



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:21 AM UTC

PDB ID : 7D94 / pdb_00007d94
Title : Crystal Structure of the Na⁺,K⁺-ATPase in the E2P state with bound one Mg²⁺ and one Rb⁺ in the presence of bufalin
Authors : Kanai, R.; Cornelius, F.; Ogawa, H.; Motoyama, K.; Vilsen, B.; Toyoshima, C.
Deposited on : 2020-10-12
Resolution : 3.50 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:

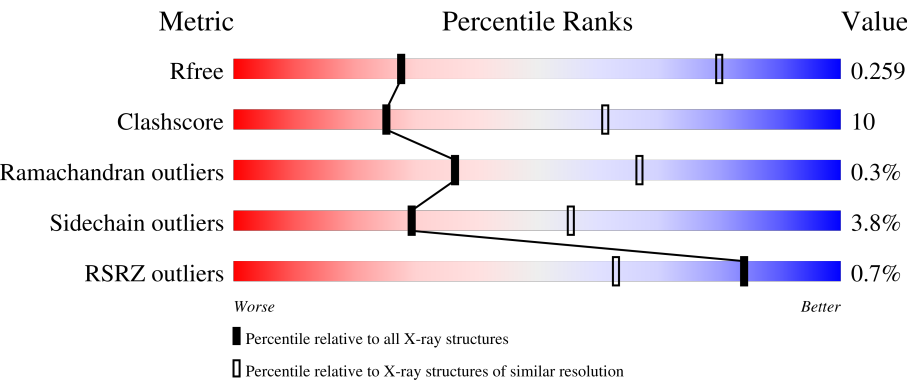
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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.



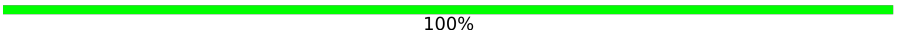
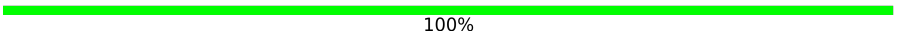
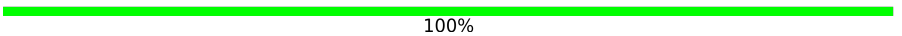
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	1016	% 74%23%..
1	C	1016	73%24%..
2	B	303	67%26%. .
2	D	303	% 63%29%. 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	E	65	 43% 5% 51%
3	G	65	 40% 9% 51%
4	F	2	 100%
4	H	2	 100%
4	I	2	 100%
4	J	2	 50% 50%

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 21218 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
1	A	996	Total	C	N	O	P	S	0	0	0
			7730	4922	1301	1459	1	47			
1	C	996	Total	C	N	O	P	S	0	0	0
			7730	4922	1301	1459	1	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				
2	D	285	Total	C	N	O	S		0	0	0
			2334	1514	383	424	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			
3	E	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	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

Continued on next page...

Continued from previous page...

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 (CCD ID: 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		

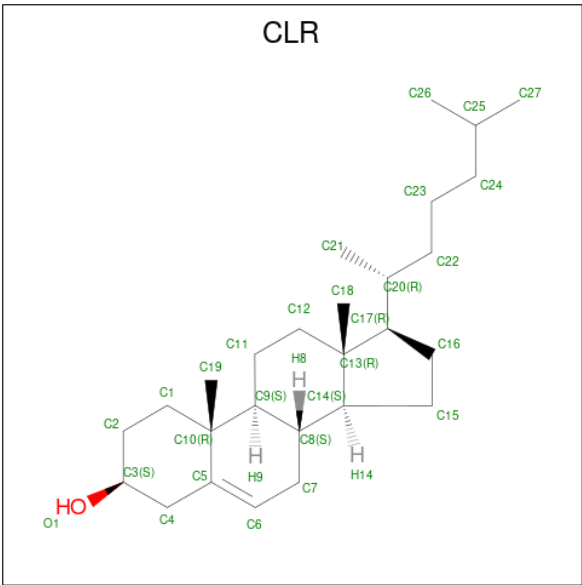
- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

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 RUBIDIUM ION (CCD ID: RB) (formula: Rb).

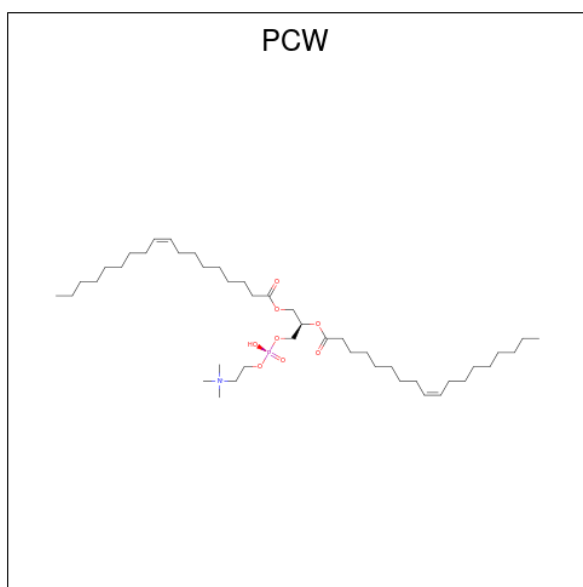
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Rb	0	0
			1	1		
7	C	1	Total	Rb	0	0
			1	1		

- Molecule 8 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



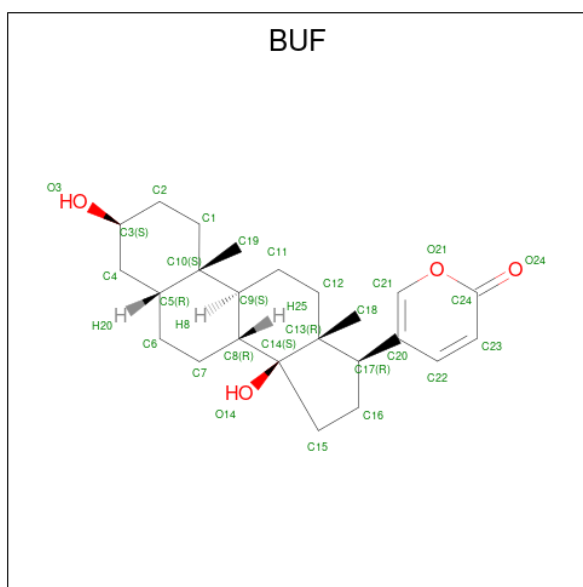
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			28	27	1		
8	G	1	Total	C	O	0	0
			28	27	1		
8	C	1	Total	C	O	0	0
			28	27	1		
8	D	1	Total	C	O	0	0
			28	27	1		
8	E	1	Total	C	O	0	0
			28	27	1		

- Molecule 9 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).



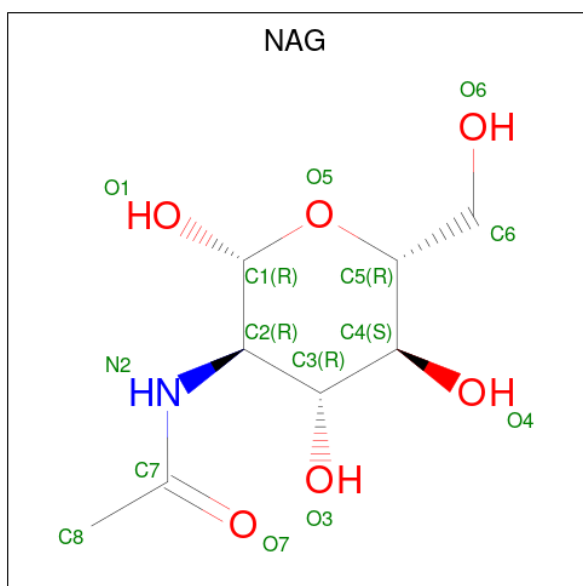
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
9	C	1	Total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

- Molecule 10 is bufalin (CCD ID: BUF) (formula: $C_{24}H_{34}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			28	24	4		
10	C	1	Total	C	O	0	0
			28	24	4		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

Continued on next page...

Continued from previous page...

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

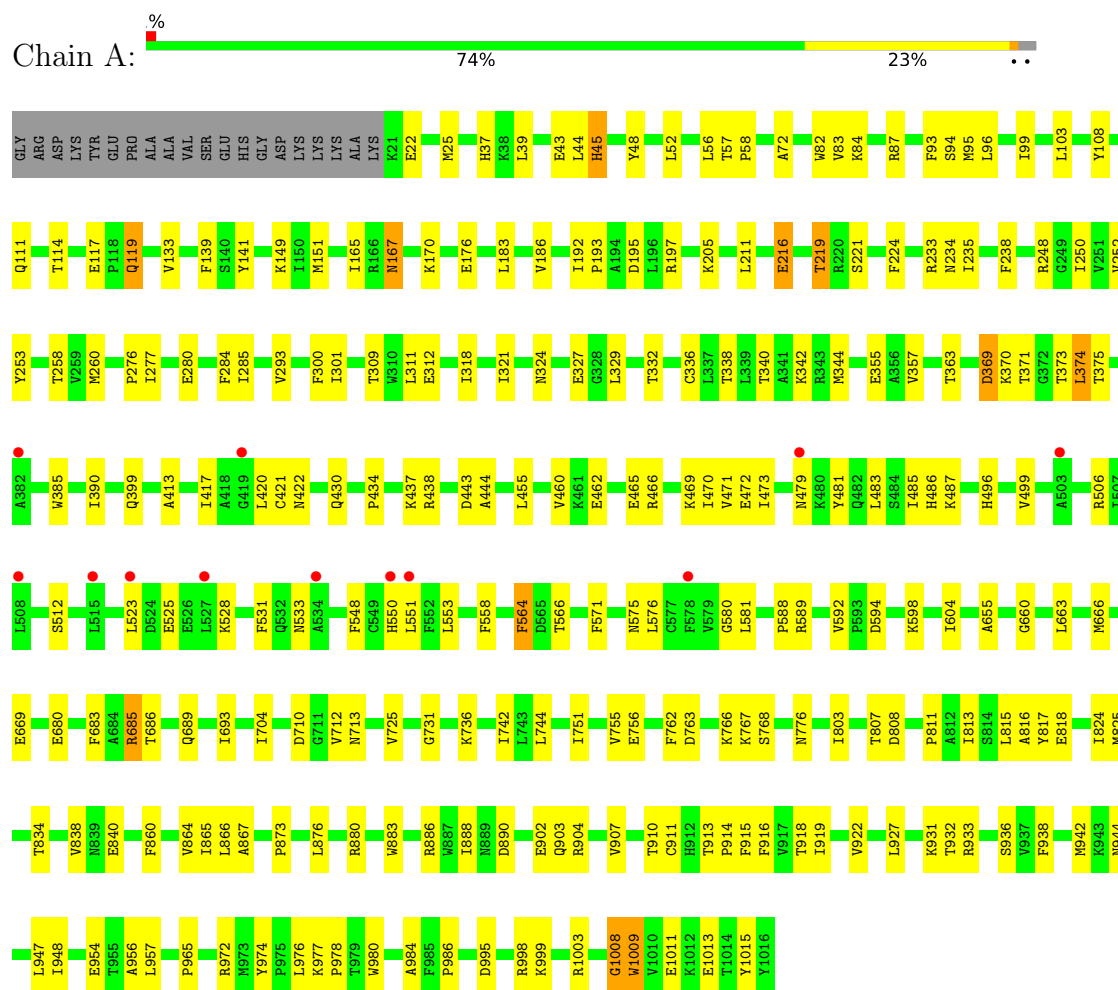
- Molecule 12 is water.

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

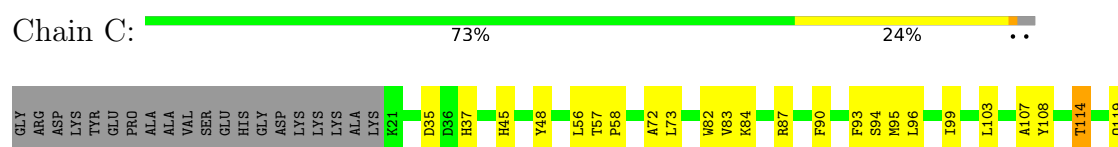
3 Residue-property plots

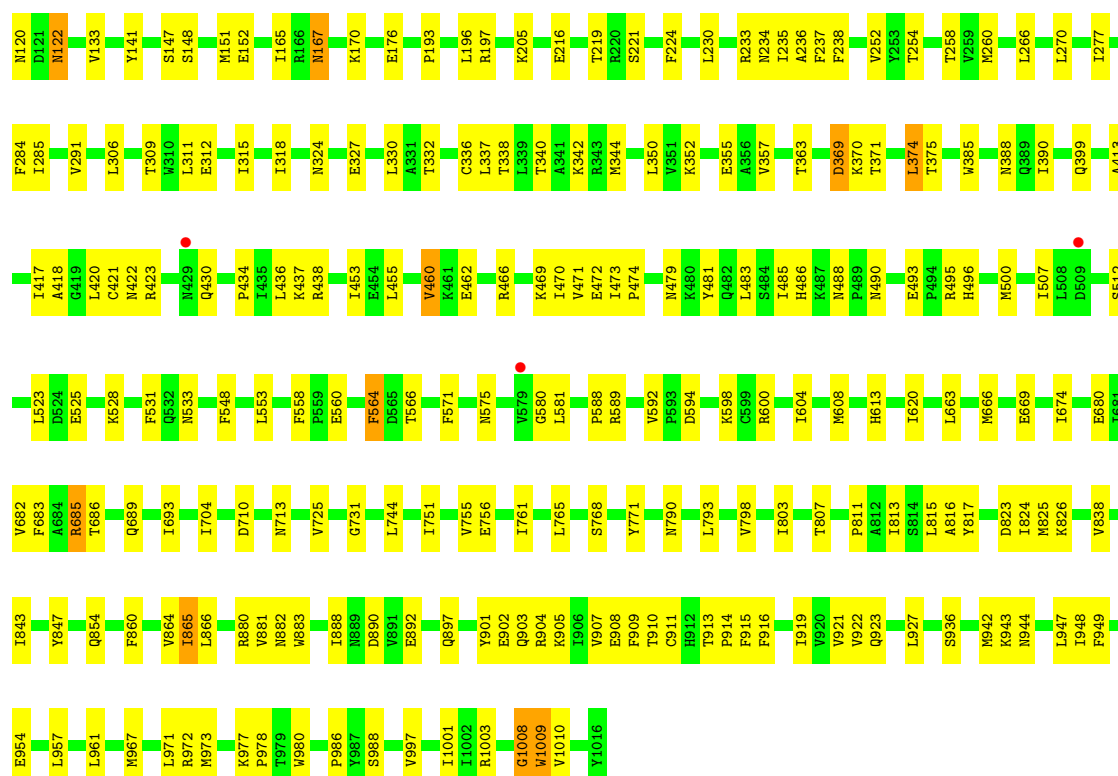
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

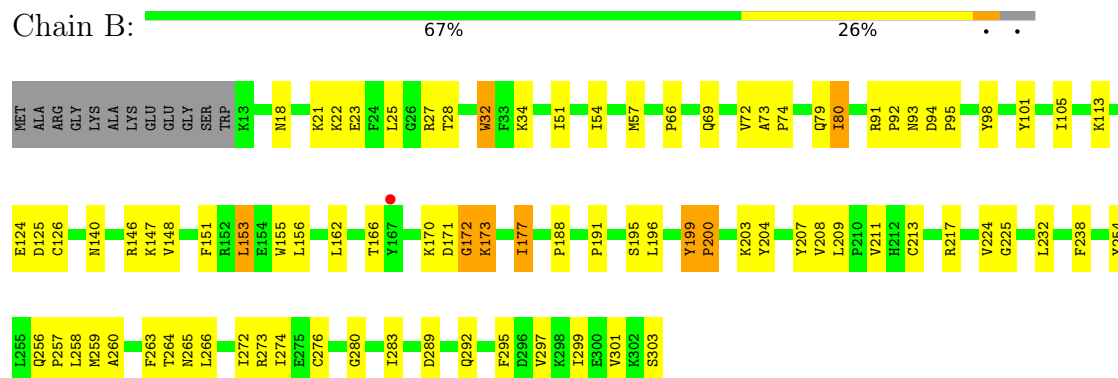


- Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

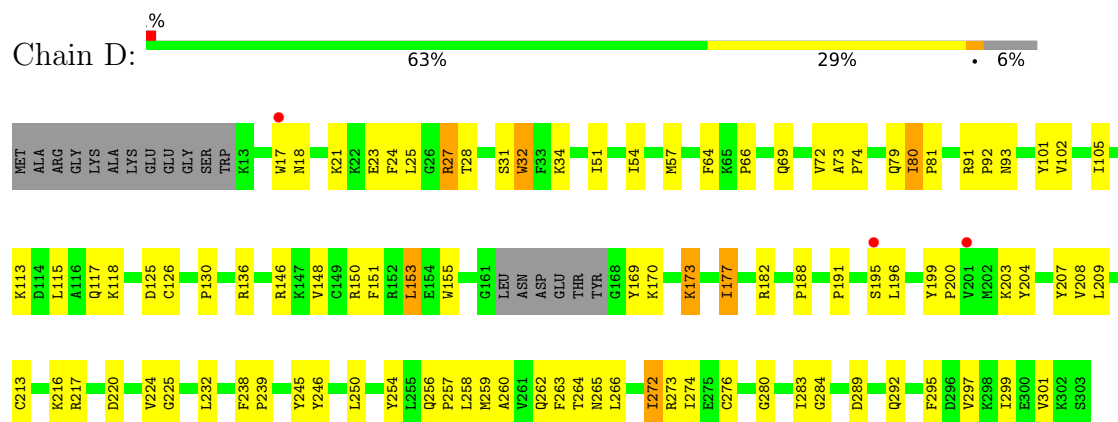




• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1



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



- Molecule 3: FXYD domain-containing ion transport regulator

Chain G:  40% 9% 51%



- Molecule 3: FXYD domain-containing ion transport regulator

Chain E:  43% 5% 51%



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

Chain F:  100%

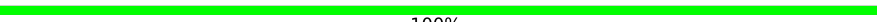


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%



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

Chain I:  100%



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

Chain J:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	115.57Å 117.31Å 490.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.50 15.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	55.5 (15.00-3.50) 55.2 (15.00-3.50)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 3.39Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.224 , 0.263 0.227 , 0.259	Depositor DCC
R_{free} test set	1966 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å ²)	93.4	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 70.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.095 for k,h,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	21218	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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: NAG, RB, BUF, PHD, MG, CLR, PCW, 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	0.22	0/7867	0.55	1/10674 (0.0%)
1	C	0.23	0/7867	0.57	2/10674 (0.0%)
2	B	0.20	0/2449	0.55	2/3301 (0.1%)
2	D	0.21	0/2395	0.55	0/3225
3	E	0.19	0/261	0.58	0/354
3	G	0.19	0/261	0.49	0/354
All	All	0.22	0/21100	0.56	5/28582 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	114	THR	N-CA-C	5.97	118.68	111.40
2	B	172	GLY	N-CA-C	-5.28	102.28	111.62
1	C	1008	GLY	N-CA-C	5.13	125.33	113.18
1	A	1008	GLY	N-CA-C	5.11	125.29	113.18
2	B	22	LYS	N-CA-C	5.08	121.62	110.80

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	7776	152	0
1	C	7730	0	7776	152	0
2	B	2386	0	2361	54	0
2	D	2334	0	2317	60	0
3	E	255	0	259	3	0
3	G	255	0	259	5	0
4	F	28	0	25	0	0
4	H	28	0	25	0	0
4	I	28	0	25	0	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	1	0	0	0	0
7	C	1	0	0	0	0
8	A	28	0	46	1	0
8	C	28	0	46	1	0
8	D	28	0	46	0	0
8	E	28	0	46	2	0
8	G	28	0	46	2	0
9	A	110	0	90	6	0
9	C	44	0	36	2	0
9	D	22	0	18	0	0
10	A	28	0	34	1	0
10	C	28	0	34	0	0
11	B	14	0	13	0	0
11	D	14	0	13	0	0
12	A	4	0	0	0	0
12	C	4	0	0	0	0
All	All	21218	0	21316	414	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 10.

The worst 5 of 414 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:430:GLN:HG3	1:A:438:ARG:HB2	1.57	0.86
2:B:80:ILE:HG12	2:B:177:ILE:HG12	1.61	0.82
2:D:80:ILE:HG12	2:D:177:ILE:HG12	1.64	0.80
1:C:986:PRO:HB3	8:C:1105:CLR:H213	1.62	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:430:GLN:HG3	1:C:438:ARG:HB2	1.64	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	993/1016 (98%)	920 (93%)	71 (7%)	2 (0%)	43	74
1	C	993/1016 (98%)	921 (93%)	69 (7%)	3 (0%)	36	67
2	B	289/303 (95%)	262 (91%)	25 (9%)	2 (1%)	18	51
2	D	281/303 (93%)	257 (92%)	22 (8%)	2 (1%)	18	51
3	E	30/65 (46%)	28 (93%)	2 (7%)	0	100	100
3	G	30/65 (46%)	28 (93%)	2 (7%)	0	100	100
All	All	2616/2768 (94%)	2416 (92%)	191 (7%)	9 (0%)	36	67

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	200	PRO
2	D	200	PRO
1	A	193	PRO
1	C	193	PRO
2	B	199	TYR

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%)	823 (97%)	23 (3%)	39	62
1	C	846/861 (98%)	823 (97%)	23 (3%)	39	62
2	B	261/269 (97%)	241 (92%)	20 (8%)	12	37
2	D	255/269 (95%)	235 (92%)	20 (8%)	11	36
3	E	26/52 (50%)	25 (96%)	1 (4%)	29	55
3	G	26/52 (50%)	26 (100%)	0	100	100
All	All	2260/2364 (96%)	2173 (96%)	87 (4%)	29	55

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	460	VAL
2	D	72	VAL
1	C	533	ASN
1	C	1009	TRP
2	D	153	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	642	ASN
2	D	262	GLN
1	C	690	GLN
2	D	69	GLN
1	A	613	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	1.01	0	9,15,17	1.15	1 (11%)
1	PHD	A	369	1,5	9,11,12	0.96	0	9,15,17	1.44	1 (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
1	PHD	C	369	1,5	-	2/8/11/13	-
1	PHD	A	369	1,5	-	2/8/11/13	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	PHD	OD1-CG-CB	3.13	118.29	110.95
1	C	369	PHD	OD1-CG-CB	2.71	117.30	110.95

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	369	PHD	CA-CB-CG-OD1
1	C	369	PHD	CA-CB-CG-OD1
1	A	369	PHD	CA-CB-CG-OD2
1	C	369	PHD	CA-CB-CG-OD2

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 ⓘ

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	0.36	0	17,19,21	0.46	0
4	NAG	F	2	4	14,14,15	0.37	0	17,19,21	0.51	0
4	NAG	H	1	2,4	14,14,15	0.57	0	17,19,21	0.68	0
4	NAG	H	2	4	14,14,15	0.41	0	17,19,21	0.41	0
4	NAG	I	1	2,4	14,14,15	0.39	0	17,19,21	0.51	0
4	NAG	I	2	4	14,14,15	0.29	0	17,19,21	0.55	0
4	NAG	J	1	2,4	14,14,15	0.62	1 (7%)	17,19,21	0.62	0
4	NAG	J	2	4	14,14,15	0.34	0	17,19,21	0.39	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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	1	NAG	O5-C1	-2.19	1.40	1.43

There are no bond angle outliers.

There are no chirality outliers.

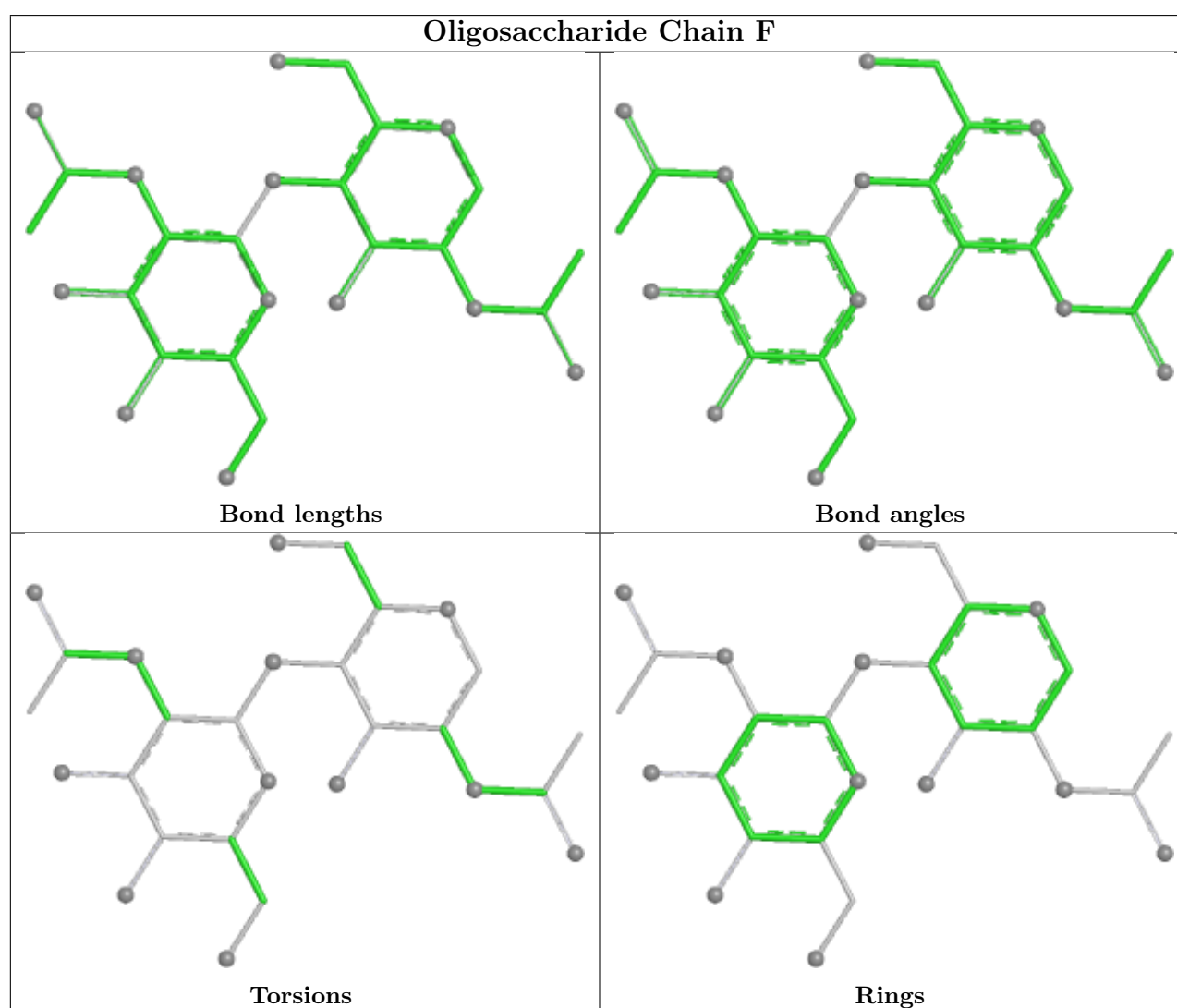
All (2) torsion outliers are listed below:

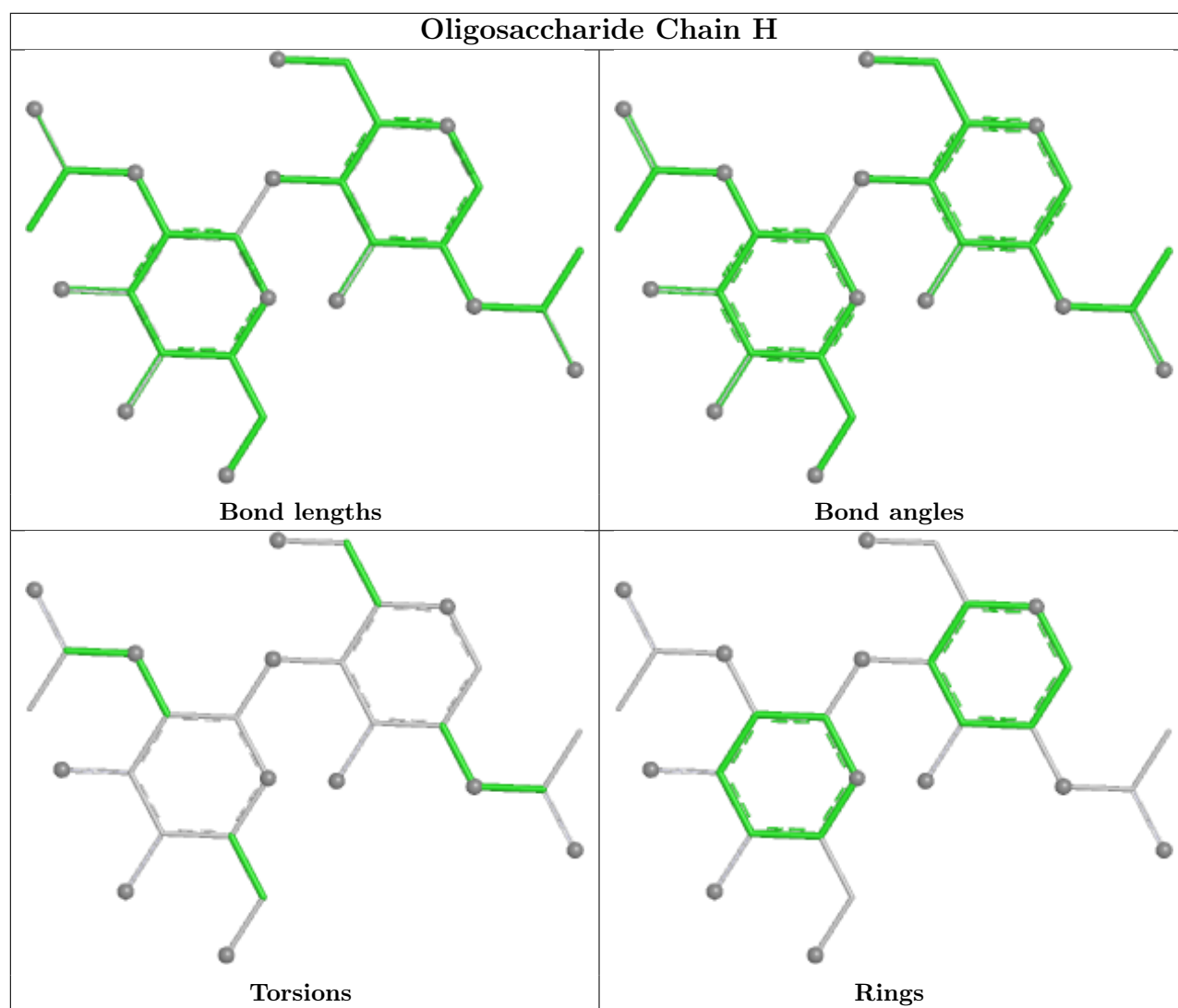
Mol	Chain	Res	Type	Atoms
4	I	1	NAG	C4-C5-C6-O6
4	I	1	NAG	O5-C5-C6-O6

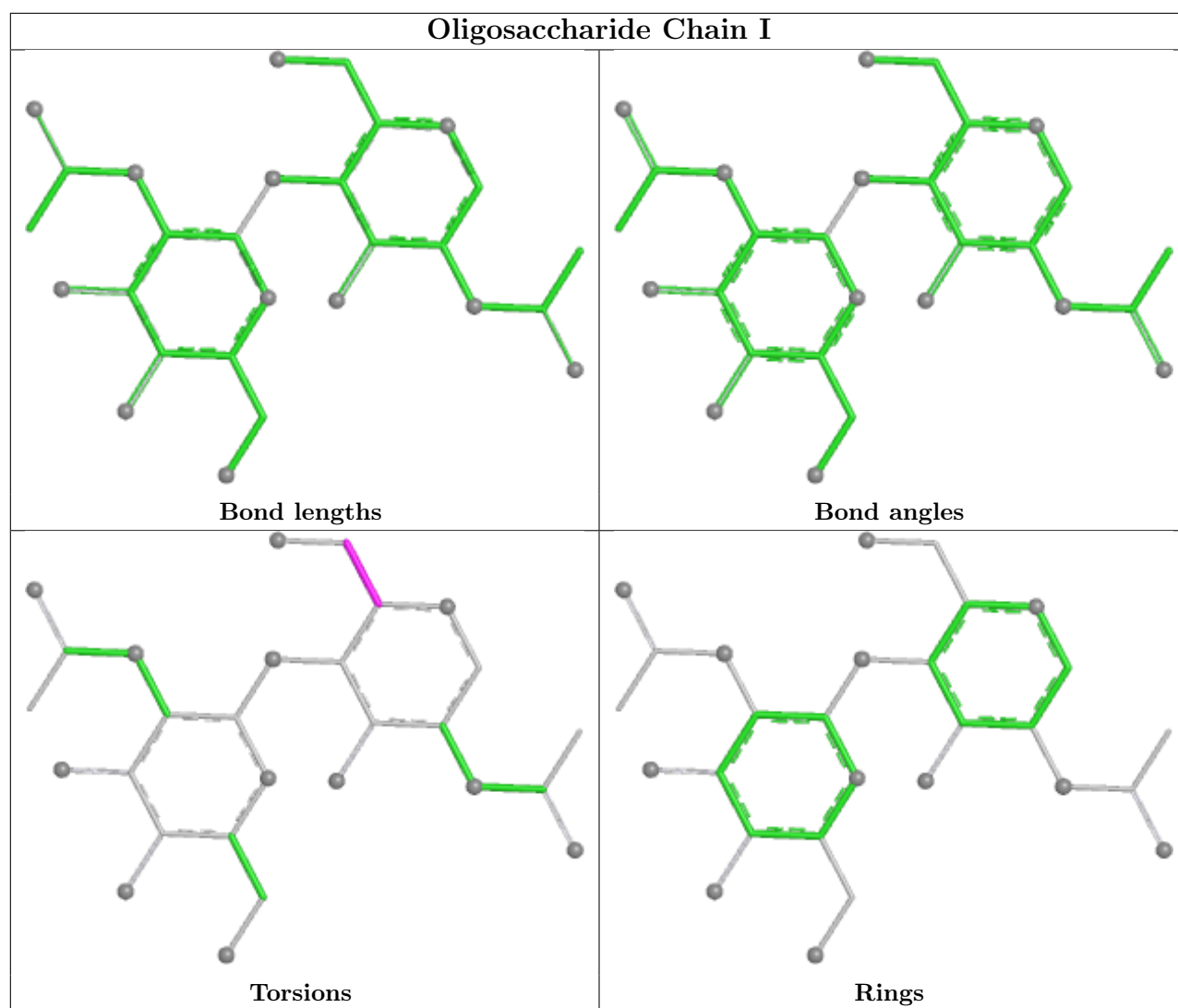
There are no ring outliers.

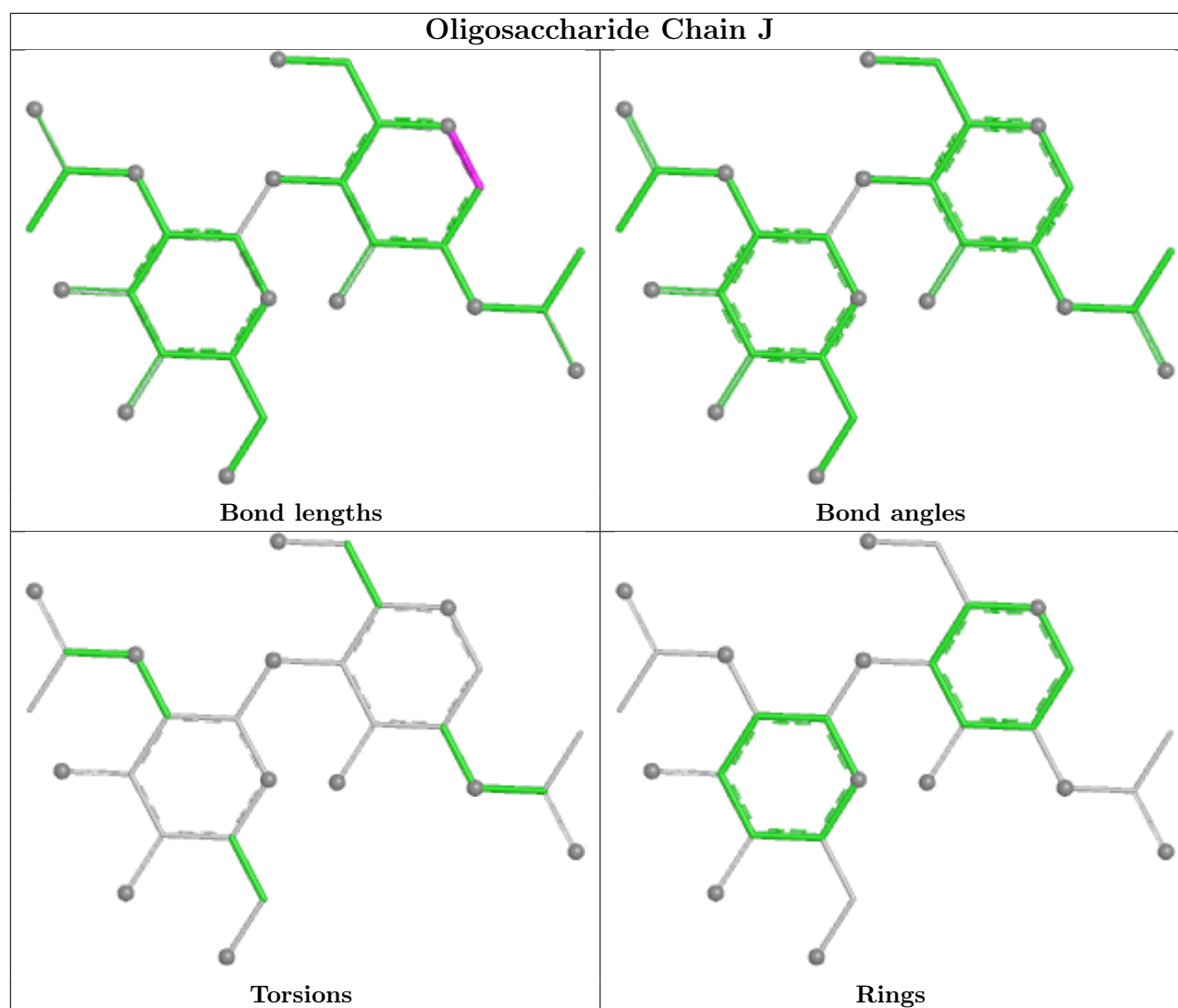
No monomer is involved in short contacts.

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 25 ligands modelled in this entry, 8 are monoatomic - leaving 17 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	$\# Z > 2$
8	CLR	A	1105	-	31,31,31	2.05	10 (32%)	48,48,48	1.59	11 (22%)
9	PCW	A	1108	-	21,21,53	1.72	6 (28%)	27,29,61	1.23	1 (3%)
9	PCW	A	1110	-	21,21,53	1.74	6 (28%)	27,29,61	1.38	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	PCW	A	1107	-	21,21,53	1.72	4 (19%)	27,29,61	1.20	1 (3%)
9	PCW	C	1107	-	21,21,53	1.73	5 (23%)	27,29,61	1.37	1 (3%)
8	CLR	C	1105	-	31,31,31	2.02	12 (38%)	48,48,48	1.58	11 (22%)
9	PCW	D	402	-	21,21,53	1.71	6 (28%)	27,29,61	1.29	1 (3%)
8	CLR	G	101	-	31,31,31	1.91	11 (35%)	48,48,48	1.73	15 (31%)
9	PCW	A	1106	-	21,21,53	1.74	6 (28%)	27,29,61	1.28	1 (3%)
10	BUF	A	1121	-	32,32,32	0.97	3 (9%)	52,52,52	1.43	9 (17%)
11	NAG	B	411	2	14,14,15	0.38	0	17,19,21	0.48	0
11	NAG	D	411	2	14,14,15	0.35	0	17,19,21	0.53	0
8	CLR	D	501	-	31,31,31	2.09	12 (38%)	48,48,48	1.54	12 (25%)
9	PCW	A	1109	-	21,21,53	1.73	6 (28%)	27,29,61	1.24	1 (3%)
10	BUF	C	1121	-	32,32,32	0.91	2 (6%)	52,52,52	1.40	9 (17%)
8	CLR	E	101	-	31,31,31	1.90	12 (38%)	48,48,48	1.63	14 (29%)
9	PCW	C	1106	-	21,21,53	1.73	6 (28%)	27,29,61	1.23	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	CLR	A	1105	-	-	4/10/68/68	0/4/4/4
9	PCW	A	1108	-	-	11/23/23/57	-
9	PCW	A	1110	-	-	11/23/23/57	-
9	PCW	A	1107	-	-	14/23/23/57	-
9	PCW	C	1107	-	-	8/23/23/57	-
8	CLR	C	1105	-	-	3/10/68/68	0/4/4/4
9	PCW	D	402	-	-	5/23/23/57	-
8	CLR	G	101	-	-	3/10/68/68	0/4/4/4
9	PCW	A	1106	-	-	12/23/23/57	-
10	BUF	A	1121	-	-	0/4/68/68	0/5/5/5
11	NAG	B	411	2	-	0/6/23/26	0/1/1/1
11	NAG	D	411	2	-	4/6/23/26	0/1/1/1
8	CLR	D	501	-	-	0/10/68/68	0/4/4/4
9	PCW	A	1109	-	-	8/23/23/57	-
10	BUF	C	1121	-	-	0/4/68/68	0/5/5/5
8	CLR	E	101	-	-	3/10/68/68	0/4/4/4

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	PCW	C	1106	-	-	10/23/23/57	-

The worst 5 of 107 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	501	CLR	C10-C9	4.89	1.63	1.56
8	G	101	CLR	C10-C5	4.65	1.61	1.52
8	G	101	CLR	C10-C9	4.19	1.62	1.56
8	E	101	CLR	C10-C5	4.02	1.60	1.52
8	A	1105	CLR	C4-C3	3.94	1.59	1.52

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	1107	PCW	O2-C31-C32	5.36	120.64	111.09
9	A	1110	PCW	O2-C31-C32	5.21	120.38	111.09
9	A	1106	PCW	O2-C31-C32	5.20	120.37	111.09
9	D	402	PCW	O2-C31-C32	5.07	120.12	111.09
9	A	1107	PCW	O2-C31-C32	4.97	119.95	111.09

There are no chirality outliers.

5 of 96 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	1106	PCW	O4P-C4-C5-N
9	A	1106	PCW	C4-O4P-P-O3P
9	A	1107	PCW	C32-C31-O2-C2
9	A	1108	PCW	C4-O4P-P-O1P
9	A	1108	PCW	C4-O4P-P-O2P

There are no ring outliers.

9 monomers are involved in 15 short contacts:

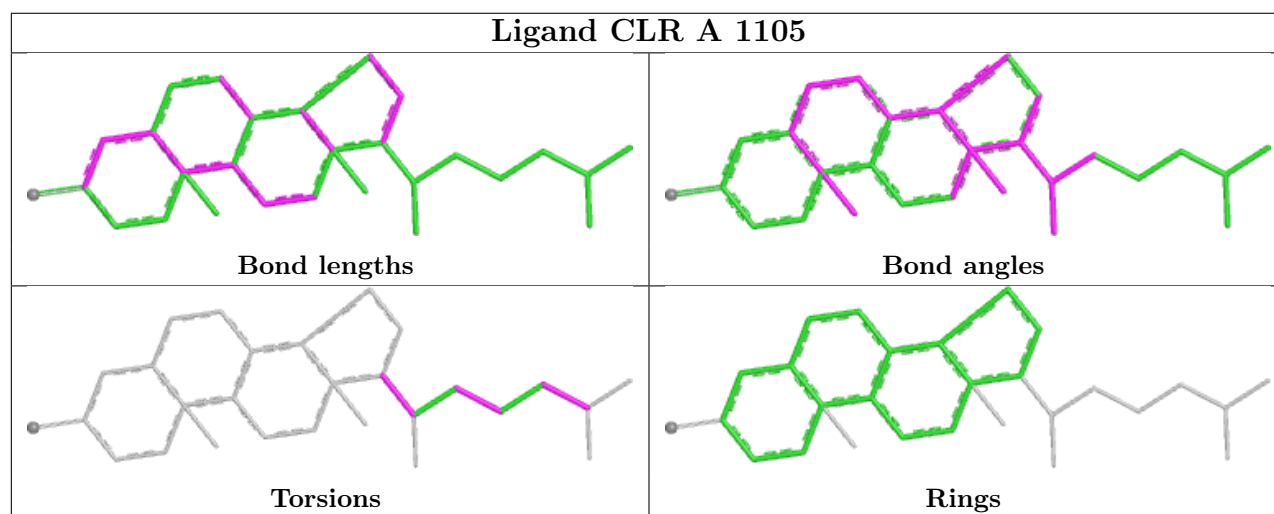
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1105	CLR	1	0
9	A	1107	PCW	1	0
9	C	1107	PCW	2	0
8	C	1105	CLR	1	0
8	G	101	CLR	2	0
9	A	1106	PCW	3	0
10	A	1121	BUF	1	0

Continued on next page...

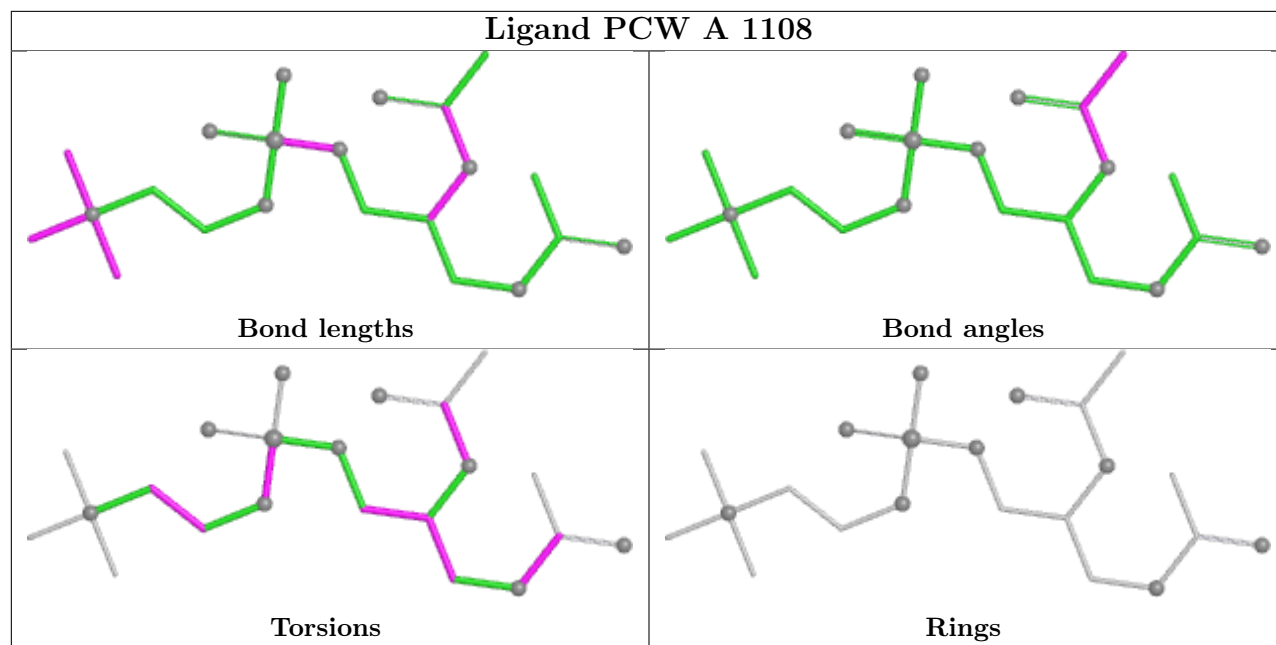
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1109	PCW	2	0
8	E	101	CLR	2	0

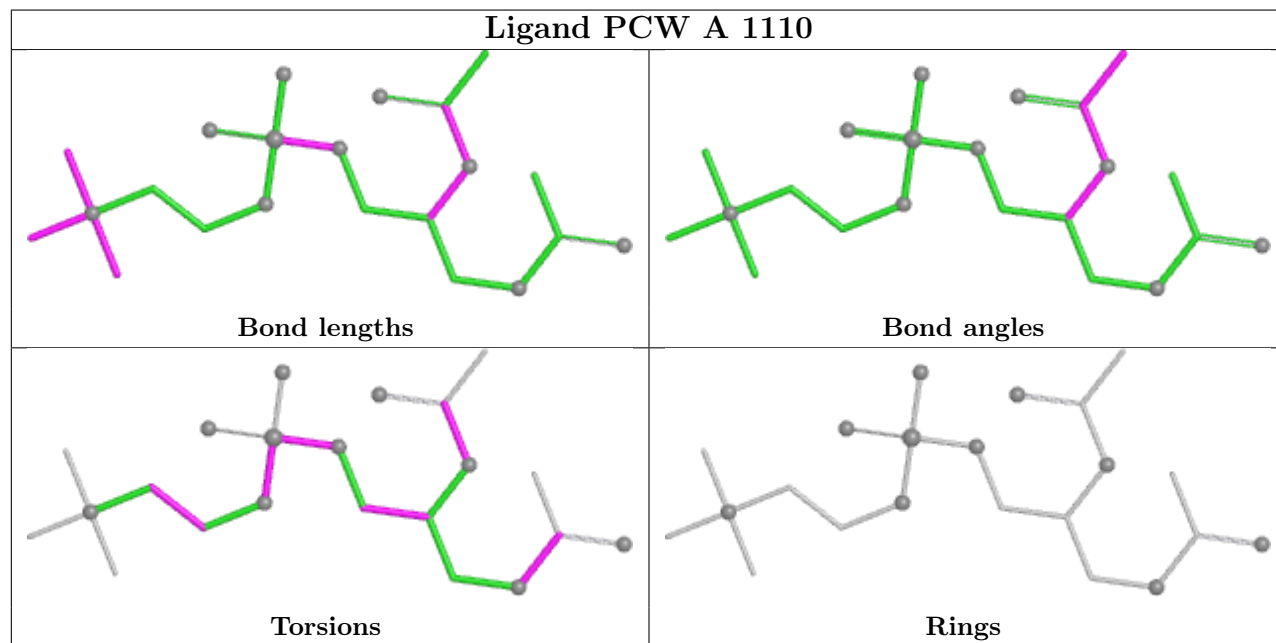
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



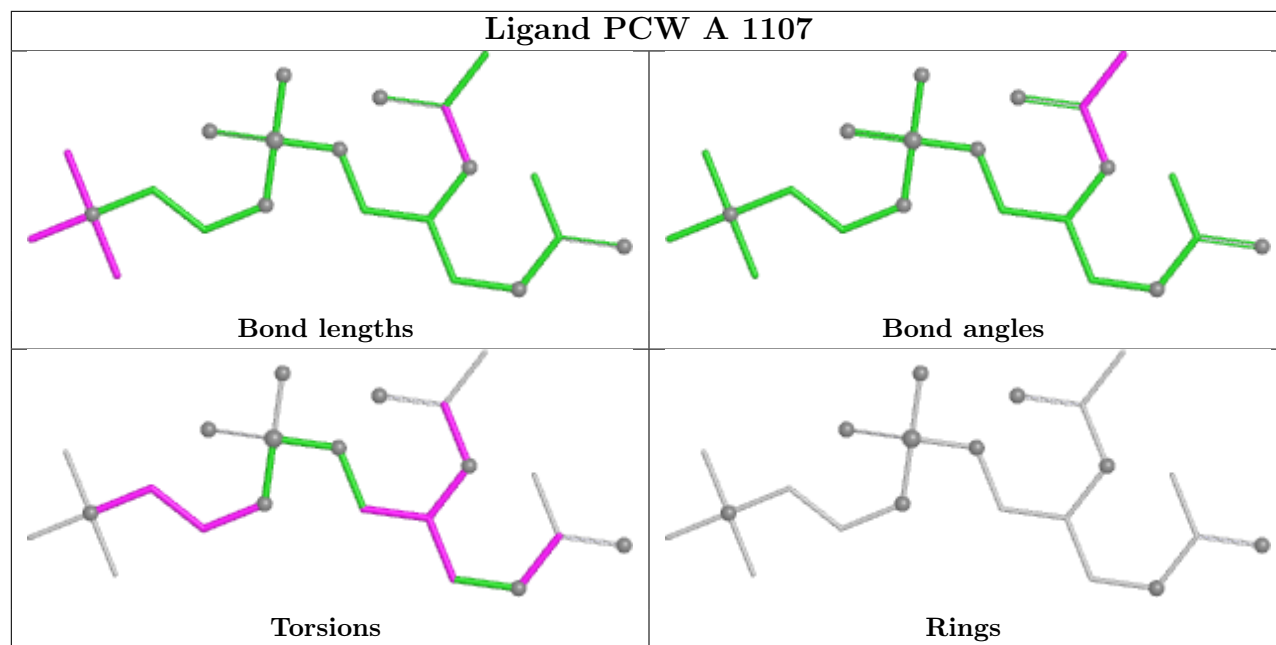
Ligand PCW A 1108



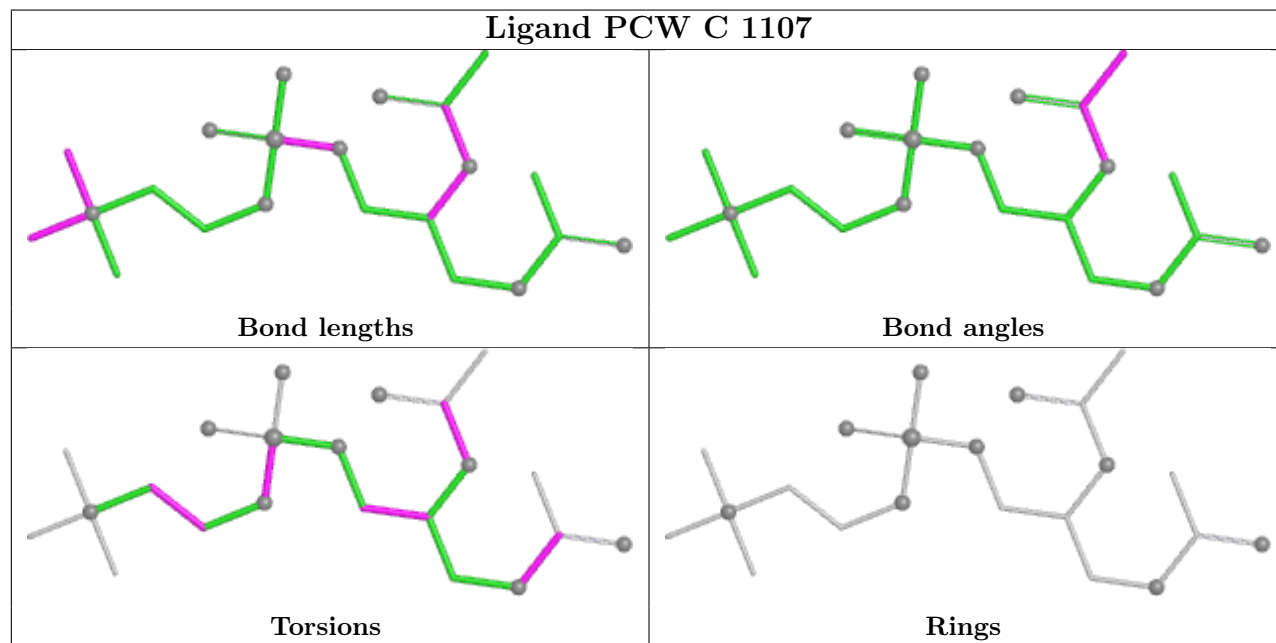
Ligand PCW A 1110

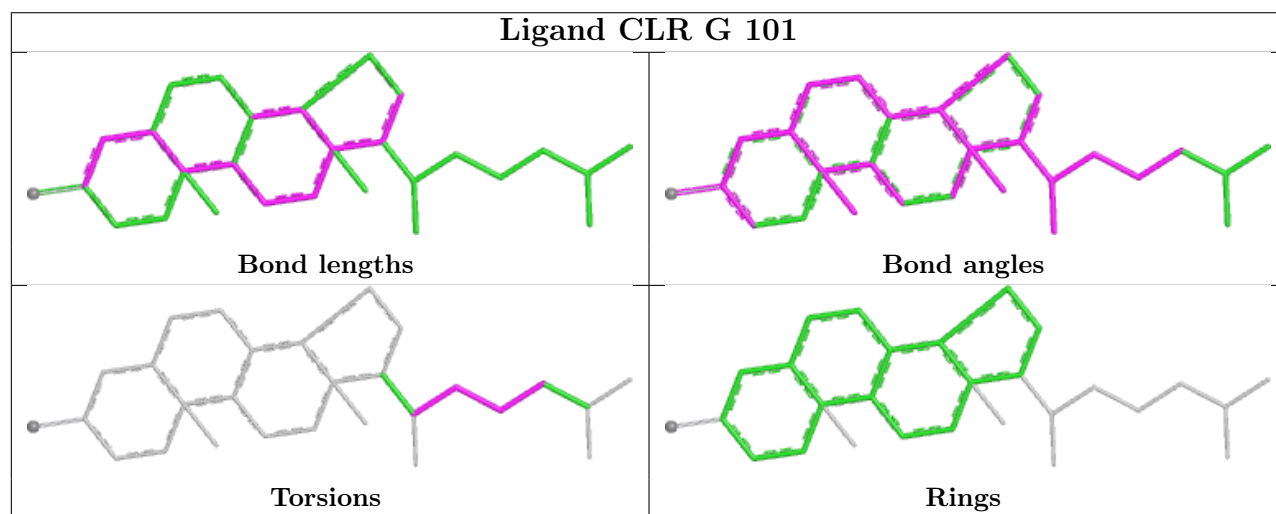
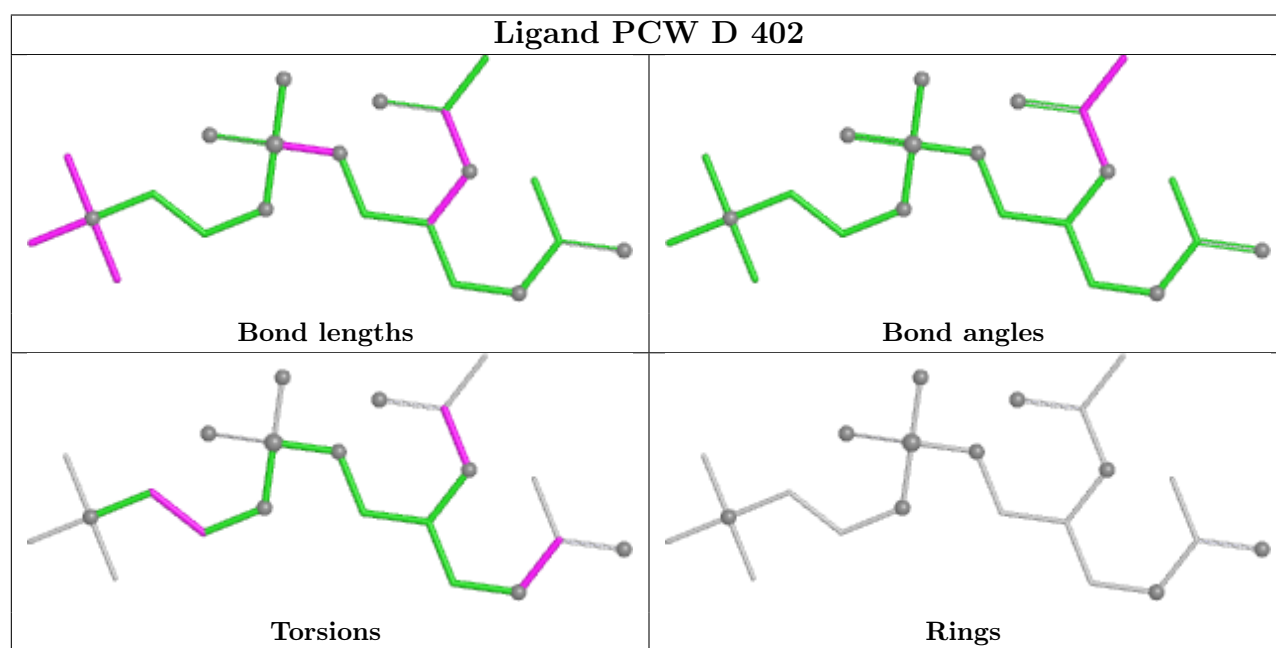
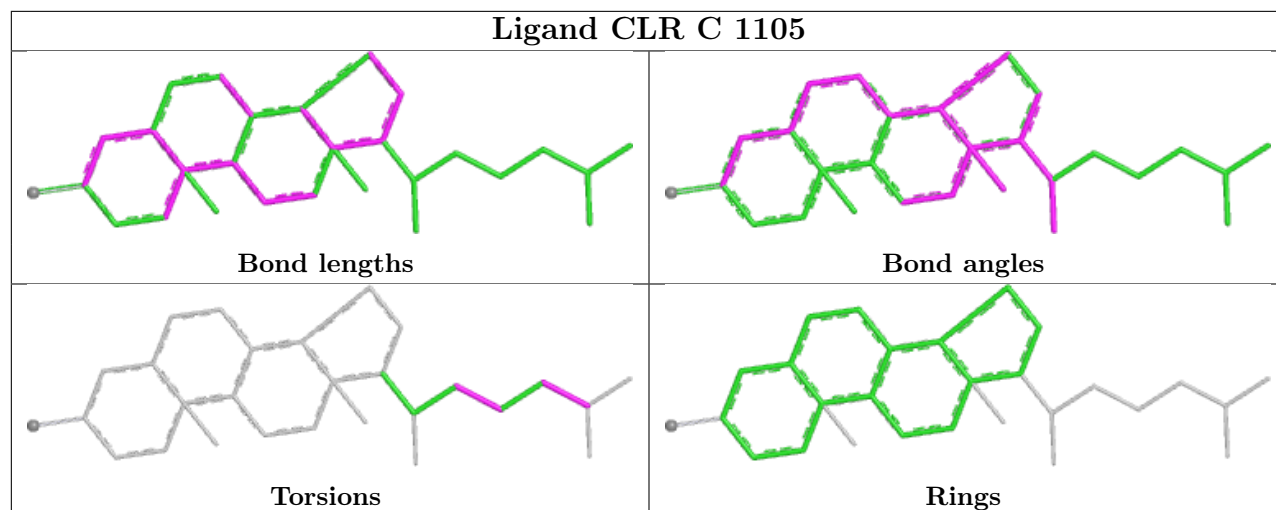


Ligand PCW A 1107

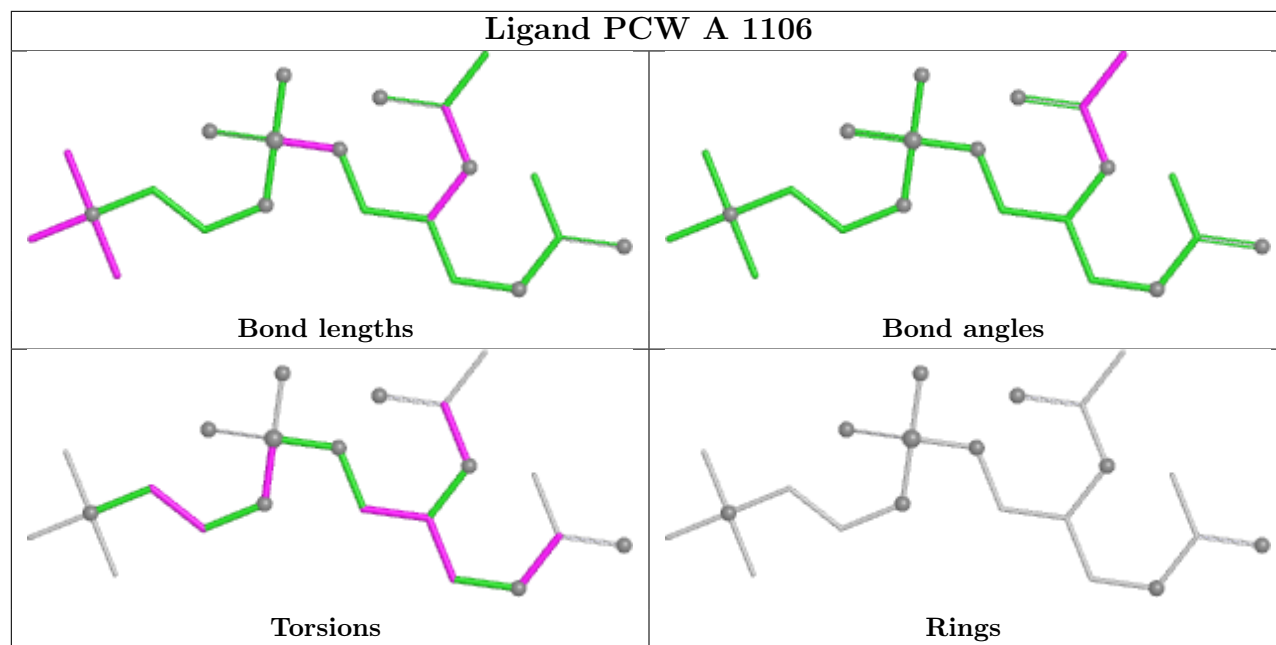


Ligand PCW C 1107

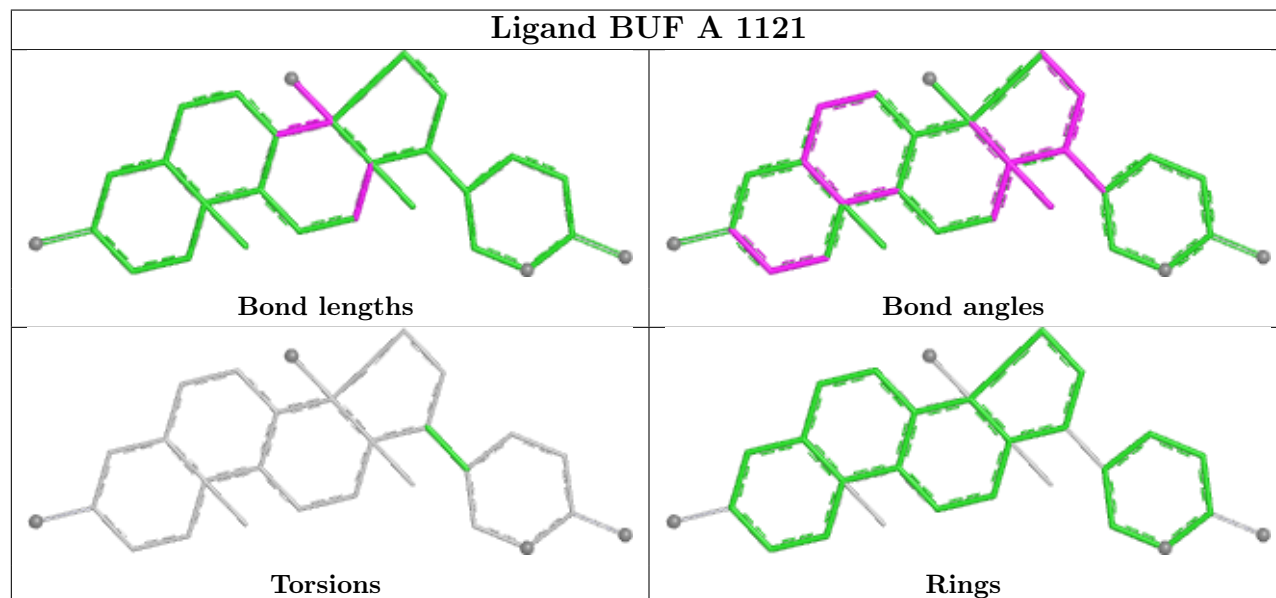




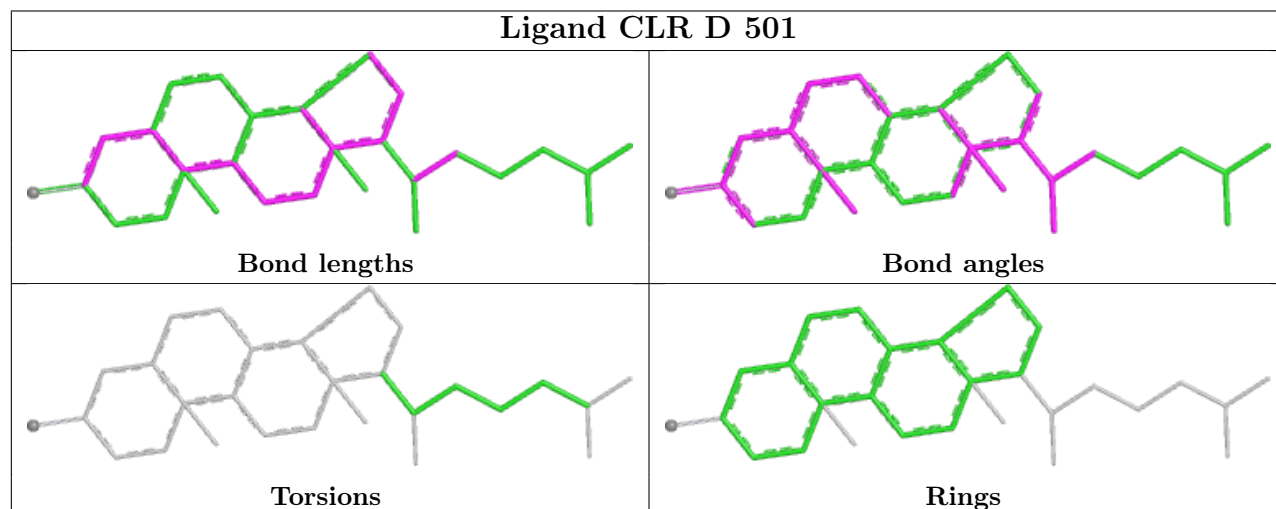
Ligand PCW A 1106



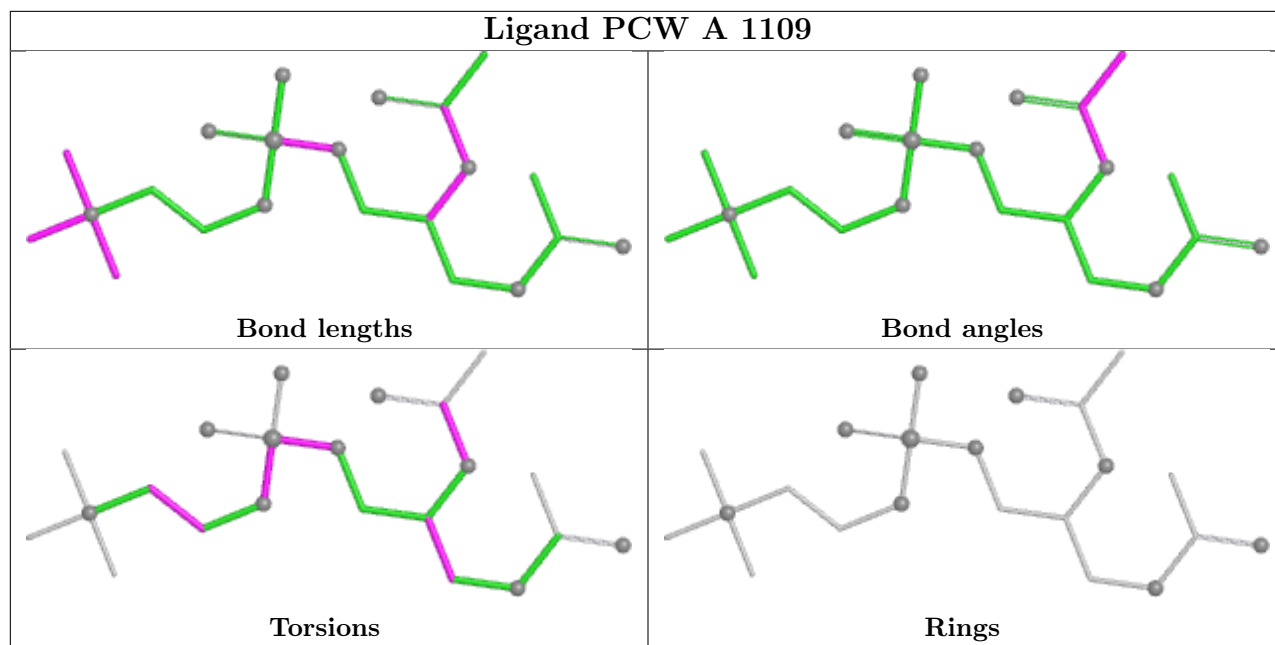
Ligand BUF A 1121



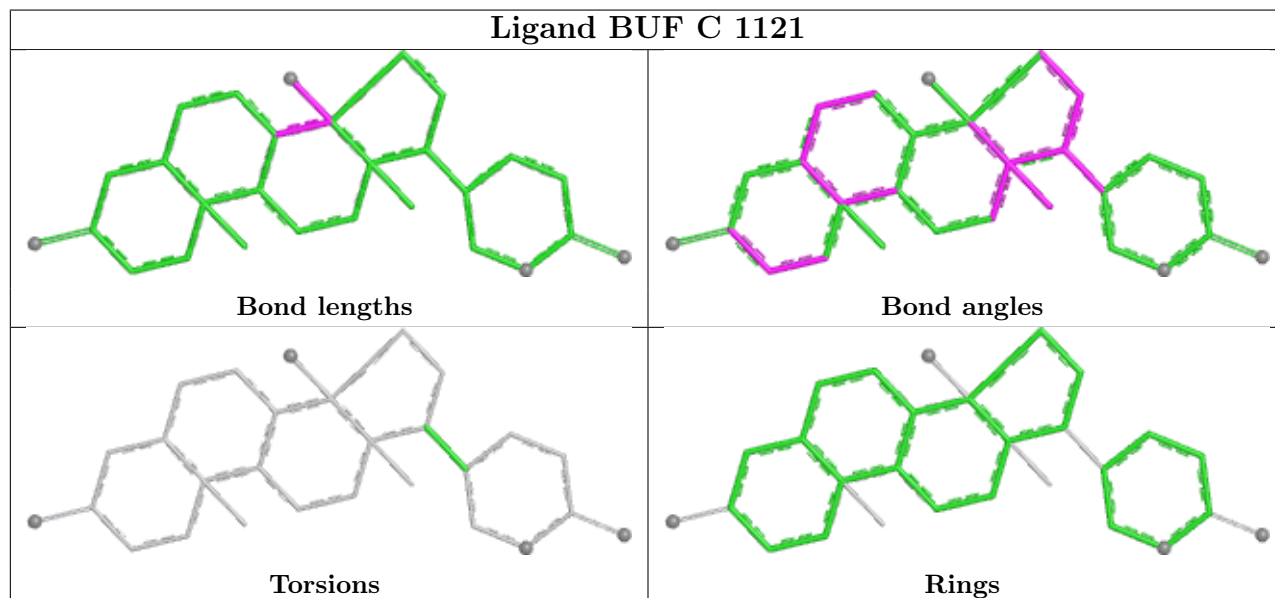
Ligand CLR D 501



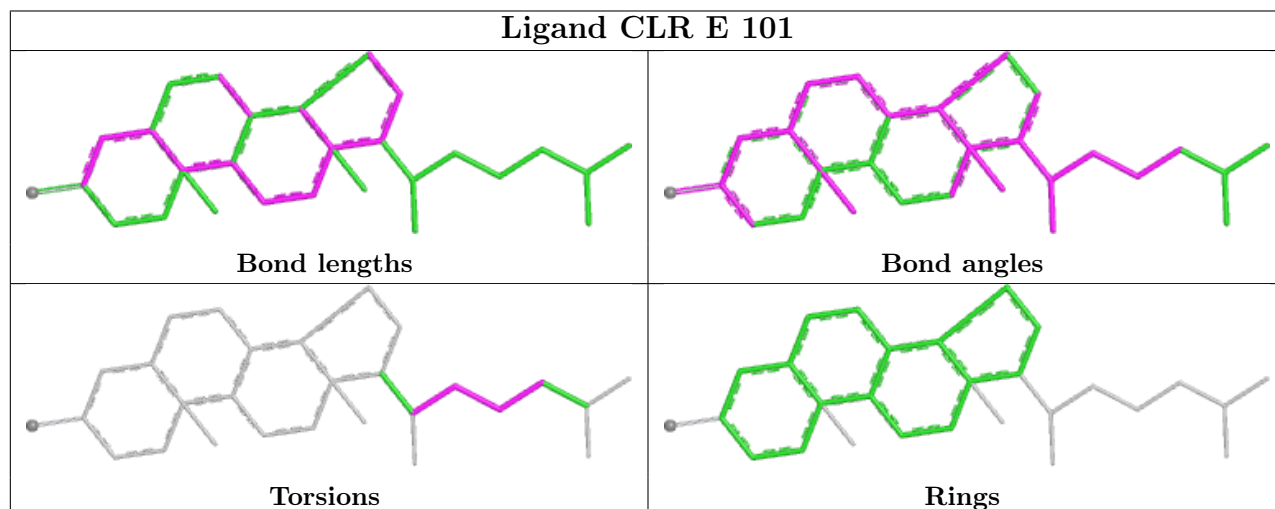
Ligand PCW A 1109

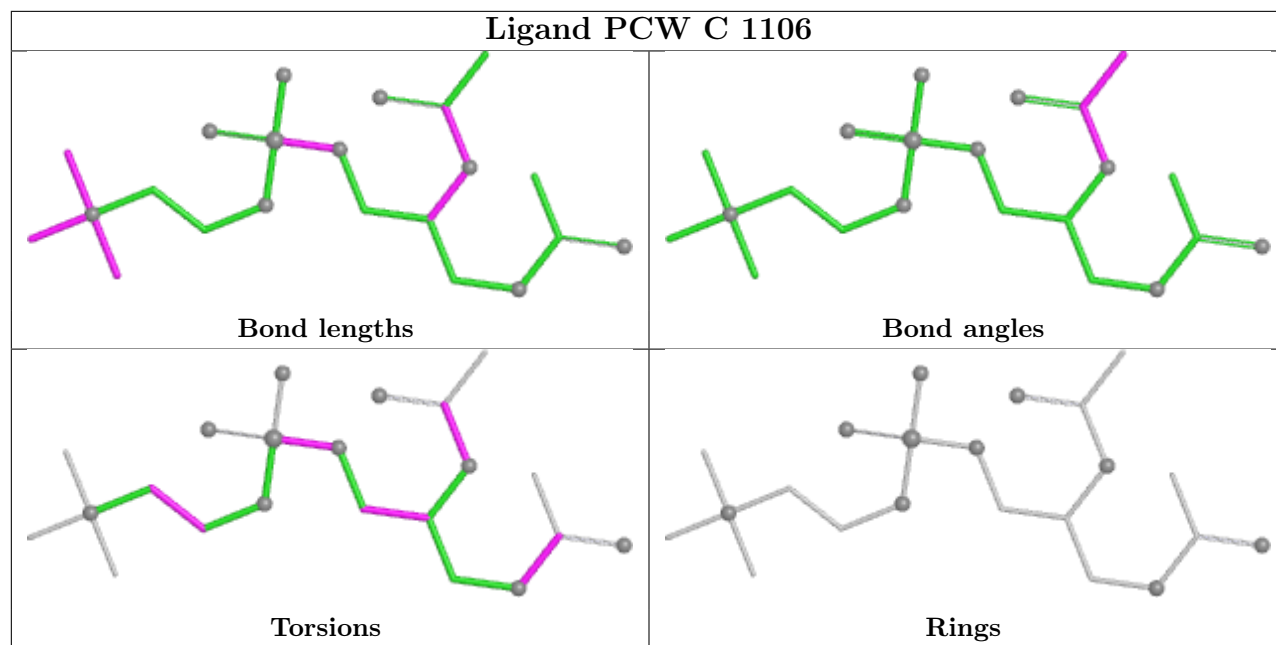


Ligand BUF C 1121



Ligand CLR E 101





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	995/1016 (97%)	-0.39	12 (1%) 76 52	40, 99, 225, 273	0
1	C	995/1016 (97%)	-0.52	3 (0%) 90 76	27, 88, 186, 241	0
2	B	291/303 (96%)	-0.23	1 (0%) 90 76	46, 121, 194, 231	0
2	D	285/303 (94%)	-0.20	3 (1%) 78 54	34, 123, 175, 217	0
3	E	32/65 (49%)	-0.76	0 100 100	34, 65, 125, 132	0
3	G	32/65 (49%)	-0.79	0 100 100	44, 73, 115, 131	0
All	All	2630/2768 (95%)	-0.41	19 (0%) 84 63	27, 101, 205, 273	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	509	ASP	3.4
1	A	508	LEU	3.1
2	D	195	SER	3.0
1	A	534	ALA	2.8
1	A	503	ALA	2.7

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.

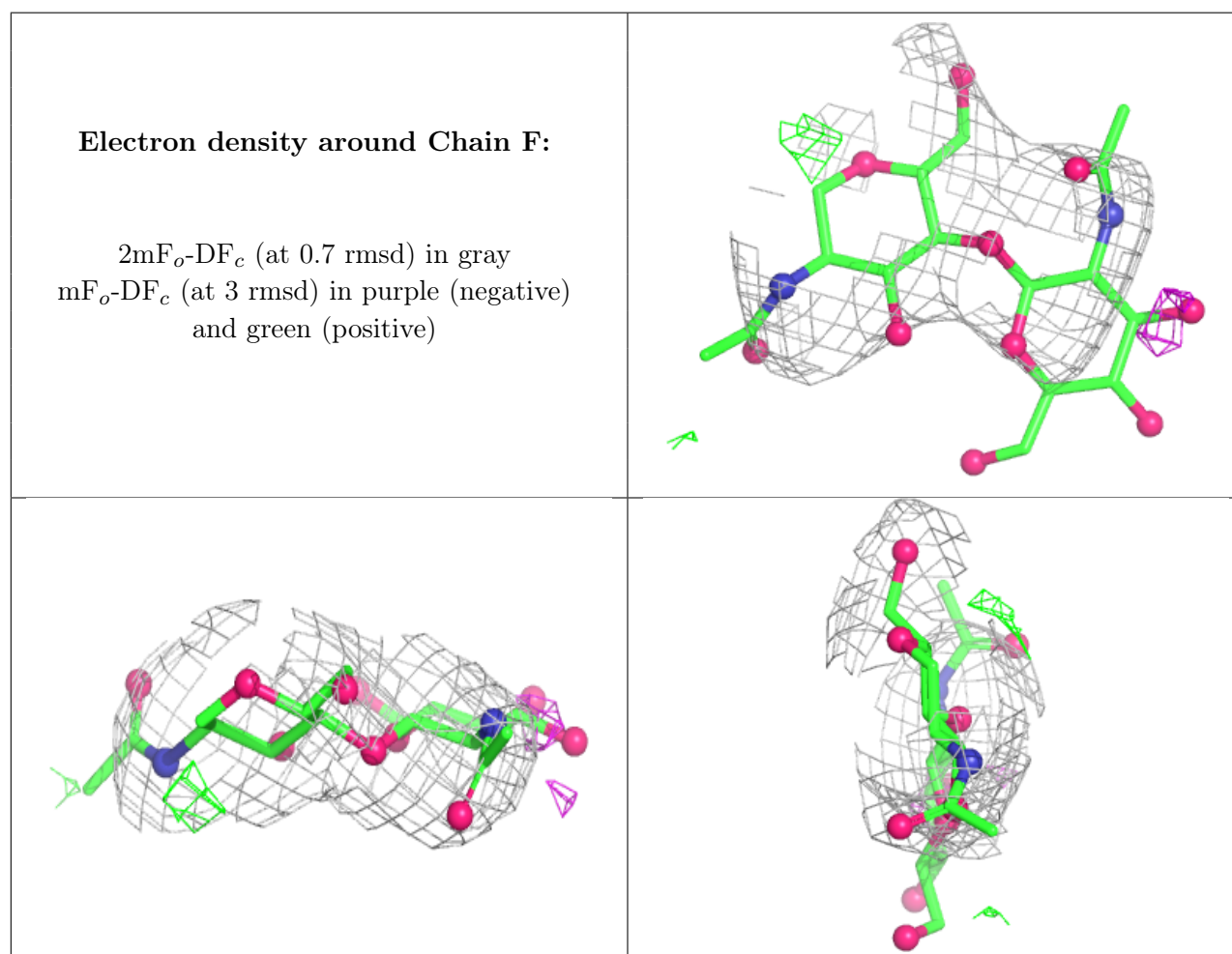
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	PHD	A	369	12/13	0.98	0.04	56,65,78,83	0
1	PHD	C	369	12/13	0.98	0.06	45,61,87,109	0

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.

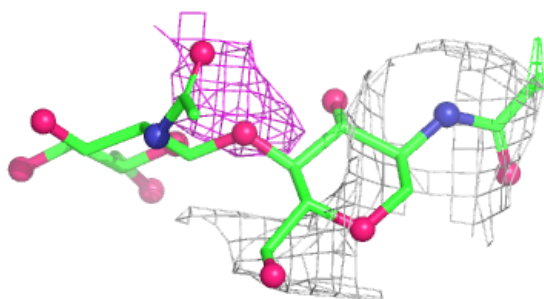
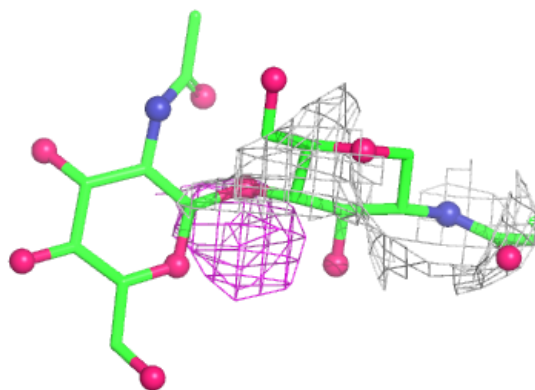
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	F	1	14/15	-	-	128,161,210,216	0
4	NAG	F	2	14/15	-	-	146,209,221,232	0
4	NAG	H	1	14/15	0.15	0.16	140,209,257,275	0
4	NAG	J	2	14/15	0.42	0.13	150,200,215,215	0
4	NAG	H	2	14/15	0.45	0.14	212,254,266,273	0
4	NAG	I	2	14/15	0.49	0.10	154,178,204,221	0
4	NAG	J	1	14/15	0.75	0.09	128,158,191,218	0
4	NAG	I	1	14/15	0.84	0.08	110,142,175,198	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.



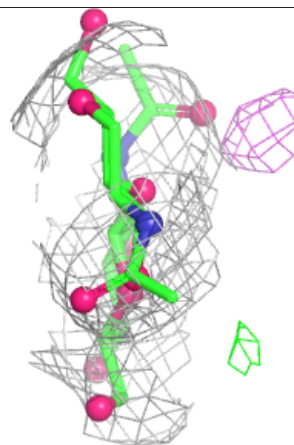
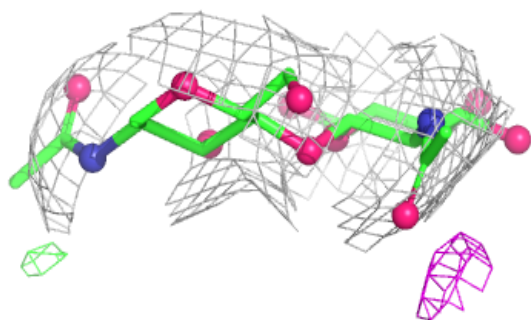
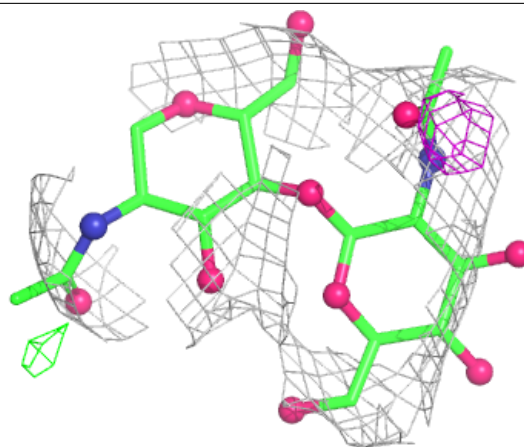
Electron density around Chain H:

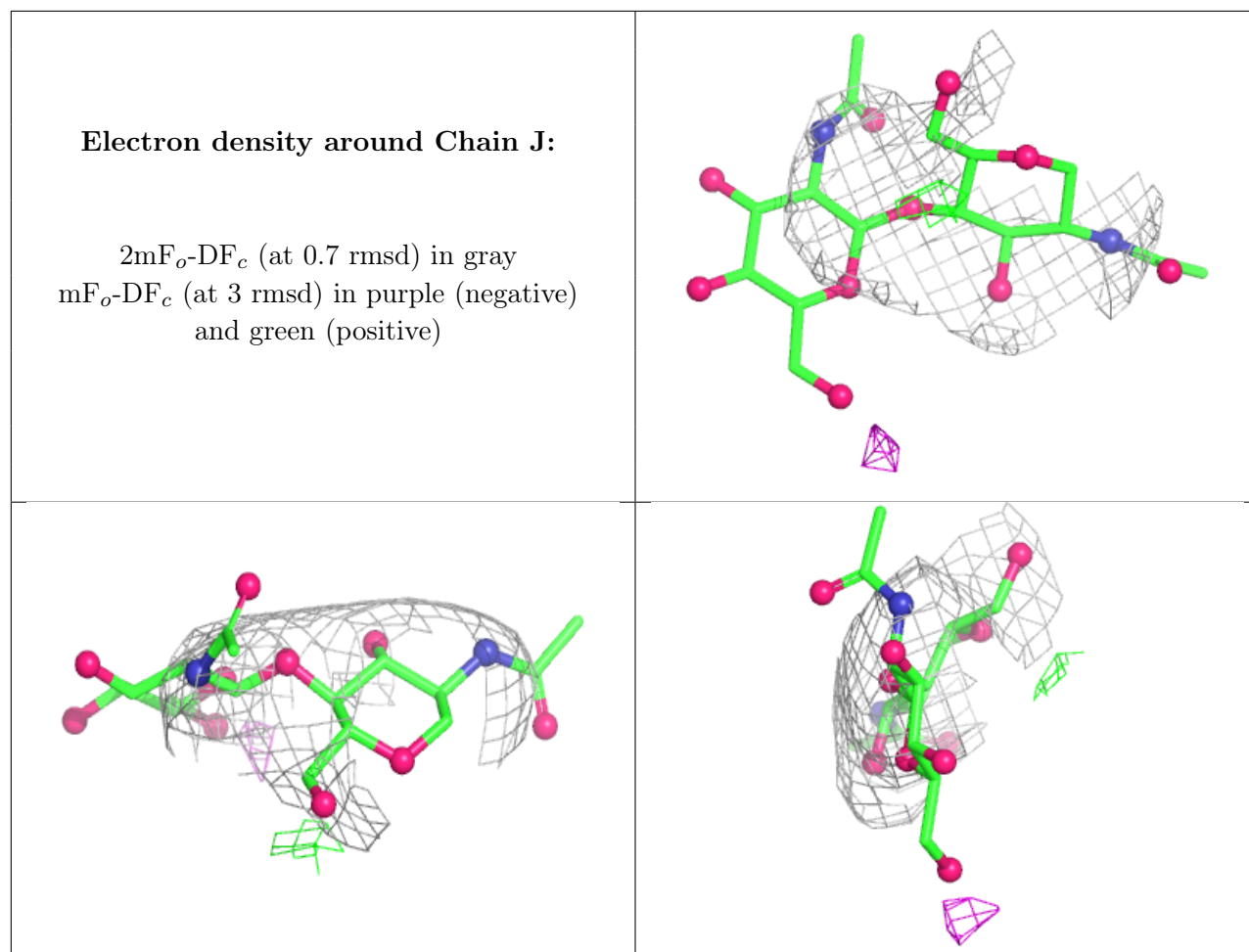
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain I:

$2mF_o - DF_c$ (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.

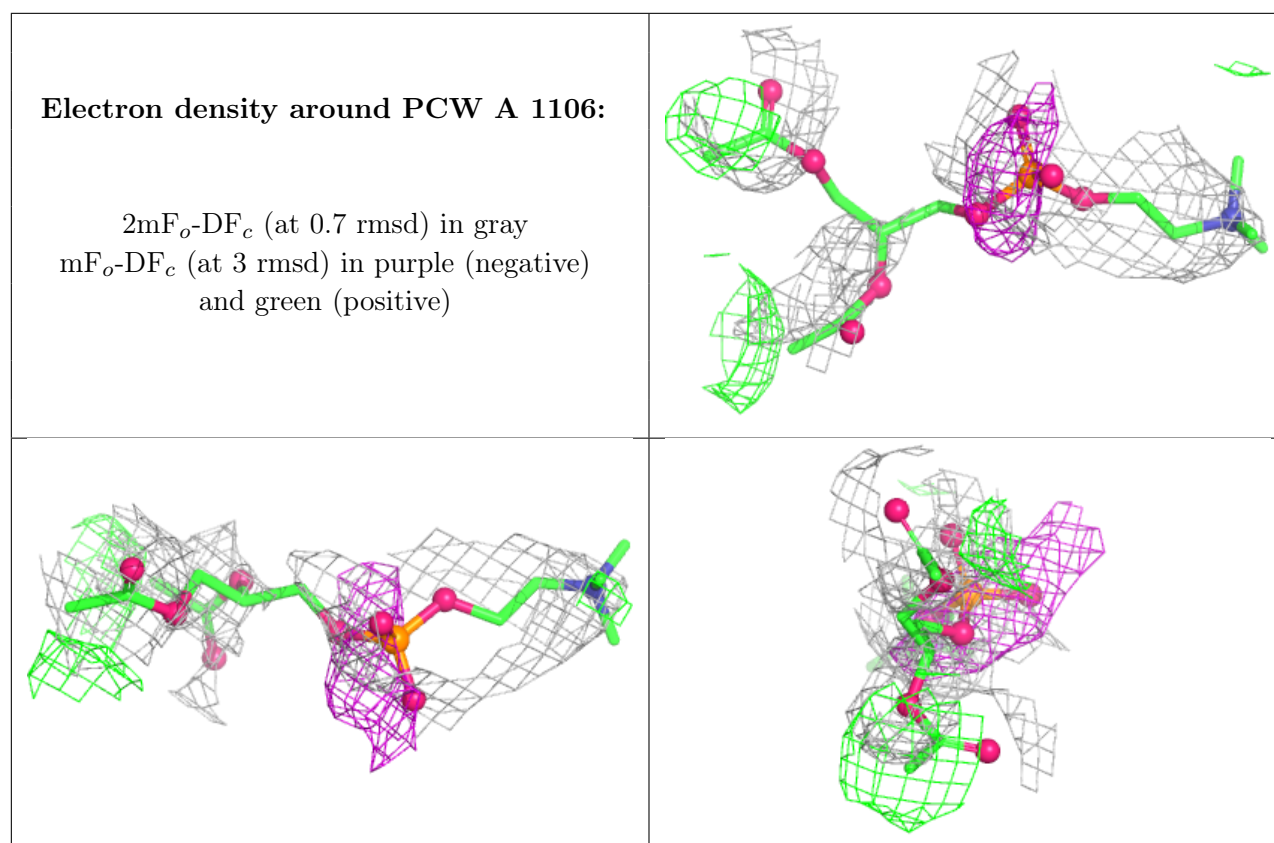
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	NAG	D	411	14/15	0.49	0.12	166,192,201,207	0
9	PCW	A	1106	22/54	0.71	0.15	90,136,158,162	0
9	PCW	D	402	22/54	0.77	0.14	129,176,202,219	0
9	PCW	A	1109	22/54	0.77	0.21	114,160,197,208	0
11	NAG	B	411	14/15	0.82	0.09	119,183,218,231	0
9	PCW	A	1107	22/54	0.83	0.15	159,192,221,223	0
9	PCW	A	1108	22/54	0.84	0.12	113,149,180,214	0
8	CLR	D	501	28/28	0.87	0.11	94,122,158,184	0
8	CLR	A	1105	28/28	0.87	0.12	68,92,141,144	0
6	NA	A	1102	1/1	0.88	0.10	25,25,25,25	0
8	CLR	C	1105	28/28	0.88	0.11	46,89,128,144	0

Continued on next page...

Continued from previous page...

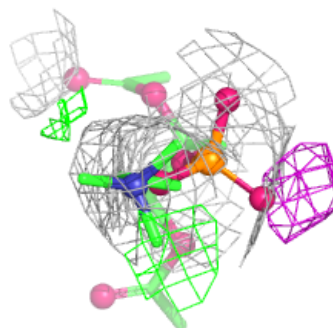
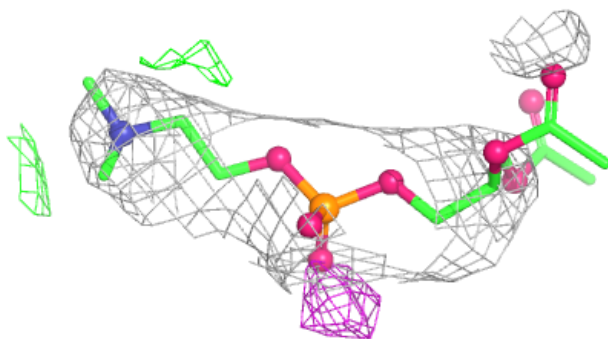
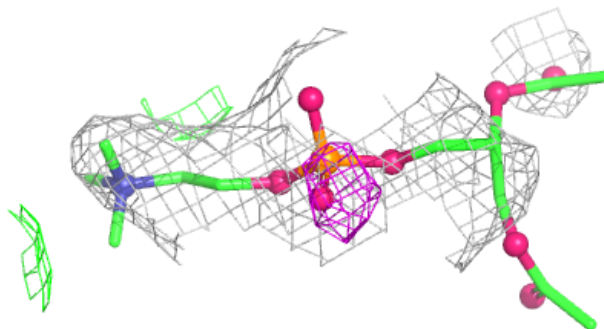
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	PCW	C	1106	22/54	0.89	0.11	106,135,163,177	0
8	CLR	G	101	28/28	0.93	0.10	34,47,93,102	0
10	BUF	A	1121	28/28	0.93	0.10	69,102,138,161	0
9	PCW	A	1110	22/54	0.95	0.10	78,103,134,173	0
9	PCW	C	1107	22/54	0.95	0.10	69,100,155,177	0
10	BUF	C	1121	28/28	0.96	0.07	49,67,111,118	0
8	CLR	E	101	28/28	0.96	0.07	17,35,75,108	0
5	MG	A	1103	1/1	0.96	0.07	50,50,50,50	0
7	RB	C	1104	1/1	0.97	0.05	99,99,99,99	0
6	NA	C	1102	1/1	0.98	0.10	9,9,9,9	0
7	RB	A	1104	1/1	0.98	0.09	101,101,101,101	0
5	MG	A	1101	1/1	0.99	0.03	70,70,70,70	0
5	MG	C	1101	1/1	0.99	0.03	63,63,63,63	0
5	MG	C	1103	1/1	0.99	0.01	28,28,28,28	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.

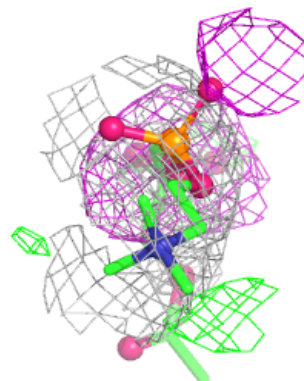
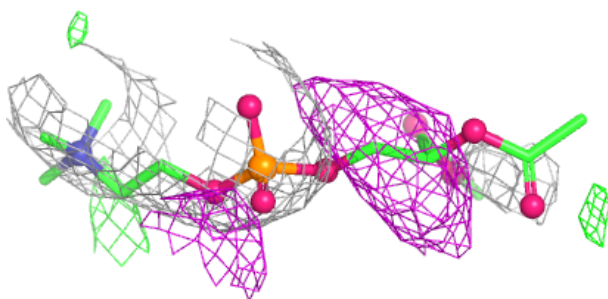
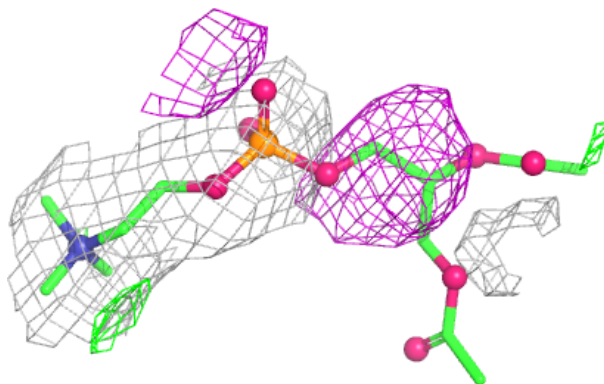


Electron density around PCW D 402:

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

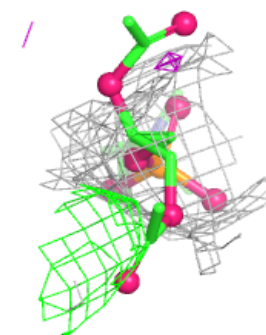
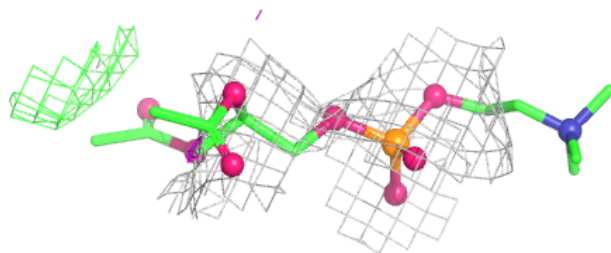
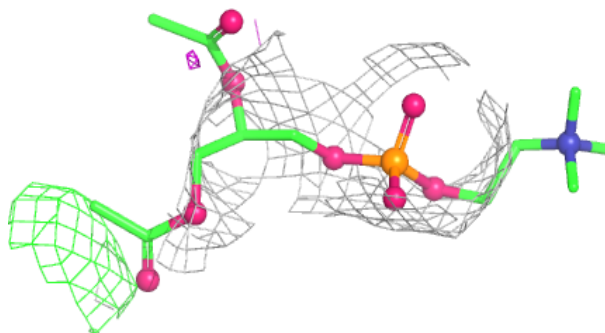
**Electron density around PCW A 1109:**

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

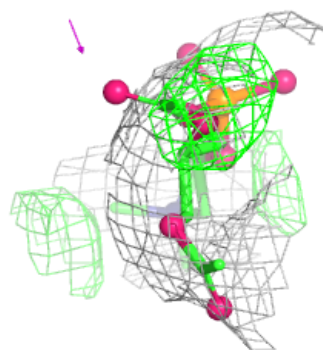
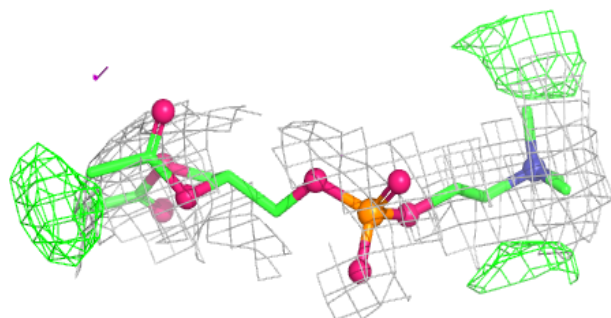
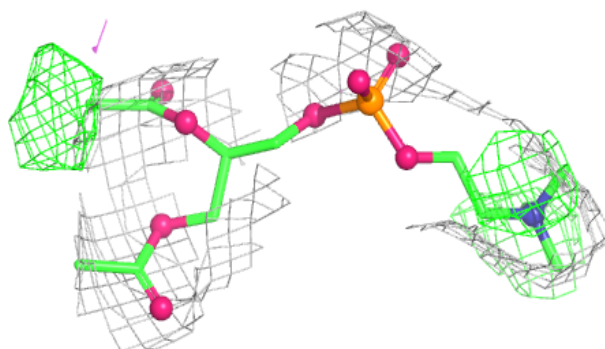


Electron density around PCW A 1107:

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

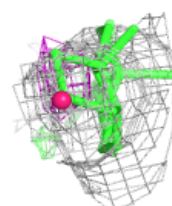
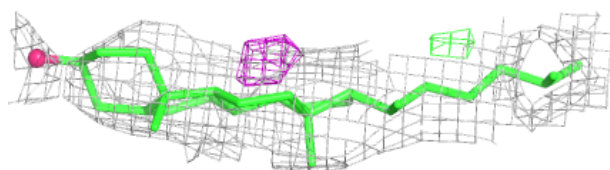
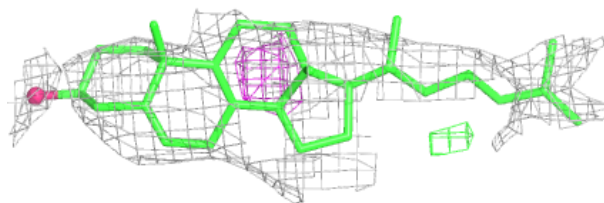
**Electron density around PCW A 1108:**

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

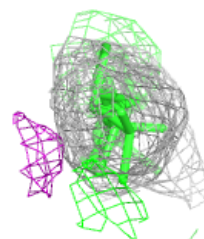
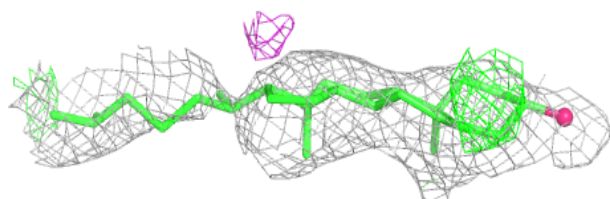
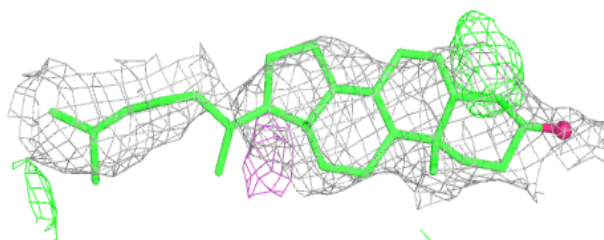


Electron density around CLR D 501:

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

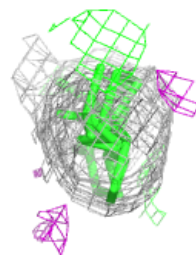
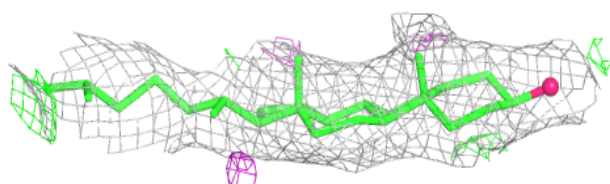
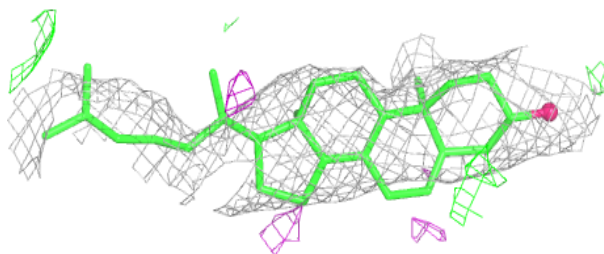
**Electron density around CLR A 1105:**

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

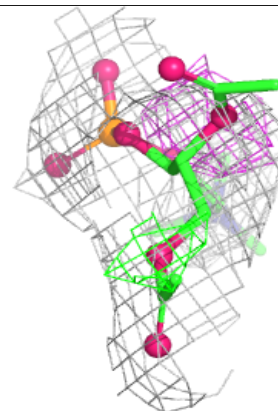
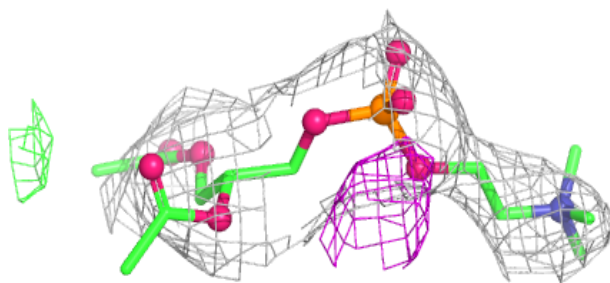
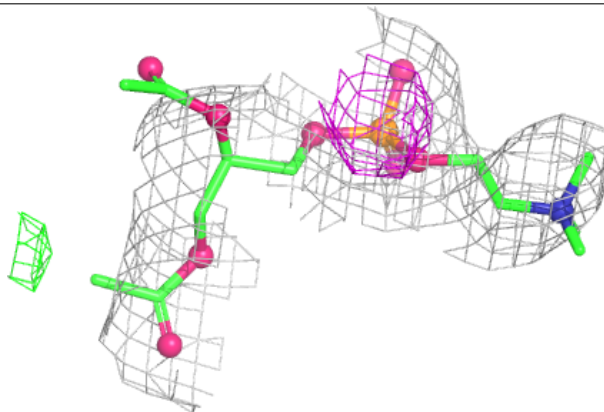


Electron density around CLR C 1105:

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

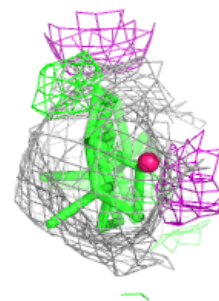
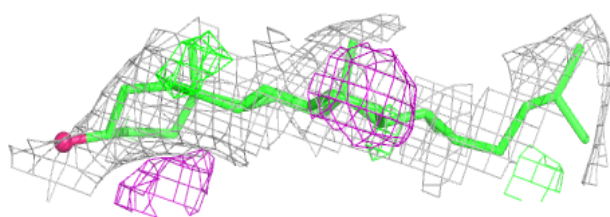
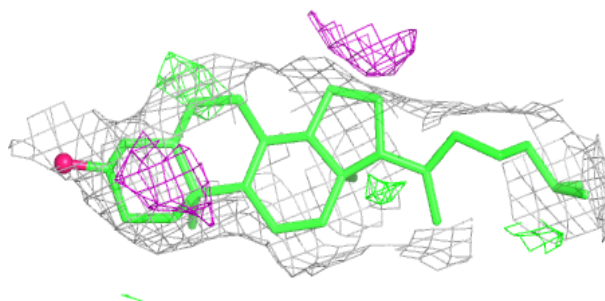
**Electron density around PCW C 1106:**

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

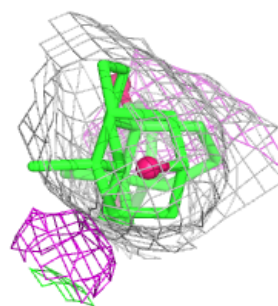
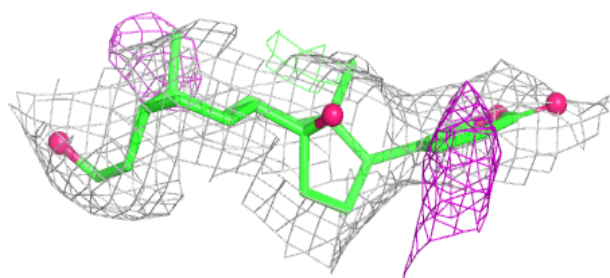
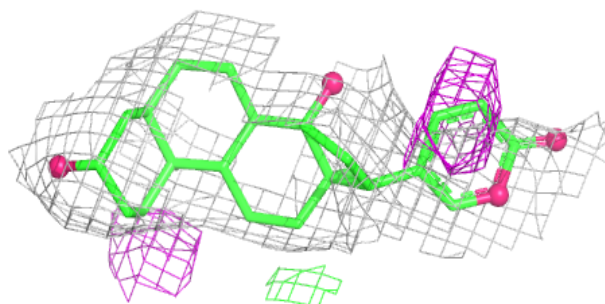


Electron density around CLR G 101:

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

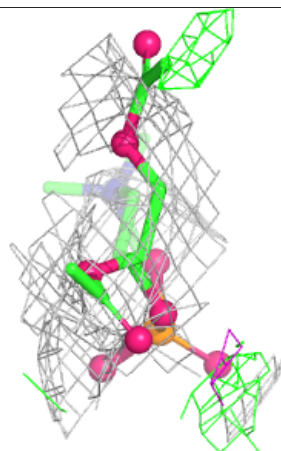
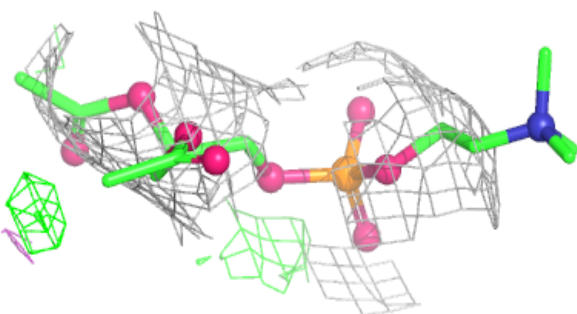
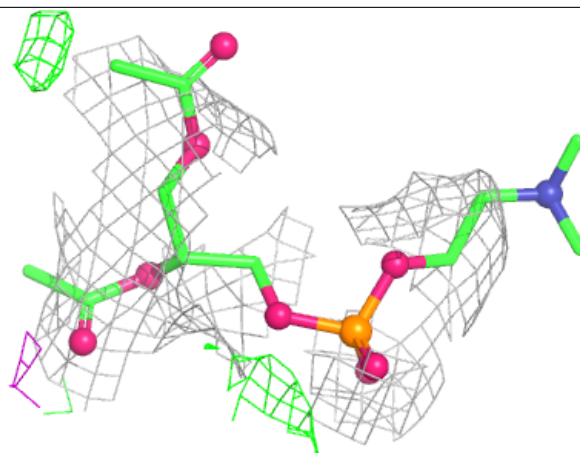
**Electron density around BUF A 1121:**

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

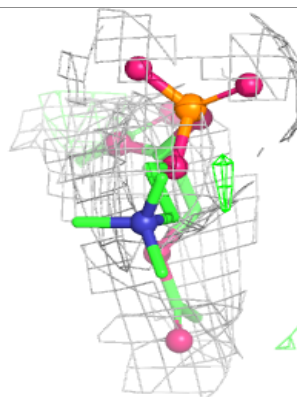
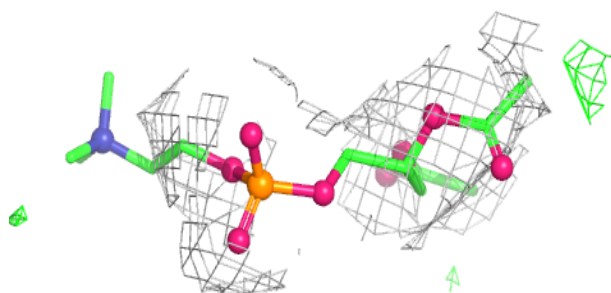
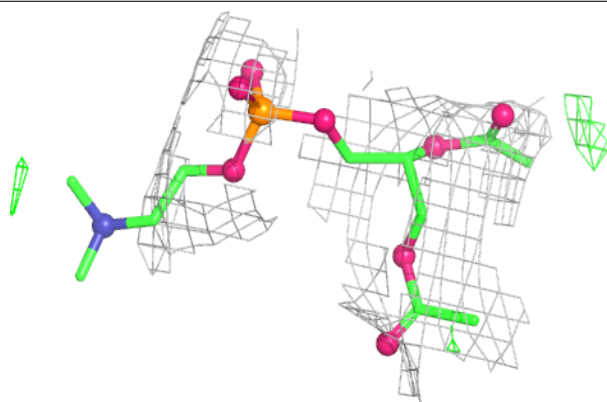


Electron density around PCW A 1110:

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

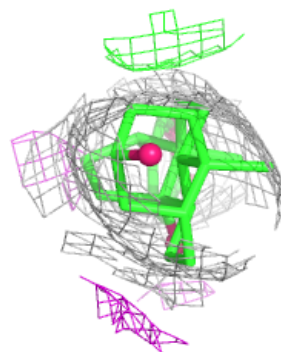
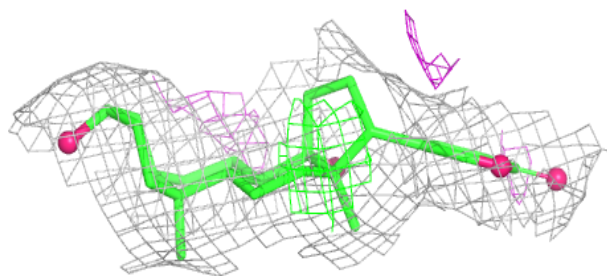
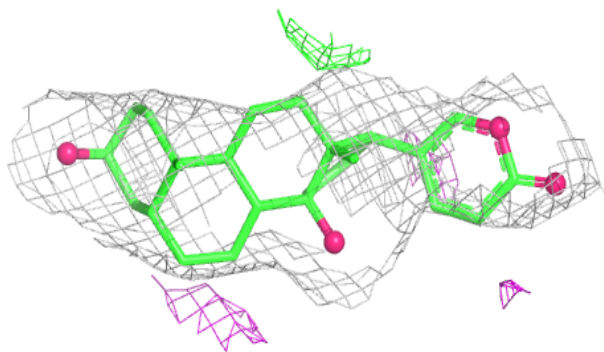
**Electron density around PCW C 1107:**

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

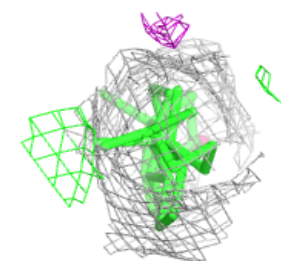
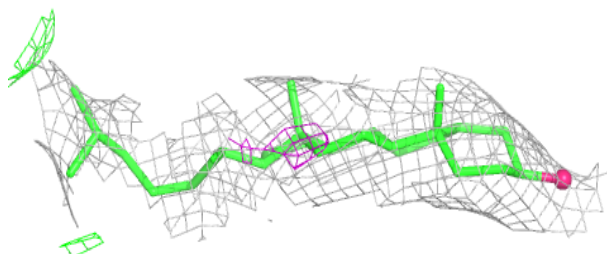


Electron density around BUF C 1121:

$2mF_o-DF_c$ (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)



6.5 Other polymers [i](#)

There are no such residues in this entry.