Full wwPDB X-ray Structure Validation Report ⓘ

Nov 29, 2021 – 02:21 PM JST

PDB ID	:	7DRJ
Title	:	Crystal structure of phosphatidylglycerol phosphate synthase in complex with phosphatidylglycerol phosphate
Authors	:	Yang, B.W.; Liu, Z.F.
Deposited on	:	2020-12-28
Resolution	:	2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see references ⓘ) were used in the production of this report:

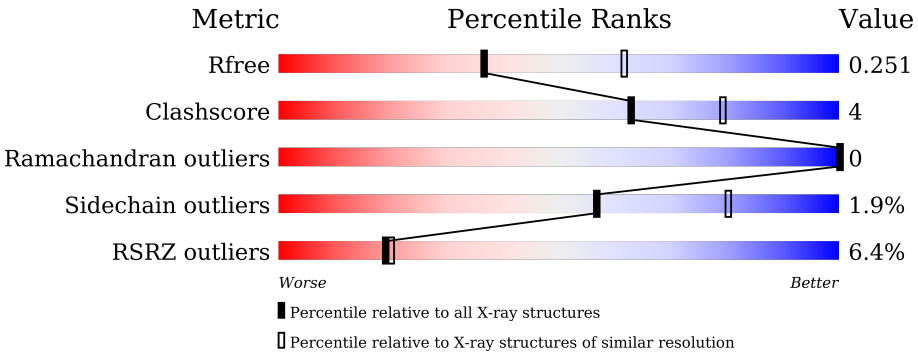
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	212	5% 79% 10% 10%
1	B	212	6% 76% 10% • 12%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 3348 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 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1468	988	229	248	3			
1	B	186	Total	C	N	O	S	0	0	0
			1431	962	224	243	2			

There are 40 discrepancies between the modelled and reference sequences:

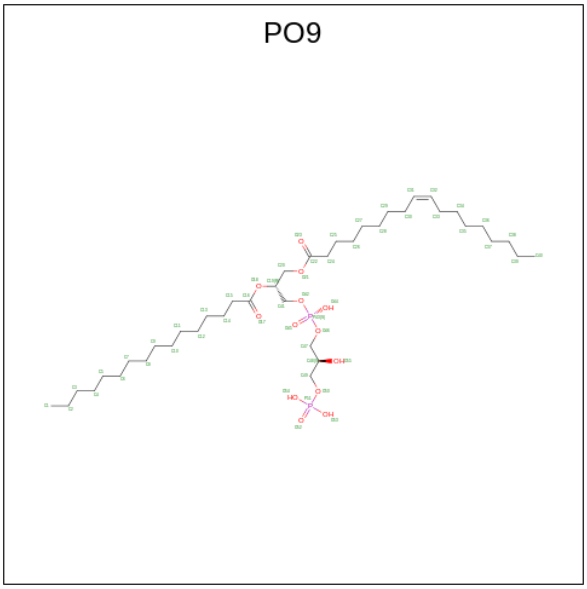
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P63756
A	-18	GLY	-	expression tag	UNP P63756
A	-17	SER	-	expression tag	UNP P63756
A	-16	SER	-	expression tag	UNP P63756
A	-15	HIS	-	expression tag	UNP P63756
A	-14	HIS	-	expression tag	UNP P63756
A	-13	HIS	-	expression tag	UNP P63756
A	-12	HIS	-	expression tag	UNP P63756
A	-11	HIS	-	expression tag	UNP P63756
A	-10	HIS	-	expression tag	UNP P63756
A	-9	SER	-	expression tag	UNP P63756
A	-8	SER	-	expression tag	UNP P63756
A	-7	GLY	-	expression tag	UNP P63756
A	-6	LEU	-	expression tag	UNP P63756
A	-5	VAL	-	expression tag	UNP P63756
A	-4	PRO	-	expression tag	UNP P63756
A	-3	ARG	-	expression tag	UNP P63756
A	-2	GLY	-	expression tag	UNP P63756
A	-1	SER	-	expression tag	UNP P63756
A	0	HIS	-	expression tag	UNP P63756
B	-19	MET	-	initiating methionine	UNP P63756
B	-18	GLY	-	expression tag	UNP P63756
B	-17	SER	-	expression tag	UNP P63756
B	-16	SER	-	expression tag	UNP P63756

Continued on next page...

Continued from previous page...

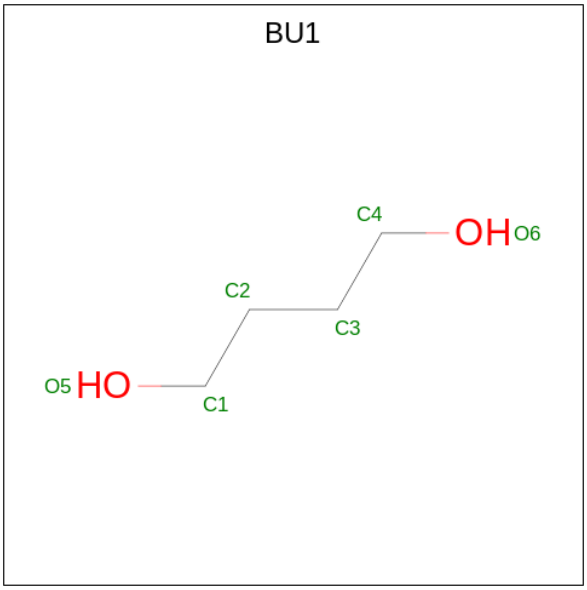
Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	expression tag	UNP P63756
B	-14	HIS	-	expression tag	UNP P63756
B	-13	HIS	-	expression tag	UNP P63756
B	-12	HIS	-	expression tag	UNP P63756
B	-11	HIS	-	expression tag	UNP P63756
B	-10	HIS	-	expression tag	UNP P63756
B	-9	SER	-	expression tag	UNP P63756
B	-8	SER	-	expression tag	UNP P63756
B	-7	GLY	-	expression tag	UNP P63756
B	-6	LEU	-	expression tag	UNP P63756
B	-5	VAL	-	expression tag	UNP P63756
B	-4	PRO	-	expression tag	UNP P63756
B	-3	ARG	-	expression tag	UNP P63756
B	-2	GLY	-	expression tag	UNP P63756
B	-1	SER	-	expression tag	UNP P63756
B	0	HIS	-	expression tag	UNP P63756

- Molecule 2 is [(2R)-2-hexadecanoyloxy-3-[oxidanyl-[(2S)-2-oxidanyl-3-phosphonooxy-propoxy]phosphoryl]oxy-propyl] (Z)-octadec-9-enoate (three-letter code: PO9) (formula: $C_{40}H_{78}O_{13}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			55	40	13	2		
2	B	1	Total	C	O	P	0	0
			55	40	13	2		

- Molecule 3 is 1,4-BUTANEDIOL (three-letter code: BU1) (formula: $C_4H_{10}O_2$).



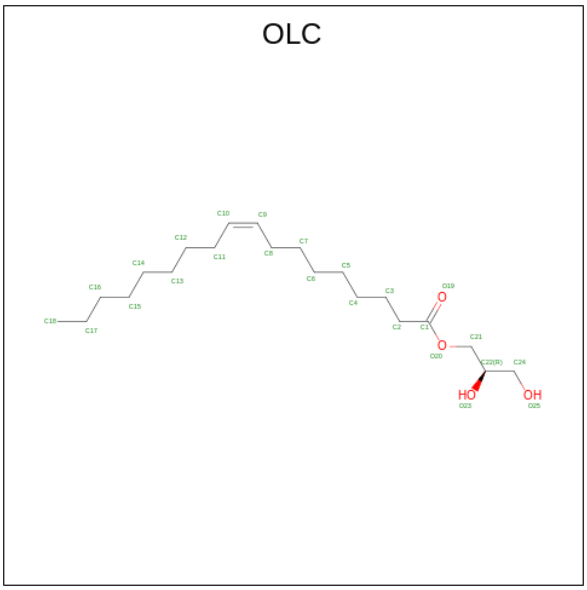
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0
3	B	1	Total C O 6 4 2	0	0
3	B	1	Total C O 6 4 2	0	0
3	B	1	Total C O 6 4 2	0	0
3	B	1	Total C O 6 4 2	0	0
3	B	1	Total C O 6 4 2	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 6 4 2	0	0

- Molecule 4 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: $C_{21}H_{40}O_4$).

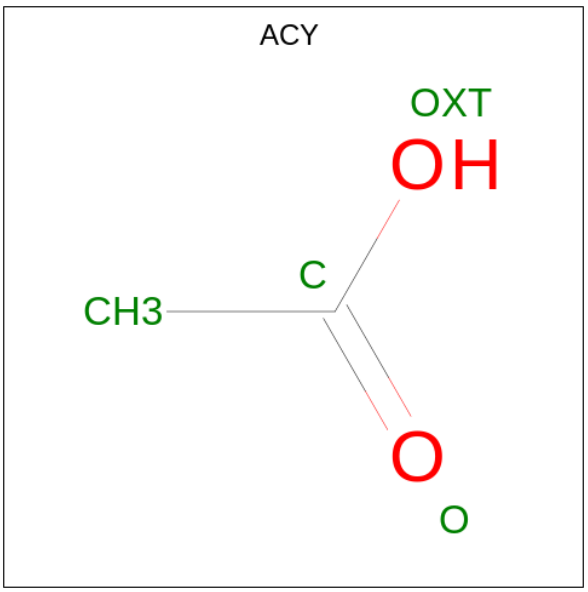


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 25 21 4	0	0
4	A	1	Total C O 25 21 4	0	0
4	B	1	Total C O 25 21 4	0	0
4	B	1	Total C O 25 21 4	0	0
4	B	1	Total C O 25 21 4	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Zn 2 2	0	0
5	B	2	Total Zn 2 2	0	0

- Molecule 6 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0

- Molecule 7 is water.

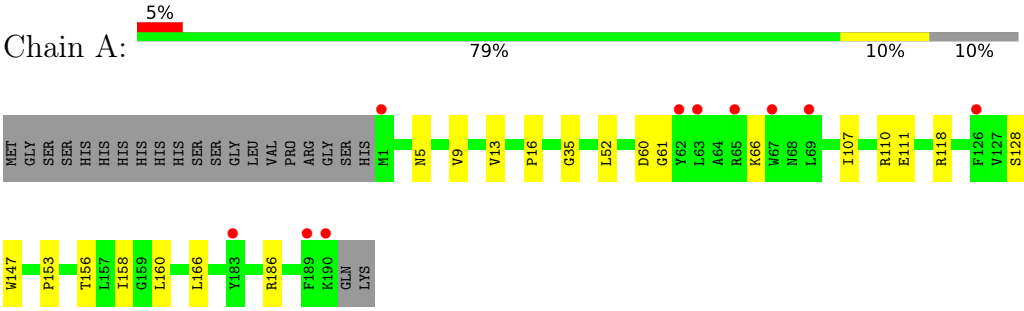
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	60	Total O 60 60	0	0
7	B	54	Total O 54 54	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

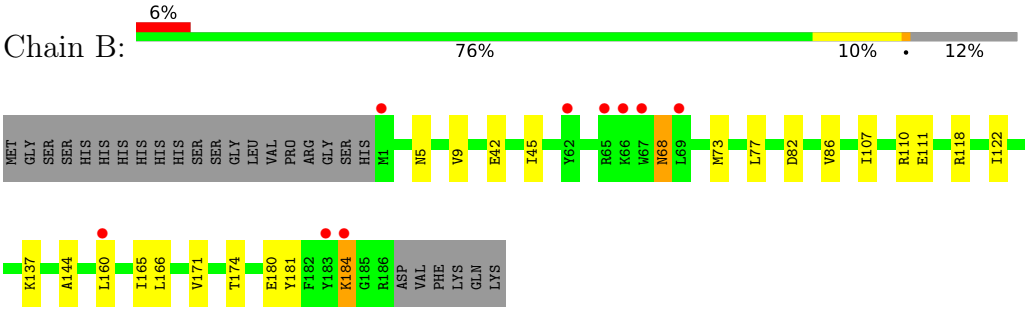
• Molecule 1: CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase

Chain A:



• Molecule 1: CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	127.54Å 59.38Å 72.98Å 90.00° 106.18° 90.00°	Depositor
Resolution (Å)	31.46 – 2.50 31.46 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.5 (31.46-2.50) 98.5 (31.46-2.50)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.42 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.212 , 0.249 0.217 , 0.251	Depositor DCC
R_{free} test set	968 reflections (5.37%)	wwPDB-VP
Wilson B-factor (Å^2)	43.4	Xtriage
Anisotropy	0.697	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 64.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3348	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PO9, ACY, BU1, OLC

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	0/1495	0.39	0/2030
1	B	0.26	0/1457	0.41	0/1981
All	All	0.26	0/2952	0.40	0/4011

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1468	0	1576	12	0
1	B	1431	0	1534	13	0
2	A	55	0	0	1	0
2	B	55	0	0	1	0
3	A	48	0	80	0	0
3	B	36	0	60	0	0
4	A	50	0	80	4	0
4	B	75	0	120	1	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	8	0	6	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	4	0	3	0	0
7	A	60	0	0	0	0
7	B	54	0	0	0	0
All	All	3348	0	3459	29	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 4.

All (29) 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:B:68:ASN:O	1:B:68:ASN:ND2	2.31	0.61
1:B:160:LEU:HD23	1:B:165:ILE:HD11	1.84	0.59
1:B:73:MET:HG3	1:B:77:LEU:HD12	1.90	0.52
1:B:118:ARG:O	1:B:122:ILE:HG13	2.12	0.49
1:B:180:GLU:O	1:B:184:LYS:HB2	2.13	0.48
1:B:5:ASN:O	1:B:9:VAL:HG23	2.13	0.48
1:B:171:VAL:O	1:B:174:THR:HG22	2.14	0.48
1:B:144:ALA:HB2	1:B:166:LEU:HB3	1.95	0.48
1:A:5:ASN:O	1:A:9:VAL:HG23	2.14	0.48
1:B:107:ILE:O	1:B:111:GLU:HG2	2.13	0.47
1:A:60:ASP:OD1	1:A:61:GLY:N	2.48	0.47
1:B:82:ASP:O	1:B:86:VAL:HG23	2.15	0.46
1:A:13:VAL:O	1:A:16:PRO:HD2	2.16	0.46
1:A:107:ILE:O	1:A:111:GLU:HG2	2.17	0.44
1:B:137:LYS:HB3	1:B:137:LYS:HE3	1.67	0.44
1:A:35:GLY:O	1:A:156:THR:OG1	2.36	0.43
1:A:118:ARG:NH2	2:A:201:PO9:O52	2.51	0.43
1:A:166:LEU:HD12	1:A:166:LEU:HA	1.90	0.43
4:A:205:OLC:H13	4:A:205:OLC:H16A	1.82	0.43
4:B:701:OLC:H4	4:B:701:OLC:H7	1.63	0.43
1:B:42:GLU:HA	1:B:45:ILE:HD12	2.01	0.43
4:A:204:OLC:H16A	4:A:204:OLC:H13	1.42	0.42
1:A:158:ILE:HG13	1:A:160:LEU:HD23	2.01	0.42
4:A:204:OLC:H18A	4:A:204:OLC:H15	1.60	0.42
1:A:144:ALA:HB2	1:A:166:LEU:HB3	2.02	0.41
1:A:66:LYS:HA	1:A:66:LYS:HD3	1.73	0.41
1:B:181:TYR:OH	2:B:702:PO9:O52	2.39	0.41
1:A:52:LEU:HD12	4:A:204:OLC:H24A	2.03	0.41
1:A:147:TRP:CD1	1:A:153:PRO:HD2	2.57	0.40

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	188/212 (89%)	186 (99%)	2 (1%)	0	100	100
1	B	184/212 (87%)	183 (100%)	1 (0%)	0	100	100
All	All	372/424 (88%)	369 (99%)	3 (1%)	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	158/177 (89%)	155 (98%)	3 (2%)	57	80
1	B	153/177 (86%)	150 (98%)	3 (2%)	55	79
All	All	311/354 (88%)	305 (98%)	6 (2%)	57	80

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	ARG
1	A	128	SER
1	A	186	ARG
1	B	68	ASN
1	B	110	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	184	LYS

Sometimes 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

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 28 ligands modelled in this entry, 4 are monoatomic - leaving 24 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	$\#\|Z\| > 2$
4	OLC	A	205	-	24,24,24	0.80	2 (8%)	25,25,25	0.98	1 (4%)
3	BU1	B	704	-	5,5,5	0.34	0	4,4,4	0.54	0
6	ACY	B	713	-	1,3,3	4.08	1 (100%)	0,3,3	-	-
3	BU1	A	203	-	5,5,5	0.35	0	4,4,4	0.54	0
3	BU1	B	705	-	5,5,5	0.34	0	4,4,4	0.53	0
4	OLC	B	703	-	24,24,24	0.80	2 (8%)	25,25,25	0.96	1 (4%)
3	BU1	A	207	-	5,5,5	0.34	0	4,4,4	0.55	0
6	ACY	A	214	-	1,3,3	4.00	1 (100%)	0,3,3	-	-
3	BU1	B	710	-	5,5,5	0.34	0	4,4,4	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	PO9	A	201	5	54,54,54	0.90	4 (7%)	59,63,63	0.87	2 (3%)
2	PO9	B	702	5	54,54,54	0.89	3 (5%)	59,63,63	0.80	2 (3%)
3	BU1	A	210	-	5,5,5	0.34	0	4,4,4	0.54	0
6	ACY	A	215	-	1,3,3	3.96	1 (100%)	0,3,3	-	-
3	BU1	A	206	-	5,5,5	0.34	0	4,4,4	0.56	0
4	OLC	B	701	-	24,24,24	0.82	2 (8%)	25,25,25	0.88	1 (4%)
3	BU1	B	707	-	5,5,5	0.34	0	4,4,4	0.55	0
3	BU1	A	209	-	5,5,5	0.34	0	4,4,4	0.55	0
3	BU1	B	706	-	5,5,5	0.35	0	4,4,4	0.55	0
3	BU1	A	211	-	5,5,5	0.34	0	4,4,4	0.52	0
4	OLC	A	204	-	24,24,24	0.81	2 (8%)	25,25,25	0.89	1 (4%)
3	BU1	B	708	-	5,5,5	0.35	0	4,4,4	0.52	0
3	BU1	A	202	-	5,5,5	0.34	0	4,4,4	0.55	0
4	OLC	B	709	-	24,24,24	0.80	2 (8%)	25,25,25	0.95	1 (4%)
3	BU1	A	208	-	5,5,5	0.34	0	4,4,4	0.55	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	OLC	A	205	-	-	12/24/24/24	-
3	BU1	B	704	-	-	2/3/3/3	-
3	BU1	A	203	-	-	2/3/3/3	-
3	BU1	B	705	-	-	1/3/3/3	-
4	OLC	B	703	-	-	12/24/24/24	-
3	BU1	A	207	-	-	1/3/3/3	-
3	BU1	B	710	-	-	1/3/3/3	-
2	PO9	A	201	5	-	25/59/59/59	-
2	PO9	B	702	5	-	26/59/59/59	-
3	BU1	A	210	-	-	0/3/3/3	-
3	BU1	A	206	-	-	2/3/3/3	-
4	OLC	B	701	-	-	13/24/24/24	-
3	BU1	B	707	-	-	1/3/3/3	-
3	BU1	A	209	-	-	1/3/3/3	-
3	BU1	B	706	-	-	0/3/3/3	-
3	BU1	A	211	-	-	1/3/3/3	-
4	OLC	A	204	-	-	13/24/24/24	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BU1	B	708	-	-	0/3/3/3	-
3	BU1	A	202	-	-	0/3/3/3	-
4	OLC	B	709	-	-	12/24/24/24	-
3	BU1	A	208	-	-	0/3/3/3	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	713	ACY	CH3-C	4.08	1.53	1.48
6	A	214	ACY	CH3-C	4.00	1.53	1.48
6	A	215	ACY	CH3-C	3.96	1.53	1.48
2	B	702	PO9	O18-C19	-2.73	1.39	1.46
2	A	201	PO9	O18-C19	-2.57	1.40	1.46
4	B	701	OLC	O20-C1	2.46	1.40	1.33
4	A	204	OLC	O20-C1	2.42	1.40	1.33
4	B	709	OLC	O20-C1	2.40	1.40	1.33
2	B	702	PO9	O21-C22	2.39	1.40	1.33
4	B	703	OLC	O20-C1	2.38	1.40	1.33
2	A	201	PO9	O21-C22	2.37	1.40	1.33
4	A	205	OLC	O20-C1	2.31	1.40	1.33
2	A	201	PO9	O21-C20	-2.21	1.40	1.45
4	B	703	OLC	O20-C21	-2.12	1.40	1.45
4	A	204	OLC	O20-C21	-2.11	1.40	1.45
4	B	701	OLC	O20-C21	-2.11	1.40	1.45
4	A	205	OLC	O20-C21	-2.10	1.40	1.45
2	A	201	PO9	O18-C16	2.10	1.40	1.34
2	B	702	PO9	O21-C20	-2.08	1.40	1.45
4	B	709	OLC	O20-C21	-2.04	1.40	1.45

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	201	PO9	O18-C16-C15	3.58	119.21	111.50
2	B	702	PO9	O18-C16-C15	3.21	118.42	111.50
4	A	205	OLC	O20-C1-C2	2.67	120.29	111.91
4	B	703	OLC	O20-C1-C2	2.60	120.08	111.91
4	B	709	OLC	O20-C1-C2	2.58	120.01	111.91
2	A	201	PO9	O21-C22-C24	2.57	119.96	111.91
4	B	701	OLC	O20-C1-C2	2.47	119.66	111.91
2	B	702	PO9	O21-C22-C24	2.46	119.63	111.91
4	A	204	OLC	O20-C1-C2	2.40	119.44	111.91

There are no chirality outliers.

All (125) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	PO9	C47-O46-P43-O42
2	A	201	PO9	C47-O46-P43-O44
2	A	201	PO9	C47-O46-P43-O45
2	B	702	PO9	O18-C19-C20-O21
2	B	702	PO9	C47-O46-P43-O44
2	B	702	PO9	C47-O46-P43-O45
2	B	702	PO9	C49-O50-P51-O53
2	B	702	PO9	C49-O50-P51-O54
4	A	205	OLC	O20-C21-C22-C24
4	A	205	OLC	O20-C21-C22-O23
4	B	701	OLC	O20-C21-C22-C24
4	B	703	OLC	C21-C22-C24-O25
4	B	709	OLC	O20-C21-C22-O23
4	B	709	OLC	C2-C1-O20-C21
4	B	709	OLC	O19-C1-O20-C21
4	B	703	OLC	C2-C1-O20-C21
4	B	703	OLC	O19-C1-O20-C21
2	A	201	PO9	O55-C48-C49-O50
2	B	702	PO9	O46-C47-C48-O55
4	B	701	OLC	O20-C21-C22-O23
4	B	701	OLC	C4-C5-C6-C7
4	A	204	OLC	C13-C14-C15-C16
2	B	702	PO9	C47-C48-C49-O50
4	B	701	OLC	C2-C1-O20-C21
2	B	702	PO9	C24-C22-O21-C20
4	A	204	OLC	C2-C1-O20-C21
2	B	702	PO9	C13-C14-C15-C16
4	A	205	OLC	C1-C2-C3-C4
4	B	703	OLC	C1-C2-C3-C4
4	B	701	OLC	O19-C1-O20-C21
2	B	702	PO9	O55-C48-C49-O50
4	A	205	OLC	C2-C1-O20-C21
2	B	702	PO9	O23-C22-O21-C20
2	B	702	PO9	C47-O46-P43-O42
2	B	702	PO9	O46-C47-C48-C49
2	A	201	PO9	C15-C16-O18-C19
2	A	201	PO9	O17-C16-O18-C19
4	A	205	OLC	C3-C4-C5-C6
4	B	701	OLC	C2-C3-C4-C5
4	A	204	OLC	O19-C1-O20-C21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	204	OLC	C12-C13-C14-C15
4	B	709	OLC	C14-C15-C16-C17
4	B	709	OLC	C12-C13-C14-C15
4	B	701	OLC	C6-C7-C8-C9
4	B	709	OLC	C10-C11-C12-C13
4	A	204	OLC	C14-C15-C16-C17
2	A	201	PO9	C11-C12-C13-C14
4	A	205	OLC	C14-C15-C16-C17
4	A	205	OLC	O19-C1-O20-C21
4	A	204	OLC	C1-C2-C3-C4
4	B	701	OLC	C3-C4-C5-C6
2	A	201	PO9	C26-C27-C28-C29
2	B	702	PO9	C34-C35-C36-C37
4	B	703	OLC	C6-C7-C8-C9
2	B	702	PO9	C12-C13-C14-C15
4	B	703	OLC	C2-C3-C4-C5
4	B	703	OLC	O20-C21-C22-C24
2	A	201	PO9	O18-C19-C41-O42
4	B	709	OLC	C5-C6-C7-C8
2	A	201	PO9	C10-C11-C12-C13
2	B	702	PO9	C6-C7-C8-C9
4	A	205	OLC	C2-C3-C4-C5
4	B	703	OLC	C5-C6-C7-C8
3	A	209	BU1	C2-C3-C4-O6
4	A	204	OLC	C4-C5-C6-C7
2	A	201	PO9	C47-C48-C49-O50
4	B	701	OLC	C14-C15-C16-C17
2	A	201	PO9	C25-C26-C27-C28
4	A	205	OLC	C4-C5-C6-C7
3	A	206	BU1	O5-C1-C2-C3
3	B	704	BU1	C2-C3-C4-O6
3	B	705	BU1	C2-C3-C4-O6
2	A	201	PO9	C9-C10-C11-C12
4	B	703	OLC	O23-C22-C24-O25
4	A	205	OLC	C11-C12-C13-C14
2	A	201	PO9	C32-C33-C34-C35
2	B	702	PO9	C28-C29-C30-C31
4	B	703	OLC	O20-C21-C22-O23
4	A	204	OLC	C15-C16-C17-C18
2	B	702	PO9	C49-O50-P51-O52
2	B	702	PO9	C7-C8-C9-C10
3	A	211	BU1	O5-C1-C2-C3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	A	201	PO9	C37-C38-C39-C40
2	A	201	PO9	C20-C19-C41-O42
2	B	702	PO9	C11-C12-C13-C14
4	B	709	OLC	O20-C21-C22-C24
4	A	204	OLC	C5-C6-C7-C8
2	B	702	PO9	C33-C34-C35-C36
4	B	709	OLC	C11-C12-C13-C14
4	A	204	OLC	C6-C7-C8-C9
2	B	702	PO9	C41-C19-C20-O21
3	A	203	BU1	O5-C1-C2-C3
2	B	702	PO9	C1-C2-C3-C4
4	B	701	OLC	C5-C6-C7-C8
3	B	710	BU1	C2-C3-C4-O6
4	A	204	OLC	C2-C3-C4-C5
4	B	703	OLC	C11-C12-C13-C14
4	B	701	OLC	C12-C13-C14-C15
2	A	201	PO9	O18-C19-C20-O21
4	B	709	OLC	C3-C4-C5-C6
2	A	201	PO9	C11-C10-C9-C8
3	B	707	BU1	C2-C3-C4-O6
3	A	207	BU1	C2-C3-C4-O6
3	A	206	BU1	C2-C3-C4-O6
2	A	201	PO9	C6-C7-C8-C9
4	B	709	OLC	C7-C8-C9-C10
4	B	709	OLC	C4-C5-C6-C7
2	A	201	PO9	C33-C34-C35-C36
4	B	701	OLC	C11-C12-C13-C14
2	A	201	PO9	O46-C47-C48-O55
2	B	702	PO9	C32-C33-C34-C35
2	A	201	PO9	C5-C6-C7-C8
4	A	205	OLC	C7-C8-C9-C10
2	B	702	PO9	C26-C27-C28-C29
4	B	701	OLC	C9-C10-C11-C12
3	B	704	BU1	O5-C1-C2-C3
2	A	201	PO9	C31-C32-C33-C34
2	A	201	PO9	C41-C19-C20-O21
2	A	201	PO9	C27-C28-C29-C30
3	A	203	BU1	C1-C2-C3-C4
2	B	702	PO9	C29-C30-C31-C32
4	B	703	OLC	C7-C8-C9-C10
4	A	204	OLC	C7-C8-C9-C10
4	A	204	OLC	C3-C4-C5-C6

Continued on next page...

Continued from previous page...

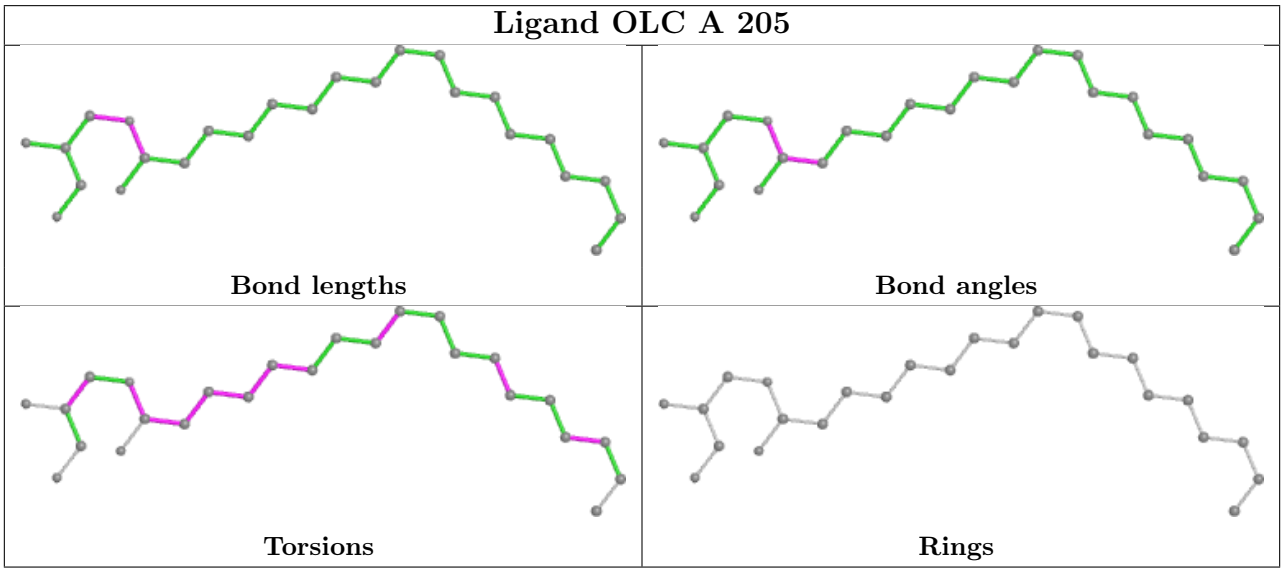
Mol	Chain	Res	Type	Atoms
4	A	205	OLC	O20-C1-C2-C3

There are no ring outliers.

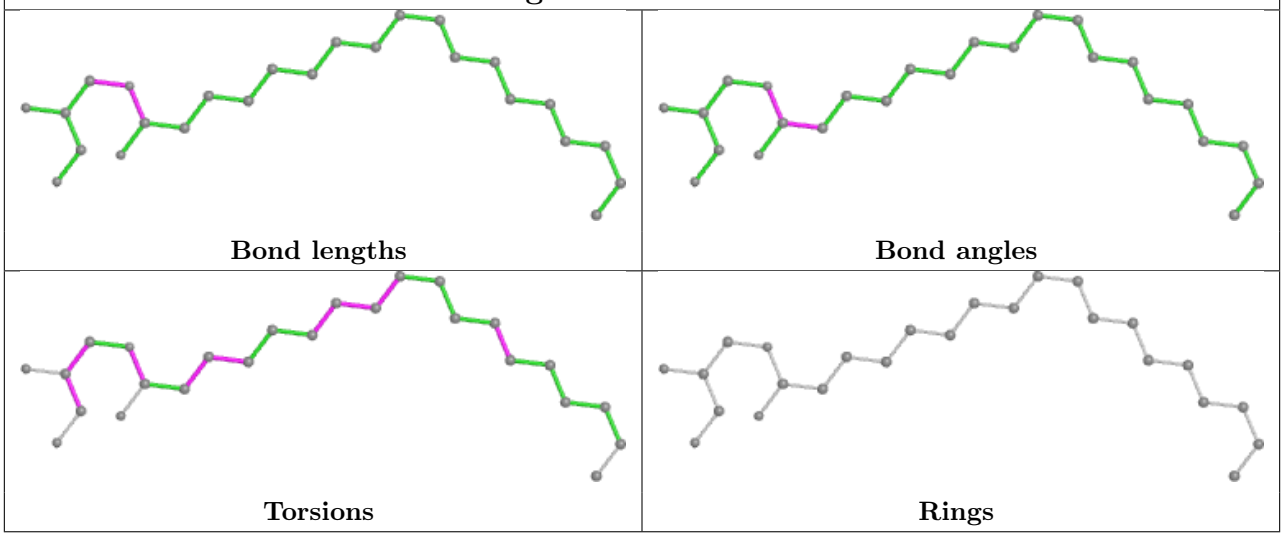
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	205	OLC	1	0
2	A	201	PO9	1	0
2	B	702	PO9	1	0
4	B	701	OLC	1	0
4	A	204	OLC	3	0

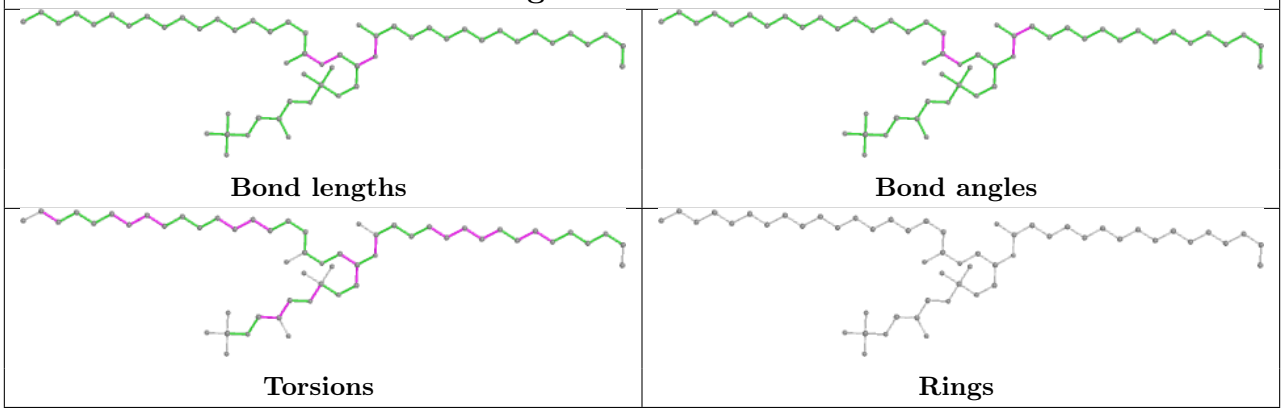
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



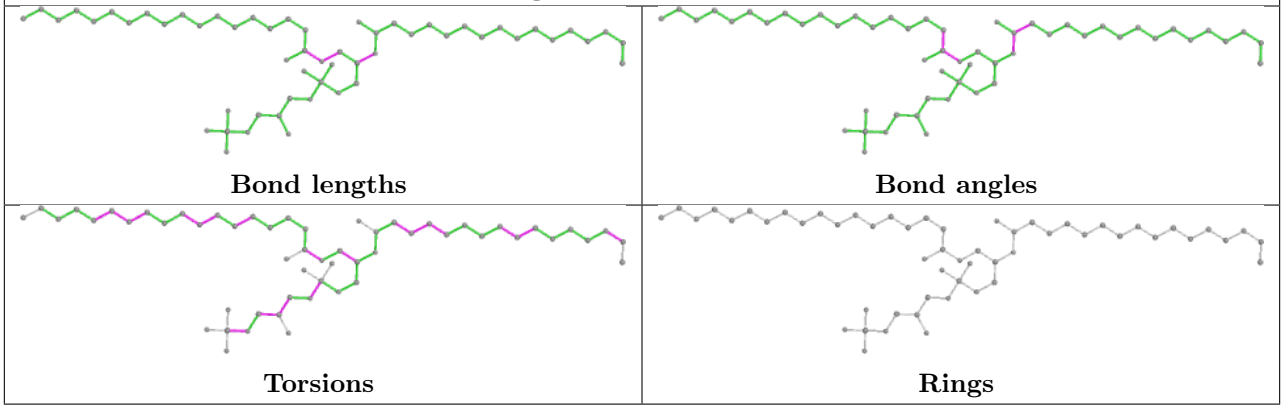
Ligand OLC B 703



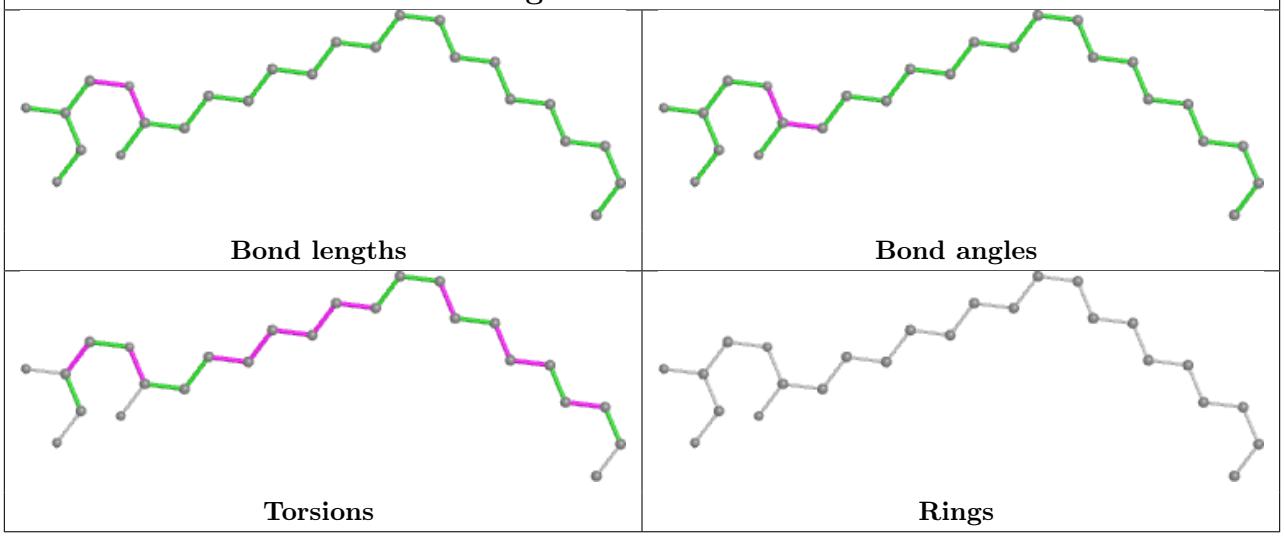
Ligand PO9 A 201



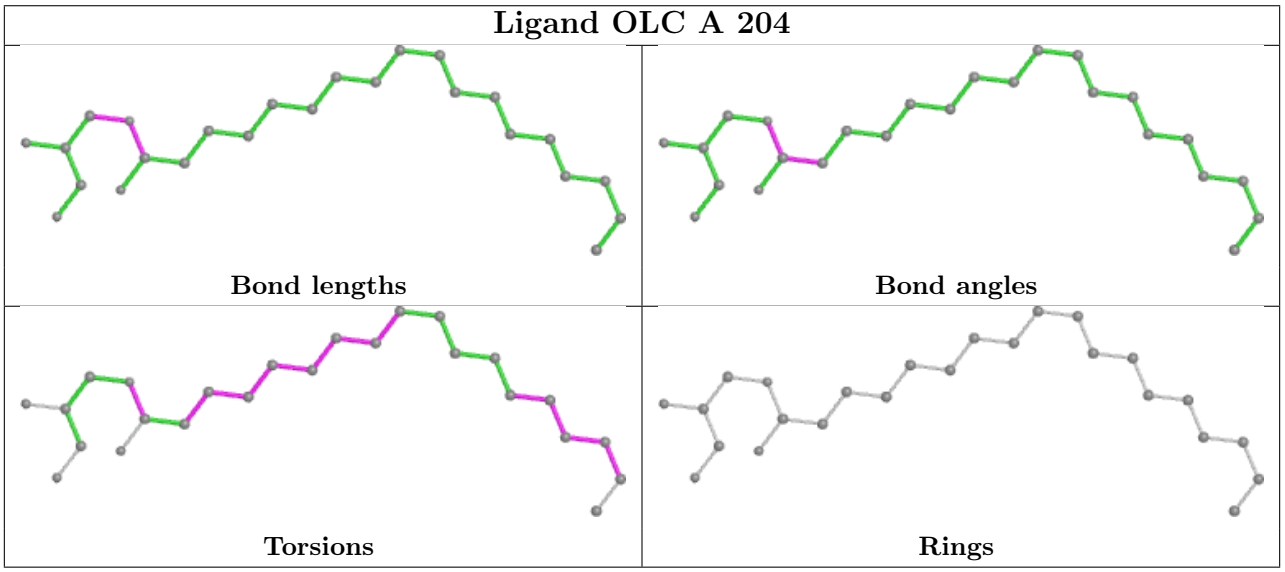
Ligand PO9 B 702



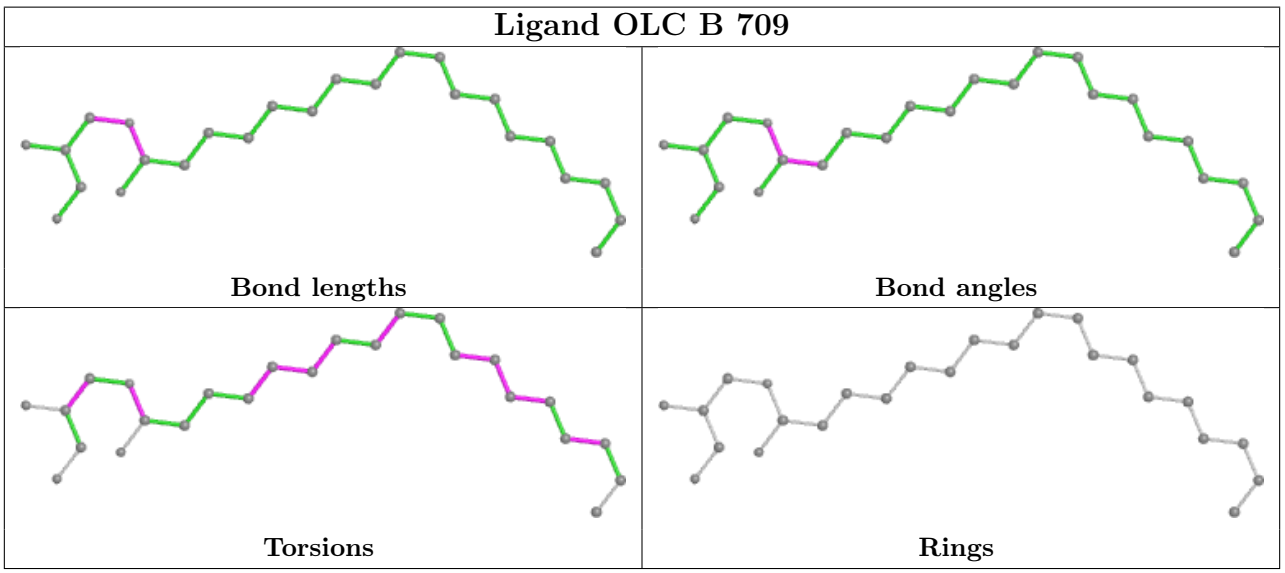
Ligand OLC B 701



Ligand OLC A 204



Ligand OLC B 709



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

6.1 Protein, DNA and RNA chains

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^{th} 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	190/212 (89%)	0.05	11 (5%)	23	24	33, 46, 94, 118	0
1	B	186/212 (87%)	0.12	13 (6%)	16	16	31, 48, 90, 137	0
All	All	376/424 (88%)	0.08	24 (6%)	19	20	31, 48, 93, 137	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	4.8
1	B	126	PHE	4.1
1	A	190	LYS	3.9
1	B	160	LEU	3.5
1	A	183	TYR	3.2
1	B	183	TYR	3.1
1	A	63	LEU	2.9
1	A	1	MET	2.9
1	A	62	TYR	2.9
1	B	66	LYS	2.9
1	B	67	TRP	2.8
1	A	69	LEU	2.8
1	B	65	ARG	2.7
1	B	129	ALA	2.7
1	B	69	LEU	2.7
1	B	184	LYS	2.7
1	A	130	ALA	2.6
1	B	127	VAL	2.6
1	A	126	PHE	2.6
1	A	189	PHE	2.5
1	B	62	TYR	2.5
1	B	130	ALA	2.4
1	A	67	TRP	2.3
1	A	65	ARG	2.2

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)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	OLC	A	205	25/25	0.71	0.33	62,71,98,102	0
4	OLC	B	701	25/25	0.75	0.28	42,49,77,88	0
6	ACY	B	713	4/4	0.77	0.37	74,74,74,74	0
3	BU1	B	707	6/6	0.80	0.23	71,75,76,77	0
4	OLC	A	204	25/25	0.83	0.32	55,74,84,91	0
6	ACY	A	214	4/4	0.83	0.23	76,76,76,76	0
3	BU1	A	209	6/6	0.83	0.20	71,74,76,78	0
6	ACY	A	215	4/4	0.84	0.28	68,69,69,69	0
3	BU1	B	710	6/6	0.84	0.21	66,67,70,72	0
4	OLC	B	703	25/25	0.85	0.23	45,65,87,93	0
5	ZN	B	711	1/1	0.86	0.07	51,51,51,51	0
3	BU1	A	207	6/6	0.87	0.18	63,65,69,80	0
3	BU1	B	706	6/6	0.88	0.20	53,55,67,67	0
3	BU1	A	211	6/6	0.88	0.24	60,60,60,61	0
3	BU1	B	708	6/6	0.88	0.19	66,72,78,82	0
3	BU1	A	203	6/6	0.89	0.18	54,60,62,62	0
3	BU1	B	705	6/6	0.89	0.25	60,63,73,78	0
4	OLC	B	709	25/25	0.89	0.21	45,57,70,77	0
5	ZN	A	213	1/1	0.89	0.11	53,53,53,53	0
3	BU1	A	206	6/6	0.91	0.18	56,66,67,70	0
3	BU1	A	210	6/6	0.92	0.17	59,59,59,59	0
2	PO9	B	702	55/55	0.92	0.20	37,58,79,86	0
3	BU1	B	704	6/6	0.92	0.19	63,68,72,72	0
3	BU1	A	208	6/6	0.93	0.27	56,62,66,70	0
2	PO9	A	201	55/55	0.93	0.18	41,51,70,73	0
3	BU1	A	202	6/6	0.95	0.21	58,65,66,67	0
5	ZN	A	212	1/1	0.97	0.08	48,48,48,48	0

Continued on next page...

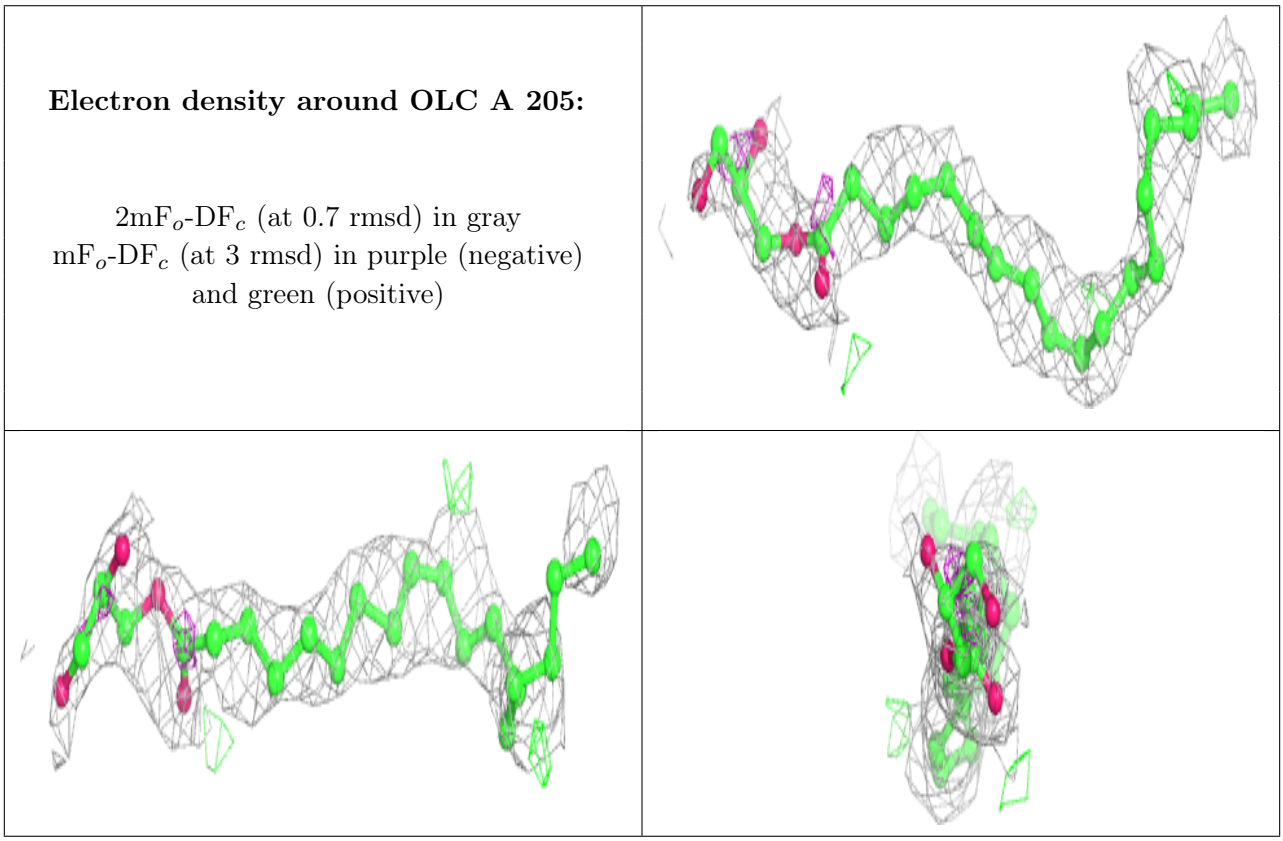
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	ZN	B	712	1/1	0.98	0.07	51,51,51,51	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.

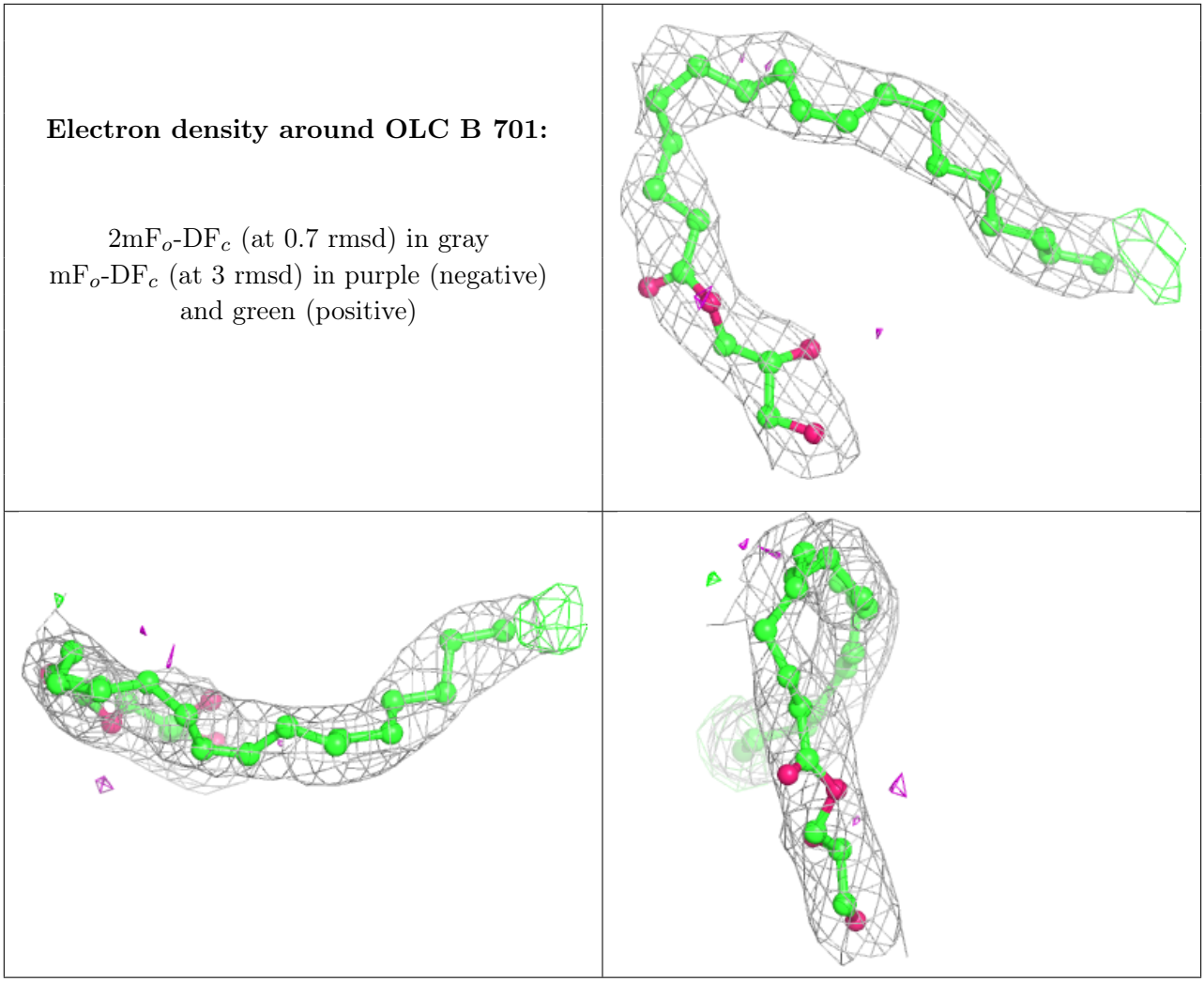
Electron density around OLC A 205:

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



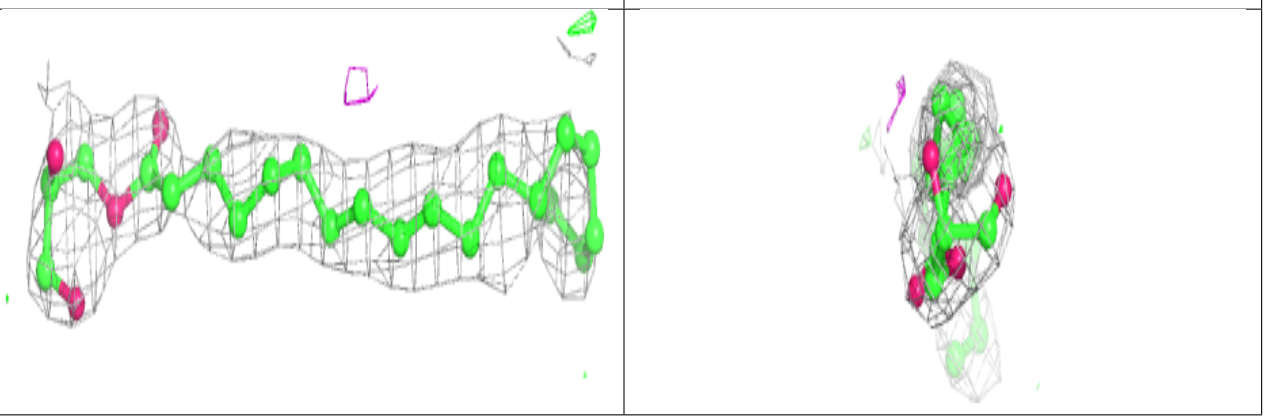
Electron density around OLC B 701:

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



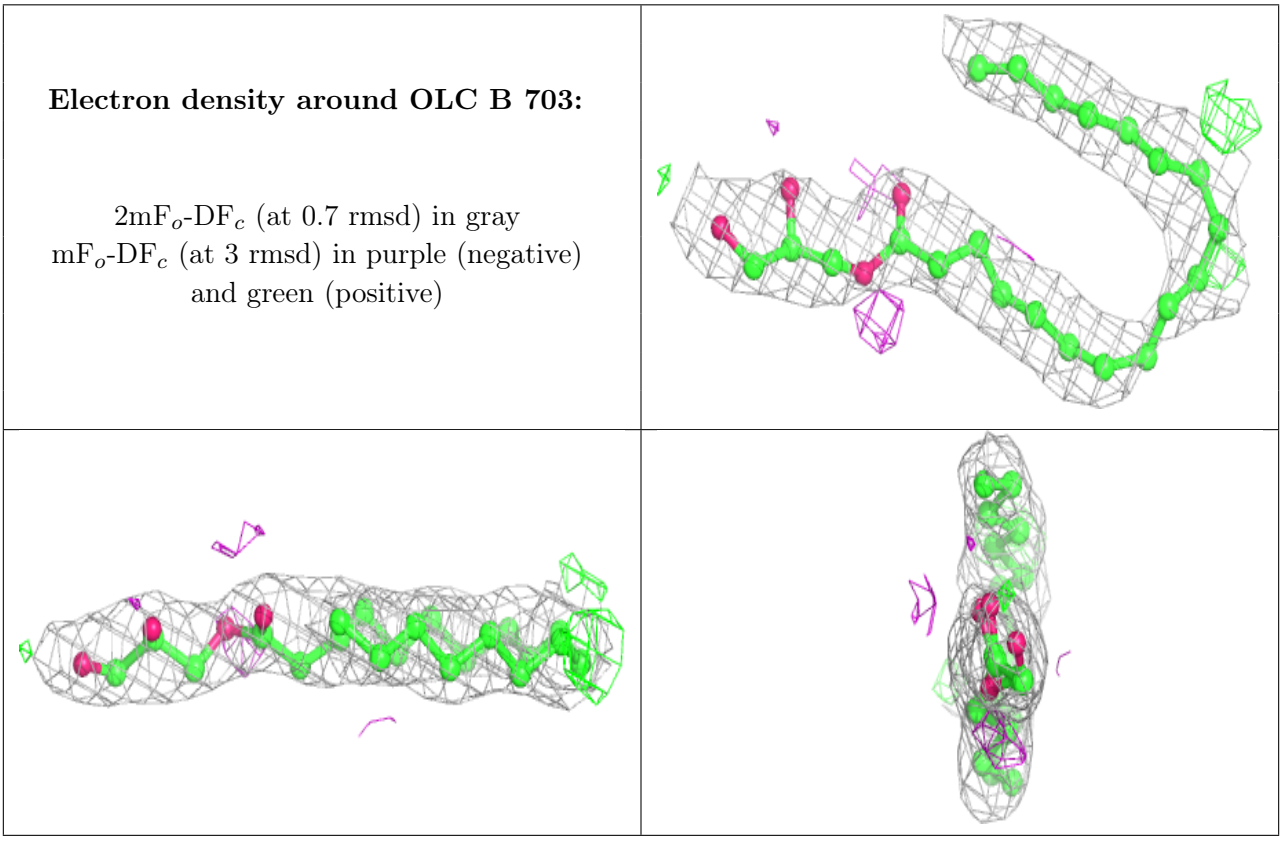
Electron density around OLC A 204:

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



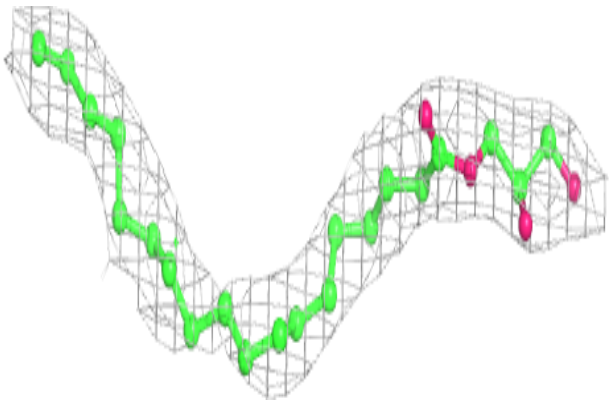
Electron density around OLC B 703:

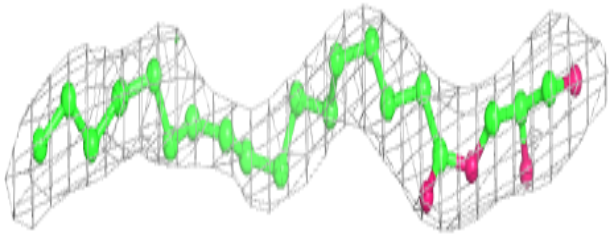
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

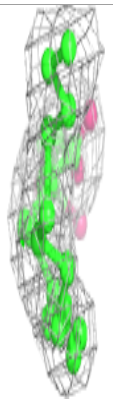


Electron density around OLC B 709:

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

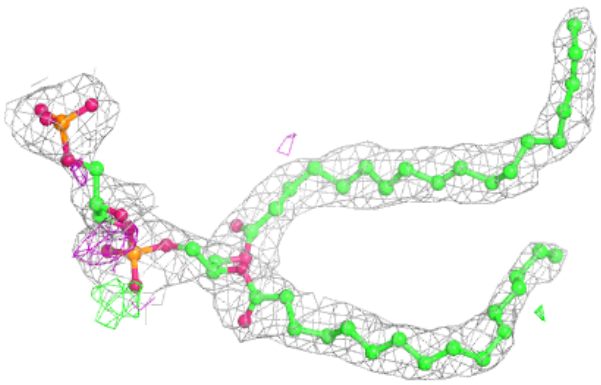


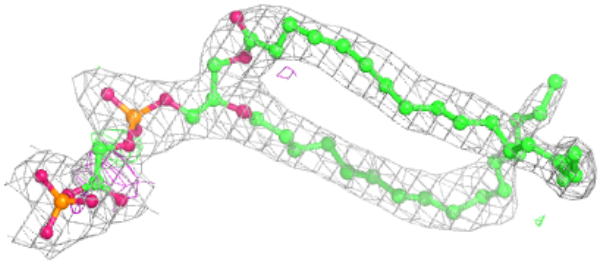




Electron density around PO9 B 702:

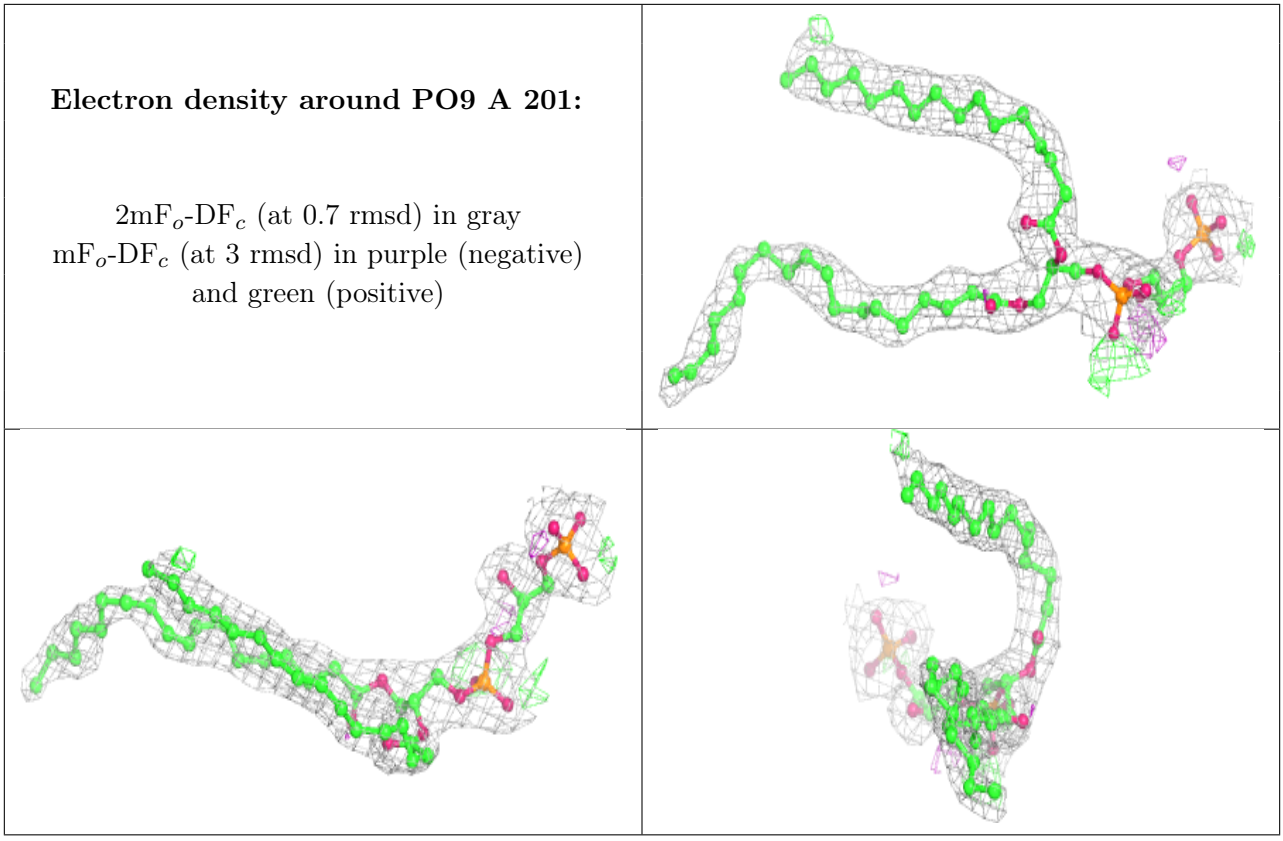
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around PO9 A 201:

$2mF_o$-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.