



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2025 – 04:23 PM JST

PDB ID : 7DDH  
Title : Crystal structures of Na<sup>+</sup>,K<sup>+</sup>-ATPase in complex with digoxin  
Authors : Ogawa, H.; Cornelius, F.; Kanai, R.; Motoyama, K.; Vilsen, B.; Toyoshima, C.  
Deposited on : 2020-10-29  
Resolution : 3.46 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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) : 1.21  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.004 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.2

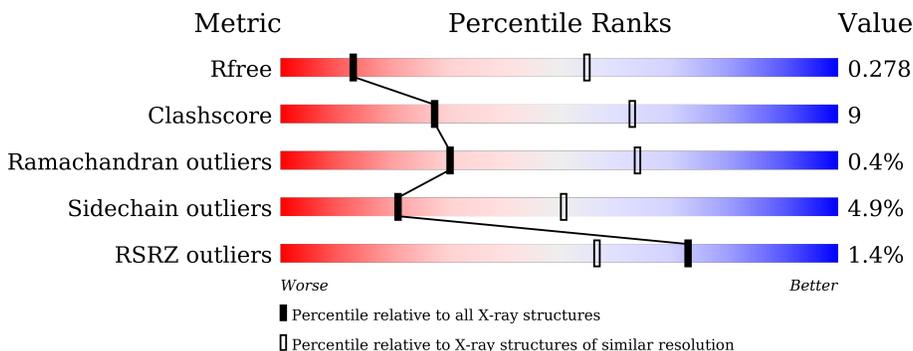
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.46 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))
$R_{free}$	164625	1597 (3.52-3.40)
Clashscore	180529	1041 (3.50-3.42)
Ramachandran outliers	177936	1026 (3.50-3.42)
Sidechain outliers	177891	1027 (3.50-3.42)
RSRZ outliers	164620	1596 (3.52-3.40)

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  $\geq 3$ , 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	1016	 % 75% 21% ..
1	C	1016	 % 75% 21% ..
2	B	303	 2% 69% 25% . .
2	D	303	 4% 64% 28% . 6%
3	E	65	 40% 9% 51%
3	G	65	 48% . 51%

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Mol	Chain	Length	Quality of chain
4	F	2	 100%
4	H	2	 50% 50%
4	I	2	 50% 50%
4	J	2	 50% 50%

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 21344 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 Sodium/potassium-transporting ATPase subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	996	7730	4922	1301	1459	1	47	0	0	0
1	C	996	7730	4922	1301	1459	1	47	0	0	0

- Molecule 2 is a protein called Sodium/potassium-transporting ATPase subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	291	2386	1546	390	437	13	0	0	0
2	D	285	2334	1514	383	424	13	0	0	0

- Molecule 3 is a protein called FXYP domain-containing ion transport regulator.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	32	255	174	37	44	0	0	0
3	E	32	255	174	37	44	0	0	0

- Molecule 4 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
			Total	C	N	O			
4	F	2	28	16	2	10	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

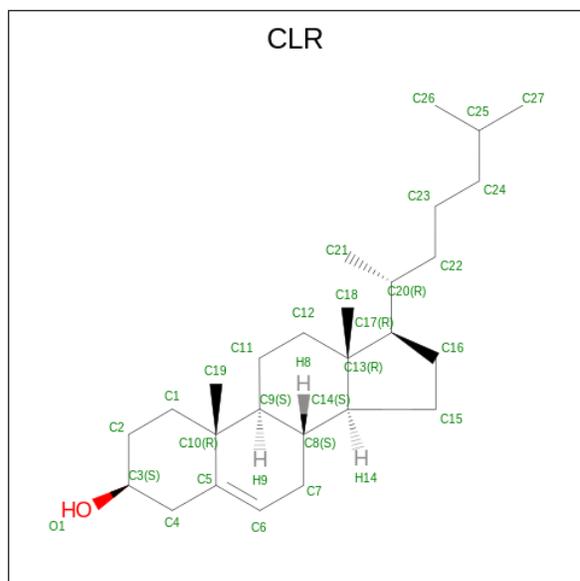
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		
5	C	2	Total	Mg	0	0
			2	2		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

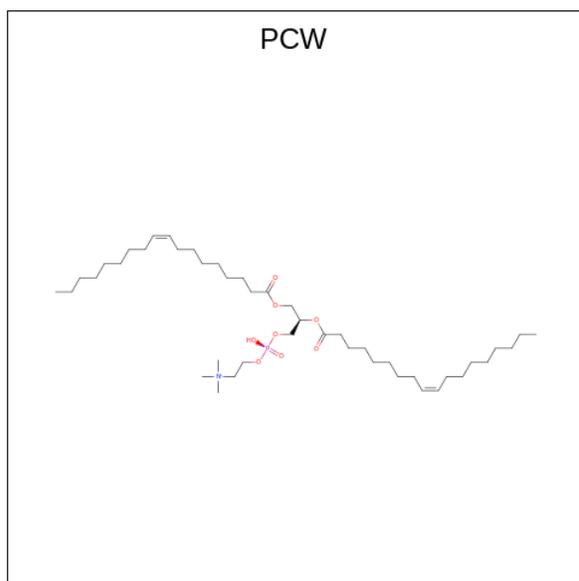
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Na	0	0
			1	1		
6	C	1	Total	Na	0	0
			1	1		

- Molecule 7 is CHOLESTEROL (three-letter code: CLR) (formula: C<sub>27</sub>H<sub>46</sub>O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			28	27	1		
7	B	1	Total	C	O	0	0
			28	27	1		
7	G	1	Total	C	O	0	0
			28	27	1		
7	C	1	Total	C	O	0	0
			28	27	1		
7	D	1	Total	C	O	0	0
			28	27	1		
7	E	1	Total	C	O	0	0
			28	27	1		

- Molecule 8 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PCW) (formula: C<sub>44</sub>H<sub>85</sub>NO<sub>8</sub>P).



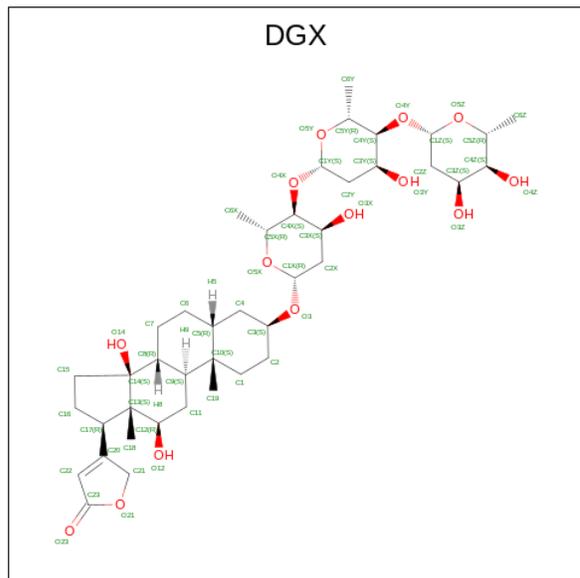
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
8	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
8	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
8	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		

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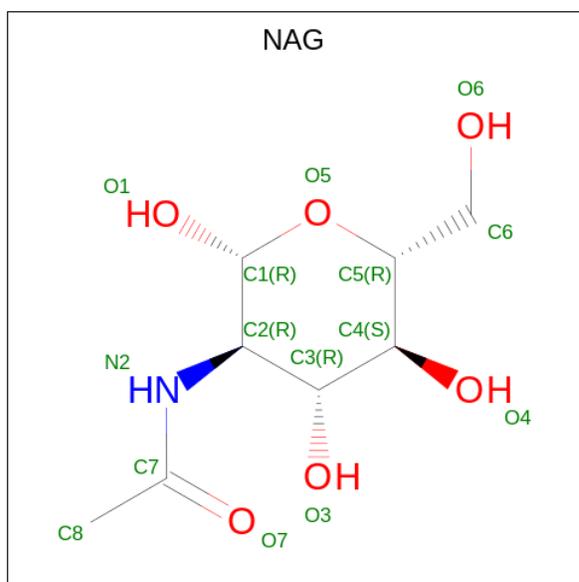
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
8	B	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
8	C	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
8	C	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
8	C	1	Total	C	N	O	P	0	0
			22	12	1	8	1		

- Molecule 9 is DIGOXIN (three-letter code: DGX) (formula:  $C_{41}H_{64}O_{14}$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			55	41	14		
9	C	1	Total	C	O	0	0
			55	41	14		

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	5	Total	O	0	0
			5	5		
11	C	5	Total	O	0	0
			5	5		

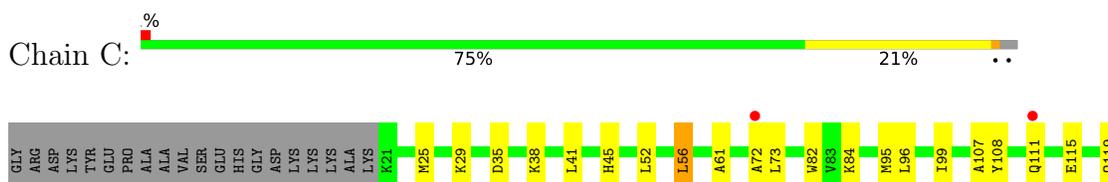
### 3 Residue-property plots [i](#)

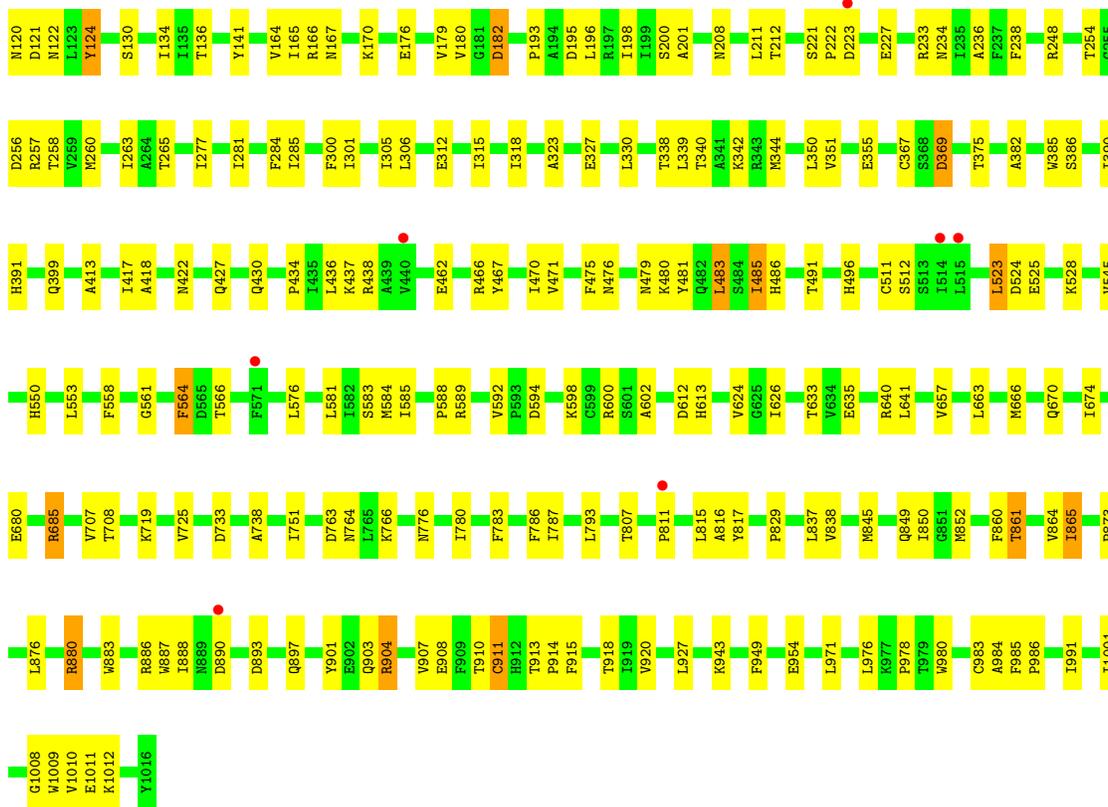
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Sodium/potassium-transporting ATPase subunit alpha-1

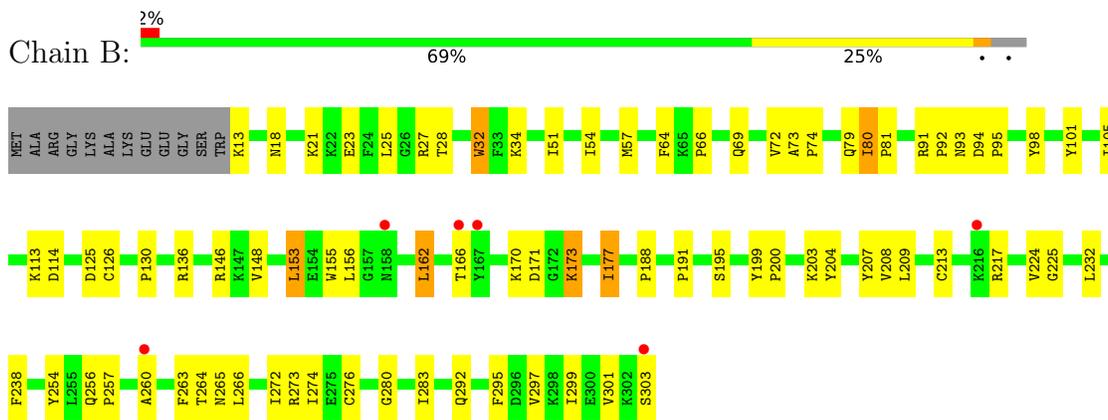


- Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

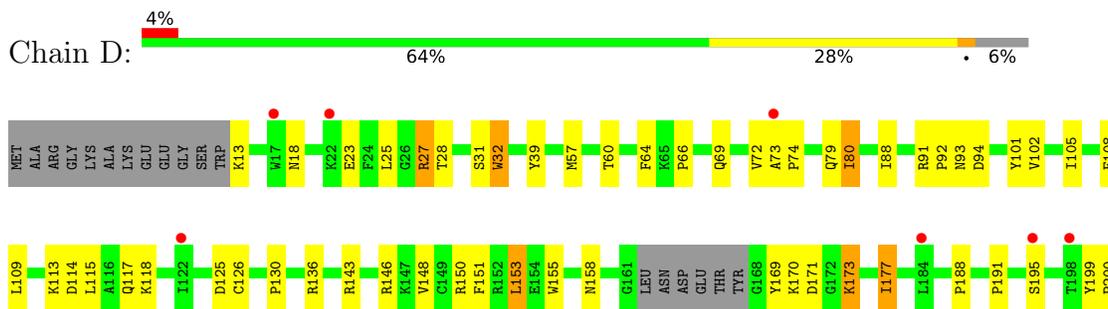




• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1



• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1

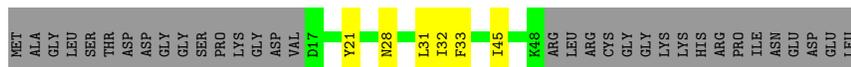




- Molecule 3: FXYP domain-containing ion transport regulator



- Molecule 3: FXYP domain-containing ion transport regulator



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



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## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.97Å 118.49Å 495.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.99 – 3.46 15.99 – 3.46	Depositor EDS
% Data completeness (in resolution range)	55.1 (15.99-3.46) 54.7 (15.99-3.46)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.70 (at 3.48Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.241 , 0.272 0.252 , 0.278	Depositor DCC
$R_{free}$ test set	4299 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	108.1	Xtrriage
Anisotropy	0.321	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 36.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.21$	Xtrriage
Estimated twinning fraction	0.068 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	21344	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	119.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CLR, DGX, NAG, PCW, PHD, NA

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	0.29	0/7867	0.50	0/10674
1	C	0.29	0/7867	0.51	0/10674
2	B	0.29	0/2449	0.54	0/3301
2	D	0.30	0/2395	0.54	0/3225
3	E	0.32	0/261	0.51	0/354
3	G	0.33	0/261	0.47	0/354
All	All	0.29	0/21100	0.51	0/28582

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	7730	0	7777	137	0
1	C	7730	0	7777	135	0
2	B	2386	0	2361	49	0
2	D	2334	0	2317	55	0
3	E	255	0	259	6	0
3	G	255	0	259	0	0
4	F	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	28	0	25	0	0
4	I	28	0	25	1	0
4	J	28	0	25	0	0
5	A	2	0	0	0	0
5	C	2	0	0	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	28	0	46	2	0
7	B	28	0	46	0	0
7	C	28	0	46	3	0
7	D	28	0	46	1	0
7	E	28	0	46	6	0
7	G	28	0	46	1	0
8	A	110	0	90	9	0
8	B	22	0	18	2	0
8	C	88	0	72	4	0
9	A	55	0	64	1	0
9	C	55	0	64	2	0
10	B	14	0	13	0	0
10	D	14	0	13	0	0
11	A	5	0	0	0	0
11	C	5	0	0	0	0
All	All	21344	0	21460	380	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 9.

The worst 5 of 380 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:84:LYS:HG3	1:A:141:TYR:HE1	1.41	0.85
1:C:978:PRO:HB3	7:E:101:CLR:H192	1.62	0.82
1:C:864:VAL:HG22	2:D:57:MET:HG3	1.63	0.81
1:C:430:GLN:HG3	1:C:438:ARG:HB2	1.65	0.78
2:B:80:ILE:HG12	2:B:177:ILE:HG12	1.66	0.78

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	993/1016 (98%)	907 (91%)	83 (8%)	3 (0%)	37	69
1	C	993/1016 (98%)	906 (91%)	84 (8%)	3 (0%)	37	69
2	B	289/303 (95%)	260 (90%)	27 (9%)	2 (1%)	19	53
2	D	281/303 (93%)	252 (90%)	27 (10%)	2 (1%)	19	53
3	E	30/65 (46%)	28 (93%)	2 (7%)	0	100	100
3	G	30/65 (46%)	26 (87%)	4 (13%)	0	100	100
All	All	2616/2768 (94%)	2379 (91%)	227 (9%)	10 (0%)	30	64

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	200	PRO
1	A	193	PRO
1	C	193	PRO
1	C	306	LEU
2	D	200	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	846/861 (98%)	813 (96%)	33 (4%)	27	58
1	C	846/861 (98%)	812 (96%)	34 (4%)	27	57
2	B	261/269 (97%)	240 (92%)	21 (8%)	10	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	255/269 (95%)	234 (92%)	21 (8%)	9	34
3	E	26/52 (50%)	25 (96%)	1 (4%)	28	58
3	G	26/52 (50%)	25 (96%)	1 (4%)	28	58
All	All	2260/2364 (96%)	2149 (95%)	111 (5%)	21	51

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	82	TRP
3	E	21	TYR
1	C	476	ASN
2	D	297	VAL
2	D	125	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	399	GLN
1	C	897	GLN
2	D	262	GLN
1	C	898	GLN
1	A	430	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues 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
1	PHD	C	369	1,5	9,11,12	0.92	0	10,15,17	1.39	2 (20%)
1	PHD	A	369	1,5	9,11,12	0.93	0	10,15,17	1.47	2 (20%)

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
1	PHD	C	369	1,5	-	0/8/11/13	-
1	PHD	A	369	1,5	-	0/8/11/13	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	C	369	PHD	CA-CB-CG	2.91	118.95	112.86
1	A	369	PHD	OD1-CG-CB	2.78	118.76	111.11
1	A	369	PHD	CA-CB-CG	2.71	118.54	112.86
1	C	369	PHD	OD1-CG-CB	2.38	117.66	111.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	369	PHD	1	0
1	A	369	PHD	2	0

## 5.5 Carbohydrates [i](#)

8 monosaccharides are modelled in this entry.

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	F	1	2,4	14,14,15	0.35	0	17,19,21	0.43	0
4	NAG	F	2	4	14,14,15	0.28	0	17,19,21	0.49	0
4	NAG	H	1	2,4	14,14,15	0.62	1 (7%)	17,19,21	0.70	0
4	NAG	H	2	4	14,14,15	0.32	0	17,19,21	0.36	0
4	NAG	I	1	2,4	14,14,15	0.39	0	17,19,21	0.46	0
4	NAG	I	2	4	14,14,15	0.31	0	17,19,21	0.48	0
4	NAG	J	1	2,4	14,14,15	0.61	1 (7%)	17,19,21	0.63	0
4	NAG	J	2	4	14,14,15	0.31	0	17,19,21	0.34	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	NAG	F	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	NAG	H	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	NAG	I	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	NAG	J	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	NAG	O5-C1	-2.18	1.40	1.43
4	J	1	NAG	O5-C1	-2.09	1.40	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

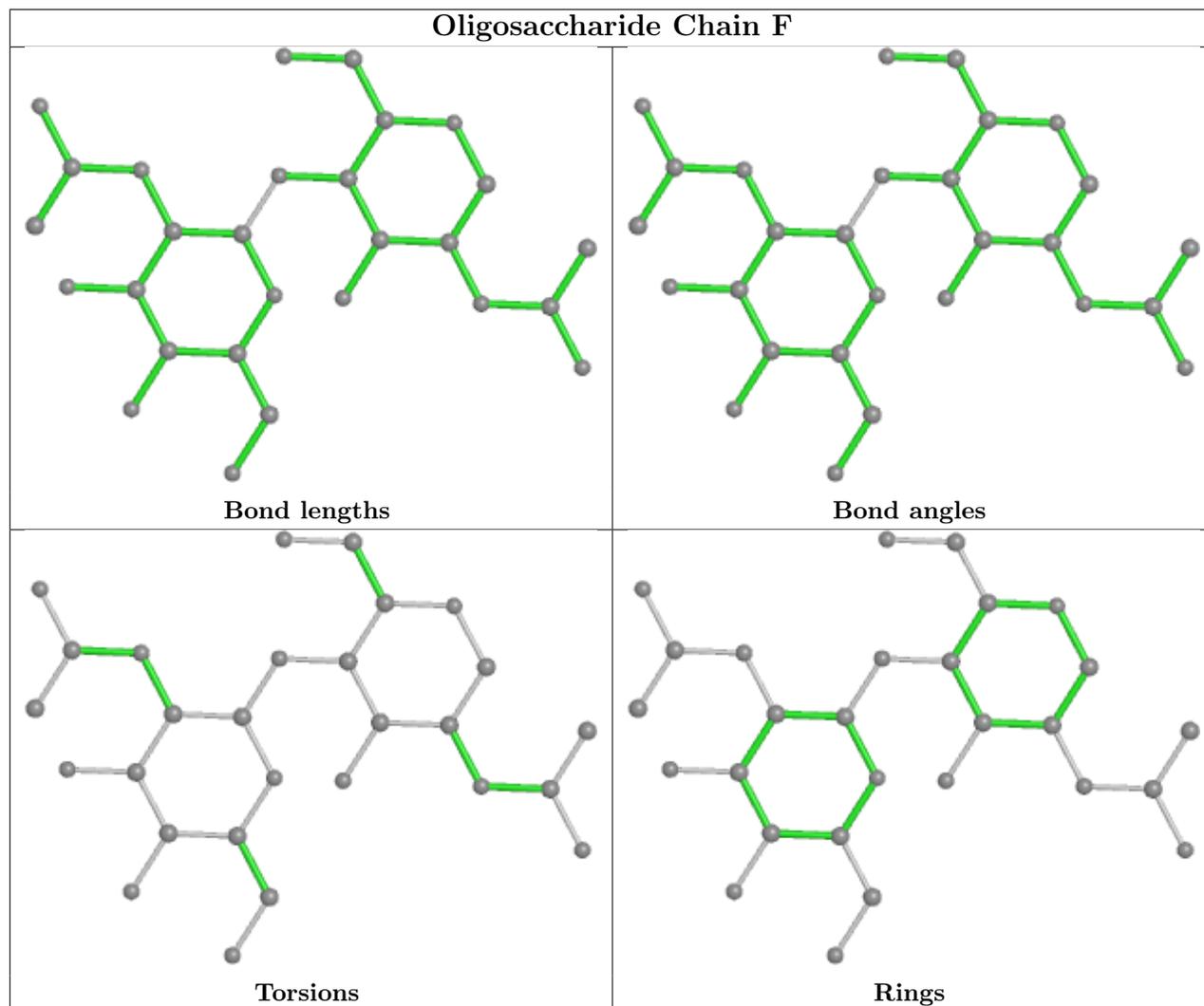
Mol	Chain	Res	Type	Atoms
4	I	1	NAG	C4-C5-C6-O6
4	I	1	NAG	O5-C5-C6-O6

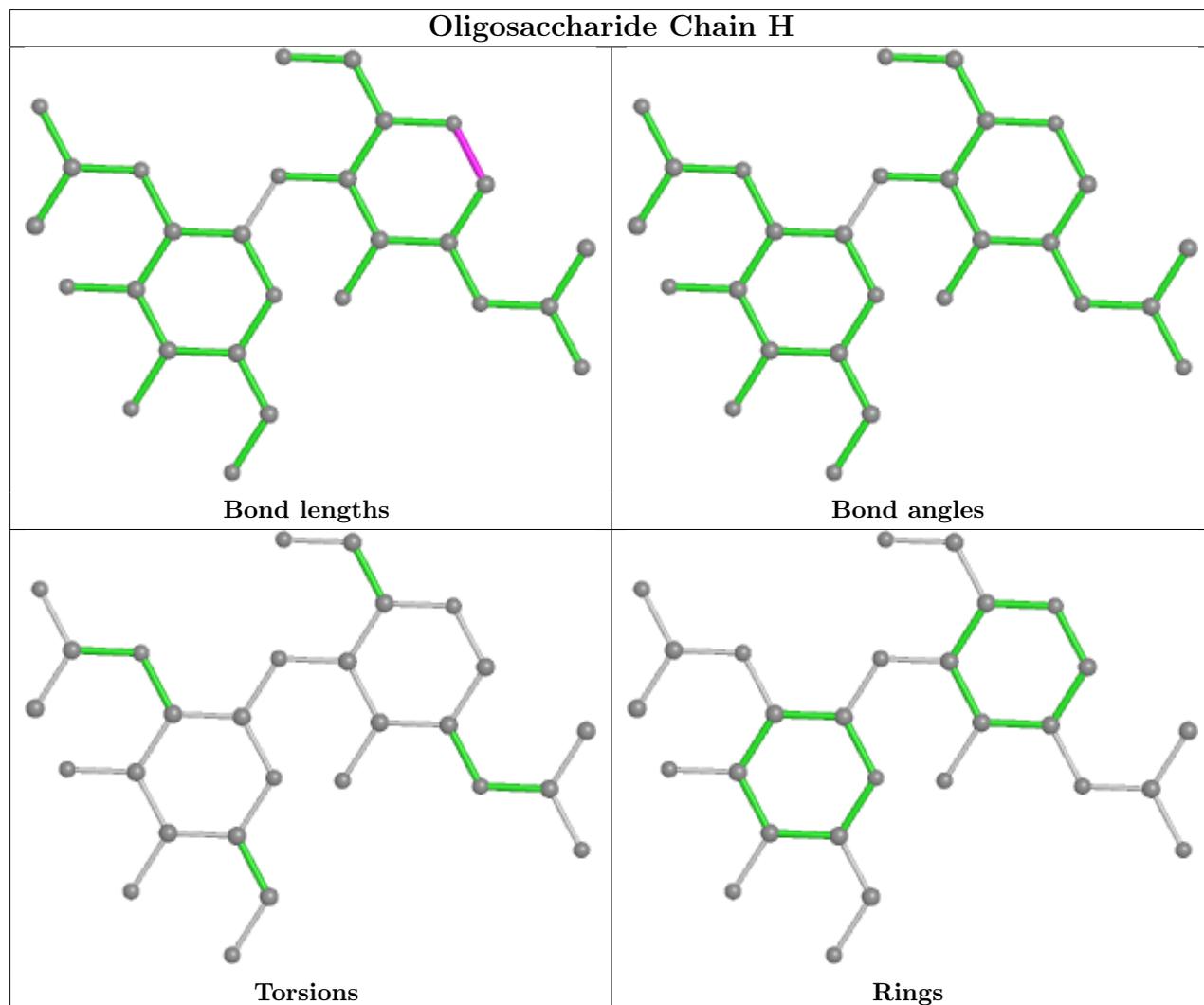
There are no ring outliers.

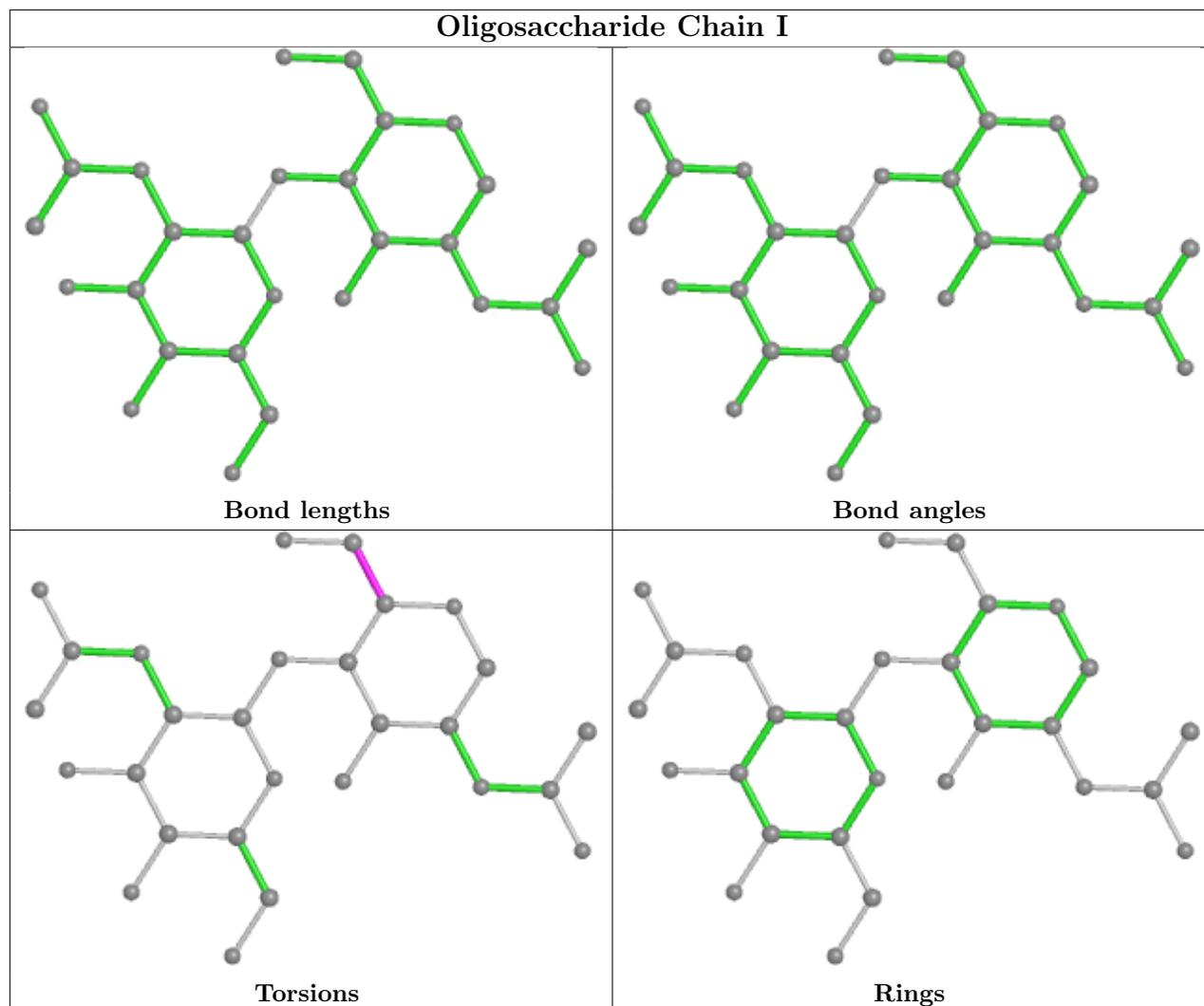
1 monomer is involved in 1 short contact:

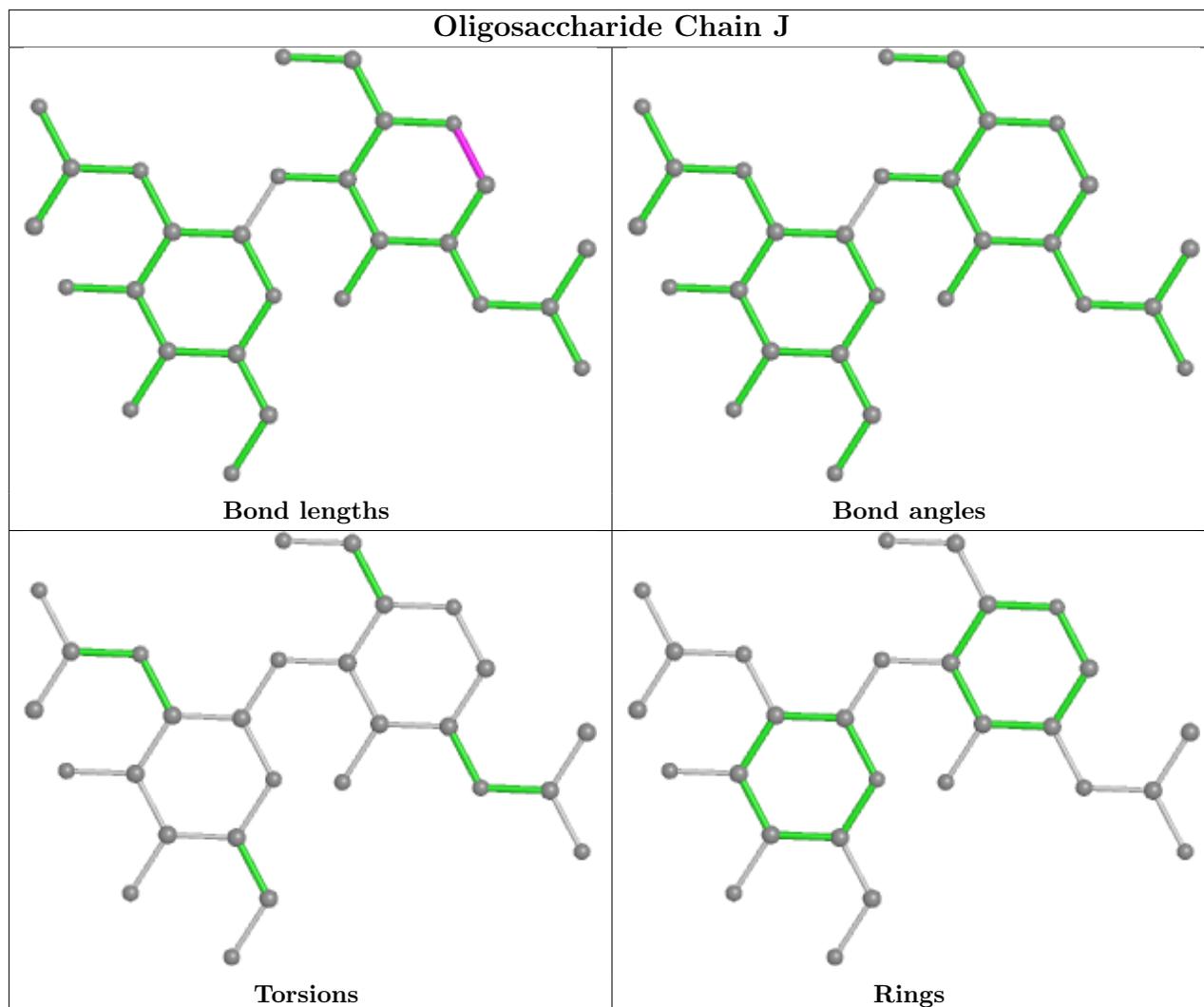
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	1	NAG	1	0

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 [i](#)

Of 26 ligands modelled in this entry, 6 are monoatomic - leaving 20 for Mogul analysis.

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$
9	DGX	A	1110	-	62,62,62	1.21	3 (4%)	89,98,98	1.29	7 (7%)
8	PCW	C	1108	-	21,21,53	1.68	6 (28%)	27,29,61	1.20	1 (3%)
8	PCW	A	1107	-	21,21,53	1.68	6 (28%)	27,29,61	1.16	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
10	NAG	D	401	2	14,14,15	0.31	0	17,19,21	0.53	0
8	PCW	C	1106	-	21,21,53	1.68	6 (28%)	27,29,61	1.23	1 (3%)
7	CLR	C	1104	-	31,31,31	1.92	9 (29%)	48,48,48	1.61	16 (33%)
7	CLR	G	101	-	31,31,31	1.77	8 (25%)	48,48,48	1.62	12 (25%)
7	CLR	A	1104	-	31,31,31	1.91	11 (35%)	48,48,48	1.57	10 (20%)
8	PCW	A	1106	-	21,21,53	1.67	4 (19%)	27,29,61	1.17	1 (3%)
8	PCW	A	1105	-	21,21,53	1.71	5 (23%)	27,29,61	1.33	1 (3%)
8	PCW	C	1107	-	21,21,53	1.69	5 (23%)	27,29,61	1.45	3 (11%)
8	PCW	C	1105	-	21,21,53	1.72	4 (19%)	27,29,61	1.15	1 (3%)
10	NAG	B	401	2	14,14,15	0.33	0	17,19,21	0.43	0
7	CLR	D	402	-	31,31,31	1.99	10 (32%)	48,48,48	1.55	12 (25%)
8	PCW	B	403	-	21,21,53	1.69	5 (23%)	27,29,61	1.23	1 (3%)
8	PCW	A	1109	-	21,21,53	1.69	5 (23%)	27,29,61	1.35	2 (7%)
9	DGX	C	1121	-	62,62,62	1.18	2 (3%)	89,98,98	1.24	8 (8%)
7	CLR	B	402	-	31,31,31	1.96	12 (38%)	48,48,48	1.63	13 (27%)
7	CLR	E	101	-	31,31,31	1.74	9 (29%)	48,48,48	1.57	11 (22%)
8	PCW	A	1108	-	21,21,53	1.68	5 (23%)	27,29,61	1.20	1 (3%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	DGX	A	1110	-	-	4/16/141/141	0/8/8/8
8	PCW	C	1108	-	-	13/23/23/57	-
8	PCW	A	1107	-	-	11/23/23/57	-
10	NAG	D	401	2	-	4/6/23/26	0/1/1/1
8	PCW	C	1106	-	-	9/23/23/57	-
7	CLR	C	1104	-	-	6/10/68/68	0/4/4/4
7	CLR	G	101	-	-	3/10/68/68	0/4/4/4
7	CLR	A	1104	-	-	6/10/68/68	0/4/4/4
8	PCW	A	1106	-	-	16/23/23/57	-
8	PCW	A	1105	-	-	12/23/23/57	-
8	PCW	C	1107	-	-	10/23/23/57	-
8	PCW	C	1105	-	-	11/23/23/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	B	401	2	-	1/6/23/26	0/1/1/1
7	CLR	D	402	-	-	1/10/68/68	0/4/4/4
8	PCW	B	403	-	-	11/23/23/57	-
8	PCW	A	1109	-	-	14/23/23/57	-
9	DGX	C	1121	-	-	4/16/141/141	0/8/8/8
7	CLR	B	402	-	-	1/10/68/68	0/4/4/4
7	CLR	E	101	-	-	3/10/68/68	0/4/4/4
8	PCW	A	1108	-	-	10/23/23/57	-

The worst 5 of 115 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	402	CLR	C10-C9	5.14	1.64	1.56
7	A	1104	CLR	C10-C9	4.90	1.64	1.56
7	D	402	CLR	C10-C9	4.77	1.64	1.56
7	C	1104	CLR	C10-C9	4.73	1.64	1.56
7	G	101	CLR	C10-C9	4.17	1.63	1.56

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1110	DGX	O21-C23-C22	5.45	115.79	108.67
9	C	1121	DGX	O21-C23-C22	5.32	115.63	108.67
8	A	1105	PCW	O2-C31-C32	5.21	120.67	111.09
8	C	1107	PCW	O2-C31-C32	5.12	120.50	111.09
8	A	1109	PCW	O2-C31-C32	4.98	120.24	111.09

There are no chirality outliers.

5 of 150 torsion outliers are listed below:

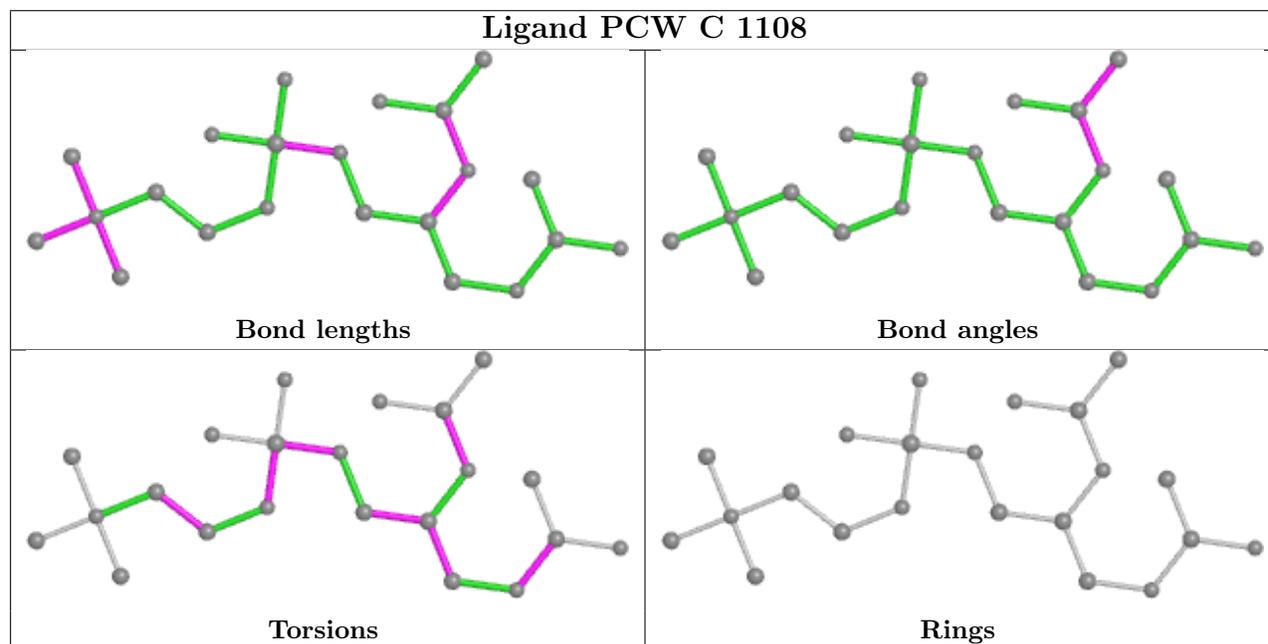
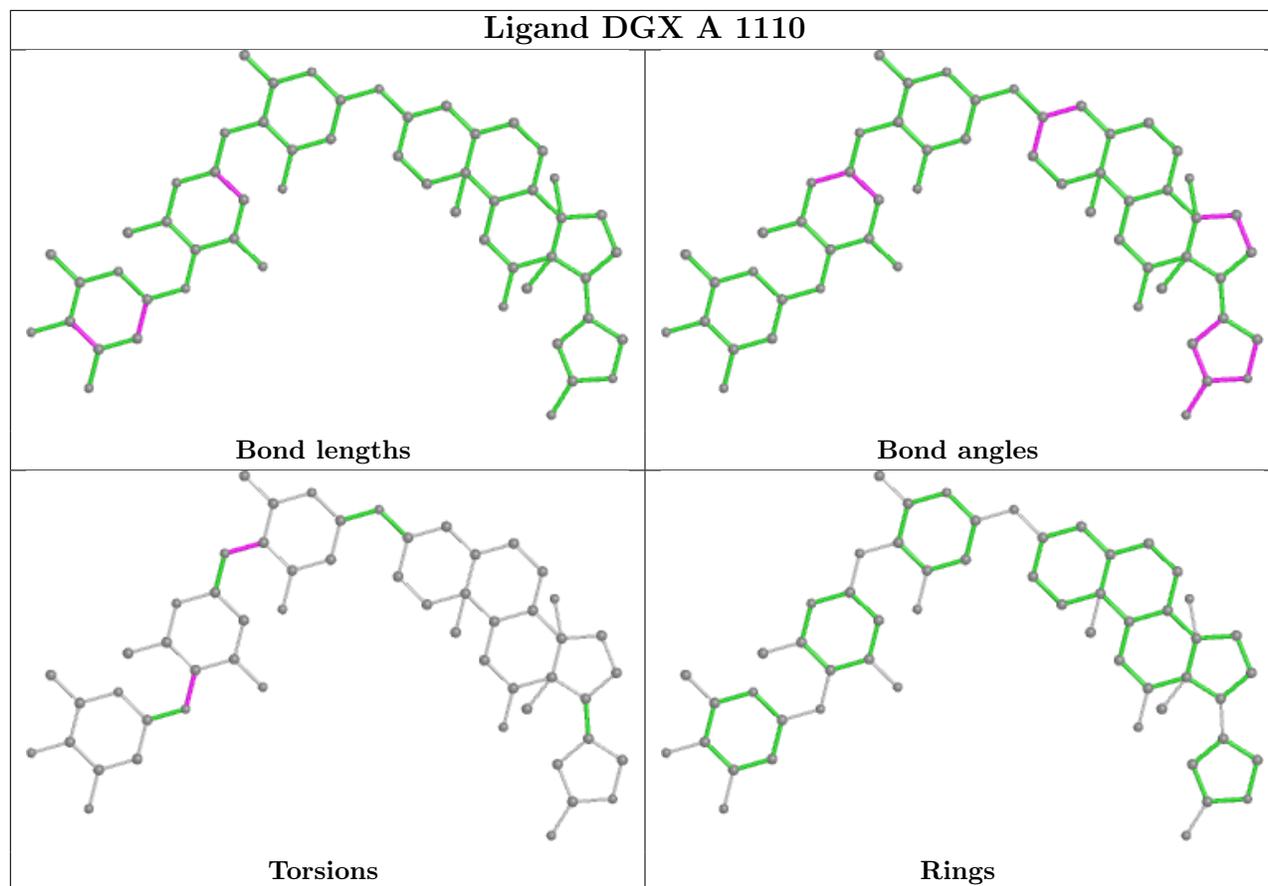
Mol	Chain	Res	Type	Atoms
8	A	1105	PCW	C4-O4P-P-O1P
8	A	1106	PCW	O4P-C4-C5-N
8	A	1107	PCW	C1-O3P-P-O2P
8	A	1108	PCW	C4-O4P-P-O1P
8	A	1108	PCW	C4-O4P-P-O2P

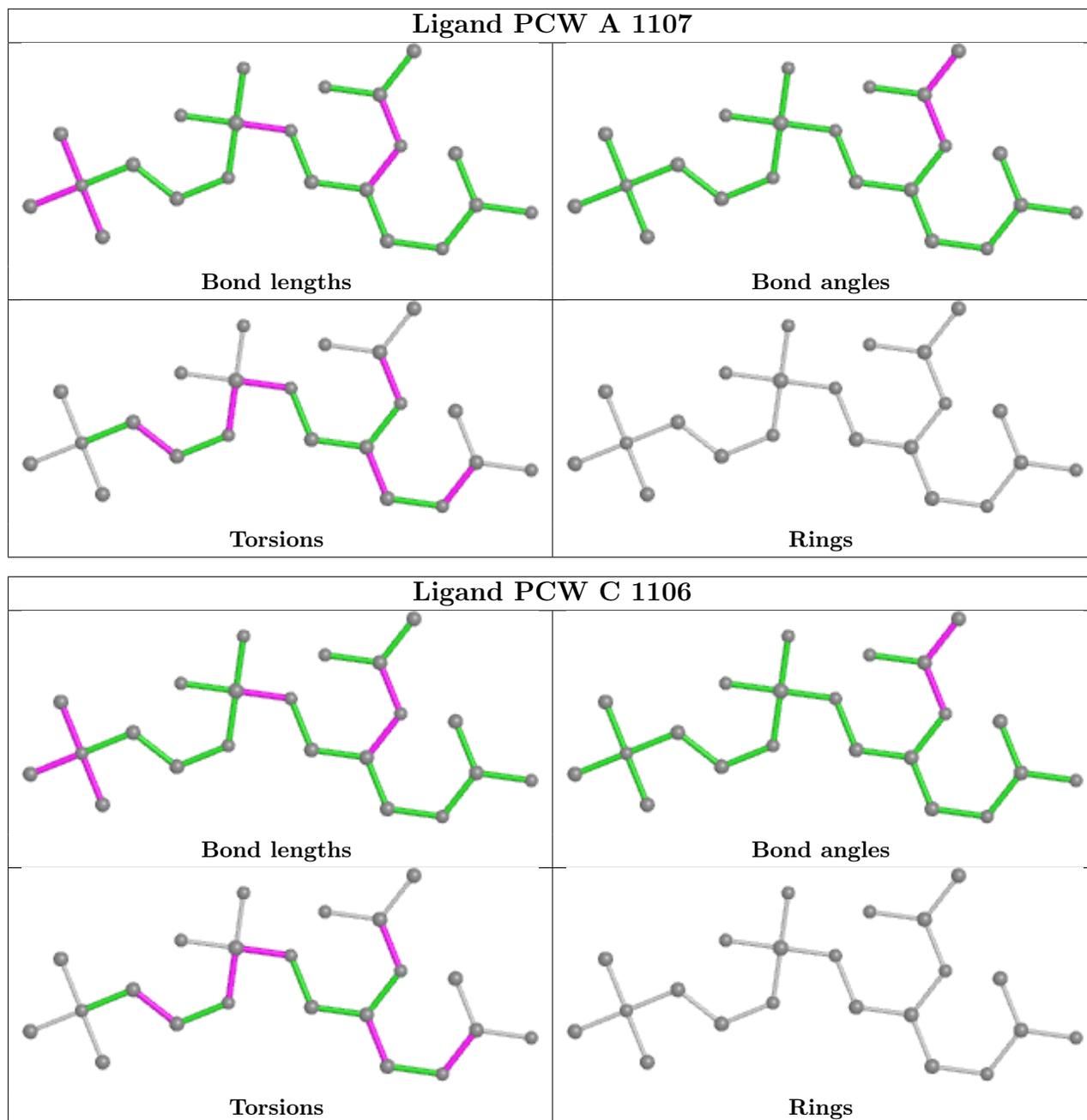
There are no ring outliers.

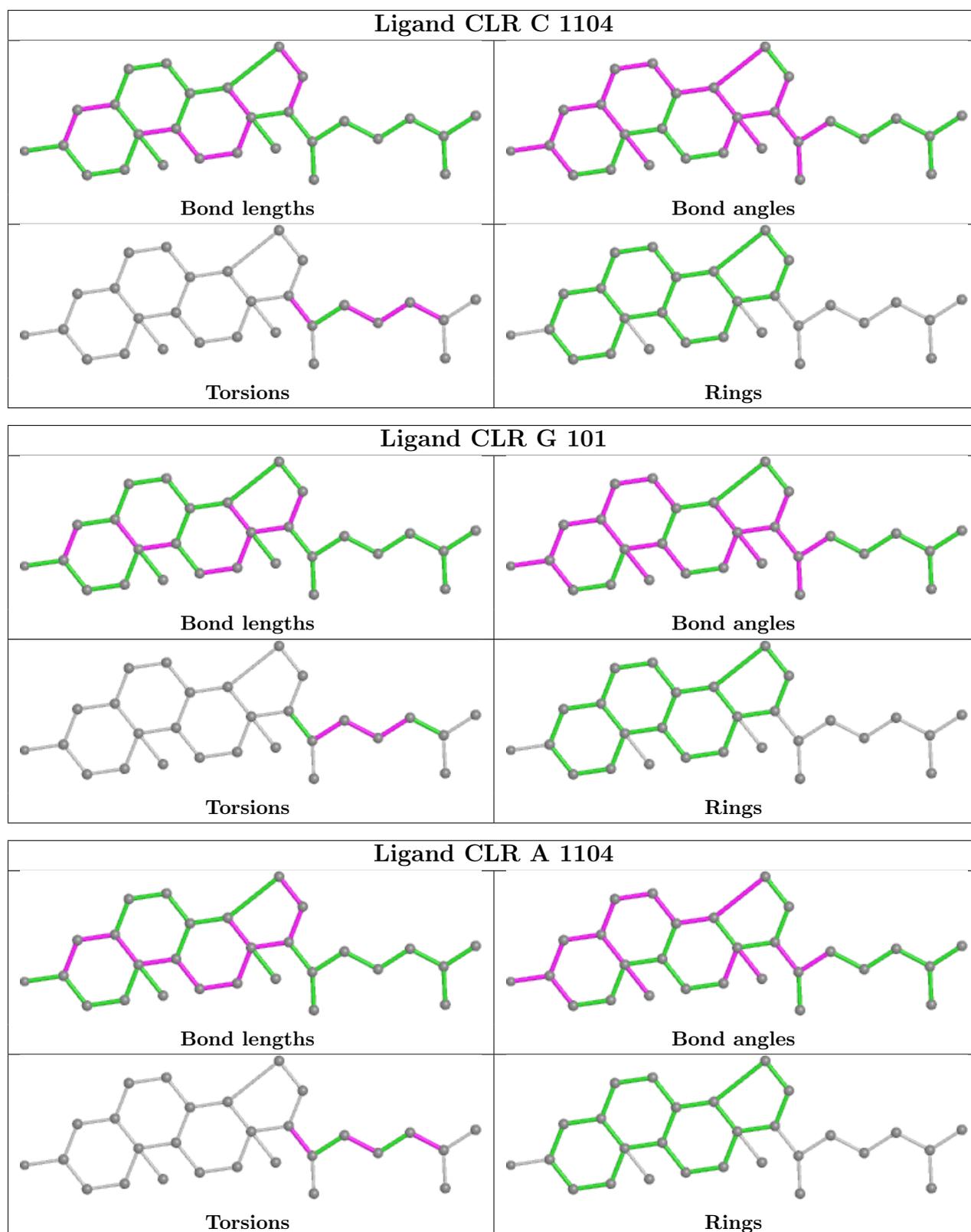
14 monomers are involved in 31 short contacts:

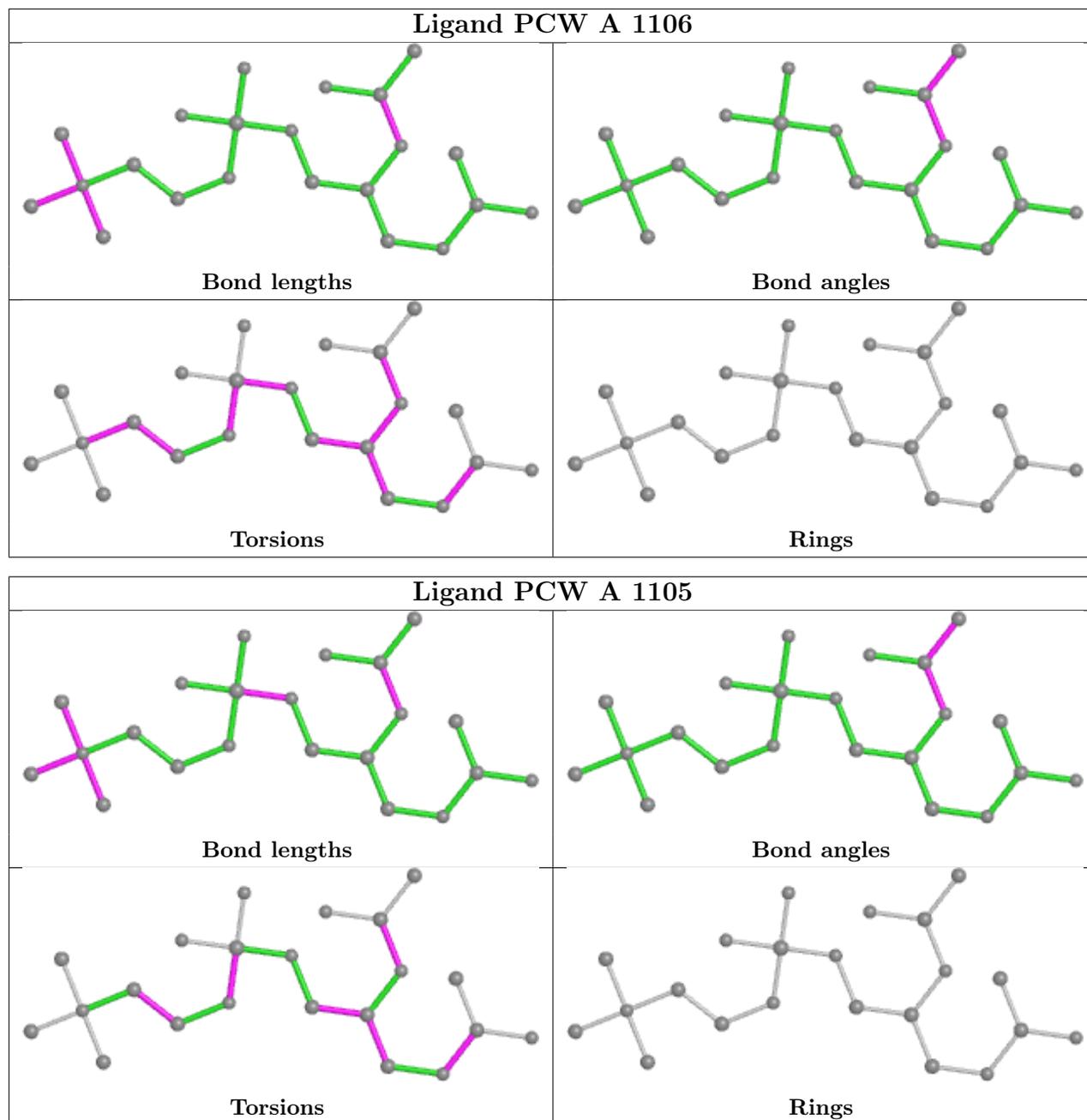
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1110	DGX	1	0
7	C	1104	CLR	3	0
7	G	101	CLR	1	0
7	A	1104	CLR	2	0
8	A	1106	PCW	4	0
8	A	1105	PCW	2	0
8	C	1107	PCW	2	0
8	C	1105	PCW	2	0
7	D	402	CLR	1	0
8	B	403	PCW	2	0
8	A	1109	PCW	1	0
9	C	1121	DGX	2	0
7	E	101	CLR	6	0
8	A	1108	PCW	2	0

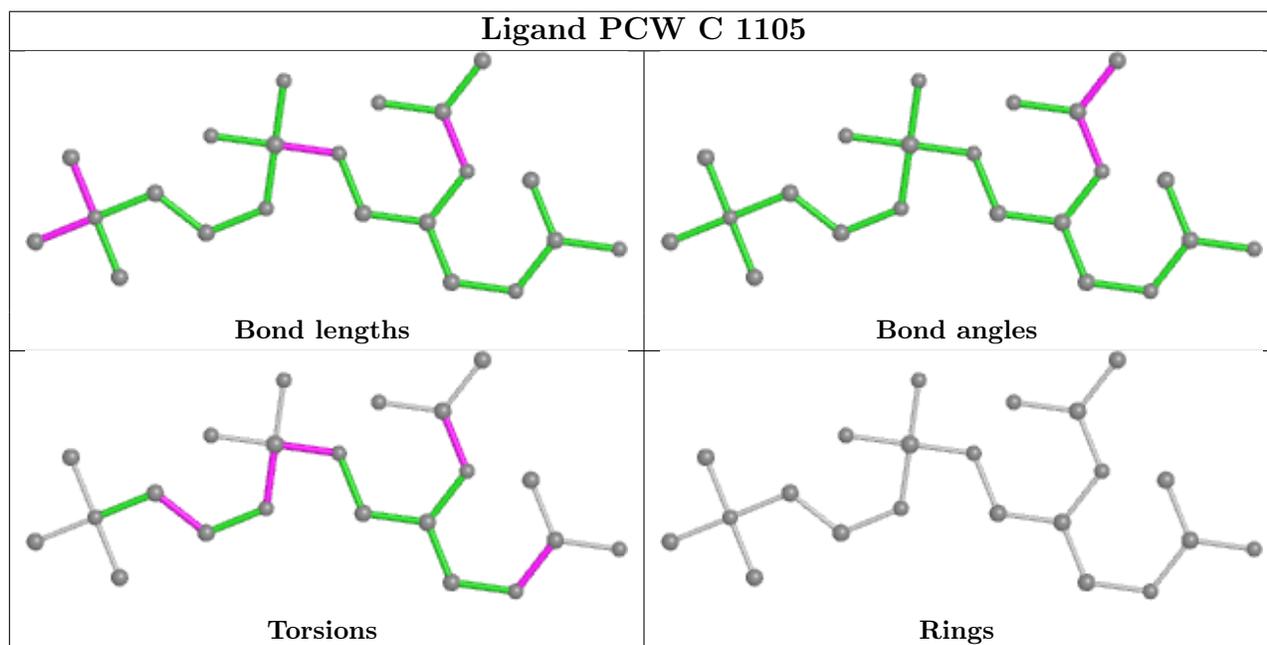
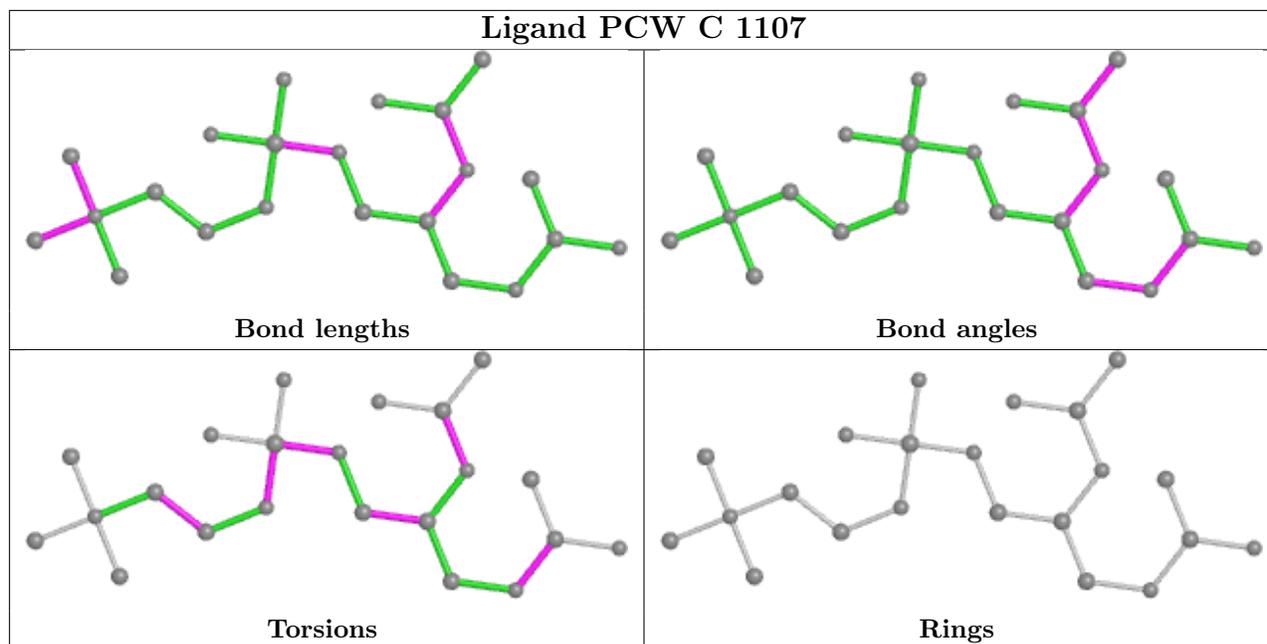
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

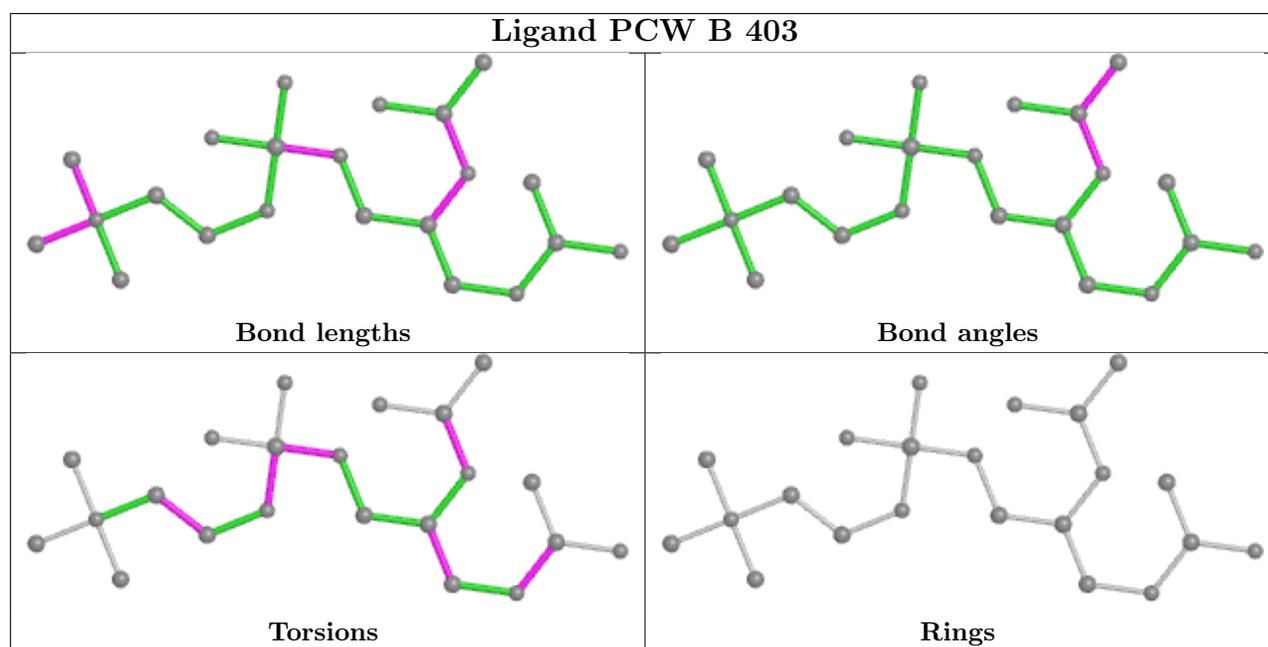
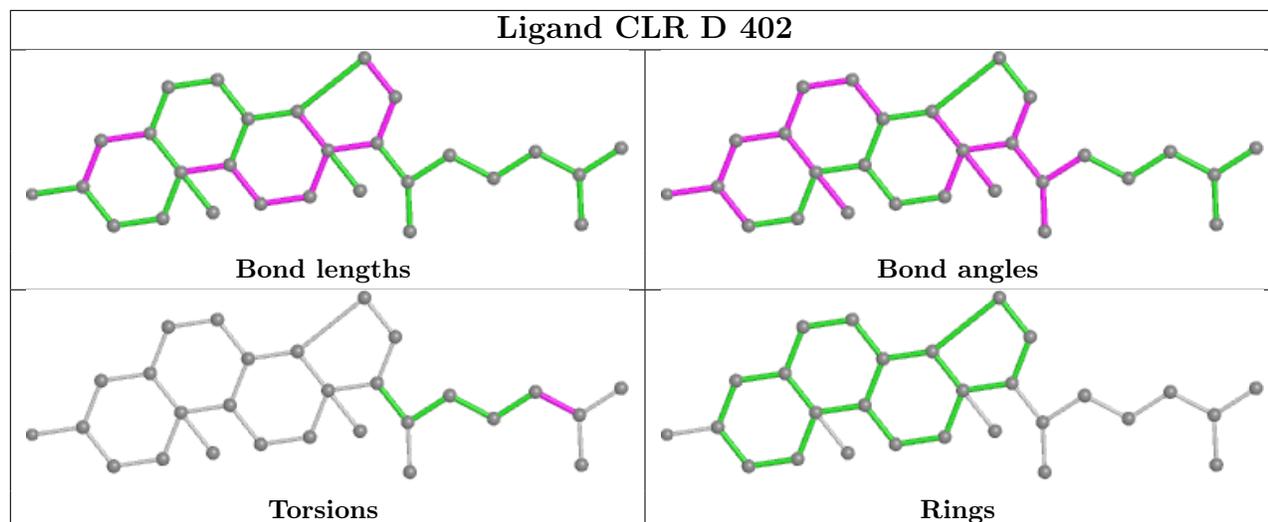


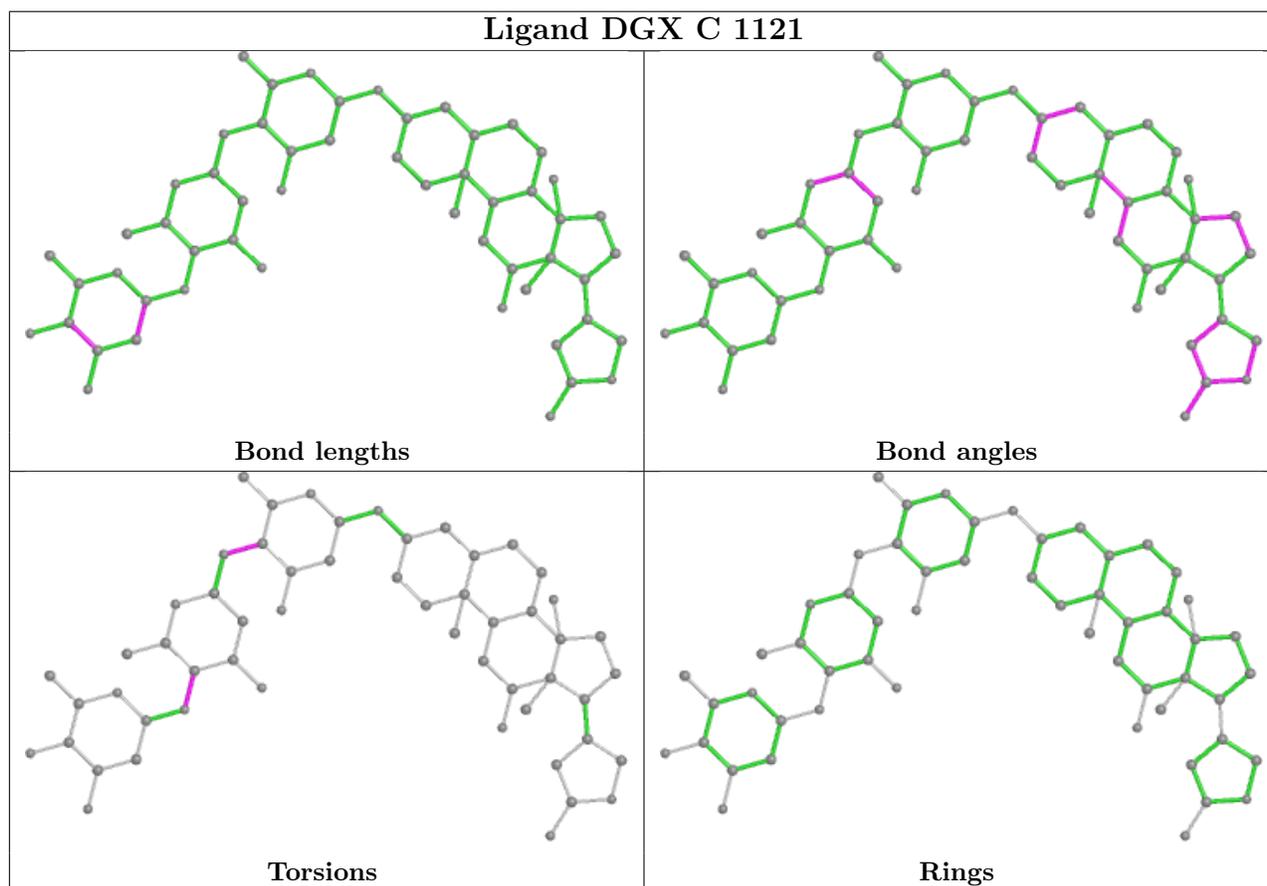
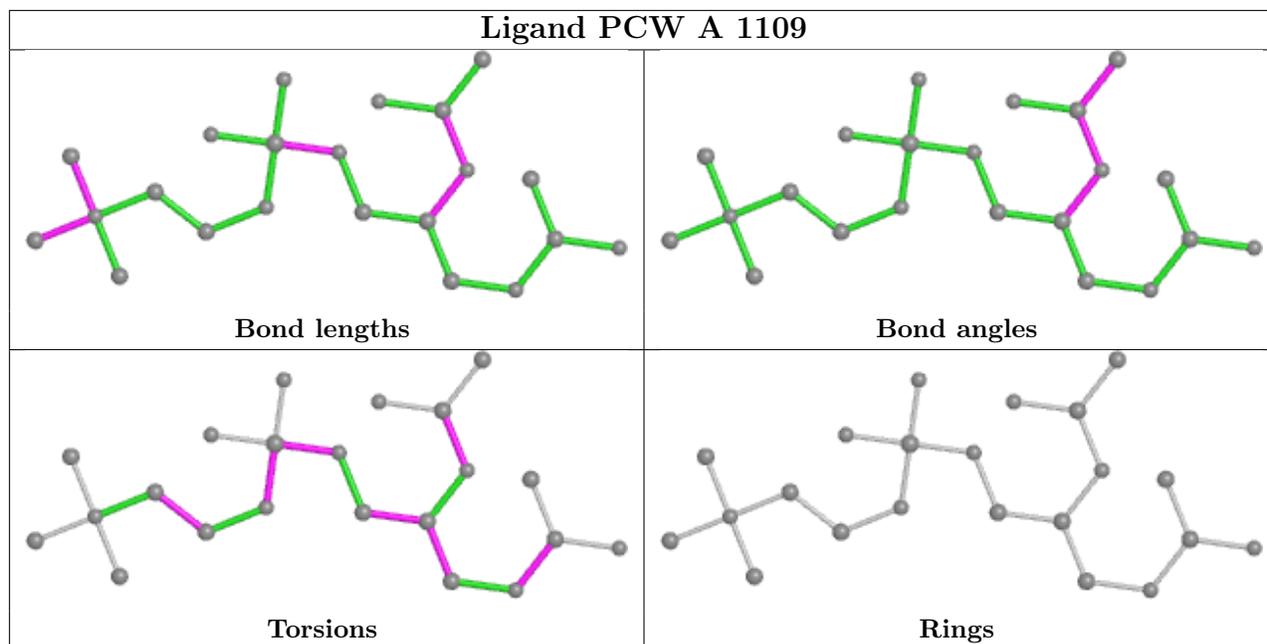


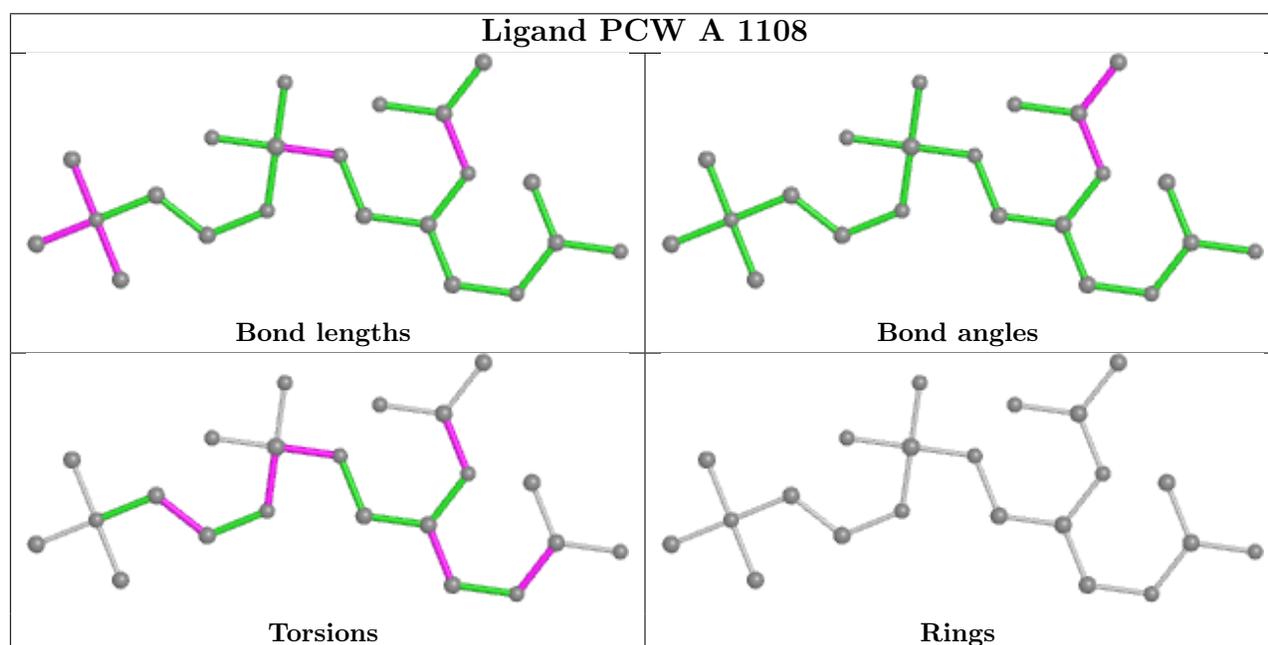
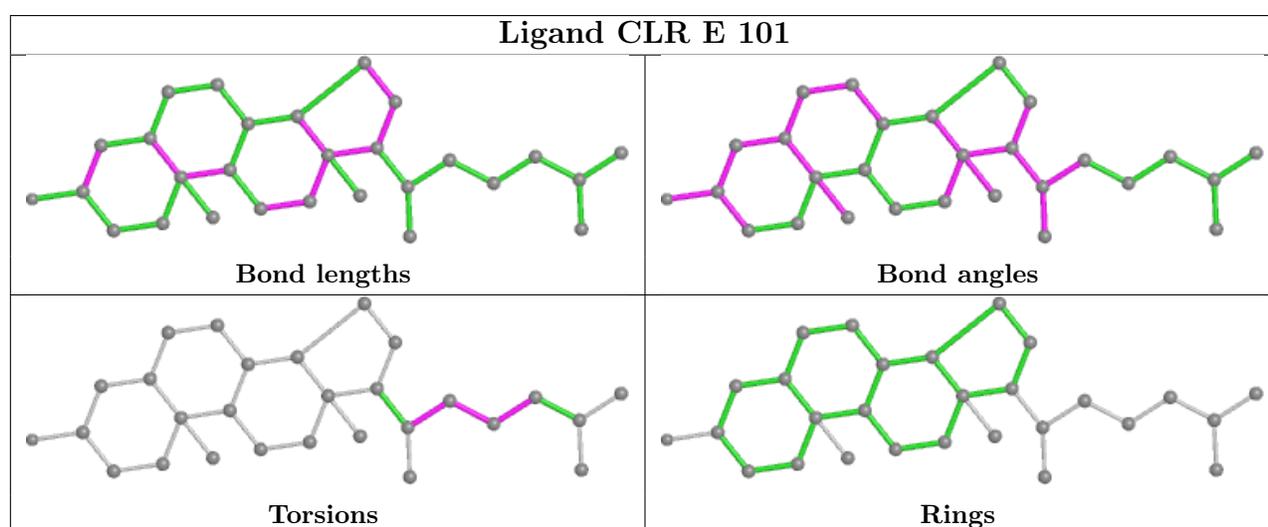
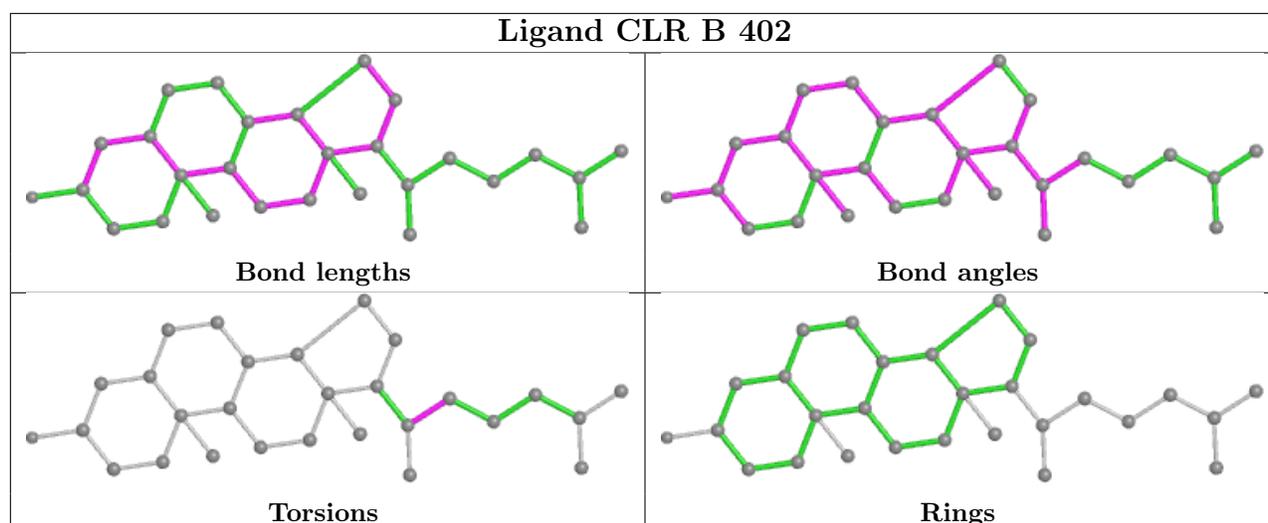












## 5.7 Other polymers

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	995/1016 (97%)	-0.37	10 (1%) 79 64	50, 103, 209, 236	0
1	C	995/1016 (97%)	-0.36	9 (0%) 81 66	51, 107, 185, 211	0
2	B	291/303 (96%)	-0.15	6 (2%) 63 47	66, 134, 178, 209	0
2	D	285/303 (94%)	-0.03	12 (4%) 41 31	58, 124, 176, 202	0
3	E	32/65 (49%)	-0.98	0 100 100	60, 84, 119, 143	0
3	G	32/65 (49%)	-0.64	0 100 100	57, 85, 120, 130	0
All	All	2630/2768 (95%)	-0.32	37 (1%) 73 57	50, 110, 196, 236	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	195	SER	6.3
2	B	167	TYR	4.4
1	A	578	PHE	3.6
2	D	122	ILE	3.5
1	C	111	GLN	3.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PHD	A	369	12/13	0.94	0.09	73,73,97,101	0
1	PHD	C	369	12/13	0.97	0.09	86,86,118,125	0

### 6.3 Carbohydrates [i](#)

SUGAR-RSR INFOmissingINFO

### 6.4 Ligands [i](#)

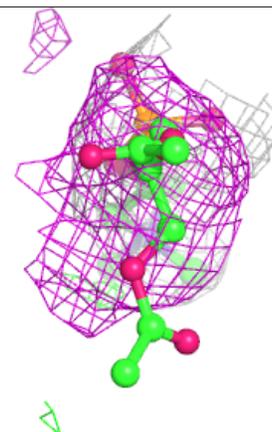
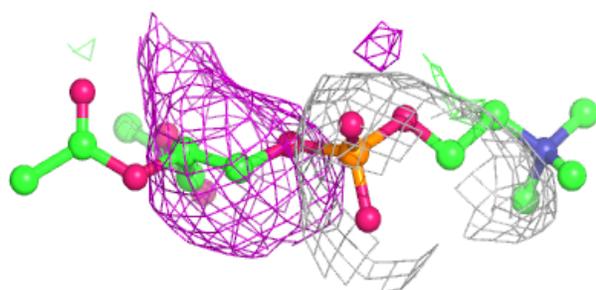
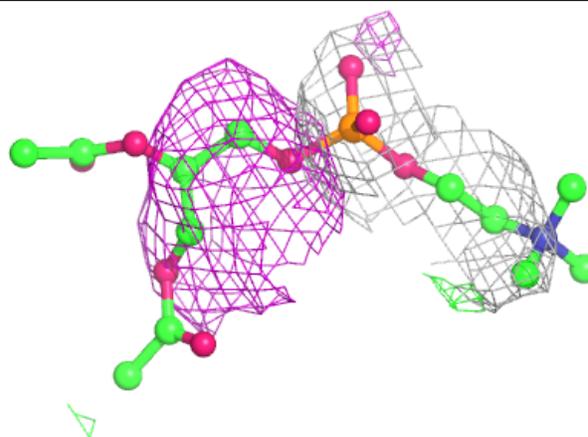
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
10	NAG	D	401	14/15	0.35	0.10	164,178,198,201	0
8	PCW	A	1108	22/54	0.63	0.18	130,163,204,216	0
8	PCW	A	1105	22/54	0.65	0.14	93,140,181,190	0
10	NAG	B	401	14/15	0.67	0.09	161,177,190,195	0
8	PCW	C	1105	22/54	0.67	0.18	119,157,191,204	0
8	PCW	A	1106	22/54	0.73	0.16	118,158,195,209	0
7	CLR	D	402	28/28	0.80	0.13	97,120,149,166	0
8	PCW	A	1107	22/54	0.80	0.12	154,180,205,211	0
8	PCW	C	1106	22/54	0.81	0.14	122,158,180,196	0
7	CLR	A	1104	28/28	0.82	0.18	83,111,135,145	0
8	PCW	B	403	22/54	0.83	0.14	118,165,189,206	0
7	CLR	B	402	28/28	0.86	0.10	107,128,142,152	0
7	CLR	C	1104	28/28	0.86	0.15	67,104,133,144	0
6	NA	C	1102	1/1	0.87	0.26	41,41,41,41	0
8	PCW	C	1108	22/54	0.89	0.09	106,125,142,161	0
9	DGX	A	1110	55/55	0.91	0.11	102,119,149,165	0
9	DGX	C	1121	55/55	0.91	0.09	80,90,126,132	0
7	CLR	E	101	28/28	0.92	0.08	54,55,75,88	0
7	CLR	G	101	28/28	0.94	0.10	61,63,95,121	0
6	NA	A	1102	1/1	0.94	0.19	50,50,50,50	0
8	PCW	A	1109	22/54	0.95	0.10	83,118,149,157	0
8	PCW	C	1107	22/54	0.95	0.09	82,112,165,171	0
5	MG	A	1101	1/1	0.99	0.03	87,87,87,87	0
5	MG	C	1103	1/1	0.99	0.02	55,55,55,55	0
5	MG	C	1101	1/1	1.00	0.08	87,87,87,87	0
5	MG	A	1103	1/1	1.00	0.07	67,67,67,67	0

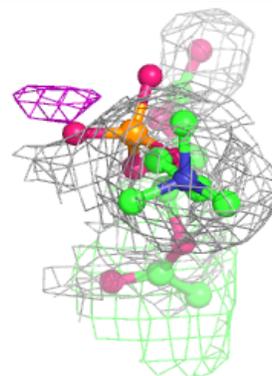
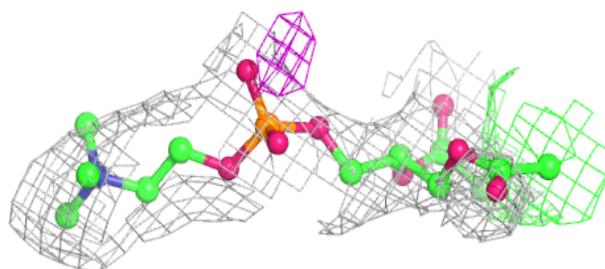
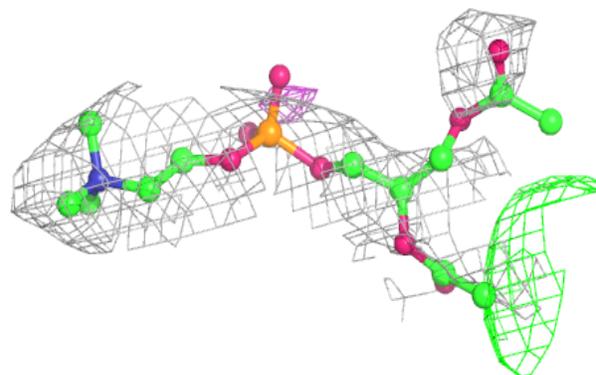
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around PCW A 1108:**

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

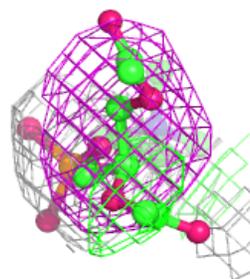
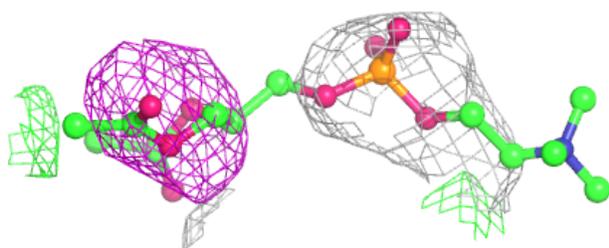
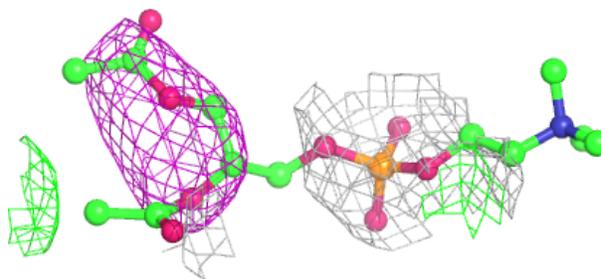
**Electron density around PCW A 1105:**

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

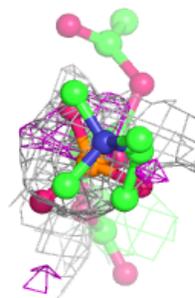
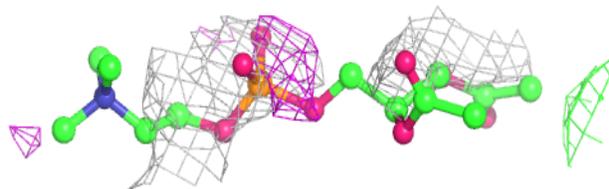
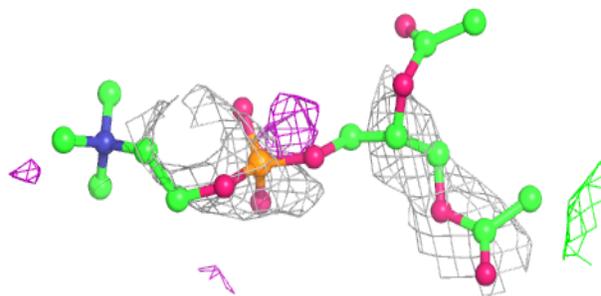


**Electron density around PCW C 1105:**

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

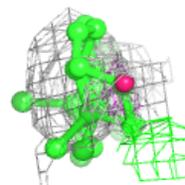
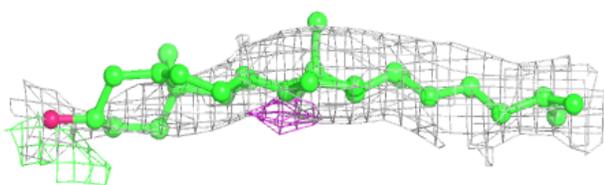
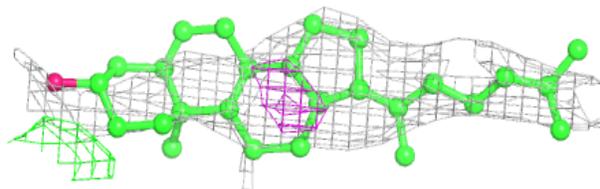
**Electron density around PCW A 1106:**

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

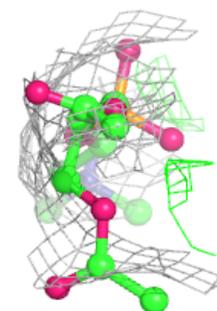
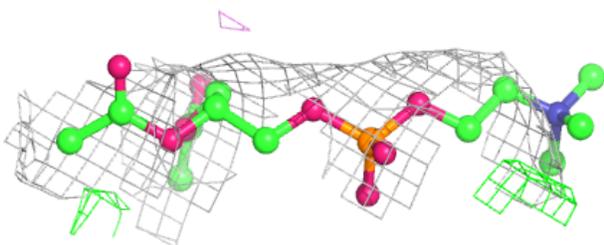
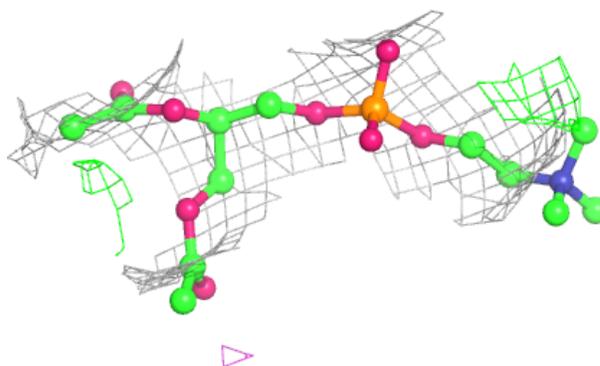


**Electron density around CLR D 402:**

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

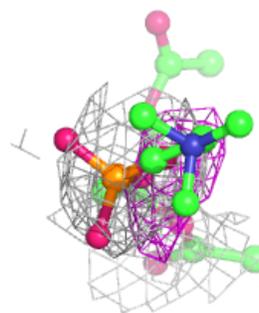
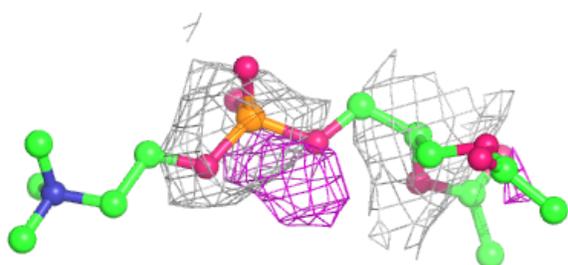
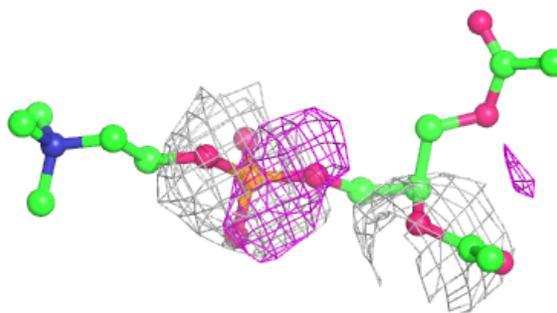
**Electron density around PCW A 1107:**

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

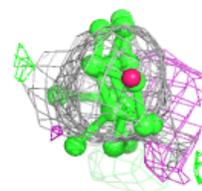
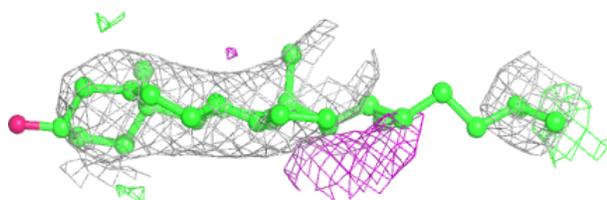
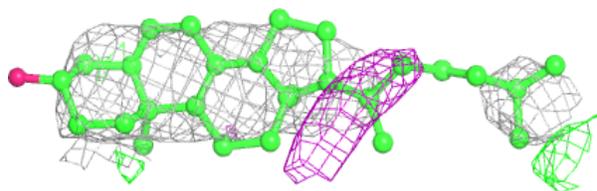


**Electron density around PCW C 1106:**

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

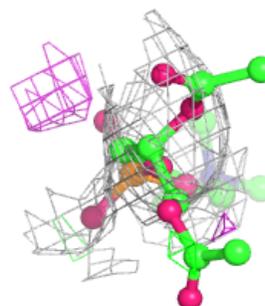
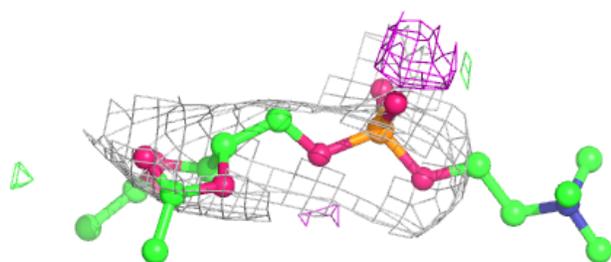
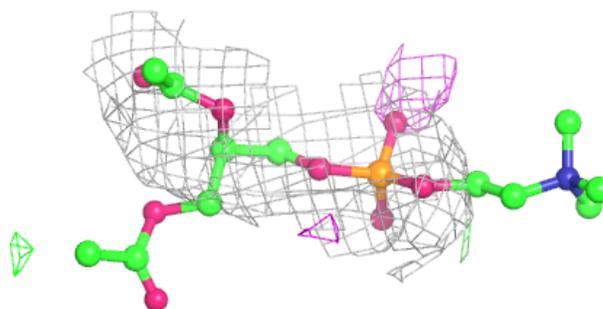
**Electron density around CLR A 1104:**

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

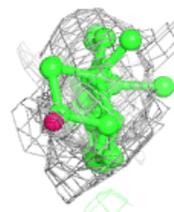
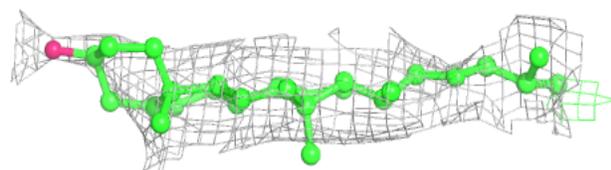
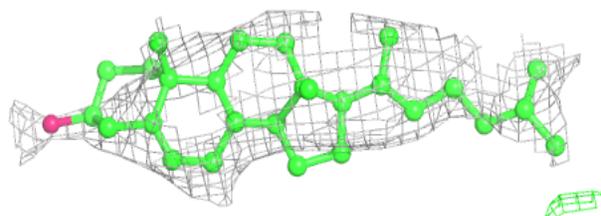


**Electron density around PCW B 403:**

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

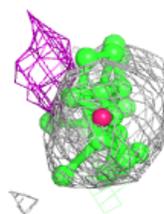
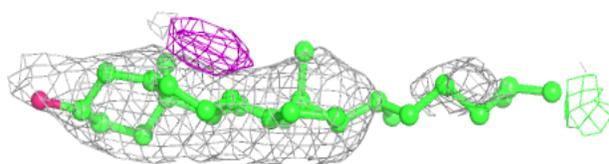
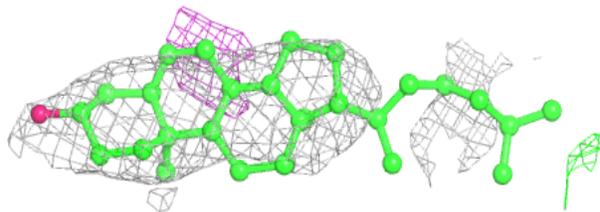
**Electron density around CLR B 402:**

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

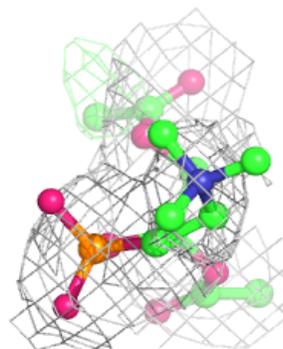
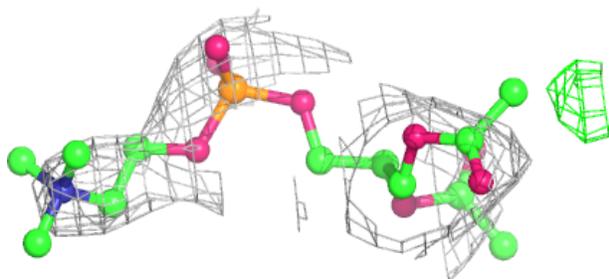
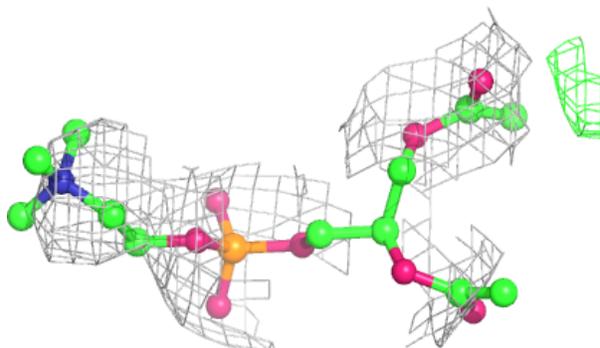


**Electron density around CLR C 1104:**

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

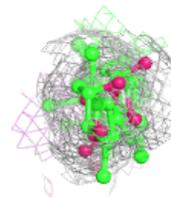
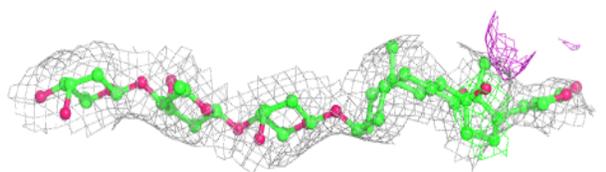
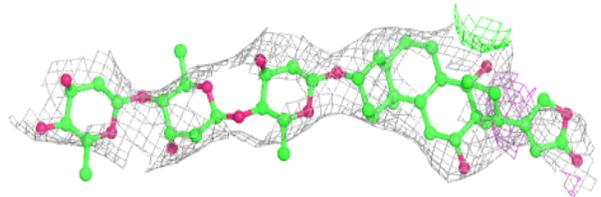
**Electron density around PCW C 1108:**

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

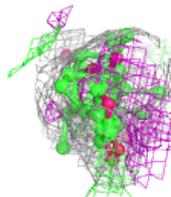
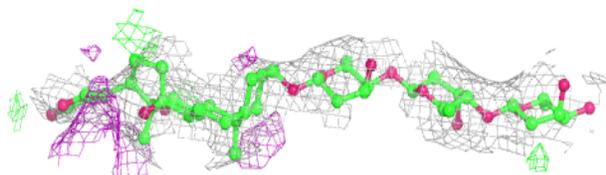
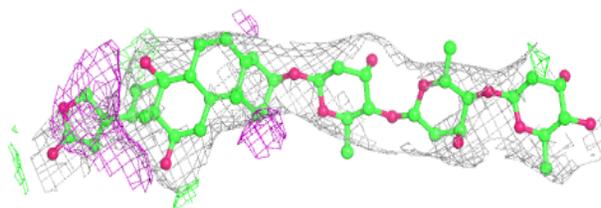


**Electron density around DGX A 1110:**

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

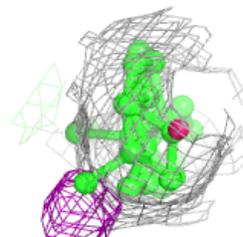
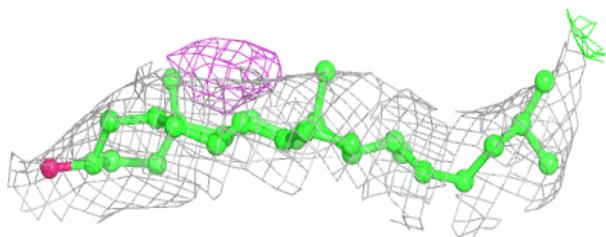
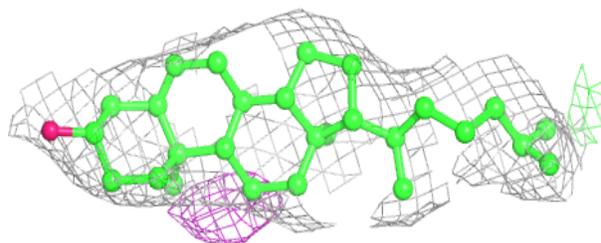
**Electron density around DGX C 1121:**

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

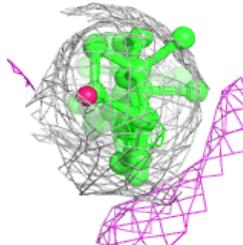
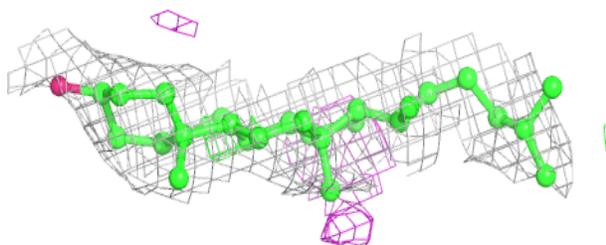
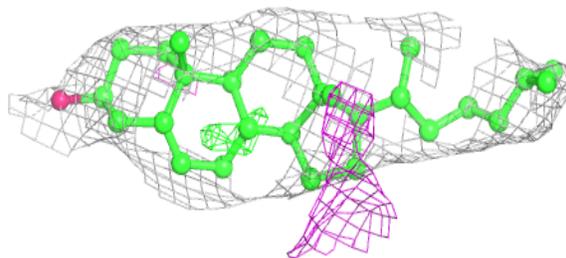


**Electron density around CLR E 101:**

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

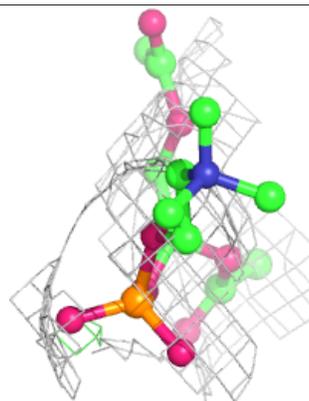
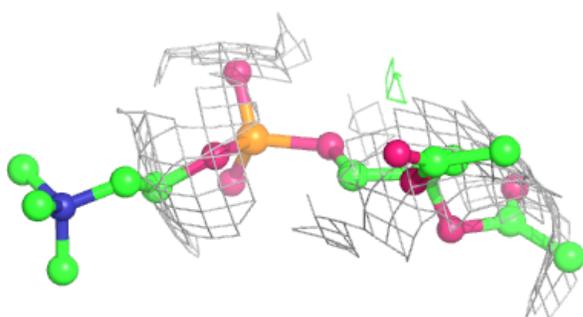
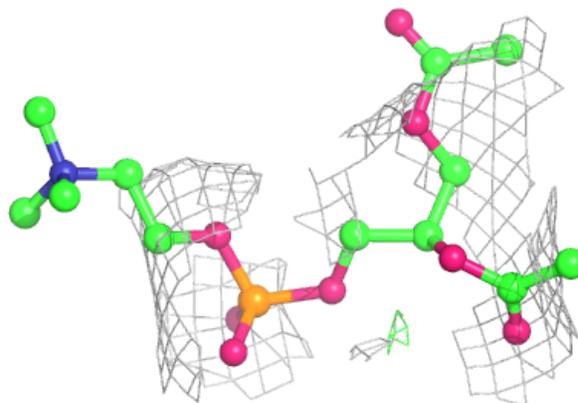
**Electron density around CLR G 101:**

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

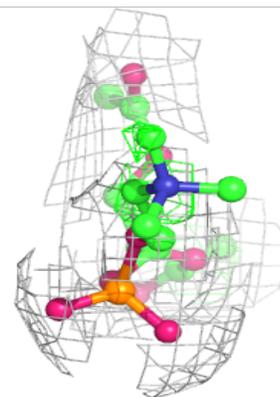
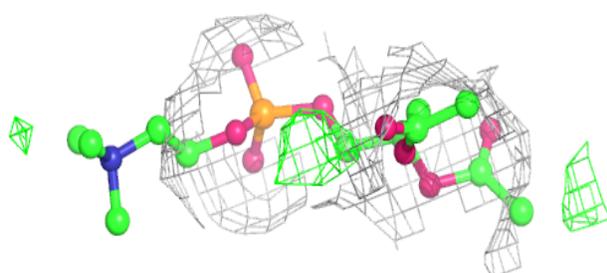
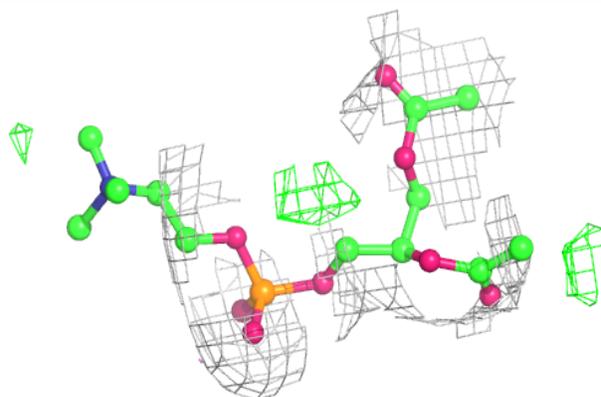


**Electron density around PCW A 1109:**

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

**Electron density around PCW C 1107:**

$2mF_o-DF_c$  (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.