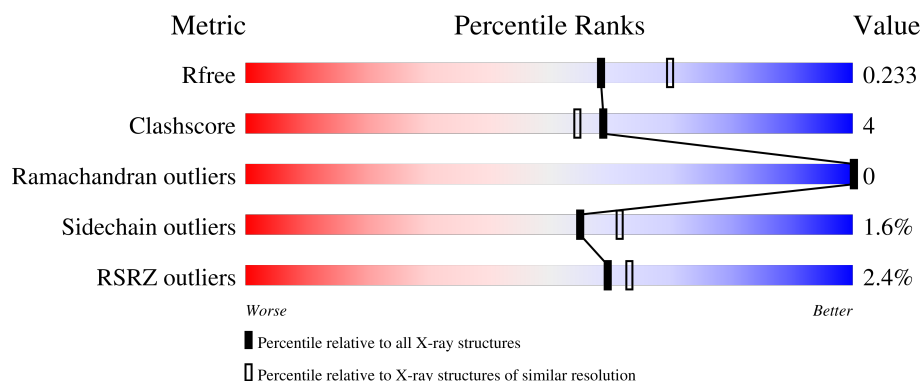
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

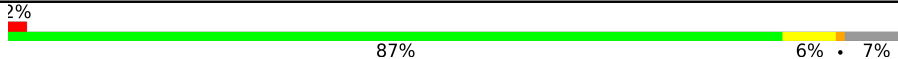
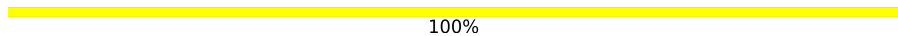
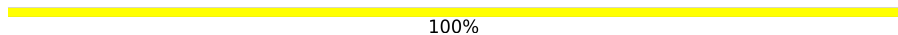
The reported resolution of this entry is 2.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	593	
1	B	593	
2	C	2	
2	E	2	
2	F	2	

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Mol	Chain	Length	Quality of chain
3	D	3	 100%

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	2	X	-	-	-
2	NAG	E	1	X	-	-	-
4	ACD	A	1	-	-	X	-
4	ACD	B	1	-	-	X	-
5	COH	A	619	X	-	-	-
9	AKR	A	9	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 10096 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	5	0
			4468	2886	743	813	26			
1	B	552	Total	C	N	O	S	0	6	0
			4469	2892	743	809	25			

There are 18 discrepancies between the modelled and reference sequences:

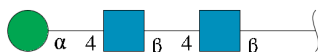
Chain	Residue	Modelled	Actual	Comment	Reference
A	27	ALA	-	expression tag	UNP Q05769
A	29	HIS	-	expression tag	UNP Q05769
A	30	HIS	-	expression tag	UNP Q05769
A	31	HIS	-	expression tag	UNP Q05769
A	32	HIS	-	expression tag	UNP Q05769
A	33	HIS	-	expression tag	UNP Q05769
A	34	HIS	-	expression tag	UNP Q05769
A	533	VAL	GLY	engineered mutation	UNP Q05769
A	594	ALA	ASN	engineered mutation	UNP Q05769
B	27	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	533	VAL	GLY	engineered mutation	UNP Q05769
B	594	ALA	ASN	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.



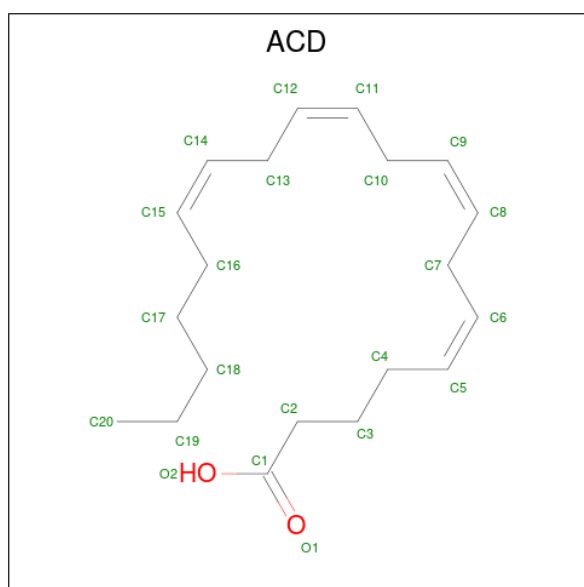
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- 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.



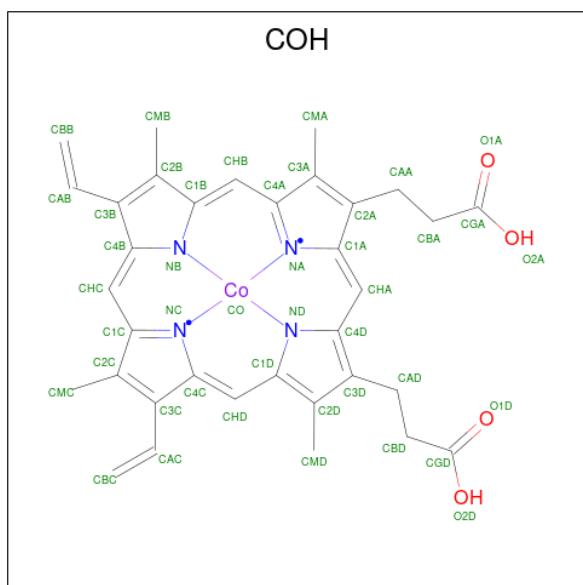
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is ARACHIDONIC ACID (CCD ID: ACD) (formula: C₂₀H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			22	20	2		
4	B	1	Total	C	O	0	0
			22	20	2		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING CO (CCD ID: COH) (formula: $C_{34}H_{32}CoN_4O_4$).



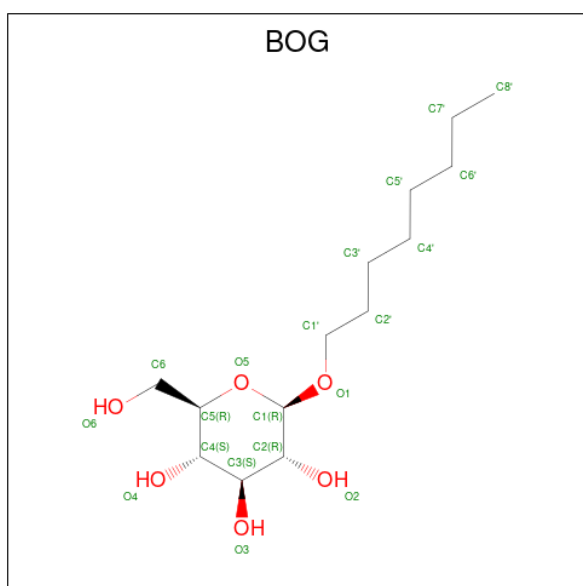
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



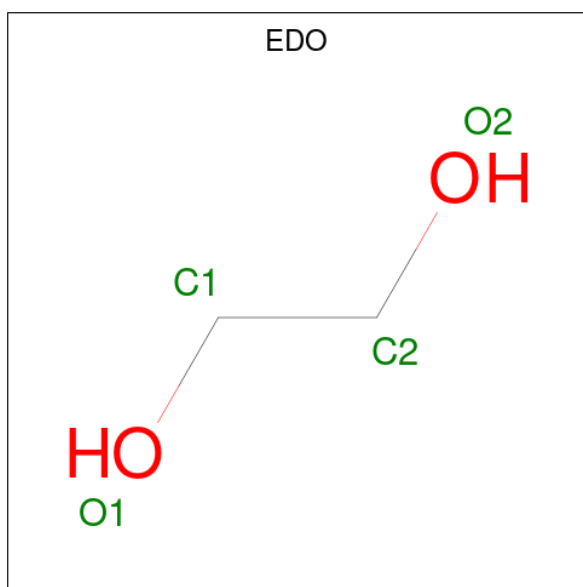
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: $C_{14}H_{28}O_6$).



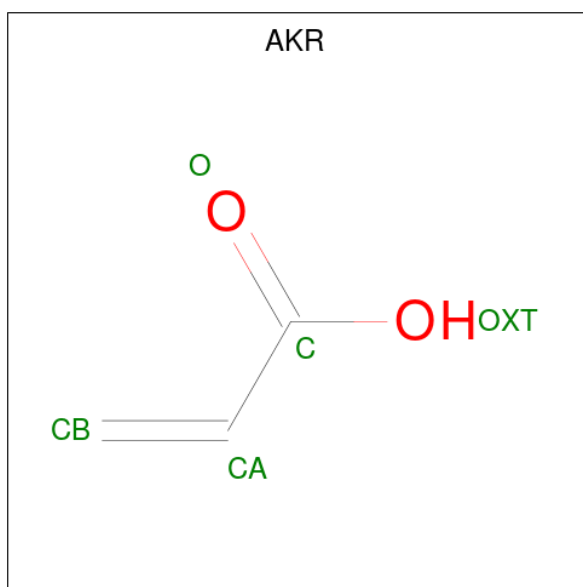
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			20	14	6		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 9 is ACRYLIC ACID (CCD ID: AKR) (formula: $C_3H_4O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			5	3	2		
9	A	1	Total	C	O	0	0
			5	3	2		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	401	Total	O	0	0
			401	401		
10	B	415	Total	O	0	0
			415	415		

MAG1
MAG2

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

Chain F:  50% 50%

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:  100%

MAG1
MAG2
MAN3

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	122.27Å 133.51Å 181.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.15 19.99 – 2.15	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.99-2.15) 99.8 (19.99-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 2.15Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.170 , 0.210 0.203 , 0.233	Depositor DCC
R_{free} test set	4039 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.1	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	0.95	EDS
Total number of atoms	10096	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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: BOG, AKR, MAN, NAG, COH, ACD, EDO

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	0.62	2/4610 (0.0%)	0.84	5/6260 (0.1%)
1	B	0.62	2/4616 (0.0%)	0.84	7/6272 (0.1%)
All	All	0.62	4/9226 (0.0%)	0.84	12/12532 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	318	GLN	CD-OE1	5.65	1.34	1.23
1	A	207	HIS	ND1-CE1	5.48	1.38	1.32
1	A	214	HIS	ND1-CE1	5.46	1.38	1.32
1	B	214	HIS	ND1-CE1	5.31	1.37	1.32

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	HIS	CB-CG-CD2	-6.54	122.70	131.20
1	B	214	HIS	CB-CG-CD2	-6.53	122.71	131.20
1	A	214	HIS	CB-CG-CD2	-6.53	122.71	131.20
1	A	121	SER	N-CA-C	6.12	118.74	111.33
1	B	121	SER	N-CA-C	5.65	117.92	111.02
1	B	504[A]	TYR	CA-C-N	-5.62	113.23	119.19
1	B	504[A]	TYR	C-N-CA	-5.62	113.23	119.19
1	B	504[B]	TYR	CA-C-N	-5.62	113.23	119.19
1	B	504[B]	TYR	C-N-CA	-5.62	113.23	119.19
1	A	207	HIS	CB-CG-ND1	5.61	131.12	122.70
1	B	214	HIS	CB-CG-ND1	5.58	131.07	122.70
1	A	214	HIS	CB-CG-ND1	5.58	131.06	122.70

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	4468	0	4308	33	0
1	B	4469	0	4286	33	0
2	C	28	0	25	0	0
2	E	28	0	25	0	0
2	F	28	0	25	3	0
3	D	39	0	34	4	0
4	A	22	0	31	11	0
4	B	22	0	31	10	0
5	A	43	0	30	0	0
5	B	43	0	30	1	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
7	A	20	0	28	1	0
8	A	8	0	12	1	0
8	B	24	0	36	1	0
9	A	10	0	6	4	0
10	A	401	0	0	4	0
10	B	415	0	0	4	0
All	All	10096	0	8933	80	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 4.

All (80) 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	2:F:2:NAG:H81	1.53	0.90
1:A:530:SER:OG	4:A:1:ACD:H192	1.73	0.89
1:B:161:THR:HG21	1:B:166:LYS:O	1.78	0.81
1:A:161:THR:HG21	1:A:166:LYS:O	1.80	0.81
1:B:530:SER:OG	4:B:1:ACD:H182	1.82	0.80
4:B:1:ACD:H11	4:B:1:ACD:H71	1.65	0.78
1:A:492:LYS:HD2	9:A:9:AKR:HA1	1.67	0.76
1:A:216:ARG:HH11	3:D:2:NAG:H83	1.50	0.74
1:B:484:GLU:HG2	1:B:485:LYS:H	1.53	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:SER:HB2	9:A:9:AKR:HB2	1.75	0.69
1:A:216:ARG:NH1	3:D:2:NAG:H83	2.08	0.69
1:B:385:TYR:OH	4:B:1:ACD:H181	1.96	0.65
1:B:263:PRO:HG2	1:B:299:MET:HE1	1.79	0.64
1:B:484:GLU:HG2	1:B:485:LYS:N	2.13	0.63
4:A:1:ACD:H72	4:A:1:ACD:H11	1.81	0.62
1:B:274:ILE:HD12	1:B:291:VAL:HG12	1.81	0.62
1:B:285[B]:PHE:HD2	1:B:299:MET:HE2	1.66	0.61
1:B:216:ARG:HH11	2:F:2:NAG:H83	1.64	0.60
4:B:1:ACD:H71	4:B:1:ACD:C11	2.32	0.60
1:A:216:ARG:HG2	3:D:2:NAG:H81	1.85	0.58
1:B:161:THR:HG23	10:B:627:HOH:O	2.03	0.58
1:B:472:LEU:HD21	1:B:524:GLU:HG3	1.85	0.58
1:B:285[B]:PHE:CD2	1:B:299:MET:HE2	2.38	0.58
4:B:1:ACD:C12	4:B:1:ACD:H162	2.34	0.57
1:B:414:LEU:HD11	1:B:419:LEU:HD12	1.86	0.56
4:B:1:ACD:C11	4:B:1:ACD:H162	2.36	0.55
4:A:1:ACD:C12	4:A:1:ACD:H162	2.38	0.54
4:B:1:ACD:C12	4:B:1:ACD:C16	2.86	0.53
1:A:349:VAL:HG13	4:A:1:ACD:H101	1.89	0.53
1:A:456:ARG:HA	8:A:2:EDO:H12	1.91	0.53
1:B:355:TYR:OH	4:B:1:ACD:H6	2.08	0.53
1:B:294:LEU:HD22	1:B:409:TYR:CD2	2.44	0.52
4:A:1:ACD:H72	4:A:1:ACD:C11	2.38	0.50
1:B:483:GLY:HA3	1:B:511:LYS:HD3	1.94	0.50
1:A:385:TYR:CE1	4:A:1:ACD:H191	2.46	0.50
5:B:619:COH:HHD	5:B:619:COH:HBC1	1.93	0.50
1:A:222:ARG:NH1	10:A:974:HOH:O	2.45	0.49
1:A:294:LEU:HG	1:A:295:VAL:CG2	2.42	0.49
1:A:161:THR:CG2	1:A:166:LYS:O	2.58	0.49
1:A:294:LEU:HG	1:A:295:VAL:HG23	1.96	0.48
1:B:161:THR:HG22	1:B:164:GLY:H	1.78	0.47
1:A:289:GLN:OE1	1:A:291:VAL:HG22	2.14	0.47
1:B:216:ARG:NH1	2:F:2:NAG:H83	2.29	0.47
1:B:364:GLU:HB3	10:B:1008:HOH:O	2.15	0.47
1:B:344:VAL:HA	1:B:348:TYR:HB3	1.96	0.46
1:B:108:LEU:O	1:B:112:ILE:HG12	2.15	0.46
1:B:294:LEU:HD22	1:B:409:TYR:HD2	1.80	0.46
1:B:234:TYR:CE2	1:B:333:ARG:HG3	2.51	0.45
1:A:477:SER:CB	9:A:9:AKR:HB2	2.45	0.45
1:A:385:TYR:HE1	4:A:1:ACD:H191	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:10:AKR:HB2	10:A:929:HOH:O	2.17	0.45
1:A:213:ASP:OD1	1:A:215:LYS:HG2	2.17	0.45
1:A:385:TYR:OH	4:A:1:ACD:H191	2.18	0.44
1:B:161:THR:CG2	1:B:166:LYS:O	2.59	0.44
4:A:1:ACD:C12	4:A:1:ACD:C16	2.96	0.44
1:A:216:ARG:HH11	3:D:2:NAG:C8	2.23	0.44
1:A:179:GLU:HB3	7:A:703:BOG:H3'2	2.01	0.43
1:B:386:HIS:HB2	1:B:504[A]:TYR:CE1	2.53	0.43
1:B:484:GLU:CG	1:B:485:LYS:N	2.81	0.43
4:A:1:ACD:H162	4:A:1:ACD:H12	2.00	0.43
1:B:532:LYS:HD2	1:B:532:LYS:HA	1.89	0.43
1:A:161:THR:HG22	1:A:164:GLY:N	2.34	0.43
1:A:364:GLU:HB3	10:A:959:HOH:O	2.18	0.43
1:A:382:ASN:O	1:A:386:HIS:HD2	2.02	0.43
1:B:161:THR:HG22	1:B:164:GLY:N	2.34	0.43
4:B:1:ACD:H102	4:B:1:ACD:H131	1.83	0.43
1:A:360:LYS:HE2	1:A:362:ASP:HB2	2.01	0.42
1:B:385:TYR:CE1	4:B:1:ACD:H181	2.54	0.42
1:B:557:LYS:HE2	10:B:943:HOH:O	2.19	0.42
1:A:263:PRO:HG2	1:A:299[B]:MET:HE1	2.01	0.42
1:A:398:GLU:HB3	1:A:399:ASP:H	1.65	0.42
1:A:532:LYS:HD2	1:A:532:LYS:HA	1.81	0.41
1:A:161:THR:HG22	1:A:164:GLY:H	1.85	0.41
8:B:7:EDO:H21	10:B:901:HOH:O	2.20	0.41
1:A:279:ILE:HG22	1:A:284:GLN:HG3	2.03	0.41
1:A:382:ASN:O	1:A:386:HIS:CD2	2.72	0.41
1:A:161:THR:HG23	10:A:25:HOH:O	2.20	0.41
1:B:34:HIS:HA	1:B:35:PRO:HD3	1.97	0.41
1:B:352:LEU:HD23	1:B:352:LEU:HA	1.90	0.41
1:A:530:SER:HG	4:A:1:ACD:H192	1.80	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	554/593 (93%)	541 (98%)	13 (2%)	0	100	100
1	B	556/593 (94%)	544 (98%)	12 (2%)	0	100	100
All	All	1110/1186 (94%)	1085 (98%)	25 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	485/531 (91%)	477 (98%)	8 (2%)	55	61
1	B	480/531 (90%)	473 (98%)	7 (2%)	57	64
All	All	965/1062 (91%)	950 (98%)	15 (2%)	55	61

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	108	LEU
1	A	111	LEU
1	A	161	THR
1	A	232	HIS
1	A	289	GLN
1	A	385	TYR
1	A	539	ILE
1	B	161	THR
1	B	224	LEU
1	B	289	GLN
1	B	306	LEU
1	B	385	TYR
1	B	409	TYR
1	B	484	GLU

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

Mol	Chain	Res	Type
1	A	105	ASN
1	A	168	ASN
1	A	270	GLN
1	A	396	ASN
1	B	168	ASN
1	B	571	ASN
1	B	583	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 ⓘ

9 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	0.63	0	17,19,21	1.01	1 (5%)
2	NAG	C	2	2	14,14,15	0.81	0	17,19,21	0.84	1 (5%)
3	NAG	D	1	1,3	14,14,15	0.51	0	17,19,21	1.40	2 (11%)
3	NAG	D	2	3	14,14,15	0.50	0	17,19,21	0.72	0
3	MAN	D	3	3	11,11,12	0.54	0	15,15,17	0.93	1 (6%)
2	NAG	E	1	1,2	14,14,15	1.49	1 (7%)	17,19,21	1.42	3 (17%)
2	NAG	E	2	2	14,14,15	0.80	1 (7%)	17,19,21	1.66	5 (29%)
2	NAG	F	1	1,2	14,14,15	0.52	0	17,19,21	1.16	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	F	2	2	14,14,15	0.58	0	17,19,21	1.29	1 (5%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	O5-C1	-5.10	1.35	1.43
2	E	2	NAG	O5-C1	-2.05	1.40	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1	NAG	C1-O5-C5	4.51	118.23	112.19
2	F	1	NAG	C1-O5-C5	3.44	116.79	112.19
2	F	2	NAG	C4-C3-C2	3.43	116.04	111.02
2	E	2	NAG	C4-C3-C2	3.33	115.90	111.02
2	E	2	NAG	C2-N2-C7	-3.17	118.65	122.90
2	E	1	NAG	C3-C4-C5	2.96	115.59	110.23
3	D	3	MAN	C1-O5-C5	2.94	116.12	112.19
2	E	1	NAG	O5-C1-C2	-2.93	106.75	111.29
2	E	2	NAG	C1-O5-C5	-2.81	108.42	112.19
3	D	1	NAG	C2-N2-C7	-2.60	119.42	122.90
2	C	2	NAG	O5-C1-C2	-2.41	107.57	111.29
2	E	1	NAG	O5-C5-C4	2.34	116.53	110.83
2	E	2	NAG	O5-C1-C2	-2.25	107.81	111.29
2	E	2	NAG	O5-C5-C6	2.10	111.74	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C3-C4-C5	-2.00	106.60	110.23

All (2) chirality outliers are listed below:

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

All (13) torsion outliers are listed below:

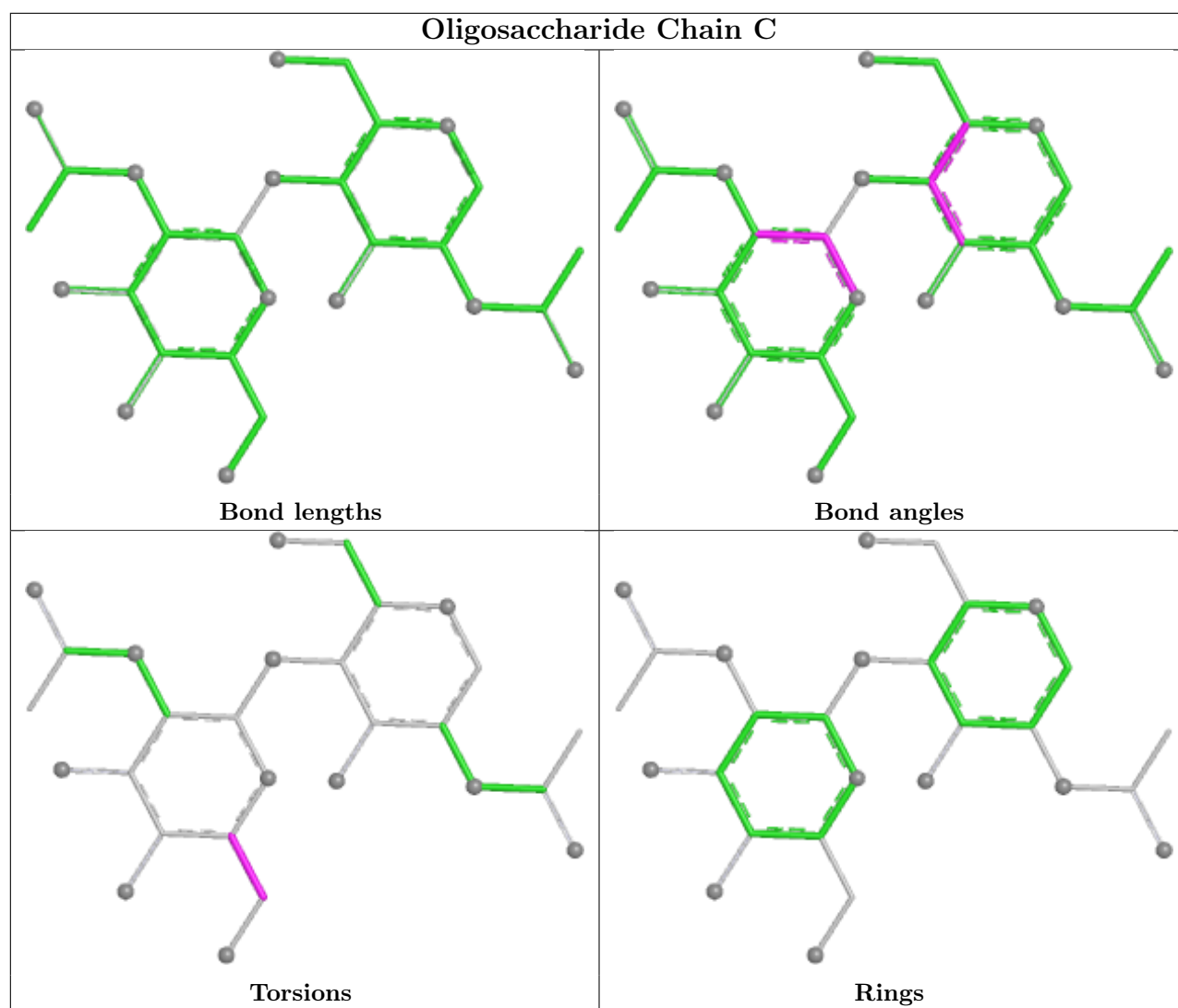
Mol	Chain	Res	Type	Atoms
2	F	2	NAG	C8-C7-N2-C2
2	F	2	NAG	O7-C7-N2-C2
2	E	2	NAG	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	D	2	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
3	D	3	MAN	O5-C5-C6-O6
3	D	3	MAN	C4-C5-C6-O6

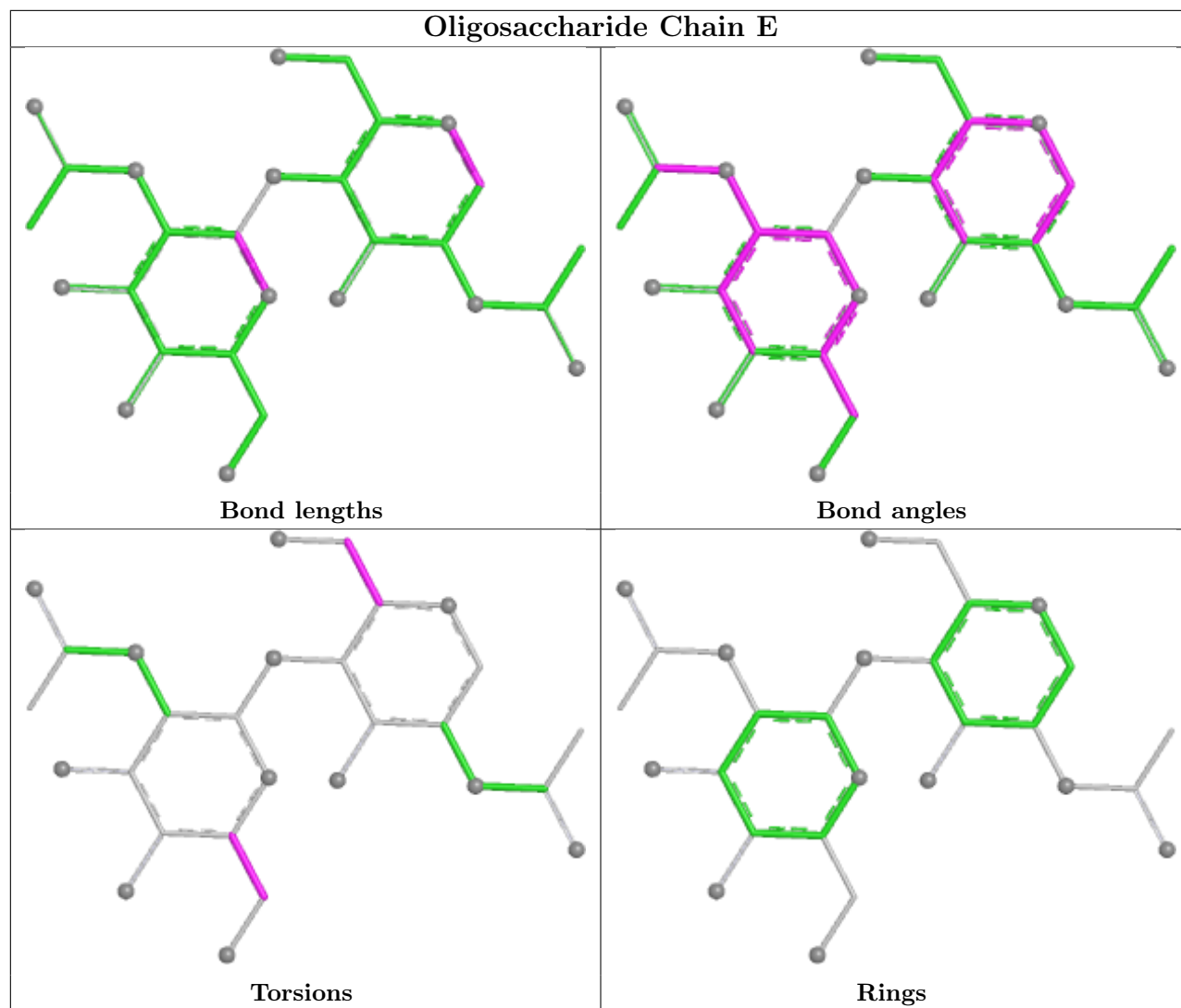
There are no ring outliers.

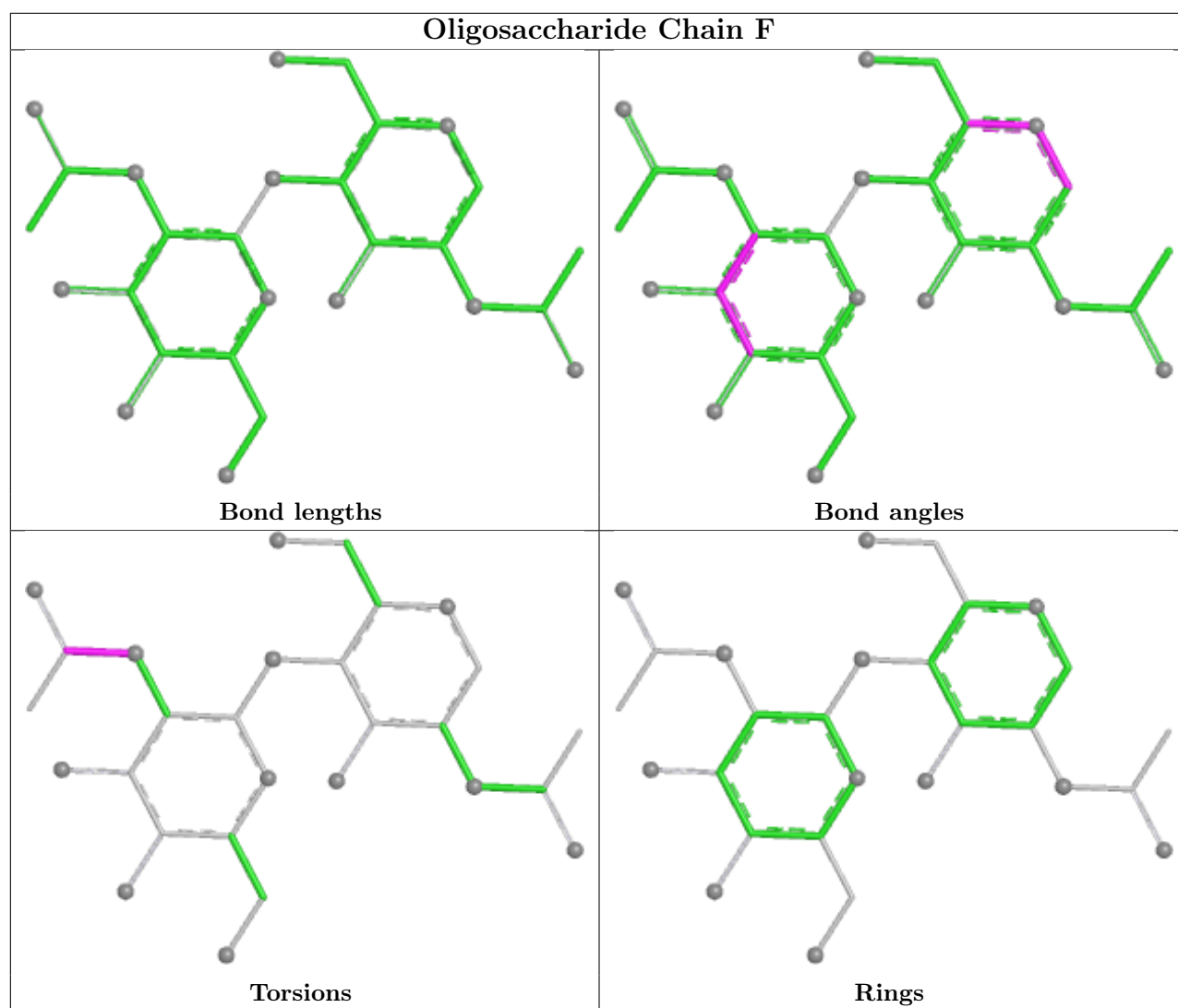
2 monomers are involved in 7 short contacts:

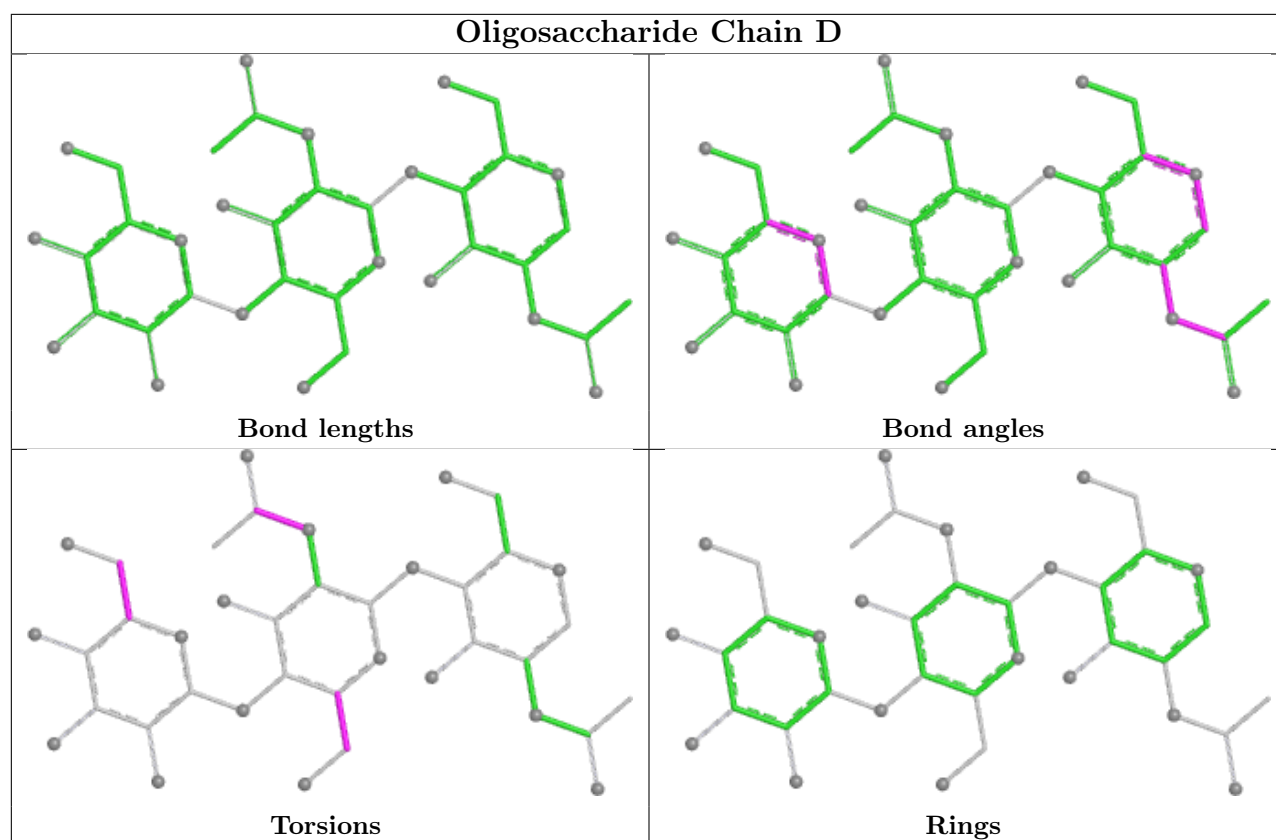
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	NAG	4	0
2	F	2	NAG	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









5.6 Ligand geometry [i](#)

17 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	$\# Z > 2$
8	EDO	B	7	-	3,3,3	0.46	0	2,2,2	0.40	0
4	ACD	A	1	-	21,21,21	0.48	0	21,21,21	0.60	0
4	ACD	B	1	-	21,21,21	0.46	0	21,21,21	0.86	1 (4%)
8	EDO	A	5	-	3,3,3	0.39	0	2,2,2	0.30	0
8	EDO	B	6	-	3,3,3	0.48	0	2,2,2	0.35	0
8	EDO	B	3	-	3,3,3	0.50	0	2,2,2	0.53	0
8	EDO	A	2	-	3,3,3	0.46	0	2,2,2	0.38	0
6	NAG	A	681	1	14,14,15	0.51	0	17,19,21	0.97	1 (5%)
8	EDO	B	620	-	3,3,3	0.49	0	2,2,2	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	EDO	B	4	-	3,3,3	0.45	0	2,2,2	0.34	0
8	EDO	B	8	-	3,3,3	0.36	0	2,2,2	0.50	0
6	NAG	B	681	1	14,14,15	0.52	0	17,19,21	1.25	1 (5%)
5	COH	A	619	1	50,50,50	1.75	11 (22%)	66,82,82	1.64	12 (18%)
7	BOG	A	703	-	20,20,20	0.48	0	25,25,25	0.67	0
9	AKR	A	9	-	4,4,4	1.98	2 (50%)	4,4,4	1.06	0
9	AKR	A	10	-	4,4,4	2.00	2 (50%)	4,4,4	0.79	0
5	COH	B	619	1	50,50,50	1.72	10 (20%)	66,82,82	1.63	12 (18%)

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
8	EDO	B	7	-	-	1/1/1/1	-
4	ACD	A	1	-	-	6/19/19/19	-
4	ACD	B	1	-	-	8/19/19/19	-
8	EDO	A	5	-	-	0/1/1/1	-
8	EDO	B	6	-	-	0/1/1/1	-
8	EDO	B	3	-	-	0/1/1/1	-
8	EDO	A	2	-	-	1/1/1/1	-
6	NAG	A	681	1	-	0/6/23/26	0/1/1/1
8	EDO	B	620	-	-	1/1/1/1	-
8	EDO	B	4	-	-	1/1/1/1	-
8	EDO	B	8	-	-	1/1/1/1	-
6	NAG	B	681	1	-	3/6/23/26	0/1/1/1
5	COH	A	619	1	1/1/3/9	4/14/54/54	-
7	BOG	A	703	-	-	5/11/31/31	0/1/1/1
9	AKR	A	9	-	-	0/2/2/2	-
9	AKR	A	10	-	-	0/2/2/2	-
5	COH	B	619	1	-	2/14/54/54	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	619	COH	C3D-C2D	5.70	1.53	1.38
5	B	619	COH	C3D-C2D	5.60	1.53	1.38
5	A	619	COH	CO-NB	4.97	2.15	1.96
5	B	619	COH	CO-NB	4.09	2.12	1.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	619	COH	CO-NA	4.05	2.11	1.96
5	A	619	COH	CO-NA	3.71	2.09	1.96
5	B	619	COH	CO-ND	3.69	2.10	1.96
5	A	619	COH	CO-ND	3.48	2.09	1.96
5	B	619	COH	CAB-C3B	3.35	1.56	1.47
5	B	619	COH	CO-NC	3.01	2.07	1.96
5	A	619	COH	CAC-C3C	2.99	1.55	1.47
5	A	619	COH	CAB-C3B	2.99	1.55	1.47
5	B	619	COH	CAC-C3C	2.81	1.54	1.47
9	A	9	AKR	CA-C	-2.70	1.39	1.46
5	A	619	COH	CO-NC	2.57	2.05	1.96
9	A	10	AKR	CA-C	-2.45	1.40	1.46
5	B	619	COH	CMA-C3A	2.40	1.55	1.50
5	A	619	COH	CMC-C2C	2.38	1.55	1.50
9	A	10	AKR	OXT-C	-2.29	1.24	1.30
5	A	619	COH	CMA-C3A	2.27	1.55	1.50
5	B	619	COH	CMC-C2C	2.24	1.55	1.50
5	A	619	COH	CMB-C2B	2.19	1.55	1.50
5	B	619	COH	CMB-C2B	2.16	1.55	1.50
9	A	9	AKR	OXT-C	-2.06	1.25	1.30
5	A	619	COH	CMD-C2D	2.01	1.54	1.50

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	619	COH	C4D-ND-C1D	5.01	112.50	105.11
5	A	619	COH	C4D-ND-C1D	4.89	112.32	105.11
5	B	619	COH	C2B-C1B-NB	-4.52	107.36	110.88
5	A	619	COH	C2C-C1C-NC	-4.45	106.33	110.96
6	B	681	NAG	C1-O5-C5	4.26	117.90	112.19
5	A	619	COH	C2B-C1B-NB	-3.77	107.95	110.88
5	A	619	COH	C4C-NC-C1C	3.71	109.84	105.12
5	B	619	COH	C3A-C4A-NA	-3.56	107.26	110.96
5	B	619	COH	C2C-C1C-NC	-3.21	107.62	110.96
5	B	619	COH	C3D-C4D-ND	-3.09	107.98	110.73
5	B	619	COH	CBA-CAA-C2A	-3.04	104.12	112.53
5	A	619	COH	C3C-C2C-C1C	3.00	108.66	106.41
5	B	619	COH	C4C-NC-C1C	2.87	108.77	105.12
6	A	681	NAG	C1-O5-C5	2.82	115.96	112.19
5	B	619	COH	CBD-CAD-C3D	-2.79	104.82	112.53
5	B	619	COH	C1A-NA-C4A	2.76	108.62	105.12
5	A	619	COH	C3A-C4A-NA	-2.69	108.17	110.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	619	COH	CHC-C4B-C3B	2.49	129.40	125.21
5	B	619	COH	C3C-C2C-C1C	2.47	108.26	106.41
5	A	619	COH	C2A-C1A-NA	-2.44	107.59	110.57
5	A	619	COH	C4B-NB-C1B	2.41	108.66	105.11
5	A	619	COH	C1A-NA-C4A	2.39	108.16	105.12
5	A	619	COH	C3D-C4D-ND	-2.37	108.62	110.73
5	B	619	COH	C4B-NB-C1B	2.25	108.43	105.11
4	B	1	ACD	C3-C2-C1	-2.16	108.87	114.51
5	B	619	COH	C2A-C1A-NA	-2.08	108.03	110.57
5	A	619	COH	CMD-C2D-C1D	2.06	128.55	125.42

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	619	COH	NB

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1	ACD	C12-C13-C14-C15
4	B	1	ACD	C12-C13-C14-C15
5	A	619	COH	C2A-CAA-CBA-CGA
7	A	703	BOG	O1-C1'-C2'-C3'
6	B	681	NAG	C8-C7-N2-C2
8	B	8	EDO	O1-C1-C2-O2
4	B	1	ACD	C16-C17-C18-C19
7	A	703	BOG	C2'-C1'-O1-C1
4	B	1	ACD	C1-C2-C3-C4
6	B	681	NAG	O7-C7-N2-C2
4	A	1	ACD	C5-C6-C7-C8
4	A	1	ACD	C11-C10-C9-C8
4	A	1	ACD	C11-C12-C13-C14
4	B	1	ACD	C5-C6-C7-C8
4	B	1	ACD	C6-C7-C8-C9
4	B	1	ACD	C2-C3-C4-C5
8	B	7	EDO	O1-C1-C2-O2
7	A	703	BOG	C4-C5-C6-O6
4	A	1	ACD	C14-C15-C16-C17
4	B	1	ACD	O2-C1-C2-C3
8	A	2	EDO	O1-C1-C2-O2
5	A	619	COH	C1A-C2A-CAA-CBA
5	A	619	COH	CAA-CBA-CGA-O1A

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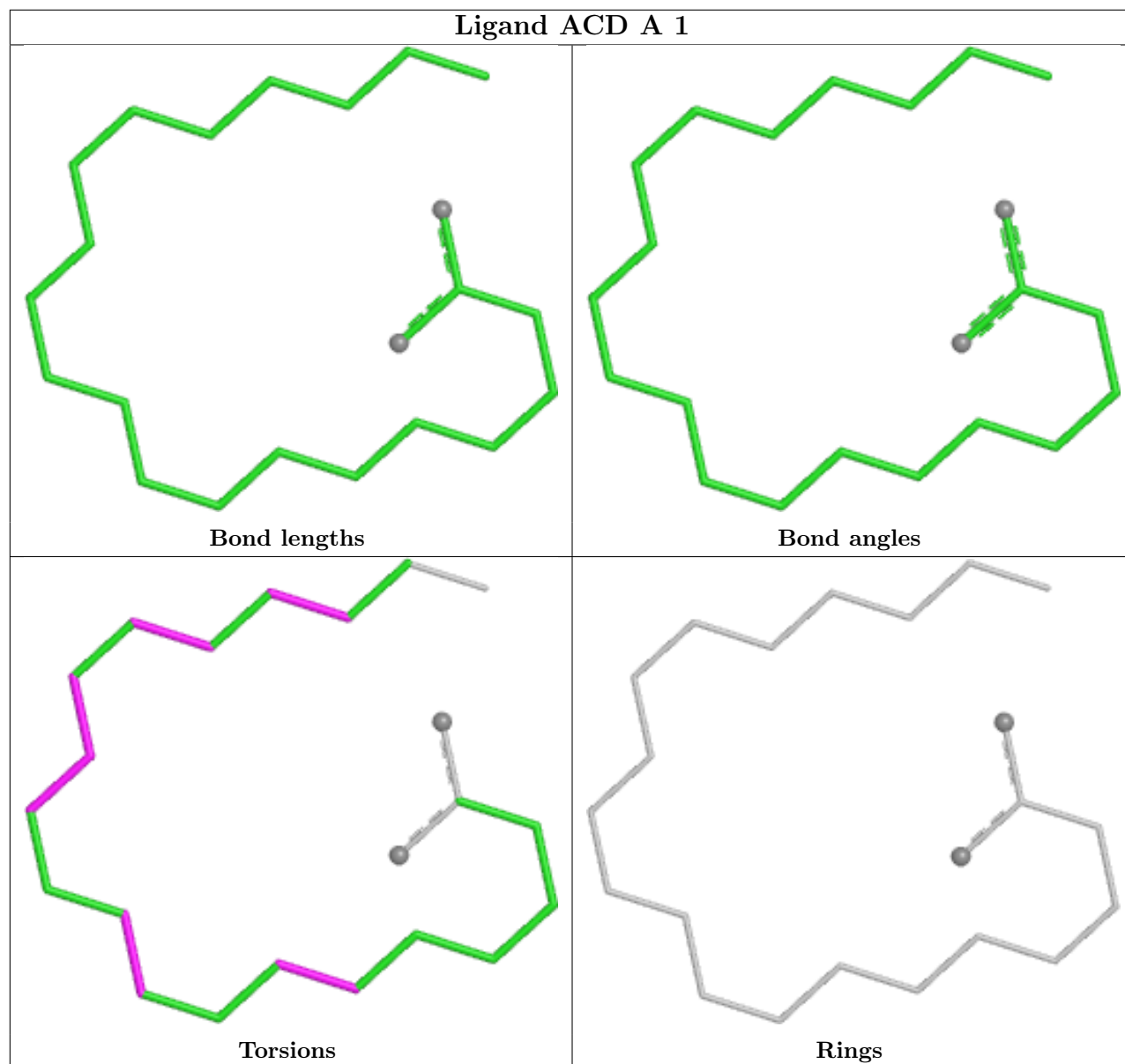
Mol	Chain	Res	Type	Atoms
4	B	1	ACD	O1-C1-C2-C3
5	B	619	COH	CAA-CBA-CGA-O1A
5	B	619	COH	CAA-CBA-CGA-O2A
4	A	1	ACD	C16-C17-C18-C19
5	A	619	COH	CAA-CBA-CGA-O2A
8	B	620	EDO	O1-C1-C2-O2
8	B	4	EDO	O1-C1-C2-O2
7	A	703	BOG	C5'-C6'-C7'-C8'
7	A	703	BOG	O5-C5-C6-O6
6	B	681	NAG	C4-C5-C6-O6

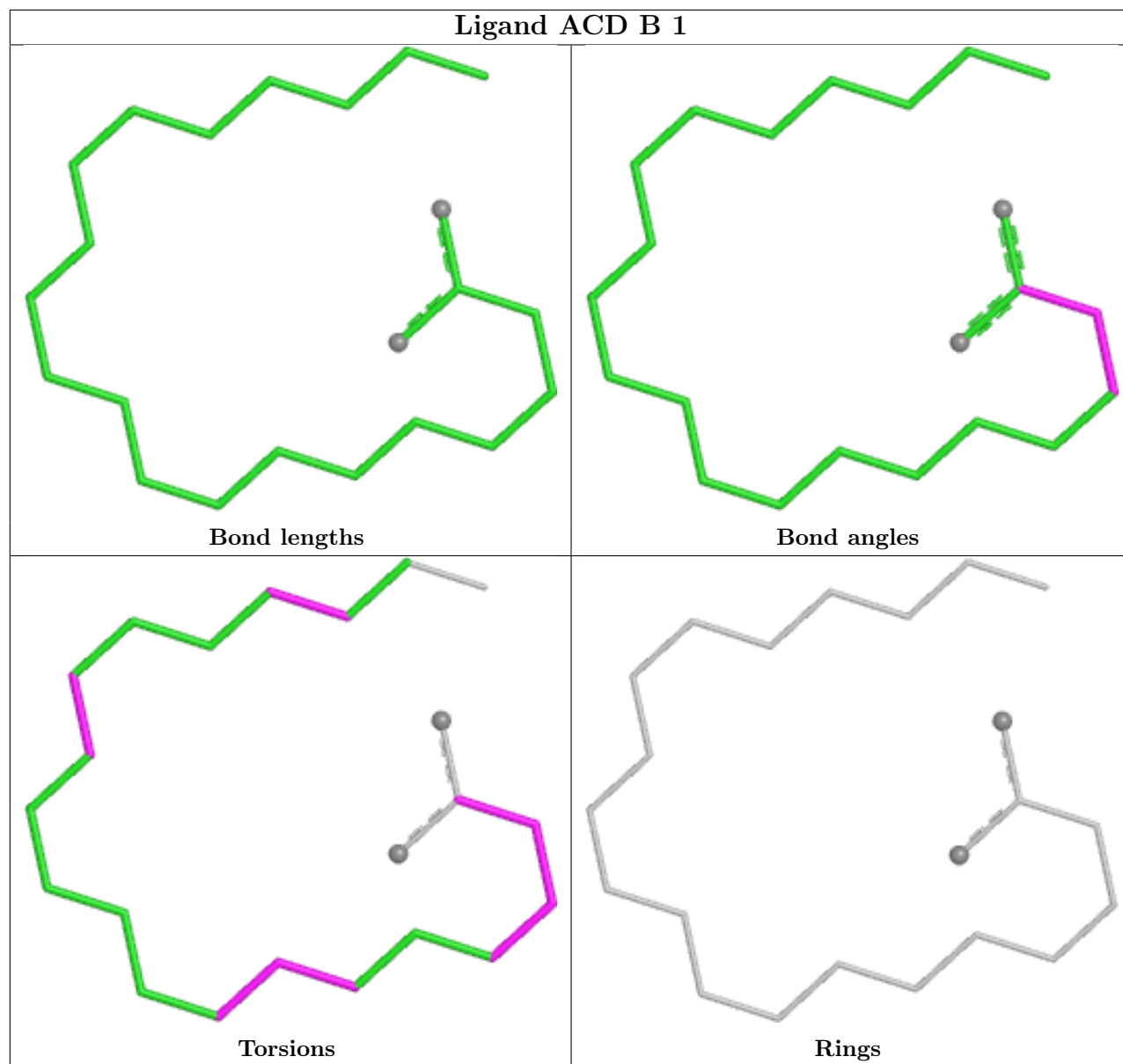
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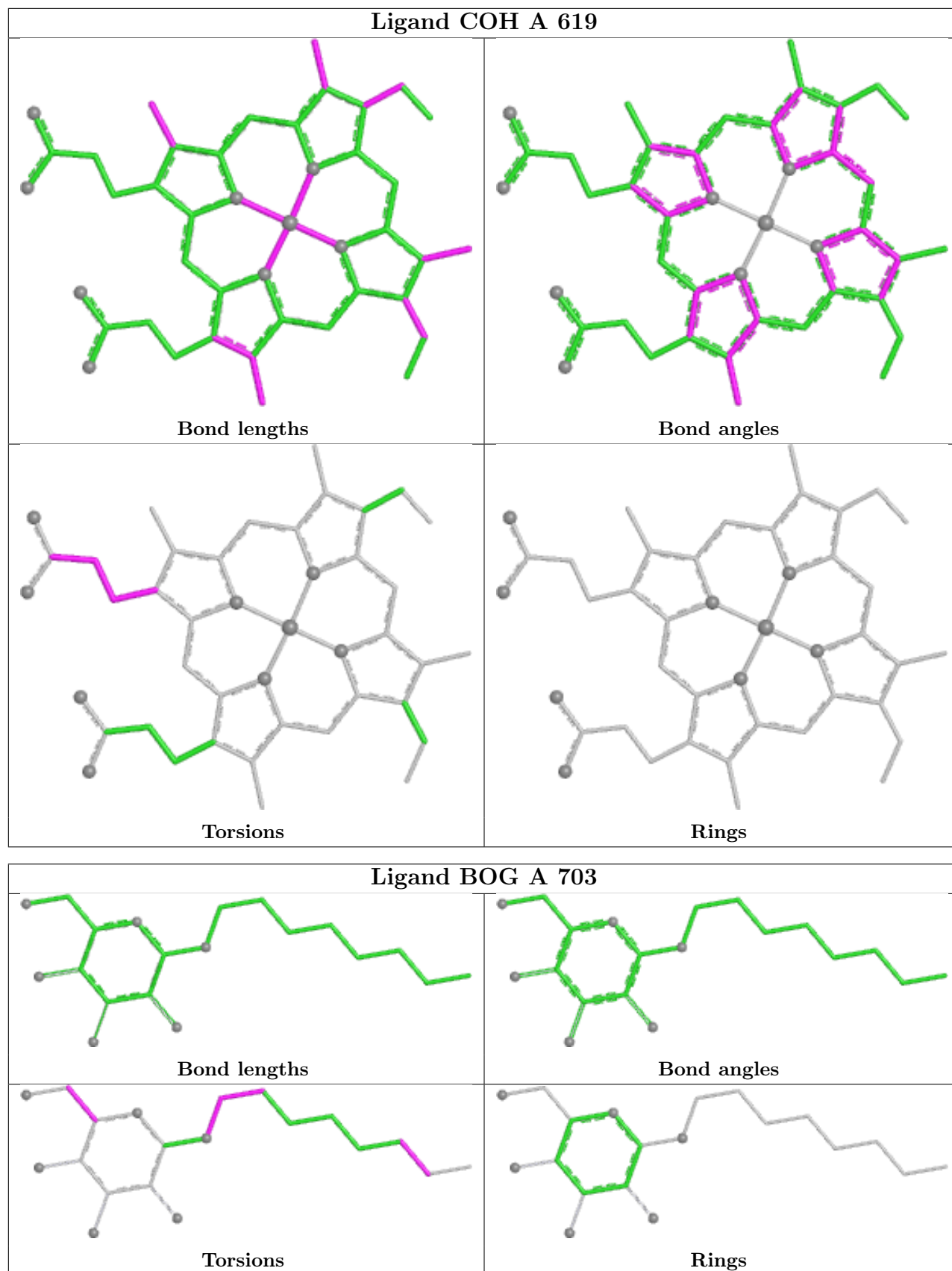
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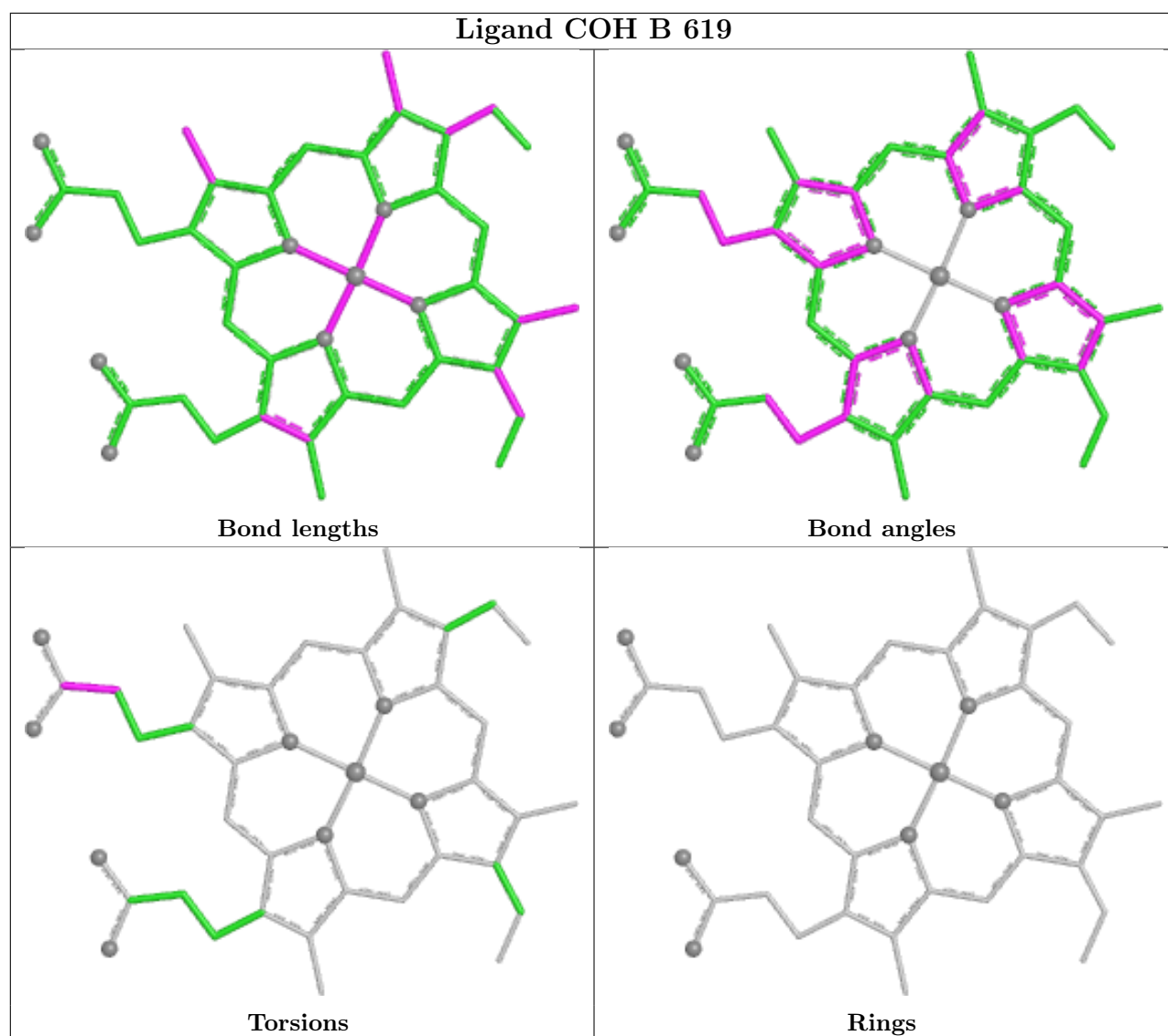
Mol	Chain	Res	Type	Clashes	Symm-Clashes
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4	A	1	ACD	11	0
4	B	1	ACD	10	0
8	A	2	EDO	1	0
7	A	703	BOG	1	0
9	A	9	AKR	3	0
9	A	10	AKR	1	0
5	B	619	COH	1	0

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	551/593 (92%)	-0.02	11 (1%) 65 69	13, 29, 39, 47	5 (0%)
1	B	552/593 (93%)	0.00	16 (2%) 53 57	13, 29, 39, 48	6 (1%)
All	All	1103/1186 (93%)	-0.01	27 (2%) 59 63	13, 29, 39, 48	11 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	74	PHE	4.6
1	A	121	SER	4.0
1	B	115	TYR	3.5
1	A	115	TYR	3.4
1	B	82	LEU	3.3
1	B	91	TYR	2.9
1	A	81	LEU	2.9
1	A	74	PHE	2.8
1	B	239	ASP	2.7
1	B	81	LEU	2.7
1	B	577[A]	PHE	2.6
1	A	122	TYR	2.6
1	A	294	LEU	2.4
1	B	65	TYR	2.4
1	B	102	ILE	2.4
1	A	108	LEU	2.3
1	A	399	ASP	2.2
1	B	101	ASN	2.2
1	B	122	TYR	2.2
1	A	107	PHE	2.2
1	B	73	GLU	2.2
1	A	101	ASN	2.2
1	B	107	PHE	2.1
1	B	409	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	96	PHE	2.1
1	A	239	ASP	2.1
1	B	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](#)

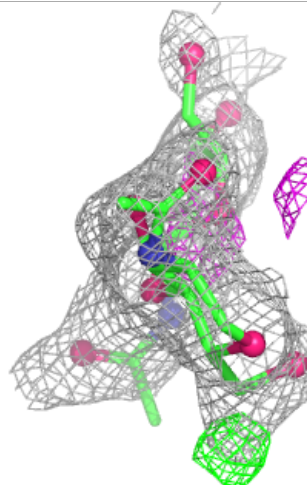
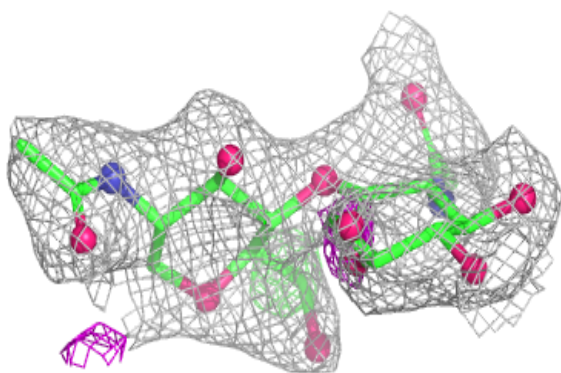
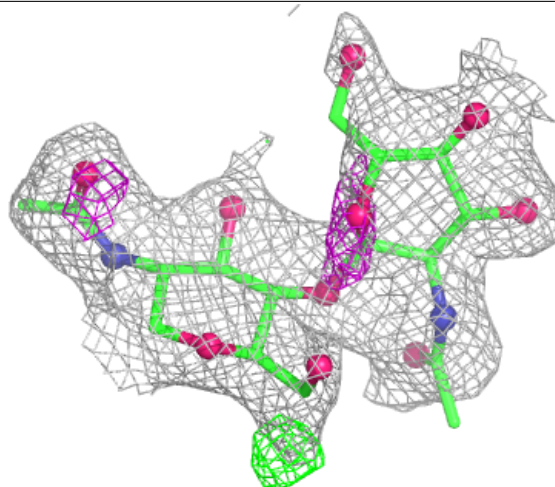
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	E	2	14/15	0.63	0.14	64,67,68,68	0
3	MAN	D	3	11/12	0.65	0.15	61,64,65,66	0
2	NAG	C	2	14/15	0.67	0.12	60,63,65,65	0
2	NAG	E	1	14/15	0.79	0.12	44,49,53,59	0
2	NAG	C	1	14/15	0.82	0.10	40,47,51,56	0
3	NAG	D	2	14/15	0.85	0.10	44,46,51,57	0
2	NAG	F	2	14/15	0.86	0.11	44,46,49,50	0
2	NAG	F	1	14/15	0.94	0.07	23,29,33,39	0
3	NAG	D	1	14/15	0.96	0.07	26,32,34,39	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.

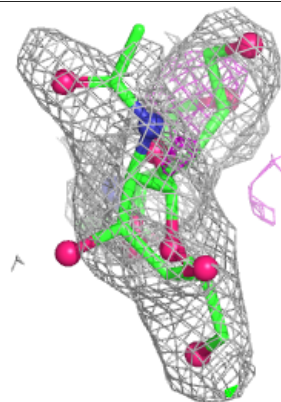
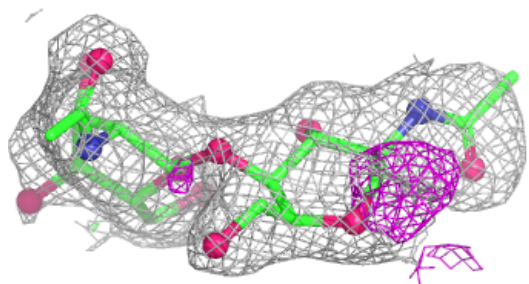
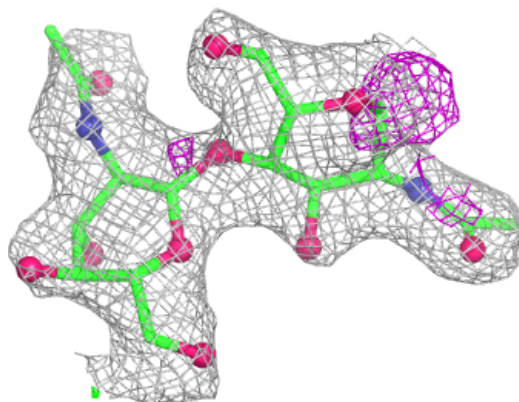
Electron density around Chain C:

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



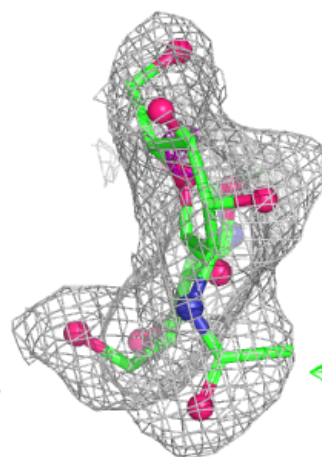
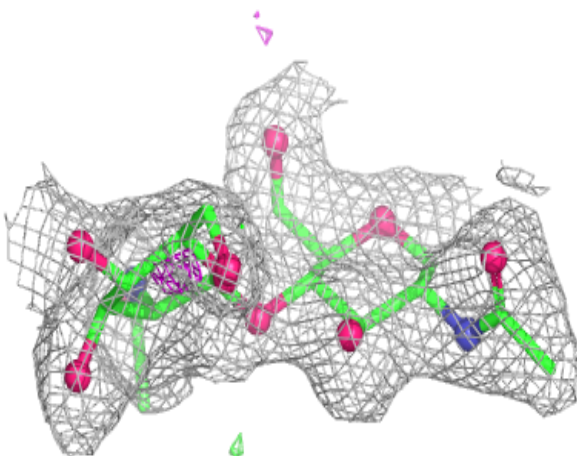
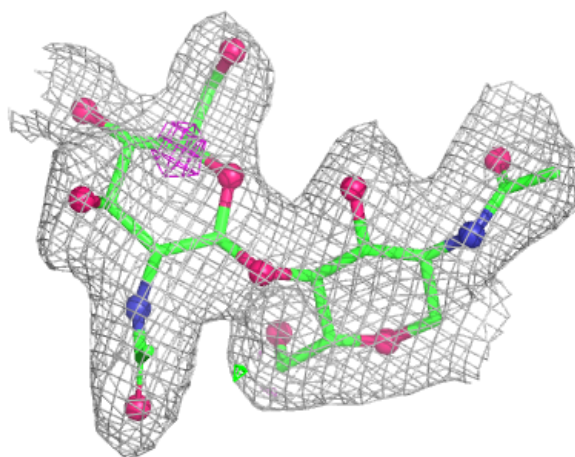
Electron density around Chain E:

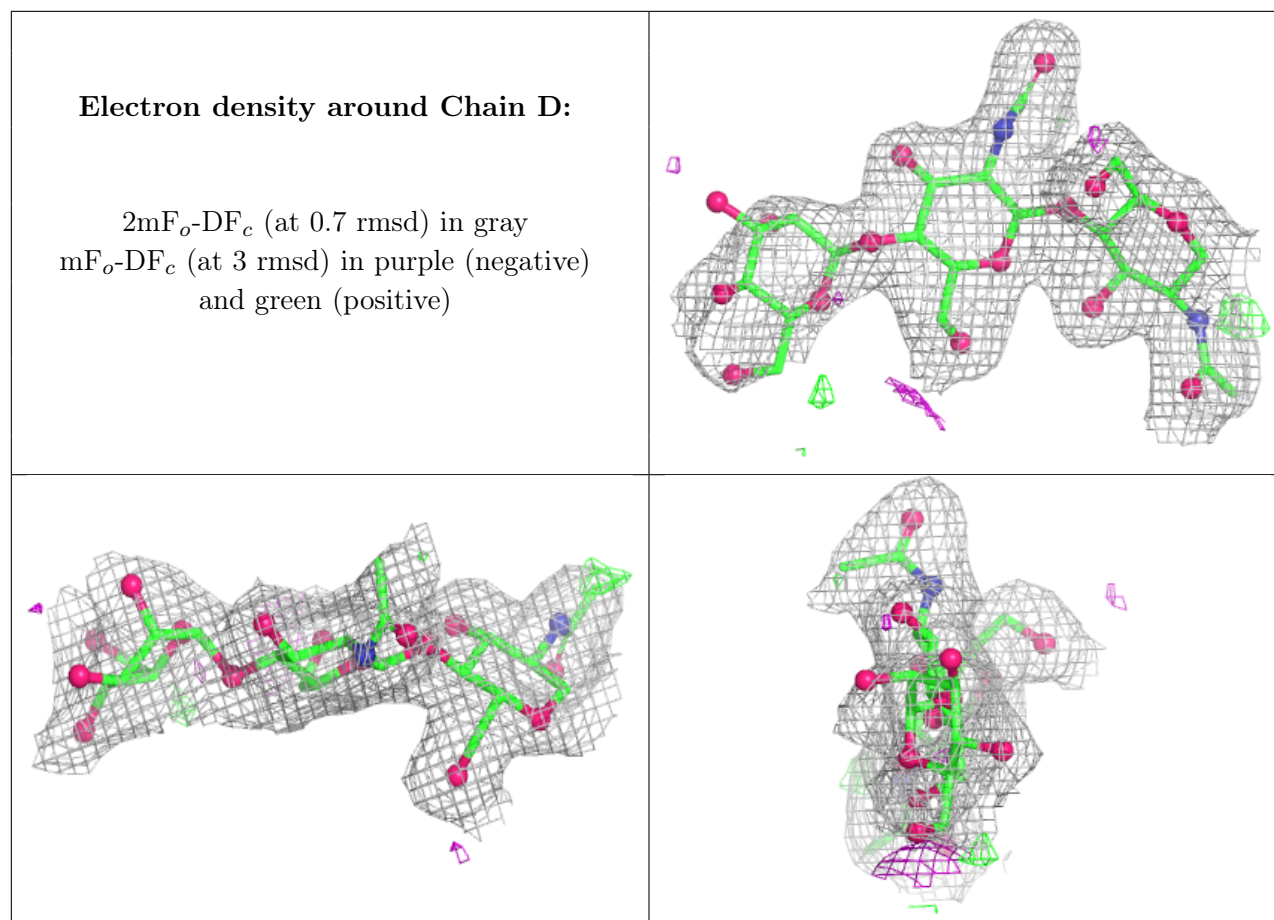
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain F:

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





6.4 Ligands [i](#)

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

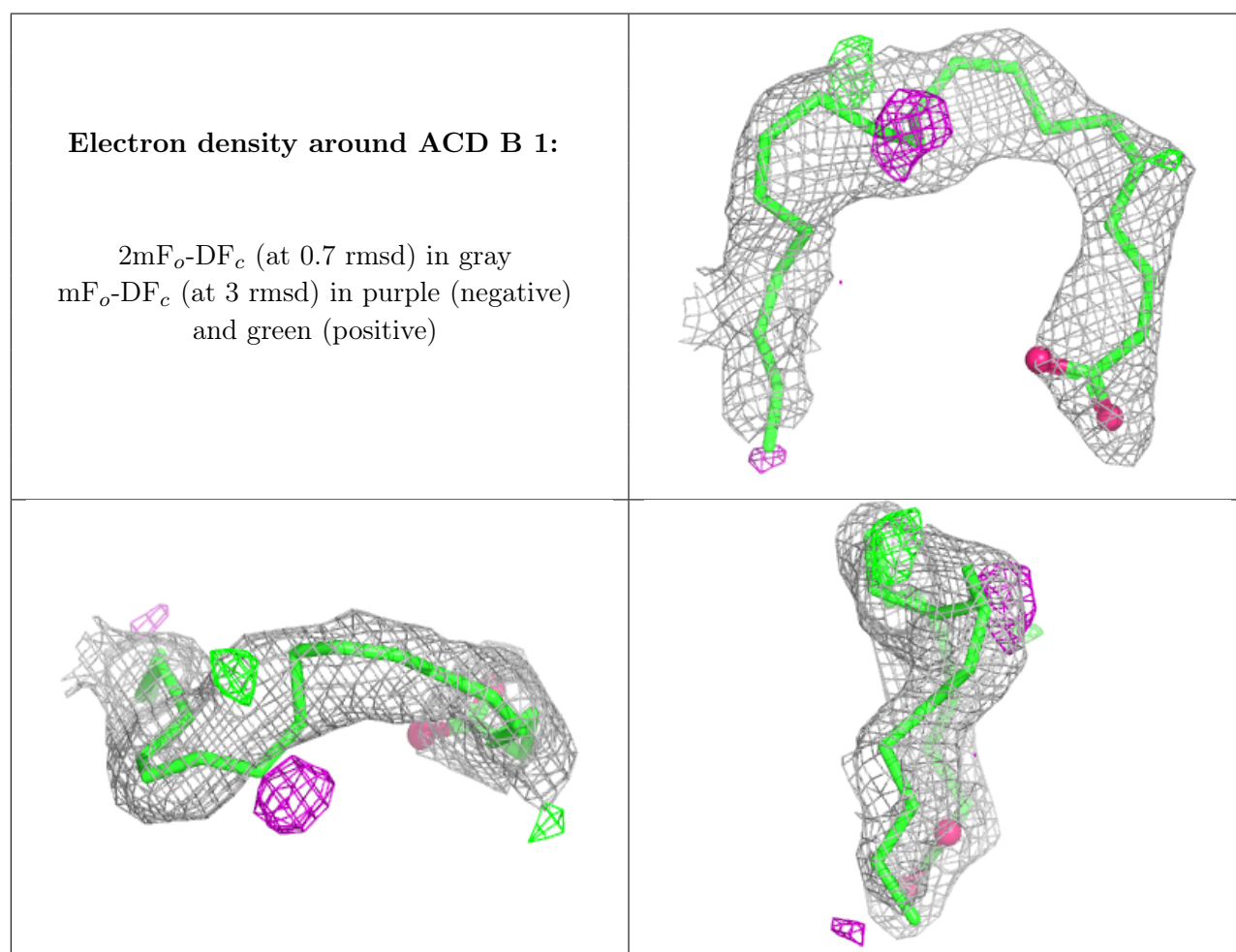
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	AKR	A	9	5/5	0.75	0.19	53,53,54,54	0
4	ACD	B	1	22/22	0.78	0.17	52,58,64,65	0
8	EDO	B	8	4/4	0.79	0.15	52,52,52,53	0
8	EDO	B	6	4/4	0.81	0.16	56,57,57,58	0
6	NAG	B	681	14/15	0.82	0.10	42,49,51,52	0
9	AKR	A	10	5/5	0.82	0.15	47,47,48,48	0
4	ACD	A	1	22/22	0.83	0.17	53,57,64,64	0
6	NAG	A	681	14/15	0.84	0.10	38,44,48,49	0
8	EDO	B	3	4/4	0.85	0.21	41,41,42,43	0
8	EDO	B	4	4/4	0.85	0.17	48,49,51,51	0
8	EDO	A	2	4/4	0.87	0.12	38,40,40,42	0
8	EDO	B	7	4/4	0.91	0.14	40,40,41,42	0

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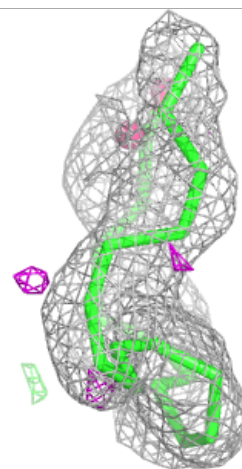
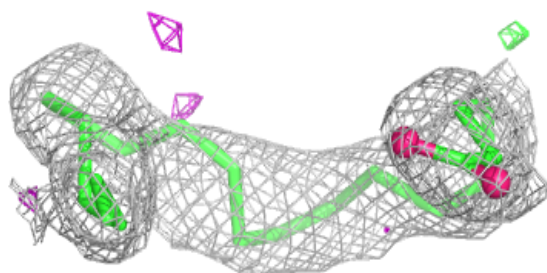
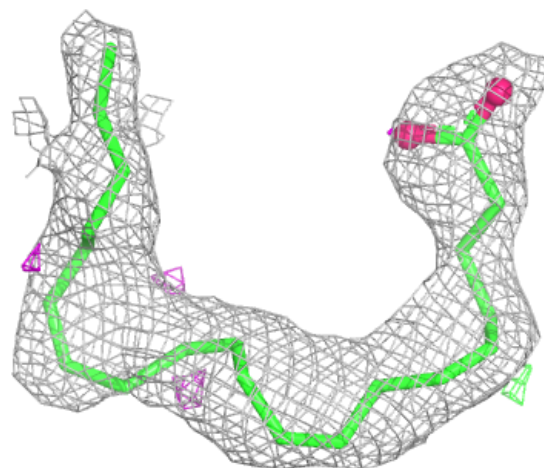
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	BOG	A	703	20/20	0.91	0.10	34,38,42,43	0
8	EDO	A	5	4/4	0.92	0.11	36,37,37,38	0
5	COH	B	619	43/43	0.94	0.10	35,37,49,53	0
8	EDO	B	620	4/4	0.95	0.08	26,32,32,34	0
5	COH	A	619	43/43	0.95	0.09	35,39,51,56	0

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.



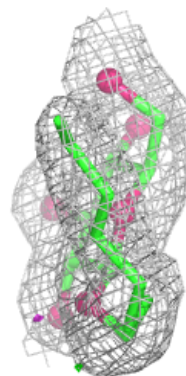
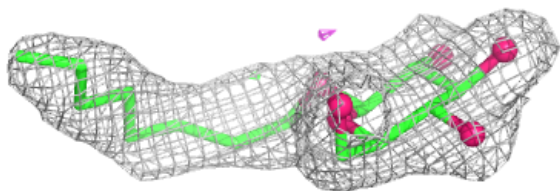
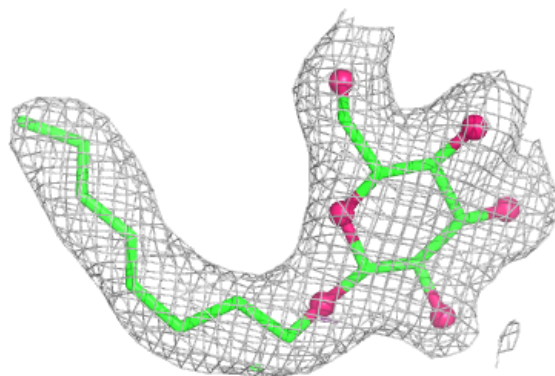
Electron density around ACD A 1:

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



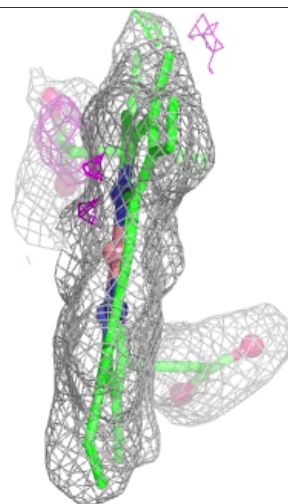
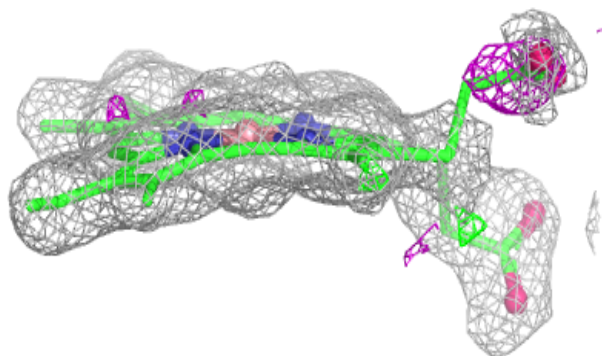
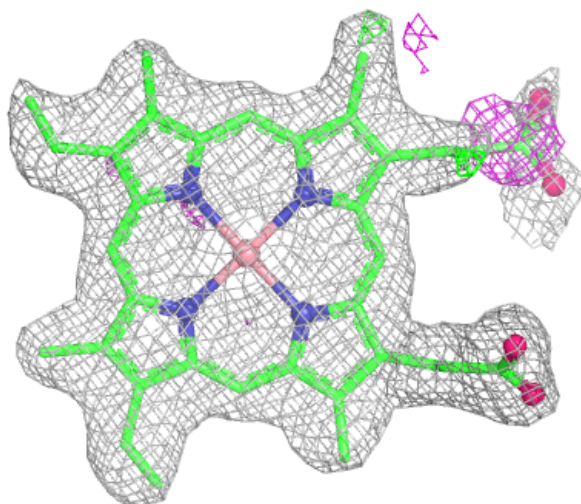
Electron density around BOG A 703:

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



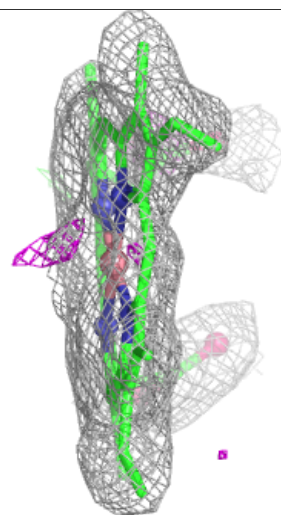
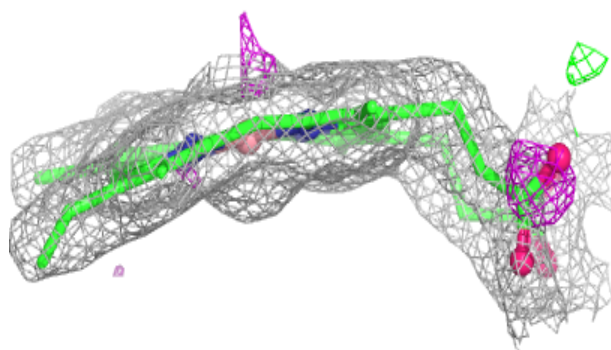
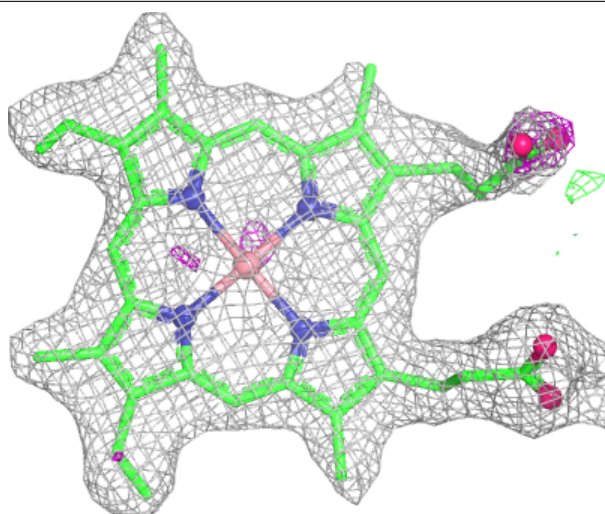
Electron density around COH B 619:

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



Electron density around COH 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.