



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 22, 2025 – 10:59 AM JST

PDB ID : 9VJ2 / pdb_00009vj2
Title : Crystal structure of palytoxin-bound Na⁺,K⁺-ATPase in the E2P state
Authors : Kanai, R.; Vilsen, B.; Cornelius, F.; Toyoshima, C.
Deposited on : 2025-06-19
Resolution : 3.79 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

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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

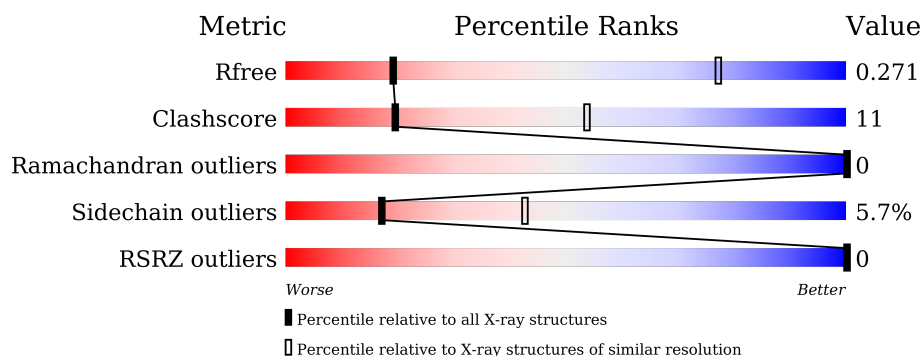
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.79 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	1025 (3.98-3.62)
Clashscore	180529	1005 (3.96-3.64)
Ramachandran outliers	177936	1044 (3.98-3.62)
Sidechain outliers	177891	1039 (3.98-3.62)
RSRZ outliers	164620	1025 (3.98-3.62)

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	1021	
2	B	303	
3	G	65	
4	C	2	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 10796 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.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	996	Total	Be	C	F	N	O	S	0	0	0
			7736	1	4929	3	1303	1453	47			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	291	Total	C	N	O	S	0	0	0
			2386	1546	390	437	13			

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

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

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

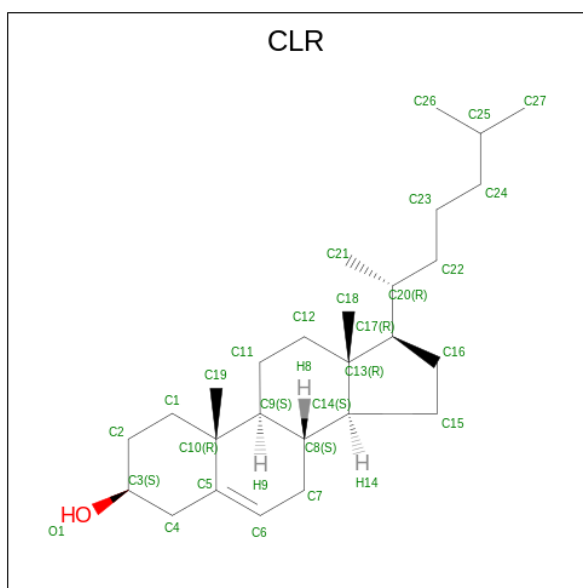


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

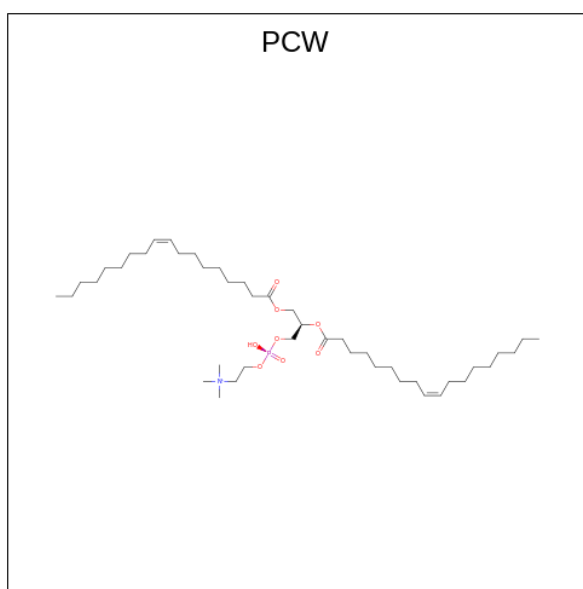
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



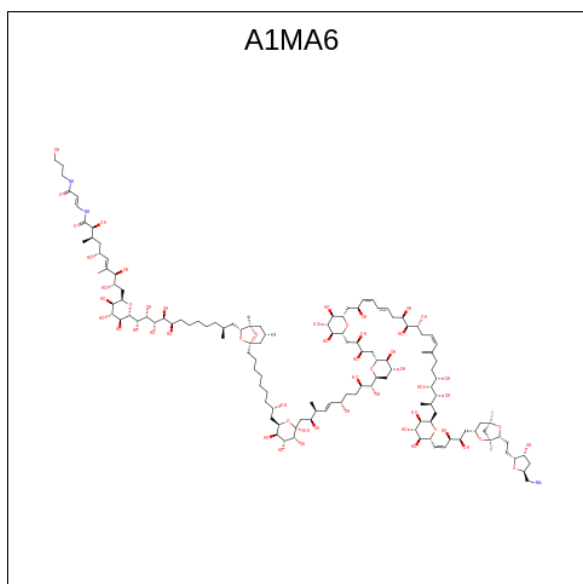
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			28	27	1		
6	A	1	Total	C	O	0	0
			28	27	1		

- Molecule 7 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: $C_{44}H_{85}NO_8P$).



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

- Molecule 8 is palytoxin (CCD ID: A1MA6) (formula: $C_{129}H_{223}N_3O_{54}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	N	O		0	0
			184	129	3	52			

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

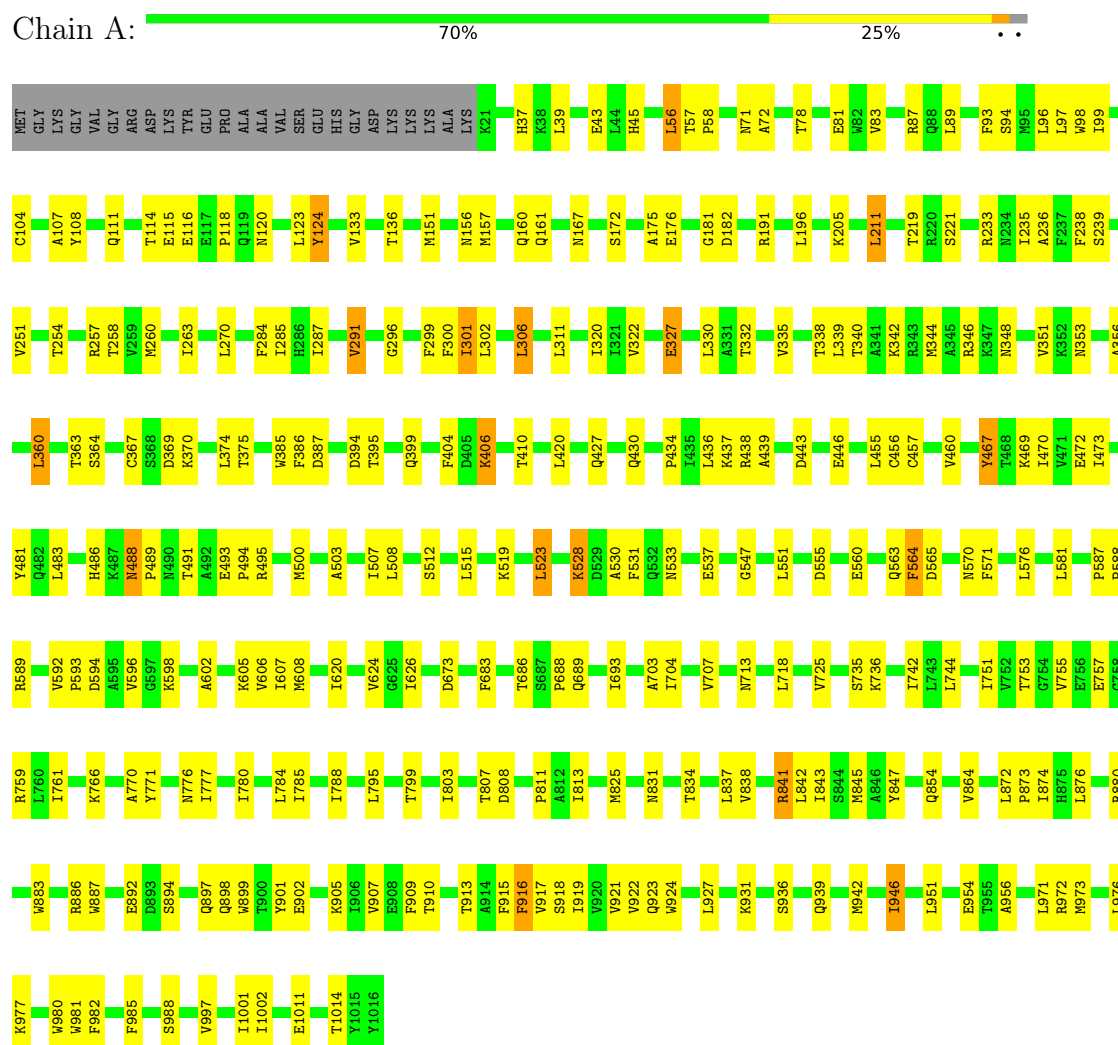
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	3	Total	O	0	0
			3	3		

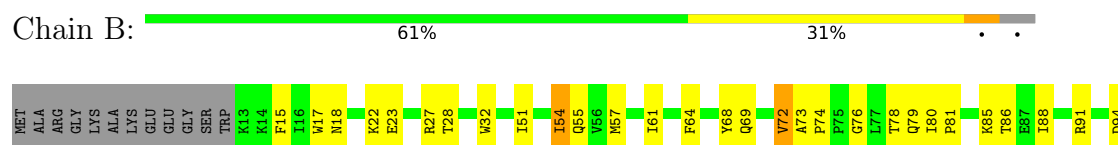
3 Residue-property plots

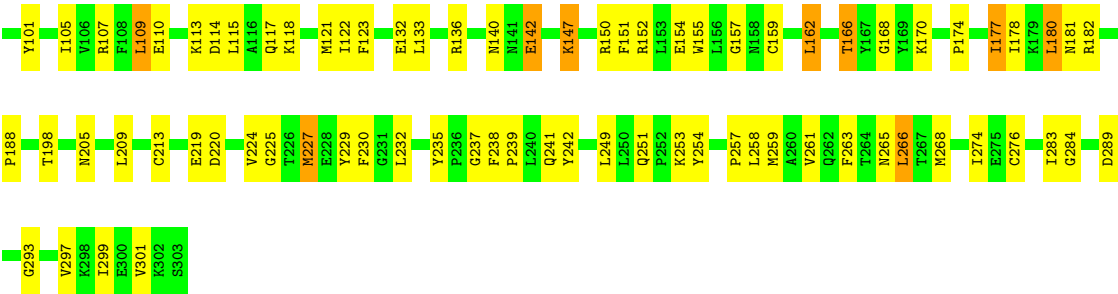
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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

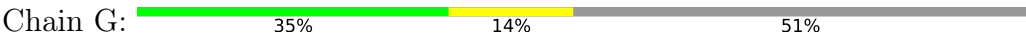


- Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1





● 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



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	85.02Å 85.02Å 646.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 3.79 10.00 – 3.79	Depositor EDS
% Data completeness (in resolution range)	44.1 (10.00-3.79) 41.4 (10.00-3.79)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.227 , 0.276 0.253 , 0.271	Depositor DCC
R_{free} test set	519 reflections (4.36%)	wwPDB-VP
Wilson B-factor (Å ²)	123.2	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 71.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10796	wwPDB-VP
Average B, all atoms (Å ²)	134.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BFD, CLR, PCW, MG, A1MA6, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.18	0/7873	0.49	0/10680
2	B	0.16	0/2449	0.47	0/3301
3	G	0.14	0/261	0.39	0/354
All	All	0.18	0/10583	0.49	0/14335

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	7736	0	7788	178	0
2	B	2386	0	2362	68	0
3	G	255	0	259	7	0
4	C	28	0	25	0	0
5	A	2	0	0	0	0
6	A	56	0	92	7	0
7	A	132	0	108	1	0
8	A	184	0	0	3	0
9	B	14	0	13	0	0
10	A	3	0	0	0	0
All	All	10796	0	10647	244	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 11.

The worst 5 of 244 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)
2:B:88:ILE:HB	2:B:299:ILE:HG22	1.55	0.89
1:A:864:VAL:HG22	2:B:57:MET:HG3	1.54	0.87
1:A:399:GLN:HE21	1:A:436:LEU:HD11	1.40	0.84
2:B:266:LEU:HD13	2:B:301:VAL:HG21	1.62	0.80
2:B:157:GLY:H	2:B:230:PHE:HB3	1.48	0.79

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	993/1021 (97%)	932 (94%)	61 (6%)	0	100	100
2	B	289/303 (95%)	273 (94%)	16 (6%)	0	100	100
3	G	30/65 (46%)	28 (93%)	2 (7%)	0	100	100
All	All	1312/1389 (94%)	1233 (94%)	79 (6%)	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	845/863 (98%)	806 (95%)	39 (5%)	23	47
2	B	261/269 (97%)	236 (90%)	25 (10%)	7	26
3	G	26/52 (50%)	25 (96%)	1 (4%)	28	52
All	All	1132/1184 (96%)	1067 (94%)	65 (6%)	17	43

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	180	LEU
2	B	219	GLU
1	A	467	TYR
1	A	460	VAL
2	B	227	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	79	GLN
2	B	181	ASN
2	B	140	ASN
2	B	212	HIS
1	A	399	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	BFD	A	369	5,1	8,11,12	1.13	0	3,15,17	2.13	1 (33%)

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	BFD	A	369	5,1	-	0/5/11/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	BFD	OD2-CG-CB	-2.97	118.16	124.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

2 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	C	1	2,4	14,14,15	0.72	0	17,19,21	1.97	4 (23%)
4	NAG	C	2	4	14,14,15	0.76	0	17,19,21	1.23	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	C	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	NAG	C1-O5-C5	3.90	117.47	112.19
4	C	1	NAG	C2-N2-C7	3.81	128.33	122.90
4	C	1	NAG	O3-C3-C2	-3.19	102.87	109.47
4	C	1	NAG	O3-C3-C4	3.17	117.69	110.35
4	C	2	NAG	C2-N2-C7	2.86	126.97	122.90

There are no chirality outliers.

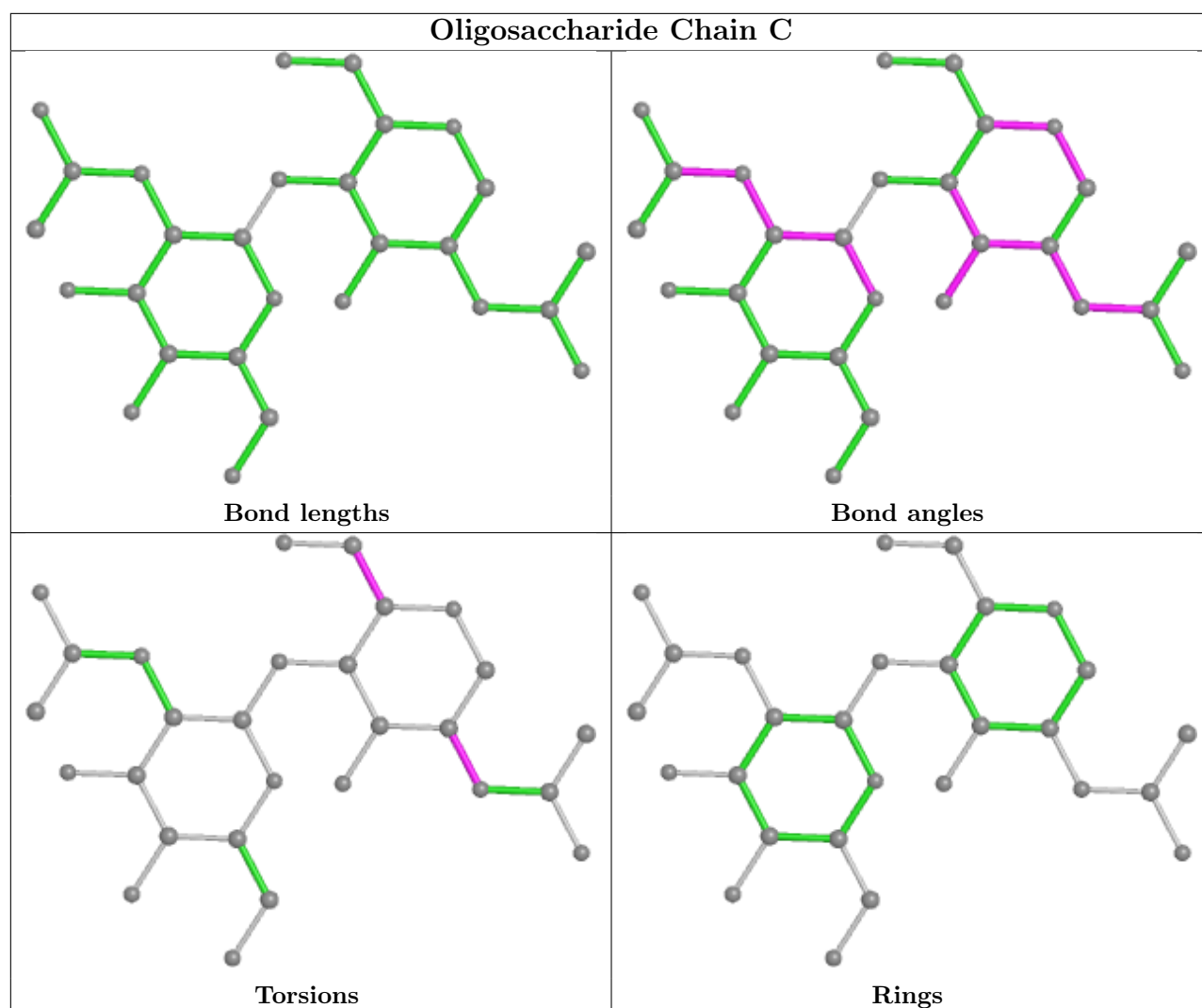
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1	NAG	C4-C5-C6-O6
4	C	1	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\# Z > 2$
7	PCW	A	1108	-	21,21,53	0.84	0	27,29,61	1.05	2 (7%)
6	CLR	A	1103	-	31,31,31	1.29	2 (6%)	48,48,48	1.33	5 (10%)
7	PCW	A	1105	-	21,21,53	0.83	0	27,29,61	0.95	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >
7	PCW	A	1106	-	21,21,53	0.85	0	27,29,61	1.21	2 (7%)
7	PCW	A	1109	-	21,21,53	0.83	0	27,29,61	1.18	3 (11%)
7	PCW	A	1107	-	21,21,53	0.84	0	27,29,61	1.22	3 (11%)
6	CLR	A	1104	-	31,31,31	1.32	5 (16%)	48,48,48	1.49	8 (16%)
8	A1MA6	A	1111	-	189,193,195	1.32	19 (10%)	218,274,278	1.72	39 (17%)
7	PCW	A	1110	-	21,21,53	0.84	0	27,29,61	0.92	1 (3%)
9	NAG	B	401	2	14,14,15	0.83	1 (7%)	17,19,21	1.53	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PCW	A	1108	-	-	6/23/23/57	-
6	CLR	A	1103	-	-	4/10/68/68	0/4/4/4
7	PCW	A	1105	-	-	9/23/23/57	-
7	PCW	A	1106	-	-	7/23/23/57	-
7	PCW	A	1109	-	-	7/23/23/57	-
7	PCW	A	1107	-	-	5/23/23/57	-
6	CLR	A	1104	-	-	4/10/68/68	0/4/4/4
8	A1MA6	A	1111	-	-	100/189/343/350	1/12/10/10
7	PCW	A	1110	-	-	9/23/23/57	-
9	NAG	B	401	2	-	1/6/23/26	0/1/1/1

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1111	A1MA6	OC2-C43	5.48	1.54	1.43
8	A	1111	A1MA6	OAO-CAP	5.44	1.57	1.45
8	A	1111	A1MA6	CBL-CBM	-5.27	1.43	1.52
8	A	1111	A1MA6	OC2-C47	5.17	1.51	1.43
8	A	1111	A1MA6	CA3-CA4	4.36	1.54	1.45

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1111	A1MA6	C97-C96-C95	-8.02	115.05	125.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1111	A1MA6	C44-O46-C47	-7.13	101.65	111.08
8	A	1111	A1MA6	CA2-CA3-CA4	-6.76	115.27	125.92
8	A	1111	A1MA6	CAH-CAG-CAF	-6.21	115.19	124.93
9	B	401	NAG	C1-O5-C5	4.96	118.92	112.19

There are no chirality outliers.

5 of 152 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1105	PCW	C1-O3P-P-O1P
7	A	1105	PCW	C1-O3P-P-O2P
7	A	1105	PCW	C1-O3P-P-O4P
7	A	1105	PCW	C4-O4P-P-O1P
7	A	1105	PCW	C4-O4P-P-O2P

All (1) ring outliers are listed below:

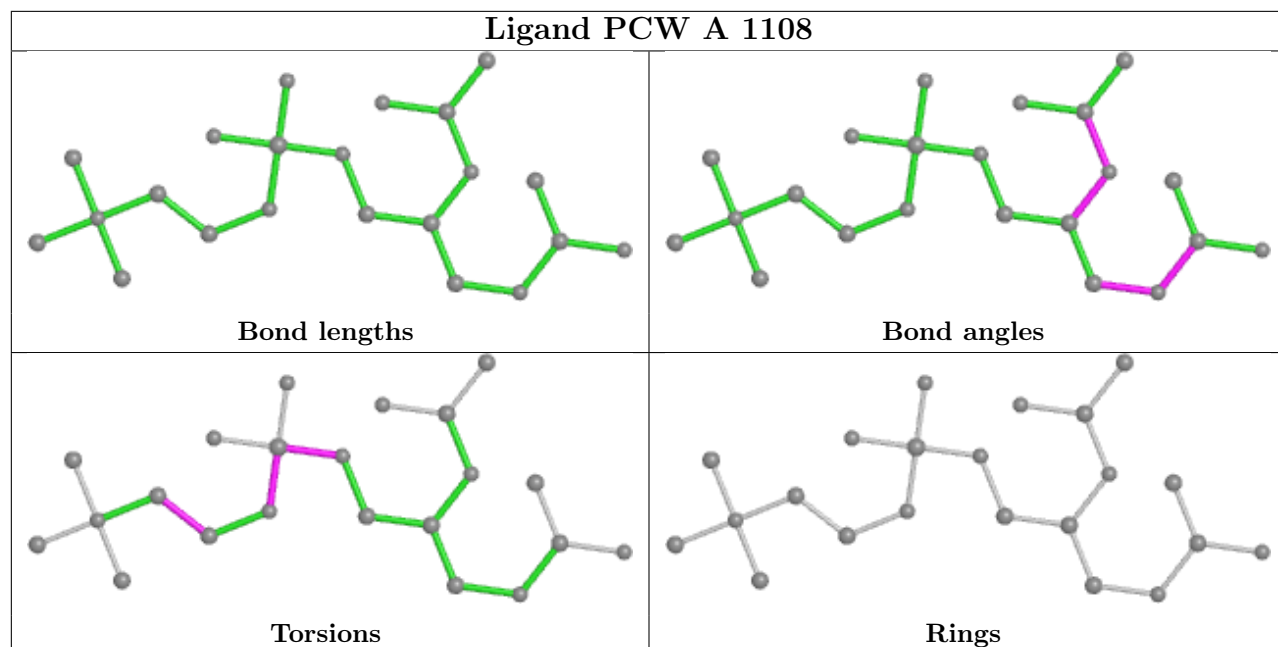
Mol	Chain	Res	Type	Atoms
8	A	1111	A1MA6	C75-C77-CBL-CBM-CBO-O76

4 monomers are involved in 11 short contacts:

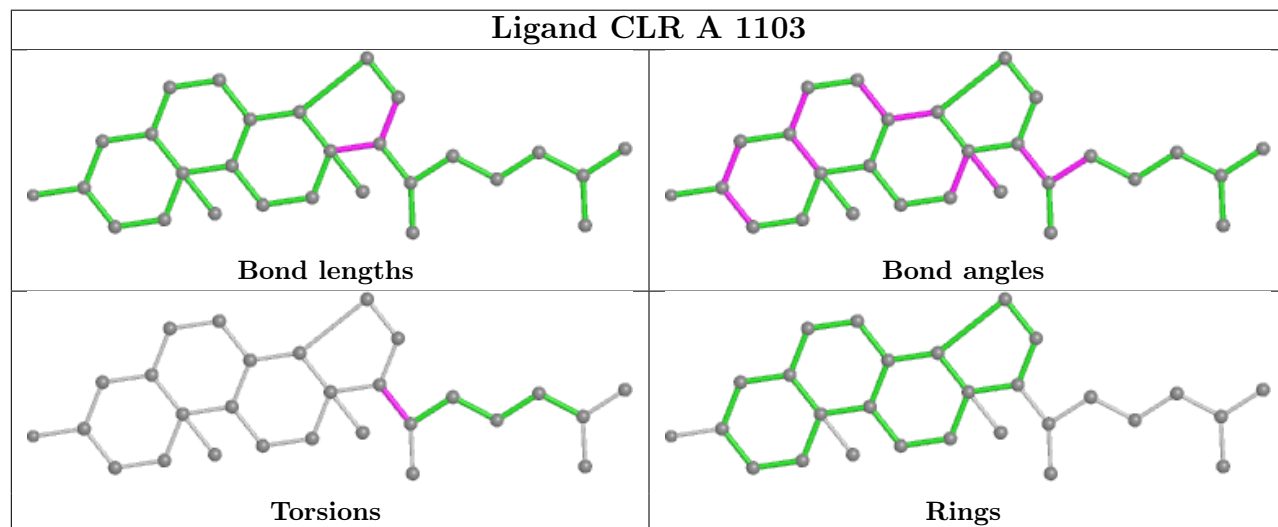
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1103	CLR	6	0
7	A	1105	PCW	1	0
6	A	1104	CLR	1	0
8	A	1111	A1MA6	3	0

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

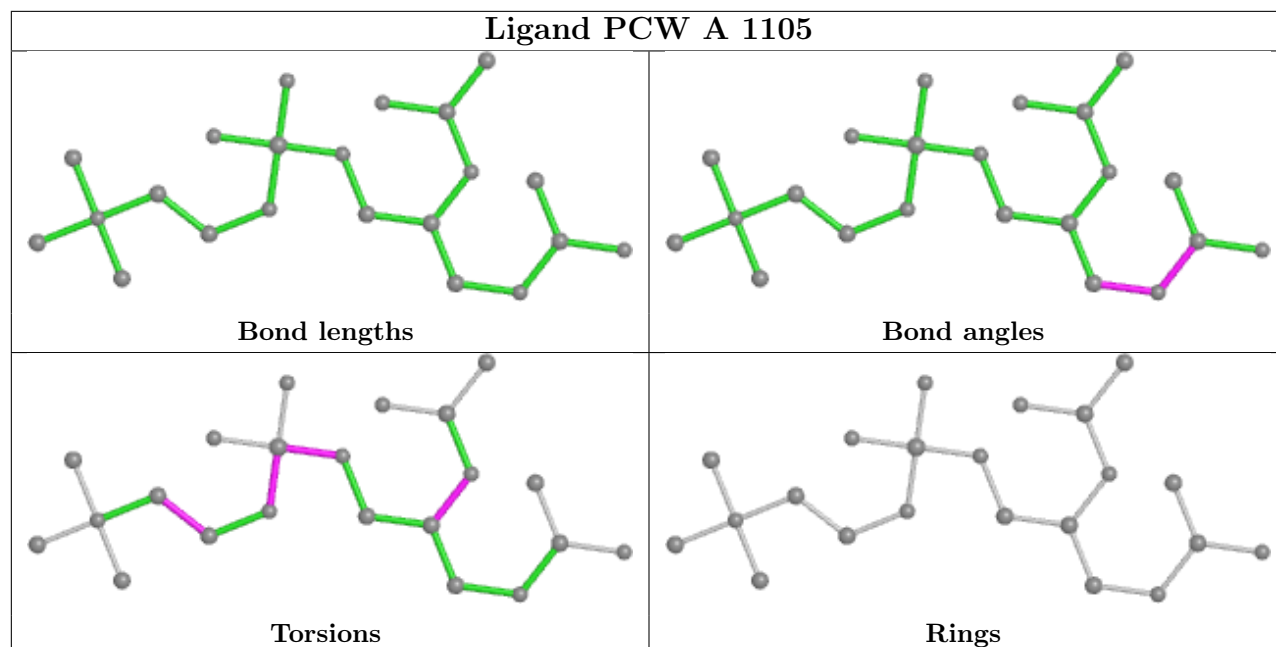
Ligand PCW A 1108



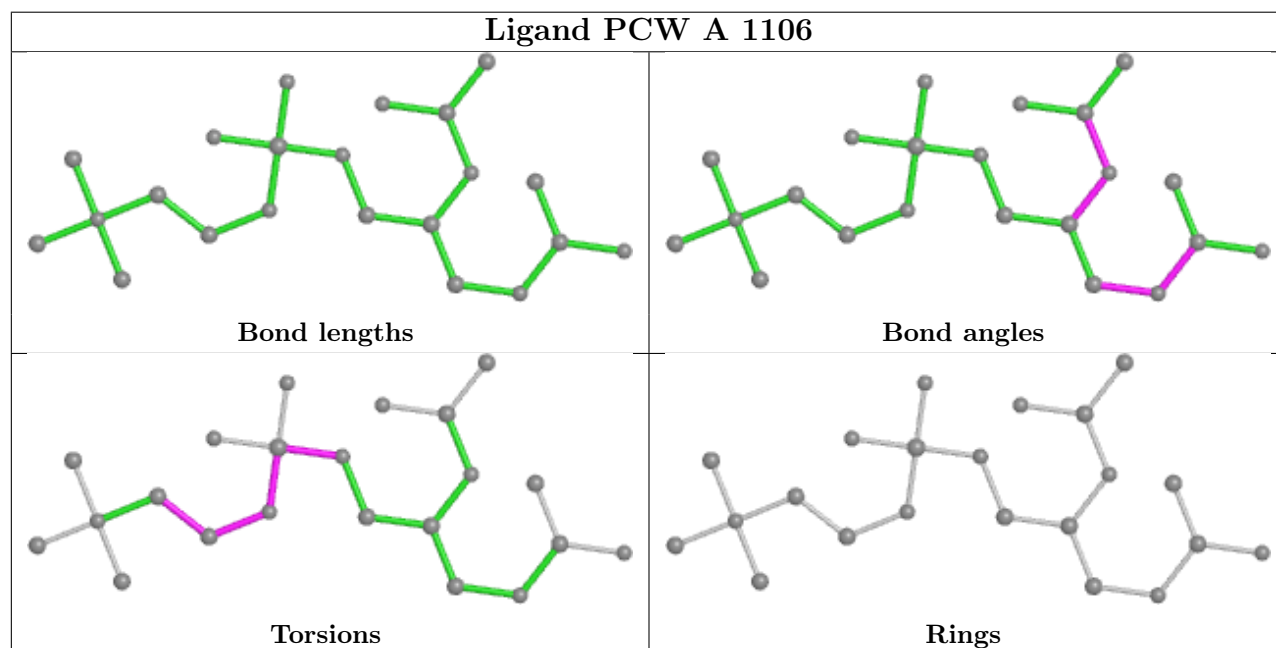
Ligand CLR A 1103



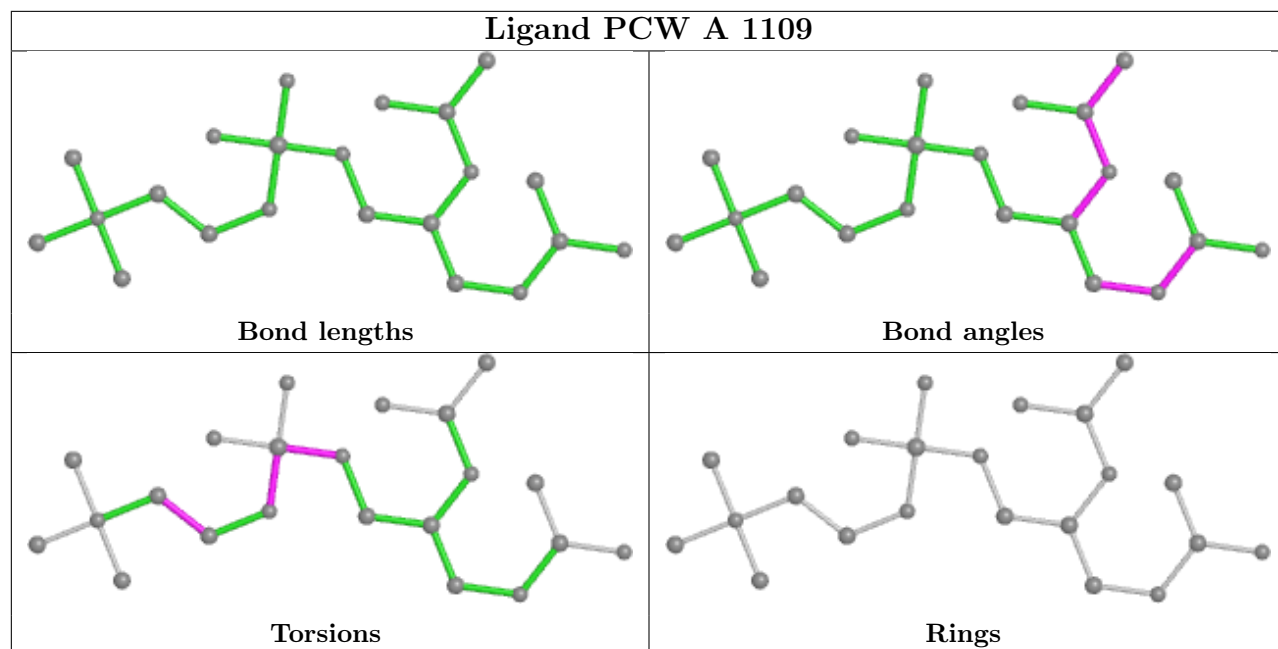
Ligand PCW A 1105



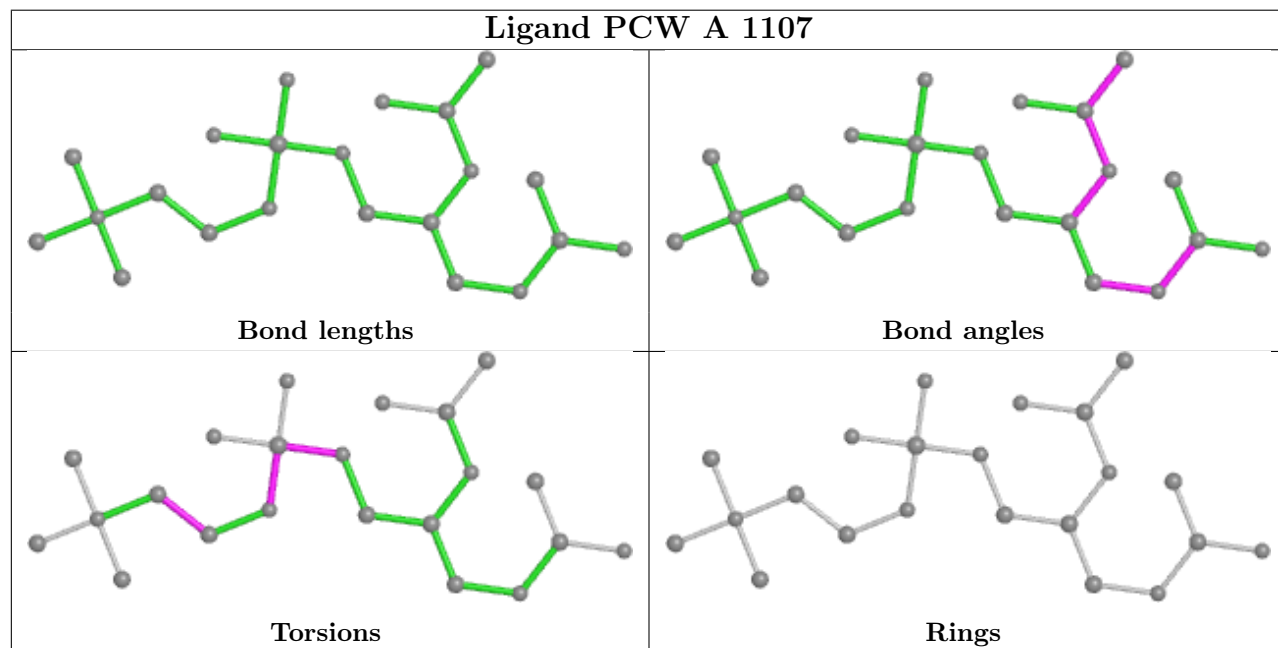
Ligand PCW A 1106

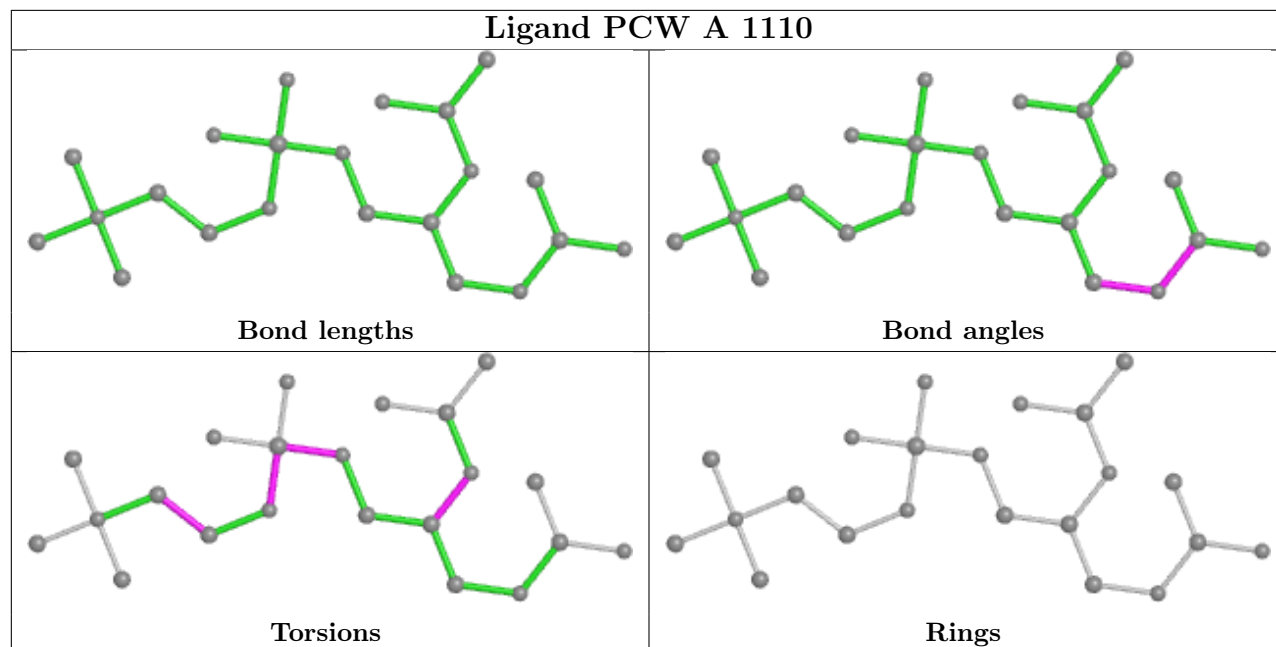
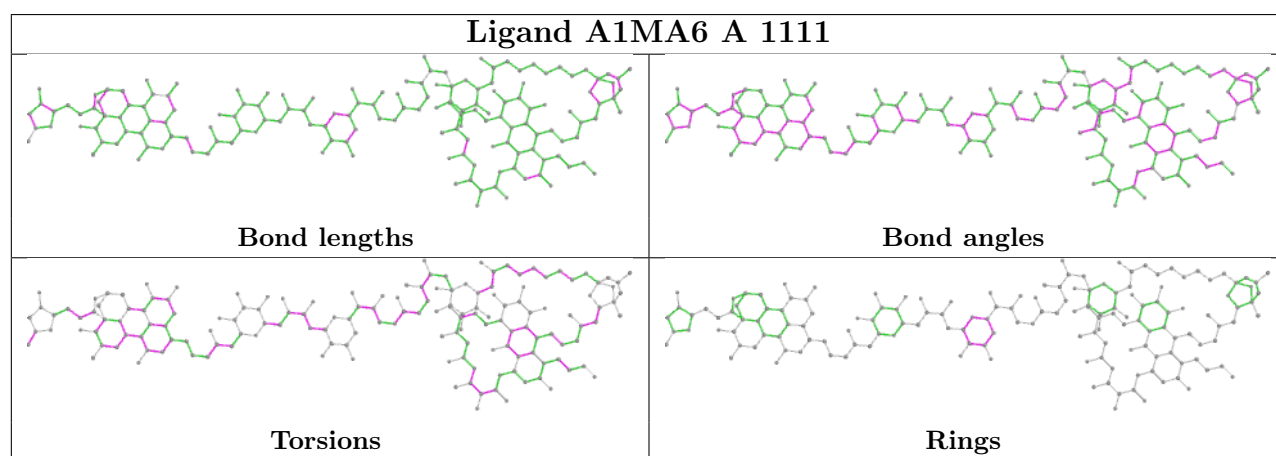
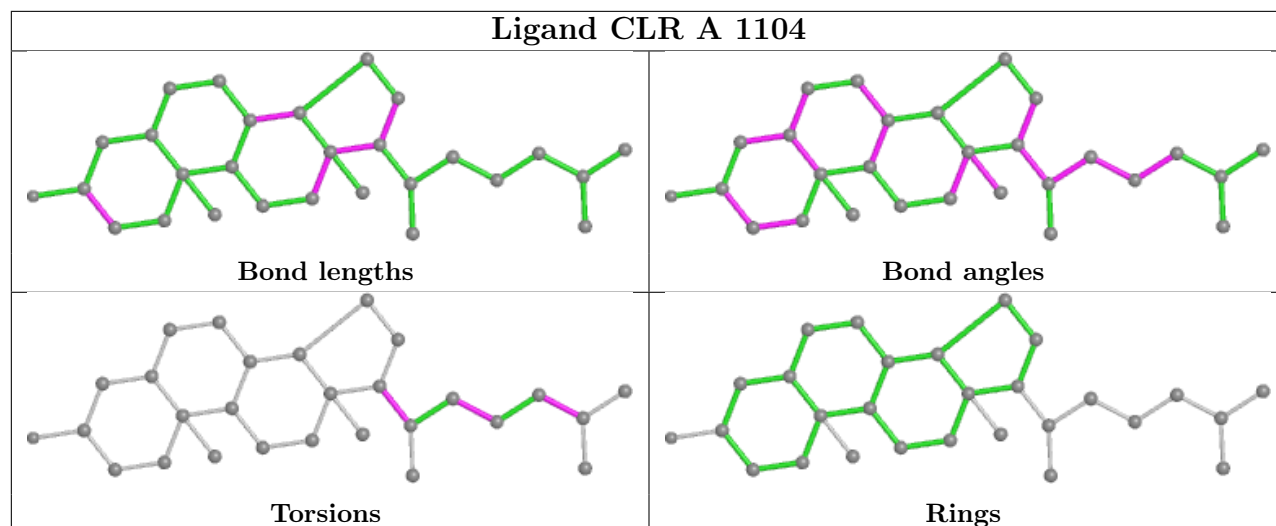


Ligand PCW A 1109



Ligand PCW A 1107





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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	995/1021 (97%)	-1.11	0 100 100	74, 126, 179, 226	0
2	B	291/303 (96%)	-1.05	0 100 100	98, 142, 184, 210	0
3	G	32/65 (49%)	-1.15	0 100 100	79, 109, 140, 167	0
All	All	1318/1389 (94%)	-1.09	0 100 100	74, 130, 180, 226	0

There are no RSRZ outliers to report.

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, 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.

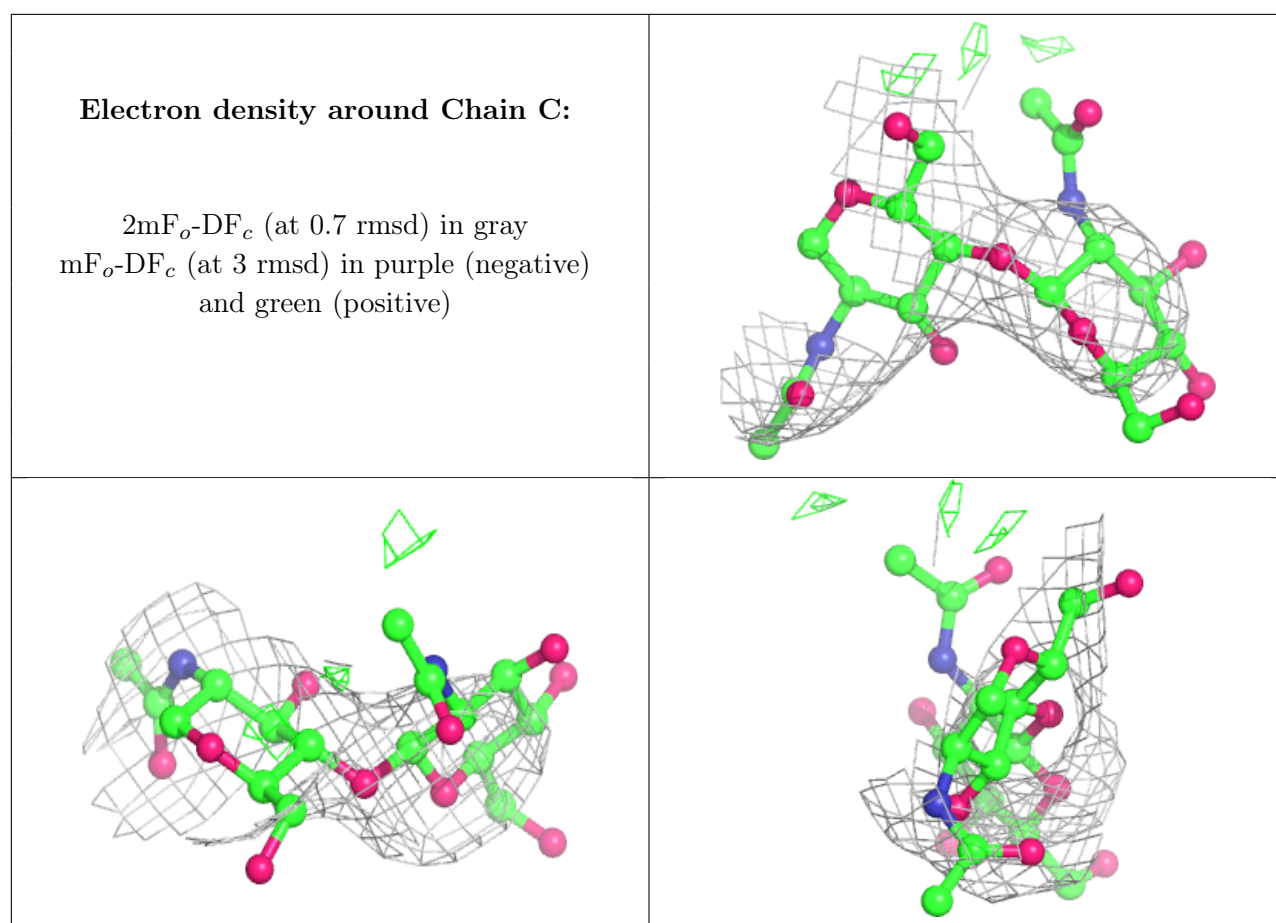
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	BFD	A	369	12/13	0.95	0.06	91,102,121,129	0

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
4	NAG	C	1	14/15	-	-	136,180,203,203	0
4	NAG	C	2	14/15	-	-	149,194,205,209	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.



6.4 Ligands [i](#)

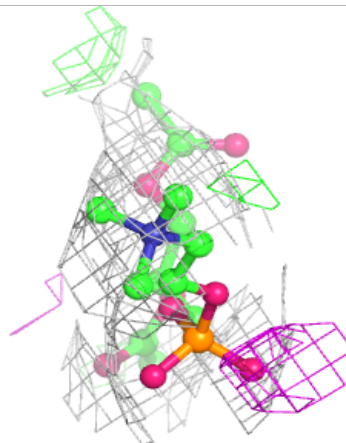
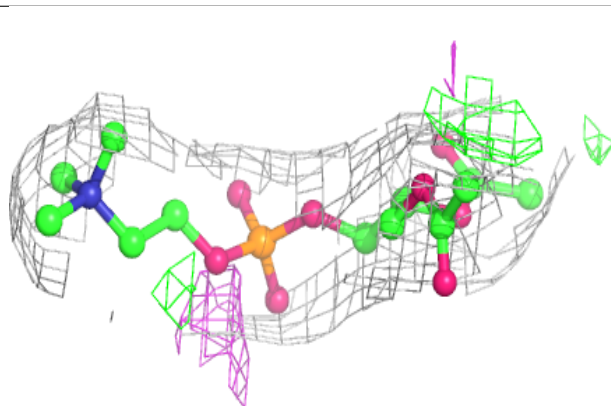
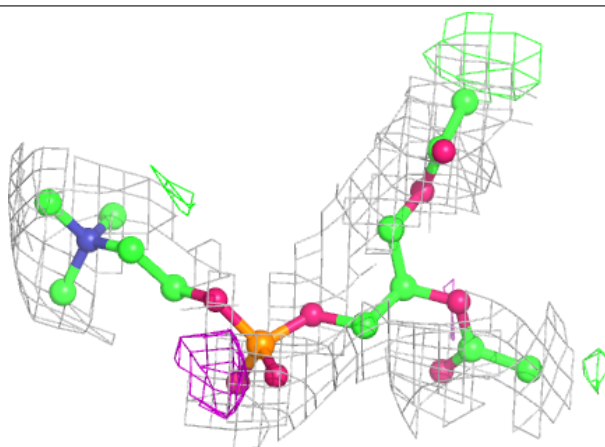
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	PCW	A	1107	22/54	0.73	0.08	128,165,205,234	0
7	PCW	A	1108	22/54	0.81	0.07	117,154,172,175	0
8	A1MA6	A	1111	184/186	0.82	0.08	130,171,213,230	0
7	PCW	A	1110	22/54	0.83	0.09	108,158,183,197	0
7	PCW	A	1109	22/54	0.83	0.07	128,161,183,193	0
7	PCW	A	1105	22/54	0.86	0.07	134,187,207,245	0
9	NAG	B	401	14/15	0.88	0.08	183,197,206,212	0
7	PCW	A	1106	22/54	0.89	0.07	127,174,202,214	0
6	CLR	A	1104	28/28	0.90	0.07	112,128,134,150	0
6	CLR	A	1103	28/28	0.91	0.08	105,121,138,161	0
5	MG	A	1102	1/1	0.98	0.10	100,100,100,100	0
5	MG	A	1101	1/1	0.99	0.03	116,116,116,116	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.

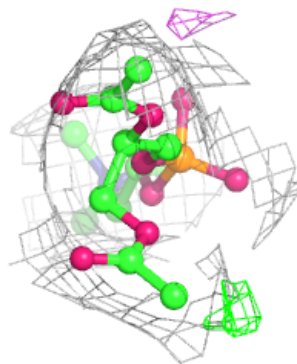
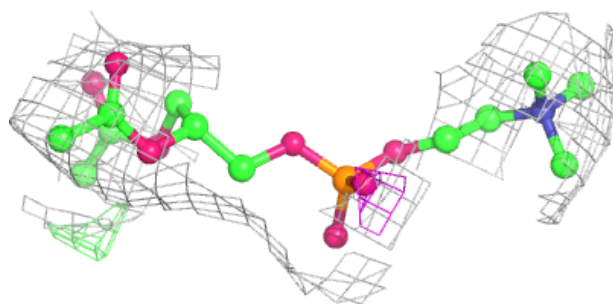
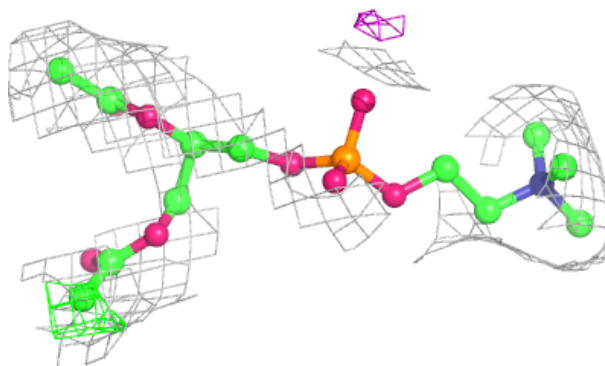
Electron density around PCW A 1107:

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



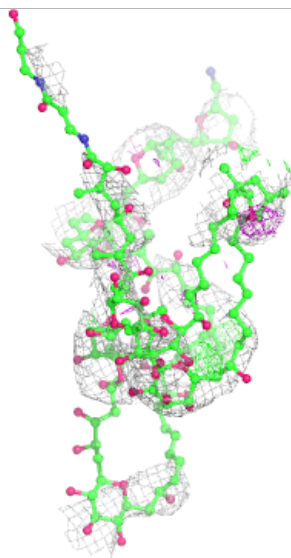
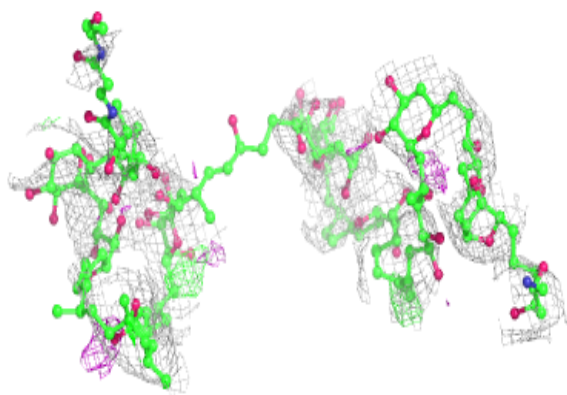
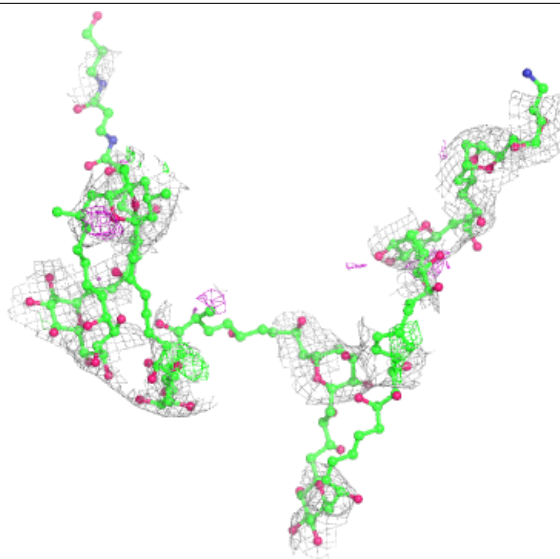
Electron density around PCW A 1108:

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



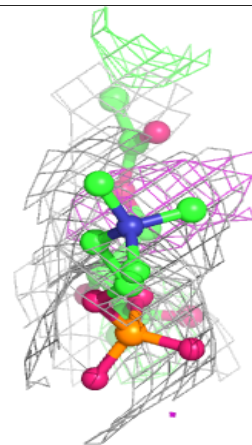
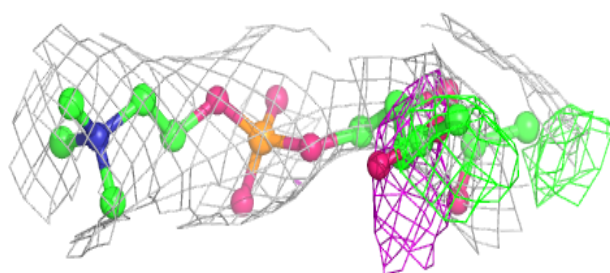
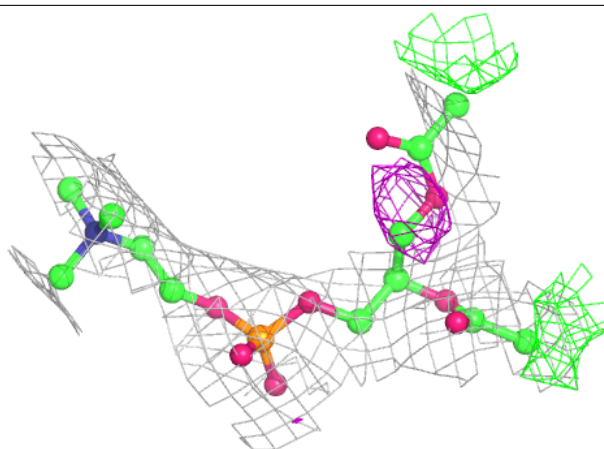
Electron density around A1MA6 A 1111:

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and green (positive)

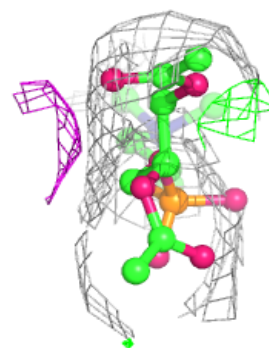
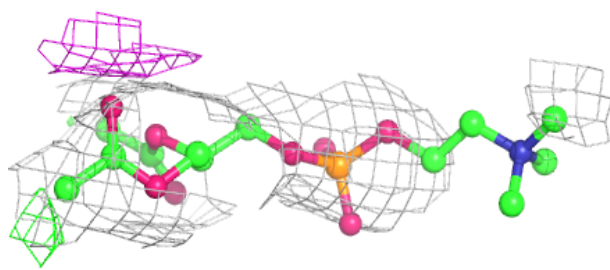
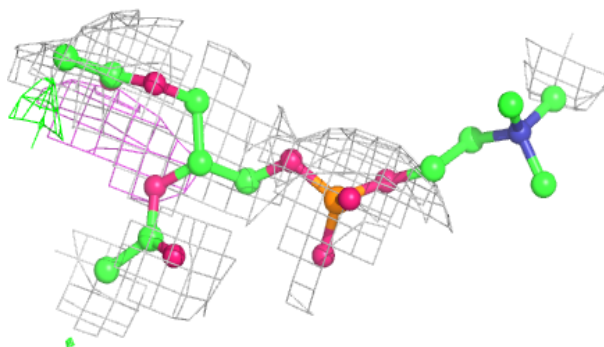


Electron density around PCW A 1110:

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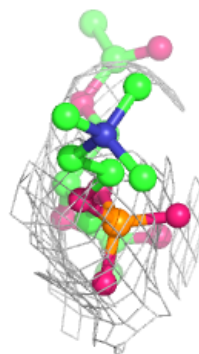
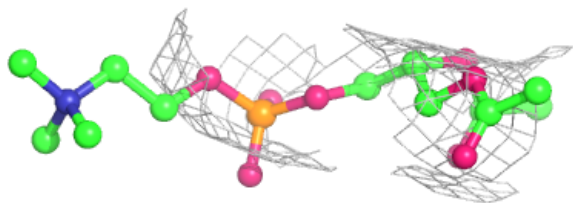
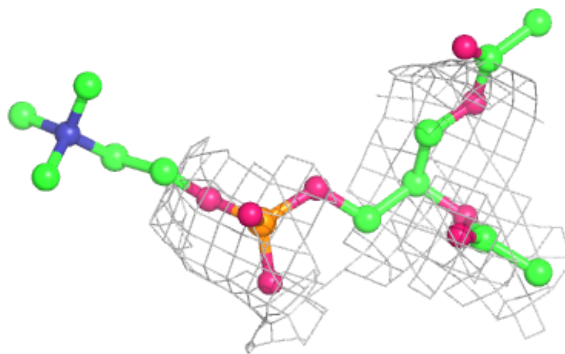
**Electron density around PCW A 1109:**

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and green (positive)

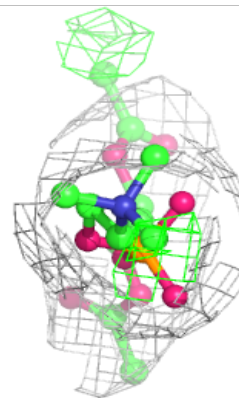
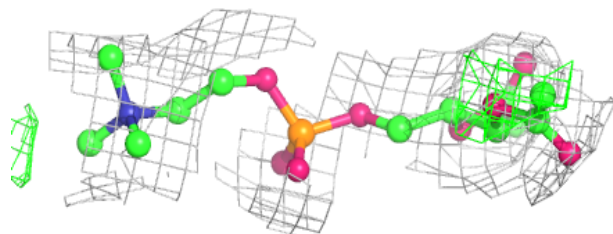
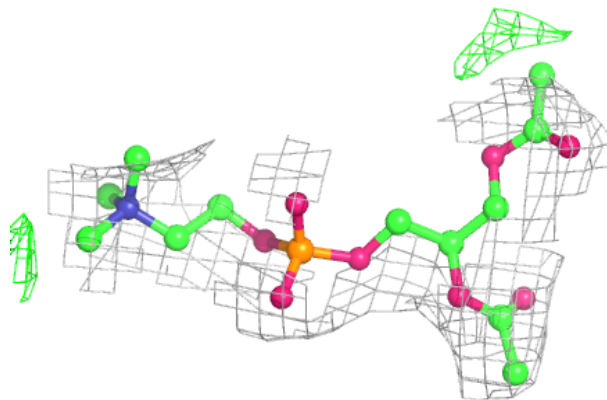


Electron density around PCW A 1105:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

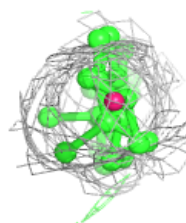
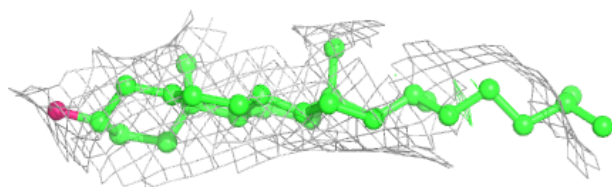
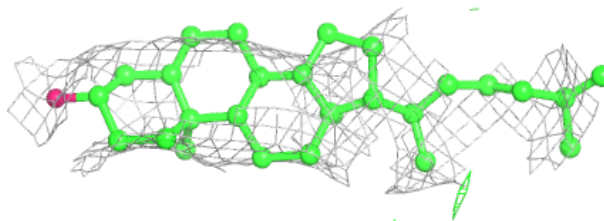
**Electron density around PCW A 1106:**

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and green (positive)

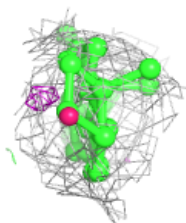
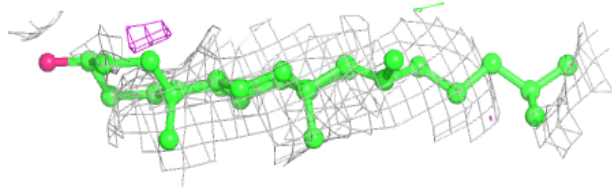
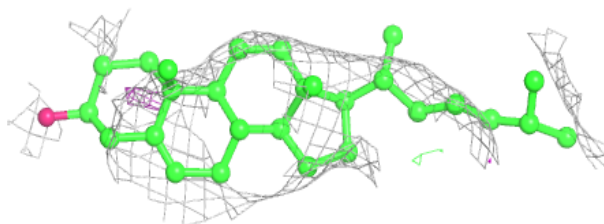


Electron density around CLR A 1104:

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and green (positive)

**Electron density around CLR A 1103:**

$2mF_o-DF_c$ (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.