wwPDB X-ray Structure Validation Summary Report (i)

Sep 24, 2023 – 04:53 AM EDT

PDB ID	:	5L0C
Title	:	Human metavinculin (residues 959-1134) in complex with PIP2
Authors	:	Chinthalapudi, K.; Izard, T.
Deposited on	:	2016-07-27
Resolution	:	3.10 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 (i) 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 (i)) were used in the production of this report:

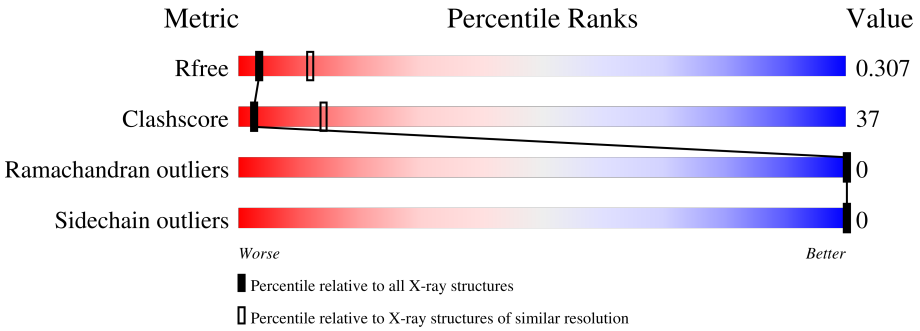
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)

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%

Mol	Chain	Length	Quality of chain
1	A	176	65% 35%
1	B	176	72% 28% .
1	C	176	58% 41% .
1	D	176	52% 42% 6%

2 Entry composition (i)

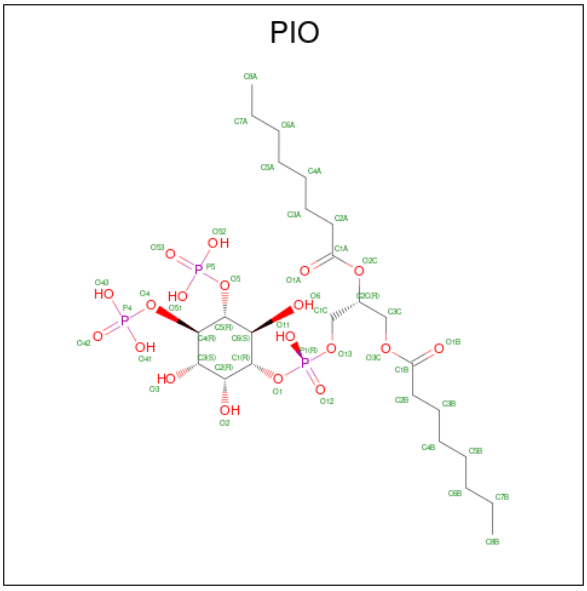
There are 4 unique types of molecules in this entry. The entry contains 5588 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Vinculin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	176	Total	C	N	O	S	0	0	0
			1368	843	257	259	9			
1	B	175	Total	C	N	O	S	0	1	0
			1362	842	255	256	9			
1	C	175	Total	C	N	O	S	0	0	0
			1358	838	255	256	9			
1	D	166	Total	C	N	O	S	0	1	0
			1299	799	246	245	9			

- Molecule 2 is [(2R)-2-octanoyloxy-3-[oxidanyl-[(1R,2R,3S,4R,5R,6S)-2,3,6-tris(oxidanyl)-4,5-diphosphonooxy-cyclohexyl]oxy-phosphoryl]oxy-propyl] octanoate (three-letter code: PIO) (formula: $C_{25}H_{49}O_{19}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			29	9	17	3		

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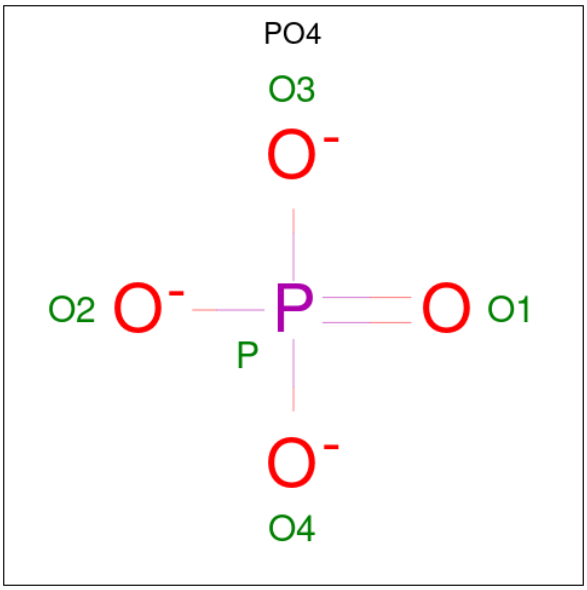
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O P 24 6 15 3	0	0
2	B	1	Total C O P 24 6 15 3	0	0
2	C	1	Total C O P 24 6 15 3	0	0
2	D	1	Total C O P 24 6 15 3	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	11	Total O 11 11	0	0
4	B	19	Total O 19 19	0	0

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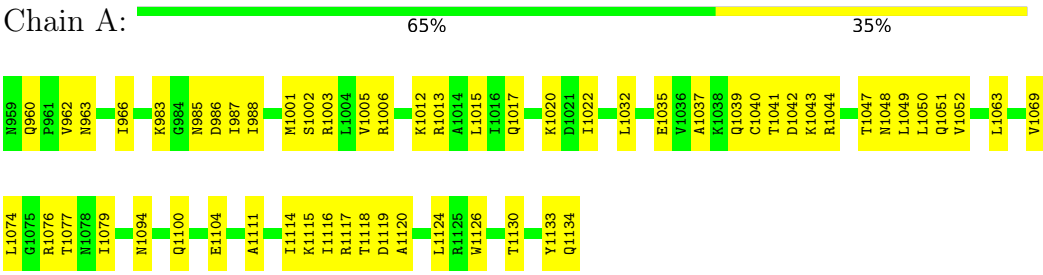
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	18	Total O 18 18	0	0
4	D	13	Total O 13 13	0	0

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. 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. 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.

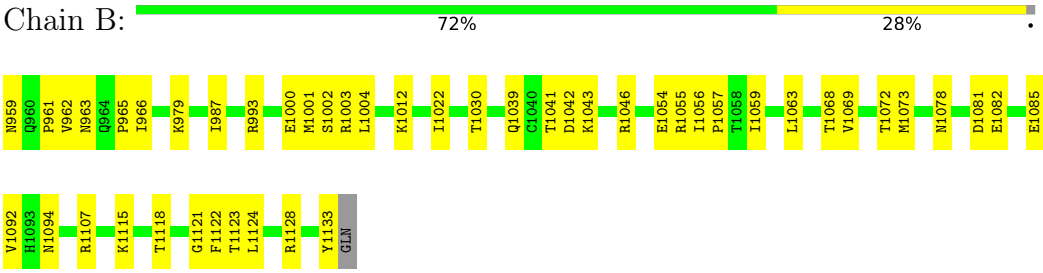
• Molecule 1: Vinculin

Chain A:



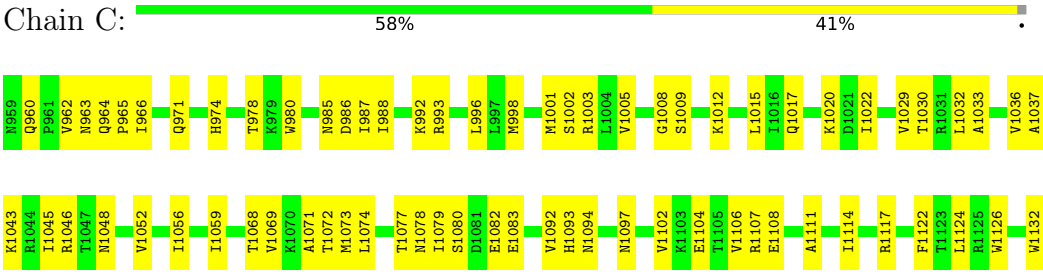
• Molecule 1: Vinculin

Chain B:



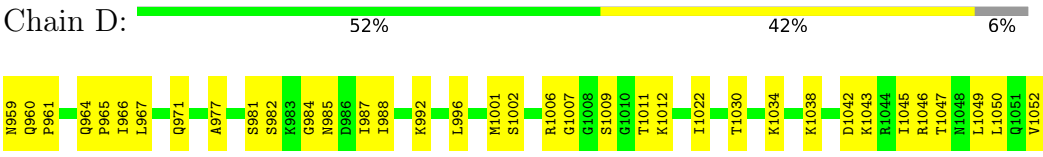
• Molecule 1: Vinculin

Chain C:



• Molecule 1: Vinculin

Chain D:




P1057
T1058
I1059
Q1062
L1063
T1068
V1069
K1070
A1071
T1072
M1073
L1074
G1075
S1080
D1081
E1082
E1083
S1084
E1085
V1092
H1093
N1094
N1097
L1098
M1099
Q1100
S1101
V1102
K1103
E1104
E1108
A1111
A1112
SER
ILE
LYS
ILE
ARG
THR
ASP
ALA
GLY
PHE
T1123
L1124
R1125
W1126
W1132
Y1133
Q1134

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	114.52Å 100.68Å 105.61Å 90.00° 122.49° 90.00°	Depositor
Resolution (Å)	30.45 – 3.10 48.30 – 3.10	Depositor EDS
% Data completeness (in resolution range)	97.9 (30.45-3.10) 97.8 (48.30-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.09 (at 3.12Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.235 , 0.261 0.301 , 0.307	Depositor DCC
R_{free} test set	924 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å^2)	106.3	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 92.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	5588	wwPDB-VP
Average B, all atoms (Å^2)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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: PIO, PO4

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	0.45	0/1381	0.68	0/1858
1	B	0.47	0/1378	0.66	0/1856
1	C	0.45	0/1371	0.64	0/1846
1	D	0.46	0/1313	0.64	0/1765
All	All	0.46	0/5443	0.66	0/7325

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	1368	0	1428	108	1
1	B	1362	0	1429	73	1
1	C	1358	0	1420	117	0
1	D	1299	0	1359	126	0
2	A	29	0	14	0	0
2	B	48	0	18	13	0
2	C	24	0	9	6	0
2	D	24	0	9	0	0
3	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	0	0
4	A	11	0	0	0	0
4	B	19	0	0	1	0
4	C	18	0	0	1	0
4	D	13	0	0	2	0
All	All	5588	0	5686	413	1

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 37.

The worst 5 of 413 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:D:1009:SER:CB	1:D:1074:LEU:HD22	1.68	1.22
1:A:1017:GLN:HE22	1:A:1020:LYS:NZ	1.45	1.14
1:C:985:ASN:ND2	1:C:988:ILE:HG12	1.61	1.13
1:C:1040:CYS:SG	1:C:1045:ILE:HD11	1.90	1.12
1:A:1073:MET:HB2	1:A:1079:ILE:CD1	1.81	1.10

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:983:LYS:NZ	1:B:1133:TYR:C[2_655]	2.19	0.01

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	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
1	B	174/176 (99%)	171 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	173/176 (98%)	168 (97%)	5 (3%)	0	100	100
1	D	163/176 (93%)	160 (98%)	3 (2%)	0	100	100
All	All	684/704 (97%)	668 (98%)	16 (2%)	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	148/148 (100%)	148 (100%)	0	100	100
1	B	148/148 (100%)	148 (100%)	0	100	100
1	C	147/148 (99%)	147 (100%)	0	100	100
1	D	141/148 (95%)	141 (100%)	0	100	100
All	All	584/592 (99%)	584 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	963	ASN
1	C	1017	GLN
1	D	1100	GLN
1	D	963	ASN
1	D	1094	ASN

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)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

8 ligands 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	$\#\|Z\| > 2$
2	PIO	D	1201	-	24,24,47	0.98	1 (4%)	36,39,65	1.24	5 (13%)
2	PIO	B	1201	-	24,24,47	0.78	0	36,39,65	1.23	4 (11%)
3	PO4	B	1204	-	4,4,4	0.92	0	6,6,6	0.43	0
2	PIO	B	1202	-	24,24,47	0.76	0	36,39,65	1.18	3 (8%)
3	PO4	A	1202	-	4,4,4	0.93	0	6,6,6	0.43	0
3	PO4	B	1203	-	4,4,4	0.92	0	6,6,6	0.43	0
2	PIO	A	1201	-	29,29,47	0.67	0	41,45,65	1.22	6 (14%)
2	PIO	C	1201	-	24,24,47	0.77	0	36,39,65	1.23	4 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PIO	D	1201	-	-	3/15/39/68	0/1/1/1
2	PIO	B	1201	-	-	4/15/39/68	0/1/1/1
2	PIO	B	1202	-	-	5/15/39/68	0/1/1/1
2	PIO	A	1201	-	-	4/23/47/68	0/1/1/1
2	PIO	C	1201	-	-	6/15/39/68	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1201	PIO	P1-O12	3.29	1.61	1.50

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1202	PIO	O5-P5-O53	-3.11	97.38	109.39
2	A	1201	PIO	O5-P5-O53	-3.10	97.42	109.39
2	A	1201	PIO	O1-P1-O12	-2.95	98.39	109.47
2	C	1201	PIO	O1-P1-O12	-2.85	98.41	109.39
2	B	1201	PIO	O1-P1-O12	-2.84	98.43	109.39

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1201	PIO	C3-C4-O4-P4
2	B	1201	PIO	C5-C4-O4-P4
2	B	1201	PIO	C4-C5-O5-P5
2	B	1201	PIO	C6-C5-O5-P5
2	B	1202	PIO	C6-C1-O1-P1

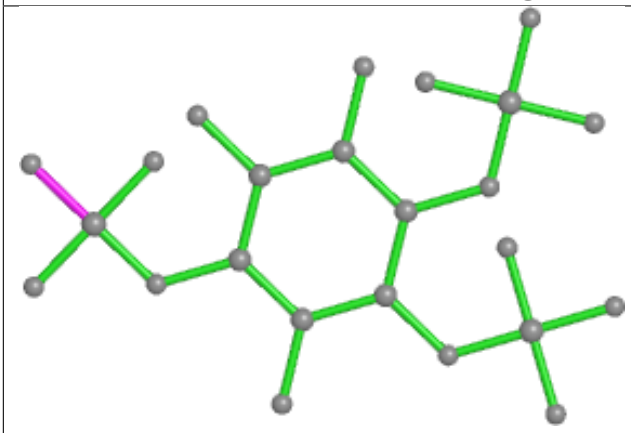
There are no ring outliers.

3 monomers are involved in 19 short contacts:

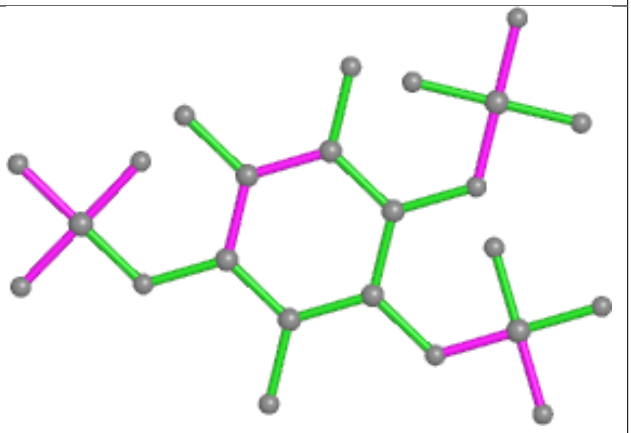
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1201	PIO	1	0
2	B	1202	PIO	12	0
2	C	1201	PIO	6	0

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.

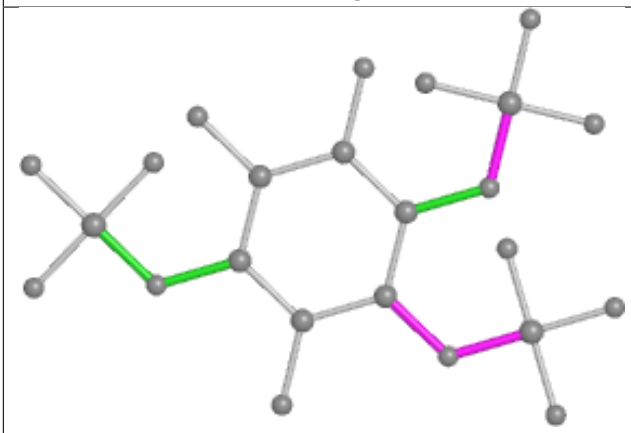
Ligand PIO D 1201



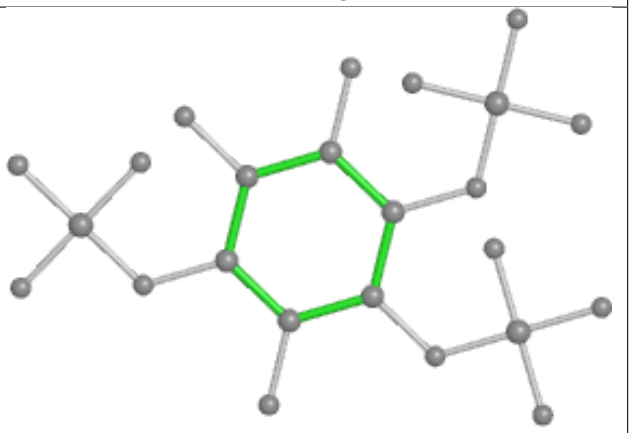
Bond lengths



Bond angles

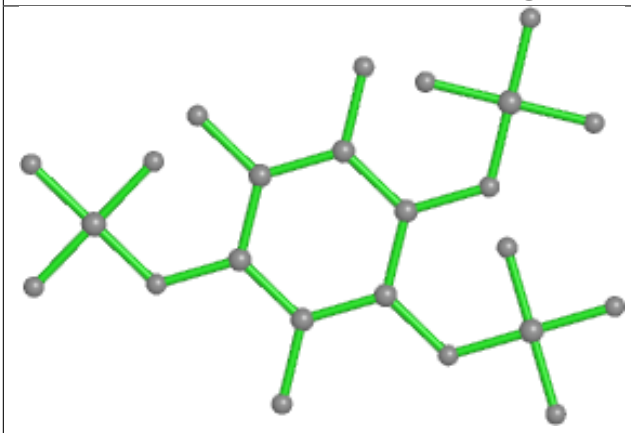


Torsions

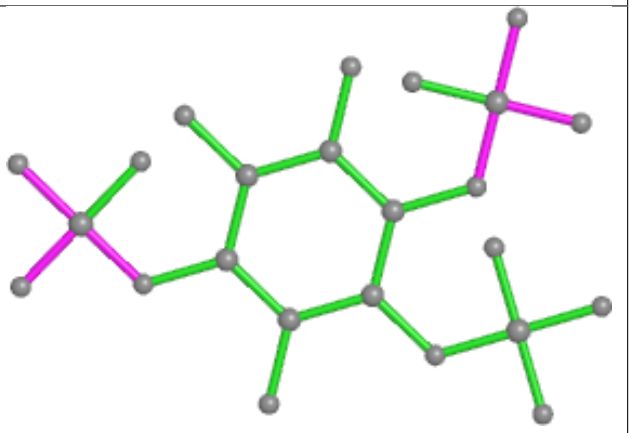


Rings

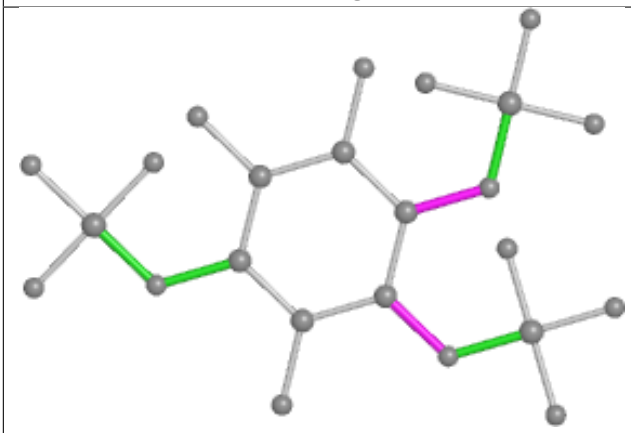
Ligand PIO B 1201



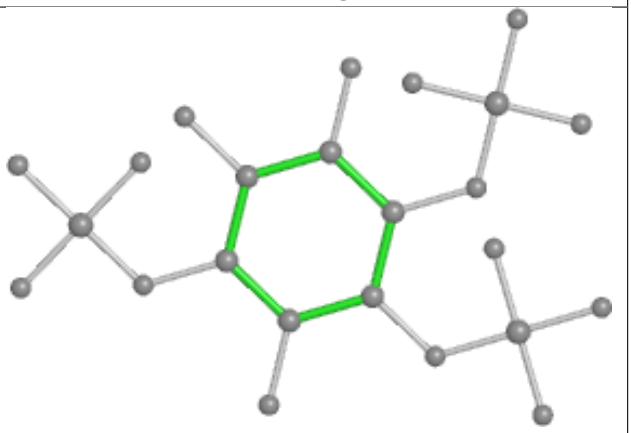
Bond lengths



Bond angles

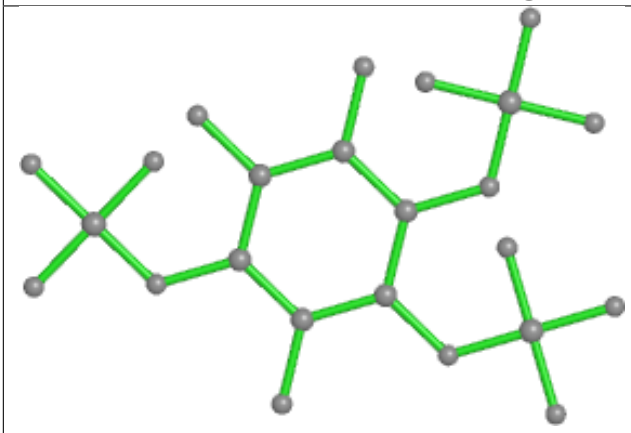


Torsions

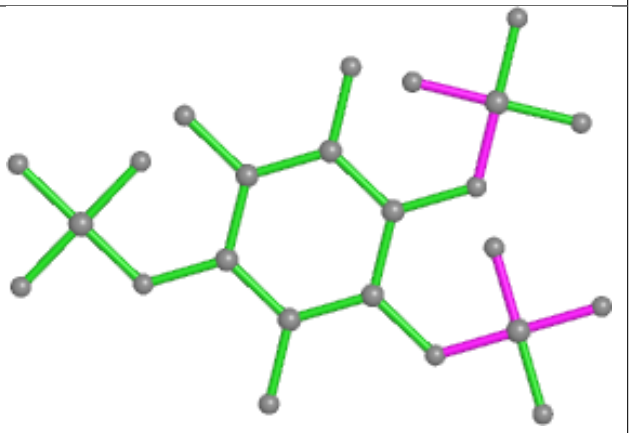


Rings

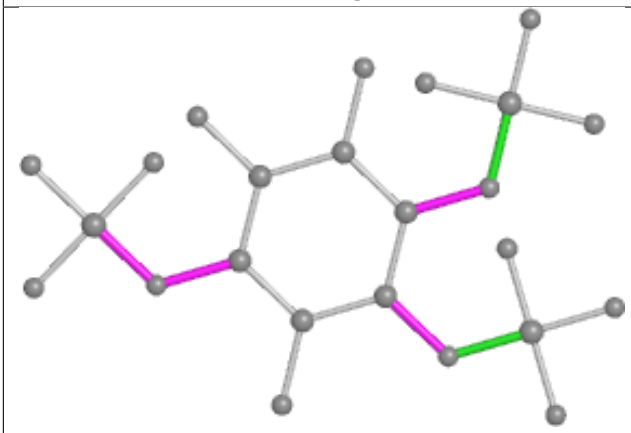
Ligand PIO B 1202



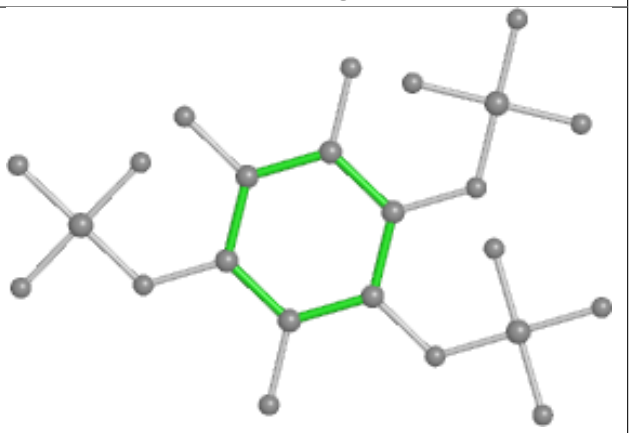
Bond lengths



Bond angles

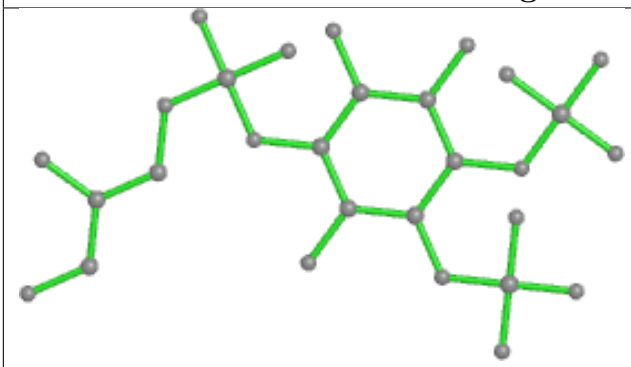


Torsions

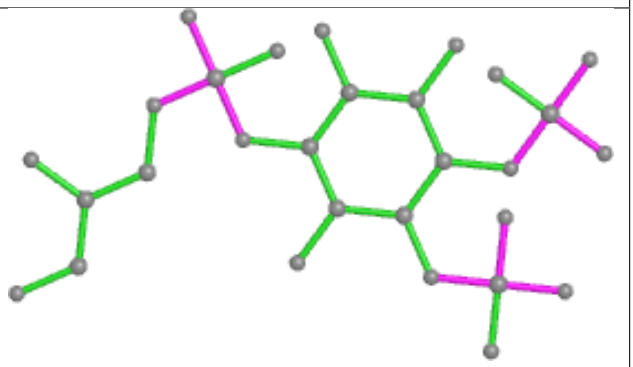


Rings

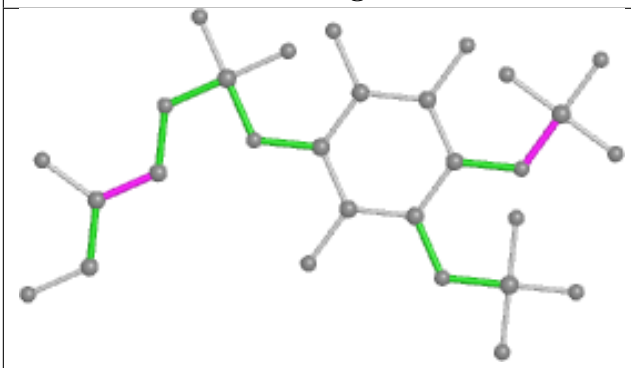
Ligand PIO A 1201



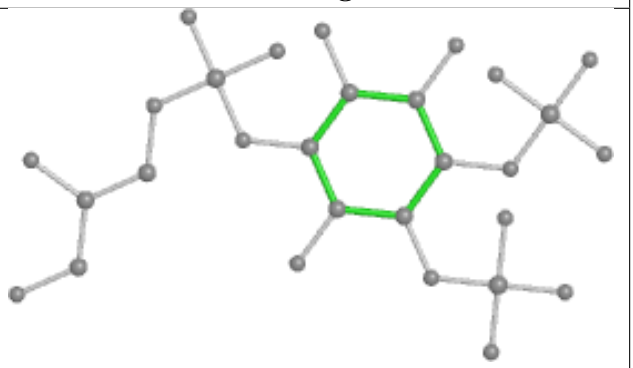
Bond lengths



Bond angles

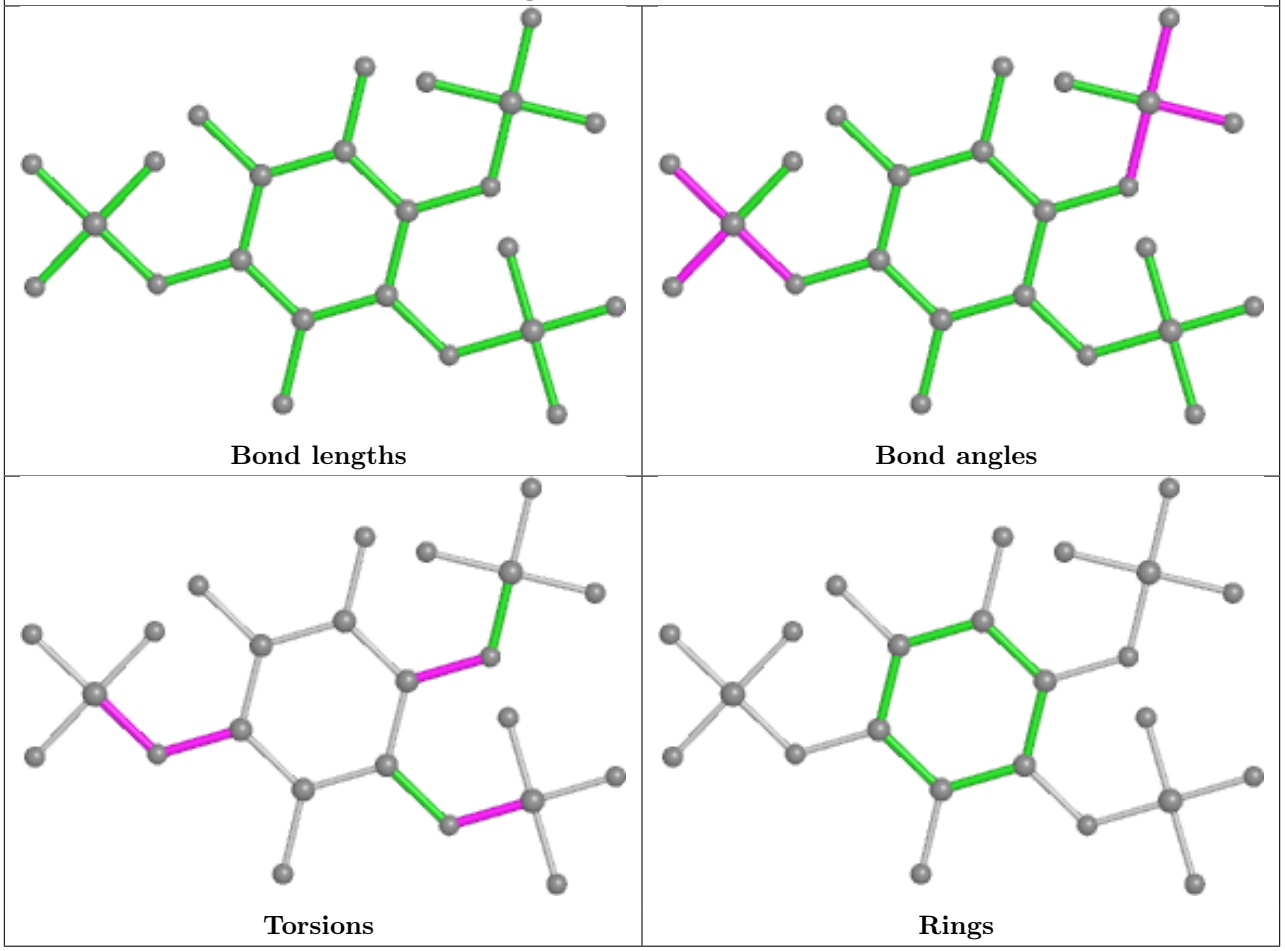


Torsions



Rings

Ligand PIO C 1201



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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

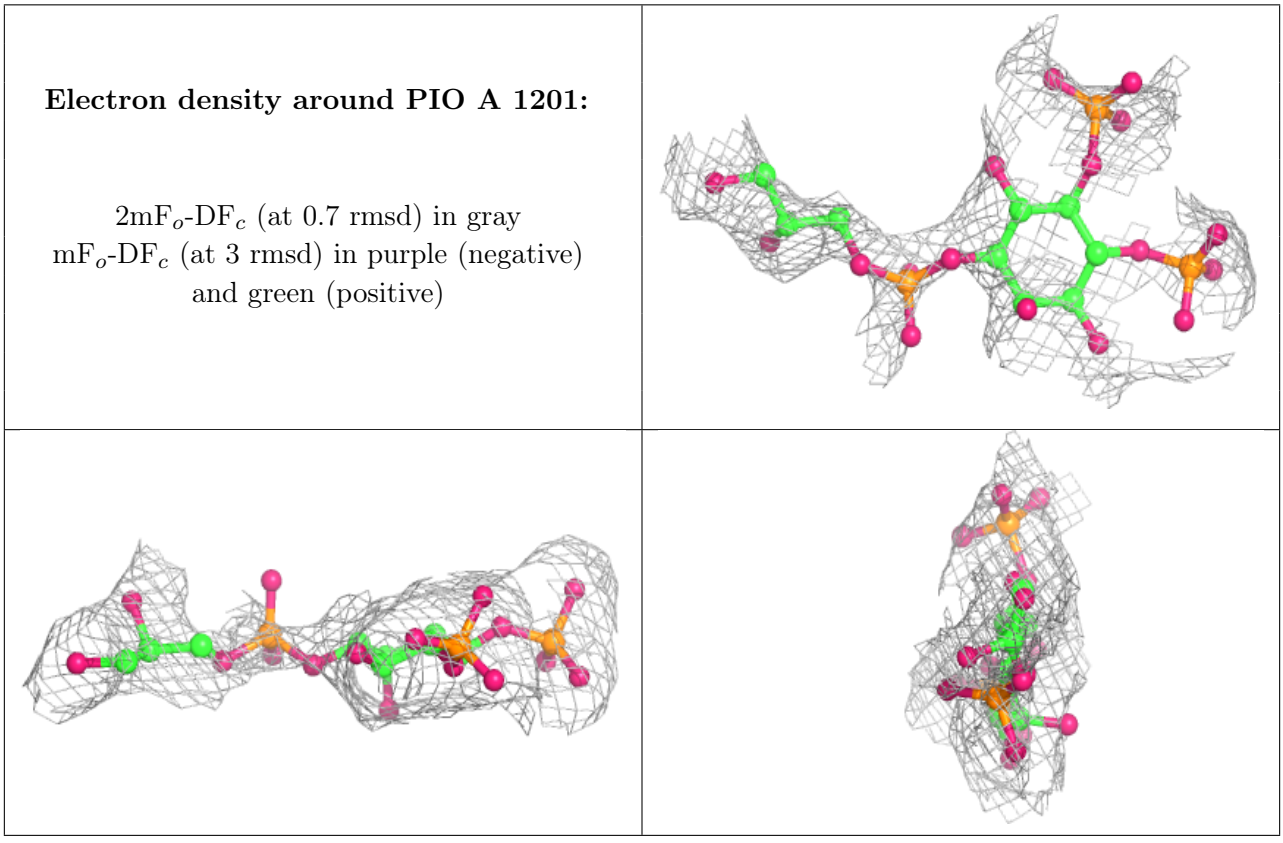
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

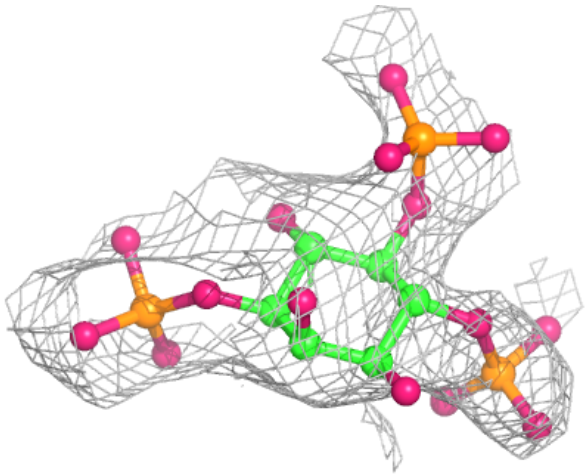
Electron density around PIO A 1201:

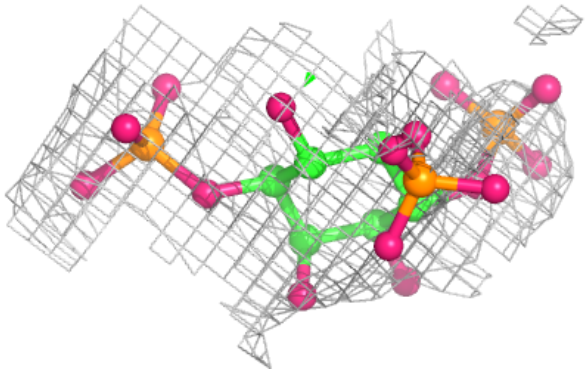
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

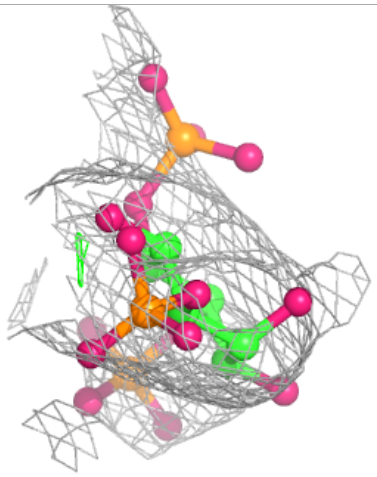


Electron density around PIO B 1201:

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

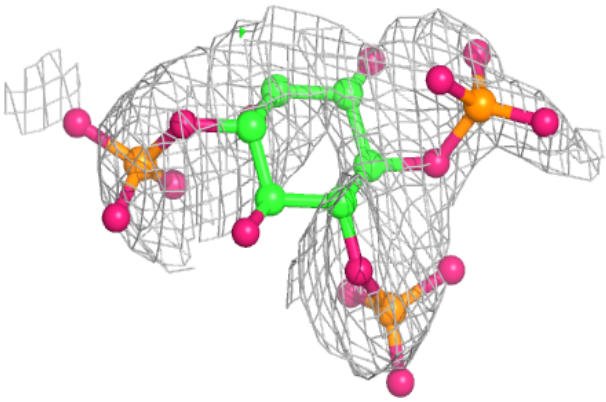


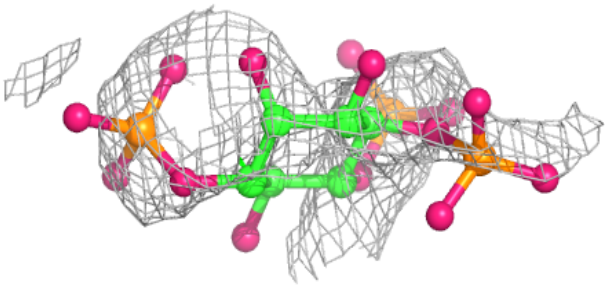


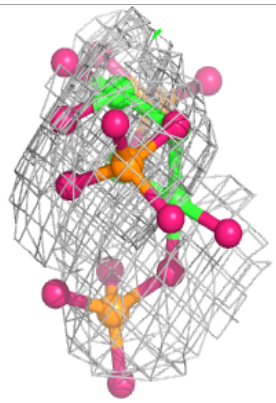


Electron density around PIO B 1202:

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

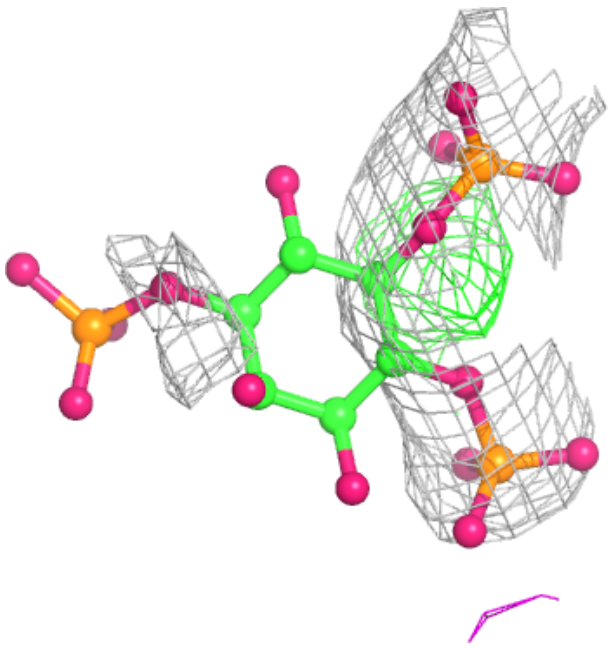


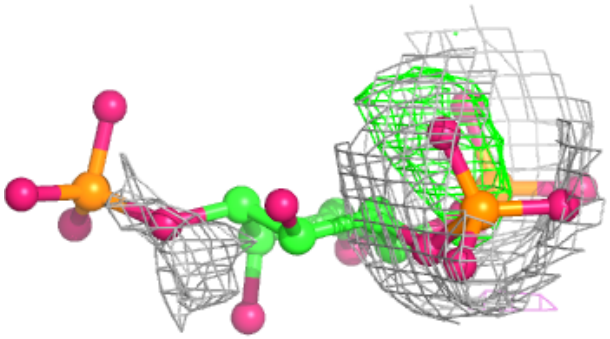


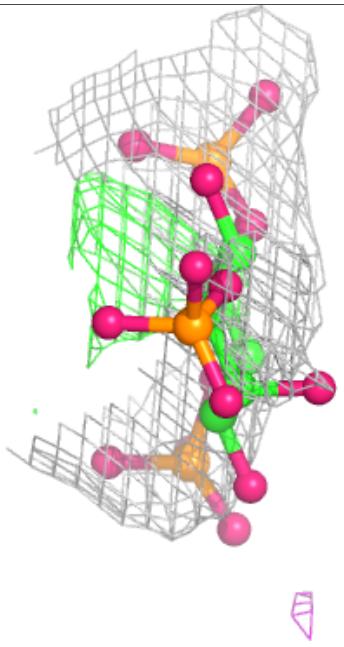


Electron density around PIO C 1201:

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

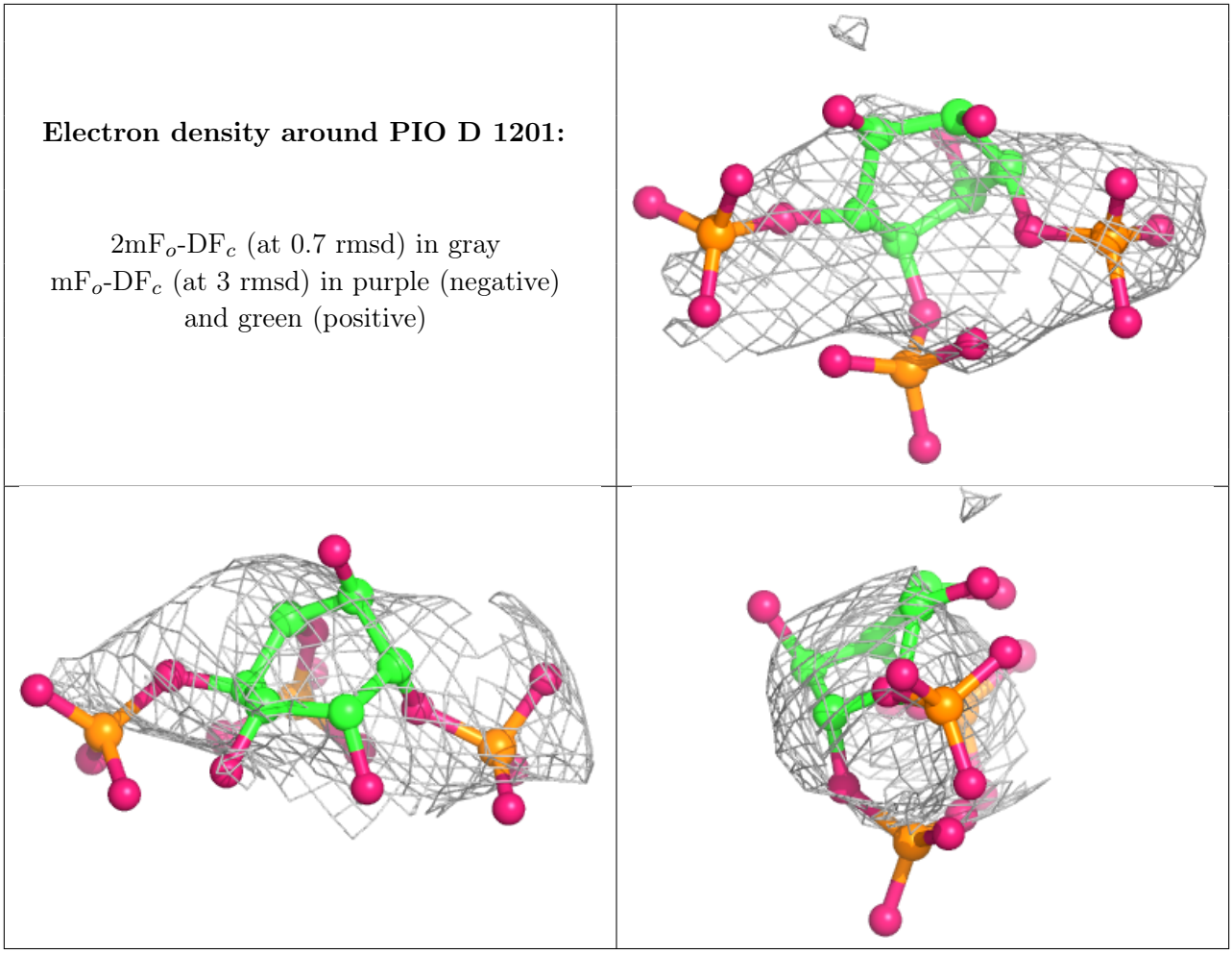






Electron density around PIO D 1201:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.