



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 07:05 PM BST

PDB ID : 5EIY  
Title : Bacterial cellulose synthase bound to a substrate analogue  
Authors : McNamara, J.T.; Zimmer, J.  
Deposited on : 2015-10-30  
Resolution : 2.95 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

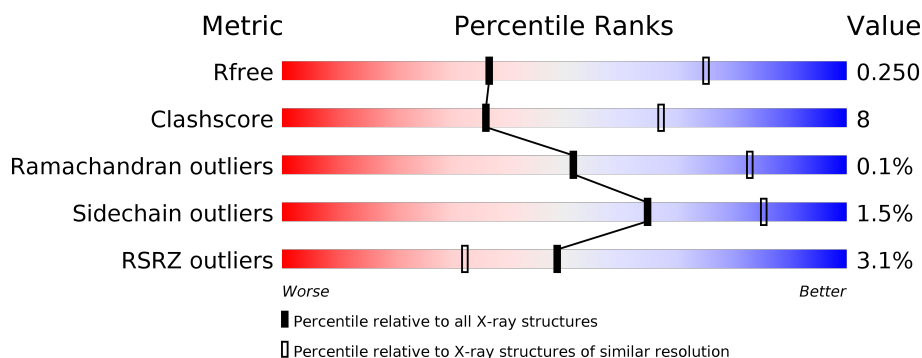
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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))
$R_{free}$	130704	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	803	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>17%</div> <div>9%</div> </div> </div>
2	B	729	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>12%</div> <div>10%</div> </div> </div>
3	D	9	<div> <div>100%</div> </div>
4	C	17	<div> <div>71%</div> <div>29%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	LDA	A	922	-	-	-	X

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 11144 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 Putative cellulose synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	0	0
			5734	3721	1000	982	31			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	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 Putative cellulose synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	658	Total	C	N	O	S	0	5	0
			4946	3134	878	918	16			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	MET	-	initiating methionine	UNP Q3J126
B	-2	LYS	-	expression tag	UNP Q3J126
B	-1	TYR	-	expression tag	UNP Q3J126
B	0	LEU	-	expression tag	UNP Q3J126
B	1	LEU	-	expression tag	UNP Q3J126
B	2	PRO	-	expression tag	UNP Q3J126
B	3	THR	-	expression tag	UNP Q3J126
B	4	ALA	-	expression tag	UNP Q3J126
B	5	ALA	-	expression tag	UNP Q3J126
B	6	ALA	-	expression tag	UNP Q3J126
B	7	GLY	-	expression tag	UNP Q3J126
B	8	LEU	-	expression tag	UNP Q3J126
B	9	LEU	-	expression tag	UNP Q3J126
B	10	LEU	-	expression tag	UNP Q3J126
B	11	LEU	-	expression tag	UNP Q3J126
B	12	ALA	-	expression tag	UNP Q3J126
B	13	ALA	-	expression tag	UNP Q3J126
B	14	GLN	-	expression tag	UNP Q3J126
B	15	PRO	-	expression tag	UNP Q3J126
B	16	ALA	-	expression tag	UNP Q3J126
B	17	MET	-	expression tag	UNP Q3J126
B	18	ALA	-	expression tag	UNP Q3J126
B	19	MET	-	expression tag	UNP Q3J126
B	20	GLY	-	expression tag	UNP Q3J126

- Molecule 3 is a protein called poly(unk).

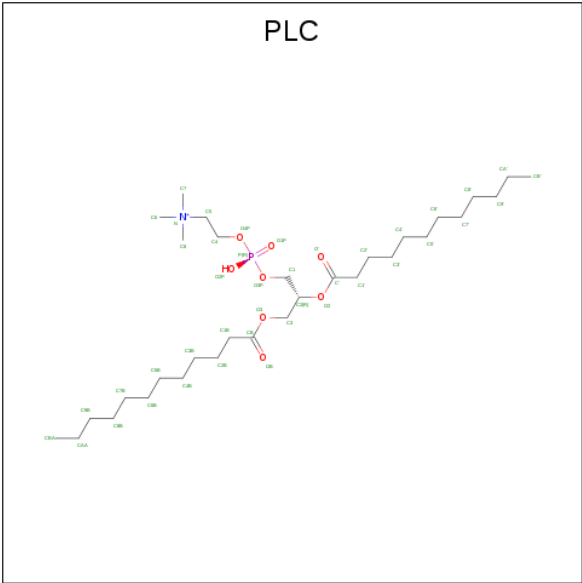
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	9	Total	C	N	O	0	0	0
			45	27	9	9			

- [illegible]



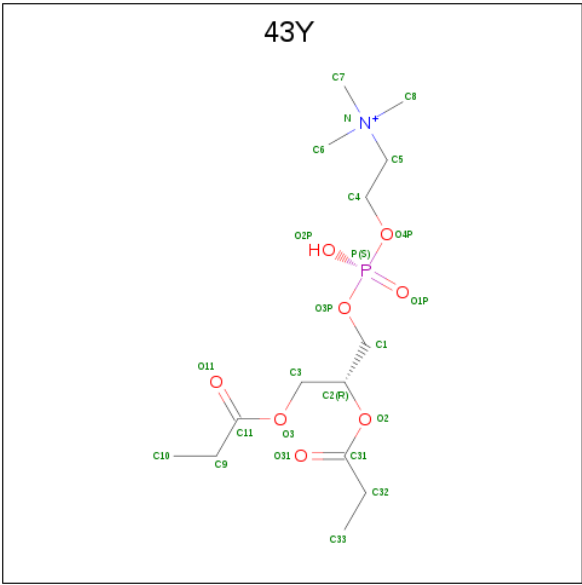
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	C	17	Total	C	O	0	0	0
			188	102	86			

- Molecule 5 is DIUNDECYL PHOSPHATIDYL CHOLINE (three-letter code: PLC) (formula: C<sub>32</sub>H<sub>65</sub>NO<sub>8</sub>P).



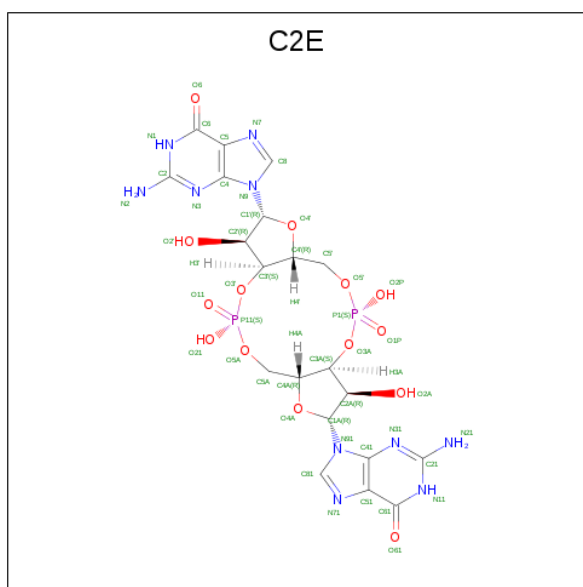
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			38	28	1	8	1		

- Molecule 6 is [(2R)-3-[oxidanyl-[2-(trimethyl- $\text{l}^{\{4\}}$ -azanyl)ethoxy]phosphoryl]oxy-2-propa noyloxy-propyl] propanoate (three-letter code: 43Y) (formula: C<sub>14</sub>H<sub>29</sub>NO<sub>8</sub>P).



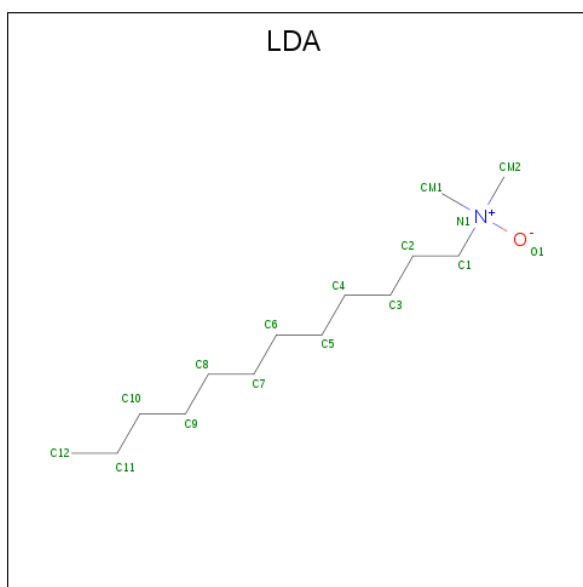
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			20	10	1	8	1		

- Molecule 7 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) (three-letter code: C2E) (formula:  $C_{20}H_{24}N_{10}O_{14}P_2$ ).



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

- Molecule 8 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:  $C_{14}H_{31}NO$ ).



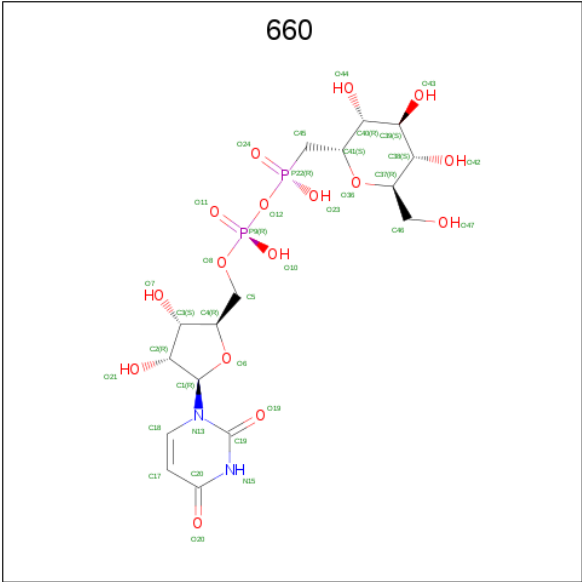
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			16	14	1	1		
8	A	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Mg	0	0
			1	1		
9	A	1	Total	Mg	0	0
			1	1		

- Molecule 10 is [[(2 {R},3 {S},4 {R},5 {R})-5-[2,4-bis(oxidanylidene)pyrimidin-1-yl]-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]oxy-[[2 {S},3 {R},4 {S},5 {S},6 {R})-6-(hydroxymethyl)-3,4,5-tris(oxidanyl)oxan-2-yl]methyl]phosphinic acid (three-letter code: 660) (formula: C<sub>16</sub>H<sub>26</sub>N<sub>2</sub>O<sub>16</sub>P<sub>2</sub>).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	N	O	P	0	0
			36	16	2	16	2		

- Molecule 11 is water.

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





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.47Å 216.65Å 221.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.92 – 2.95 34.92 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.92-2.95) 99.8 (34.92-2.95)	Depositor EDS
$R_{merge}$	0.28	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.73 (at 2.95Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.222 , 0.248 0.225 , 0.250	Depositor DCC
$R_{free}$ test set	3482 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	75.5	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 49.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.006 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	11144	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: MG, BGC, 43Y, LDA, 660, GAL, PLC, C2E

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	0.25	0/5880	0.45	1/7997 (0.0%)
2	B	0.22	0/5065	0.45	1/6945 (0.0%)
All	All	0.24	0/10945	0.45	2/14942 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	3
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	189	SER	CB-CA-C	5.50	120.54	110.10
2	B	74	LEU	O-C-N	-5.19	114.40	122.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	135	GLN	Peptide
2	B	643	ARG	Sidechain
2	B	74	LEU	Mainchain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5734	0	5846	112	0
2	B	4946	0	5023	66	0
3	D	45	0	12	0	0
4	C	188	0	155	7	0
5	A	38	0	53	0	0
6	A	20	0	15	1	0
7	A	92	0	41	5	0
8	A	32	0	62	2	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	36	0	0	2	0
11	A	11	0	0	0	0
All	All	11144	0	11207	178	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 8.

The worst 5 of 178 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)
7:A:921:C2E:O4'	7:A:921:C2E:C4'	1.64	1.21
7:A:920:C2E:O4'	7:A:920:C2E:C4'	1.64	1.20
1:A:134:LEU:O	1:A:134:LEU:HD12	1.58	1.04
2:B:140:LEU:HB3	2:B:144:VAL:HG11	1.42	1.00
2:B:643:ARG:HD3	2:B:643:ARG:N	1.82	0.94

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	726/803 (90%)	700 (96%)	25 (3%)	1 (0%)	51	83
2	B	659/729 (90%)	646 (98%)	13 (2%)	0	100	100
All	All	1385/1532 (90%)	1346 (97%)	38 (3%)	1 (0%)	51	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	189	SER

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	598/661 (90%)	590 (99%)	8 (1%)	69	87
2	B	525/573 (92%)	516 (98%)	9 (2%)	60	83
All	All	1123/1234 (91%)	1106 (98%)	17 (2%)	65	85

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	617	LEU
2	B	86	PHE
2	B	477	ASP
1	A	615	VAL
2	B	597	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

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	12,12,12	2.11	3 (25%)	17,17,17	1.68	4 (23%)
4	BGC	C	10	4	11,11,12	2.60	2 (18%)	15,15,17	1.92	4 (26%)
4	BGC	C	11	4	11,11,12	2.63	3 (27%)	15,15,17	1.23	2 (13%)
4	BGC	C	12	4	11,11,12	2.68	3 (27%)	15,15,17	1.23	2 (13%)
4	BGC	C	13	4	11,11,12	2.55	2 (18%)	15,15,17	1.38	2 (13%)
4	BGC	C	14	4	11,11,12	2.62	3 (27%)	15,15,17	1.97	2 (13%)
4	BGC	C	15	4	11,11,12	2.62	4 (36%)	15,15,17	1.39	2 (13%)
4	BGC	C	16	4	11,11,12	2.72	3 (27%)	15,15,17	1.85	4 (26%)
4	GAL	C	17	4	11,11,12	0.58	0	15,15,17	0.90	0
4	BGC	C	2	4	11,11,12	2.62	4 (36%)	15,15,17	1.84	4 (26%)
4	BGC	C	3	4	11,11,12	2.66	2 (18%)	15,15,17	2.31	5 (33%)
4	BGC	C	4	4	11,11,12	2.70	5 (45%)	15,15,17	2.14	5 (33%)
4	BGC	C	5	4	11,11,12	2.55	3 (27%)	15,15,17	2.14	4 (26%)
4	BGC	C	6	4	11,11,12	2.93	5 (45%)	15,15,17	1.01	1 (6%)
4	BGC	C	7	4	11,11,12	2.66	4 (36%)	15,15,17	1.35	2 (13%)
4	BGC	C	8	4	11,11,12	2.52	4 (36%)	15,15,17	1.95	5 (33%)
4	BGC	C	9	4	11,11,12	2.61	1 (9%)	15,15,17	1.58	1 (6%)

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	-	2/2/22/22	0/1/1/1
4	BGC	C	10	4	-	1/2/19/22	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	-	1/2/19/22	0/1/1/1
4	BGC	C	14	4	-	0/2/19/22	0/1/1/1
4	BGC	C	15	4	-	2/2/19/22	0/1/1/1
4	BGC	C	16	4	-	2/2/19/22	0/1/1/1
4	GAL	C	17	4	-	2/2/19/22	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	-	0/2/19/22	0/1/1/1
4	BGC	C	6	4	-	1/2/19/22	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	-	0/2/19/22	0/1/1/1

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	6	BGC	O5-C1	8.00	1.56	1.43
4	C	12	BGC	O5-C1	7.34	1.55	1.43
4	C	7	BGC	O5-C1	7.34	1.55	1.43
4	C	3	BGC	O5-C1	7.30	1.55	1.43
4	C	11	BGC	O5-C1	7.27	1.55	1.43

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	14	BGC	C1-C2-C3	6.19	117.28	109.67
4	C	5	BGC	C1-C2-C3	5.58	116.52	109.67
4	C	3	BGC	C1-C2-C3	5.22	116.08	109.67
4	C	10	BGC	C1-C2-C3	5.02	115.84	109.67
4	C	4	BGC	C2-C3-C4	4.78	119.17	110.89

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	16	BGC	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	C	4	BGC	O5-C5-C6-O6
4	C	7	BGC	O5-C5-C6-O6
4	C	2	BGC	O5-C5-C6-O6
4	C	16	BGC	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	5	BGC	1	0
4	C	14	BGC	1	0
4	C	17	GAL	1	0
4	C	6	BGC	3	0
4	C	4	BGC	1	0
4	C	10	BGC	1	0

## 5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 2 are 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
7	C2E	A	921	-	44,52,52	5.10	29 (65%)	54,82,82	2.49	16 (29%)
8	LDA	A	922	-	12,15,15	2.10	1 (8%)	14,17,17	0.45	0
8	LDA	A	923	-	12,15,15	2.09	1 (8%)	14,17,17	0.58	0
10	660	A	925	-	32,38,38	3.07	11 (34%)	37,58,58	1.21	5 (13%)
7	C2E	A	920	-	44,52,52	5.11	29 (65%)	54,82,82	2.48	16 (29%)
6	43Y	A	902	-	19,19,23	1.36	3 (15%)	22,24,31	1.48	2 (9%)
5	PLC	A	901	-	37,37,41	1.11	4 (10%)	43,45,49	1.03	2 (4%)

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	C2E	A	921	-	-	3/22/62/62	0/6/7/7
8	LDA	A	922	-	-	5/13/13/13	-
8	LDA	A	923	-	-	8/13/13/13	-
10	660	A	925	-	-	9/18/59/59	0/3/3/3
7	C2E	A	920	-	-	7/22/62/62	0/6/7/7
6	43Y	A	902	-	-	6/22/22/27	-
5	PLC	A	901	-	-	23/41/41/45	-

The worst 5 of 78 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	920	C2E	C2A-C3A	-13.85	1.22	1.52
7	A	921	C2E	C2A-C3A	-13.76	1.22	1.52
10	A	925	660	C18-N13	10.70	1.49	1.35
7	A	921	C2E	C3'-C4'	-9.87	1.26	1.52
7	A	920	C2E	C3'-C4'	-9.69	1.26	1.52

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	921	C2E	C1'-N9-C4	-11.14	107.07	126.64
7	A	920	C2E	C1'-N9-C4	-10.87	107.54	126.64
7	A	921	C2E	C1A-N91-C41	-5.31	117.31	126.64
7	A	920	C2E	N3-C2-N1	-5.26	120.20	127.22
7	A	920	C2E	N31-C21-N11	-5.25	120.22	127.22

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

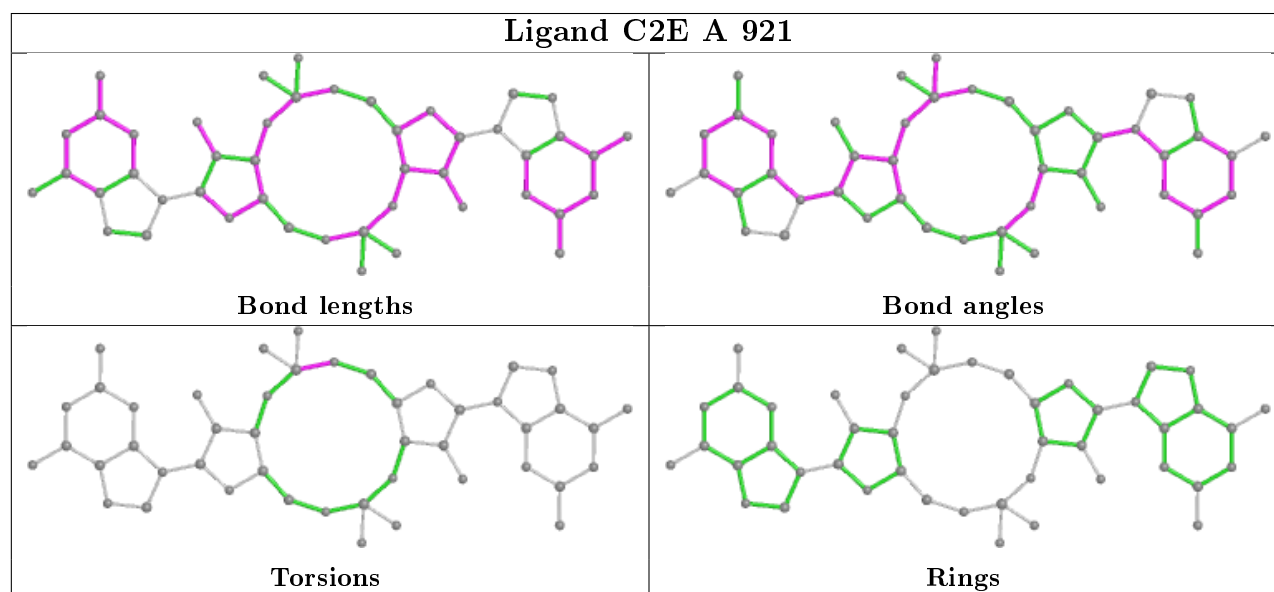
Mol	Chain	Res	Type	Atoms
7	A	921	C2E	C5A-O5A-P11-O11
10	A	925	660	C2-C1-N13-C18
10	A	925	660	O6-C1-N13-C18
10	A	925	660	C41-C45-P22-O12
10	A	925	660	C41-C45-P22-O23

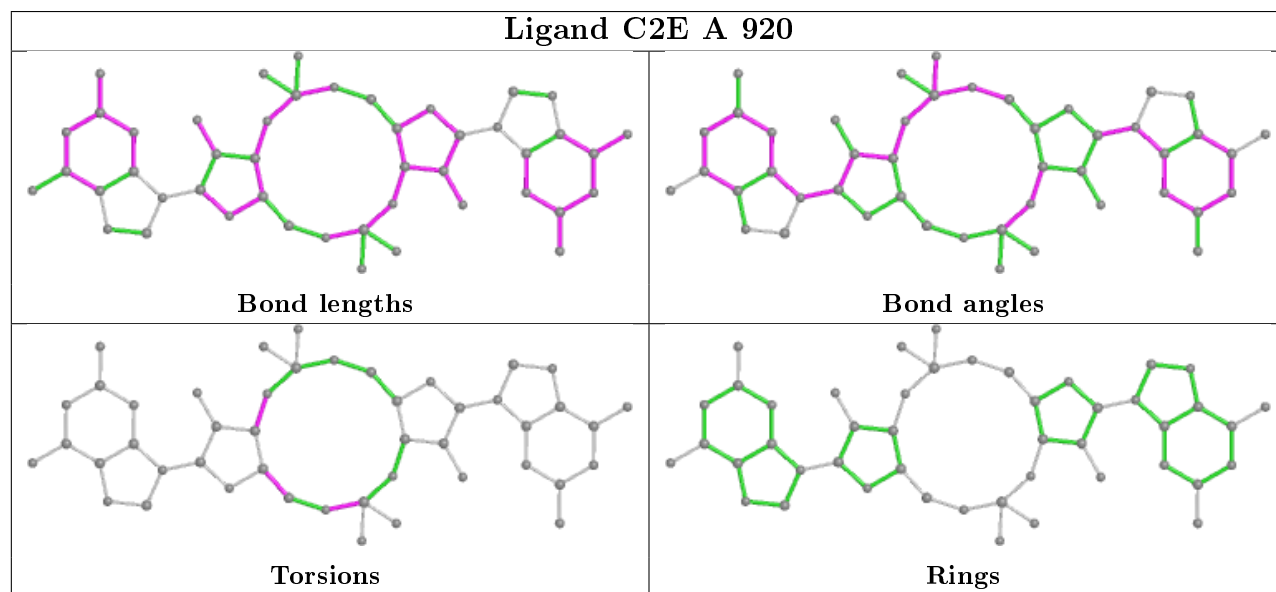
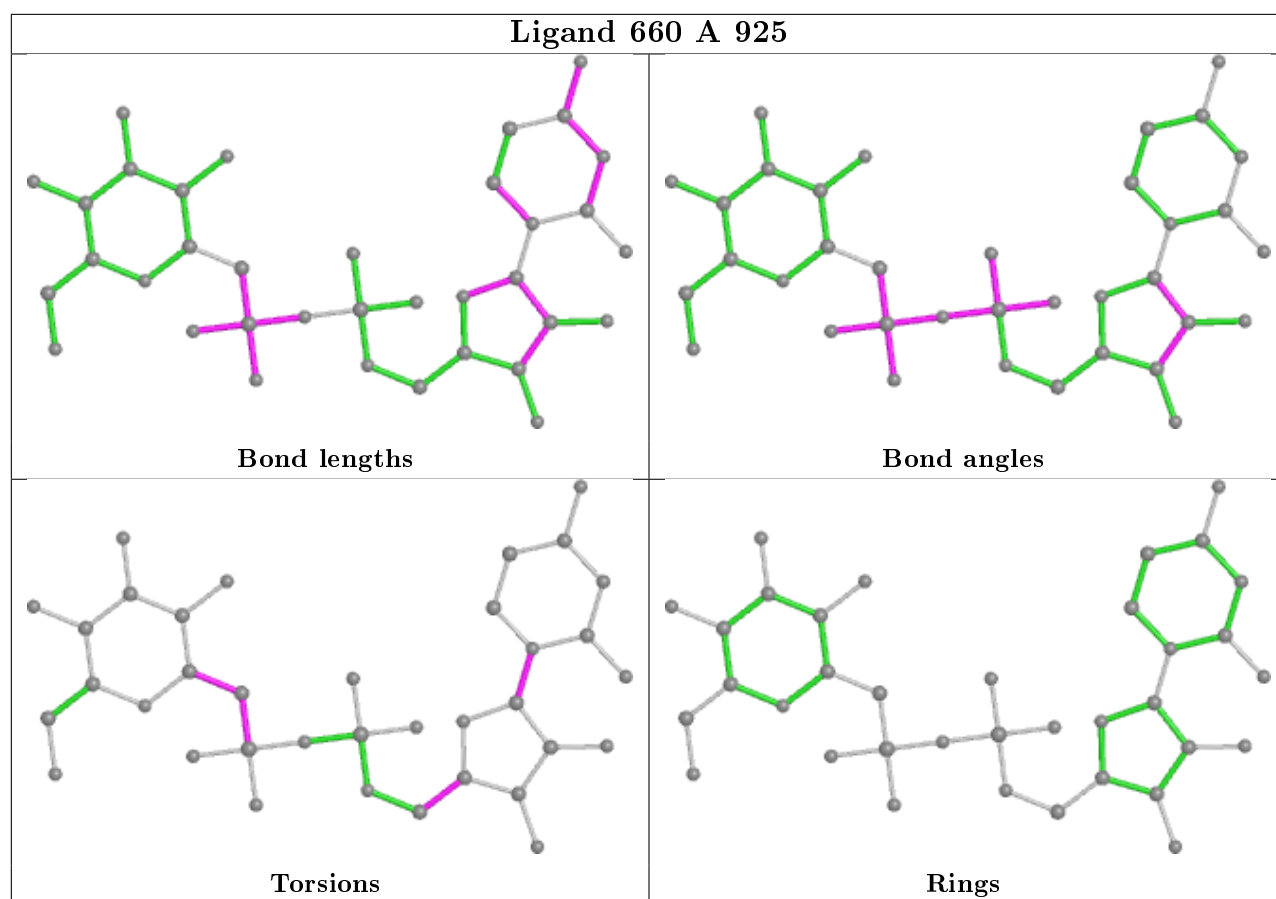
There are no ring outliers.

5 monomers are involved in 10 short contacts:

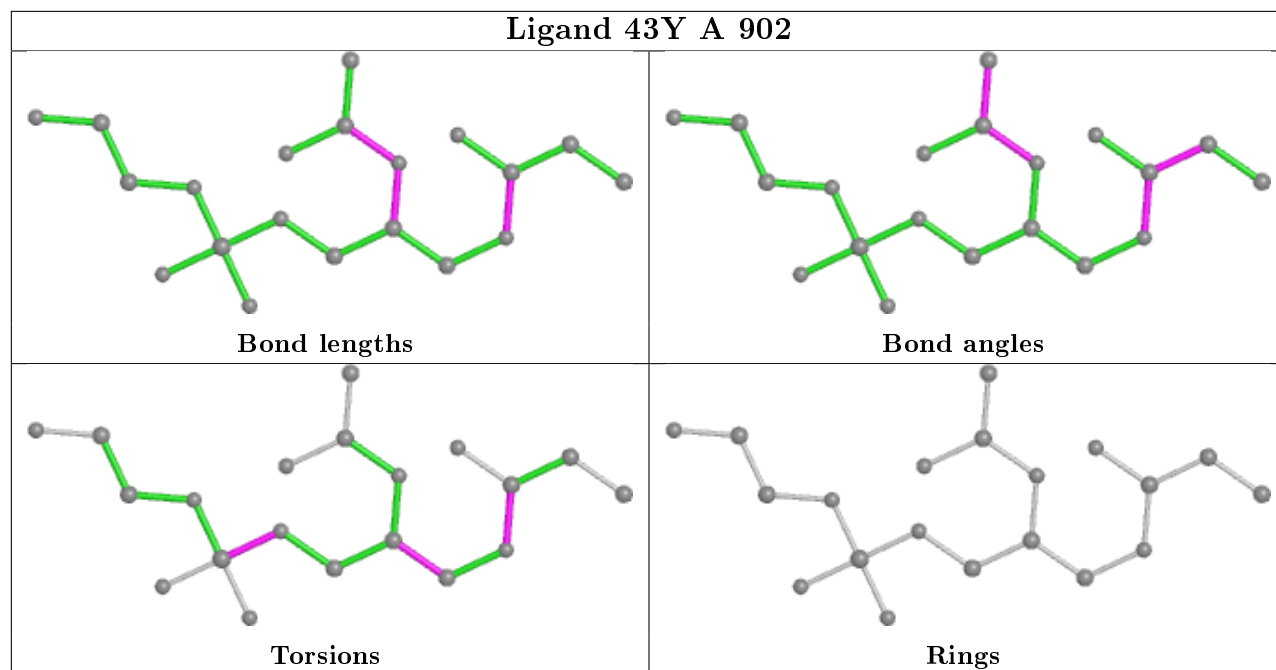
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	921	C2E	4	0
8	A	923	LDA	2	0
10	A	925	660	2	0
7	A	920	C2E	2	0
6	A	902	43Y	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

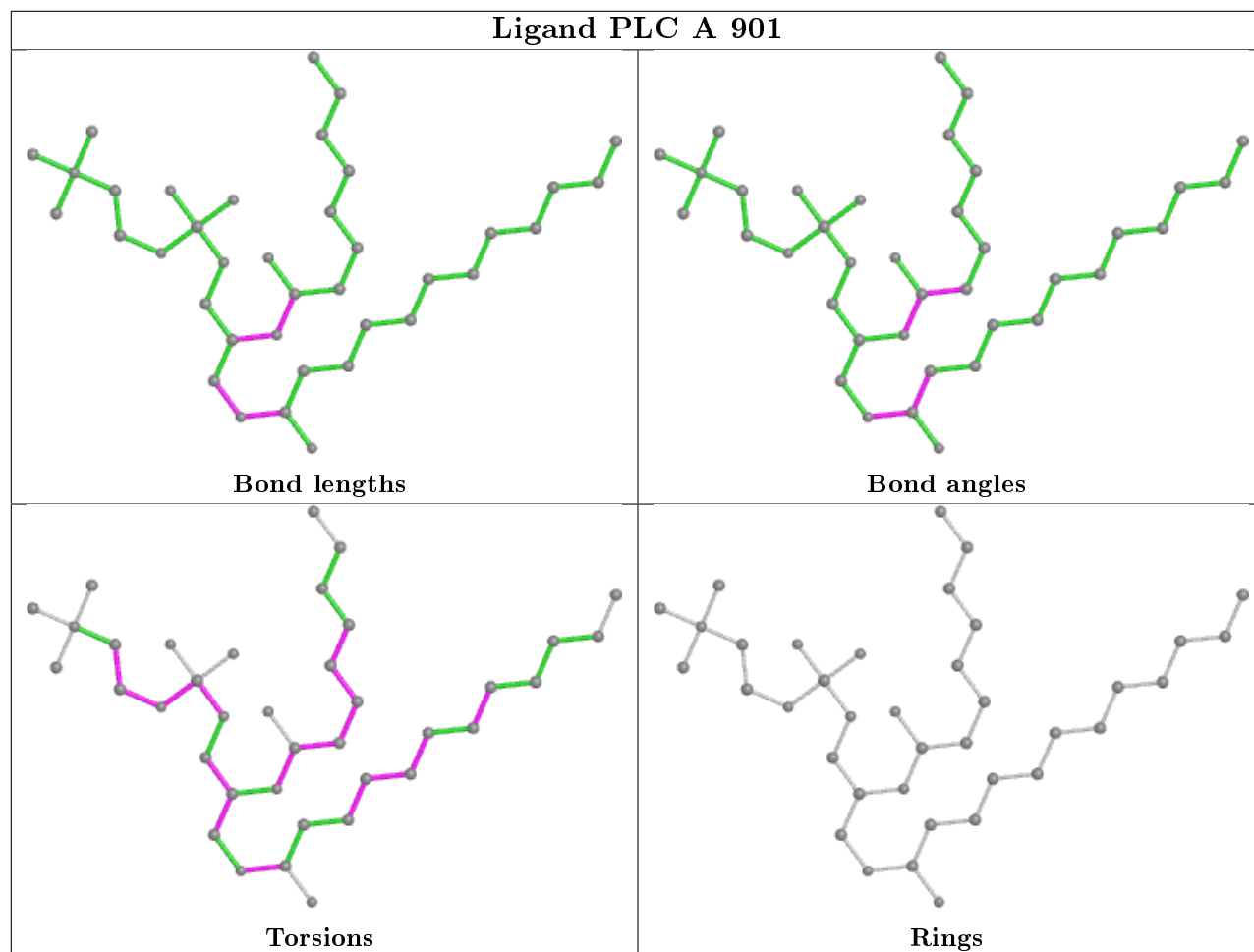




## Ligand 43Y A 902



## Ligand PLC A 901



## 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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	728/803 (90%)	0.06	28 (3%) 40 26	47, 80, 140, 234	0
2	B	658/729 (90%)	-0.09	15 (2%) 60 43	47, 74, 123, 188	0
3	D	0/9	-	-	-	-
All	All	1386/1541 (89%)	-0.01	43 (3%) 49 32	47, 77, 132, 234	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	502	ARG	5.5
1	A	496	LEU	5.0
2	B	77[A]	GLN	4.8
1	A	509	ASP	3.9
1	A	318	CYS	3.8

### 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	BGC	C	1	12/12	0.73	0.34	161,171,185,205	0
4	BGC	C	2	11/12	0.83	0.25	105,120,134,148	0
4	BGC	C	6	11/12	0.88	0.19	53,63,85,108	0
4	BGC	C	7	11/12	0.90	0.17	49,65,72,81	0

*Continued on next page...*



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	BGC	C	3	11/12	0.90	0.20	92,109,121,126	0
4	BGC	C	8	11/12	0.93	0.21	72,76,97,117	0
4	BGC	C	5	11/12	0.93	0.18	49,55,64,105	0
4	BGC	C	14	11/12	0.94	0.28	65,81,86,87	0
4	BGC	C	4	11/12	0.94	0.19	56,69,114,142	0
4	BGC	C	13	11/12	0.95	0.30	63,80,85,85	0
4	BGC	C	11	11/12	0.96	0.20	82,89,93,95	0
4	BGC	C	12	11/12	0.96	0.23	63,73,83,87	0
4	GAL	C	17	11/12	0.96	0.33	65,80,96,98	0
4	BGC	C	10	11/12	0.96	0.23	71,77,92,98	0
4	BGC	C	9	11/12	0.97	0.20	69,74,79,88	0
4	BGC	C	16	11/12	0.97	0.30	59,69,86,93	0
4	BGC	C	15	11/12	0.97	0.26	59,68,73,73	0

## 6.4 Ligands ⓘ

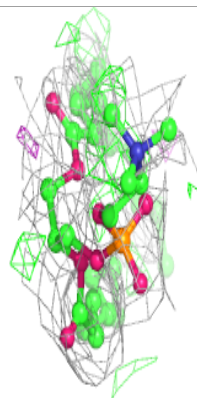
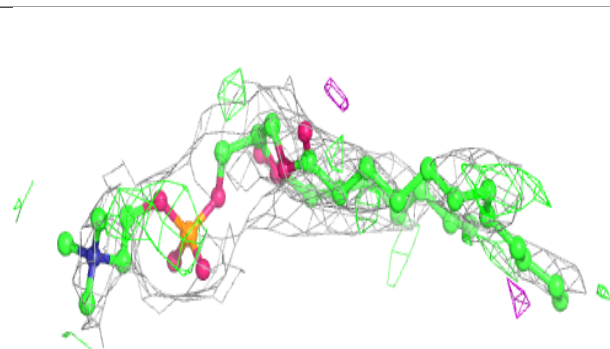
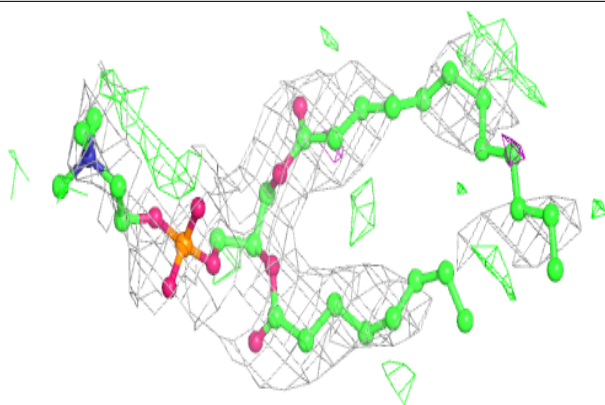
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
8	LDA	A	922	16/16	0.61	0.48	52,67,83,85	16
8	LDA	A	923	16/16	0.62	0.28	76,91,111,119	16
9	MG	B	801	1/1	0.73	0.19	54,54,54,54	0
5	PLC	A	901	38/42	0.82	0.42	106,129,151,152	0
9	MG	A	924	1/1	0.88	1.45	83,83,83,83	0
10	660	A	925	36/36	0.92	0.33	67,78,89,95	36
6	43Y	A	902	20/24	0.93	0.27	88,105,122,129	0
7	C2E	A	921	46/46	0.95	0.12	53,76,86,95	0
7	C2E	A	920	46/46	0.96	0.13	51,67,82,82	0

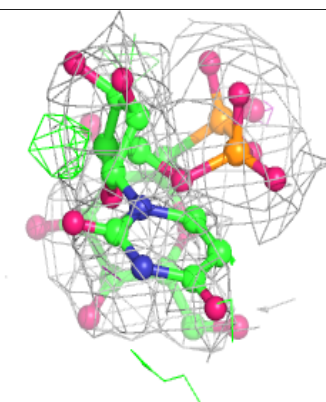
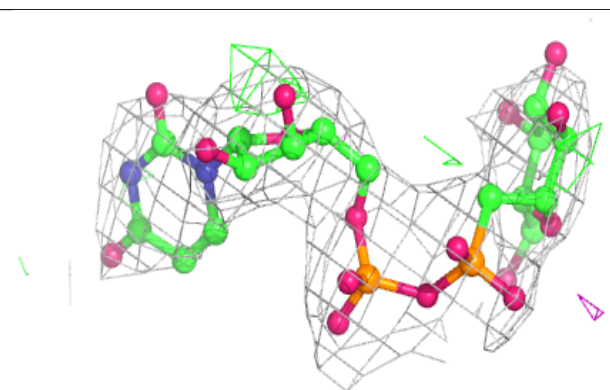
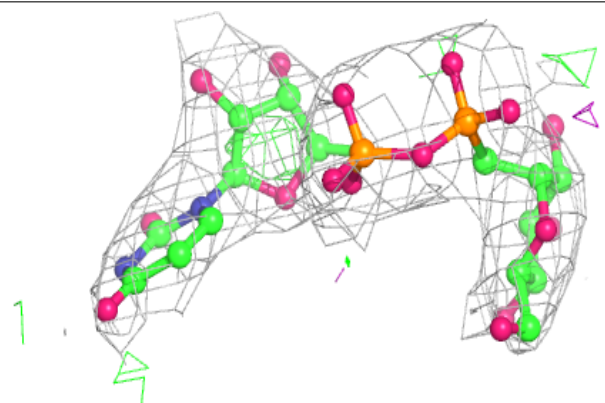
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around PLC A 901:**

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

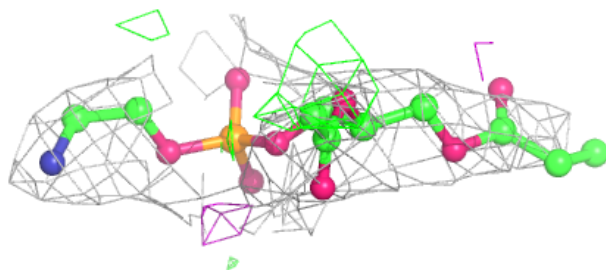
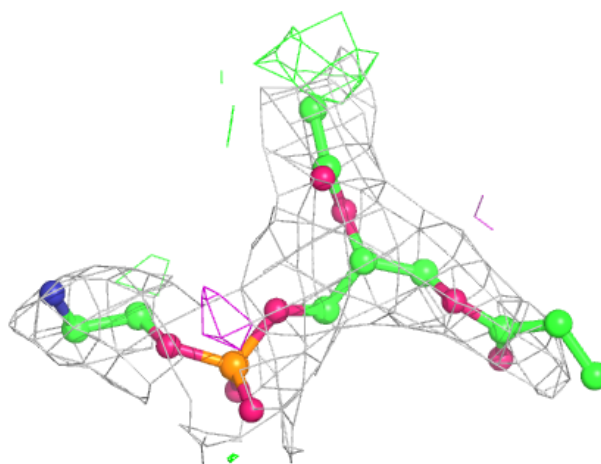
**Electron density around 660 A 925:**

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



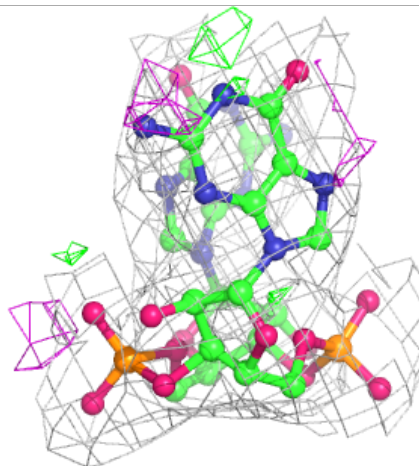
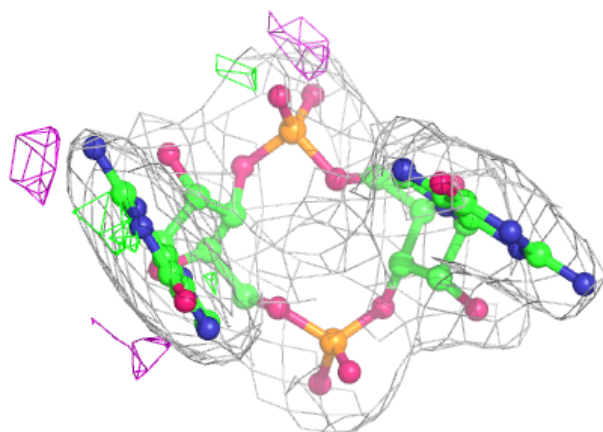
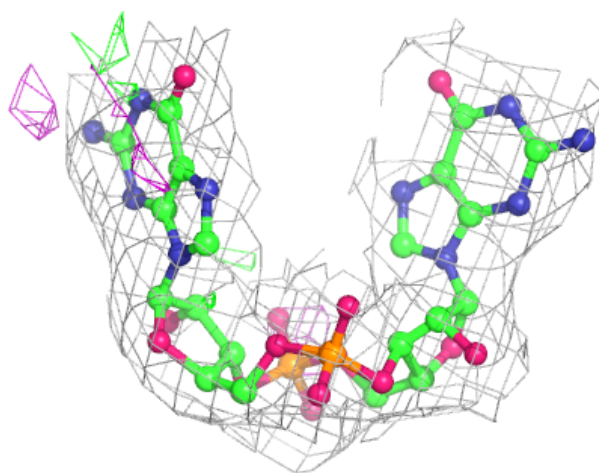
**Electron density around 43Y A 902:**

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



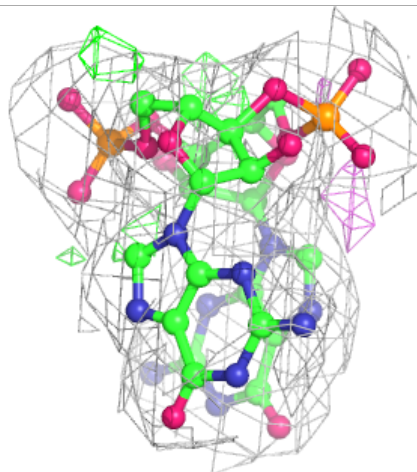
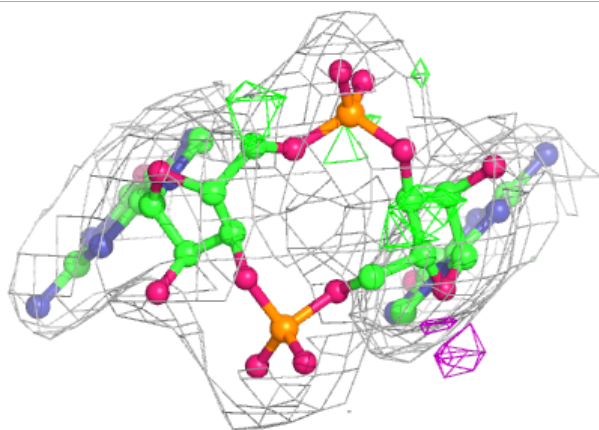
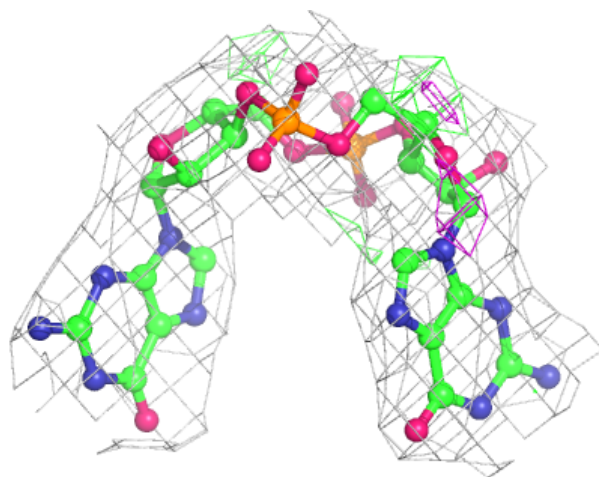
**Electron density around C2E A 921:**

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



**Electron density around C2E A 920:**

$2mF_o-DF_c$  (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.