



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 10:37 PM UTC

PDB ID : 6ZOH / pdb_00006zoh
Title : 3-Formylrifamycin SV binding to the access pocket of AcrB-G619P_G621P L and T protomers
Authors : Tam, H.K.; Foong, W.E.; Pos, K.M.
Deposited on : 2020-07-07
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

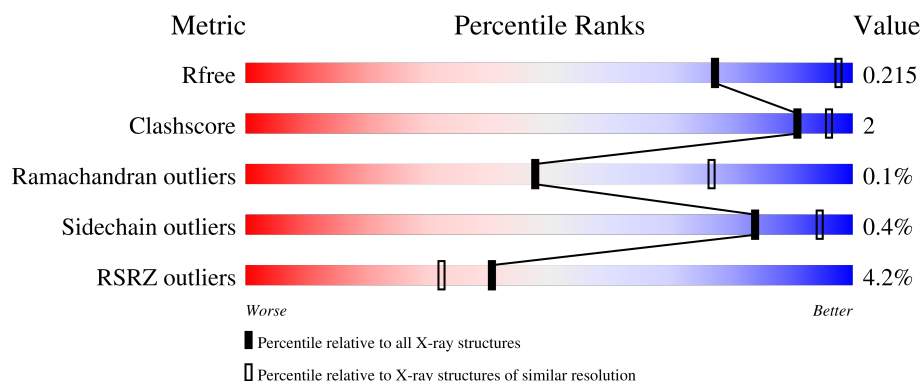
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	1057	6% 91% 7%
1	B	1057	5% 93% 5%
1	C	1057	% 93% 5%
2	D	169	2% 91% 9%
2	E	169	7% 91% 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	D12	A	1208	-	-	-	X
7	DDQ	A	1206	-	-	-	X

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 26785 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 Multidrug efflux pump subunit AcrB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1034	Total	C	N	O	S	0	2	0
			7875	5070	1299	1462	44			
1	B	1034	Total	C	N	O	S	0	1	0
			7866	5065	1296	1460	45			
1	C	1033	Total	C	N	O	S	0	0	0
			7855	5058	1295	1458	44			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	619	PRO	GLY	engineered mutation	UNP P31224
A	621	PRO	GLY	engineered mutation	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	619	PRO	GLY	engineered mutation	UNP P31224
B	621	PRO	GLY	engineered mutation	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	619	PRO	GLY	engineered mutation	UNP P31224
C	621	PRO	GLY	engineered mutation	UNP P31224
C	1050	LEU	-	expression tag	UNP P31224

Continued on next page...

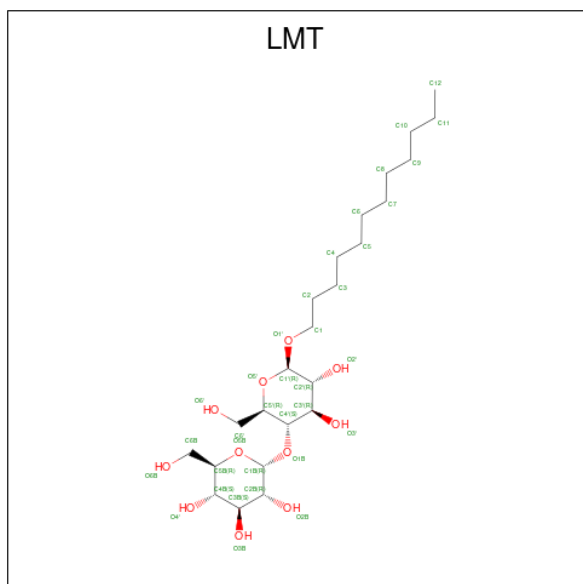
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	1051	GLU	-	expression tag	UNP P31224
C	1052	HIS	-	expression tag	UNP P31224
C	1053	HIS	-	expression tag	UNP P31224
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	154	Total	C	N	O	S	0	0	0
			1167	736	204	226	1			
2	E	153	Total	C	N	O	S	0	0	0
			1159	732	203	223	1			

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



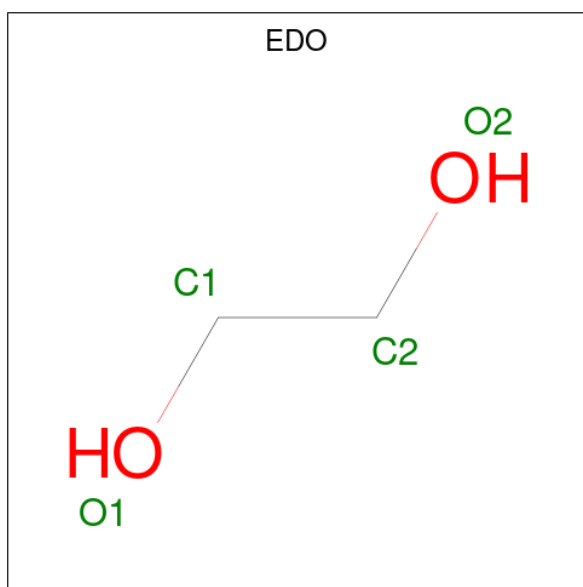
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			35	24	11		
3	A	1	Total	C	O	0	0
			35	24	11		
3	A	1	Total	C	O	0	0
			35	24	11		
3	B	1	Total	C	O	0	0
			35	24	11		

Continued on next page...

Continued from previous page...

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	C	1	Total	C	O	0	0
			35	24	11		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

Continued on next page...

Continued from previous page...

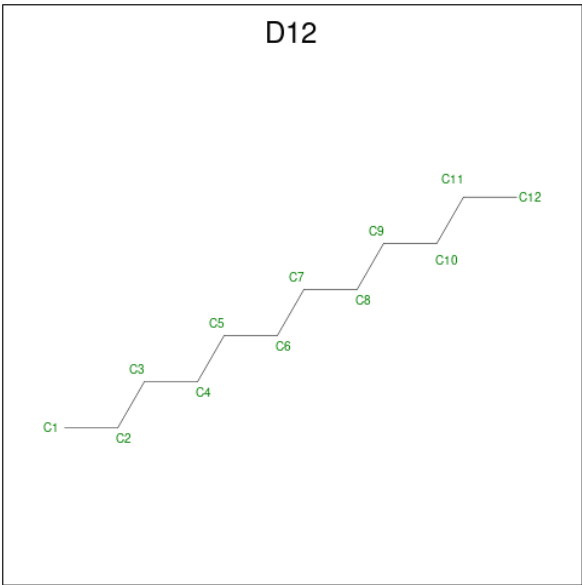
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



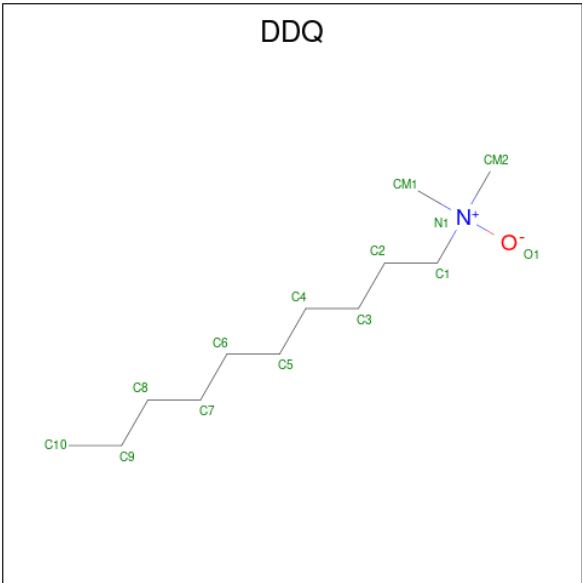
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is DODECANE (CCD ID: D12) (formula: $C_{12}H_{26}$).



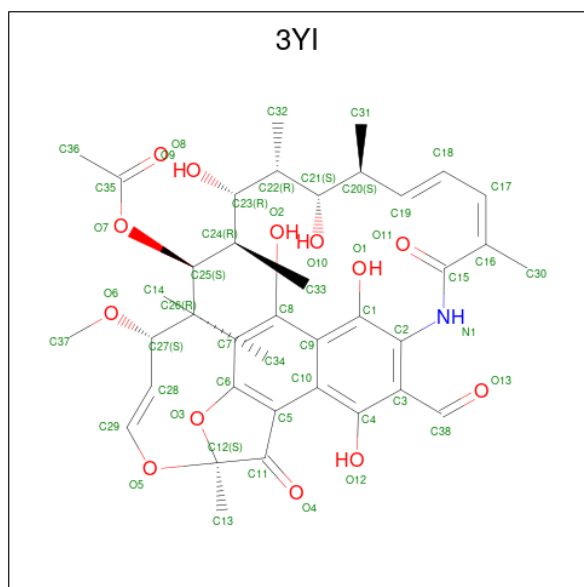
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C 12 12	0	0
6	A	1	Total C 12 12	0	0
6	C	1	Total C 12 12	0	0
6	C	1	Total C 12 12	0	0

- Molecule 7 is DECYLAMINE-N,N-DIMETHYL-N-OXIDE (CCD ID: DDQ) (formula: C₁₂H₂₇NO).



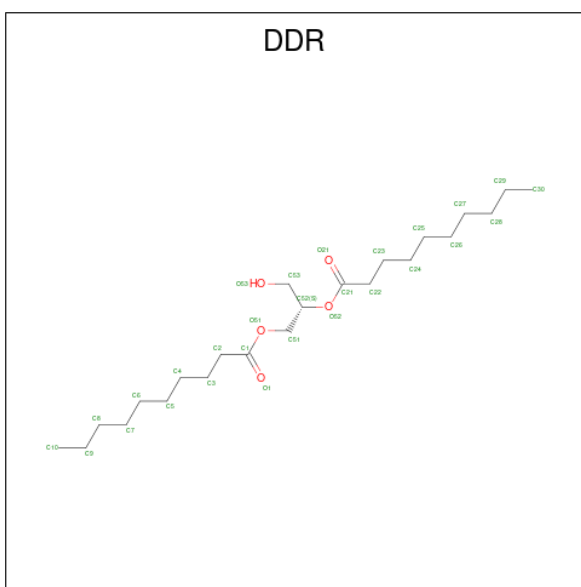
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	12	1	1		
7	B	1	Total	C	N	O	0	0
			14	12	1	1		

- Molecule 8 is (2S,12Z,14E,16S,17S,18R,19R,20R,21S,22R,23S,24E)-8-formyl-5,6,9,17,19-pentahydroxy-23-methoxy-2,4,12,16,18,20,22-heptamethyl-1,11-dioxo-1,2-dihydro-2,7-(epoxypentadeca[1,11,13]trienoimino)naphtho[2,1-b]furan-21-yl acetate (CCD ID: 3YI) (formula: $C_{38}H_{47}NO_{13}$) (labeled as "Ligand of Interest" by depositor).



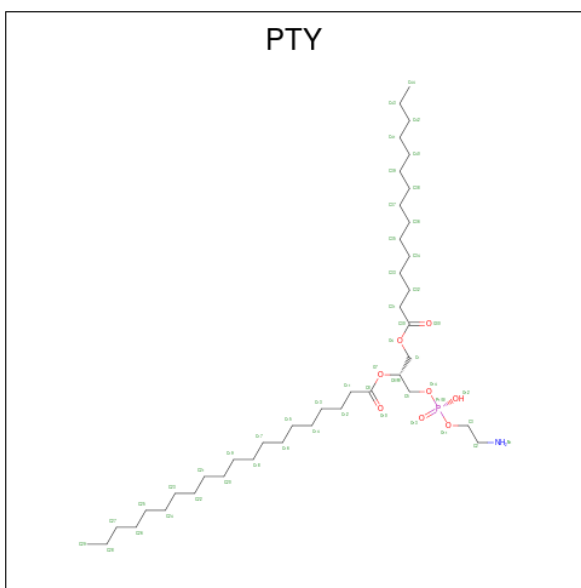
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			52	38	1	13		
8	B	1	Total	C	N	O	0	0
			52	38	1	13		

- Molecule 9 is (2S)-3-hydroxypropane-1,2-diyl didecanoate (CCD ID: DDR) (formula: $C_{23}H_{44}O_5$).



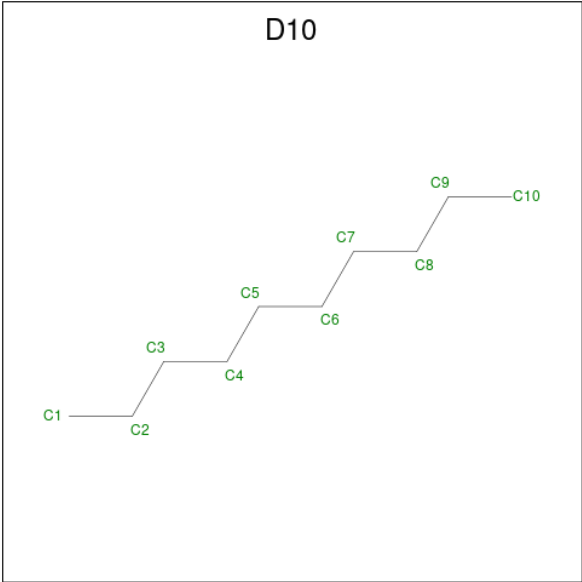
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			28	23	5		

- Molecule 10 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula: $C_{40}H_{80}NO_8P$).



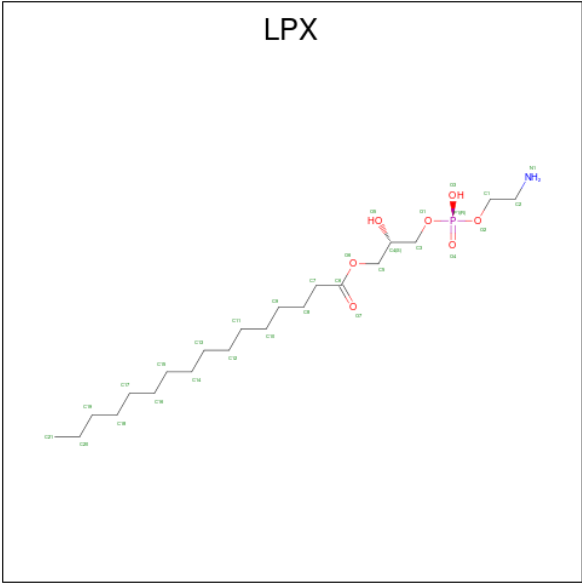
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	C	1	Total	C	N	O	P	0	0
			50	40	1	8	1		

- Molecule 11 is DECANE (CCD ID: D10) (formula: $\text{C}_{10}\text{H}_{22}$).



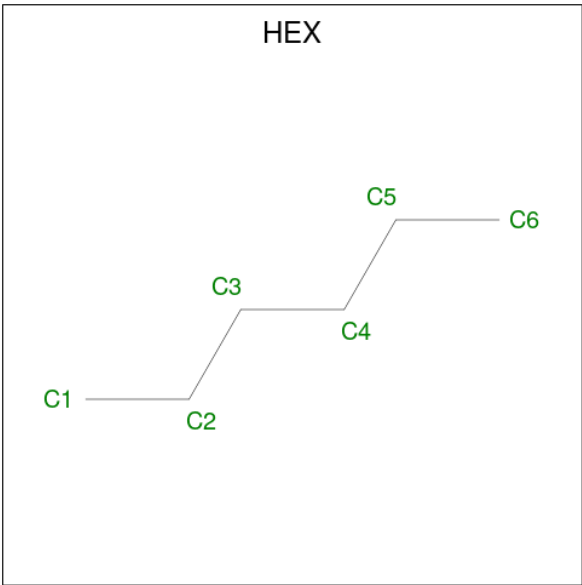
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	C	1	Total	C			0	0
			10	10				

- Molecule 12 is (2S)-3-{[(R)-(2-aminoethoxy)(hydroxy)phosphoryl]oxy}-2-hydroxypropyl hexadecanoate (CCD ID: LPX) (formula: C₂₁H₄₄NO₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	C	1	Total	C	N	O	P	0	0
			30	21	1	7	1		

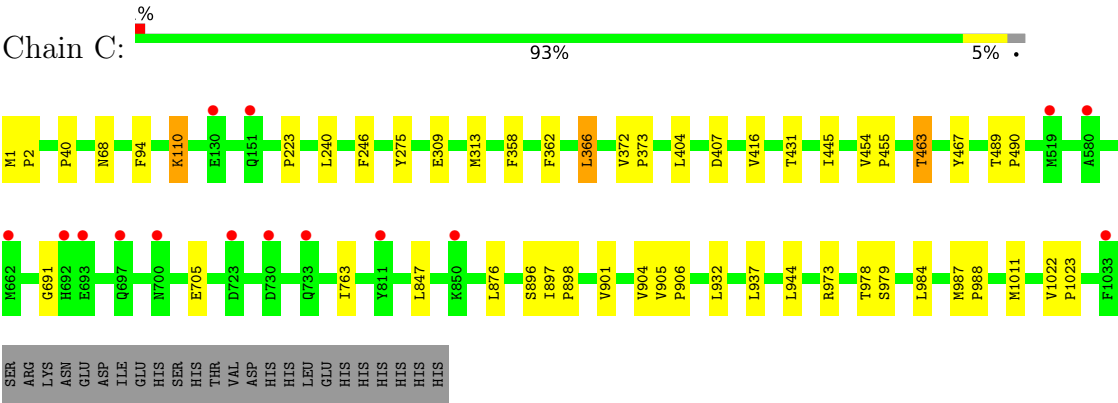
- Molecule 13 is HEXANE (CCD ID: HEX) (formula: C₆H₁₄).



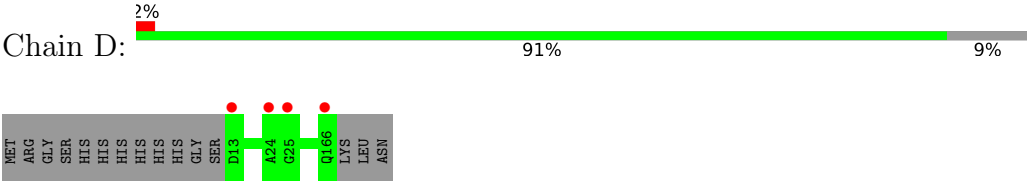
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	C	1	Total C 6 6	0	0
13	C	1	Total C 6 6	0	0

- Molecule 14 is water.

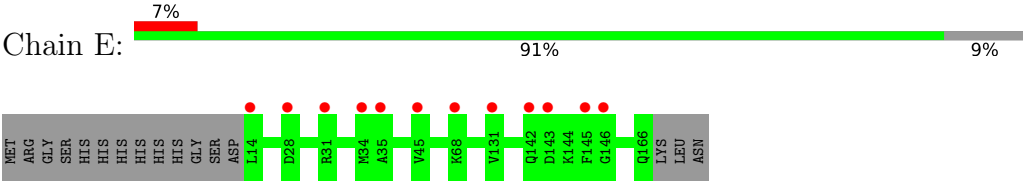
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	A	78	Total O 78 78	0	0
14	B	67	Total O 69 69	0	2
14	C	68	Total O 69 69	0	1
14	D	17	Total O 18 18	0	1
14	E	8	Total O 10 10	0	2



• Molecule 2: DARPIN



• Molecule 2: DARPIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	145.14Å 160.13Å 243.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.19 – 2.80 49.19 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.19-2.80) 100.0 (49.19-2.80)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.223 , 0.245 (Not available) , 0.215	Depositor DCC
R_{free} test set	6765 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	57.5	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	26785	wwPDB-VP
Average B, all atoms (Å ²)	64.0	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: LPX, HEX, 3YI, GOL, PTY, D10, DDR, LMT, EDO, D12, DDQ

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	1.03	0/8033	1.56	3/10911 (0.0%)
1	B	1.03	0/8021	1.56	5/10895 (0.0%)
1	C	1.02	0/8007	1.55	5/10877 (0.0%)
2	D	1.02	0/1186	1.57	0/1613
2	E	1.03	0/1178	1.58	0/1602
All	All	1.02	0/26425	1.56	13/35898 (0.0%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	896	SER	CA-C-N	7.30	124.84	120.24
1	A	896	SER	C-N-CA	7.30	124.84	120.24
1	A	691	GLY	CA-C-O	-5.81	118.26	122.45
1	C	691	GLY	CA-C-O	-5.81	118.27	122.45
1	B	691	GLY	CA-C-O	-5.60	118.28	122.37

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	7875	0	8033	42	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	7866	0	8023	28	0
1	C	7855	0	8009	26	0
2	D	1167	0	1151	0	0
2	E	1159	0	1147	0	0
3	A	105	0	138	0	0
3	B	35	0	46	0	0
3	C	105	0	138	0	0
4	A	16	0	24	0	0
4	B	8	0	12	0	0
4	C	16	0	24	0	0
5	A	6	0	8	0	0
5	B	6	0	8	0	0
5	C	12	0	16	0	0
6	A	24	0	52	0	0
6	C	24	0	52	0	0
7	A	14	0	27	1	0
7	B	14	0	27	0	0
8	A	52	0	0	1	0
8	B	52	0	0	1	0
9	B	28	0	44	0	0
10	C	50	0	79	0	0
11	C	10	0	22	0	0
12	C	30	0	43	0	0
13	C	12	0	28	0	0
14	A	78	0	0	0	0
14	B	69	0	0	0	0
14	C	69	0	0	0	0
14	D	18	0	0	0	0
14	E	10	0	0	0	0
All	All	26785	0	27151	93	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 2.

The worst 5 of 93 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:209:ALA:HB1	1:B:743:ILE:HG21	1.71	0.72
1:A:968:VAL:HG11	1:A:1023:PRO:HG3	1.73	0.71
1:A:85:THR:HG21	1:A:621:PRO:HD2	1.80	0.64
1:C:372:VAL:HB	1:C:373:PRO:HD3	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:979:SER:HA	1:C:1011:MET:HE3	1.81	0.62

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	1034/1057 (98%)	998 (96%)	33 (3%)	3 (0%)	36	66
1	B	1033/1057 (98%)	1005 (97%)	28 (3%)	0	100	100
1	C	1031/1057 (98%)	1007 (98%)	24 (2%)	0	100	100
2	D	152/169 (90%)	150 (99%)	2 (1%)	0	100	100
2	E	151/169 (89%)	147 (97%)	4 (3%)	0	100	100
All	All	3401/3509 (97%)	3307 (97%)	91 (3%)	3 (0%)	48	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	622	GLN
1	A	621	PRO
1	A	126	GLY

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	844/865 (98%)	842 (100%)	2 (0%)	87	96
1	B	843/865 (98%)	837 (99%)	6 (1%)	76	91
1	C	841/865 (97%)	838 (100%)	3 (0%)	84	94
2	D	119/132 (90%)	119 (100%)	0	100	100
2	E	118/132 (89%)	118 (100%)	0	100	100
All	All	2765/2859 (97%)	2754 (100%)	11 (0%)	84	94

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	801	PHE
1	C	110	LYS
1	C	984	LEU
1	C	463	THR
1	B	556	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	58	GLN
2	E	155	ASN
1	C	120	GLN
2	D	92	HIS
1	C	81	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 oligosaccharides in this entry.

5.6 Ligand geometry

35 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
5	GOL	B	1103	-	5,5,5	0.09	0	5,5,5	0.24	0
5	GOL	C	1116	-	5,5,5	0.10	0	5,5,5	0.29	0
6	D12	C	1104	-	11,11,11	0.09	0	10,10,10	0.06	0
4	EDO	C	1108	-	3,3,3	0.05	0	2,2,2	0.07	0
6	D12	A	1205	-	11,11,11	0.08	0	10,10,10	0.09	0
11	D10	C	1105	-	9,9,9	0.08	0	8,8,8	0.06	0
12	LPX	C	1106	-	29,29,29	0.29	0	31,33,33	0.36	0
4	EDO	B	1104	-	3,3,3	0.07	0	2,2,2	0.11	0
4	EDO	A	1203	-	3,3,3	0.06	0	2,2,2	0.08	0
3	LMT	A	1201	-	36,36,36	0.46	0	47,47,47	0.58	0
9	DDR	B	1105	-	27,27,27	0.25	0	29,29,29	0.24	0
6	D12	A	1208	-	11,11,11	0.08	0	10,10,10	0.09	0
4	EDO	A	1207	-	3,3,3	0.06	0	2,2,2	0.11	0
7	DDQ	B	1106	-	11,13,13	0.12	0	12,15,15	0.30	0
10	PTY	C	1101	-	49,49,49	0.26	0	52,54,54	0.33	0
13	HEX	C	1115	-	5,5,5	0.13	0	4,4,4	0.08	0
3	LMT	B	1101	-	36,36,36	0.49	1 (2%)	47,47,47	0.73	1 (2%)
6	D12	C	1103	-	11,11,11	0.08	0	10,10,10	0.07	0
3	LMT	C	1114	-	36,36,36	0.51	1 (2%)	47,47,47	0.77	1 (2%)
4	EDO	A	1212	-	3,3,3	0.06	0	2,2,2	0.13	0
5	GOL	C	1112	-	5,5,5	0.09	0	5,5,5	0.29	0
7	DDQ	A	1206	-	11,13,13	0.14	0	12,15,15	0.42	0
3	LMT	A	1202	-	36,36,36	0.52	1 (2%)	47,47,47	0.75	0
3	LMT	C	1113	-	36,36,36	0.54	1 (2%)	47,47,47	0.75	2 (4%)
4	EDO	C	1107	-	3,3,3	0.07	0	2,2,2	0.07	0
4	EDO	C	1109	-	3,3,3	0.07	0	2,2,2	0.12	0
13	HEX	C	1111	-	5,5,5	0.13	0	4,4,4	0.10	0
8	3YI	A	1210	-	55,55,55	0.99	2 (3%)	82,83,83	1.46	9 (10%)
8	3YI	B	1107	-	55,55,55	0.99	2 (3%)	82,83,83	1.50	9 (10%)
4	EDO	C	1110	-	3,3,3	0.07	0	2,2,2	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	LMT	A	1211	-	36,36,36	0.49	0	47,47,47	0.65	1 (2%)
4	EDO	A	1209	-	3,3,3	0.07	0	2,2,2	0.14	0
5	GOL	A	1204	-	5,5,5	0.08	0	5,5,5	0.26	0
3	LMT	C	1102	-	36,36,36	0.45	0	47,47,47	0.73	1 (2%)
4	EDO	B	1102	-	3,3,3	0.07	0	2,2,2	0.14	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
5	GOL	B	1103	-	-	1/4/4/4	-
5	GOL	C	1116	-	-	0/4/4/4	-
6	D12	C	1104	-	-	2/9/9/9	-
4	EDO	C	1108	-	-	1/1/1/1	-
6	D12	A	1205	-	-	6/9/9/9	-
11	D10	C	1105	-	-	2/7/7/7	-
12	LPX	C	1106	-	-	11/31/31/31	-
4	EDO	B	1104	-	-	0/1/1/1	-
4	EDO	A	1203	-	-	0/1/1/1	-
3	LMT	A	1201	-	-	7/21/61/61	0/2/2/2
9	DDR	B	1105	-	-	12/29/29/29	-
6	D12	A	1208	-	-	2/9/9/9	-
4	EDO	A	1207	-	-	1/1/1/1	-
7	DDQ	B	1106	-	-	5/11/11/11	-
10	PTY	C	1101	-	-	29/53/53/53	-
13	HEX	C	1115	-	-	1/3/3/3	-
3	LMT	B	1101	-	-	7/21/61/61	0/2/2/2
6	D12	C	1103	-	-	5/9/9/9	-
3	LMT	C	1114	-	-	14/21/61/61	0/2/2/2
4	EDO	A	1212	-	-	0/1/1/1	-
5	GOL	C	1112	-	-	1/4/4/4	-
7	DDQ	A	1206	-	-	7/11/11/11	-
3	LMT	A	1202	-	-	9/21/61/61	0/2/2/2
3	LMT	C	1113	-	-	12/21/61/61	0/2/2/2
4	EDO	C	1107	-	-	1/1/1/1	-
4	EDO	C	1109	-	-	1/1/1/1	-
13	HEX	C	1111	-	-	0/3/3/3	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	3YI	A	1210	-	-	14/57/72/72	0/4/4/4
8	3YI	B	1107	-	-	14/57/72/72	0/4/4/4
4	EDO	C	1110	-	-	1/1/1/1	-
3	LMT	A	1211	-	-	12/21/61/61	0/2/2/2
4	EDO	A	1209	-	-	1/1/1/1	-
5	GOL	A	1204	-	-	4/4/4/4	-
3	LMT	C	1102	-	-	12/21/61/61	0/2/2/2
4	EDO	B	1102	-	-	1/1/1/1	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	1107	3YI	C15-N1	4.35	1.44	1.35
8	A	1210	3YI	C15-N1	4.11	1.44	1.35
3	C	1113	LMT	O1'-C1'	2.31	1.44	1.40
3	A	1202	LMT	O1'-C1'	2.19	1.43	1.40
8	B	1107	3YI	C14-C7	-2.18	1.47	1.51

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	1107	3YI	C2-C3-C4	6.27	123.17	119.19
8	A	1210	3YI	C2-C3-C4	6.01	123.00	119.19
8	B	1107	3YI	C4-C3-C38	-5.14	112.78	119.83
8	A	1210	3YI	C4-C3-C38	-4.73	113.35	119.83
8	B	1107	3YI	C3-C2-C1	-4.03	117.82	120.68

There are no chirality outliers.

5 of 196 torsion outliers are listed below:

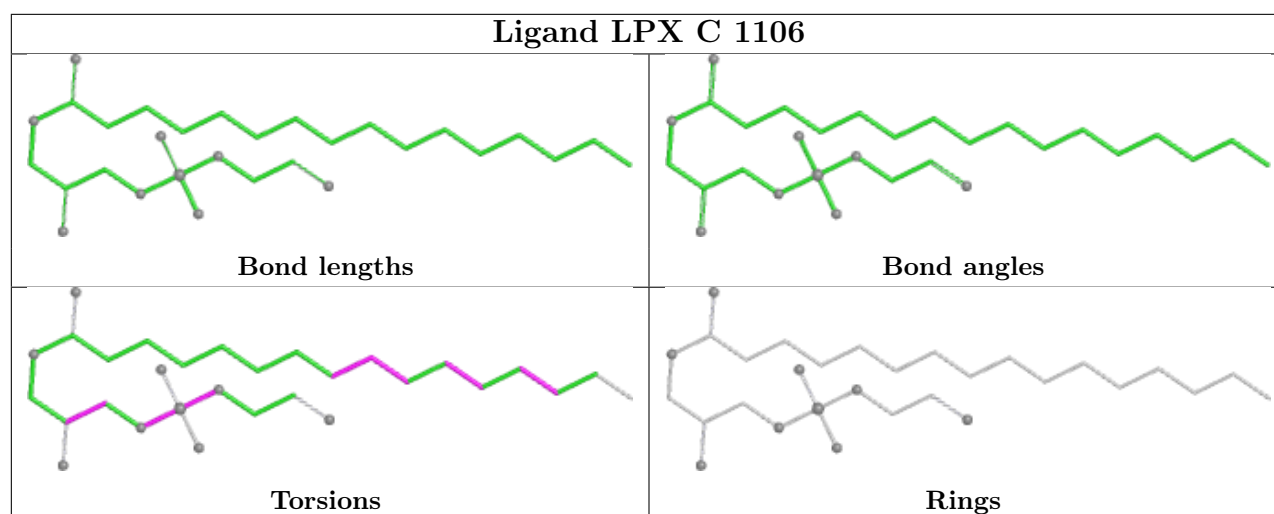
Mol	Chain	Res	Type	Atoms
3	A	1202	LMT	O5'-C1'-O1'-C1
3	A	1211	LMT	O5'-C1'-O1'-C1
3	B	1101	LMT	O5'-C1'-O1'-C1
3	C	1102	LMT	C2'-C1'-O1'-C1
3	C	1102	LMT	C2-C1-O1'-C1'

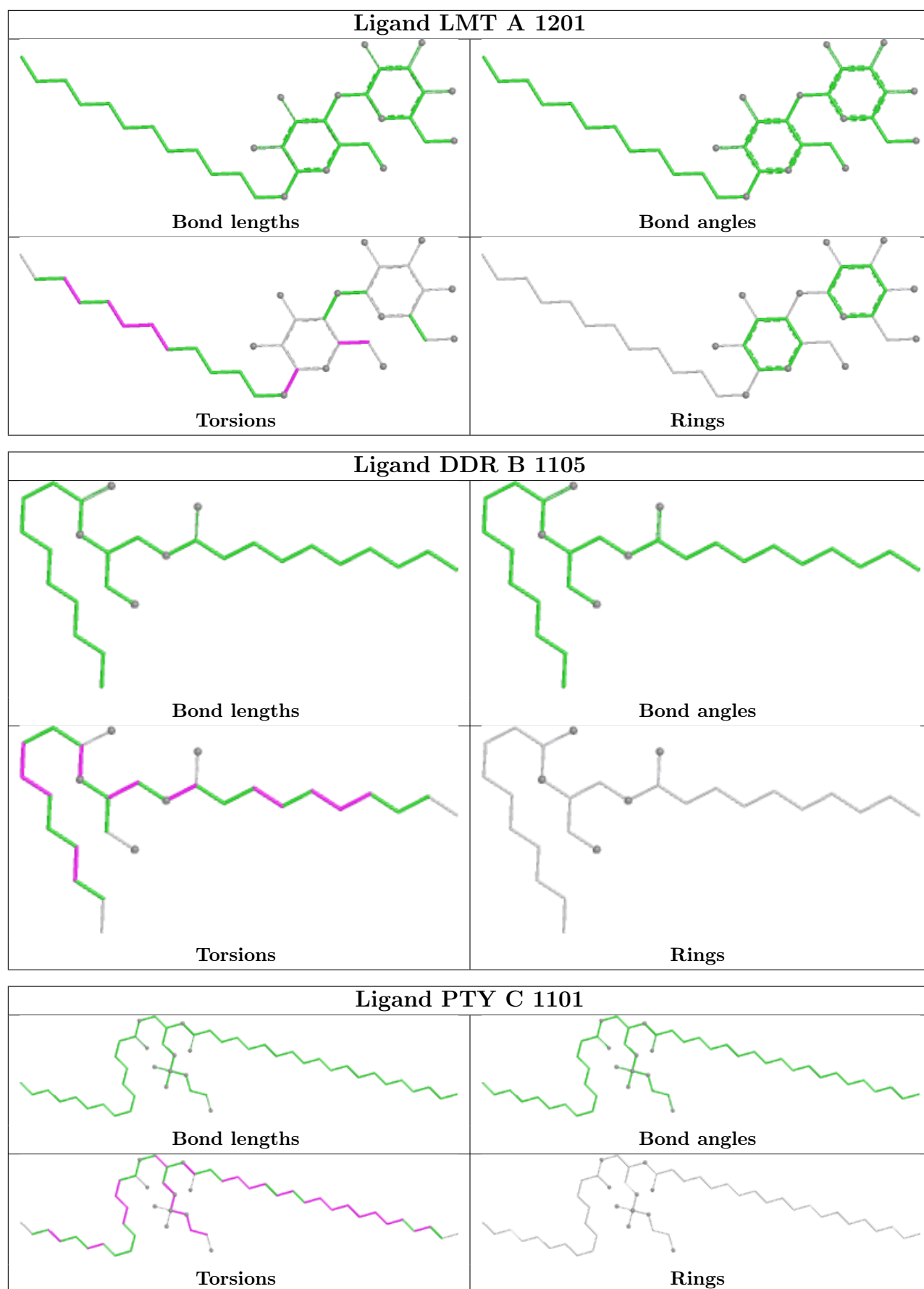
There are no ring outliers.

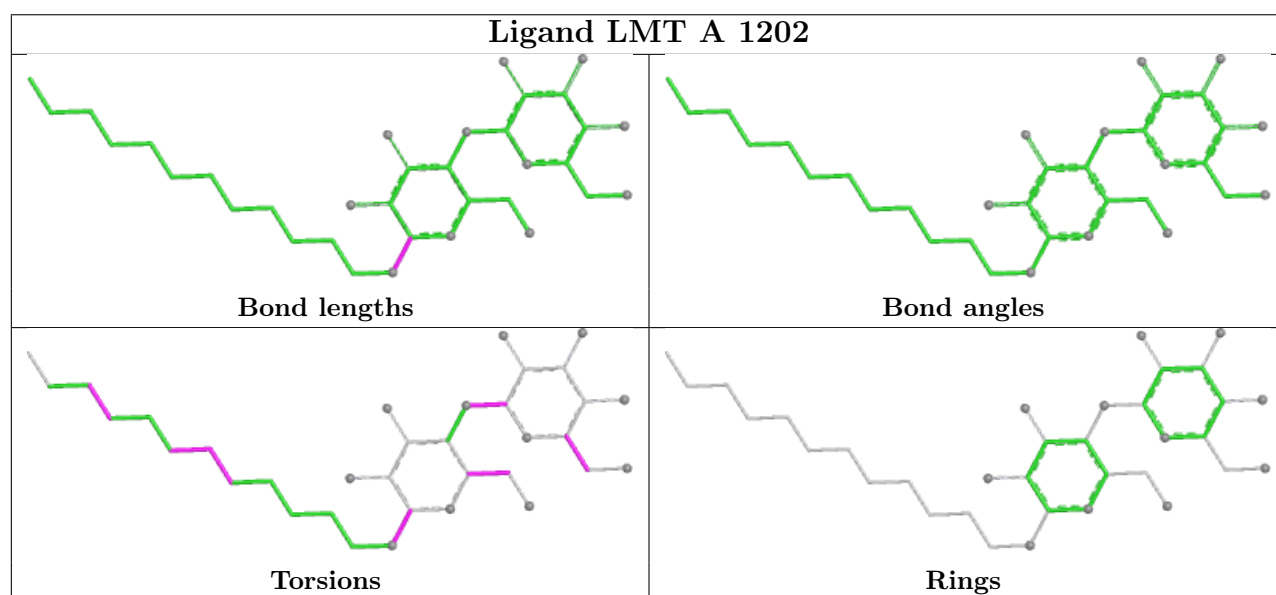
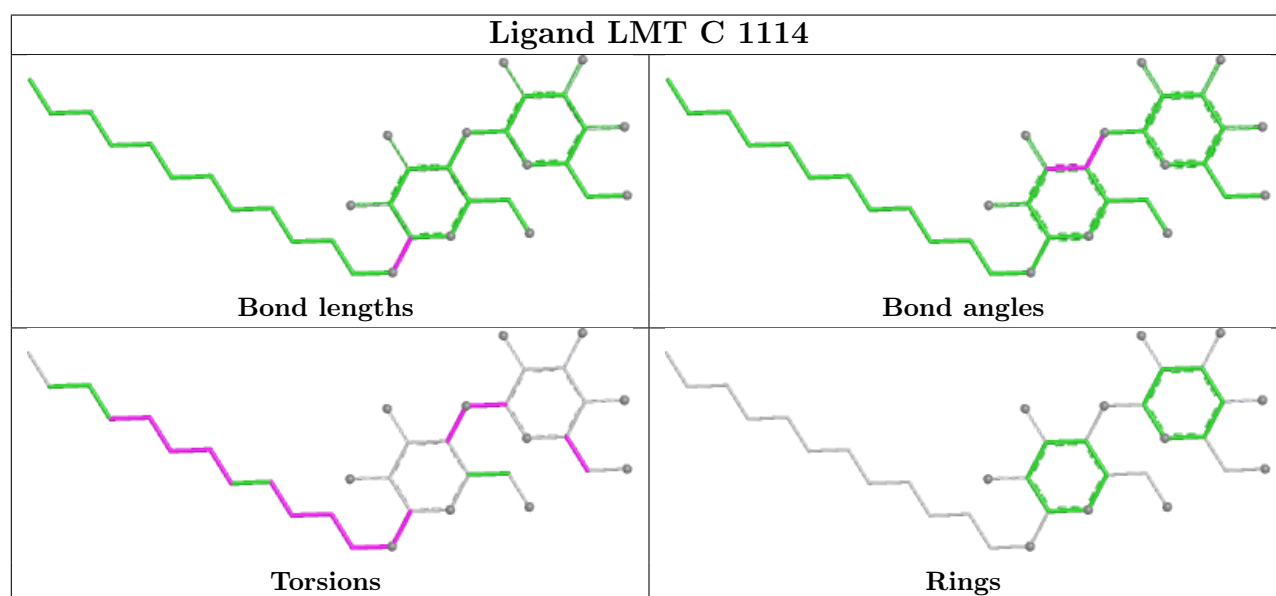
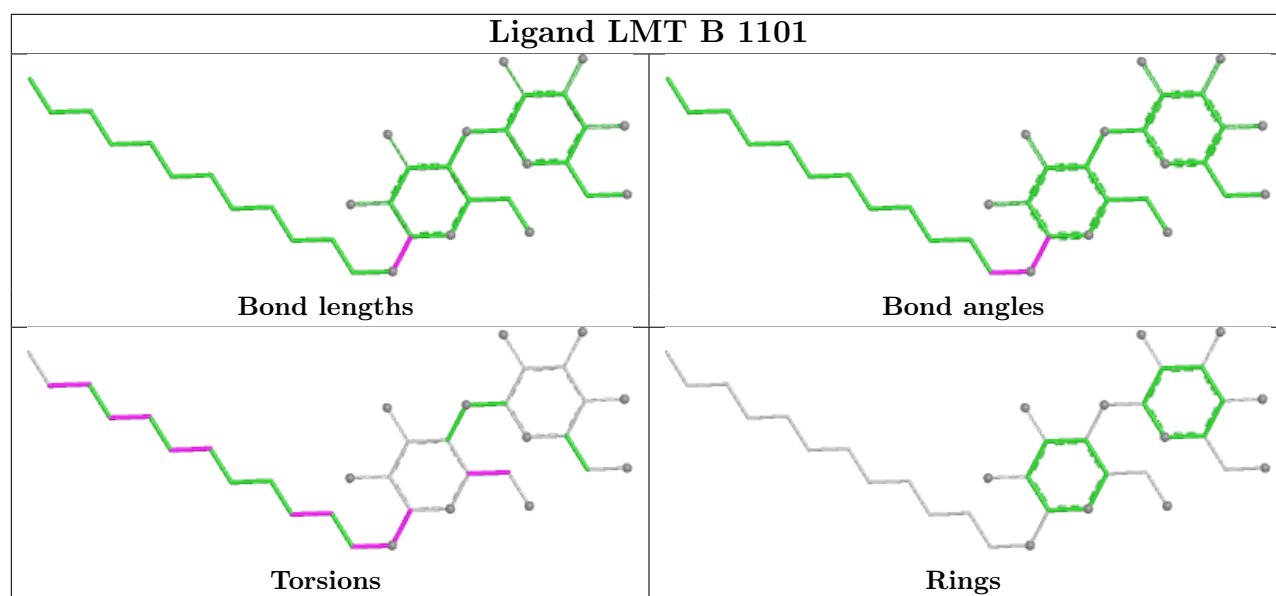
3 monomers are involved in 3 short contacts:

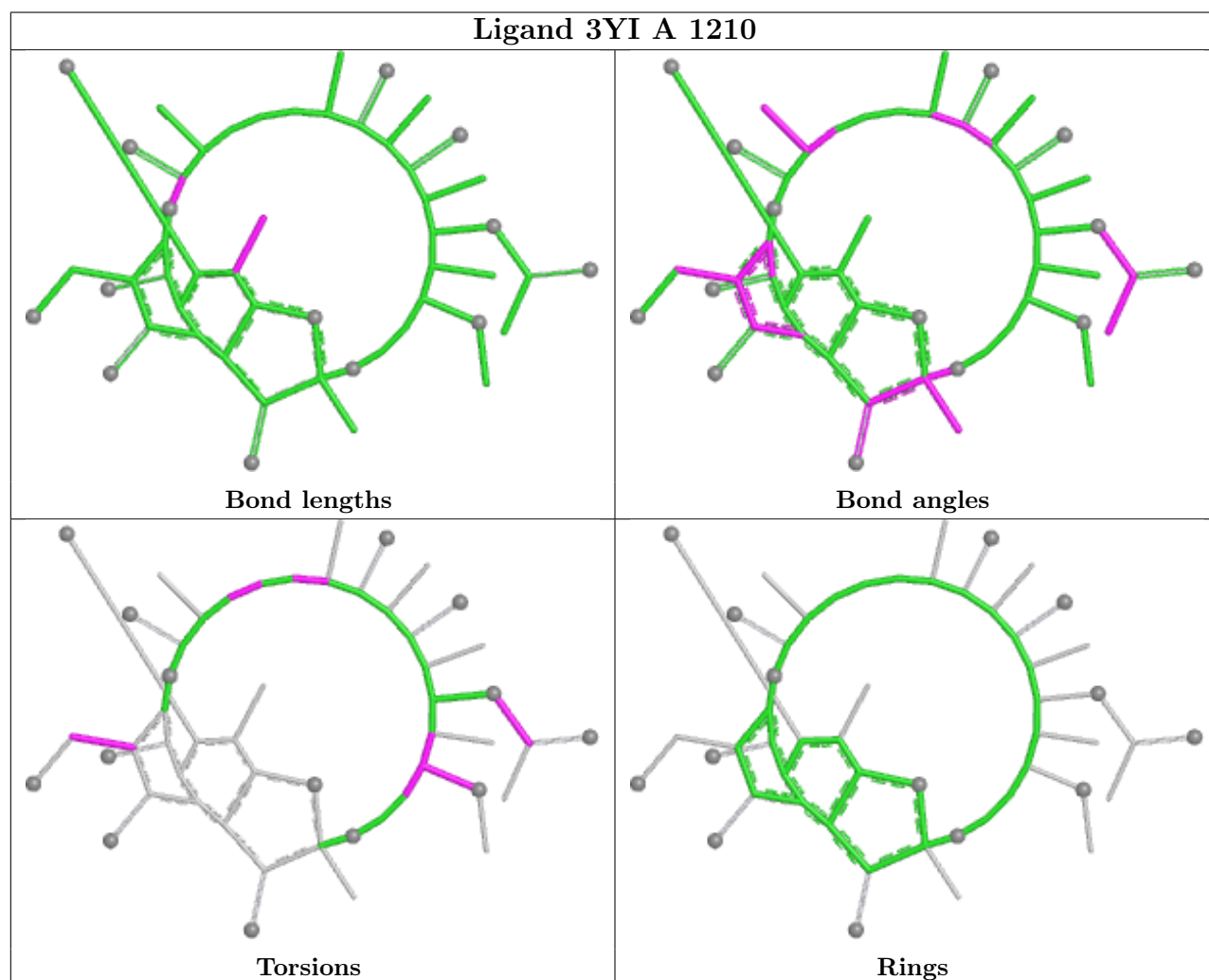
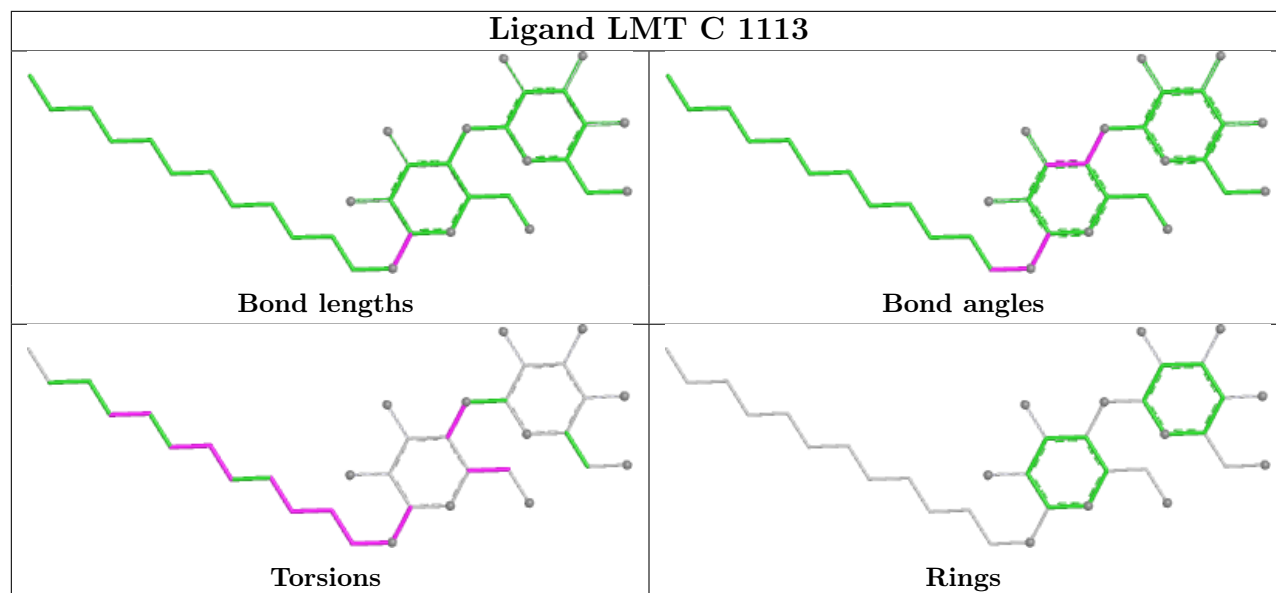
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1206	DDQ	1	0
8	A	1210	3YI	1	0
8	B	1107	3YI	1	0

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.

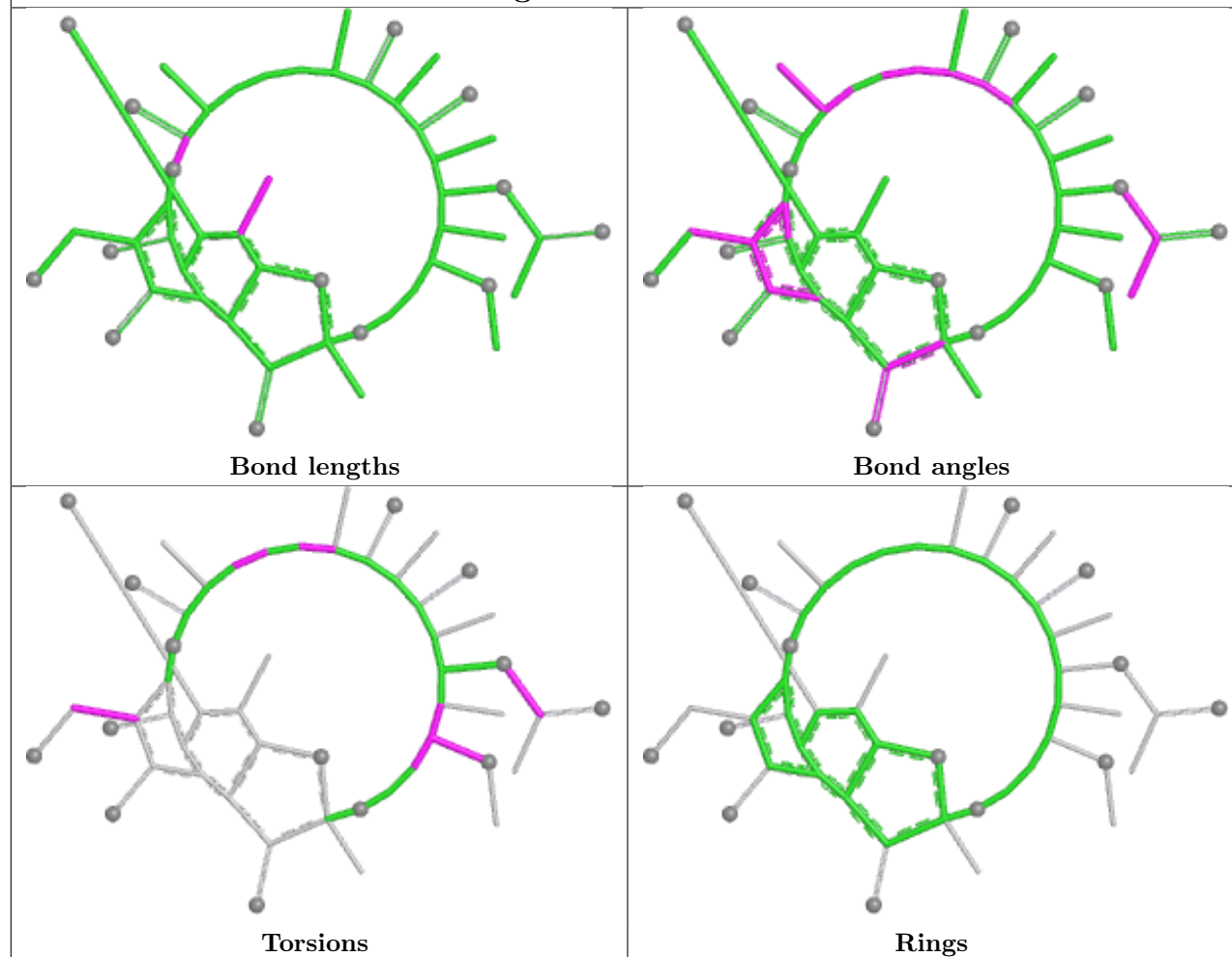




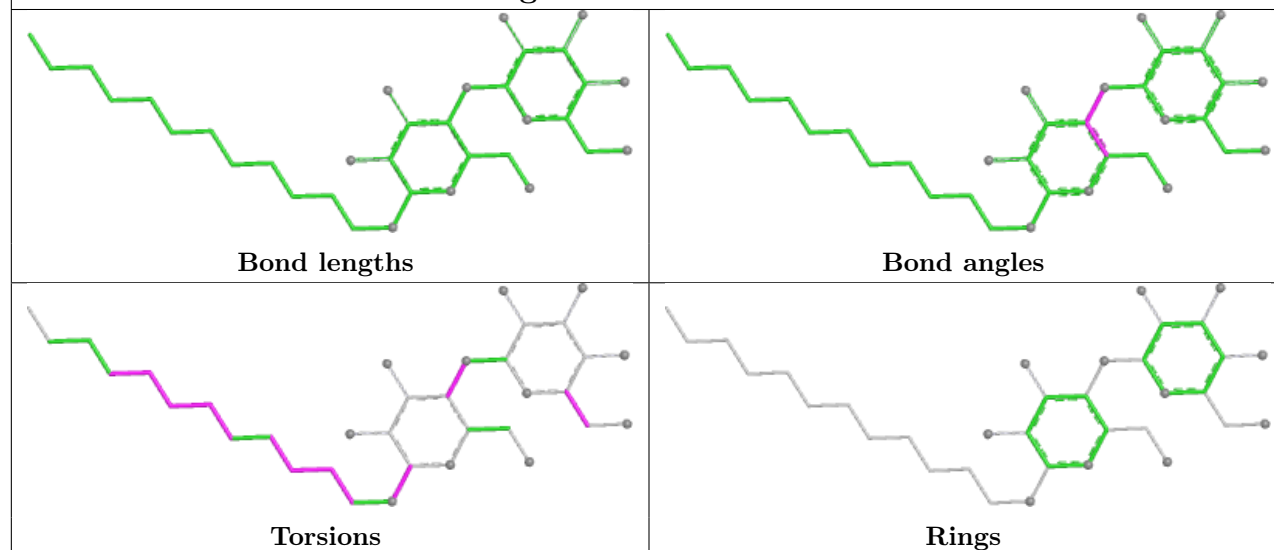


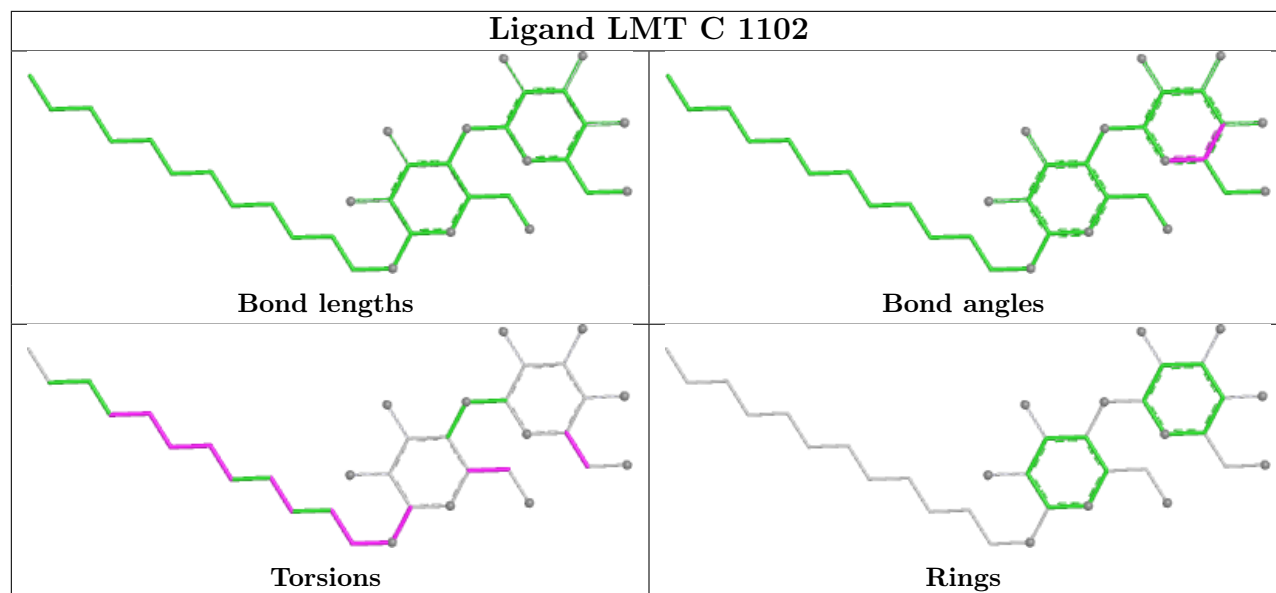


Ligand 3YI B 1107



Ligand LMT A 1211





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	1034/1057 (97%)	0.46	60 (5%)	29	22	28, 64, 103, 127	9 (0%)
1	B	1034/1057 (97%)	0.46	52 (5%)	34	26	36, 62, 94, 111	6 (0%)
1	C	1033/1057 (97%)	0.11	15 (1%)	72	63	37, 54, 79, 101	0
2	D	154/169 (91%)	0.31	4 (2%)	57	47	50, 62, 84, 93	0
2	E	153/169 (90%)	0.79	12 (7%)	19	14	60, 78, 100, 109	0
All	All	3408/3509 (97%)	0.36	143 (4%)	40	32	28, 60, 96, 127	15 (0%)

The worst 5 of 143 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	868	LEU	6.2
1	B	566	ASP	4.9
1	A	668	LEU	4.8
1	B	617	PHE	4.5
2	E	14	LEU	4.4

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 oligosaccharides 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,

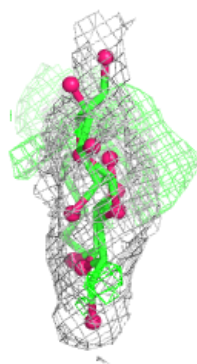
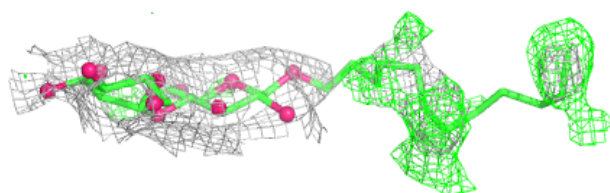
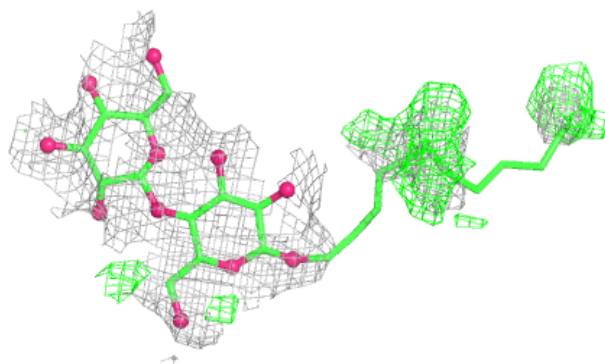
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	C	1110	4/4	0.49	0.34	88,89,89,90	0
3	LMT	C	1114	35/35	0.64	0.23	122,126,138,139	0
5	GOL	C	1116	6/6	0.68	0.33	84,86,86,86	0
7	DDQ	A	1206	14/14	0.68	0.40	110,115,121,121	0
6	D12	A	1208	12/12	0.75	0.40	79,83,84,85	0
4	EDO	A	1207	4/4	0.75	0.23	76,77,78,80	0
3	LMT	A	1201	35/35	0.77	0.19	104,110,119,119	0
6	D12	C	1104	12/12	0.78	0.35	73,74,75,75	0
7	DDQ	B	1106	14/14	0.78	0.30	74,86,97,97	0
4	EDO	A	1212	4/4	0.79	0.28	71,71,72,72	0
4	EDO	B	1102	4/4	0.79	0.30	82,83,83,83	0
13	HEX	C	1111	6/6	0.80	0.32	69,69,70,70	0
13	HEX	C	1115	6/6	0.81	0.31	61,62,62,62	0
10	PTY	C	1101	50/50	0.82	0.26	84,91,118,122	0
3	LMT	C	1113	35/35	0.82	0.24	116,128,132,133	0
4	EDO	A	1209	4/4	0.82	0.21	67,67,68,68	0
6	D12	C	1103	12/12	0.83	0.28	66,68,71,72	0
3	LMT	A	1211	35/35	0.84	0.20	87,103,116,117	0
3	LMT	B	1101	35/35	0.84	0.20	94,96,106,107	0
4	EDO	C	1107	4/4	0.85	0.24	56,57,57,57	0
3	LMT	A	1202	35/35	0.86	0.19	90,116,132,132	0
12	LPX	C	1106	30/30	0.86	0.22	88,93,96,97	0
6	D12	A	1205	12/12	0.87	0.35	93,97,97,98	0
4	EDO	A	1203	4/4	0.88	0.15	66,67,67,68	0
5	GOL	A	1204	6/6	0.90	0.18	70,70,71,71	0
8	3YI	A	1210	52/52	0.90	0.16	80,86,90,90	0
4	EDO	C	1108	4/4	0.91	0.26	71,71,72,73	0
9	DDR	B	1105	28/28	0.91	0.22	93,104,111,112	0
3	LMT	C	1102	35/35	0.91	0.12	72,74,76,76	0
11	D10	C	1105	10/10	0.92	0.19	66,67,68,68	0
8	3YI	B	1107	52/52	0.92	0.14	70,77,79,80	0
4	EDO	C	1109	4/4	0.93	0.15	52,53,53,54	0
4	EDO	B	1104	4/4	0.93	0.16	59,60,60,60	0
5	GOL	C	1112	6/6	0.94	0.12	58,59,59,60	0
5	GOL	B	1103	6/6	0.94	0.12	62,63,64,65	0

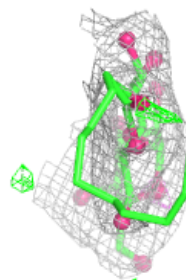
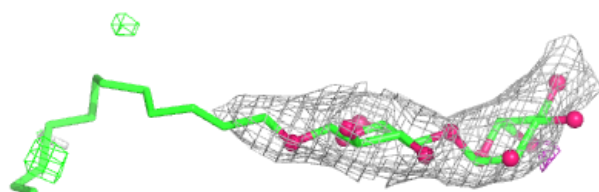
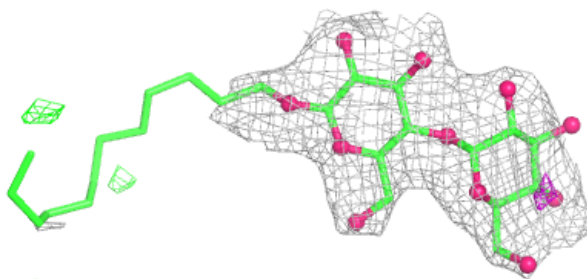
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LMT C 1114:

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

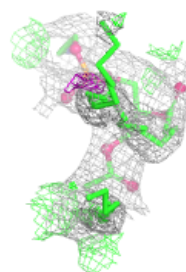
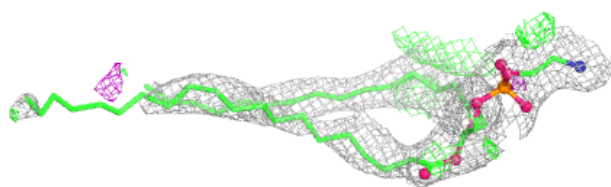
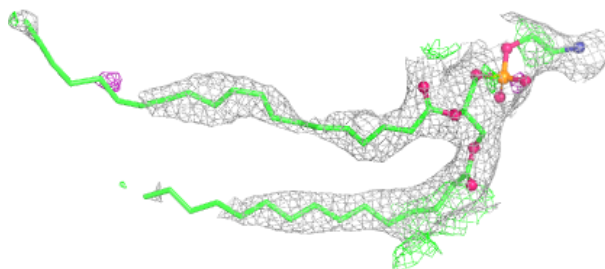
**Electron density around LMT A 1201:**

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

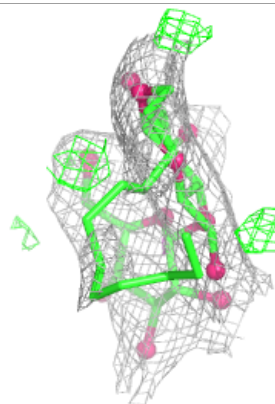
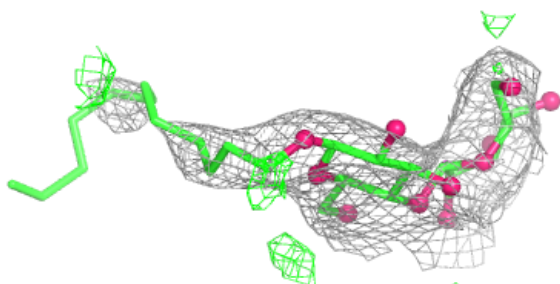
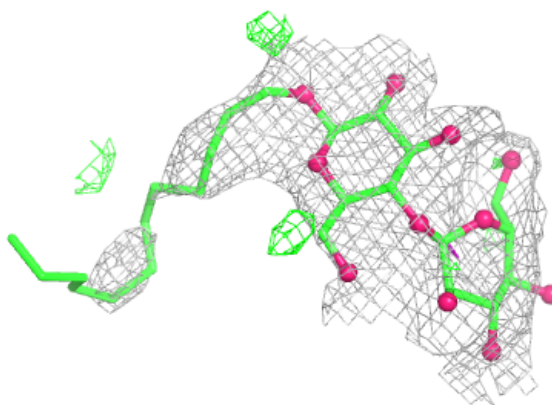


Electron density around PTY C 1101:

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

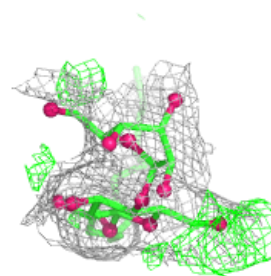
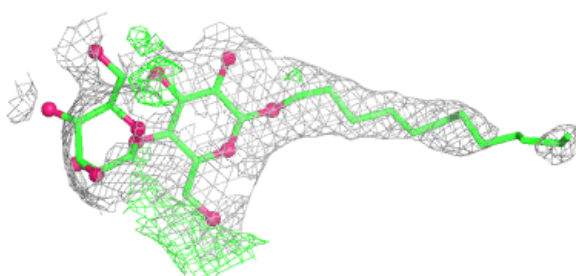
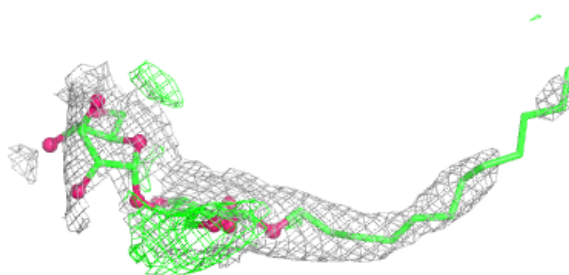
**Electron density around LMT C 1113:**

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

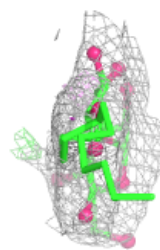
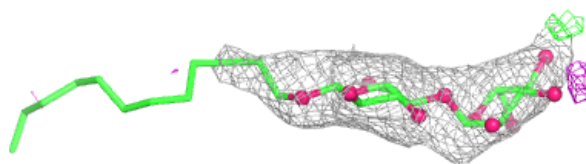
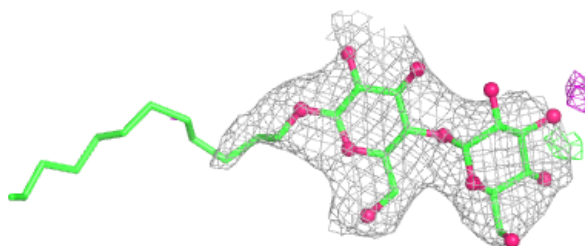


Electron density around LMT A 1211:

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

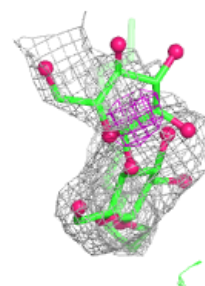
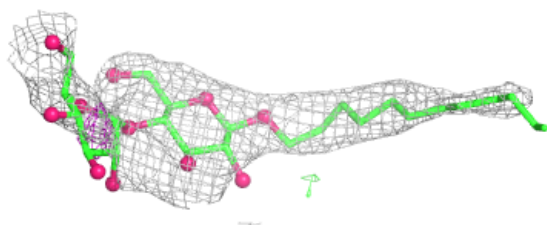
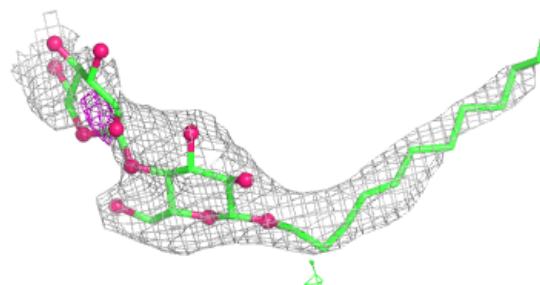
**Electron density around LMT B 1101:**

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

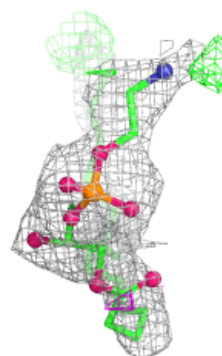
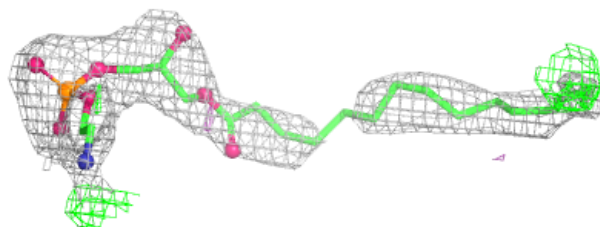
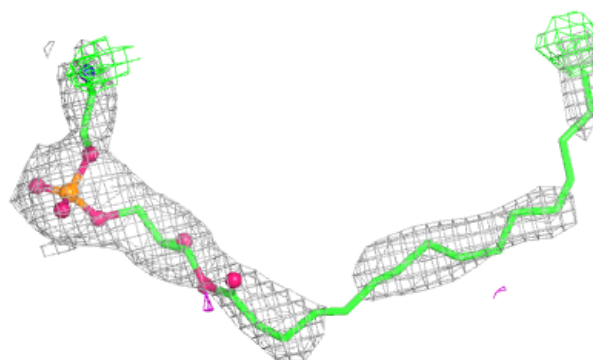


Electron density around LMT A 1202:

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

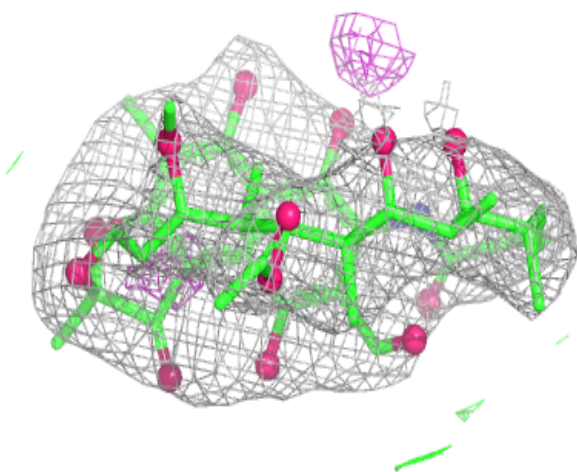
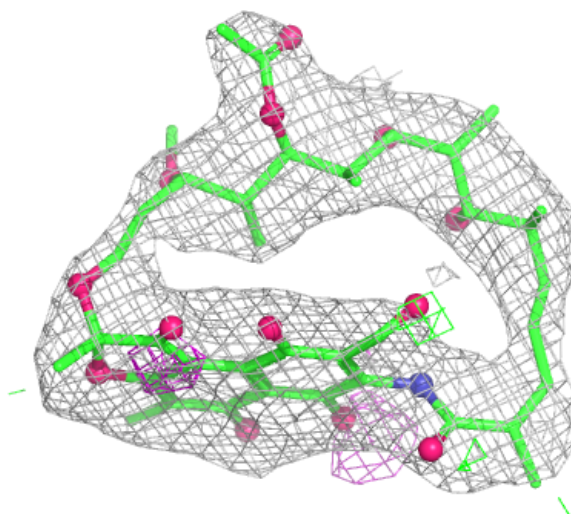
**Electron density around LPX C 1106:**

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



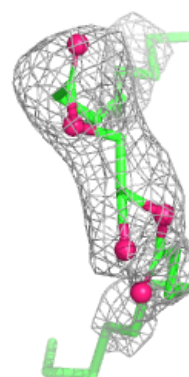
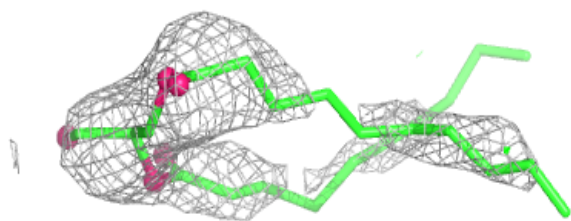
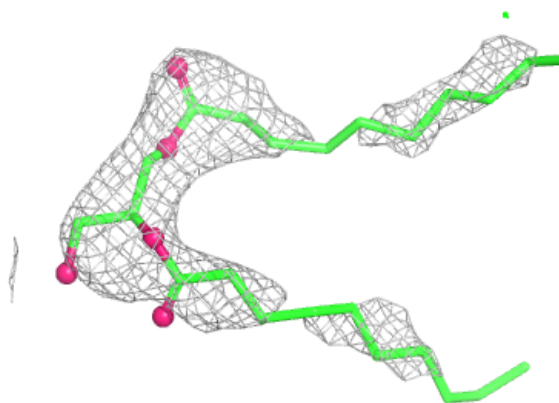
Electron density around 3YI A 1210:

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



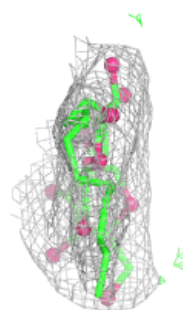
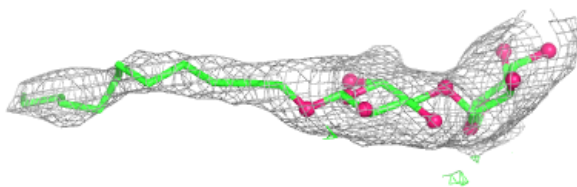
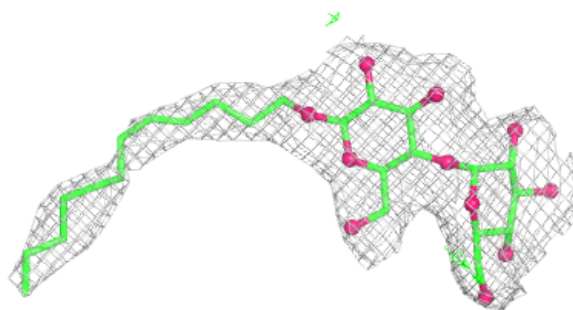
Electron density around DDR B 1105:

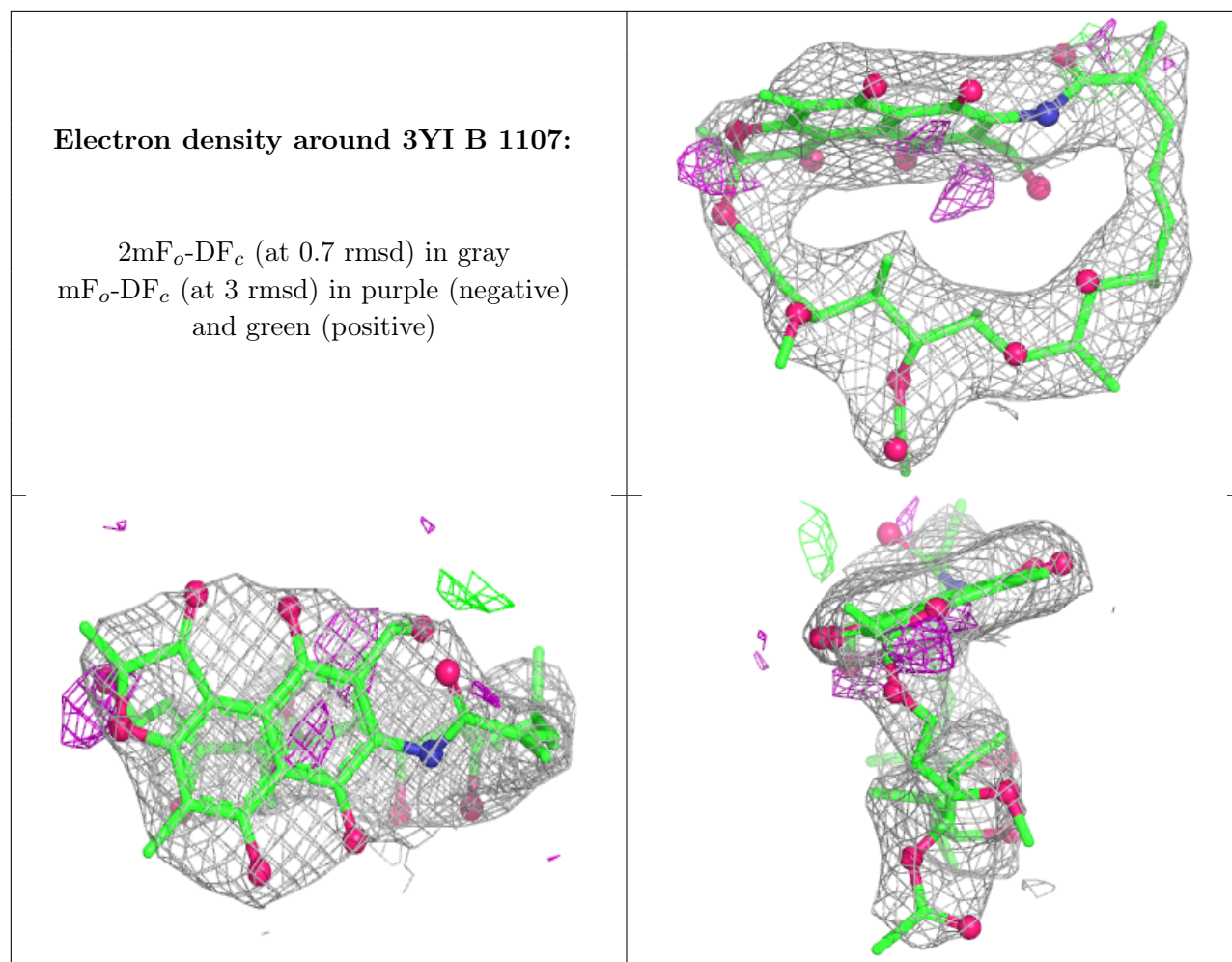
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.5 Other polymers [i](#)

There are no such residues in this entry.