



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 04:41 AM UTC

PDB ID : 6T1Z / pdb_00006t1z
Title : LmrP from *L. lactis*, in an outward-open conformation, bound to Hoechst 33342
Authors : Hutchin, A.; Debruycker, V.; Masureel, M.; Legrand, P.; Remaut, H.; Goovaerts, C.
Deposited on : 2019-10-07
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

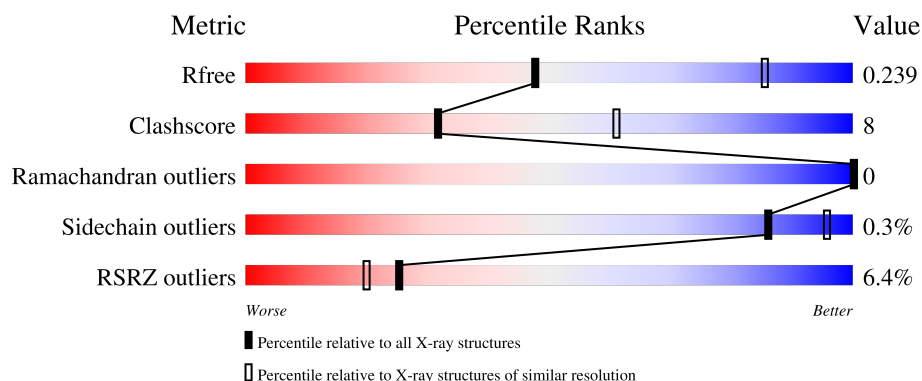
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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 ≥ 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	411	6% 76% 18% ••

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3164 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.

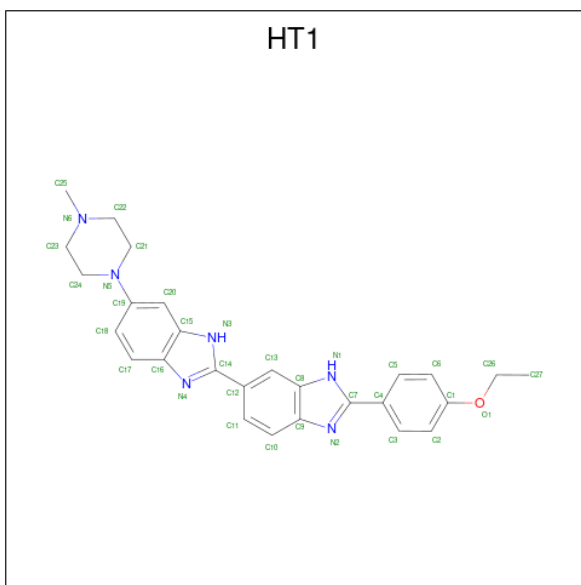
- Molecule 1 is a protein called LmrP integral membrane protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			2981	1986	467	513	15			

There are 12 discrepancies between the modelled and reference sequences:

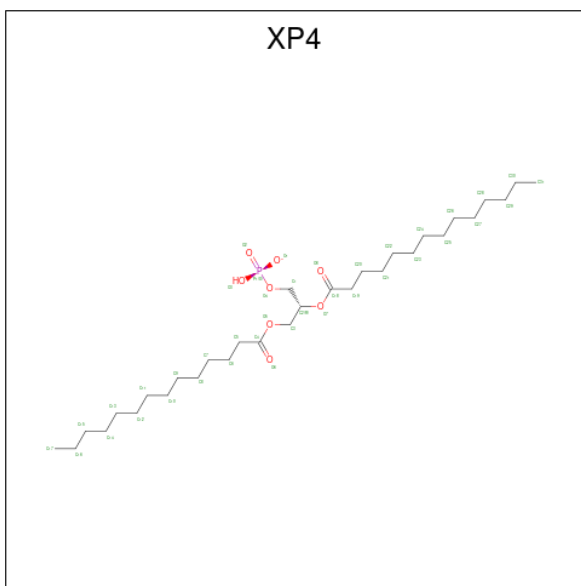
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q48658
A	?	-	GLU	deletion	UNP Q48658
A	?	-	LYS	deletion	UNP Q48658
A	?	-	ALA	deletion	UNP Q48658
A	?	-	GLU	deletion	UNP Q48658
A	409	LEU	-	expression tag	UNP Q48658
A	410	GLU	-	expression tag	UNP Q48658
A	411	VAL	-	expression tag	UNP Q48658
A	412	LEU	-	expression tag	UNP Q48658
A	413	PHE	-	expression tag	UNP Q48658
A	414	GLN	-	expression tag	UNP Q48658
A	415	GLY	-	expression tag	UNP Q48658

- Molecule 2 is 2'-(4-ETHOXYPHENYL)-5-(4-METHYL-1-PIPERAZINYL)-2,5'-BI-BENZIMIDAZOLE (CCD ID: HT1) (formula: C₂₇H₂₈N₆O) (labeled as "Ligand of Interest" by depositor).



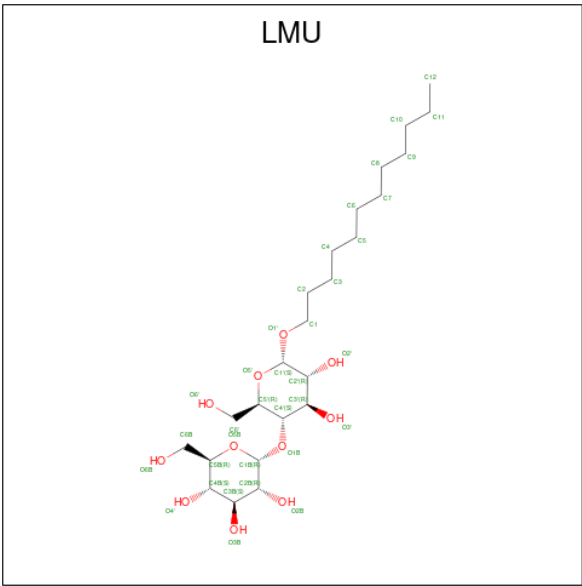
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			34	27	6	1		

- Molecule 3 is 1,2-DIMYRISTOYL-SN-GLYCERO-3-PHOSPHATE (CCD ID: XP4) (formula: $\text{C}_{31}\text{H}_{60}\text{O}_8\text{P}$) (labeled as "Ligand of Interest" by depositor).



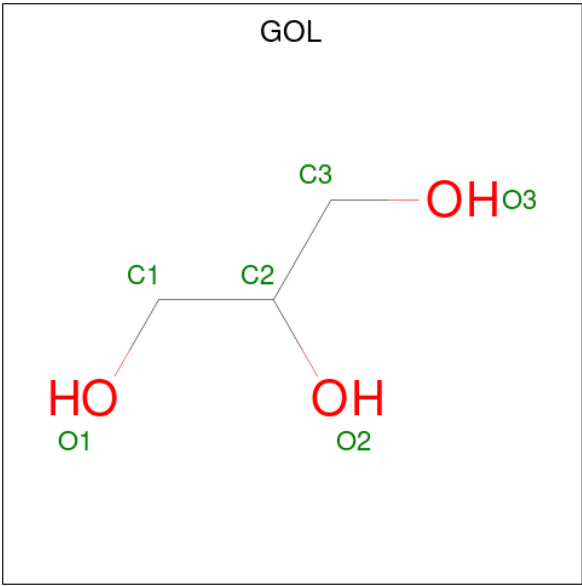
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 32	C 23	O 8	P 1	0	0
3	A	1	Total 40	C 31	O 8	P 1	0	0

- Molecule 4 is DODECYL-ALPHA-D-MALTOSIDE (CCD ID: LMU) (formula: C₂₄H₄₆O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			35	24	11		
4	A	1	Total	C	O	0	0
			33	22	11		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

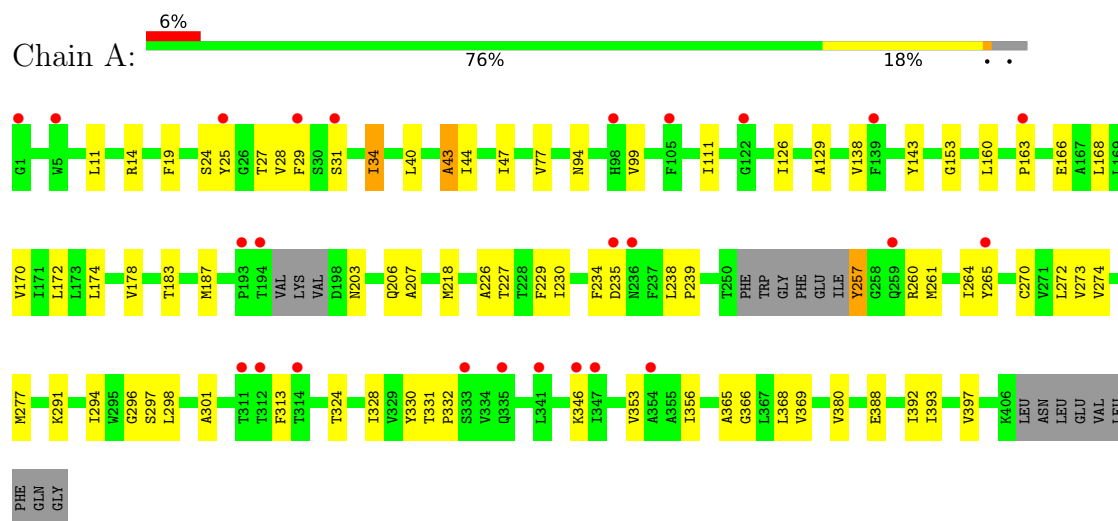
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		

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: LmrP integral membrane protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	104.76Å 139.99Å 115.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	66.3 (20.00-2.90) 66.1 (20.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.88Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.225 , 0.238 (Not available) , 0.239	Depositor DCC
R_{free} test set	654 reflections (3.41%)	wwPDB-VP
Wilson B-factor (Å ²)	89.6	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3164	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HT1, XP4, LMU, GOL

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	0.86	0/3044	1.46	7/4146 (0.2%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366	GLY	CA-C-N	5.80	128.05	120.28
1	A	366	GLY	C-N-CA	5.80	128.05	120.28
1	A	43	ALA	N-CA-C	-5.24	105.64	111.36
1	A	34	ILE	CA-C-N	5.10	127.87	120.79
1	A	34	ILE	C-N-CA	5.10	127.87	120.79
1	A	291	LYS	CA-C-N	5.07	125.70	120.03
1	A	291	LYS	C-N-CA	5.07	125.70	120.03

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2981	0	3069	48	0
2	A	34	0	28	1	0
3	A	72	0	98	3	0
4	A	68	0	84	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	6	0	8	0	0
6	A	3	0	0	0	0
All	All	3164	0	3287	52	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 8.

All (52) 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:218:MET:HA	1:A:218:MET:HE2	1.69	0.74
1:A:365:ALA:O	1:A:369:VAL:HG23	1.90	0.71
3:A:502:XP4:O5	3:A:502:XP4:H11	1.93	0.66
1:A:261:MET:HA	1:A:264:ILE:HD12	1.87	0.57
4:A:504:LMU:H6D	4:A:505:LMU:C7	2.35	0.56
4:A:504:LMU:H6D	4:A:505:LMU:C8	2.36	0.56
1:A:353:VAL:O	1:A:356:ILE:HG12	2.06	0.56
1:A:29:PHE:CE1	3:A:502:XP4:H22	2.42	0.54
1:A:235:ASP:OD2	2:A:501:HT1:H13	2.07	0.54
4:A:505:LMU:O2B	4:A:505:LMU:H4'	2.09	0.52
1:A:77:VAL:HG22	1:A:183:THR:HG22	1.92	0.52
1:A:294:ILE:HG23	1:A:392:ILE:HD12	1.92	0.52
1:A:331:THR:HB	1:A:332:PRO:HD3	1.91	0.51
1:A:294:ILE:O	1:A:298:LEU:HB2	2.11	0.50
1:A:257:TYR:HB2	1:A:260:ARG:HD2	1.92	0.50
1:A:143:TYR:CD1	1:A:331:THR:HG21	2.47	0.49
1:A:226:ALA:O	1:A:229:PHE:HB3	2.12	0.49
1:A:11:LEU:HD21	1:A:129:ALA:HB3	1.95	0.49
1:A:43:ALA:O	1:A:47:ILE:HG12	2.13	0.49
1:A:126:ILE:HG23	1:A:138:VAL:HG11	1.95	0.49
1:A:166:GLU:O	1:A:170:VAL:HG23	2.13	0.48
1:A:24:SER:HB3	1:A:172:LEU:HD12	1.96	0.48
1:A:294:ILE:HG12	1:A:392:ILE:HD12	1.95	0.48
1:A:238:LEU:N	1:A:239:PRO:HD2	2.29	0.47
1:A:227:THR:HG22	1:A:297:SER:HB2	1.96	0.47
1:A:234:PHE:HE2	1:A:265:TYR:HD2	1.62	0.46
1:A:14:ARG:HE	1:A:126:ILE:HD11	1.80	0.46
1:A:301:ALA:HB2	1:A:388:GLU:HG3	1.98	0.45
1:A:272:LEU:HB2	1:A:324:THR:HG21	1.99	0.45
1:A:143:TYR:CD2	1:A:277:MET:HE1	2.51	0.44
1:A:94:ASN:ND2	1:A:99:VAL:HG13	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:PHE:C	1:A:313:PHE:CD1	2.96	0.44
1:A:28:VAL:HG22	1:A:168:LEU:HB3	2.00	0.43
1:A:111:ILE:HD13	1:A:172:LEU:HD21	2.01	0.43
1:A:19:PHE:CD1	1:A:19:PHE:C	2.96	0.43
1:A:227:THR:HA	1:A:230:ILE:HD12	2.00	0.43
1:A:160:LEU:HA	1:A:163:PRO:HG2	1.99	0.43
1:A:368:LEU:HD21	1:A:380:VAL:HG13	2.00	0.43
1:A:174:LEU:O	1:A:178:VAL:HG23	2.18	0.43
1:A:207:ALA:HA	1:A:346:LYS:NZ	2.34	0.43
1:A:203:ASN:HB3	1:A:206:GLN:HB2	2.00	0.42
1:A:25:TYR:HB2	3:A:502:XP4:H20	2.01	0.42
1:A:183:THR:HA	1:A:187:MET:HE3	2.01	0.42
1:A:31:SER:O	1:A:34:ILE:HB	2.21	0.41
1:A:25:TYR:OH	4:A:505:LMU:H11	2.21	0.41
1:A:27:THR:HG23	1:A:153:GLY:HA2	2.02	0.41
1:A:270:CYS:O	1:A:274:VAL:HG23	2.21	0.41
1:A:40:LEU:HB3	1:A:44:ILE:HG21	2.03	0.41
1:A:234:PHE:CE2	1:A:265:TYR:HD2	2.38	0.41
1:A:296:GLY:HA3	1:A:330:TYR:HB2	2.03	0.41
1:A:393:ILE:O	1:A:397:VAL:HG23	2.20	0.41
1:A:273:VAL:HG22	1:A:328:ILE:HG12	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	387/411 (94%)	372 (96%)	15 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	310/343 (90%)	309 (100%)	1 (0%)	86	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	224	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 [i](#)

6 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	XP4	A	503	-	39,39,39	0.35	0	42,44,44	1.06	2 (4%)
5	GOL	A	506	-	5,5,5	0.10	0	5,5,5	0.18	0
4	LMU	A	504	-	36,36,36	0.69	1 (2%)	47,47,47	1.09	3 (6%)
2	HT1	A	501	-	39,39,39	0.40	0	56,56,56	0.56	0
3	XP4	A	502	-	31,31,39	0.36	0	34,36,44	0.82	2 (5%)
4	LMU	A	505	-	34,34,36	0.95	3 (8%)	45,45,47	2.54	11 (24%)

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	XP4	A	503	-	-	23/41/41/41	-
5	GOL	A	506	-	-	2/4/4/4	-
4	LMU	A	504	-	-	7/21/61/61	0/2/2/2
2	HT1	A	501	-	-	0/15/25/25	0/6/6/6
3	XP4	A	502	-	-	10/33/33/41	-
4	LMU	A	505	-	-	9/19/59/61	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	505	LMU	O1'-C1'	2.66	1.44	1.40
4	A	505	LMU	C4'-C5'	2.66	1.60	1.52
4	A	505	LMU	C1'-C2'	-2.18	1.46	1.52
4	A	504	LMU	O1'-C1'	2.06	1.43	1.40

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	505	LMU	C3'-C4'-C5'	-9.28	90.36	110.93
4	A	505	LMU	O2'-C2'-C1'	6.78	126.23	110.08
3	A	503	XP4	O5-C3-C2	5.62	124.60	108.40
4	A	505	LMU	O1B-C1B-C2B	5.56	121.78	108.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	505	LMU	O2'-C2'-C3'	-4.71	99.26	110.38
4	A	505	LMU	C6'-C5'-C4'	4.58	126.27	113.38
4	A	505	LMU	O5'-C1'-C2'	4.42	119.45	110.37
4	A	504	LMU	C1B-O1B-C4'	-3.87	108.81	117.98
4	A	505	LMU	O3'-C3'-C4'	3.76	119.58	109.94
3	A	502	XP4	O5-C3-C2	3.04	117.15	108.40
4	A	505	LMU	O5'-C5'-C4'	2.88	115.69	109.72
4	A	505	LMU	C5-C4-C3	-2.82	100.13	114.37
3	A	502	XP4	C3-C2-C1	-2.37	106.27	111.78
4	A	505	LMU	O1'-C1-C2	-2.32	101.50	109.37
4	A	504	LMU	O5'-C1'-O1'	-2.30	104.60	110.04
4	A	504	LMU	O1B-C1B-C2B	2.23	113.57	108.09
4	A	505	LMU	C1'-O5'-C5'	-2.10	109.62	113.72
3	A	503	XP4	O7-C2-C1	2.01	115.55	108.34

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	XP4	C1-O4-P1-O1
3	A	503	XP4	O4-C1-C2-O7
4	A	504	LMU	C2-C1-O1'-C1'
4	A	505	LMU	C2B-C1B-O1B-C4'
4	A	504	LMU	C4B-C5B-C6B-O6B
4	A	505	LMU	C4B-C5B-C6B-O6B
4	A	505	LMU	C4'-C5'-C6'-O6'
4	A	504	LMU	C4'-C5'-C6'-O6'
4	A	505	LMU	O5B-C5B-C6B-O6B
4	A	504	LMU	O5B-C5B-C6B-O6B
4	A	505	LMU	C1-C2-C3-C4
4	A	505	LMU	C4-C5-C6-C7
4	A	504	LMU	O5'-C5'-C6'-O6'
3	A	503	XP4	C5-C4-O5-C3
3	A	503	XP4	O6-C4-O5-C3
4	A	504	LMU	C3-C4-C5-C6
4	A	504	LMU	C7-C8-C9-C10
4	A	505	LMU	C6-C7-C8-C9
4	A	505	LMU	O5'-C5'-C6'-O6'
3	A	502	XP4	C18-C19-C20-C21
5	A	506	GOL	C1-C2-C3-O3
3	A	503	XP4	C10-C11-C12-C13
5	A	506	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	503	XP4	C4-C5-C6-C7
3	A	502	XP4	C5-C6-C7-C8
3	A	503	XP4	C9-C10-C11-C12
3	A	503	XP4	C2-C3-O5-C4
3	A	503	XP4	C19-C18-O7-C2
3	A	503	XP4	C21-C22-C23-C24
3	A	502	XP4	C22-C23-C24-C25
3	A	502	XP4	O4-C1-C2-C3
3	A	503	XP4	O4-C1-C2-C3
3	A	503	XP4	C18-C19-C20-C21
3	A	503	XP4	O8-C18-O7-C2
3	A	503	XP4	C1-O4-P1-O2
3	A	503	XP4	O7-C2-C3-O5
3	A	503	XP4	C11-C10-C9-C8
3	A	503	XP4	C1-O4-P1-O3
3	A	503	XP4	C20-C21-C22-C23
3	A	502	XP4	O4-C1-C2-O7
3	A	503	XP4	C1-C2-C3-O5
4	A	505	LMU	O5B-C1B-O1B-C4'
3	A	503	XP4	C22-C23-C24-C25
3	A	502	XP4	C5-C4-O5-C3
3	A	503	XP4	C7-C8-C9-C10
3	A	502	XP4	C20-C21-C22-C23
3	A	502	XP4	C10-C11-C12-C13
3	A	502	XP4	O7-C18-C19-C20
3	A	503	XP4	C19-C20-C21-C22
3	A	503	XP4	C27-C28-C29-C30
3	A	502	XP4	O8-C18-C19-C20

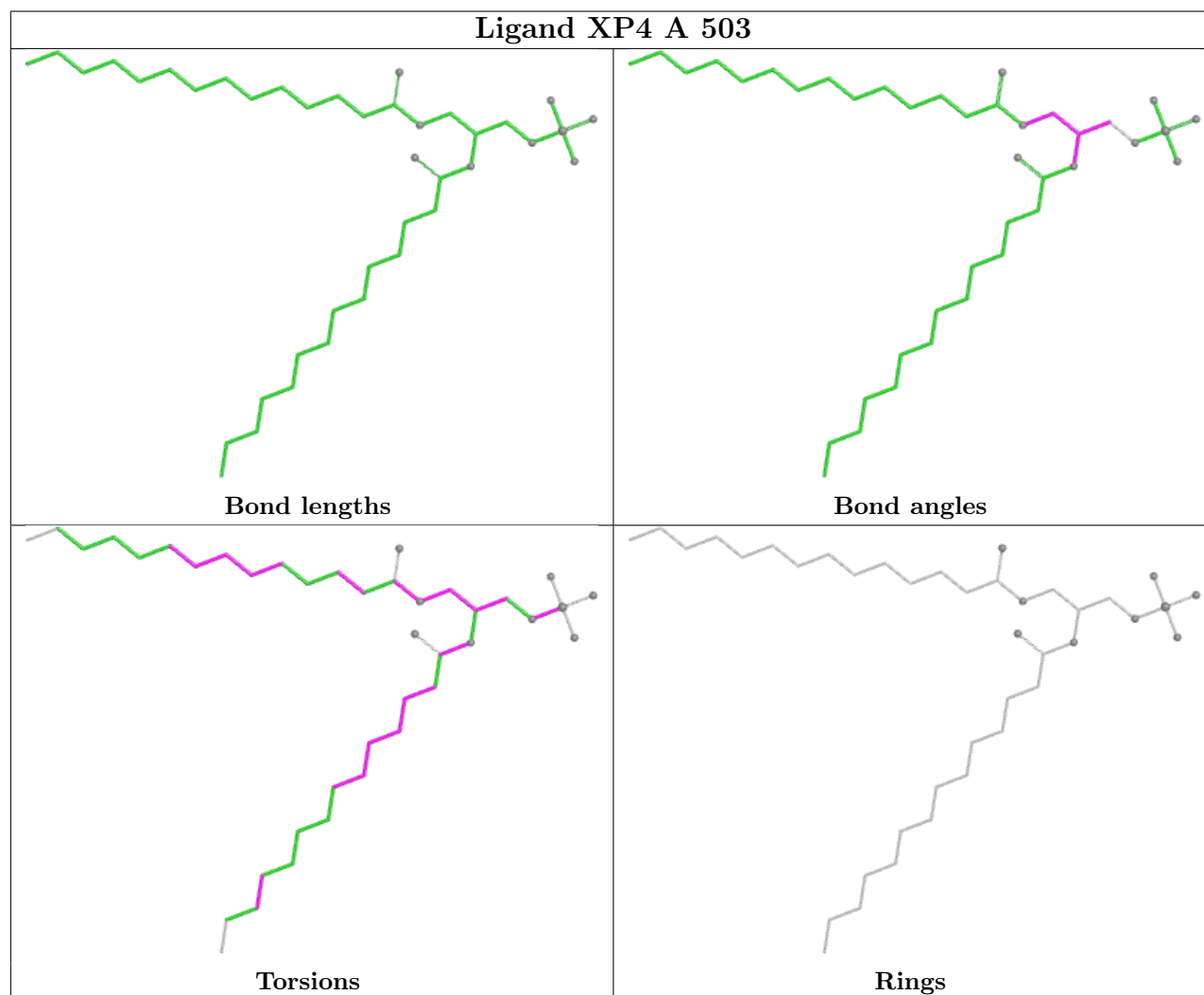
There are no ring outliers.

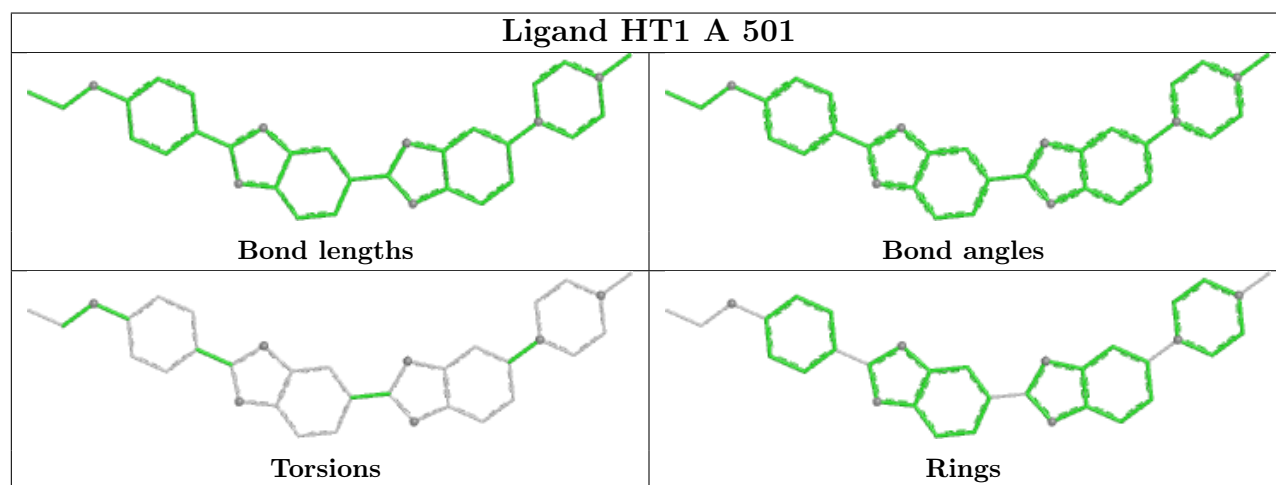
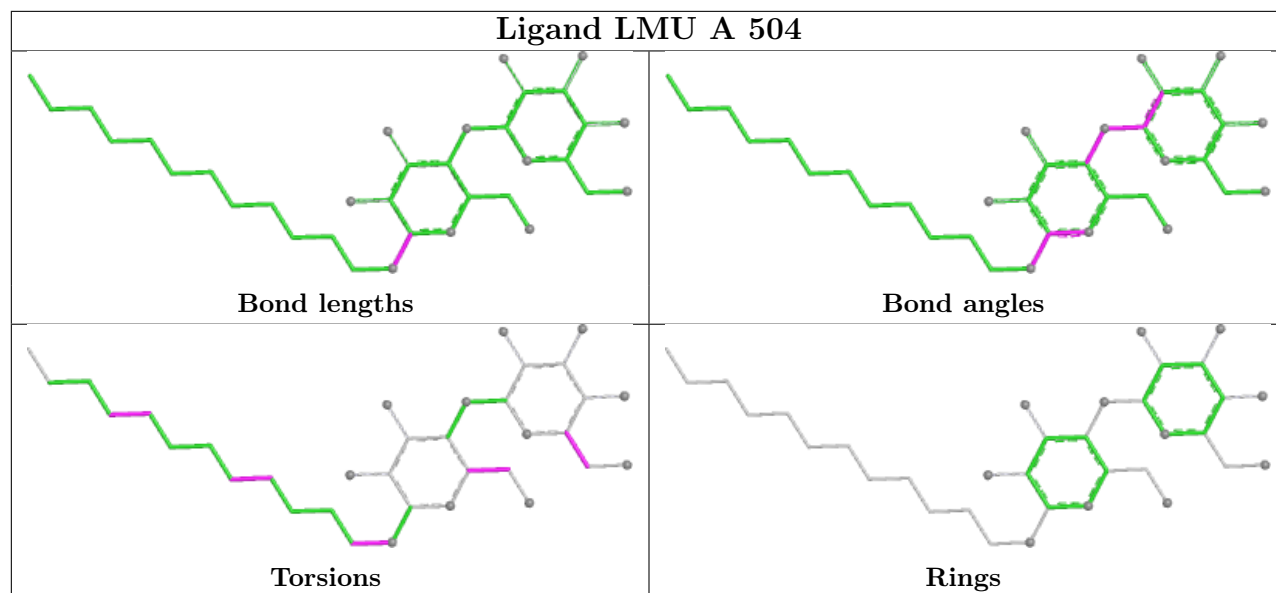
4 monomers are involved in 8 short contacts:

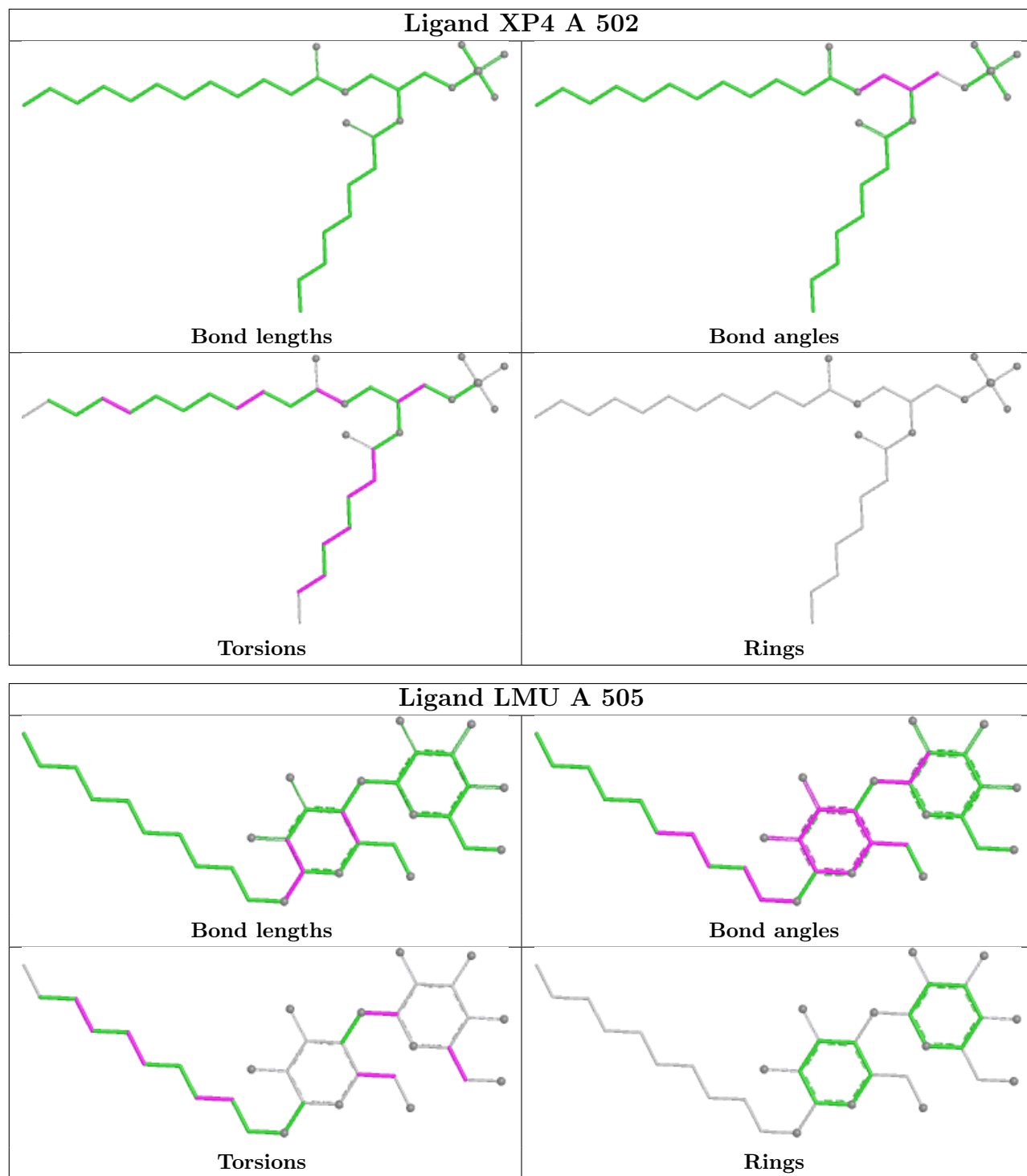
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	LMU	2	0
2	A	501	HT1	1	0
3	A	502	XP4	3	0
4	A	505	LMU	4	0

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 ⓘ

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, 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	393/411 (95%)	0.47	25 (6%)	25 20	48, 80, 111, 143	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	236	ASN	5.8
1	A	194	THR	4.3
1	A	235	ASP	4.1
1	A	163	PRO	4.0
1	A	29	PHE	3.3
1	A	265	TYR	3.1
1	A	31	SER	2.9
1	A	25	TYR	2.7
1	A	105	PHE	2.7
1	A	335	GLN	2.6
1	A	259	GLN	2.6
1	A	333	SER	2.5
1	A	311	THR	2.5
1	A	5	TRP	2.4
1	A	1	GLY	2.3
1	A	312	THR	2.3
1	A	122	GLY	2.3
1	A	354	ALA	2.2
1	A	139	PHE	2.2
1	A	347	ILE	2.2
1	A	341	LEU	2.2
1	A	193	PRO	2.1
1	A	346	LYS	2.1
1	A	98	HIS	2.1
1	A	314	THR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

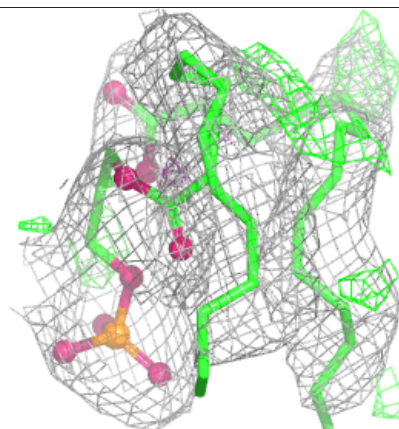
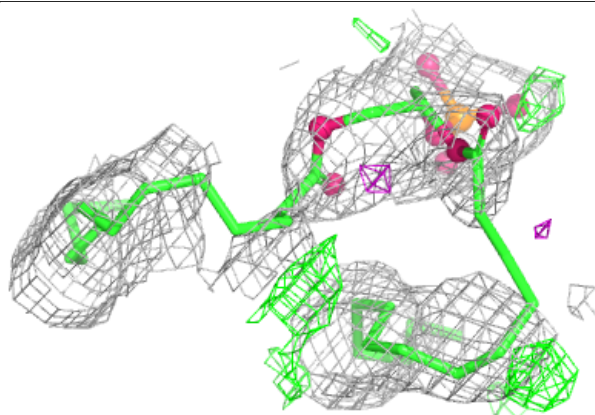
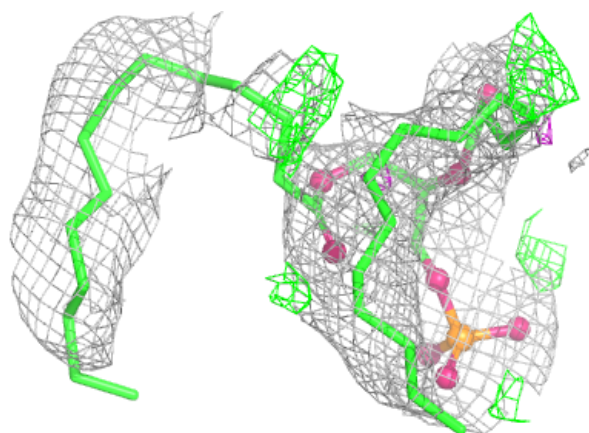
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	XP4	A	503	40/40	0.78	0.23	100,109,138,139	0
4	LMU	A	505	33/35	0.78	0.22	82,114,120,122	0
3	XP4	A	502	32/40	0.79	0.20	57,85,139,141	0
4	LMU	A	504	35/35	0.80	0.18	94,115,125,126	0
5	GOL	A	506	6/6	0.86	0.11	94,96,96,97	0
2	HT1	A	501	34/34	0.94	0.09	61,74,87,90	0

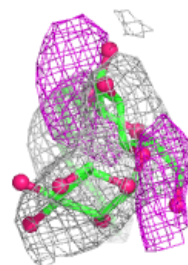
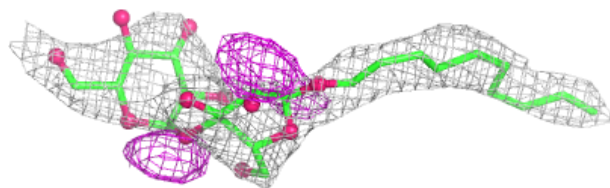
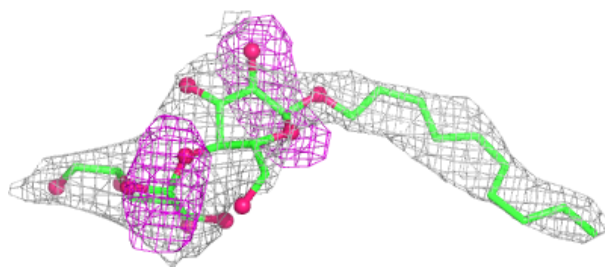
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around XP4 A 503:

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

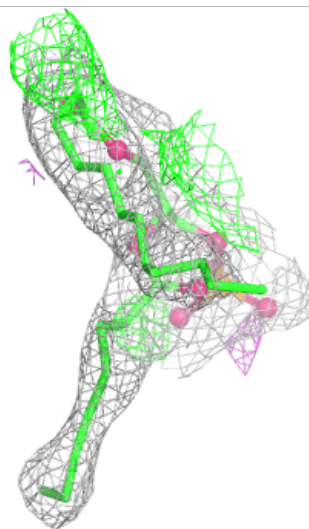
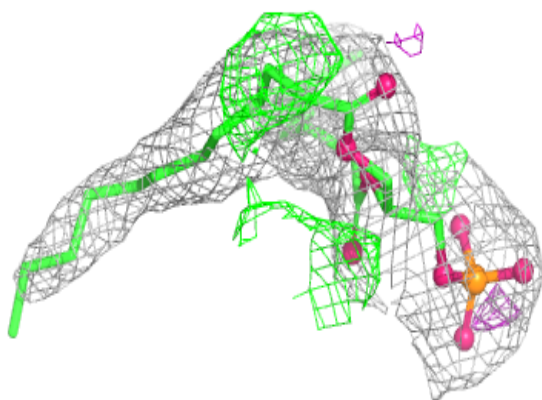
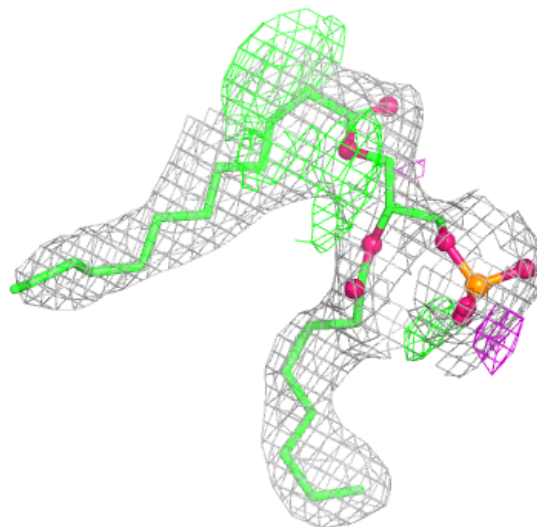
**Electron density around LMU A 505:**

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



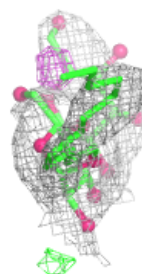
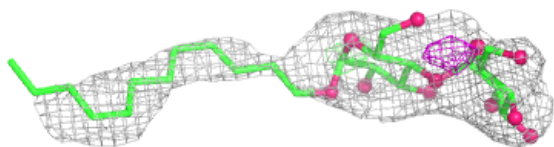
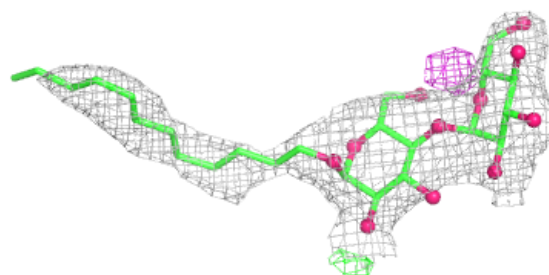
Electron density around XP4 A 502:

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

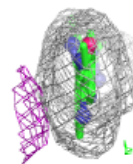
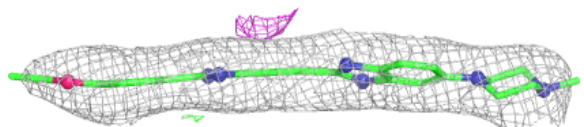
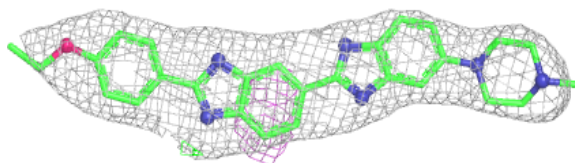


Electron density around LMU A 504:

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

**Electron density around HT1 A 501:**

$2mF_o-DF_c$ (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.