



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:48 PM UTC

PDB ID : 4P02 / pdb_00004p02
Title : Structure of Bacterial Cellulose Synthase with cyclic-di-GMP bound.
Authors : Morgan, J.L.W.; McNamara, J.T.; Zimmer, J.
Deposited on : 2014-02-20
Resolution : 2.65 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

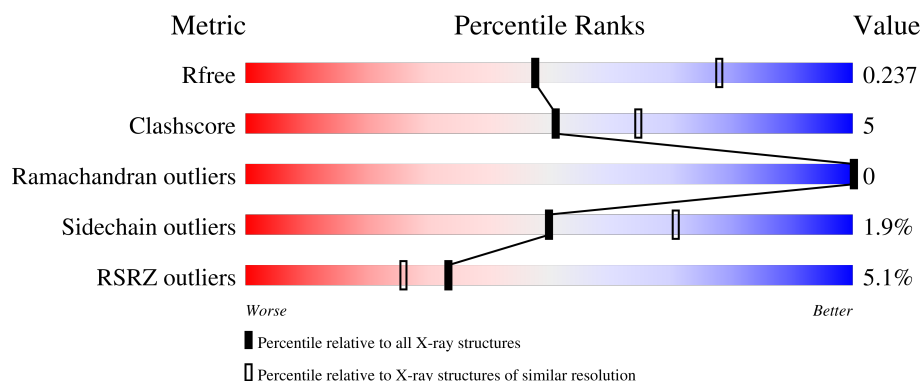
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	803	5% 78% 12% • 9%
2	B	724	4% 77% 13% 10%
3	D	9	100%
4	C	17	29% 47% 24%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BGC	C	5	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11040 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 Cellulose Synthase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	1	0
			5739	3725	1000	982	32			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q3J125
A	1	GLY	-	expression tag	UNP Q3J125
A	789	HIS	-	expression tag	UNP Q3J125
A	790	HIS	-	expression tag	UNP Q3J125
A	791	HIS	-	expression tag	UNP Q3J125
A	792	HIS	-	expression tag	UNP Q3J125
A	793	HIS	-	expression tag	UNP Q3J125
A	794	HIS	-	expression tag	UNP Q3J125
A	795	LYS	-	expression tag	UNP Q3J125
A	796	LEU	-	expression tag	UNP Q3J125
A	797	HIS	-	expression tag	UNP Q3J125
A	798	HIS	-	expression tag	UNP Q3J125
A	799	HIS	-	expression tag	UNP Q3J125
A	800	HIS	-	expression tag	UNP Q3J125
A	801	HIS	-	expression tag	UNP Q3J125
A	802	HIS	-	expression tag	UNP Q3J125

- Molecule 2 is a protein called Cellulose Synthase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	655	Total	C	N	O	S	0	0	0
			4887	3100	864	907	16			

- Molecule 3 is a protein called unidentified peptide.

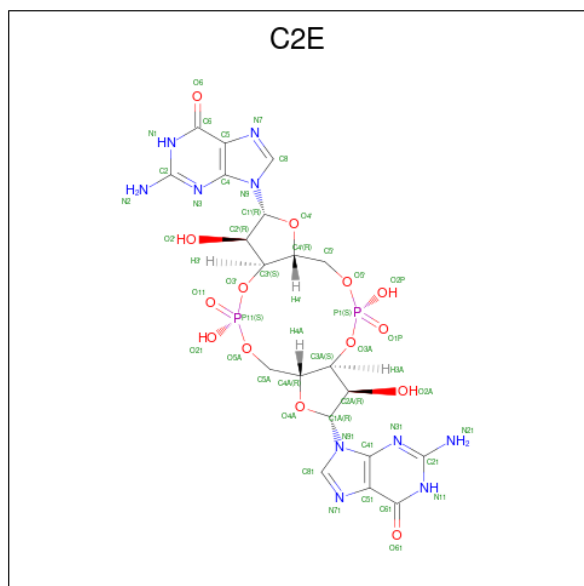
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	9	Total	C	N	O	0	0	0
			45	27	9	9			

- [illegible]



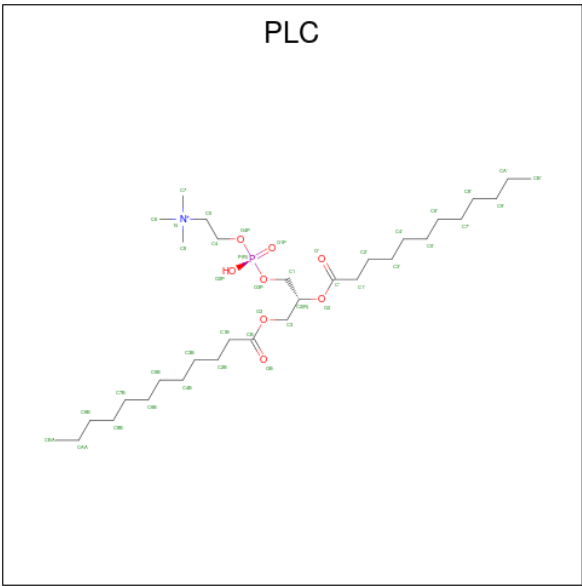
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	C	17	Total	C	O	0	0	0
			187	102	85			

- Molecule 5 is 9,9'-[(2R,3R,3aS,5S,7aR,9R,10R,10aS,12S,14aR)-3,5,10,12-tetrahydroxy-5,12-dioxidoctahydro-2H,7H-difuro[3,2-d:3',2'-j][1,3,7,9,2,8]tetraoxadiphosphacyclododecine-2,9-diyl]bis(2-amino-1,9-dihydro-6H-purin-6-one) (CCD ID: C2E) (formula: C₂₀H₂₄N₁₀O₁₄P₂).



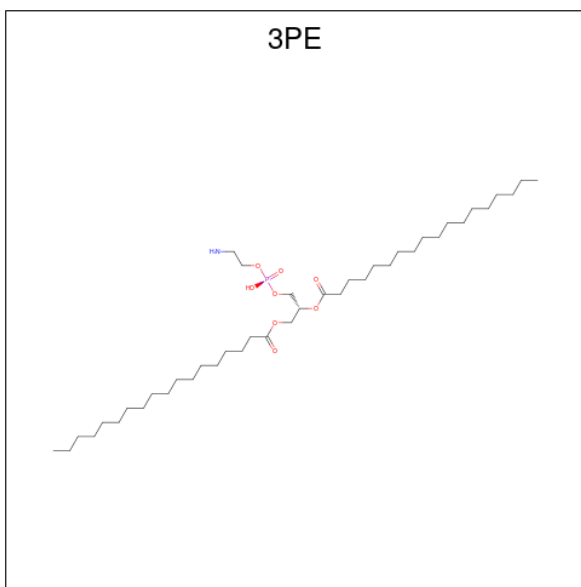
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 46	C 20	N 10	O 14	P 2	0	0
5	A	1	Total 46	C 20	N 10	O 14	P 2	0	0

- Molecule 6 is DIUNDECYL PHOSPHATIDYL CHOLINE (CCD ID: PLC) (formula: C₃₂H₆₅NO₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 38	C 28	N 1	O 8	P 1	0	0
6	B	1	Total C 11 11					0	0
6	B	1	Total C 9 9					0	0
6	B	1	Total C 11 11					0	0

- Molecule 7 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			20	10	1	8	1		

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Mg	0	0
			1	1		

- Molecule 1: Cellulose Synthase subunit A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.64Å 214.66Å 220.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.65 19.99 – 2.65	Depositor EDS
% Data completeness (in resolution range)	91.4 (19.99-2.65) 91.1 (19.99-2.65)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 2.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.199 , 0.230 0.212 , 0.237	Depositor DCC
R_{free} test set	4314 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	59.5	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11040	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% 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: 3PE, C2E, MG, PLC, BGC

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	0.30	0/5888	0.74	4/8007 (0.0%)
2	B	0.31	0/5006	0.77	4/6865 (0.1%)
All	All	0.30	0/10894	0.75	8/14872 (0.1%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	107	LEU	CA-C-N	6.01	125.50	119.24
2	B	107	LEU	C-N-CA	6.01	125.50	119.24
1	A	225	ALA	CB-CA-C	-5.78	109.90	116.54
2	B	516	GLU	CB-CA-C	-5.27	109.52	115.79
2	B	563	PRO	O-C-N	5.23	123.72	121.31

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	5739	0	5855	58	0
2	B	4887	0	4966	56	0
3	D	45	0	12	0	0
4	C	187	0	154	16	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	92	0	44	0	0
6	A	38	0	53	0	0
6	B	31	0	56	0	0
7	A	20	0	14	0	0
8	B	1	0	0	0	0
All	All	11040	0	11154	116	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 5.

The worst 5 of 116 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)
4:C:4:BGC:O3	4:C:5:BGC:O5	1.85	0.94
4:C:5:BGC:O3	4:C:6:BGC:O5	1.90	0.88
2:B:390:ARG:NH2	4:C:5:BGC:O6	2.07	0.84
4:C:1:BGC:H6C1	4:C:2:BGC:O2	1.78	0.84
1:A:243:VAL:HG22	1:A:323:VAL:HG22	1.66	0.77

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	727/803 (90%)	706 (97%)	21 (3%)	0	100	100
2	B	651/724 (90%)	635 (98%)	16 (2%)	0	100	100
All	All	1378/1527 (90%)	1341 (97%)	37 (3%)	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	599/661 (91%)	585 (98%)	14 (2%)	44	66
2	B	520/572 (91%)	513 (99%)	7 (1%)	61	77
All	All	1119/1233 (91%)	1098 (98%)	21 (2%)	50	71

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	158	ARG
2	B	383	VAL
2	B	514	ASN
2	B	448	VAL
2	B	326	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	77	GLN
2	B	129	GLN
2	B	472	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

17 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	BGC	C	1	4	11,11,12	0.29	0	15,15,17	0.60	0
4	BGC	C	10	4	11,11,12	0.27	0	15,15,17	0.80	1 (6%)
4	BGC	C	11	4	11,11,12	0.29	0	15,15,17	0.59	0
4	BGC	C	12	4	11,11,12	0.29	0	15,15,17	0.75	0
4	BGC	C	13	4	11,11,12	0.36	0	15,15,17	0.66	0
4	BGC	C	14	4	11,11,12	0.37	0	15,15,17	0.99	1 (6%)
4	BGC	C	15	4	11,11,12	0.28	0	15,15,17	0.72	0
4	BGC	C	16	4	11,11,12	0.34	0	15,15,17	1.02	1 (6%)
4	BGC	C	17	4	11,11,12	0.29	0	15,15,17	0.70	0
4	BGC	C	2	4	11,11,12	0.34	0	15,15,17	0.85	0
4	BGC	C	3	4	11,11,12	0.30	0	15,15,17	0.64	0
4	BGC	C	4	4	11,11,12	0.37	0	15,15,17	0.99	1 (6%)
4	BGC	C	5	4	11,11,12	0.51	0	15,15,17	1.63	3 (20%)
4	BGC	C	6	4	11,11,12	0.26	0	15,15,17	0.98	1 (6%)
4	BGC	C	7	4	11,11,12	0.21	0	15,15,17	0.66	0
4	BGC	C	8	4	11,11,12	0.42	0	15,15,17	1.38	3 (20%)
4	BGC	C	9	4	11,11,12	0.30	0	15,15,17	0.68	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	BGC	C	1	4	-	2/2/19/22	0/1/1/1
4	BGC	C	10	4	-	2/2/19/22	0/1/1/1
4	BGC	C	11	4	-	0/2/19/22	0/1/1/1
4	BGC	C	12	4	-	0/2/19/22	0/1/1/1
4	BGC	C	13	4	-	0/2/19/22	0/1/1/1
4	BGC	C	14	4	-	2/2/19/22	0/1/1/1
4	BGC	C	15	4	-	0/2/19/22	0/1/1/1
4	BGC	C	16	4	-	2/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BGC	C	17	4	-	0/2/19/22	0/1/1/1
4	BGC	C	2	4	-	2/2/19/22	0/1/1/1
4	BGC	C	3	4	-	1/2/19/22	0/1/1/1
4	BGC	C	4	4	-	2/2/19/22	0/1/1/1
4	BGC	C	5	4	-	2/2/19/22	0/1/1/1
4	BGC	C	6	4	-	2/2/19/22	0/1/1/1
4	BGC	C	7	4	-	2/2/19/22	0/1/1/1
4	BGC	C	8	4	-	2/2/19/22	0/1/1/1
4	BGC	C	9	4	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	5	BGC	C1-C2-C3	3.75	115.11	109.64
4	C	14	BGC	C1-C2-C3	3.12	114.19	109.64
4	C	5	BGC	C1-O5-C5	-2.98	108.19	112.19
4	C	8	BGC	C3-C4-C5	2.82	115.34	110.23
4	C	4	BGC	C1-C2-C3	2.80	113.73	109.64

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	7	BGC	O5-C5-C6-O6
4	C	2	BGC	C4-C5-C6-O6
4	C	4	BGC	O5-C5-C6-O6
4	C	2	BGC	O5-C5-C6-O6
4	C	5	BGC	O5-C5-C6-O6

There are no ring outliers.

9 monomers are involved in 16 short contacts:

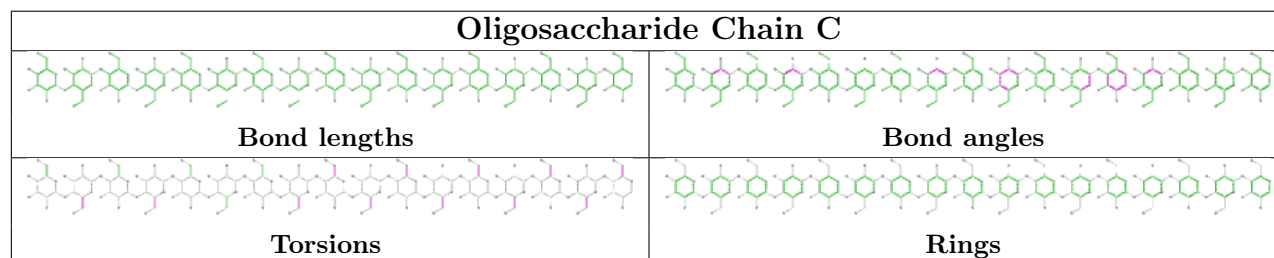
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	17	BGC	1	0
4	C	14	BGC	1	0
4	C	6	BGC	3	0
4	C	3	BGC	1	0
4	C	2	BGC	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	7	BGC	3	0
4	C	1	BGC	1	0
4	C	4	BGC	4	0
4	C	5	BGC	8	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 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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
6	PLC	B	802	-	10,10,41	0.26	0	9,9,49	0.54	0
5	C2E	A	919	-	52,52,52	1.16	6 (11%)	78,82,82	1.87	16 (20%)
7	3PE	A	921	-	19,19,50	1.63	2 (10%)	22,24,55	1.66	4 (18%)
6	PLC	B	804	-	10,10,41	0.25	0	9,9,49	0.54	0
6	PLC	A	920	-	37,37,41	1.13	2 (5%)	43,45,49	1.11	3 (6%)
5	C2E	A	918	-	52,52,52	1.15	5 (9%)	78,82,82	1.89	15 (19%)
6	PLC	B	803	-	8,8,41	0.25	0	7,7,49	0.50	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
6	PLC	B	802	-	-	1/8/8/45	-
5	C2E	A	919	-	-	0/30/62/62	0/6/7/7
7	3PE	A	921	-	-	4/22/22/54	-
6	PLC	B	804	-	-	5/8/8/45	-
6	PLC	A	920	-	-	21/41/41/45	-
5	C2E	A	918	-	-	2/30/62/62	0/6/7/7
6	PLC	B	803	-	-	2/6/6/45	-

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	921	3PE	O21-C21	4.91	1.46	1.35
7	A	921	3PE	O31-C31	4.38	1.46	1.33
6	A	920	PLC	O3-CB	4.28	1.45	1.33
6	A	920	PLC	O2-C'	4.20	1.46	1.34
5	A	919	C2E	C5-C4	3.18	1.47	1.38

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	918	C2E	C5-C4-N3	-6.18	118.55	128.39
5	A	919	C2E	C51-C41-N31	-6.15	118.60	128.39
5	A	919	C2E	C5-C4-N3	-6.12	118.64	128.39
5	A	918	C2E	C51-C41-N31	-5.99	118.86	128.39
7	A	921	3PE	O21-C21-C22	5.30	120.54	111.09

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

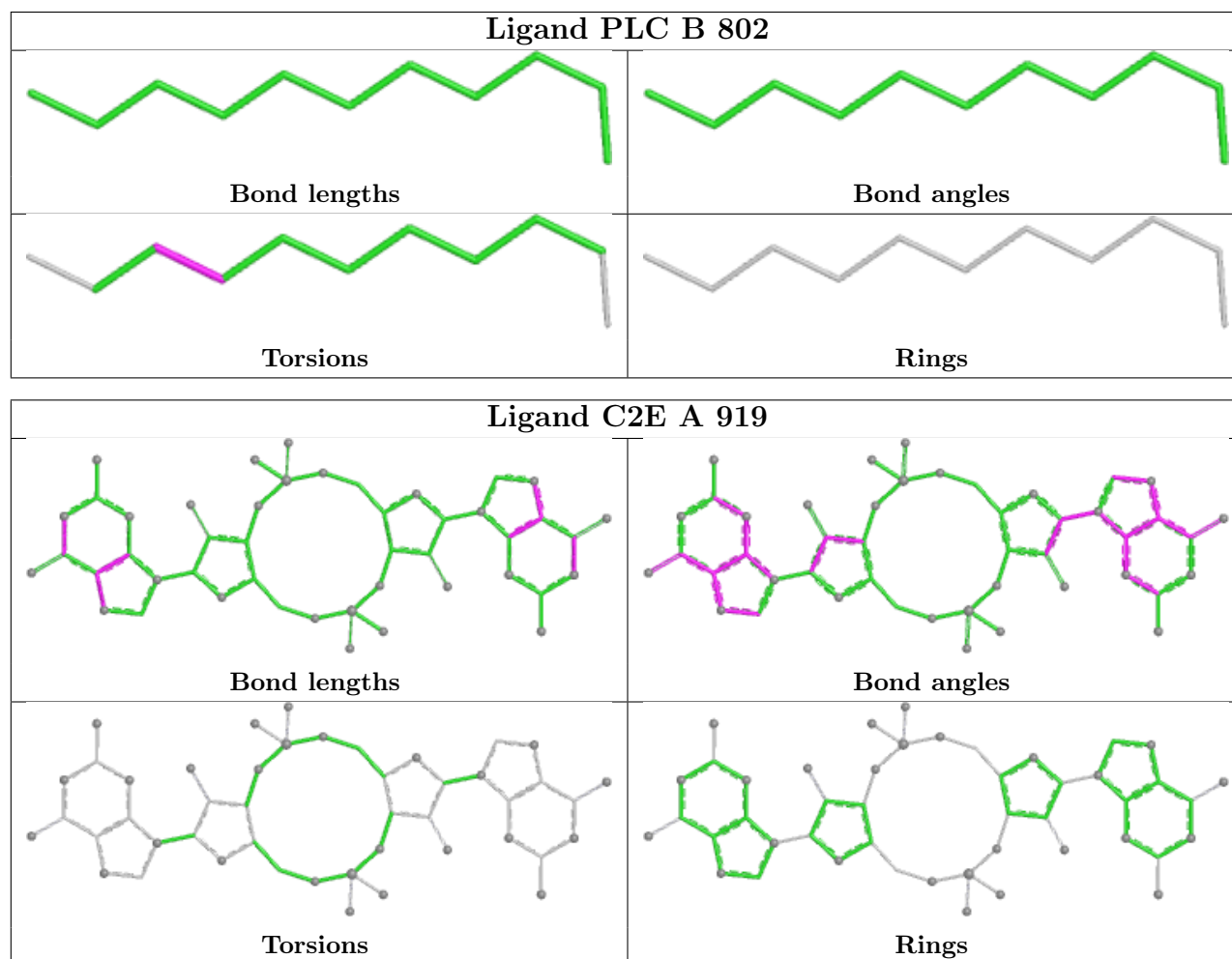
Mol	Chain	Res	Type	Atoms
6	A	920	PLC	O2-C2-C3-O3
6	A	920	PLC	O4P-C4-C5-N
6	A	920	PLC	C5-C4-O4P-P
6	A	920	PLC	C4-O4P-P-O1P
7	A	921	3PE	O32-C31-O31-C3

There are no ring outliers.

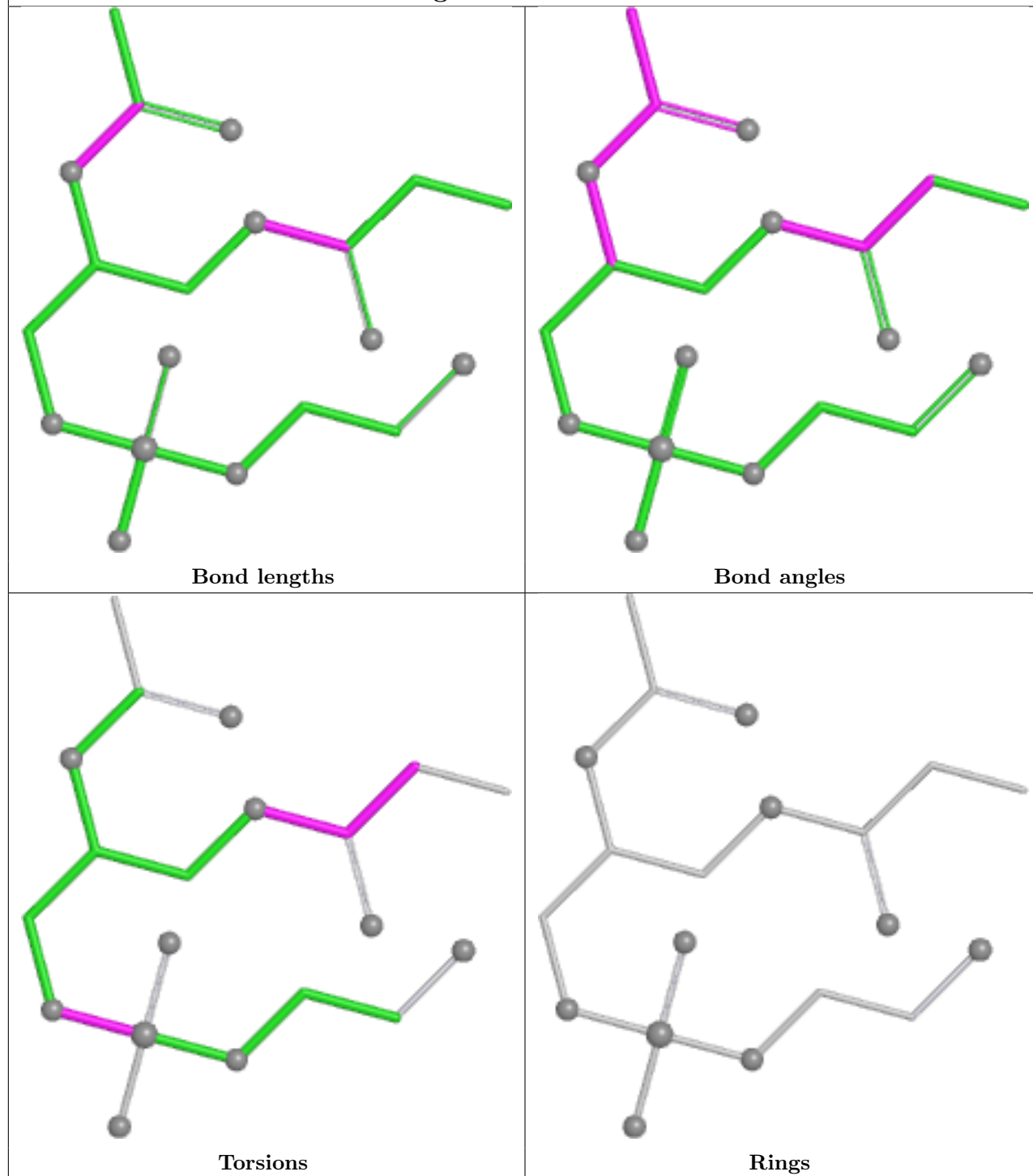
No monomer is involved in short contacts.

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

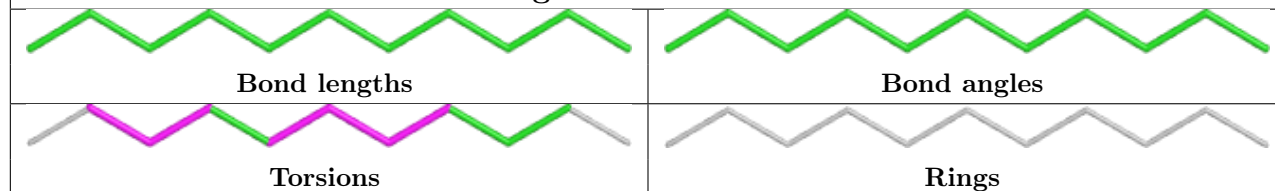
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

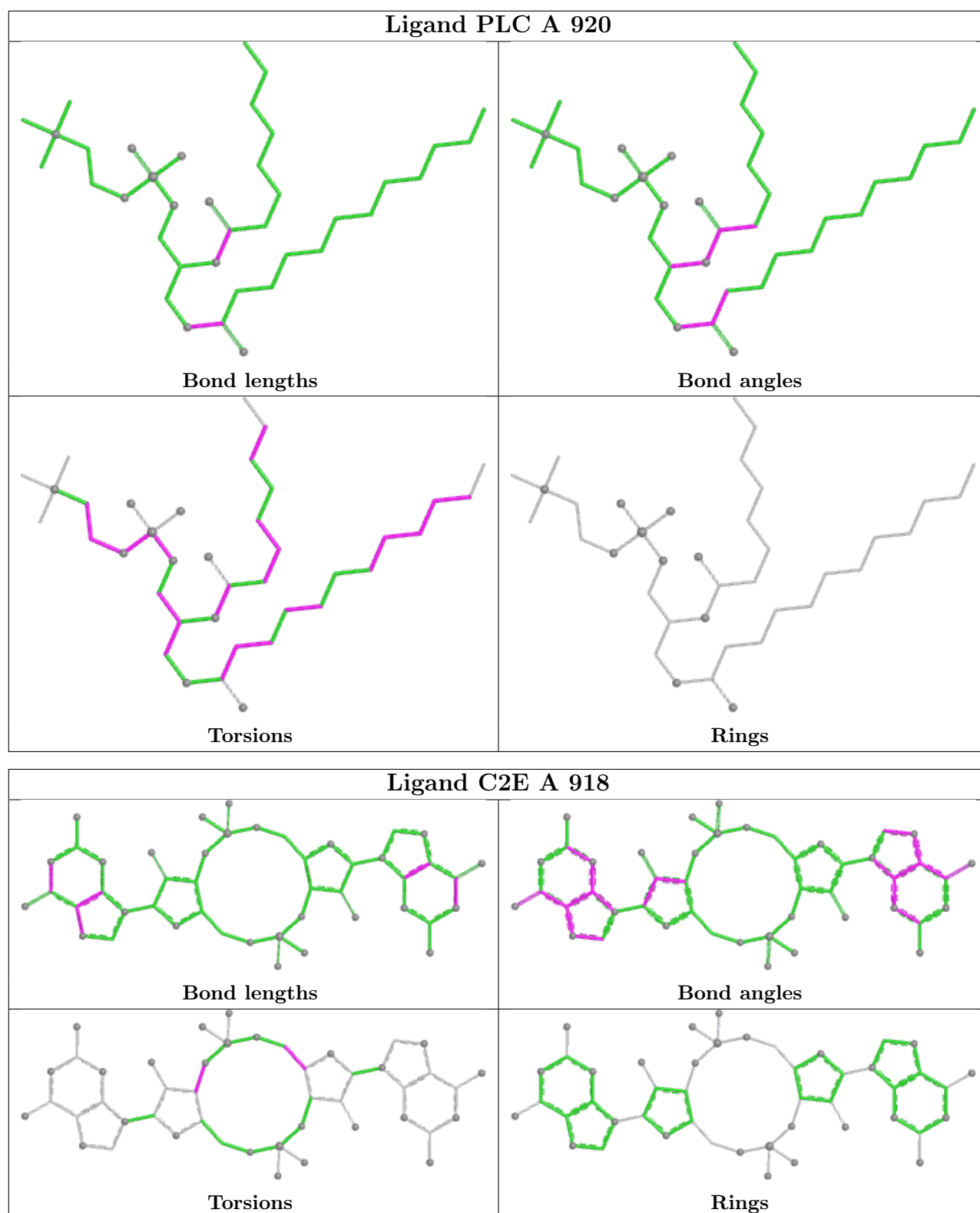


Ligand 3PE A 921



Ligand PLC B 804





Ligand PLC B 803	
 Bond lengths	 Bond angles
 Torsions	 Rings

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	728/803 (90%)	0.20	41 (5%) 30 24	43, 69, 112, 162	1 (0%)
2	B	655/724 (90%)	0.08	29 (4%) 39 31	43, 61, 103, 148	0
3	D	0/9	-	-	-	-
All	All	1383/1536 (90%)	0.14	70 (5%) 33 26	43, 66, 109, 162	1 (0%)

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	77	GLN	8.0
1	A	13	VAL	6.4
1	A	512	LEU	5.6
2	B	76	GLY	5.3
2	B	248	SER	5.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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

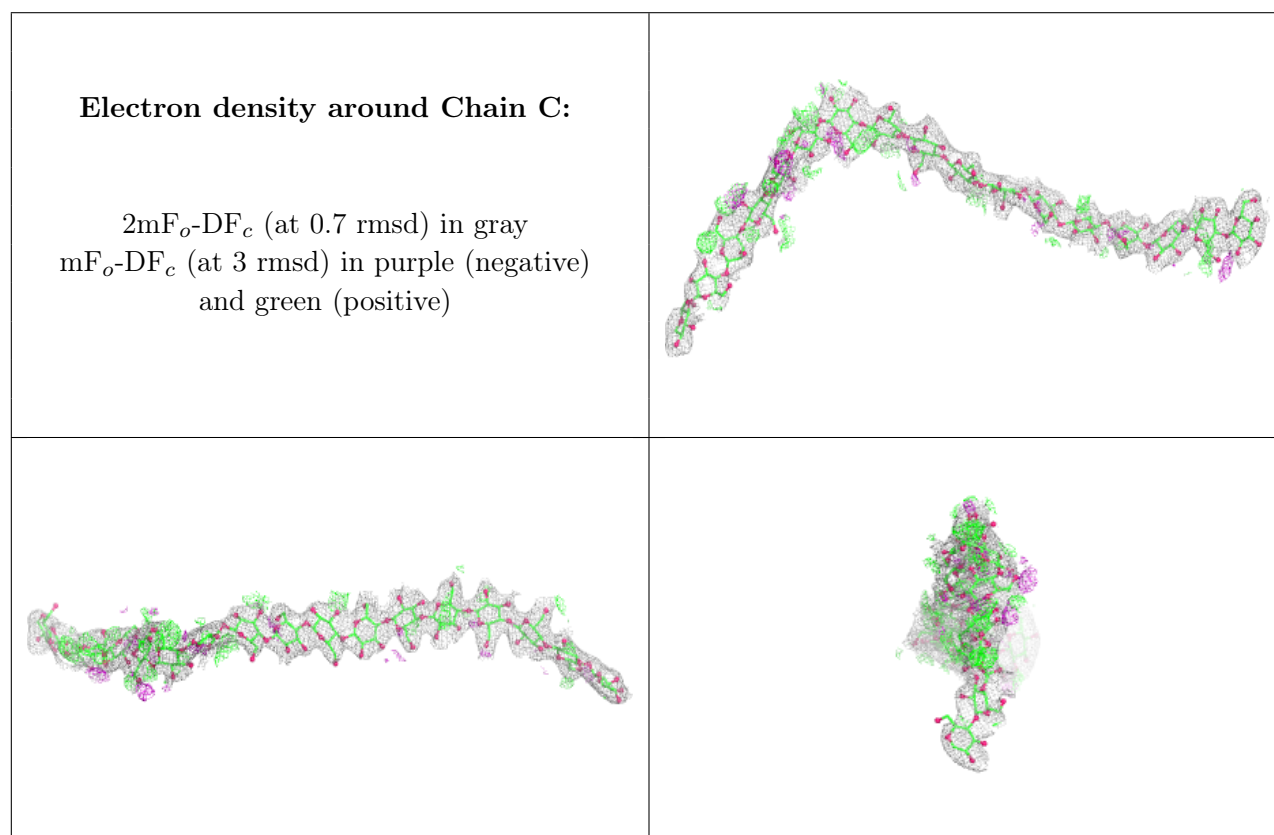
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BGC	C	1	11/12	-	-	106,136,161,167	0
4	BGC	C	2	11/12	-	-	107,118,143,154	0
4	BGC	C	3	11/12	-	-	66,93,110,122	0
4	BGC	C	4	11/12	-	-	45,56,132,152	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BGC	C	5	11/12	-	-	34,48,64,66	0
4	BGC	C	6	11/12	-	-	20,38,84,108	0
4	BGC	C	7	11/12	-	-	32,40,62,67	0
4	BGC	C	8	11/12	-	-	37,54,91,98	0
4	BGC	C	9	11/12	-	-	45,59,76,92	0
4	BGC	C	10	11/12	-	-	53,63,80,85	0
4	BGC	C	11	11/12	-	-	42,57,75,83	0
4	BGC	C	12	11/12	-	-	43,52,63,73	0
4	BGC	C	13	11/12	-	-	49,55,64,65	0
4	BGC	C	14	11/12	-	-	49,58,75,77	0
4	BGC	C	15	11/12	-	-	43,45,70,71	0
4	BGC	C	16	11/12	-	-	48,62,87,117	0
4	BGC	C	17	11/12	-	-	50,60,70,85	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,

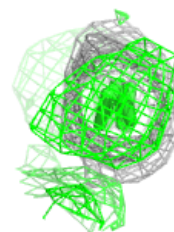
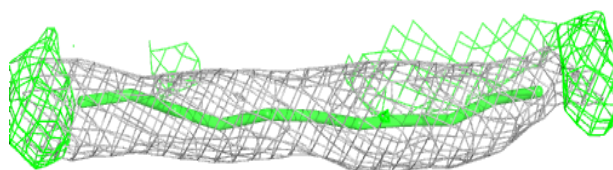
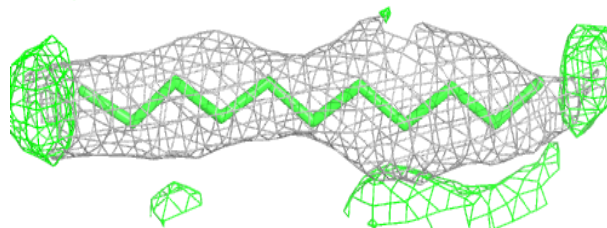
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	PLC	B	802	11/42	0.78	0.22	56,68,80,82	0
6	PLC	A	920	38/42	0.79	0.27	77,105,134,161	0
6	PLC	B	803	9/42	0.84	0.19	50,78,86,89	0
6	PLC	B	804	11/42	0.88	0.17	65,74,86,87	0
7	3PE	A	921	20/51	0.88	0.16	65,78,125,128	0
5	C2E	A	919	46/46	0.95	0.09	36,51,63,75	0
8	MG	B	801	1/1	0.96	0.09	38,38,38,38	0
5	C2E	A	918	46/46	0.97	0.09	37,46,58,65	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.

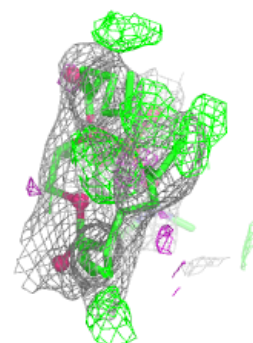
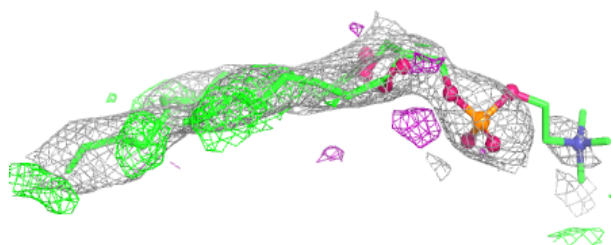
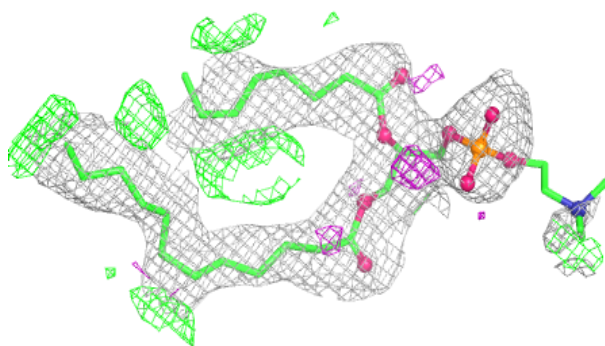
Electron density around PLC B 802:

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

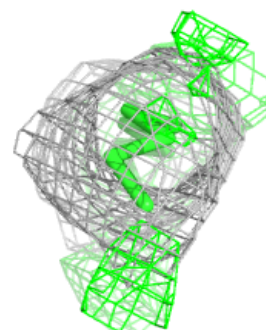
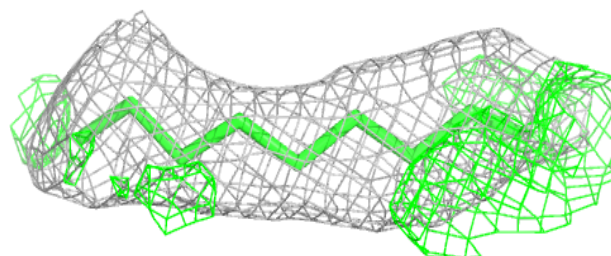
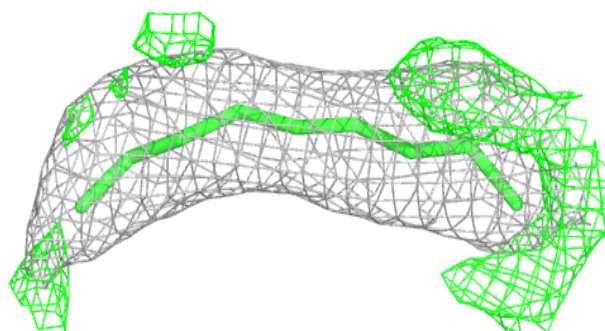


Electron density around PLC A 920:

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

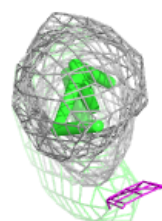
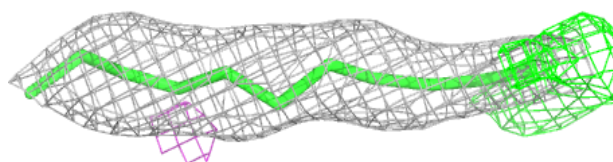
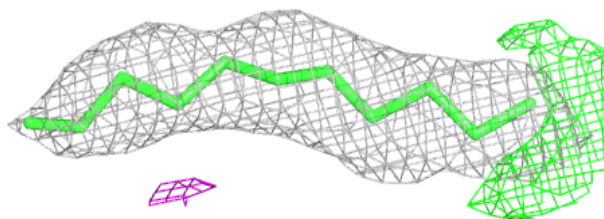
**Electron density around PLC B 803:**

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

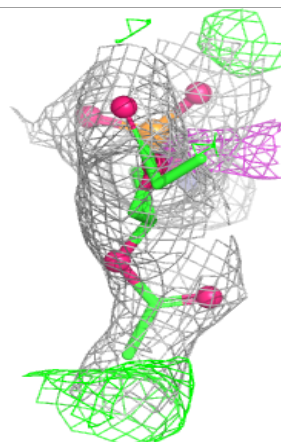
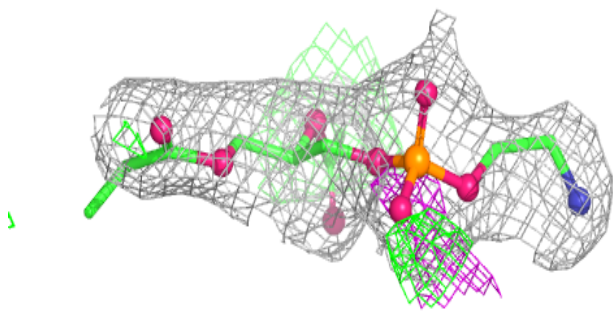
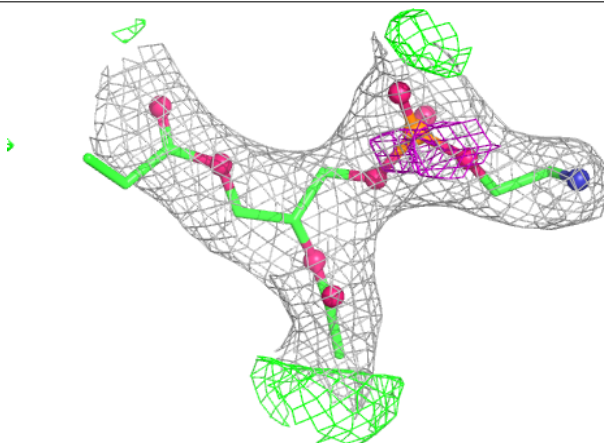


Electron density around PLC B 804:

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

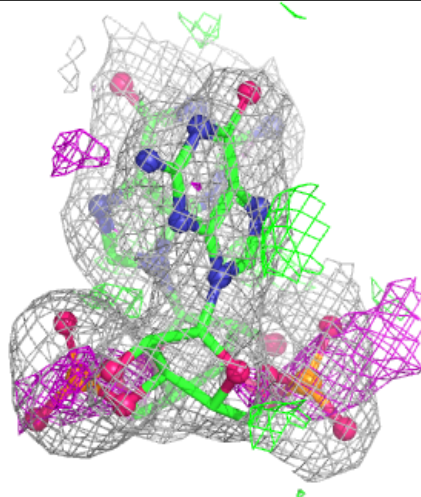
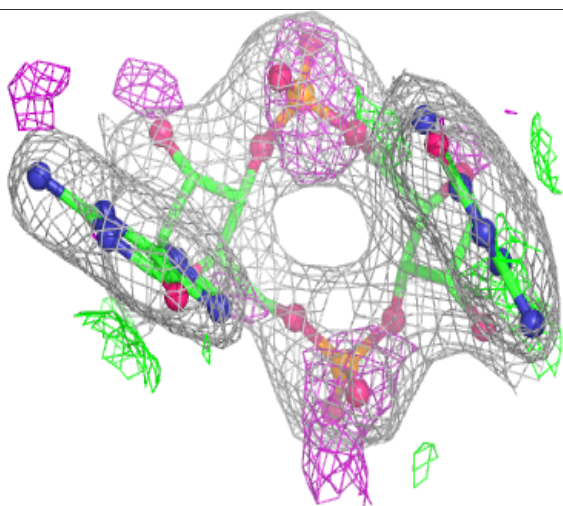
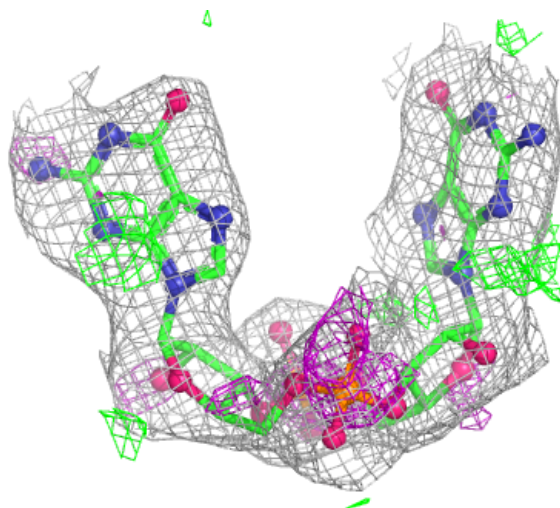
**Electron density around 3PE A 921:**

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



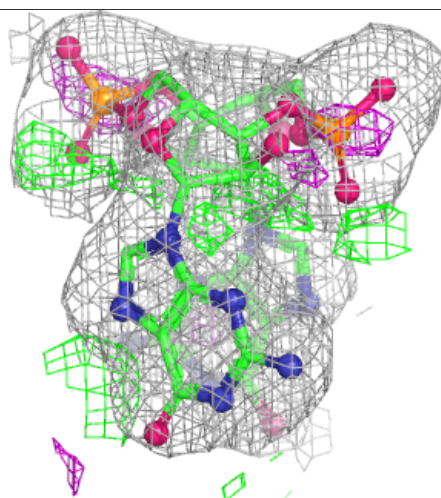
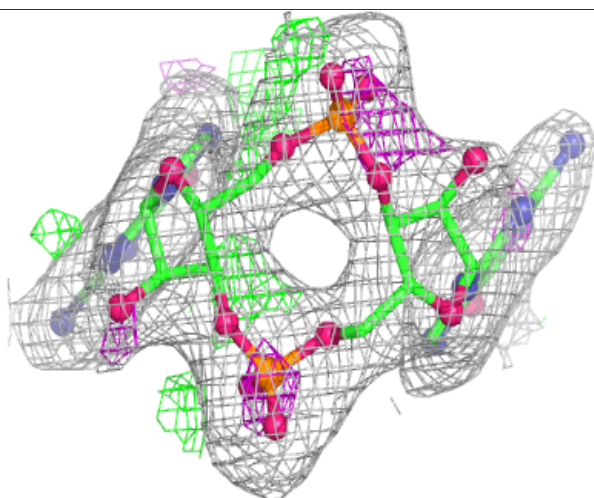
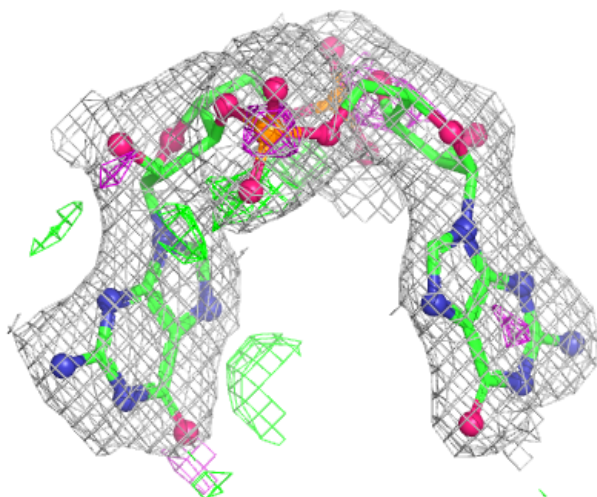
Electron density around C2E A 919:

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



Electron density around C2E A 918:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.