



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 07:23 am BST

PDB ID : 4DX6
Title : Transport of drugs by the multidrug transporter AcrB involves an access and a deep binding pocket that are separated by a switch-loop
Authors : Eicher, T.; Cha, H.; Seeger, M.A.; Brandstaetter, L.; El-Delik, J.; Bohnert, J.A.; Kern, W.V.; Verrey, F.; Gruetter, M.G.; Diederichs, K.; Pos, K.M.
Deposited on : 2012-02-27
Resolution : 2.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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 : 2.11
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) : 2.11

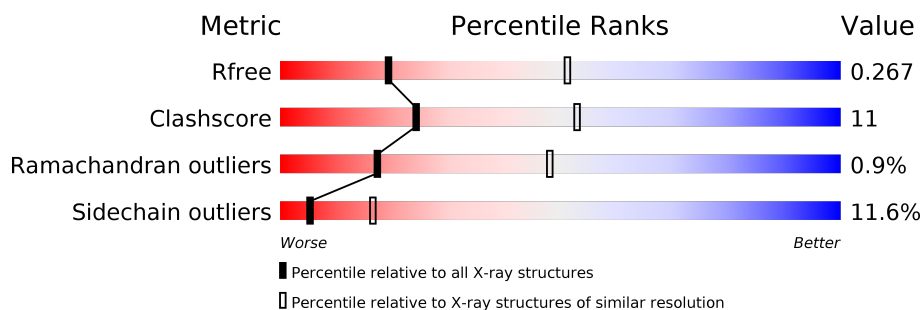
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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 ≥ 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1057	<div> <div style="width: 65%; background-color: green;"></div> <div style="width: 29%; background-color: yellow;"></div> <div style="width: 6%; background-color: orange;"></div> <div style="width: 0%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>65% 29% . .</div>
1	B	1057	<div> <div style="width: 70%; background-color: green;"></div> <div style="width: 24%; background-color: yellow;"></div> <div style="width: 4%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>70% 24% . .</div>
1	C	1057	<div> <div style="width: 67%; background-color: green;"></div> <div style="width: 27%; background-color: yellow;"></div> <div style="width: 4%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>67% 27% . .</div>
2	D	169	<div> <div style="width: 72%; background-color: green;"></div> <div style="width: 18%; background-color: yellow;"></div> <div style="width: 7%; background-color: orange;"></div> <div style="width: 3%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>72% 18% . 8%</div>
2	E	169	<div> <div style="width: 54%; background-color: green;"></div> <div style="width: 29%; background-color: yellow;"></div> <div style="width: 7%; background-color: orange;"></div> <div style="width: 10%; background-color: grey;"></div> </div> <div>54% 29% 7% 10%</div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 26232 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 Acriflavine resistance protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1044	Total	C	N	O	S	0	0	0
			7947	5108	1316	1479	44			
1	B	1033	Total	C	N	O	S	0	0	0
			7853	5054	1296	1459	44			
1	C	1034	Total	C	N	O	S	0	0	0
			7859	5057	1297	1461	44			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	616	ASN	GLY	CONFLICT	UNP P31224
A	1050	LEU	-	EXPRESSION TAG	UNP P31224
A	1051	GLU	-	EXPRESSION TAG	UNP P31224
A	1052	HIS	-	EXPRESSION TAG	UNP P31224
A	1053	HIS	-	EXPRESSION TAG	UNP P31224
A	1054	HIS	-	EXPRESSION TAG	UNP P31224
A	1055	HIS	-	EXPRESSION TAG	UNP P31224
A	1056	HIS	-	EXPRESSION TAG	UNP P31224
A	1057	HIS	-	EXPRESSION TAG	UNP P31224
B	616	ASN	GLY	CONFLICT	UNP P31224
B	1050	LEU	-	EXPRESSION TAG	UNP P31224
B	1051	GLU	-	EXPRESSION TAG	UNP P31224
B	1052	HIS	-	EXPRESSION TAG	UNP P31224
B	1053	HIS	-	EXPRESSION TAG	UNP P31224
B	1054	HIS	-	EXPRESSION TAG	UNP P31224
B	1055	HIS	-	EXPRESSION TAG	UNP P31224
B	1056	HIS	-	EXPRESSION TAG	UNP P31224
B	1057	HIS	-	EXPRESSION TAG	UNP P31224
C	616	ASN	GLY	CONFLICT	UNP P31224
C	1050	LEU	-	EXPRESSION TAG	UNP P31224
C	1051	GLU	-	EXPRESSION TAG	UNP P31224
C	1052	HIS	-	EXPRESSION TAG	UNP P31224
C	1053	HIS	-	EXPRESSION TAG	UNP P31224

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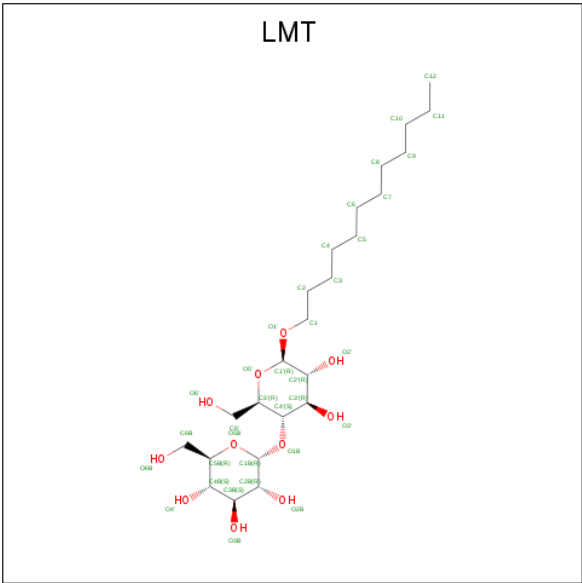
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Chain	Residue	Modelled	Actual	Comment	Reference
C	1054	HIS	-	EXPRESSION TAG	UNP P31224
C	1055	HIS	-	EXPRESSION TAG	UNP P31224
C	1056	HIS	-	EXPRESSION TAG	UNP P31224
C	1057	HIS	-	EXPRESSION TAG	UNP P31224

- Molecule 2 is a protein called DARPIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	156	Total	C	N	O	S	0	0	0
			1177	741	206	229	1			
2	E	152	Total	C	N	O	S	0	0	0
			1151	726	202	222	1			

- Molecule 3 is DODECYL-BETA-D-MALTOSIDE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			35	24	11		
3	A	1	Total	C	O	0	0
			35	24	11		
3	B	1	Total	C	O	0	0
			35	24	11		
3	B	1	Total	C	O	0	0
			35	24	11		
3	B	1	Total	C	O	0	0
			35	24	11		

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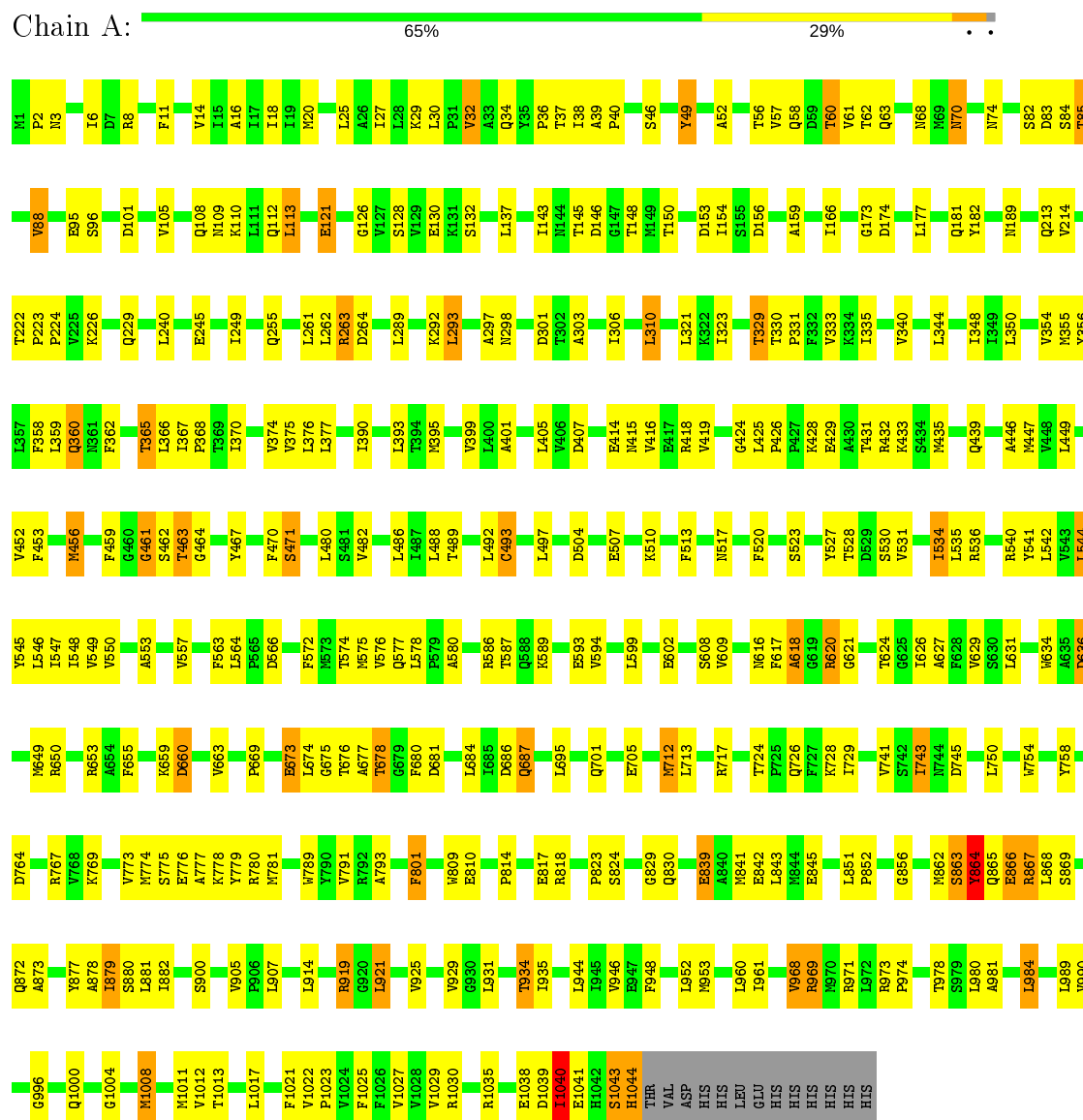
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			35	24	11		
3	C	1	Total	C	O	0	0
			35	24	11		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Acriflavine resistance protein B





Response	Percentage
Doing a good job	67%
Doing a bad job	27%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	145.69Å 165.45Å 245.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.28 – 2.90 49.28 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.28-2.90) 95.0 (49.28-2.29)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.7.3 _928	Depositor
R, R_{free}	0.209 , 0.270 0.204 , 0.267	Depositor DCC
R_{free} test set	12616 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.359	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	26232	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LMT

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	0.44	0/8099	0.64	0/10997
1	B	0.41	0/8003	0.60	1/10869 (0.0%)
1	C	0.44	0/8009	0.63	2/10877 (0.0%)
2	D	0.38	0/1196	0.58	0/1626
2	E	0.42	0/1170	0.63	0/1591
All	All	0.43	0/26477	0.62	3/35960 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	867	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	C	564	LEU	CA-CB-CG	5.20	127.27	115.30
1	B	250	LEU	CA-CB-CG	5.18	127.20	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7947	0	8087	211	0
1	B	7853	0	8004	154	0
1	C	7859	0	8009	174	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1177	0	1159	24	0
2	E	1151	0	1136	39	0
3	A	70	0	92	4	0
3	B	105	0	138	4	0
3	C	70	0	92	3	0
All	All	26232	0	26717	583	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 11.

The worst 5 of 583 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:GLY:H	1:A:624:THR:HG21	1.31	0.95
1:A:968:VAL:HG21	1:A:1023:PRO:HG3	1.57	0.86
1:C:57:VAL:HG21	1:C:86:GLY:HA2	1.59	0.84
1:C:616:ASN:HB3	1:C:618:ALA:H	1.41	0.84
1:A:764:ASP:OD2	1:A:769:LYS:NZ	2.16	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1042/1057 (99%)	963 (92%)	63 (6%)	16 (2%)	10	34
1	B	1031/1057 (98%)	954 (92%)	66 (6%)	11 (1%)	14	42
1	C	1032/1057 (98%)	963 (93%)	66 (6%)	3 (0%)	41	71
2	D	154/169 (91%)	144 (94%)	10 (6%)	0	100	100
2	E	150/169 (89%)	139 (93%)	10 (7%)	1 (1%)	22	54
All	All	3409/3509 (97%)	3163 (93%)	215 (6%)	31 (1%)	17	48

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	462	SER
1	A	864	TYR
1	A	866	GLU
1	A	1040	ILE
1	B	510	LYS

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	851/864 (98%)	747 (88%)	104 (12%)	5	15
1	B	840/864 (97%)	748 (89%)	92 (11%)	6	19
1	C	841/864 (97%)	742 (88%)	99 (12%)	5	16
2	D	120/132 (91%)	111 (92%)	9 (8%)	13	37
2	E	117/132 (89%)	101 (86%)	16 (14%)	3	11
All	All	2769/2856 (97%)	2449 (88%)	320 (12%)	5	16

5 of 320 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	569	GLN
1	B	880	SER
2	D	28	ASP
1	B	578	LEU
1	B	715	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	237	GLN
2	E	125	HIS
1	C	577	GLN
1	C	104	GLN

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Mol	Chain	Res	Type
1	C	439	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

7 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$
3	LMT	A	1101	-	36,36,36	1.18	3 (8%)	47,47,47	1.44	7 (14%)
3	LMT	B	1103	-	36,36,36	1.17	4 (11%)	47,47,47	1.64	14 (29%)
3	LMT	C	1101	-	36,36,36	1.13	3 (8%)	47,47,47	1.15	3 (6%)
3	LMT	A	1102	-	36,36,36	1.15	3 (8%)	47,47,47	1.48	7 (14%)
3	LMT	B	1102	-	36,36,36	1.17	3 (8%)	47,47,47	1.39	8 (17%)
3	LMT	C	1102	-	36,36,36	1.19	4 (11%)	47,47,47	1.28	5 (10%)
3	LMT	B	1101	-	36,36,36	1.17	3 (8%)	47,47,47	1.30	8 (17%)

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
3	LMT	A	1101	-	-	12/21/61/61	0/2/2/2
3	LMT	B	1103	-	-	16/21/61/61	0/2/2/2
3	LMT	C	1101	-	-	13/21/61/61	0/2/2/2
3	LMT	A	1102	-	-	13/21/61/61	0/2/2/2
3	LMT	B	1102	-	-	15/21/61/61	0/2/2/2
3	LMT	C	1102	-	-	10/21/61/61	0/2/2/2
3	LMT	B	1101	-	-	6/21/61/61	0/2/2/2

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1101	LMT	O5B-C1B	4.13	1.52	1.41
3	B	1101	LMT	O5B-C1B	4.02	1.52	1.41
3	B	1102	LMT	O5B-C1B	3.99	1.52	1.41
3	B	1103	LMT	O5B-C1B	3.98	1.52	1.41
3	C	1102	LMT	O5B-C1B	3.83	1.51	1.41

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1102	LMT	C1-O1'-C1'	5.08	122.27	113.84
3	A	1102	LMT	C3B-C4B-C5B	4.83	118.86	110.24
3	A	1102	LMT	C1-O1'-C1'	3.97	120.42	113.84
3	A	1101	LMT	O5'-C1'-C2'	3.68	118.14	110.35
3	A	1102	LMT	O5B-C5B-C4B	3.67	116.36	109.69

There are no chirality outliers.

5 of 85 torsion outliers are listed below:

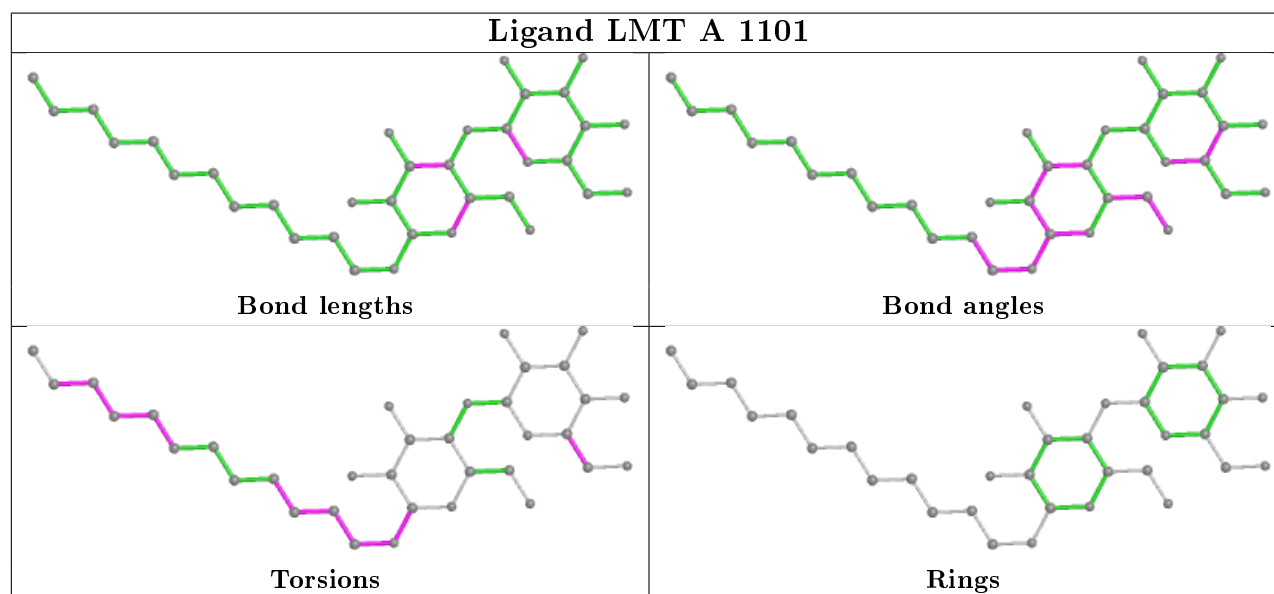
Mol	Chain	Res	Type	Atoms
3	A	1101	LMT	C2'-C1'-O1'-C1
3	B	1103	LMT	C2'-C1'-O1'-C1
3	B	1103	LMT	O5'-C1'-O1'-C1
3	C	1101	LMT	O5'-C1'-O1'-C1
3	C	1101	LMT	C2-C1-O1'-C1'

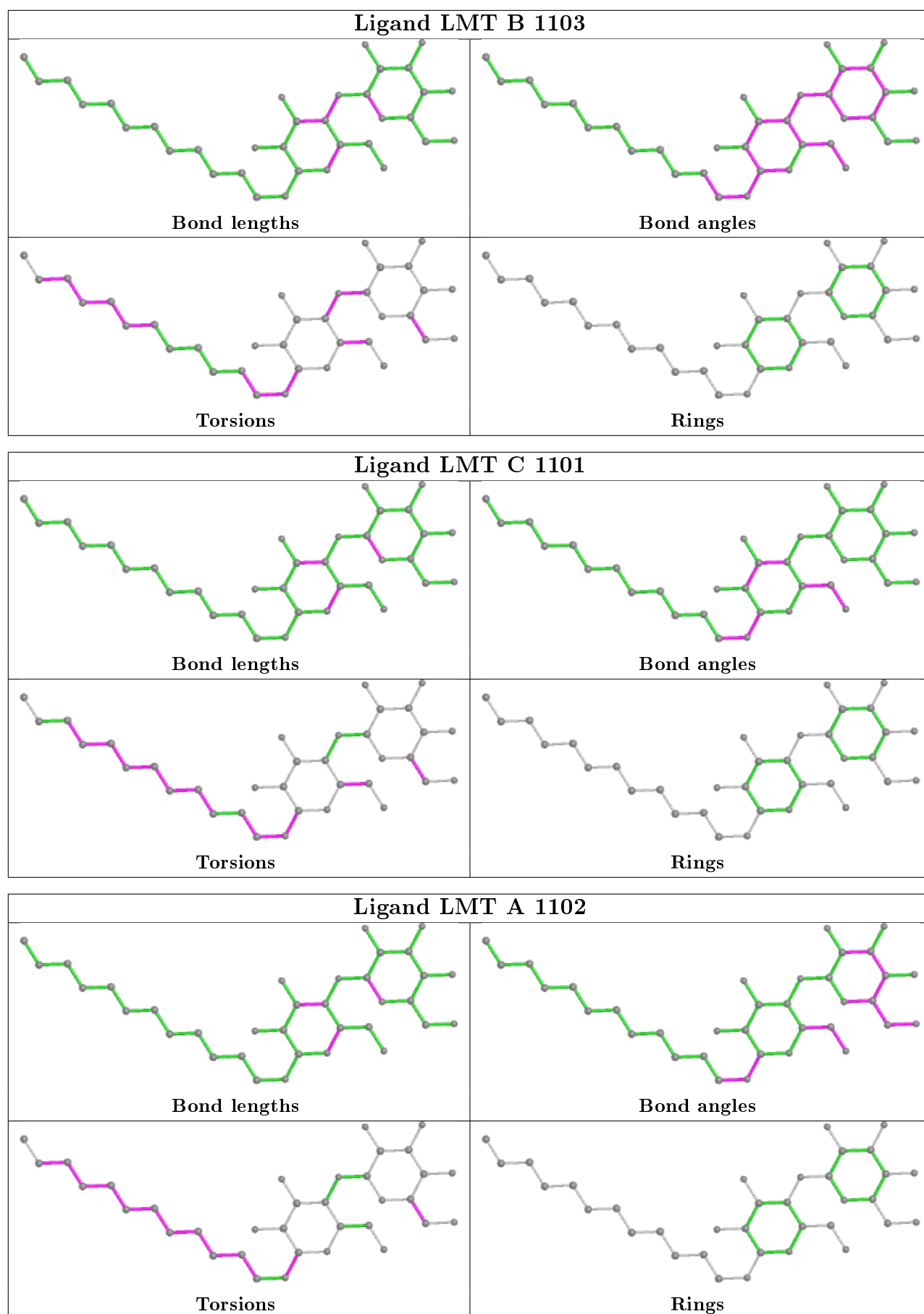
There are no ring outliers.

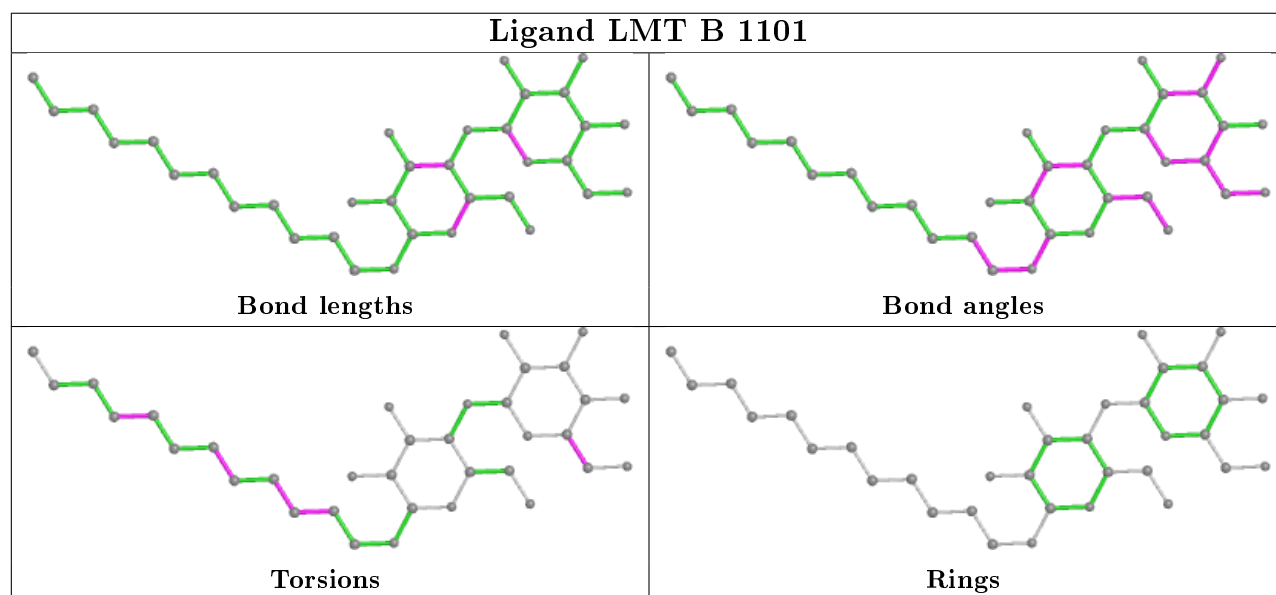
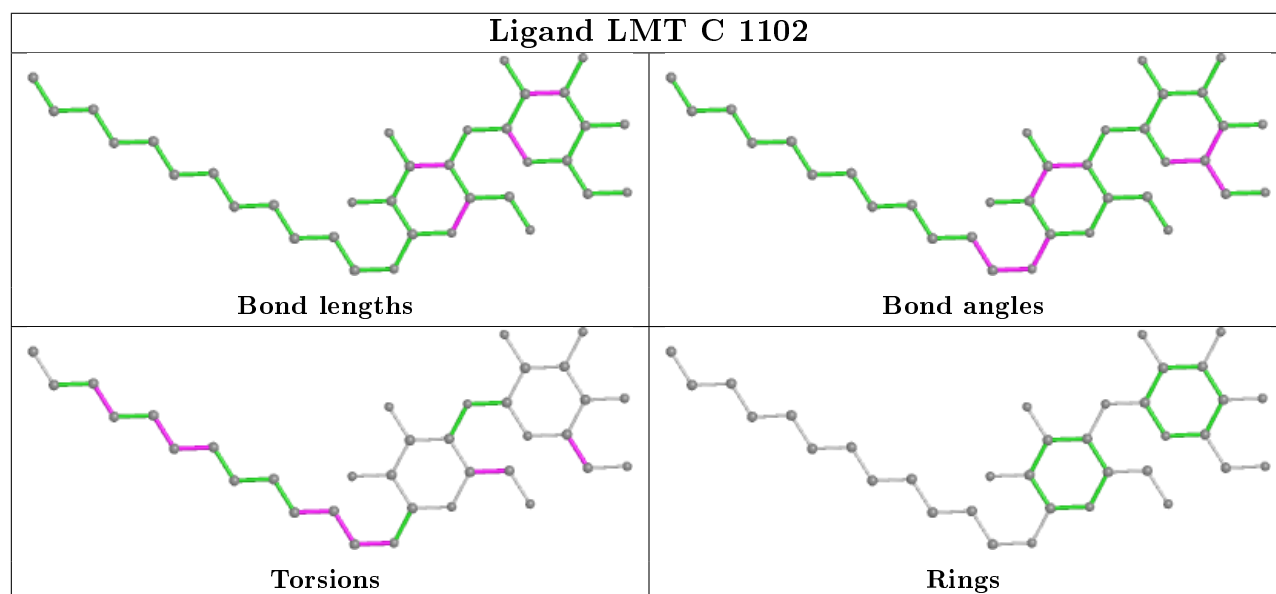
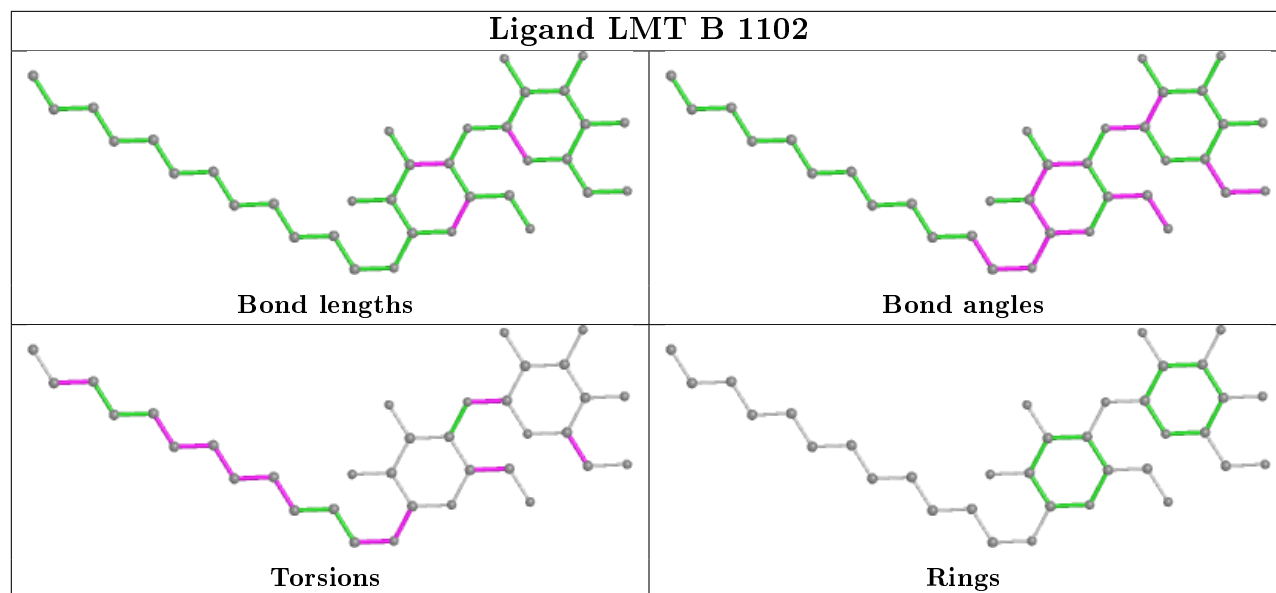
6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1101	LMT	2	0
3	B	1103	LMT	2	0
3	C	1101	LMT	1	0
3	A	1102	LMT	2	0
3	B	1102	LMT	2	0
3	C	1102	LMT	2	0

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







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](#)

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

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

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

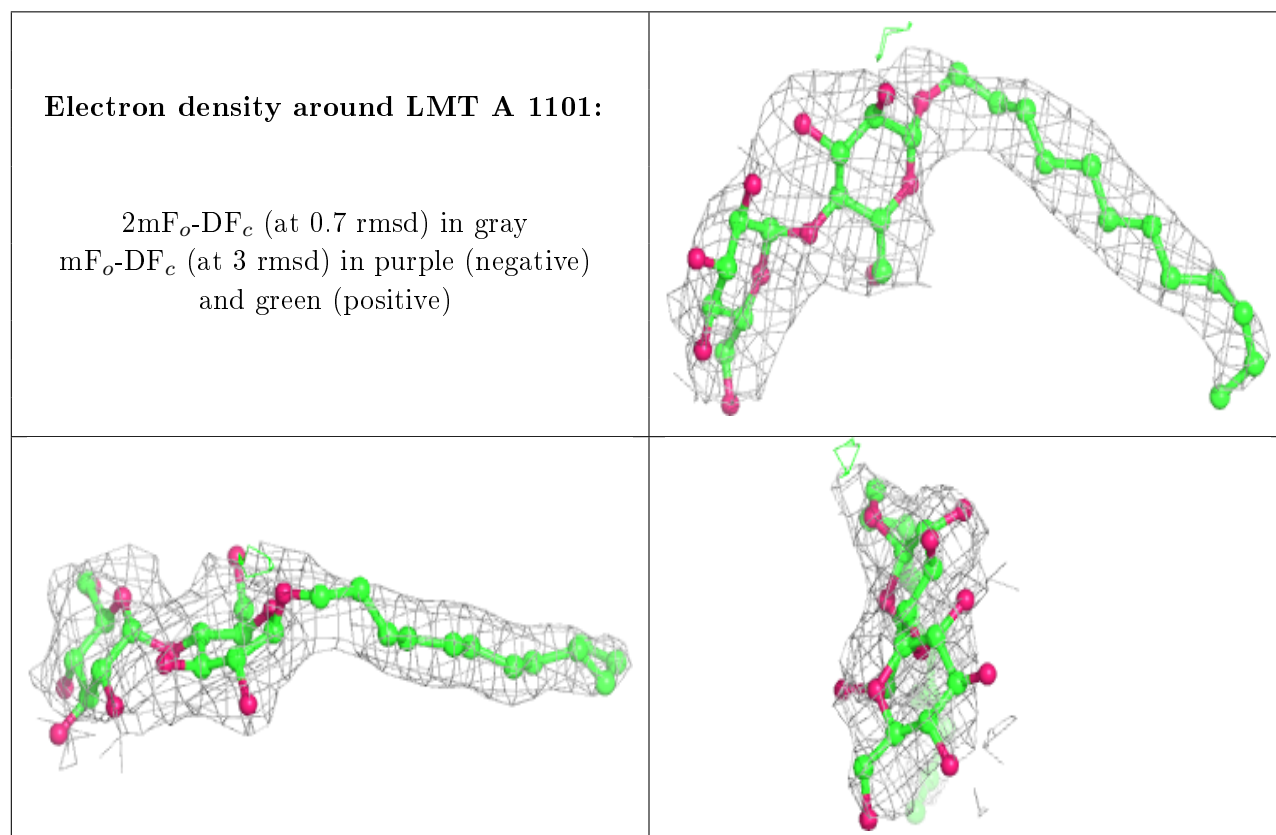
6.3 Carbohydrates [i](#)

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

6.4 Ligands [i](#)

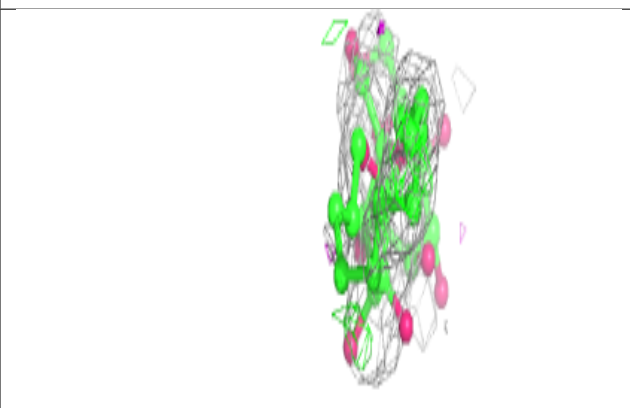
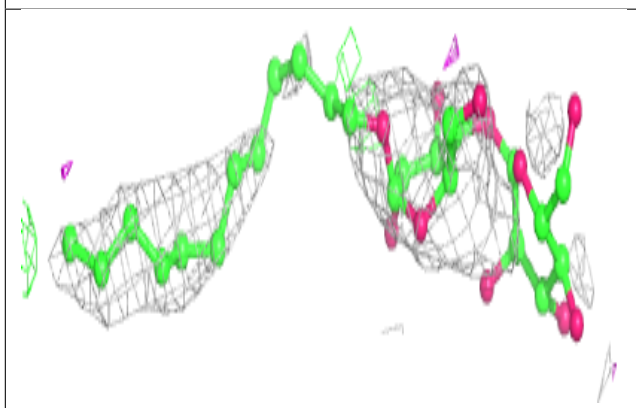
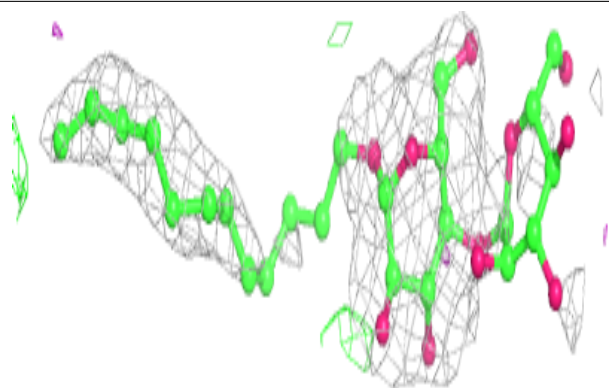
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

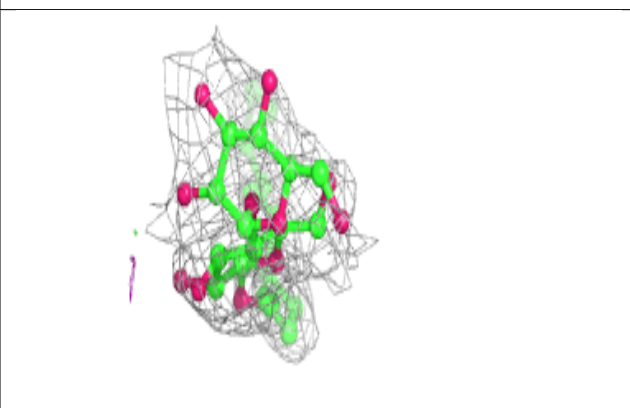
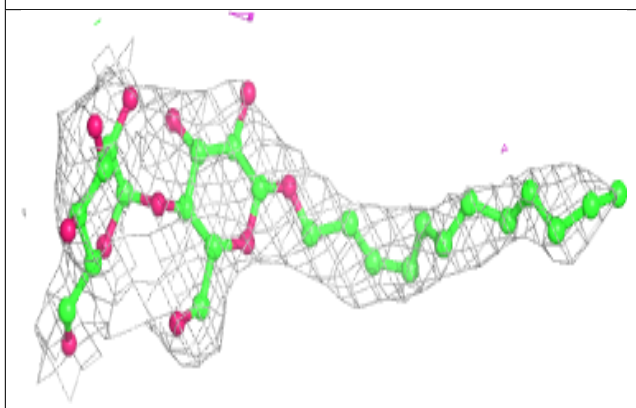
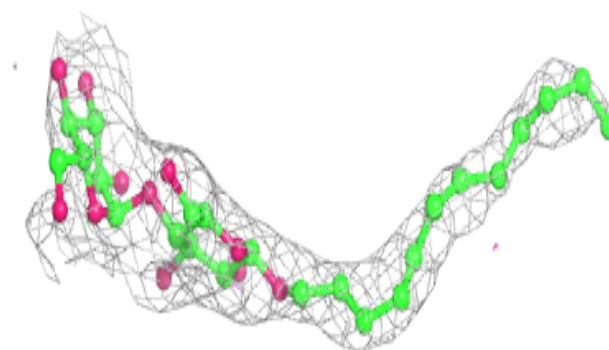


Electron density around LMT B 1103:

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

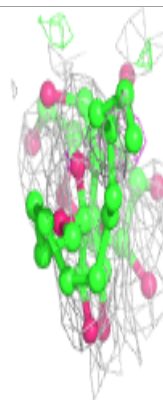
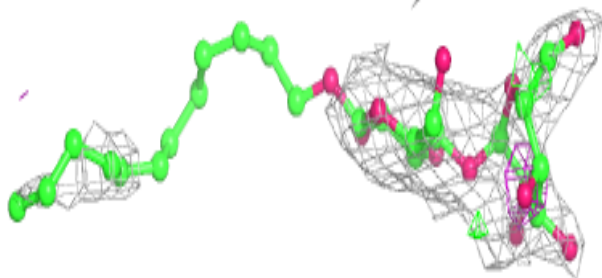
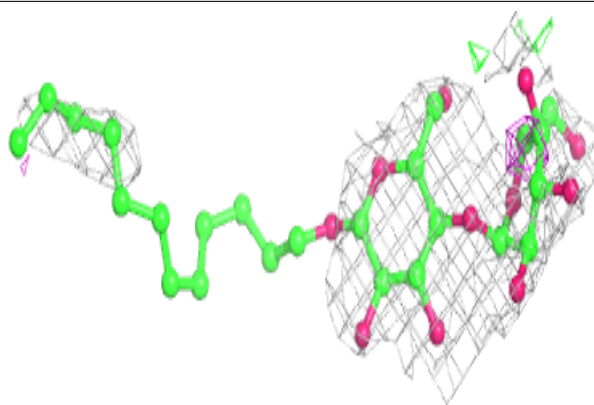
**Electron density around LMT C 1101:**

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

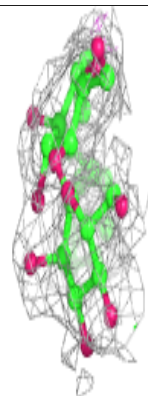
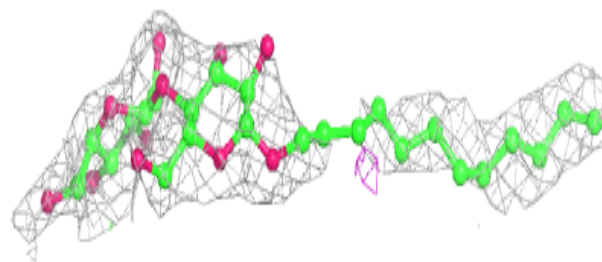
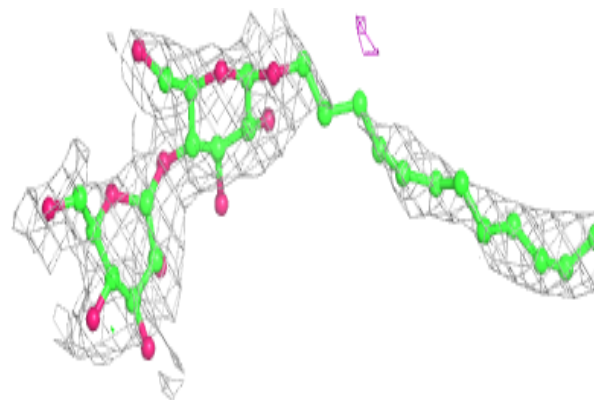


Electron density around LMT A 1102:

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

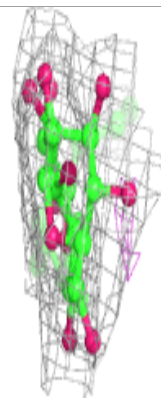
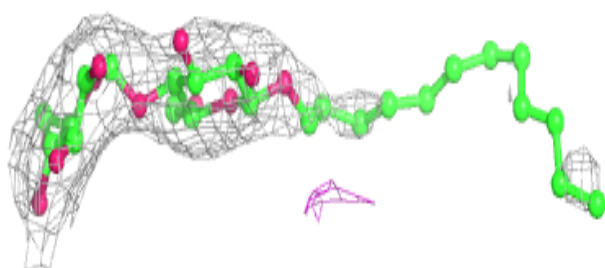
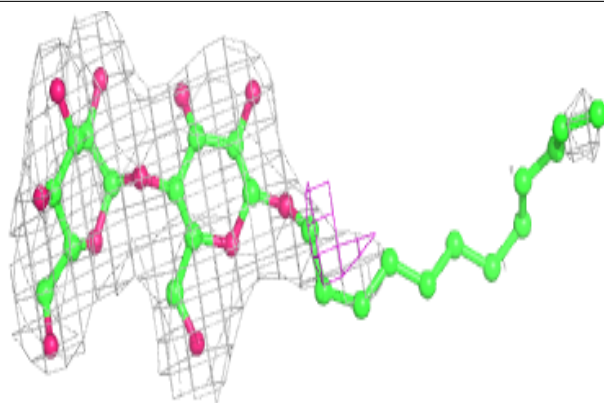
**Electron density around LMT B 1102:**

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

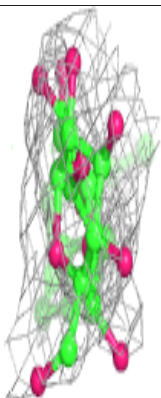
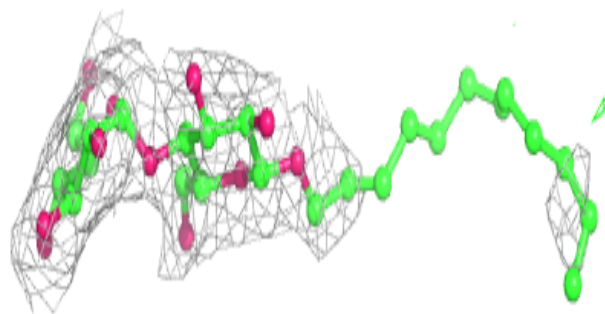
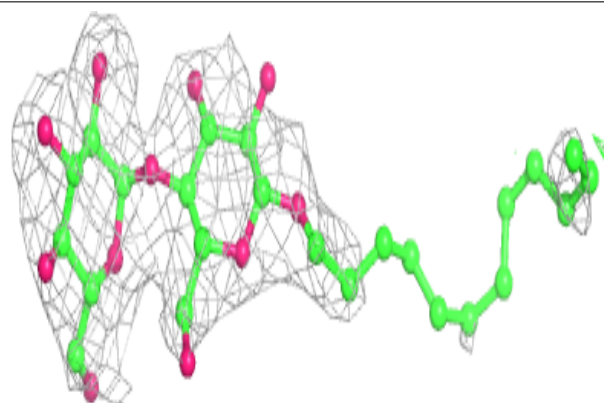


Electron density around LMT C 1102:

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

**Electron density around LMT B 1101:**

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



6.5 Other polymers

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