



# Full wwPDB X-ray Structure Validation Report ⓘ

May 11, 2021 – 10:19 am BST

PDB ID : 6ZOC  
Title : Erythromycin binding to the access pocket of AcrB-G616P L protomer and 3-formylrifamycin SV binding to the access pocket of AcrB-G616P T protomer  
Authors : Tam, H.K.; Foong, W.E.; Pos, K.M.  
Deposited on : 2020-07-07  
Resolution : 2.89 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.18  
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) : 2.18

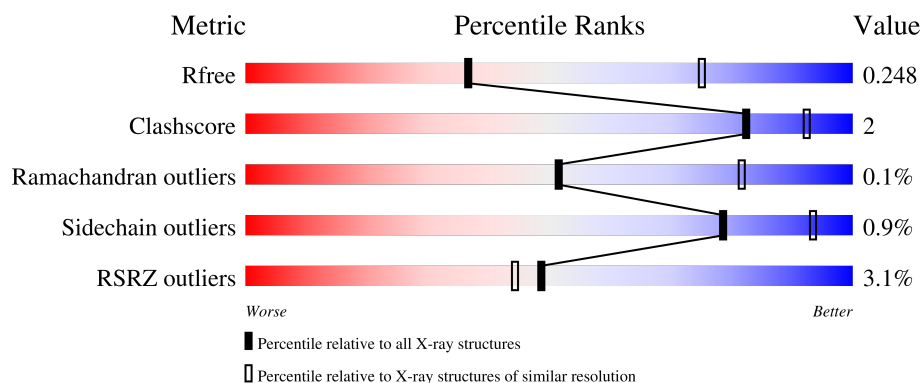
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.89 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)
RSRZ outliers	127900	1906 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1057	 3% 90% 8% .
1	B	1057	 3% 91% 7% .
1	C	1057	 % 90% 8% .
2	D	169	 3% 85% 7% 8%
2	E	169	 13% 83% 8% 9%

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 26894 atoms, of which 277 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	0	0
			7858	5058	1296	1460	44			
1	B	1033	Total	C	N	O	S	0	0	0
			7852	5055	1295	1458	44			
1	C	1034	Total	C	N	O	S	0	0	0
			7858	5058	1296	1460	44			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	616	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	616	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	616	PRO	GLY	engineered mutation	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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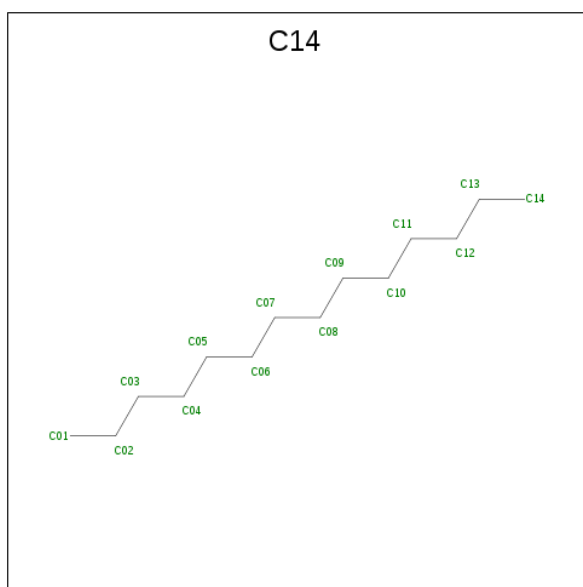
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Chain	Residue	Modelled	Actual	Comment	Reference
C	1054	HIS	-	expression tag	UNP P31224
C	1055	HIS	-	expression tag	UNP P31224
C	1056	HIS	-	expression tag	UNP P31224
C	1057	HIS	-	expression tag	UNP P31224

- Molecule 2 is a protein called DARPIN.

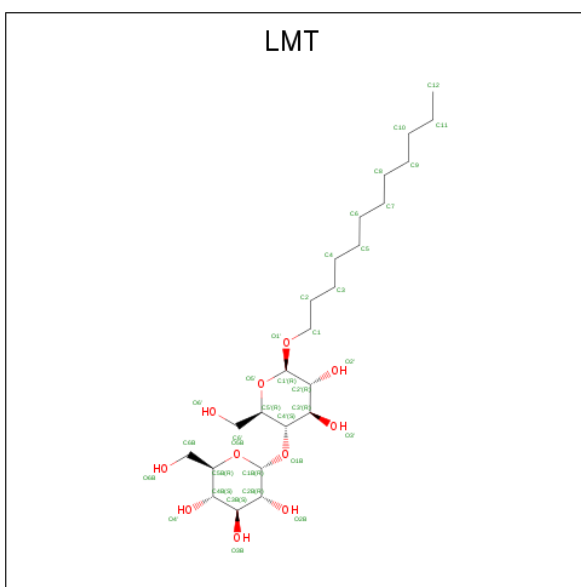
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	155	Total	C	N	O	S	0	0	0
			1168	736	204	227	1			
2	E	154	Total	C	N	O	S	0	0	0
			1167	736	204	226	1			

- Molecule 3 is TETRADECANE (three-letter code: C14) (formula: C<sub>14</sub>H<sub>30</sub>).



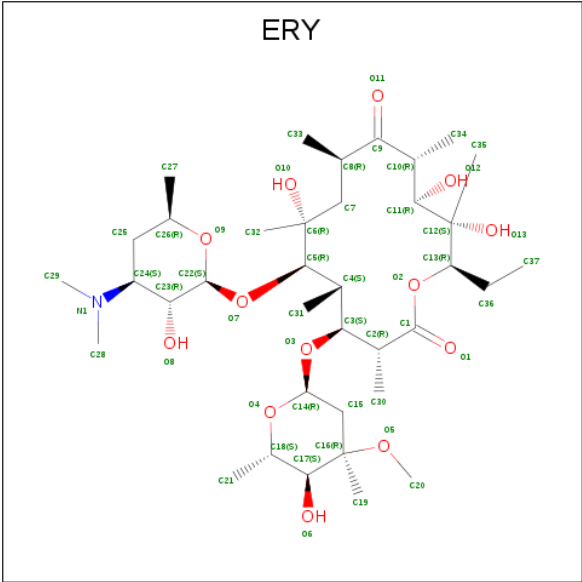
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C H	0	0
			44	14 30		
3	C	1	Total	C	0	0
			14	14		

- Molecule 4 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: C<sub>24</sub>H<sub>46</sub>O<sub>11</sub>).



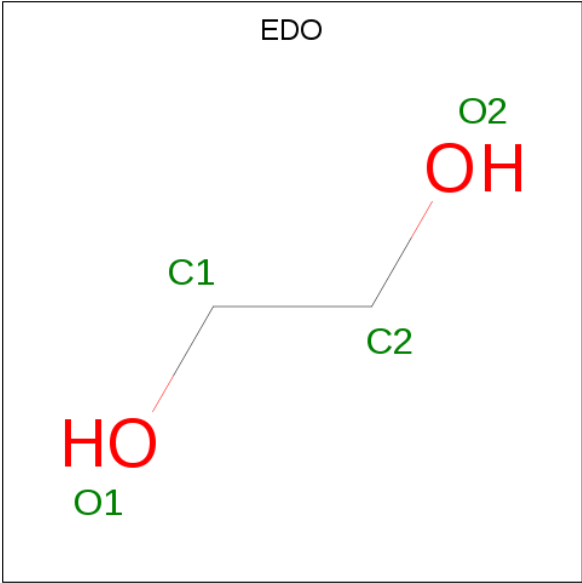
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 35	C 24	O 11	0	0
4	B	1	Total 35	C 24	O 11	0	0
4	B	1	Total 35	C 24	O 11	0	0
4	C	1	Total 35	C 24	O 11	0	0
4	C	1	Total 35	C 24	O 11	0	0

- Molecule 5 is ERYTHROMYCIN A (three-letter code: ERY) (formula:  $C_{37}H_{67}NO_{13}$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			51	37	1	13		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



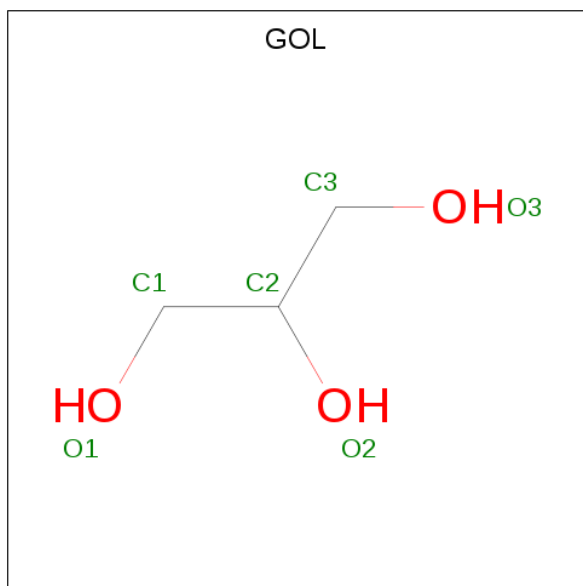
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	C	1	Total	C	H	O	0	0
			10	2	6	2		
6	C	1	Total	C	H	O	0	0
			10	2	6	2		
6	C	1	Total	C	H	O	0	0
			10	2	6	2		
6	C	1	Total	C	H	O	0	0
			10	2	6	2		
6	E	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



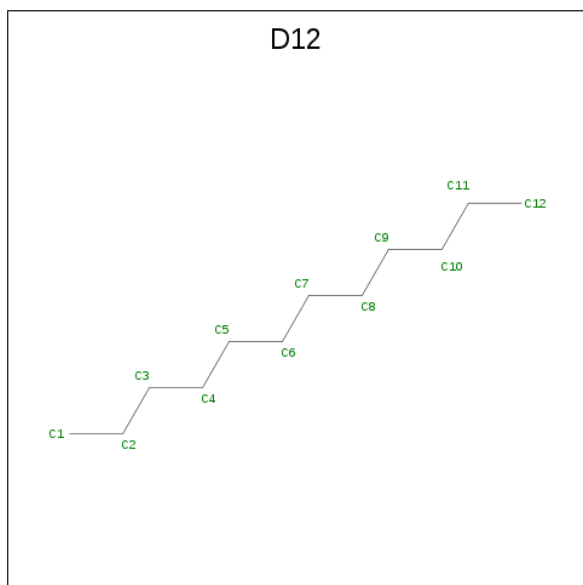
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			14	3	8	3		
7	A	1	Total	C	H	O	0	0
			14	3	8	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			14	3	8	3		
7	C	1	Total	C	H	O	0	0
			14	3	8	3		
7	C	1	Total	C	H	O	0	0
			14	3	8	3		

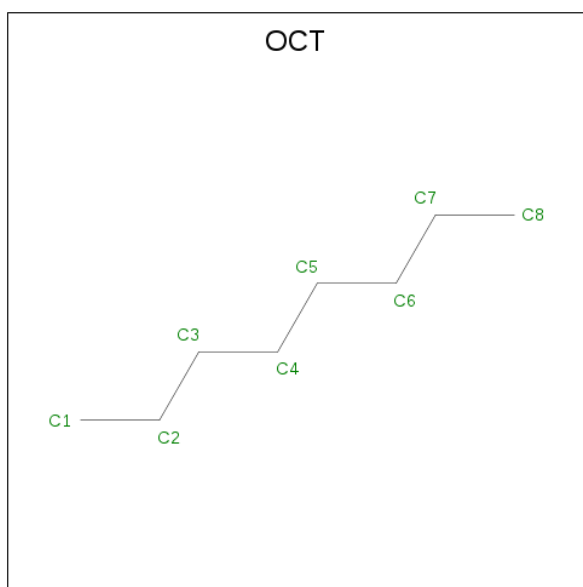
- Molecule 8 is DODECANE (three-letter code: D12) (formula:  $C_{12}H_{26}$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C		0	0
			12	12			
8	B	1	Total	C	H	0	0
			38	12	26		

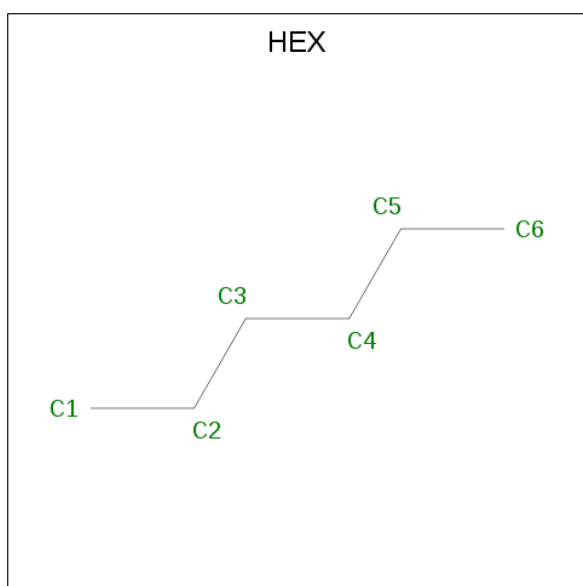
- Molecule 9 is N-OCTANE (three-letter code: OCT) (formula:  $C_8H_{18}$ ).





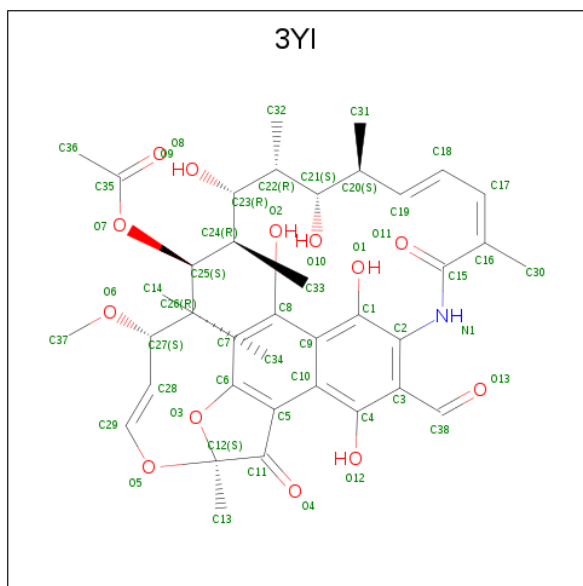
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	H	0	0
			26	8	18		
9	C	1	Total	C	H	0	0
			26	8	18		

- Molecule 10 is HEXANE (three-letter code: HEX) (formula:  $C_6H_{14}$ ).



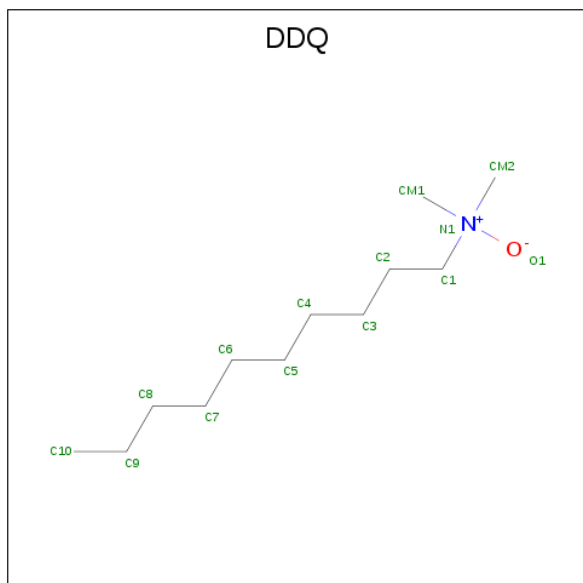
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	H	0	0
			20	6	14		
10	C	1	Total	C	H	0	0
			20	6	14		

- Molecule 11 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 (three-letter code: 3YI) (formula:  $C_{38}H_{47}NO_{13}$ ) (labeled as "Ligand of Interest" by depositor).



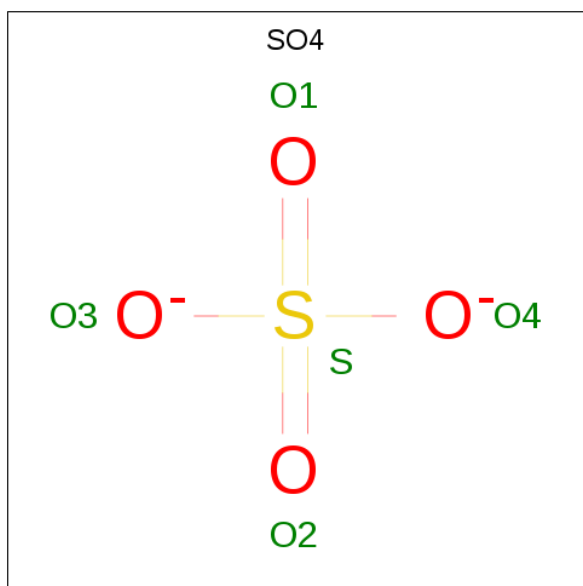
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	0	0
			52	38	1	13		

- Molecule 12 is DECYLAMINE-N,N-DIMETHYL-N-OXIDE (three-letter code: DDQ) (formula:  $C_{12}H_{27}NO$ ).



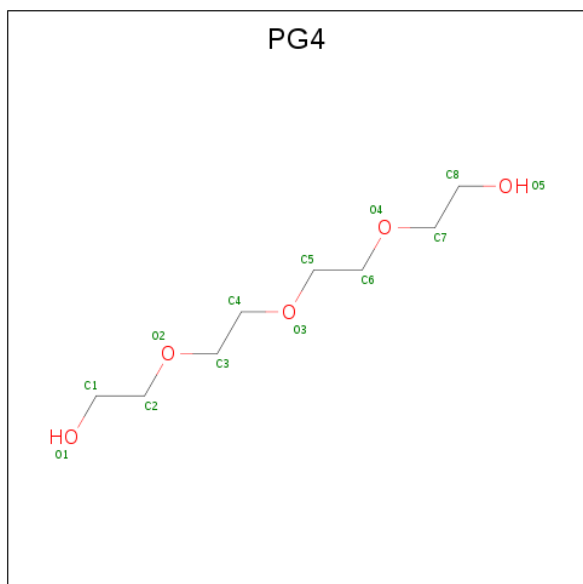
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	B	1	Total	C	H	N	O	0	0
			41	12	27	1	1		

- Molecule 13 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



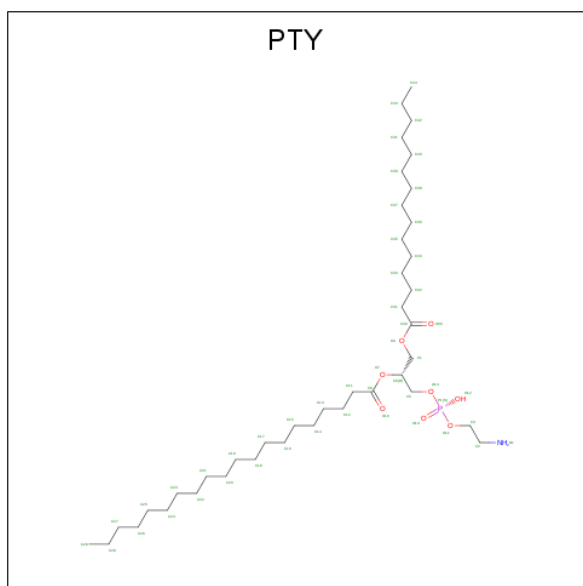
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	O	S	0	0
			5	4	1		
13	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 14 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
14	C	1	Total	C	H	O	0	0
			31	8	18	5		

- Molecule 15 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula:  $C_{40}H_{80}NO_8P$ ).



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

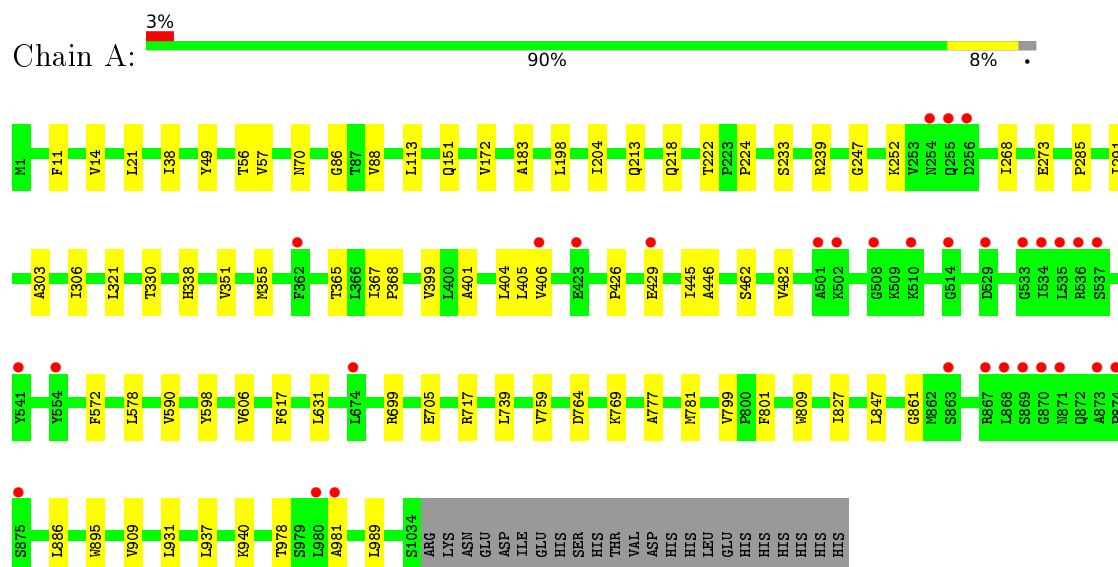
- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	65	Total	O	0	1
			66	66		
16	B	50	Total	O	0	1
			51	51		
16	C	59	Total	O	0	0
			59	59		
16	D	5	Total	O	0	0
			5	5		
16	E	10	Total	O	0	0
			10	10		

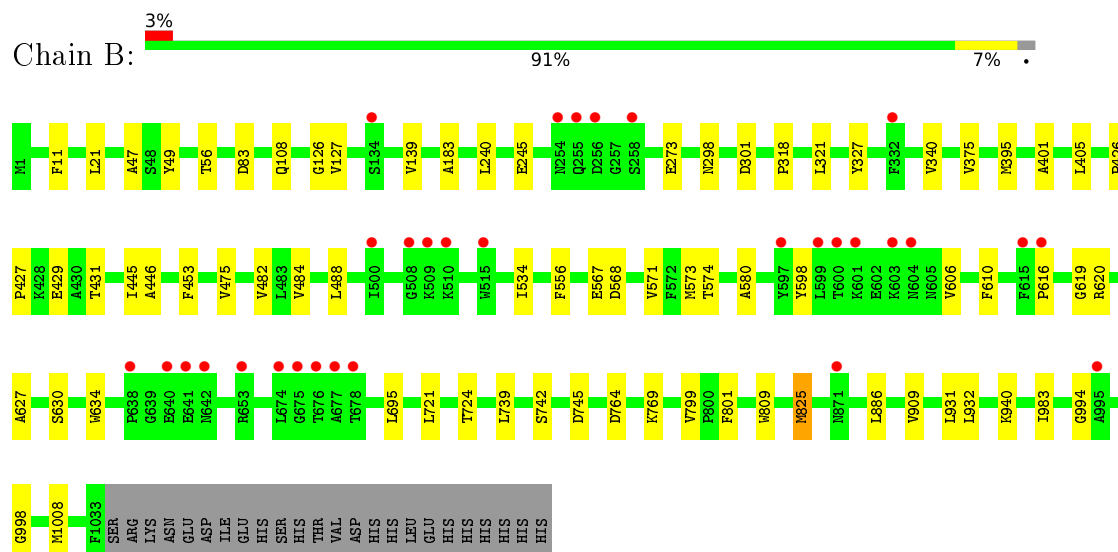
### 3 Residue-property plots [i](#)

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.

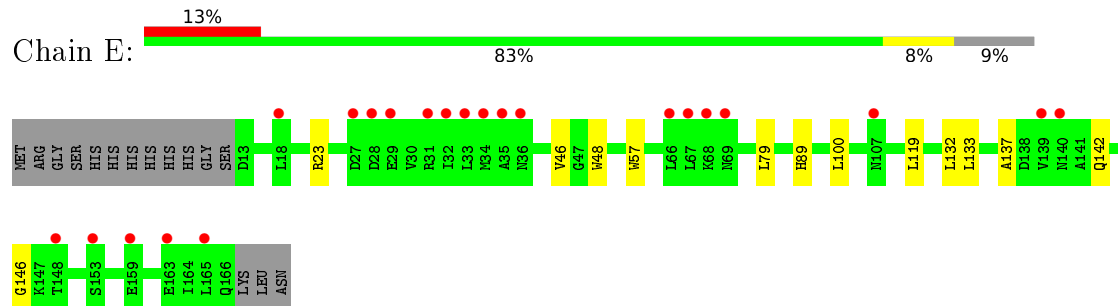
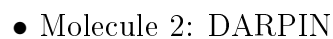
- Molecule 1: Multidrug efflux pump subunit AcrB



- Molecule 1: Multidrug efflux pump subunit AcrB



- Molecule 1: Multidrug efflux pump subunit AcrB



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.33Å 161.26Å 244.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.37 – 2.89 49.37 – 2.87	Depositor EDS
% Data completeness (in resolution range)	67.7 (49.37-2.89) 67.7 (49.37-2.87)	Depositor EDS
$R_{merge}$	0.60	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 2.86Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.218 , 0.238 0.233 , 0.248	Depositor DCC
$R_{free}$ test set	4399 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.7	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 28.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	26894	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: 3YI, D12, LMT, OCT, PG4, GOL, SO4, EDO, HEX, C14, ERY, PTY, 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	0.26	0/8009	0.32	0/10878
1	B	0.25	0/8003	0.31	0/10870
1	C	0.26	0/8009	0.32	0/10878
2	D	0.26	0/1187	0.30	0/1614
2	E	0.26	0/1186	0.29	0/1613
All	All	0.26	0/26394	0.31	0/35853

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 [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	7858	0	8010	45	0
1	B	7852	0	8005	39	0
1	C	7858	0	8010	45	0
2	D	1168	0	1151	7	0
2	E	1167	0	1151	7	0
3	A	14	30	30	0	0
3	C	14	0	30	0	0
4	A	35	0	46	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	70	0	92	1	0
4	C	70	0	92	1	0
5	A	51	0	67	2	0
6	A	20	30	30	0	0
6	B	4	6	6	0	0
6	C	20	30	30	0	0
6	E	4	6	6	0	0
7	A	18	24	24	0	0
7	C	12	16	16	2	0
8	A	12	0	26	1	0
8	B	12	26	26	0	0
9	B	8	18	18	0	0
9	C	8	18	18	0	0
10	B	6	14	14	1	0
10	C	6	14	14	0	0
11	B	52	0	0	0	0
12	B	14	27	27	0	0
13	B	5	0	0	0	0
13	D	5	0	0	0	0
14	C	13	18	18	0	0
15	C	50	0	79	3	0
16	A	66	0	0	0	0
16	B	51	0	0	0	0
16	C	59	0	0	0	0
16	D	5	0	0	0	0
16	E	10	0	0	0	0
All	All	26617	277	27036	133	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.

All (133) 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:616:PRO:HA	1:B:620:ARG:HB3	1.23	1.14
1:B:809:TRP:CD1	2:D:79:LEU:HD12	2.08	0.89
1:C:895:TRP:HB2	15:C:1113:PTY:HC6	1.56	0.88
1:B:126:GLY:HA3	1:C:116:PRO:HB3	1.68	0.75
1:C:57:VAL:HG21	1:C:86:GLY:HA2	1.76	0.66
1:C:84:SER:HB3	1:C:814:PRO:HA	1.77	0.65
1:B:616:PRO:HA	1:B:620:ARG:CB	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:580:ALA:HB1	1:B:724:THR:HG22	1.82	0.61
1:B:932:LEU:HD11	10:B:1104:HEX:H42	1.83	0.60
1:A:355:MET:HB2	1:A:365:THR:HG23	1.84	0.60
1:A:351:VAL:HG12	1:A:981:ALA:HB1	1.85	0.59
1:C:616:PRO:HD3	1:C:626:ILE:HB	1.85	0.58
2:E:133:LEU:HD23	2:E:137:ALA:HB3	1.86	0.57
1:B:340:VAL:HG21	1:B:395:MET:HB3	1.84	0.57
1:B:534:ILE:HD11	4:B:1101:LMT:H11	1.86	0.57
1:A:446:ALA:HB2	1:A:482:VAL:HG21	1.86	0.56
1:B:574:THR:HB	1:B:627:ALA:HB3	1.88	0.56
1:A:113:LEU:HD21	1:C:128:SER:HB3	1.88	0.55
2:D:67:LEU:HD11	2:D:99:LEU:HD23	1.89	0.55
1:C:34:GLN:HB2	1:C:333:VAL:HG13	1.88	0.54
1:C:445:ILE:HD11	1:C:944:LEU:HD21	1.89	0.54
1:A:351:VAL:O	1:A:355:MET:HG2	2.08	0.54
1:A:247:GLY:HA2	1:A:268:ILE:HD13	1.91	0.53
1:A:38:ILE:HG23	1:A:462:SER:HB3	1.91	0.53
2:E:89:HIS:ND1	2:E:119:LEU:HD22	2.24	0.52
1:A:895:TRP:HE1	8:A:1210:D12:H12	1.74	0.52
1:C:351:VAL:HG21	1:C:402:ILE:HG22	1.92	0.52
1:C:222:THR:HA	1:C:224:PRO:HD3	1.92	0.51
1:A:406:VAL:HG23	1:A:978:THR:HG23	1.93	0.51
1:C:426:PRO:HD2	1:C:429:GLU:HB2	1.93	0.51
1:A:426:PRO:HD2	1:A:429:GLU:HB2	1.93	0.51
1:A:809:TRP:CD1	2:E:79:LEU:HD12	2.45	0.51
1:C:895:TRP:HE1	15:C:1113:PTY:C35	2.22	0.51
1:B:298:ASN:HB3	1:B:301:ASP:HB2	1.93	0.51
1:B:446:ALA:HB2	1:B:482:VAL:HG21	1.93	0.51
1:A:183:ALA:HB2	1:A:273:GLU:HG2	1.92	0.50
1:A:399:VAL:HG11	1:A:989:LEU:HD11	1.93	0.50
1:C:372:VAL:HB	1:C:373:PRO:HD3	1.94	0.50
1:A:739:LEU:HD13	1:A:799:VAL:HG11	1.94	0.50
1:A:909:VAL:HG22	1:A:931:LEU:HD11	1.94	0.50
1:C:303:ALA:HB2	1:C:330:THR:HG21	1.94	0.50
1:A:172:VAL:HG13	1:A:291:ILE:HG23	1.92	0.50
1:A:57:VAL:HG21	1:A:86:GLY:HA2	1.94	0.49
1:A:222:THR:HA	1:A:224:PRO:HD3	1.94	0.49
1:C:139:VAL:HB	1:C:327:TYR:HB3	1.94	0.48
1:C:204:ILE:HG23	1:C:759:VAL:HG13	1.94	0.48
1:C:876:LEU:HD21	1:C:932:LEU:HD11	1.94	0.48
1:A:886:LEU:HB3	1:C:14:VAL:HG13	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:142:GLN:HB3	2:D:146:GLY:HA2	1.95	0.48
2:D:72:ASP:HB3	2:D:75:ALA:HB2	1.95	0.48
1:A:56:THR:HA	1:C:213:GLN:HG2	1.96	0.48
1:A:291:ILE:HD13	1:A:306:ILE:HD13	1.96	0.48
1:C:182:TYR:HB3	1:C:270:LEU:HD22	1.96	0.48
1:C:888:LEU:HD21	1:C:943:ILE:HD11	1.95	0.48
1:B:318:PRO:HD2	1:B:321:LEU:HD22	1.96	0.47
2:E:23:ARG:HG3	2:E:57:TRP:NE1	2.28	0.47
2:E:100:LEU:HD11	2:E:132:LEU:HD23	1.96	0.47
1:A:705:GLU:HB3	1:A:847:LEU:HD22	1.97	0.47
1:A:303:ALA:HB2	1:A:330:THR:HG21	1.96	0.47
1:C:898:PRO:O	1:C:902:MET:HG2	2.14	0.47
1:B:21:LEU:HD21	15:C:1113:PTY:H252	1.97	0.47
1:A:861:GLY:HA3	5:A:1203:ERY:H203	1.98	0.46
1:C:398:MET:O	1:C:402:ILE:HG12	2.16	0.46
1:C:705:GLU:HB3	1:C:847:LEU:HD22	1.97	0.46
1:C:841:MET:HE2	1:C:859:TRP:CE2	2.51	0.46
1:A:404:LEU:HD23	1:A:937:LEU:HD13	1.98	0.46
1:B:426:PRO:HD2	1:B:429:GLU:HB2	1.98	0.46
1:B:453:PHE:HB2	1:B:475:VAL:HG23	1.98	0.46
1:C:298:ASN:HB3	1:C:301:ASP:HB2	1.97	0.46
1:B:375:VAL:HG11	1:B:405:LEU:HD22	1.99	0.45
1:C:168:ARG:HB2	7:C:1106:GOL:H2	1.98	0.45
1:A:777:ALA:O	1:A:781:MET:HG2	2.16	0.45
1:C:161:ASN:HD21	7:C:1105:GOL:H31	1.82	0.45
1:A:57:VAL:HG13	1:A:88:VAL:HG22	1.99	0.45
1:C:904:VAL:HG21	1:C:942:ALA:HB2	1.98	0.45
2:E:46:VAL:HG23	2:E:48:TRP:CD1	2.52	0.44
1:B:764:ASP:HB3	1:B:769:LYS:HD2	1.99	0.44
1:C:420:MET:HB3	1:C:500:ILE:HB	2.00	0.44
1:C:411:VAL:HG12	1:C:438:ILE:HD12	2.00	0.44
1:C:281:PHE:O	1:C:284:GLN:HG2	2.19	0.43
1:B:445:ILE:HG21	1:B:940:LYS:HE3	1.99	0.43
1:A:445:ILE:HG21	1:A:940:LYS:HE3	2.00	0.43
1:A:699:ARG:HG3	1:A:827:ILE:HD11	2.01	0.43
1:A:895:TRP:NE1	1:C:10:ILE:HG12	2.33	0.43
1:A:198:LEU:HD21	1:A:252:LYS:HD2	2.00	0.43
1:B:183:ALA:HB2	1:B:273:GLU:HG2	2.00	0.43
1:B:567:GLU:HG2	1:B:998:GLY:HA3	2.00	0.43
1:B:809:TRP:NE1	2:D:79:LEU:HD12	2.32	0.43
1:B:695:LEU:HG	1:B:825:MET:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:909:VAL:HG22	1:B:931:LEU:HD22	1.99	0.43
1:C:187:TRP:HB2	1:C:267:LYS:HB3	2.00	0.43
1:A:218:GLN:HG2	1:A:233:SER:HA	2.00	0.43
1:B:598:TYR:HB3	1:B:606:VAL:HG21	2.01	0.42
1:A:401:ALA:O	1:A:405:LEU:HG	2.20	0.42
1:C:598:TYR:HB3	1:C:606:VAL:HG11	1.99	0.42
1:A:70:ASN:HB2	1:C:167:SER:HB3	2.01	0.42
1:A:578:LEU:HD11	1:A:590:VAL:HG21	2.01	0.42
5:A:1203:ERY:H322	5:A:1203:ERY:O9	2.20	0.42
1:C:78:MET:HG3	1:C:92:LEU:HG	2.02	0.42
1:C:987:MET:N	1:C:988:PRO:HD2	2.34	0.42
1:B:445:ILE:HD13	1:B:940:LYS:HG3	2.02	0.42
1:C:655:PHE:HB3	1:C:663:VAL:HB	2.02	0.42
1:B:401:ALA:O	1:B:405:LEU:HG	2.20	0.42
1:A:204:ILE:HG23	1:A:759:VAL:HG13	2.02	0.42
1:B:47:ALA:HB2	1:B:127:VAL:HG13	2.01	0.42
1:B:571:VAL:HG12	1:B:630:SER:HA	2.01	0.42
1:B:739:LEU:HD13	1:B:799:VAL:HG11	2.00	0.42
1:C:143:ILE:HG22	1:C:286:ALA:HB2	2.02	0.42
2:E:142:GLN:HB3	2:E:146:GLY:HA2	2.01	0.42
1:A:572:PHE:HE2	1:A:631:LEU:HD21	1.84	0.41
1:B:983:ILE:HG23	1:B:1008:MET:HG3	2.01	0.41
1:A:151:GLN:HB2	1:A:285:PRO:HB3	2.03	0.41
1:B:619:GLY:HA3	1:B:721:LEU:HD11	2.02	0.41
1:A:213:GLN:HG2	1:B:56:THR:HA	2.02	0.41
1:A:367:ILE:HB	1:A:368:PRO:HD3	2.01	0.41
1:C:559:LEU:HA	1:C:560:PRO:HD3	1.98	0.41
1:B:568:ASP:O	1:B:634:TRP:NE1	2.44	0.41
1:B:742:SER:HB3	1:B:745:ASP:HB2	2.03	0.41
1:C:572:PHE:HE2	1:C:631:LEU:HD21	1.86	0.41
2:D:42:ALA:O	2:D:50:PRO:HD3	2.20	0.41
1:A:14:VAL:HG13	1:B:886:LEU:HB3	2.03	0.41
1:B:139:VAL:HB	1:B:327:TYR:HB3	2.02	0.41
1:B:484:VAL:HG13	1:B:488:LEU:HB3	2.01	0.41
1:C:445:ILE:HG23	1:C:940:LYS:HG3	2.03	0.41
1:A:213:GLN:HB2	1:A:239:ARG:HG2	2.03	0.41
1:C:213:GLN:HB2	1:C:239:ARG:HG3	2.03	0.41
1:C:384:ALA:HB1	4:C:1108:LMT:H3'	2.03	0.41
1:A:598:TYR:HB3	1:A:606:VAL:HG11	2.04	0.40
1:A:764:ASP:HB3	1:A:769:LYS:HD2	2.02	0.40
1:B:427:PRO:O	1:B:431:THR:OG1	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:598:TYR:HB3	1:A:606:VAL:HG21	2.03	0.40
1:B:240:LEU:HD22	1:B:245:GLU:HB3	2.04	0.40
2:D:51:LEU:HD11	2:D:63:VAL:HG13	2.02	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	1032/1057 (98%)	1002 (97%)	29 (3%)	1 (0%)	51	82
1	B	1031/1057 (98%)	1001 (97%)	29 (3%)	1 (0%)	51	82
1	C	1032/1057 (98%)	998 (97%)	34 (3%)	0	100	100
2	D	153/169 (90%)	151 (99%)	2 (1%)	0	100	100
2	E	152/169 (90%)	147 (97%)	5 (3%)	0	100	100
All	All	3400/3509 (97%)	3299 (97%)	99 (3%)	2 (0%)	51	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	617	PHE
1	B	994	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	841/864 (97%)	834 (99%)	7 (1%)	81	94
1	B	840/864 (97%)	831 (99%)	9 (1%)	73	92
1	C	841/864 (97%)	834 (99%)	7 (1%)	81	94
2	D	119/132 (90%)	118 (99%)	1 (1%)	81	94
2	E	119/132 (90%)	119 (100%)	0	100	100
All	All	2760/2856 (97%)	2736 (99%)	24 (1%)	78	93

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	PHE
1	A	21	LEU
1	A	49	TYR
1	A	321	LEU
1	A	338	HIS
1	A	717	ARG
1	A	801	PHE
1	B	11	PHE
1	B	49	TYR
1	B	83	ASP
1	B	108	GLN
1	B	556	PHE
1	B	573	MET
1	B	610	PHE
1	B	801	PHE
1	B	825	MET
1	C	11	PHE
1	C	49	TYR
1	C	219	LEU
1	C	811	TYR
1	C	948	PHE
1	C	951	ASP
1	C	1011	MET
2	D	23	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	437	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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

37 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$
7	GOL	A	1206	-	5,5,5	0.03	0	5,5,5	0.11	0
8	D12	A	1210	-	11,11,11	0.24	0	10,10,10	0.55	0
10	HEX	B	1104	-	5,5,5	0.12	0	4,4,4	0.07	0
9	OCT	C	1102	-	7,7,7	0.10	0	6,6,6	0.07	0
9	OCT	B	1103	-	7,7,7	0.11	0	6,6,6	0.07	0
4	LMT	B	1101	-	36,36,36	0.44	0	47,47,47	0.64	1 (2%)
4	LMT	A	1202	-	36,36,36	0.58	1 (2%)	47,47,47	0.99	4 (8%)
10	HEX	C	1114	-	5,5,5	0.14	0	4,4,4	0.08	0
12	DDQ	B	1108	-	10,13,13	2.25	1 (10%)	12,15,15	0.58	0
5	ERY	A	1203	-	53,53,53	0.98	1 (1%)	82,82,82	1.60	15 (18%)
6	EDO	C	1112	-	3,3,3	0.05	0	2,2,2	0.15	0
4	LMT	C	1108	-	36,36,36	0.44	0	47,47,47	0.66	0
6	EDO	A	1205	-	3,3,3	0.06	0	2,2,2	0.16	0
11	3YI	B	1107	-	55,55,55	0.75	2 (3%)	82,83,83	0.44	1 (1%)
13	SO4	D	201	-	4,4,4	0.15	0	6,6,6	0.04	0
15	PTY	C	1113	-	49,49,49	0.94	2 (4%)	52,54,54	1.03	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	EDO	A	1209	-	3,3,3	0.06	0	2,2,2	0.15	0
7	GOL	C	1105	-	5,5,5	0.09	0	5,5,5	0.14	0
13	SO4	B	1109	-	4,4,4	0.14	0	6,6,6	0.05	0
3	C14	A	1201	-	13,13,13	0.08	0	12,12,12	0.05	0
6	EDO	A	1204	-	3,3,3	0.04	0	2,2,2	0.19	0
6	EDO	C	1110	-	3,3,3	0.06	0	2,2,2	0.15	0
6	EDO	C	1107	-	3,3,3	0.06	0	2,2,2	0.19	0
6	EDO	C	1109	-	3,3,3	0.06	0	2,2,2	0.16	0
6	EDO	B	1102	-	3,3,3	0.05	0	2,2,2	0.16	0
7	GOL	C	1106	-	5,5,5	0.06	0	5,5,5	0.13	0
4	LMT	B	1105	-	36,36,36	0.58	0	47,47,47	1.45	9 (19%)
6	EDO	C	1111	-	3,3,3	0.06	0	2,2,2	0.18	0
4	LMT	C	1101	-	36,36,36	0.43	0	47,47,47	0.65	1 (2%)
6	EDO	A	1212	-	3,3,3	0.06	0	2,2,2	0.19	0
14	PG4	C	1104	-	12,12,12	0.20	0	11,11,11	0.13	0
8	D12	B	1106	-	11,11,11	0.25	0	10,10,10	0.58	0
6	EDO	A	1208	-	3,3,3	0.06	0	2,2,2	0.16	0
6	EDO	E	201	-	3,3,3	0.06	0	2,2,2	0.13	0
7	GOL	A	1211	-	5,5,5	0.06	0	5,5,5	0.17	0
7	GOL	A	1207	-	5,5,5	0.08	0	5,5,5	0.24	0
3	C14	C	1103	-	13,13,13	0.08	0	12,12,12	0.08	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
7	GOL	A	1206	-	-	0/4/4/4	-
8	D12	A	1210	-	-	0/9/9/9	-
10	HEX	B	1104	-	-	0/3/3/3	-
9	OCT	C	1102	-	-	0/5/5/5	-
9	OCT	B	1103	-	-	0/5/5/5	-
4	LMT	B	1101	-	-	6/21/61/61	0/2/2/2
4	LMT	A	1202	-	-	12/21/61/61	0/2/2/2
10	HEX	C	1114	-	-	0/3/3/3	-
12	DDQ	B	1108	-	-	2/11/11/11	-
5	ERY	A	1203	-	-	17/72/107/107	0/3/3/3
6	EDO	C	1112	-	-	0/1/1/1	-
4	LMT	C	1108	-	-	6/21/61/61	0/2/2/2
6	EDO	A	1205	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	3YI	B	1107	-	-	6/57/72/72	0/4/4/4
15	PTY	C	1113	-	-	20/53/53/53	-
6	EDO	A	1209	-	-	1/1/1/1	-
7	GOL	C	1105	-	-	0/4/4/4	-
3	C14	A	1201	-	-	4/11/11/11	-
6	EDO	A	1204	-	-	0/1/1/1	-
6	EDO	C	1110	-	-	0/1/1/1	-
6	EDO	C	1107	-	-	0/1/1/1	-
6	EDO	C	1109	-	-	0/1/1/1	-
6	EDO	B	1102	-	-	0/1/1/1	-
7	GOL	C	1106	-	-	1/4/4/4	-
4	LMT	B	1105	-	-	10/21/61/61	0/2/2/2
6	EDO	C	1111	-	-	0/1/1/1	-
4	LMT	C	1101	-	-	6/21/61/61	0/2/2/2
6	EDO	A	1212	-	-	0/1/1/1	-
14	PG4	C	1104	-	-	3/10/10/10	-
8	D12	B	1106	-	-	4/9/9/9	-
6	EDO	A	1208	-	-	0/1/1/1	-
6	EDO	E	201	-	-	0/1/1/1	-
7	GOL	A	1211	-	-	1/4/4/4	-
7	GOL	A	1207	-	-	0/4/4/4	-
3	C14	C	1103	-	-	0/11/11/11	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	1108	DDQ	O1-N1	-7.10	1.25	1.42
5	A	1203	ERY	O2-C1	5.37	1.46	1.34
15	C	1113	PTY	O4-C30	4.23	1.45	1.33
15	C	1113	PTY	O7-C8	4.14	1.46	1.34
11	B	1107	3YI	C26-C27	2.32	1.62	1.54
4	A	1202	LMT	O1'-C1'	2.04	1.43	1.40
11	B	1107	3YI	O5-C12	2.02	1.51	1.42

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1203	ERY	O5-C16-C15	-4.82	105.24	112.96
4	B	1105	LMT	C1B-O5B-C5B	4.39	122.31	113.69
15	C	1113	PTY	O7-C8-C11	4.01	120.15	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1105	LMT	O5B-C5B-C4B	3.85	116.69	109.69
5	A	1203	ERY	O5-C16-C17	3.75	109.36	103.81
5	A	1203	ERY	C20-O5-C16	3.71	125.30	117.55
5	A	1203	ERY	O2-C1-C2	3.53	119.30	111.56
5	A	1203	ERY	C25-C24-C23	3.49	115.00	109.97
5	A	1203	ERY	C22-C23-C24	3.34	114.66	109.19
4	A	1202	LMT	O5B-C5B-C4B	3.32	115.72	109.69
5	A	1203	ERY	C15-C16-C17	3.32	113.62	107.67
5	A	1203	ERY	O13-C12-C13	3.27	112.54	107.28
5	A	1203	ERY	C22-O9-C26	3.26	118.07	112.91
5	A	1203	ERY	O12-C11-C12	3.18	112.61	106.68
4	B	1105	LMT	C2'-C3'-C4'	2.88	116.26	109.68
5	A	1203	ERY	O4-C18-C17	2.80	115.03	110.03
4	A	1202	LMT	O1B-C4'-C3'	2.80	114.72	107.28
4	B	1105	LMT	O5'-C1'-C2'	2.77	116.21	110.35
4	B	1105	LMT	C1B-O1B-C4'	-2.75	111.16	117.96
4	A	1202	LMT	C1B-C2B-C3B	2.64	115.50	110.00
15	C	1113	PTY	O4-C30-C31	2.62	120.13	111.91
4	B	1105	LMT	O5B-C1B-C2B	2.45	115.54	110.35
15	C	1113	PTY	C6-O7-C8	-2.43	111.80	117.79
4	B	1105	LMT	C4B-C3B-C2B	-2.42	106.59	110.82
4	C	1101	LMT	C1B-O1B-C4'	-2.36	112.11	117.96
5	A	1203	ERY	C14-O4-C18	2.35	120.17	113.84
4	A	1202	LMT	C1B-O5B-C5B	2.35	118.30	113.69
5	A	1203	ERY	O2-C13-C12	2.28	111.01	107.29
5	A	1203	ERY	O7-C5-C6	2.25	109.17	106.39
11	B	1107	3YI	C3-C4-C10	2.23	123.04	121.20
4	B	1105	LMT	C3B-C4B-C5B	2.19	114.14	110.24
5	A	1203	ERY	C13-O2-C1	-2.16	114.34	118.18
4	B	1105	LMT	C1'-C2'-C3'	2.07	114.31	110.00
4	B	1101	LMT	C1B-O1B-C4'	-2.05	112.88	117.96

There are no chirality outliers.

All (99) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1202	LMT	C2'-C1'-O1'-C1
4	A	1202	LMT	O5'-C1'-O1'-C1
5	A	1203	ERY	C35-C12-C13-C36
5	A	1203	ERY	O13-C12-C13-O2
5	A	1203	ERY	O13-C12-C13-C36
5	A	1203	ERY	C15-C16-O5-C20

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Mol	Chain	Res	Type	Atoms
5	A	1203	ERY	C17-C16-O5-C20
5	A	1203	ERY	C19-C16-O5-C20
11	B	1107	3YI	C25-C26-C27-C28
15	C	1113	PTY	C3-O11-P1-O12
15	C	1113	PTY	C3-O11-P1-O13
15	C	1113	PTY	C3-O11-P1-O14
15	C	1113	PTY	C5-O14-P1-O12
4	B	1101	LMT	O5'-C5'-C6'-O6'
4	B	1101	LMT	C4'-C5'-C6'-O6'
4	C	1108	LMT	C2'-C1'-O1'-C1
15	C	1113	PTY	C11-C8-O7-C6
4	C	1101	LMT	C4'-C5'-C6'-O6'
15	C	1113	PTY	C30-C31-C32-C33
14	C	1104	PG4	O2-C3-C4-O3
4	A	1202	LMT	C3'-C4'-O1B-C1B
4	B	1105	LMT	O5'-C1'-O1'-C1
4	C	1108	LMT	O5'-C1'-O1'-C1
15	C	1113	PTY	O10-C8-O7-C6
15	C	1113	PTY	C5-O14-P1-O11
4	B	1105	LMT	O1'-C1-C2-C3
15	C	1113	PTY	C22-C23-C24-C25
4	A	1202	LMT	C7-C8-C9-C10
4	C	1108	LMT	C3-C4-C5-C6
4	C	1108	LMT	C5-C6-C7-C8
4	A	1202	LMT	C6-C7-C8-C9
4	C	1108	LMT	C2-C3-C4-C5
4	C	1101	LMT	O5'-C5'-C6'-O6'
4	B	1101	LMT	C3-C4-C5-C6
7	A	1211	GOL	O1-C1-C2-C3
7	C	1106	GOL	O1-C1-C2-C3
4	B	1105	LMT	C4-C5-C6-C7
4	B	1101	LMT	C11-C10-C9-C8
4	B	1105	LMT	C2-C1-O1'-C1'
15	C	1113	PTY	C21-C22-C23-C24
4	B	1101	LMT	C4-C5-C6-C7
8	B	1106	D12	C11-C10-C9-C8
4	B	1105	LMT	C7-C8-C9-C10
4	B	1105	LMT	C2-C3-C4-C5
15	C	1113	PTY	C36-C37-C38-C39
11	B	1107	3YI	C34-C26-C27-O6
11	B	1107	3YI	C34-C26-C27-C28
4	C	1101	LMT	O5B-C5B-C6B-O6B

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Mol	Chain	Res	Type	Atoms
5	A	1203	ERY	C35-C12-C13-O2
5	A	1203	ERY	C11-C12-C13-O2
5	A	1203	ERY	C11-C12-C13-C36
11	B	1107	3YI	C25-C26-C27-O6
12	B	1108	DDQ	C4-C5-C6-C7
4	B	1101	LMT	C2-C3-C4-C5
3	A	1201	C14	C05-C06-C07-C08
4	A	1202	LMT	C11-C10-C9-C8
8	B	1106	D12	C1-C2-C3-C4
4	B	1105	LMT	O5B-C5B-C6B-O6B
4	A	1202	LMT	C5'-C4'-O1B-C1B
14	C	1104	PG4	O1-C1-C2-O2
5	A	1203	ERY	C12-C13-C36-C37
4	C	1101	LMT	C2-C3-C4-C5
8	B	1106	D12	C3-C4-C5-C6
4	C	1101	LMT	C1-C2-C3-C4
11	B	1107	3YI	C28-C27-O6-C37
15	C	1113	PTY	O4-C1-C6-C5
5	A	1203	ERY	O9-C22-O7-C5
15	C	1113	PTY	C20-C21-C22-C23
15	C	1113	PTY	O4-C1-C6-O7
5	A	1203	ERY	O2-C13-C36-C37
4	C	1108	LMT	C4-C5-C6-C7
4	A	1202	LMT	C3-C4-C5-C6
8	B	1106	D12	C4-C5-C6-C7
4	A	1202	LMT	O1'-C1-C2-C3
5	A	1203	ERY	C9-C10-C11-C12
5	A	1203	ERY	C34-C10-C11-C12
4	A	1202	LMT	C4-C5-C6-C7
15	C	1113	PTY	O14-C5-C6-O7
14	C	1104	PG4	O4-C7-C8-O5
15	C	1113	PTY	C11-C12-C13-C14
3	A	1201	C14	C06-C07-C08-C09
15	C	1113	PTY	O14-C5-C6-C1
12	B	1108	DDQ	C2-C3-C4-C5
4	A	1202	LMT	C2-C3-C4-C5
3	A	1201	C14	C02-C03-C04-C05
15	C	1113	PTY	C23-C24-C25-C26
11	B	1107	3YI	C26-C27-O6-C37
4	B	1105	LMT	C6-C7-C8-C9
4	C	1101	LMT	C5-C6-C7-C8
5	A	1203	ERY	C32-C6-C7-C8

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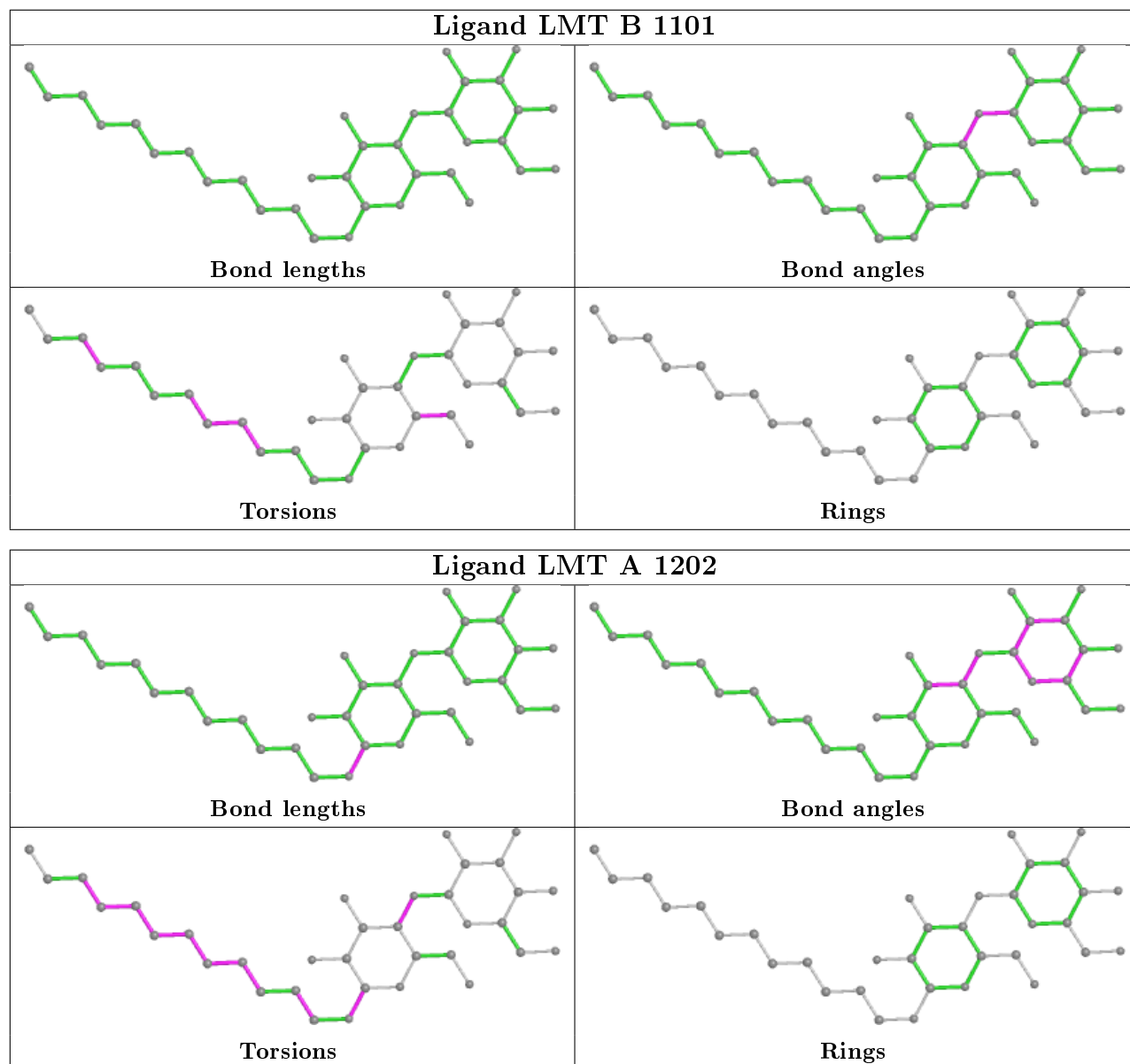
Mol	Chain	Res	Type	Atoms
3	A	1201	C14	C03-C04-C05-C06
6	A	1209	EDO	O1-C1-C2-O2
15	C	1113	PTY	C8-C11-C12-C13
15	C	1113	PTY	C31-C32-C33-C34
5	A	1203	ERY	C23-C22-O7-C5
5	A	1203	ERY	O4-C14-O3-C3
4	A	1202	LMT	C5-C6-C7-C8
4	B	1105	LMT	C3'-C4'-O1B-C1B
4	B	1105	LMT	C5-C6-C7-C8

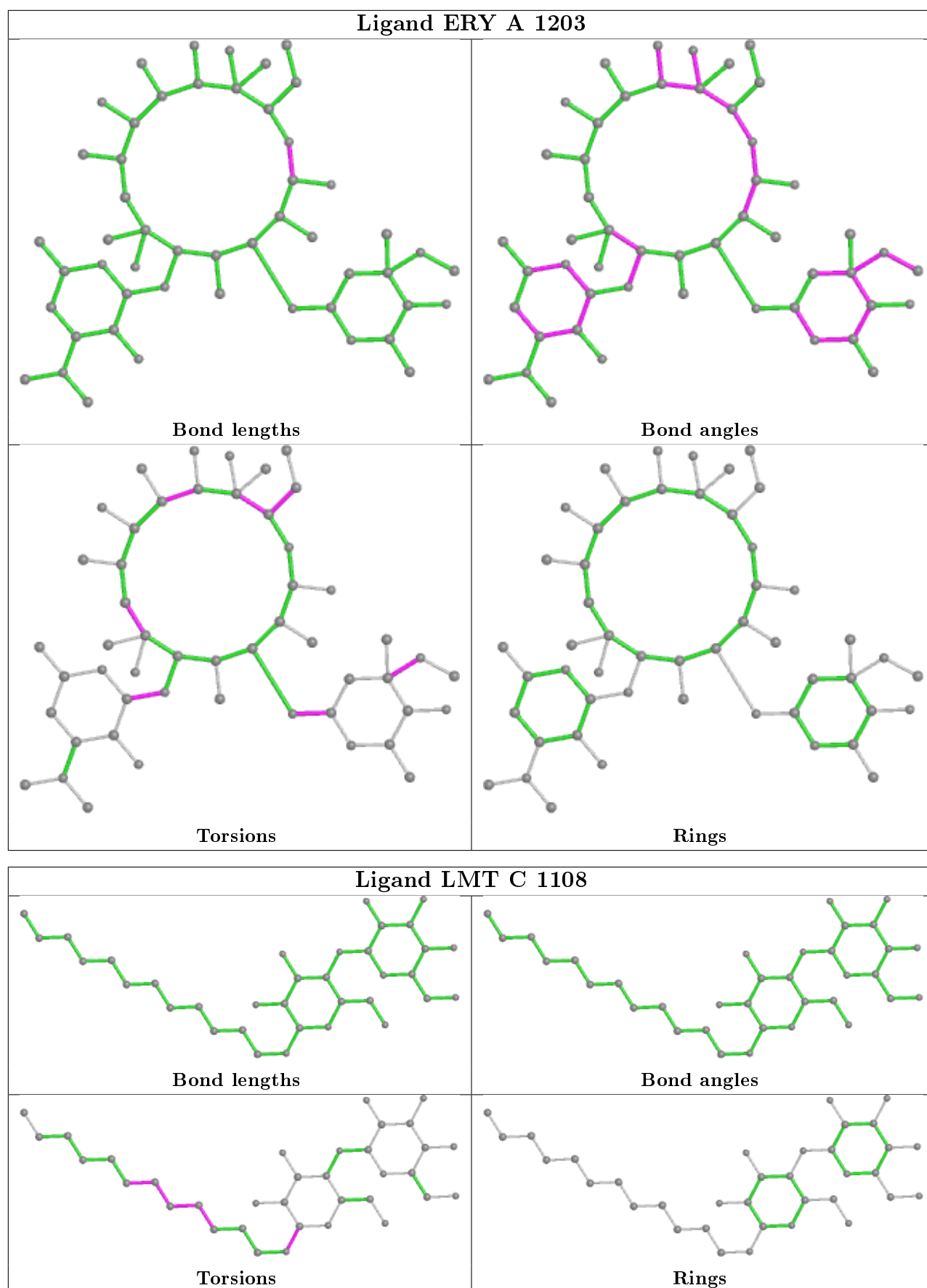
There are no ring outliers.

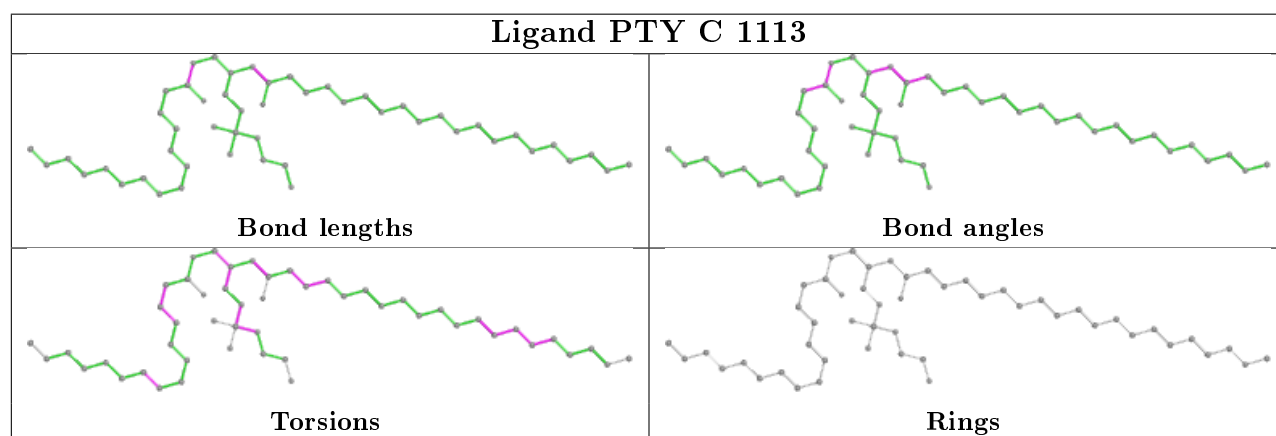
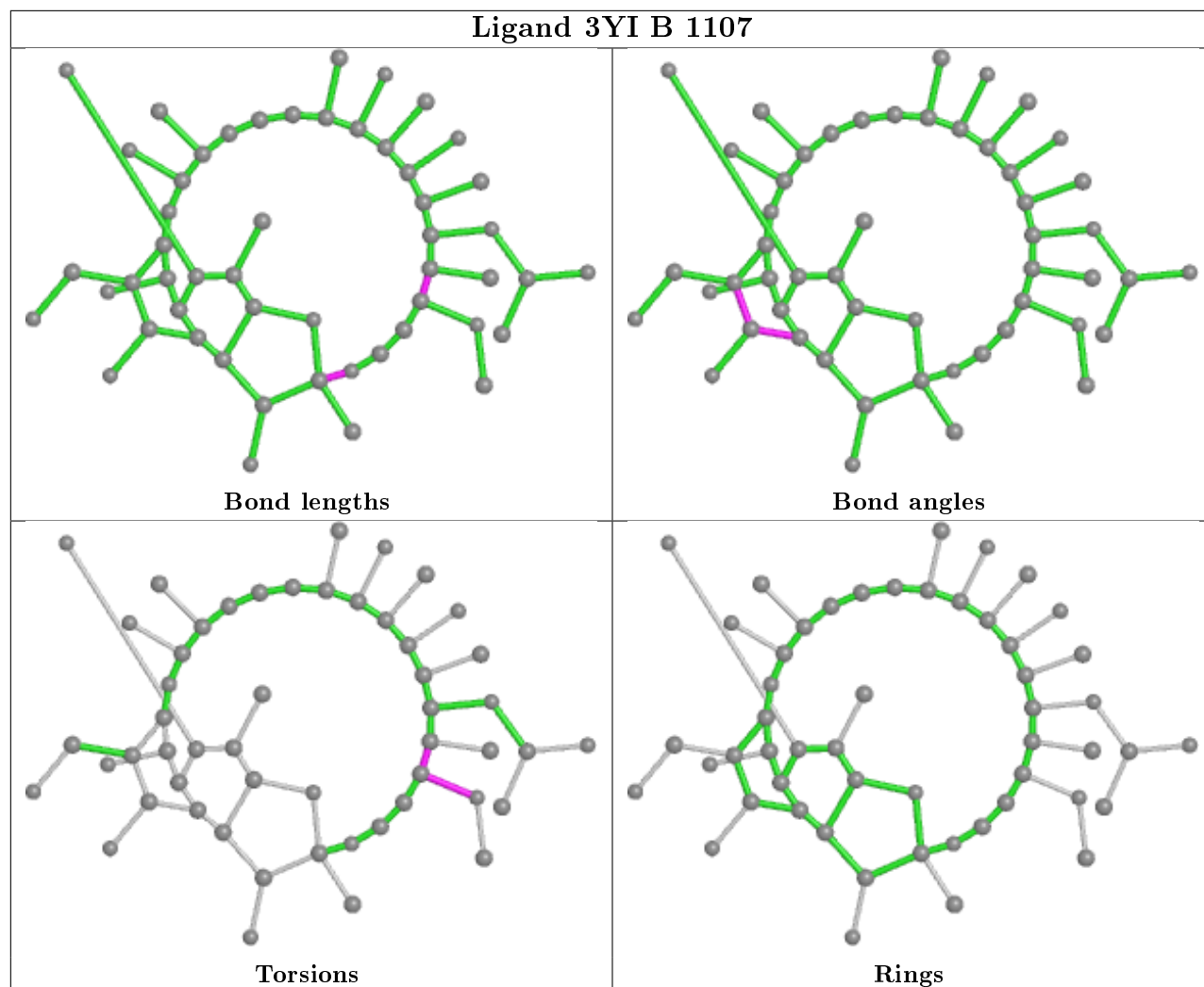
8 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1210	D12	1	0
10	B	1104	HEX	1	0
4	B	1101	LMT	1	0
5	A	1203	ERY	2	0
4	C	1108	LMT	1	0
15	C	1113	PTY	3	0
7	C	1105	GOL	1	0
7	C	1106	GOL	1	0

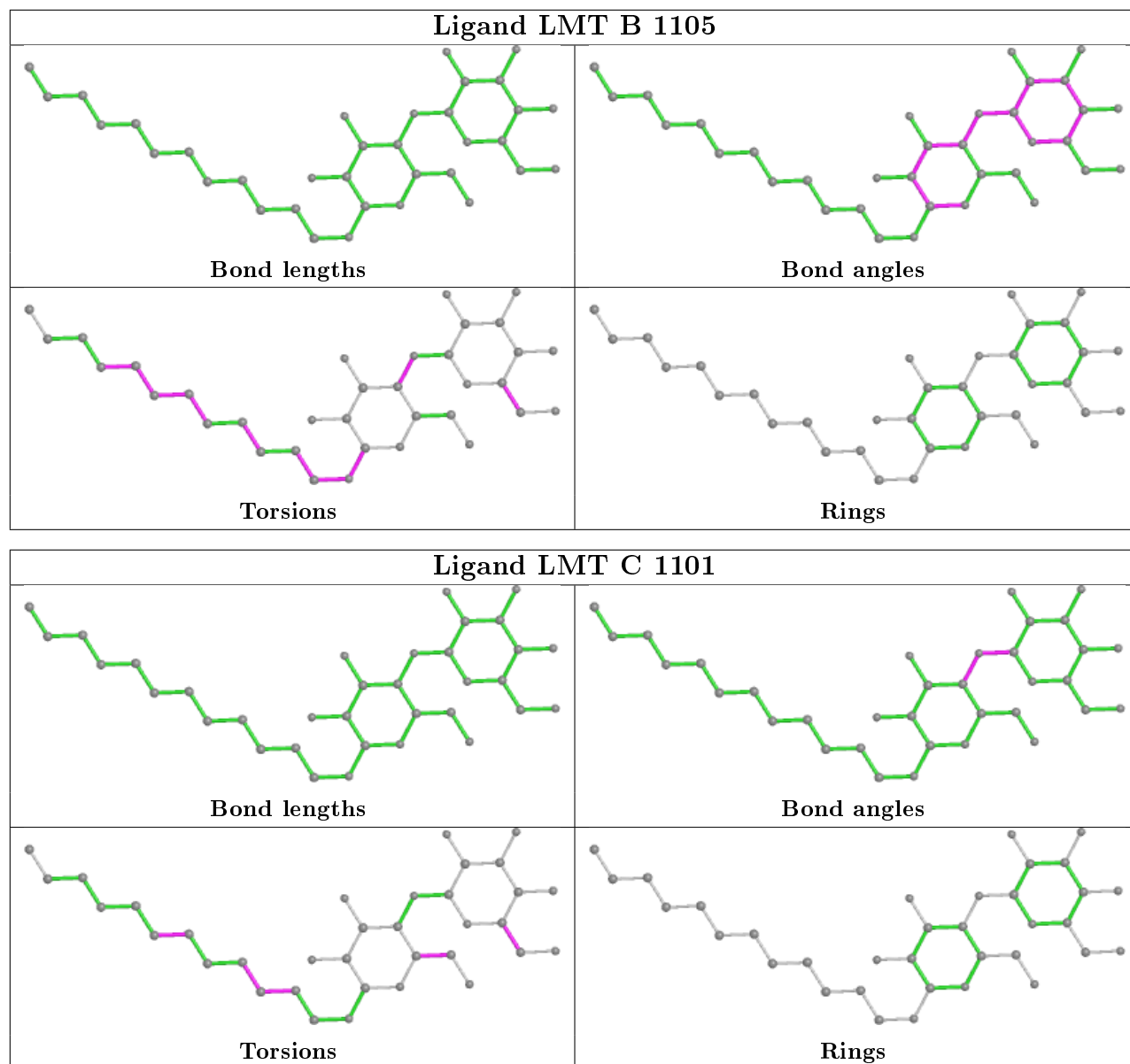
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
1	A	1034/1057 (97%)	-0.08	32 (3%)	49	44	10, 35, 73, 94	0
1	B	1033/1057 (97%)	-0.03	31 (3%)	50	45	8, 39, 64, 75	0
1	C	1034/1057 (97%)	-0.16	15 (1%)	73	73	14, 28, 51, 65	8 (0%)
2	D	155/169 (91%)	0.11	5 (3%)	47	43	33, 42, 57, 72	0
2	E	154/169 (91%)	0.85	22 (14%)	2	2	40, 59, 76, 85	0
All	All	3410/3509 (97%)	-0.04	105 (3%)	49	44	8, 36, 65, 94	8 (0%)

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	616	PRO	6.0
2	E	28	ASP	5.2
1	A	871	ASN	5.0
1	A	873	ALA	4.9
1	A	874	PRO	4.9
1	A	875	SER	4.0
1	A	869	SER	3.8
2	D	11	GLY	3.8
1	B	510	LYS	3.8
1	B	677	ALA	3.6
1	A	868	LEU	3.6
1	A	501	ALA	3.4
1	B	678	THR	3.4
1	B	600	THR	3.3
2	E	35	ALA	3.3
1	B	674	LEU	3.3
2	E	31	ARG	3.3
1	A	255	GLN	3.3
2	E	36	ASN	3.3
1	C	363	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	509	LYS	3.2
1	B	871	ASN	3.2
1	B	615	PHE	3.2
1	A	674	LEU	3.1
1	B	676	THR	3.1
2	D	159	GLU	3.1
1	C	510	LYS	3.0
1	B	640	GLU	3.0
1	A	362	PHE	3.0
1	B	256	ASP	3.0
1	B	641	GLU	2.9
2	E	140	ASN	2.9
1	C	797	GLN	2.9
1	B	638	PRO	2.9
1	B	254	ASN	2.9
2	E	27	ASP	2.9
1	C	501	ALA	2.9
1	B	332	PHE	2.9
1	B	255	GLN	2.8
2	E	153	SER	2.8
2	E	34	MET	2.8
2	E	29	GLU	2.8
2	E	32	ILE	2.8
1	A	534	ILE	2.8
1	A	867	ARG	2.7
1	B	653	ARG	2.7
2	E	139	VAL	2.7
1	A	254	ASN	2.7
1	C	1033	PHE	2.7
1	A	406	VAL	2.7
1	B	258	SER	2.6
1	B	603	LYS	2.6
1	A	533	GLY	2.6
1	B	134	SER	2.6
1	B	642	ASN	2.6
2	E	159	GLU	2.6
1	B	675	GLY	2.5
1	B	995	ALA	2.5
2	E	148	THR	2.5
1	A	980	LEU	2.5
1	A	981	ALA	2.4
2	E	33	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
2	E	163	GLU	2.4
2	E	107	ASN	2.4
1	A	256	ASP	2.4
1	A	508	GLY	2.4
2	E	69	ASN	2.4
2	E	68	LYS	2.4
1	A	870	GLY	2.4
2	D	163	GLU	2.4
1	C	255	GLN	2.4
2	D	165	LEU	2.3
1	B	508	GLY	2.3
2	E	67	LEU	2.3
1	A	429	GLU	2.3
1	A	529	ASP	2.3
1	C	616	PRO	2.3
1	B	500	ILE	2.3
2	D	150	PHE	2.3
1	C	122	VAL	2.2
1	B	601	LYS	2.2
1	C	621	GLY	2.2
1	A	423	GLU	2.2
1	A	541	TYR	2.2
1	C	515	TRP	2.2
2	E	66	LEU	2.2
1	A	510	LYS	2.2
1	B	597	TYR	2.2
1	C	253	VAL	2.2
1	A	536	ARG	2.2
1	A	554	TYR	2.1
1	A	514	GLY	2.1
1	A	863	SER	2.1
1	B	604	ASN	2.1
1	C	362	PHE	2.1
1	A	502	LYS	2.1
1	C	513	PHE	2.1
1	A	535	LEU	2.1
1	A	537	SER	2.1
1	C	794	ALA	2.1
1	B	515	TRP	2.0
1	C	254	ASN	2.0
1	B	599	LEU	2.0
2	E	18	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
2	E	165	LEU	2.0

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

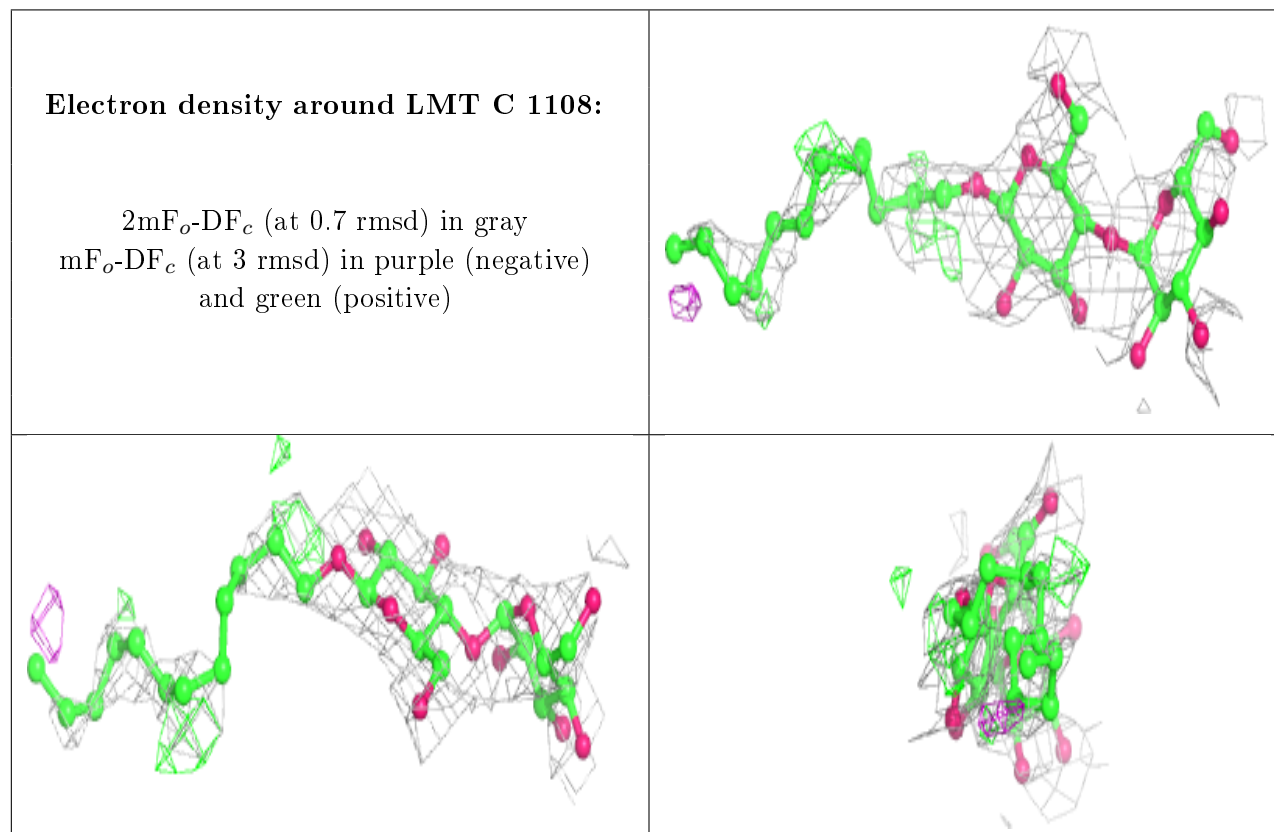
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	LMT	C	1108	35/35	0.67	0.38	128,129,130,130	0
7	GOL	A	1207	6/6	0.73	0.29	62,78,80,80	0
6	EDO	B	1102	4/4	0.81	0.22	37,44,44,44	0
15	PTY	C	1113	50/50	0.81	0.37	73,76,78,78	0
4	LMT	B	1105	35/35	0.83	0.28	72,73,73,73	35
8	D12	B	1106	12/12	0.84	0.27	40,51,54,54	0
4	LMT	B	1101	35/35	0.84	0.32	84,84,84,84	0
6	EDO	C	1111	4/4	0.85	0.40	48,65,66,67	0
6	EDO	A	1212	4/4	0.85	0.26	38,48,49,49	0
9	OCT	C	1102	8/8	0.86	0.28	39,53,56,57	0
13	SO4	B	1109	5/5	0.86	0.23	93,93,93,93	0
4	LMT	A	1202	35/35	0.86	0.21	60,62,63,63	0
5	ERY	A	1203	51/51	0.87	0.27	31,32,32,32	51
10	HEX	B	1104	6/6	0.87	0.18	34,43,44,44	0
14	PG4	C	1104	13/13	0.88	0.27	41,50,53,53	31
7	GOL	A	1211	6/6	0.88	0.22	68,84,85,85	0
6	EDO	A	1205	4/4	0.89	0.18	54,84,86,86	0
4	LMT	C	1101	35/35	0.89	0.26	60,62,63,63	0
11	3YI	B	1107	52/52	0.90	0.25	55,55,55,55	0
3	C14	A	1201	14/14	0.90	0.27	42,53,54,55	0
6	EDO	A	1208	4/4	0.90	0.19	45,56,56,57	0
10	HEX	C	1114	6/6	0.90	0.24	32,45,47,47	0

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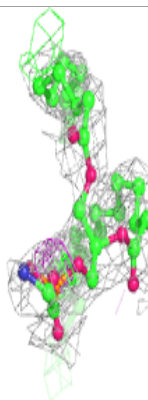
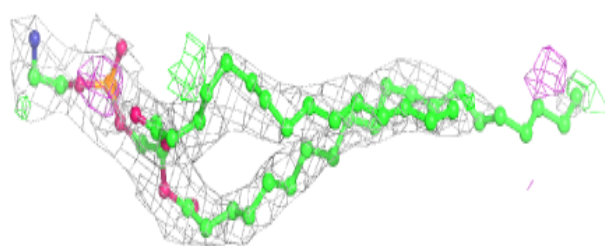
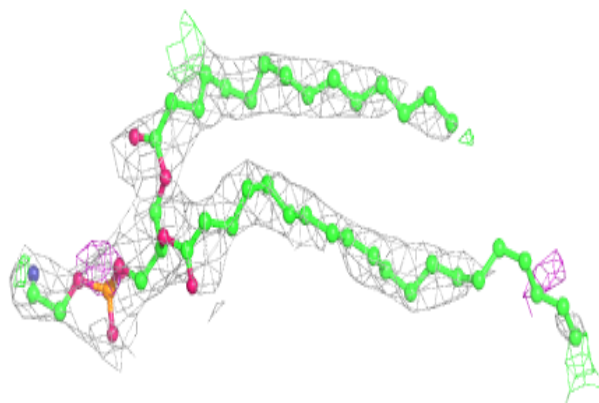
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	C14	C	1103	14/14	0.91	0.17	25,25,26,26	0
9	OCT	B	1103	8/8	0.92	0.30	27,34,35,36	0
12	DDQ	B	1108	14/14	0.92	0.32	51,66,71,71	0
7	GOL	C	1105	6/6	0.92	0.17	48,57,58,58	0
8	D12	A	1210	12/12	0.92	0.25	18,18,19,19	0
6	EDO	C	1107	4/4	0.92	0.25	44,60,61,61	0
6	EDO	E	201	4/4	0.93	0.22	34,41,46,47	0
7	GOL	A	1206	6/6	0.93	0.17	41,50,51,51	0
6	EDO	A	1204	4/4	0.93	0.19	26,37,38,39	0
6	EDO	C	1112	4/4	0.93	0.17	41,48,48,48	0
7	GOL	C	1106	6/6	0.94	0.27	42,50,50,50	0
13	SO4	D	201	5/5	0.94	0.23	90,90,90,90	0
6	EDO	C	1110	4/4	0.95	0.23	53,65,66,67	0
6	EDO	C	1109	4/4	0.96	0.15	26,29,30,30	0
6	EDO	A	1209	4/4	0.96	0.09	25,28,29,29	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.

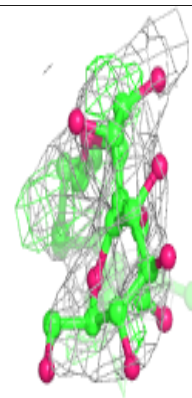
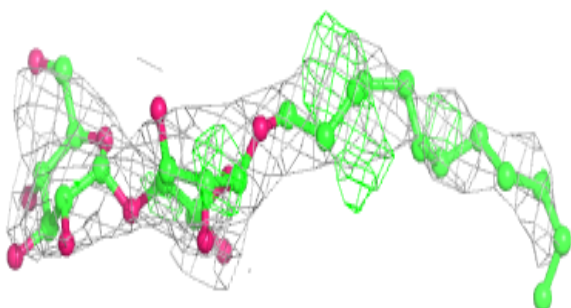
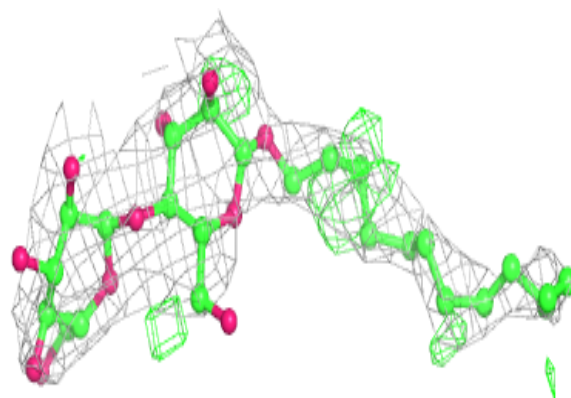


**Electron density around PTY C 1113:**

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

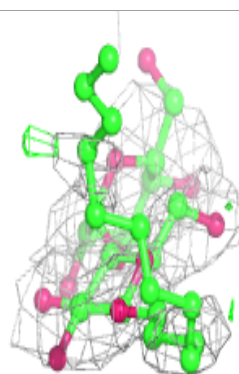
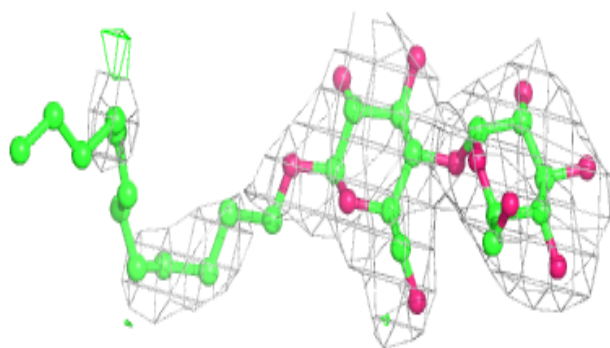
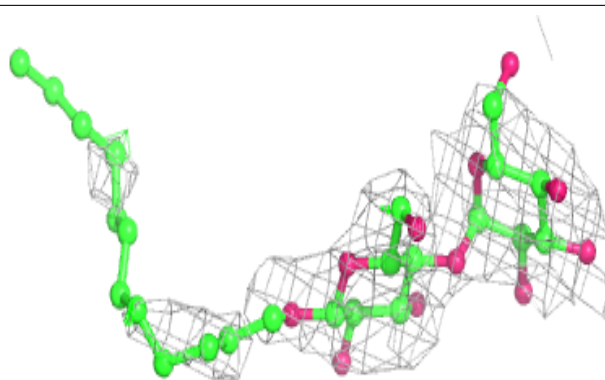
**Electron density around LMT B 1105:**

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

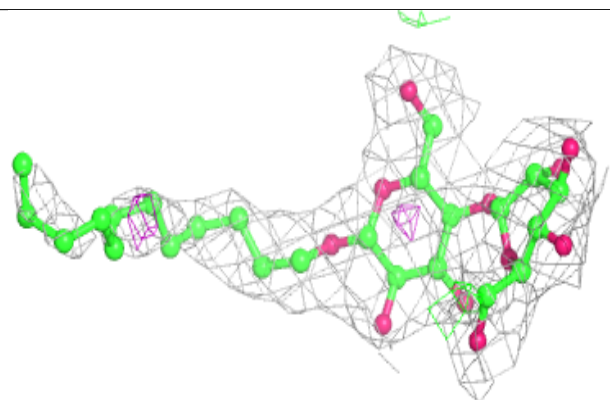
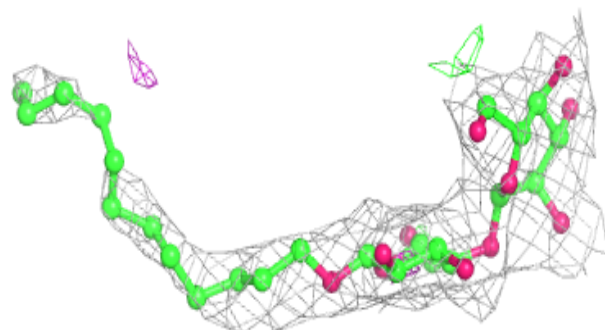


**Electron density around LMT B 1101:**

$2mF_o-DF_c$  (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:**

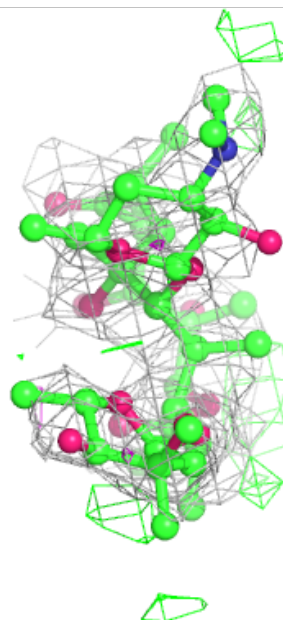
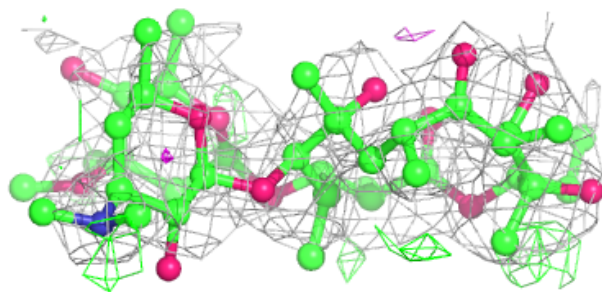
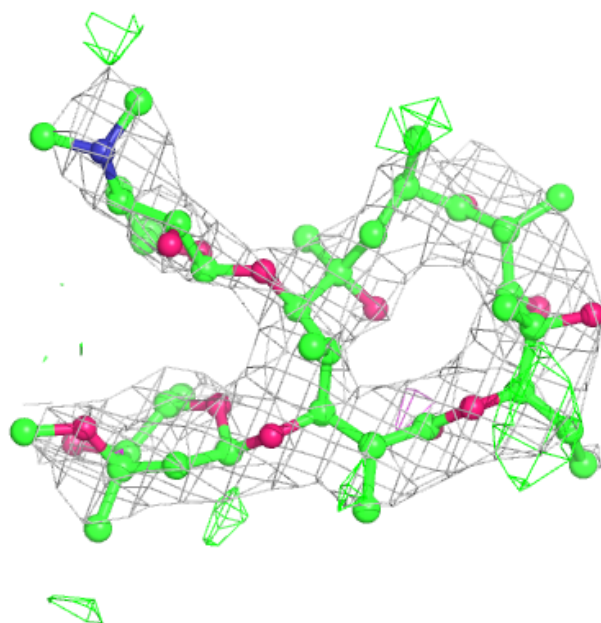
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





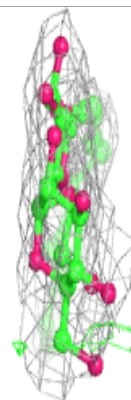
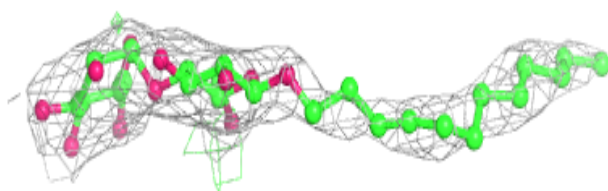
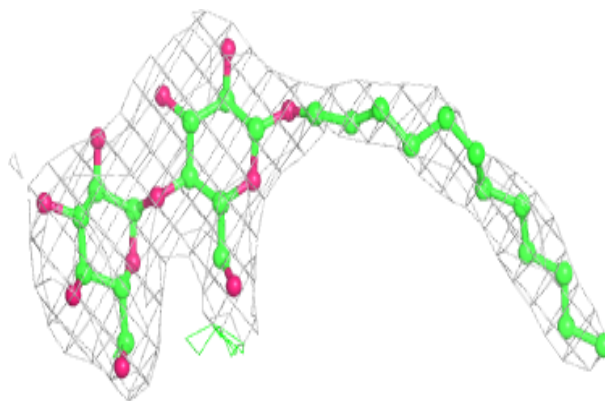
**Electron density around ERY A 1203:**

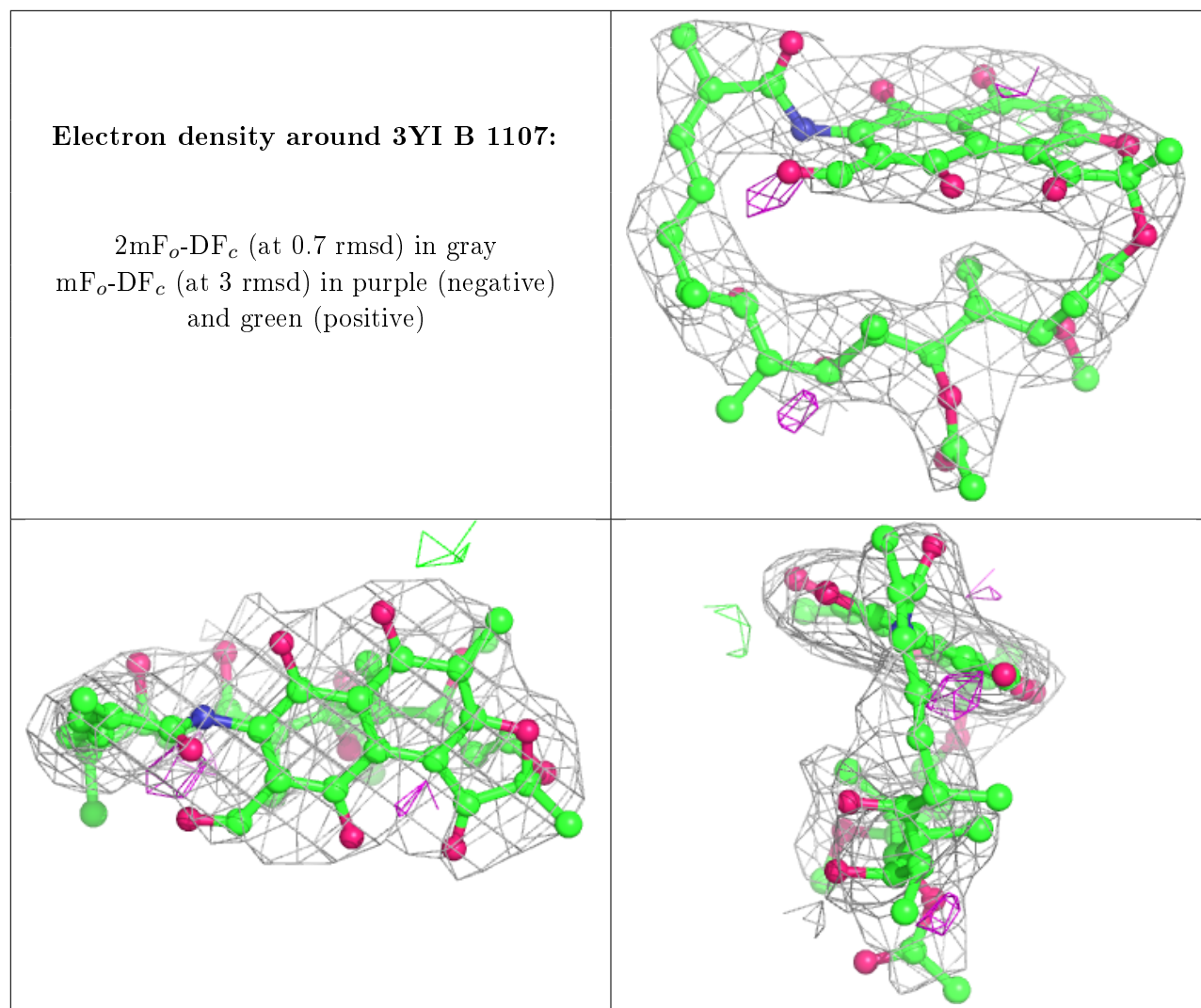
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.