



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:06 AM UTC

PDB ID : 2UUH / pdb_00002uuh
Title : Crystal structure of Human Leukotriene C4 Synthase in complex with substrate glutathione
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Deposited on : 2007-03-02
Resolution : 2.15 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

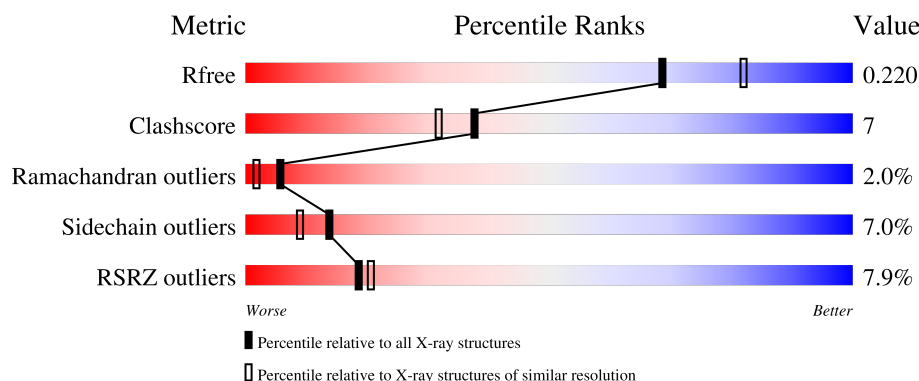
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	156	8% 78% 15% ...

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
3	LMU	A	1149	X	-	-	-
4	GSH	A	1150	X	-	-	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 1440 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.

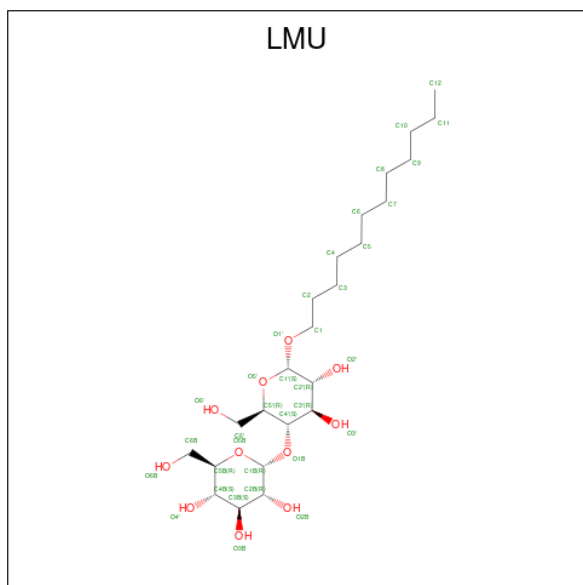
- Molecule 1 is a protein called LEUKOTRIENE C4 SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	0	2	1
			1195	791	215	187	2			

- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

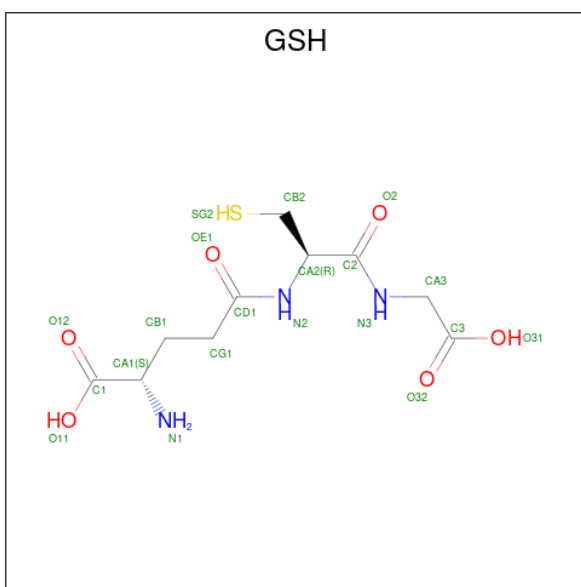
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ni	0	0
			2	2		

- Molecule 3 is DODECYL-ALPHA-D-MALTOSIDE (CCD ID: LMU) (formula: C₂₄H₄₆O₁₁).



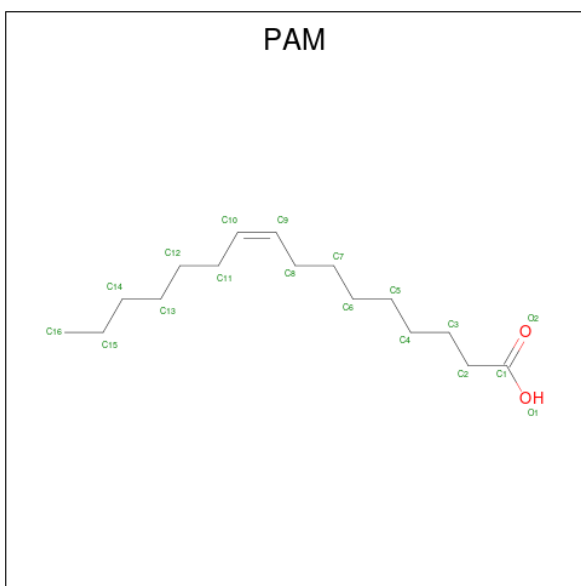
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			35	24	11		

- Molecule 4 is GLUTATHIONE (CCD ID: GSH) (formula: C₁₀H₁₇N₃O₆S).



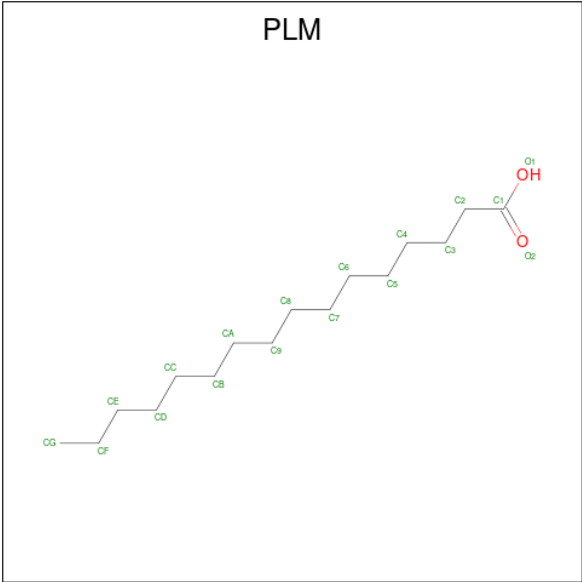
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			20	10	3	6	1		

- Molecule 5 is PALMITOLEIC ACID (CCD ID: PAM) (formula: $C_{16}H_{30}O_2$).



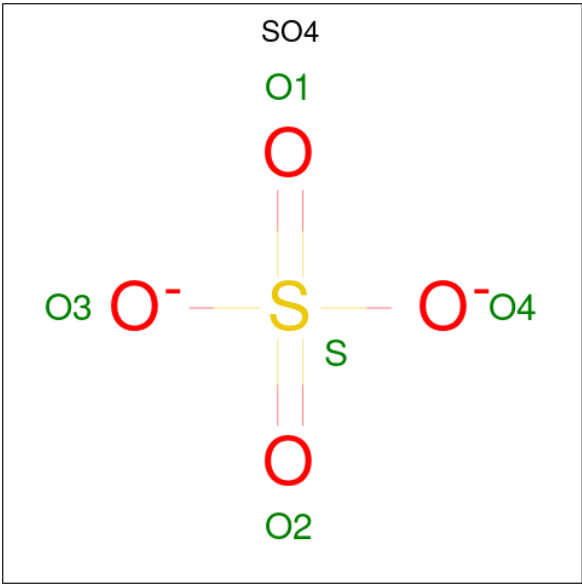
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			18	16	2		

- Molecule 6 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C 10 10	0	0
6	A	1	Total C 10 10	0	0
6	A	1	Total C 8 8	0	0
6	A	1	Total C 10 10	0	0
6	A	1	Total C 5 5	0	0

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		

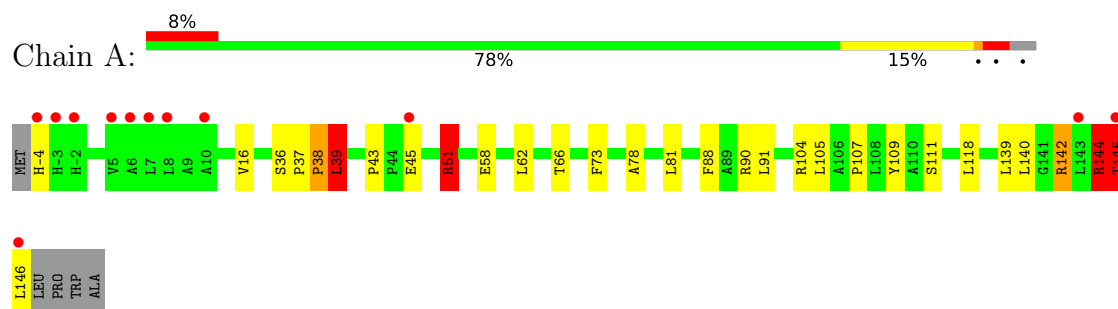
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	122	Total	O	0	0
			122	122		

3 Residue-property plots

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: LEUKOTRIENE C4 SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, α , β , γ	169.94Å 169.94Å 169.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.03 – 2.15 49.03 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.03-2.15) 99.6 (49.03-2.15)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.183 , 0.220 0.184 , 0.220	Depositor DCC
R_{free} test set	1129 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.059 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	1440	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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: LMU, GSH, NI, PLM, PAM, SO4

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	1.52	9/1236 (0.7%)	1.40	12/1686 (0.7%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	LEU	N-CA	14.28	1.64	1.46
1	A	145	THR	C-N	-7.82	1.22	1.33
1	A	51	ARG	CD-NE	-6.92	1.36	1.46
1	A	16	VAL	CA-CB	6.90	1.63	1.54
1	A	111	SER	CA-C	5.38	1.59	1.52
1	A	37	PRO	CA-C	5.30	1.57	1.52
1	A	88	PHE	N-CA	-5.26	1.39	1.46
1	A	43	PRO	CA-C	5.09	1.56	1.52
1	A	78	ALA	C-O	5.09	1.30	1.24

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	38	PRO	CA-C-N	-10.49	101.51	121.54
1	A	38	PRO	C-N-CA	-10.49	101.51	121.54
1	A	51	ARG	NE-CZ-NH2	-9.99	110.21	119.20
1	A	-4	HIS	CA-C-N	6.75	133.86	121.70
1	A	-4	HIS	C-N-CA	6.75	133.86	121.70
1	A	145	THR	O-C-N	-6.44	112.69	123.00
1	A	51	ARG	NE-CZ-NH1	6.33	127.83	121.50
1	A	73	PHE	CA-C-N	-5.33	116.09	122.44
1	A	73	PHE	C-N-CA	-5.33	116.09	122.44
1	A	140	LEU	CA-C-N	5.29	125.85	119.98
1	A	140	LEU	C-N-CA	5.29	125.85	119.98
1	A	107	PRO	N-CA-C	5.06	120.20	113.57

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	1195	0	1236	19	0
2	A	2	0	0	0	0
3	A	35	0	46	4	0
4	A	20	0	14	2	0
5	A	18	0	29	0	0
6	A	43	0	66	0	0
7	A	5	0	0	0	0
8	A	122	0	0	3	0
All	All	1440	0	1391	19	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 7.

All (19) 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:38:PRO:O	1:A:39:LEU:CB	1.84	1.09
1:A:38:PRO:O	1:A:39:LEU:HB2	1.41	1.08
1:A:66[A]:THR:HG22	1:A:118:LEU:HB3	1.59	0.83
1:A:144:ARG:N	8:A:2116:HOH:O	2.01	0.77
1:A:104:ARG:HH22	3:A:1149:LMU:H3B	1.50	0.76
1:A:51:ARG:HD3	4:A:1150:GSH:O32	1.84	0.76
1:A:38:PRO:O	1:A:39:LEU:HB3	1.85	0.76
1:A:109:TYR:HE1	3:A:1149:LMU:H22	1.51	0.75
1:A:145:THR:O	8:A:2117:HOH:O	2.12	0.68
1:A:45:GLU:HG3	8:A:2087:HOH:O	1.94	0.67
1:A:144:ARG:O	1:A:144:ARG:HD2	1.95	0.66
1:A:144:ARG:O	1:A:144:ARG:NH1	2.42	0.52
1:A:66[A]:THR:CG2	1:A:118:LEU:HB3	2.38	0.50
1:A:104:ARG:HH22	3:A:1149:LMU:C3B	2.26	0.45
1:A:58:GLU:OE2	4:A:1150:GSH:N1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ARG:NH1	1:A:146:LEU:N	2.68	0.42
1:A:105:LEU:HD11	3:A:1149:LMU:H2B	2.01	0.41
1:A:90:ARG:HD3	1:A:90:ARG:HA	1.86	0.41
1:A:142:ARG:HH21	1:A:142:ARG:HG2	1.86	0.41

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	151/156 (97%)	144 (95%)	4 (3%)	3 (2%)	6 2

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	ARG
1	A	145	THR
1	A	39	LEU

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	117/120 (98%)	109 (93%)	8 (7%)	14 10

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	SER
1	A	51	ARG
1	A	62	LEU
1	A	81	LEU
1	A	91	LEU
1	A	139	LEU
1	A	142	ARG
1	A	144	ARG

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	0	HIS
1	A	25	GLN

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](#)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 for Mogul analysis.

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
6	PLM	A	1154	-	7,7,17	0.26	0	6,6,17	0.82	0
5	PAM	A	1151	-	17,17,17	1.17	1 (5%)	17,17,17	1.13	1 (5%)
6	PLM	A	1153	-	9,9,17	0.55	0	8,8,17	0.43	0
6	PLM	A	1152	-	9,9,17	0.28	0	8,8,17	0.73	0
3	LMU	A	1149	-	36,36,36	1.14	3 (8%)	47,47,47	2.33	16 (34%)
6	PLM	A	1157	-	4,4,17	0.43	0	3,3,17	0.45	0
7	SO4	A	1155	-	4,4,4	0.56	0	6,6,6	0.70	0
6	PLM	A	1156	-	9,9,17	0.58	0	8,8,17	0.60	0
4	GSH	A	1150	-	18,19,19	2.43	4 (22%)	21,24,24	2.79	9 (42%)

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
6	PLM	A	1154	-	-	1/5/5/15	-
5	PAM	A	1151	-	-	5/15/15/15	-
6	PLM	A	1153	-	-	1/7/7/15	-
6	PLM	A	1152	-	-	6/7/7/15	-
3	LMU	A	1149	-	2/2/10/10	9/21/61/61	0/2/2/2
6	PLM	A	1157	-	-	0/2/2/15	-
6	PLM	A	1156	-	-	2/7/7/15	-
4	GSH	A	1150	-	1/1/6/8	5/24/24/24	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1150	GSH	O2-C2	6.50	1.35	1.23
4	A	1150	GSH	OE1-CD1	6.48	1.36	1.23
5	A	1151	PAM	C10-C9	4.11	1.55	1.31
3	A	1149	LMU	O5'-C1'	2.60	1.48	1.41
4	A	1150	GSH	CB2-CA2	2.47	1.55	1.53
4	A	1150	GSH	CA2-N2	2.30	1.50	1.45
3	A	1149	LMU	O1'-C1'	2.24	1.43	1.40
3	A	1149	LMU	C4B-C5B	2.07	1.57	1.53

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1149	LMU	C1B-O5B-C5B	-7.21	99.65	113.72
4	A	1150	GSH	CB1-CA1-C1	6.32	127.21	110.45
4	A	1150	GSH	CB1-CG1-CD1	-5.84	100.04	113.06
3	A	1149	LMU	C6B-C5B-C4B	4.92	125.09	113.02
3	A	1149	LMU	C1B-O1B-C4'	-4.84	106.51	117.98
4	A	1150	GSH	OE1-CD1-N2	-4.80	114.83	122.95
3	A	1149	LMU	C3'-C4'-C5'	4.11	120.04	110.93
3	A	1149	LMU	O5'-C5'-C6'	3.96	116.27	106.44
4	A	1150	GSH	CG1-CD1-N2	3.84	122.63	115.86
3	A	1149	LMU	O1'-C1'-C2'	3.52	113.62	108.27
3	A	1149	LMU	O5'-C1'-C2'	3.31	117.17	110.37
4	A	1150	GSH	O2-C2-N3	-2.98	116.68	122.98
3	A	1149	LMU	C1-O1'-C1'	-2.94	108.66	113.68
4	A	1150	GSH	O31-C3-CA3	2.78	123.39	112.81
3	A	1149	LMU	O5B-C1B-C2B	2.76	116.04	110.37
3	A	1149	LMU	O1B-C1B-C2B	2.72	114.79	108.09
3	A	1149	LMU	O5B-C5B-C6B	2.69	113.09	106.44
3	A	1149	LMU	C1B-C2B-C3B	2.57	115.41	110.01
4	A	1150	GSH	CA2-C2-N3	2.54	121.98	116.54
3	A	1149	LMU	O3B-C3B-C2B	-2.51	104.45	110.38
4	A	1150	GSH	CB2-CA2-C2	-2.38	104.32	109.50
4	A	1150	GSH	CB1-CA1-N1	2.37	116.29	110.12
3	A	1149	LMU	O2'-C2'-C1'	2.34	115.66	110.08
3	A	1149	LMU	O3B-C3B-C4B	2.15	115.45	110.38
5	A	1151	PAM	C8-C9-C10	-2.15	108.71	124.83
3	A	1149	LMU	C5-C4-C3	-2.07	103.91	114.37

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1149	LMU	C5B
3	A	1149	LMU	C2B
4	A	1150	GSH	CA1

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1150	GSH	C1-CA1-CB1-CG1
3	A	1149	LMU	O5B-C5B-C6B-O6B
4	A	1150	GSH	O11-C1-CA1-CB1
4	A	1150	GSH	CA1-CB1-CG1-CD1
6	A	1152	PLM	C5-C6-C7-C8
3	A	1149	LMU	O1'-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
6	A	1152	PLM	C3-C4-C5-C6
6	A	1152	PLM	C2-C3-C4-C5
4	A	1150	GSH	O12-C1-CA1-CB1
3	A	1149	LMU	C4B-C5B-C6B-O6B
3	A	1149	LMU	C11-C10-C9-C8
3	A	1149	LMU	C5-C6-C7-C8
3	A	1149	LMU	C6-C7-C8-C9
6	A	1153	PLM	C5-C6-C7-C8
6	A	1152	PLM	C7-C8-C9-CA
5	A	1151	PAM	C13-C14-C15-C16
6	A	1152	PLM	C1-C2-C3-C4
3	A	1149	LMU	C2'-C1'-O1'-C1
3	A	1149	LMU	C1-C2-C3-C4
5	A	1151	PAM	C3-C4-C5-C6
5	A	1151	PAM	C10-C11-C12-C13
6	A	1154	PLM	C2-C3-C4-C5
6	A	1156	PLM	C6-C7-C8-C9
6	A	1156	PLM	C3-C4-C5-C6
5	A	1151	PAM	C7-C8-C9-C10
4	A	1150	GSH	C3-CA3-N3-C2
6	A	1152	PLM	C6-C7-C8-C9
5	A	1151	PAM	C6-C7-C8-C9
3	A	1149	LMU	C3'-C4'-O1B-C1B

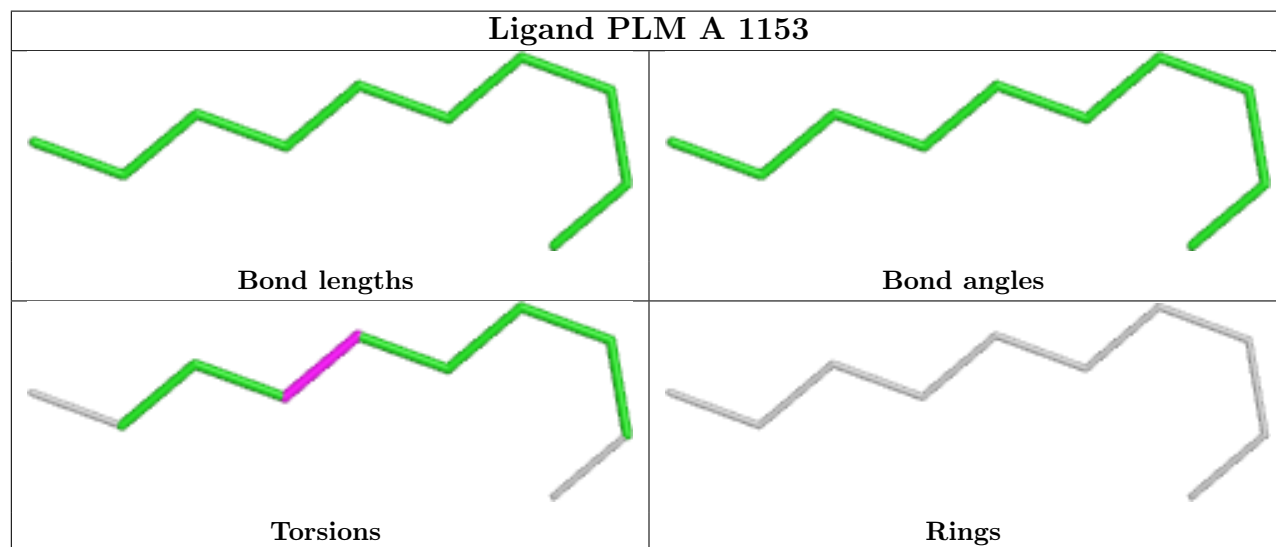
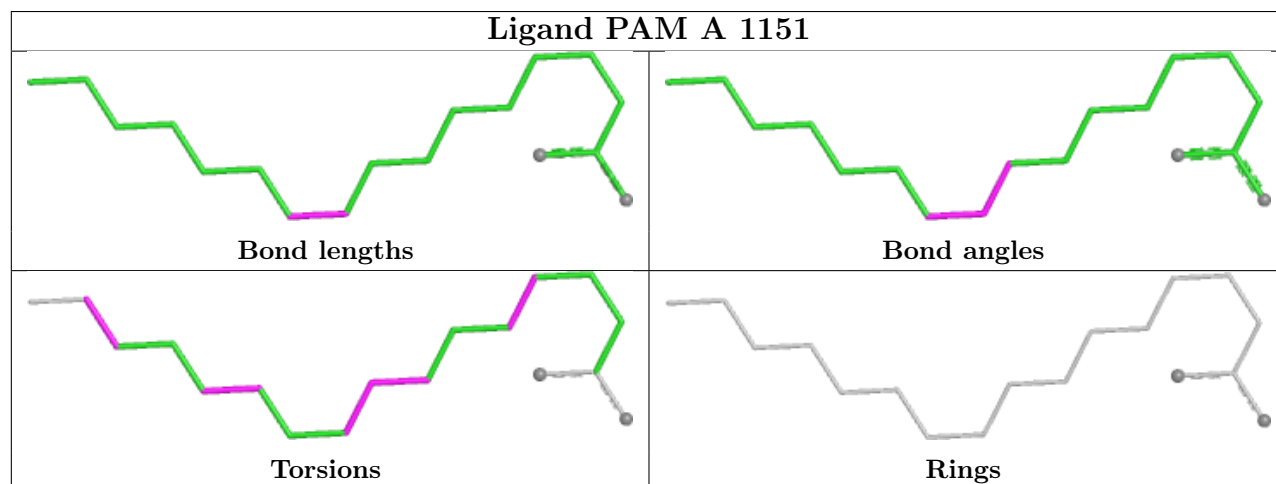
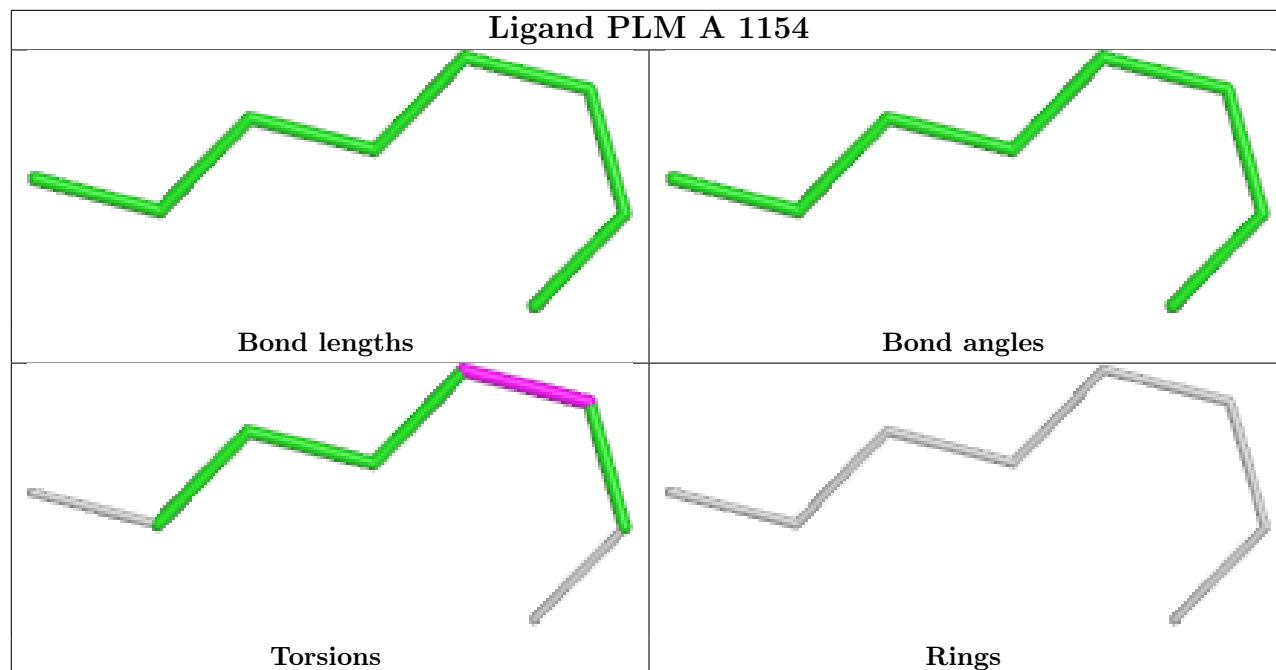
There are no ring outliers.

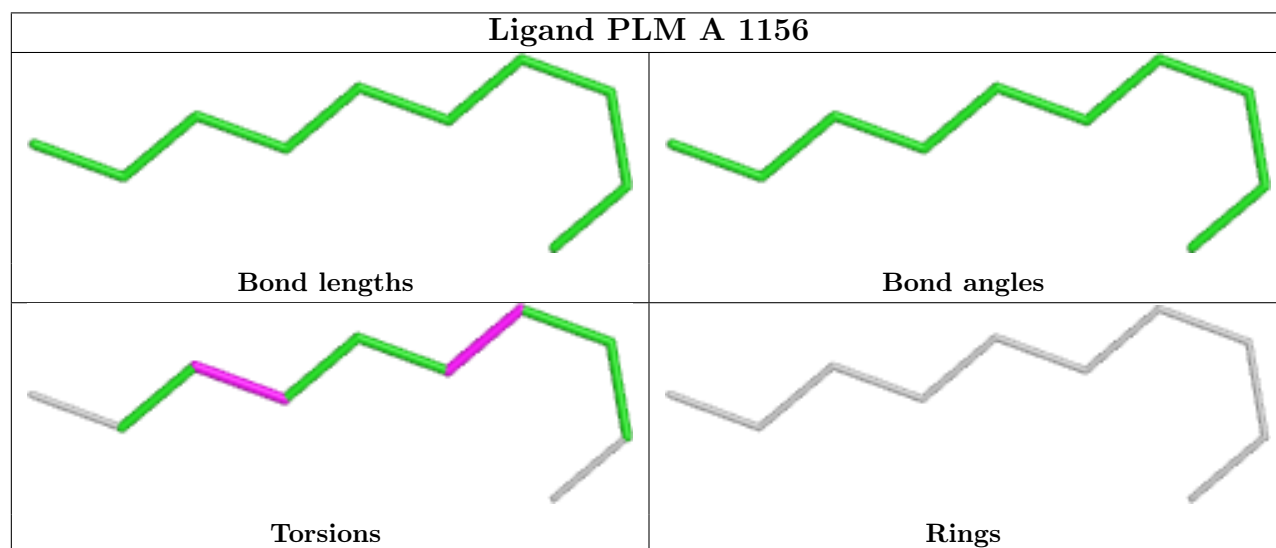
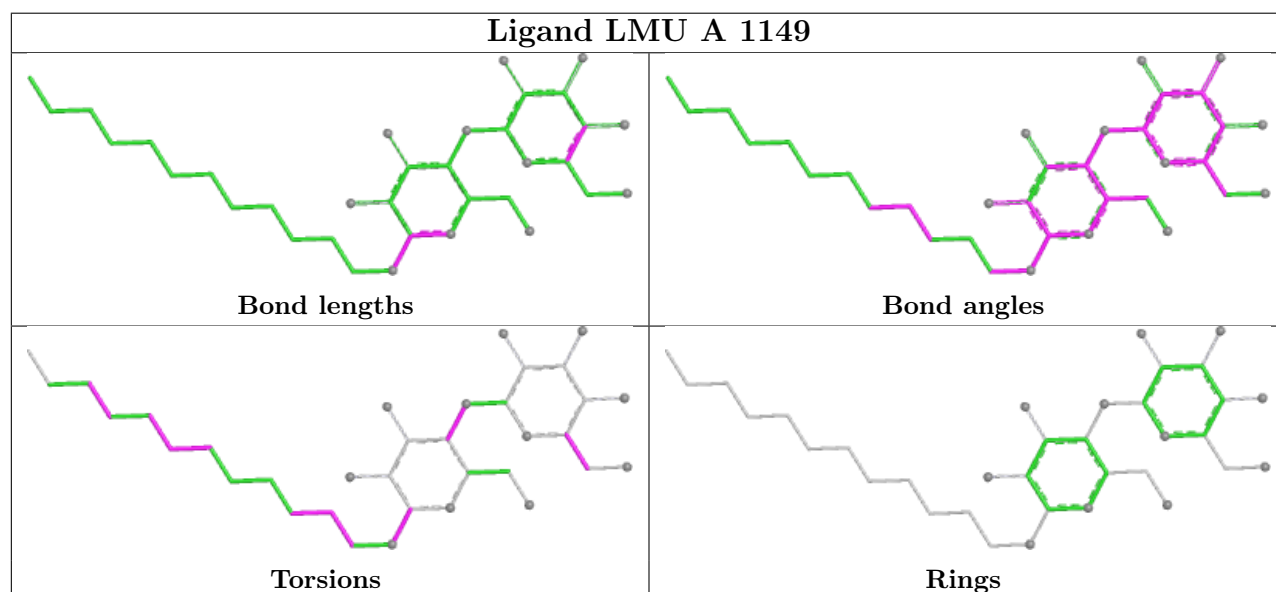
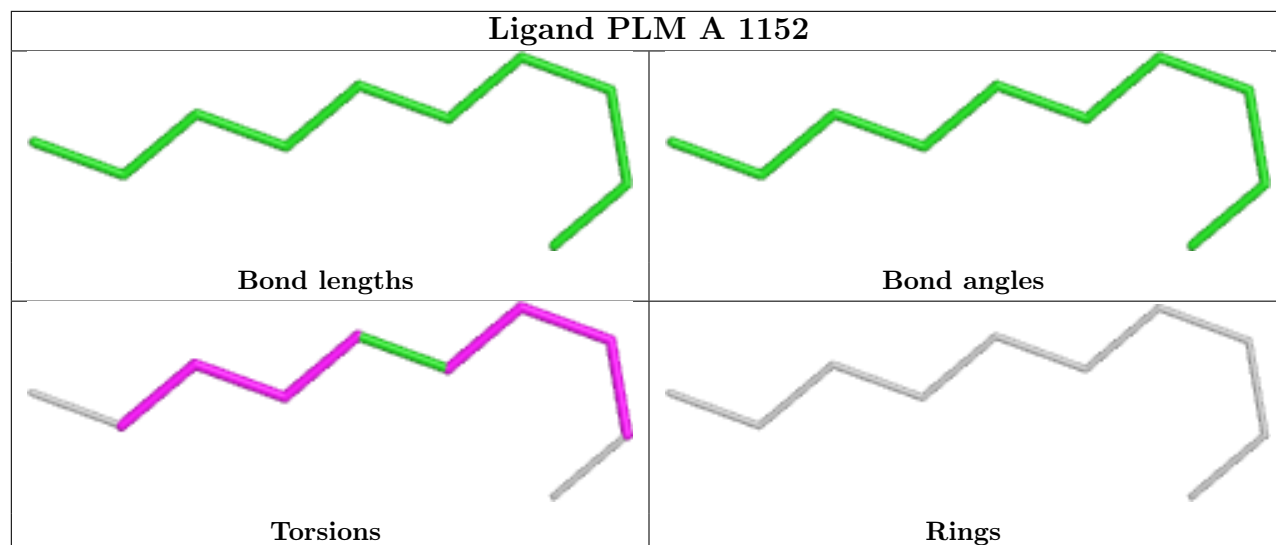
2 monomers are involved in 6 short contacts:

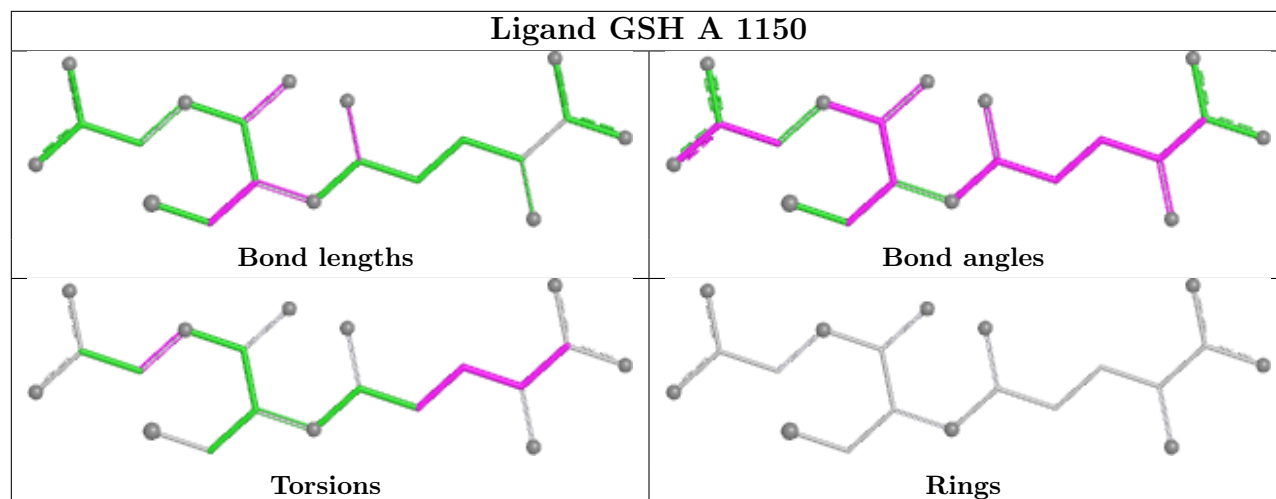
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1149	LMU	4	0
4	A	1150	GSH	2	0

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

equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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	151/156 (96%)	0.14	12 (7%)	18 20	8, 15, 35, 44	2 (1%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	LEU	3.9
1	A	5	VAL	3.5
1	A	145	THR	3.2
1	A	-3	HIS	3.2
1	A	8	LEU	3.0
1	A	143[A]	LEU	2.8
1	A	10	ALA	2.8
1	A	-4	HIS	2.7
1	A	6	ALA	2.6
1	A	-2	HIS	2.5
1	A	7	LEU	2.3
1	A	45	GLU	2.2

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,

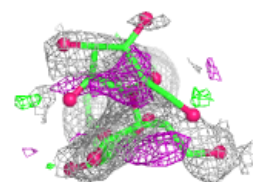
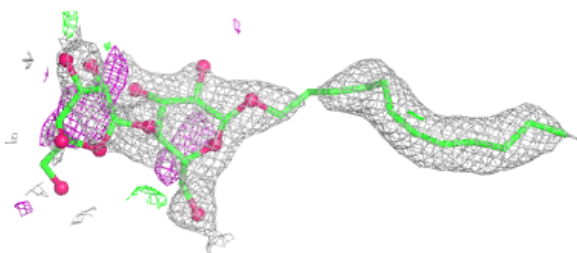
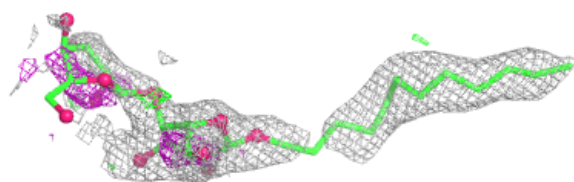
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	LMU	A	1149	35/35	0.81	0.24	38,65,94,99	0
6	PLM	A	1157	5/18	0.81	0.34	48,48,54,55	0
5	PAM	A	1151	18/18	0.89	0.17	33,47,66,66	0
6	PLM	A	1156	10/18	0.91	0.15	35,37,44,48	0
6	PLM	A	1154	8/18	0.91	0.16	38,42,49,49	0
6	PLM	A	1153	10/18	0.92	0.14	36,39,45,45	0
6	PLM	A	1152	10/18	0.93	0.12	35,39,44,47	0
7	SO4	A	1155	5/5	0.95	0.12	30,32,37,38	5
4	GSH	A	1150	20/20	0.97	0.06	14,19,23,23	0
2	NI	A	1148	1/1	1.00	0.03	34,34,34,34	1
2	NI	A	1147	1/1	1.00	0.09	43,43,43,43	1

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.

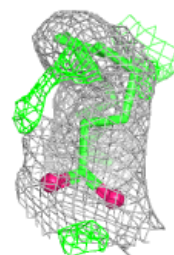
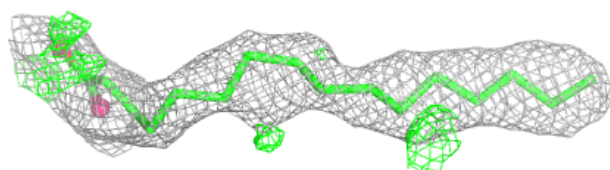
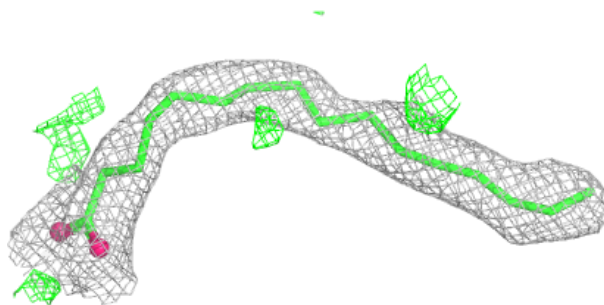
Electron density around LMU A 1149:

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

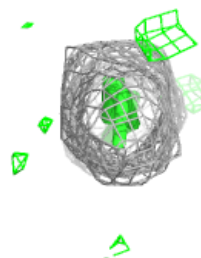
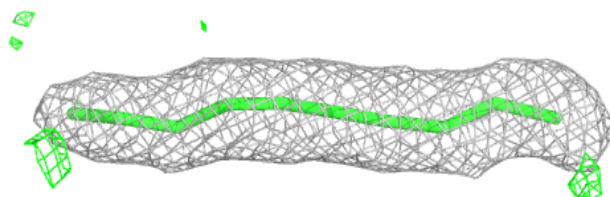
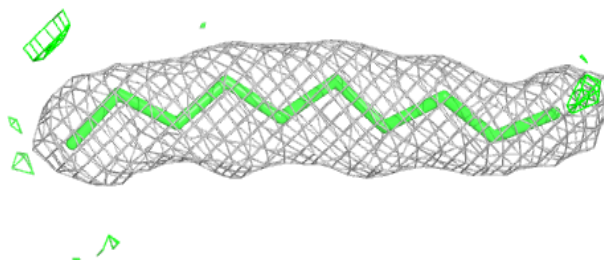


Electron density around PAM A 1151:

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

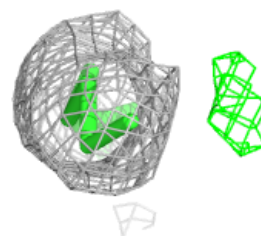
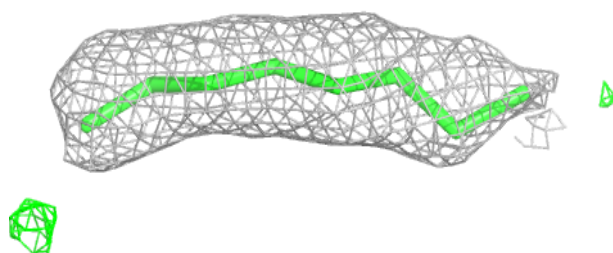
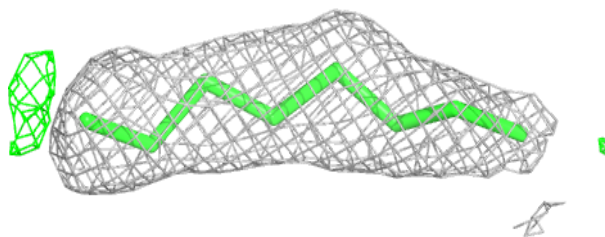
**Electron density around PLM A 1156:**

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

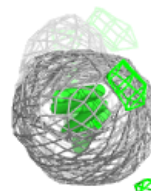
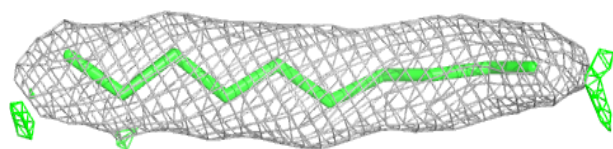
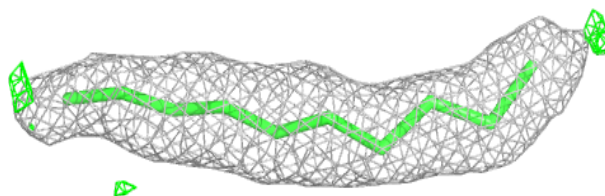


Electron density around PLM A 1154:

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

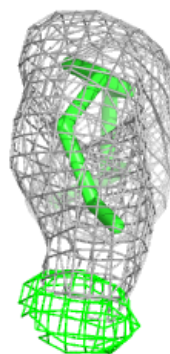
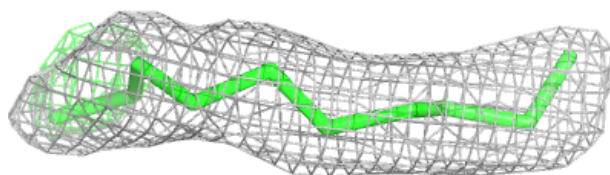
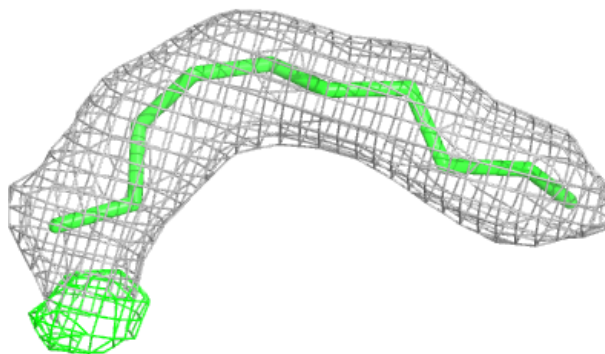
**Electron density around PLM A 1153:**

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



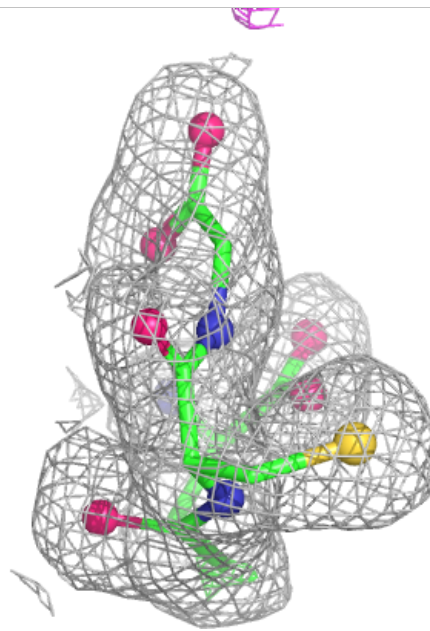
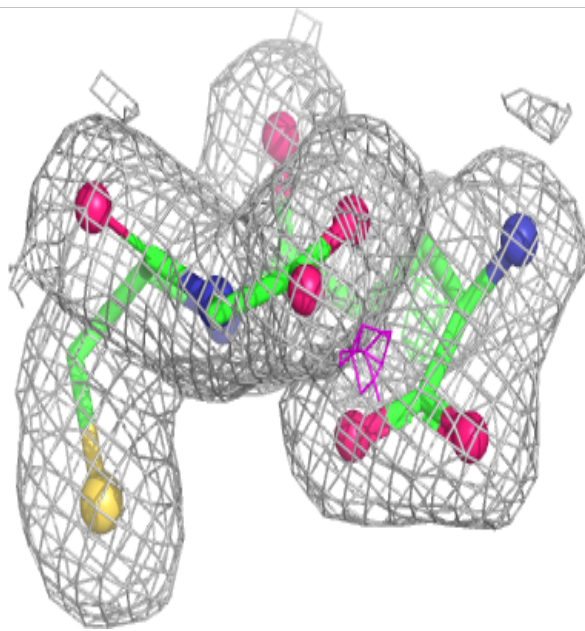
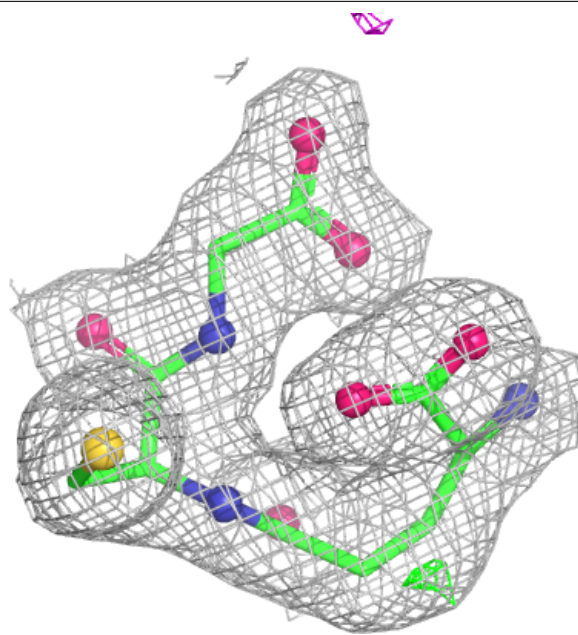
Electron density around PLM A 1152:

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



Electron density around GSH A 1150:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.