



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 02:52 AM BST

PDB ID : 3ZK1
Title : Crystal structure of the sodium binding rotor ring at pH 5.3
Authors : Schulz, S.; Meier, T.; Yildiz, O.
Deposited on : 2013-01-21
Resolution : 2.20 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 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 : 2.13.1
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) : 2.13.1

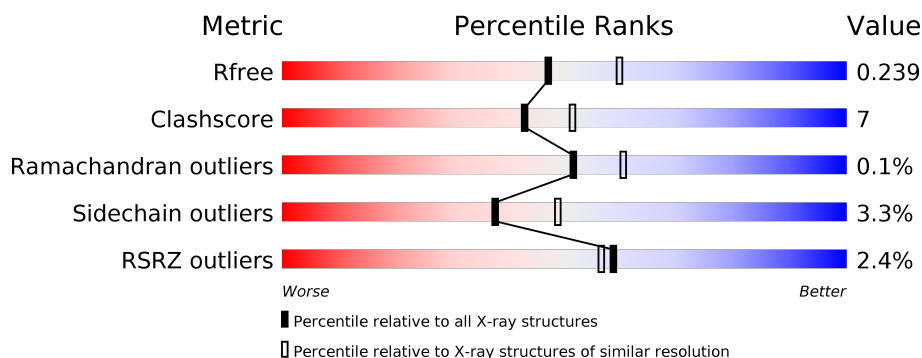
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	89	<div> <div>89%</div> <div>11%</div> </div>
1	B	89	<div>2%</div> <div>87%</div> <div>12%</div> <div>.</div>
1	C	89	<div>2%</div> <div>90%</div> <div>10%</div>
1	D	89	<div>4%</div> <div>94%</div> <div>6%</div>
1	E	89	<div>%</div> <div>93%</div> <div>6%</div> <div>.</div>
1	F	89	<div>3%</div> <div>94%</div> <div>.</div> <div>.</div>

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Mol	Chain	Length	Quality of chain
1	G	89	
1	H	89	
1	I	89	
1	J	89	
1	K	89	
1	L	89	
1	M	89	
1	N	89	
1	O	89	
1	P	89	
1	Q	89	
1	R	89	
1	S	89	
1	T	89	
1	U	89	
1	V	89	

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	DMU	B	92	-	-	-	X
3	DMU	C	92	-	-	-	X
3	DMU	D	92	-	-	-	X
3	DMU	E	92	-	-	-	X
3	DMU	F	92	-	-	-	X
3	DMU	I	92	-	-	-	X
3	DMU	J	92	-	-	-	X
3	DMU	K	92	-	-	-	X
3	DMU	M	92	-	-	-	X
3	DMU	N	92	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DMU	O	92	-	-	-	X
3	DMU	P	92	-	-	-	X
3	DMU	S	92	-	-	-	X
3	DMU	T	92	-	-	-	X
3	DMU	U	92	-	-	-	X
4	LMT	B	1090	-	-	-	X
4	LMT	C	1091	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14836 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 ATP SYNTHASE SUBUNIT C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	B	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	C	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	D	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	E	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	F	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	G	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	H	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	I	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	J	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	K	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	L	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	M	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	N	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	O	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			
1	P	89	Total	C	N	O	S	0	0	0
			620	398	101	117	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	89	Total 620	C 398	N 101	O 117	S 4	0	0	0
1	R	89	Total 620	C 398	N 101	O 117	S 4	0	0	0
1	S	89	Total 620	C 398	N 101	O 117	S 4	0	0	0
1	T	89	Total 620	C 398	N 101	O 117	S 4	0	0	0
1	U	89	Total 620	C 398	N 101	O 117	S 4	0	0	0
1	V	89	Total 620	C 398	N 101	O 117	S 4	0	0	0

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

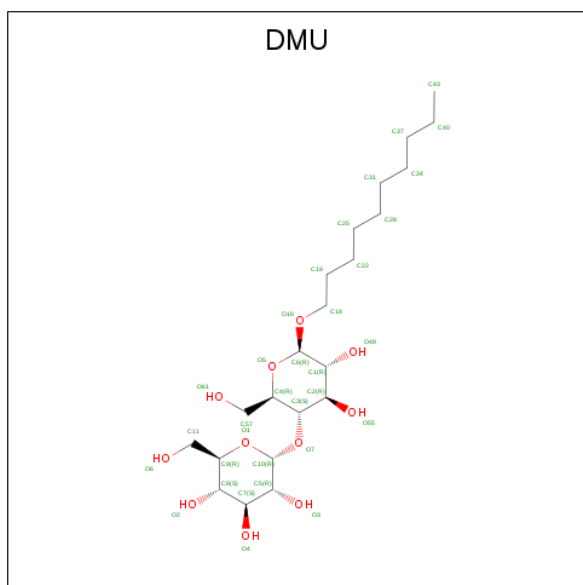
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	1	Total 1	Na 1	0	0
2	K	1	Total 1	Na 1	0	0
2	B	1	Total 1	Na 1	0	0
2	N	1	Total 1	Na 1	0	0
2	S	1	Total 1	Na 1	0	0
2	J	1	Total 1	Na 1	0	0
2	E	1	Total 1	Na 1	0	0
2	V	1	Total 1	Na 1	0	0
2	A	1	Total 1	Na 1	0	0
2	R	1	Total 1	Na 1	0	0
2	M	1	Total 1	Na 1	0	0
2	D	1	Total 1	Na 1	0	0
2	I	1	Total 1	Na 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	U	1	Total	Na	0	0
			1	1		
2	L	1	Total	Na	0	0
			1	1		
2	G	1	Total	Na	0	0
			1	1		
2	Q	1	Total	Na	0	0
			1	1		
2	H	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		
2	T	1	Total	Na	0	0
			1	1		
2	O	1	Total	Na	0	0
			1	1		
2	F	1	Total	Na	0	0
			1	1		

- Molecule 3 is DECYL-BETA-D-MALTOPYRANOSIDE (three-letter code: DMU) (formula: $C_{22}H_{42}O_{11}$).



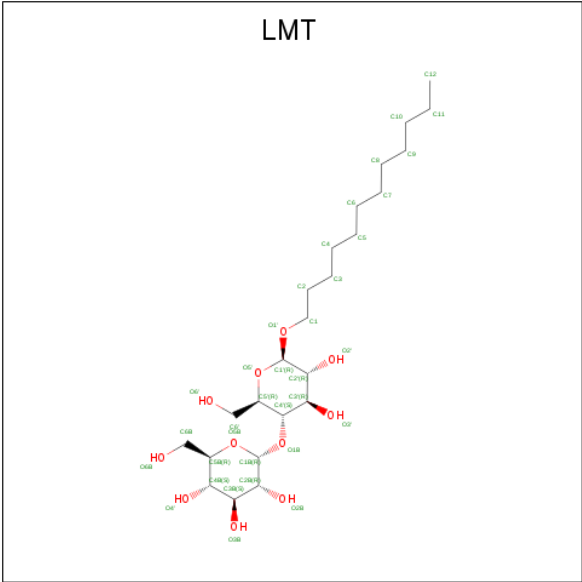
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			33	22	11		
3	B	1	Total	C	O	0	0
			33	22	11		

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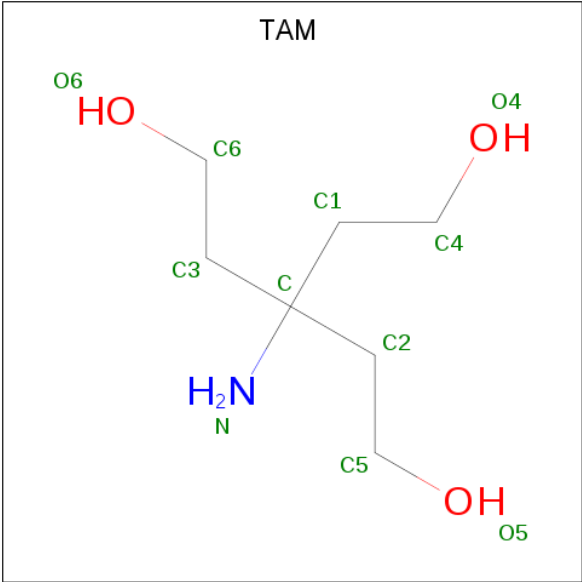
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total 33	C 22	O 11	0	0
3	D	1	Total 33	C 22	O 11	0	0
3	E	1	Total 33	C 22	O 11	0	0
3	F	1	Total 33	C 22	O 11	0	0
3	G	1	Total 33	C 22	O 11	0	0
3	H	1	Total 33	C 22	O 11	0	0
3	I	1	Total 33	C 22	O 11	0	0
3	J	1	Total 33	C 22	O 11	0	0
3	K	1	Total 33	C 22	O 11	0	0
3	L	1	Total 33	C 22	O 11	0	0
3	M	1	Total 33	C 22	O 11	0	0
3	N	1	Total 33	C 22	O 11	0	0
3	O	1	Total 33	C 22	O 11	0	0
3	P	1	Total 33	C 22	O 11	0	0
3	Q	1	Total 33	C 22	O 11	0	0
3	R	1	Total 33	C 22	O 11	0	0
3	S	1	Total 33	C 22	O 11	0	0
3	T	1	Total 33	C 22	O 11	0	0
3	U	1	Total 33	C 22	O 11	0	0
3	V	1	Total 33	C 22	O 11	0	0

- Molecule 4 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: C₂₄H₄₆O₁₁).



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

- Molecule 5 is TRIS(HYDROXYETHYL)AMINOMETHANE (three-letter code: TAM) (formula: C₇H₁₇NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	M	1	Total	C	N	O	0	0
			11	7	1	3		
5	R	1	Total	C	N	O	0	0
			11	7	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	28	Total	O	0	0
			28	28		
6	B	17	Total	O	0	0
			17	17		
6	C	13	Total	O	0	0
			13	13		
6	D	20	Total	O	0	0
			20	20		
6	E	14	Total	O	0	0
			14	14		
6	F	21	Total	O	0	0
			21	21		
6	G	17	Total	O	0	0
			17	17		
6	H	16	Total	O	0	0
			16	16		
6	I	14	Total	O	0	0
			14	14		
6	J	16	Total	O	0	0
			16	16		
6	K	18	Total	O	0	0
			18	18		
6	L	13	Total	O	0	0
			13	13		
6	M	13	Total	O	0	0
			13	13		
6	N	12	Total	O	0	0
			12	12		
6	O	20	Total	O	0	0
			20	20		
6	P	17	Total	O	0	0
			17	17		
6	Q	10	Total	O	0	0
			10	10		
6	R	16	Total	O	0	0
			16	16		

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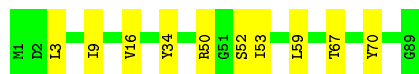
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	S	6	Total 6	O 6	0	0
6	T	9	Total 9	O 9	0	0
6	U	8	Total 8	O 8	0	0
6	V	3	Total 3	O 3	0	0

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.

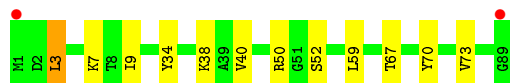
- Molecule 1: ATP SYNTHASE SUBUNIT C

Chain A: 

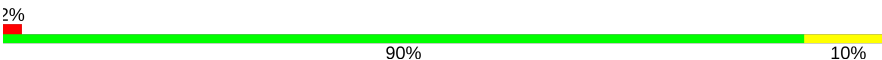


- Molecule 1: ATP SYNTHASE SUBUNIT C

Chain B: 



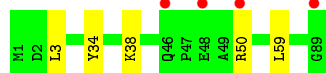
- Molecule 1: ATP SYNTHASE SUBUNIT C

Chain C: 



- Molecule 1: ATP SYNTHASE SUBUNIT C

Chain D: 



- Molecule 1: ATP SYNTHASE SUBUNIT C

Chain E: 



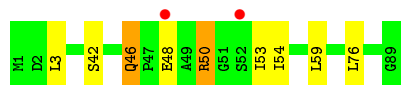
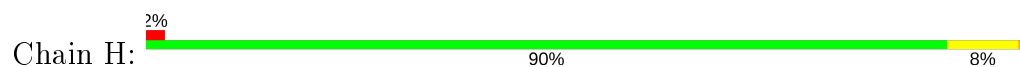
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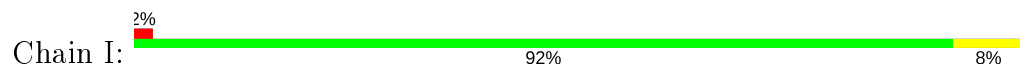
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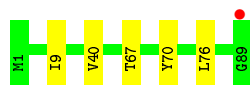
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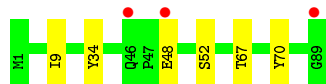
- Molecule 1: ATP SYNTHASE SUBUNIT C



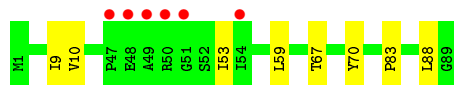
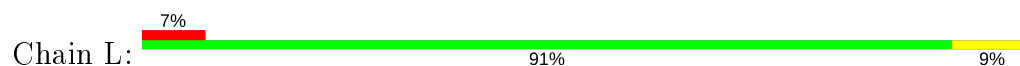
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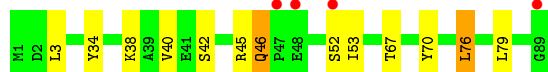
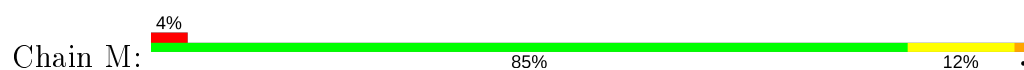
- Molecule 1: ATP SYNTHASE SUBUNIT C



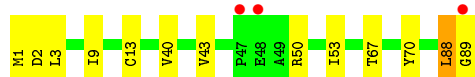
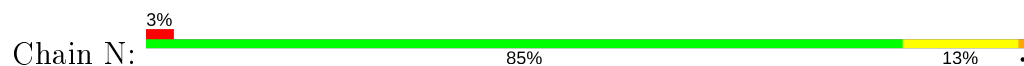
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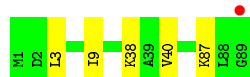
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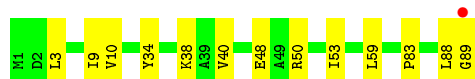
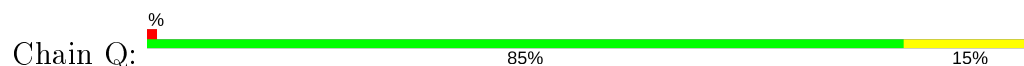
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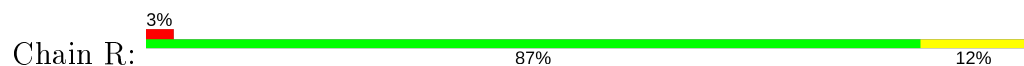
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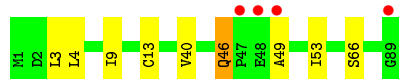
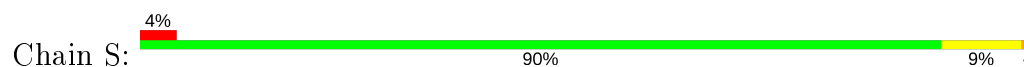
- Molecule 1: ATP SYNTHASE SUBUNIT C



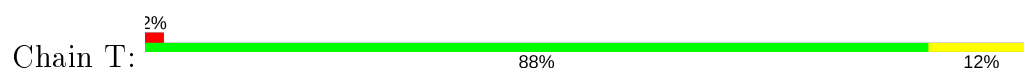
- Molecule 1: ATP SYNTHASE SUBUNIT C



- Molecule 1: ATP SYNTHASE SUBUNIT C



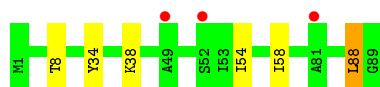
- Molecule 1: ATP SYNTHASE SUBUNIT C



- Molecule 1: ATP SYNTHASE SUBUNIT C



- Molecule 1: ATP SYNTHASE SUBUNIT C



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.77Å 83.90Å 150.99Å 90.00° 112.85° 90.00°	Depositor
Resolution (Å)	29.75 – 2.20 29.75 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.75-2.20) 99.7 (29.75-2.20)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.20Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.208 , 0.234 0.212 , 0.239	Depositor DCC
R_{free} test set	7919 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 61.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14836	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.23% 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: NA, LMT, DMU, TAM

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	0.23	0/626	0.44	0/846
1	B	0.22	0/626	0.43	0/846
1	C	0.22	0/626	0.41	0/846
1	D	0.23	0/626	0.42	0/846
1	E	0.22	0/626	0.41	0/846
1	F	0.23	0/626	0.43	0/846
1	G	0.22	0/626	0.40	0/846
1	H	0.22	0/626	0.42	0/846
1	I	0.23	0/626	0.41	0/846
1	J	0.22	0/626	0.41	0/846
1	K	0.22	0/626	0.41	0/846
1	L	0.22	0/626	0.41	0/846
1	M	0.22	0/626	0.42	0/846
1	N	0.23	0/626	0.42	0/846
1	O	0.22	0/626	0.39	0/846
1	P	0.22	0/626	0.40	0/846
1	Q	0.22	0/626	0.40	0/846
1	R	0.22	0/626	0.43	0/846
1	S	0.23	0/626	0.40	0/846
1	T	0.22	0/626	0.40	0/846
1	U	0.22	0/626	0.40	0/846
1	V	0.22	0/626	0.42	0/846
All	All	0.22	0/13772	0.41	0/18612

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 ⓘ

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	620	0	662	7	0
1	B	620	0	662	9	0
1	C	620	0	662	4	0
1	D	620	0	662	1	0
1	E	620	0	662	7	0
1	F	620	0	662	3	0
1	G	620	0	662	3	0
1	H	620	0	662	3	0
1	I	620	0	662	4	0
1	J	620	0	662	3	0
1	K	620	0	662	4	0
1	L	620	0	662	5	0
1	M	620	0	662	8	0
1	N	620	0	662	9	0
1	O	620	0	662	4	0
1	P	620	0	662	5	0
1	Q	620	0	662	9	0
1	R	620	0	662	13	0
1	S	620	0	662	7	0
1	T	620	0	662	8	0
1	U	620	0	662	6	0
1	V	620	0	662	5	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
2	U	1	0	0	0	0
2	V	1	0	0	0	0
3	A	33	0	42	6	0
3	B	33	0	42	5	0
3	C	33	0	42	3	0
3	D	33	0	42	8	0
3	E	33	0	42	13	0
3	F	33	0	42	5	0
3	G	33	0	42	7	0
3	H	33	0	42	3	0
3	I	33	0	42	6	0
3	J	33	0	40	4	0
3	K	33	0	42	4	0
3	L	33	0	42	10	0
3	M	33	0	42	12	0
3	N	33	0	42	4	0
3	O	33	0	42	13	0
3	P	33	0	40	12	0
3	Q	33	0	42	10	0
3	R	33	0	42	7	0
3	S	33	0	42	7	0
3	T	33	0	41	2	0
3	U	33	0	42	5	0
3	V	33	0	41	1	0
4	B	35	0	46	0	0
4	C	70	0	92	5	0
5	M	11	0	17	2	0
5	R	11	0	17	5	0
6	A	28	0	0	2	0
6	B	17	0	0	0	0
6	C	13	0	0	0	0
6	D	20	0	0	0	0
6	E	14	0	0	0	0
6	F	21	0	0	2	0
6	G	17	0	0	0	0
6	H	16	0	0	0	0
6	I	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	J	16	0	0	0	0
6	K	18	0	0	0	0
6	L	13	0	0	0	0
6	M	13	0	0	0	0
6	N	12	0	0	1	0
6	O	20	0	0	0	0
6	P	17	0	0	1	0
6	Q	10	0	0	0	0
6	R	16	0	0	0	0
6	S	6	0	0	0	0
6	T	9	0	0	0	0
6	U	8	0	0	0	0
6	V	3	0	0	0	0
All	All	14836	0	15654	204	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 (204) 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)
3:E:92:DMU:C7	3:E:92:DMU:C5	1.74	1.62
3:M:92:DMU:C5	3:M:92:DMU:C7	1.79	1.60
3:P:92:DMU:O5	3:P:92:DMU:C6	1.66	1.44
3:O:92:DMU:C9	3:O:92:DMU:C10	1.94	1.41
3:D:92:DMU:C10	3:D:92:DMU:C9	1.98	1.39
3:L:92:DMU:C9	3:L:92:DMU:C10	1.95	1.38
3:Q:92:DMU:C10	3:Q:92:DMU:C9	2.01	1.36
3:L:92:DMU:O1	3:L:92:DMU:C10	1.75	1.33
3:Q:92:DMU:C10	3:Q:92:DMU:O1	1.79	1.30
3:O:92:DMU:O1	3:O:92:DMU:C10	1.77	1.30
3:D:92:DMU:C10	3:D:92:DMU:O1	1.80	1.29
3:E:92:DMU:C8	3:E:92:DMU:C5	2.17	1.20
3:M:92:DMU:C8	3:M:92:DMU:C5	2.18	1.20
3:P:92:DMU:C4	3:P:92:DMU:C6	2.33	1.06
3:O:92:DMU:H35	3:O:92:DMU:C10	2.00	0.92
3:P:92:DMU:O5	3:P:92:DMU:H5	1.71	0.91
3:L:92:DMU:C10	3:L:92:DMU:H35	1.99	0.90
3:G:92:DMU:H30	3:H:92:DMU:H30	1.56	0.88
3:D:92:DMU:C10	3:D:92:DMU:H35	2.05	0.86
3:L:92:DMU:O7	3:L:92:DMU:H35	1.76	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:92:DMU:O3	3:E:92:DMU:O2	1.96	0.84
3:E:92:DMU:C7	3:E:92:DMU:H32	2.03	0.83
3:Q:92:DMU:C10	3:Q:92:DMU:H35	2.06	0.81
3:O:92:DMU:H35	3:O:92:DMU:O7	1.83	0.79
1:K:9:ILE:HG12	3:K:92:DMU:H13	1.65	0.78
3:M:92:DMU:H32	3:M:92:DMU:C7	2.11	0.76
3:A:92:DMU:O3	6:A:2002:HOH:O	2.05	0.74
3:P:92:DMU:H30	3:Q:92:DMU:H3	1.69	0.74
3:D:92:DMU:H35	3:D:92:DMU:O7	1.86	0.73
3:P:92:DMU:H4	3:P:92:DMU:C6	2.18	0.73
3:M:92:DMU:H38	3:M:92:DMU:H37	0.74	0.72
3:P:92:DMU:C4	3:P:92:DMU:H5	2.21	0.70
3:L:92:DMU:C9	3:L:92:DMU:O7	2.37	0.69
3:M:92:DMU:O3	3:M:92:DMU:O2	1.95	0.69
3:U:92:DMU:H29	3:V:92:DMU:H8	1.74	0.68
3:M:92:DMU:C5	3:M:92:DMU:H37	2.08	0.67
3:L:92:DMU:H6	3:L:92:DMU:O49	1.94	0.67
3:F:92:DMU:H3	3:G:92:DMU:H2	1.78	0.65
1:S:9:ILE:HG12	3:S:92:DMU:H19	1.80	0.63
1:R:9:ILE:HD11	3:R:92:DMU:H12	1.81	0.62
3:Q:92:DMU:O7	3:Q:92:DMU:H35	2.00	0.61
1:A:52:SER:OG	1:B:50:ARG:NH1	2.33	0.61
3:D:92:DMU:O55	3:D:92:DMU:H32	2.01	0.60
3:P:92:DMU:H4	3:P:92:DMU:H5	1.81	0.60
3:B:92:DMU:H34	3:C:92:DMU:H40	1.83	0.60
3:M:92:DMU:H42	3:M:92:DMU:H39	1.42	0.60
3:L:92:DMU:O2	3:L:92:DMU:O3	2.03	0.60
1:R:50:ARG:HH12	5:R:1090:TAM:H11	1.66	0.60
3:A:92:DMU:H35	3:K:92:DMU:H41	1.84	0.59
3:E:92:DMU:O4	3:E:92:DMU:H40	2.00	0.59
1:P:45:ARG:NH1	6:P:2007:HOH:O	2.34	0.59
3:I:92:DMU:O49	3:I:92:DMU:H7	2.01	0.59
3:O:92:DMU:O2	3:O:92:DMU:O3	2.10	0.59
1:A:50:ARG:NH1	1:K:52:SER:OG	2.36	0.58
3:N:92:DMU:H29	3:O:92:DMU:O5	2.04	0.58
1:S:13:CYS:SG	3:T:92:DMU:H20	2.43	0.58
1:P:9:ILE:HG12	3:P:92:DMU:H15	1.86	0.57
1:R:53:ILE:HG23	1:S:40:VAL:HG13	1.87	0.57
1:I:53:ILE:HG23	1:J:40:VAL:HG13	1.87	0.57
1:P:52:SER:HB2	1:Q:50:ARG:HD2	1.85	0.57
3:H:92:DMU:O3	3:I:92:DMU:H1	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:92:DMU:O3	3:E:92:DMU:C8	2.50	0.56
3:F:92:DMU:H30	3:G:92:DMU:O3	2.06	0.56
1:E:5:THR:HG21	3:E:92:DMU:H29	1.87	0.56
1:R:43:VAL:HG13	1:R:50:ARG:HG2	1.86	0.56
3:P:92:DMU:O61	3:Q:92:DMU:O6	2.01	0.56
3:D:92:DMU:C9	3:D:92:DMU:O7	2.45	0.56
3:P:92:DMU:O55	3:P:92:DMU:O5	2.15	0.55
1:R:1:MET:N	3:S:92:DMU:O55	2.19	0.55
3:U:92:DMU:O55	3:U:92:DMU:H36	2.06	0.55
3:F:92:DMU:H3	3:G:92:DMU:C2	2.37	0.55
3:O:92:DMU:H40	3:P:92:DMU:H40	1.88	0.55
3:I:92:DMU:H2	3:J:92:DMU:H1	1.88	0.55
1:U:5:THR:HG21	3:U:92:DMU:O61	2.07	0.55
1:Q:3:LEU:HD22	1:Q:89:GLY:HA2	1.87	0.55
3:R:92:DMU:H29	3:S:92:DMU:H5	1.89	0.54
1:Q:9:ILE:HD13	3:R:92:DMU:H15	1.89	0.54
3:N:92:DMU:O61	3:N:92:DMU:H35	2.08	0.54
6:N:2004:HOH:O	1:O:38:LYS:NZ	2.34	0.53
1:B:52:SER:OG	1:C:50:ARG:NH2	2.38	0.53
3:O:92:DMU:C9	3:O:92:DMU:O7	2.42	0.53
3:H:92:DMU:H26	3:H:92:DMU:H17	1.91	0.53
1:R:2:ASP:OD1	1:R:2:ASP:N	2.36	0.53
1:B:3:LEU:HD22	1:B:7:LYS:HE3	1.91	0.53
1:H:53:ILE:HG23	1:I:40:VAL:HG13	1.90	0.52
1:S:46:GLN:HB2	1:S:49:ALA:HB3	1.90	0.52
1:U:10:VAL:HG23	1:V:8:THR:HG23	1.92	0.52
1:N:13:CYS:SG	3:O:92:DMU:H23	2.50	0.52
1:G:1:MET:HA	3:G:92:DMU:O6	2.10	0.51
1:M:53:ILE:HG23	1:N:40:VAL:HG13	1.92	0.51
3:I:92:DMU:H6	3:J:92:DMU:H15	1.93	0.51
1:B:9:ILE:HG12	3:B:92:DMU:H11	1.93	0.51
1:J:9:ILE:HG12	3:J:92:DMU:H19	1.92	0.50
3:G:92:DMU:H7	3:G:92:DMU:O49	2.12	0.50
1:Q:53:ILE:HG23	1:R:40:VAL:HG13	1.92	0.50
3:R:92:DMU:H29	3:S:92:DMU:H2	1.94	0.50
6:A:2012:HOH:O	1:B:50:ARG:NH2	2.45	0.49
1:C:81:ALA:HB2	4:C:1091:LMT:H5'	1.93	0.49
1:L:53:ILE:HG23	1:M:40:VAL:HG13	1.93	0.49
5:M:1090:TAM:N	5:M:1090:TAM:O5	2.46	0.49
1:T:66:SER:OG	1:U:65:GLU:OE2	2.30	0.49
1:T:9:ILE:HD13	3:U:92:DMU:H8	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:5:THR:OG1	3:E:92:DMU:H29	2.13	0.48
1:B:67:THR:HA	1:B:70:TYR:CD2	2.48	0.48
3:E:92:DMU:C5	3:E:92:DMU:O2	2.52	0.48
1:H:50:ARG:HH11	1:H:54:ILE:HD11	1.78	0.48
1:M:52:SER:OG	1:N:50:ARG:NH2	2.47	0.48
1:A:16:VAL:HG21	3:A:92:DMU:H24	1.95	0.48
3:L:92:DMU:H4	3:M:92:DMU:H2	1.95	0.47
3:B:92:DMU:O55	3:B:92:DMU:H36	2.14	0.47
1:J:67:THR:HA	1:J:70:TYR:CD2	2.49	0.47
1:Q:59:LEU:HD22	5:R:1090:TAM:H51	1.95	0.47
3:A:92:DMU:O7	3:A:92:DMU:O61	2.27	0.47
3:Q:92:DMU:O55	3:R:92:DMU:O49	2.33	0.47
4:C:1090:LMT:O6'	4:C:1091:LMT:O2B	2.16	0.47
1:M:42:SER:O	1:M:46:GLN:N	2.48	0.46
1:N:2:ASP:H	3:N:92:DMU:C11	2.28	0.46
1:E:5:THR:CG2	3:E:92:DMU:H29	2.46	0.46
3:M:92:DMU:O3	3:M:92:DMU:C7	2.55	0.46
1:Q:83:PRO:HG3	1:R:79:LEU:HB3	1.97	0.46
1:L:10:VAL:HG21	1:L:88:LEU:HD11	1.98	0.46
1:P:53:ILE:HG23	1:Q:40:VAL:HG13	1.97	0.46
1:N:53:ILE:HG23	1:O:40:VAL:HG13	1.97	0.45
1:Q:10:VAL:HG21	1:Q:88:LEU:HD11	1.97	0.45
1:V:54:ILE:HG23	1:V:58:ILE:HD13	1.99	0.45
1:E:67:THR:HA	1:E:70:TYR:CD2	2.52	0.45
1:C:34:TYR:O	1:C:38:LYS:HG2	2.17	0.45
3:M:92:DMU:O55	3:M:92:DMU:H36	2.16	0.45
1:T:13:CYS:SG	3:T:92:DMU:H25	2.56	0.45
3:M:92:DMU:H35	3:M:92:DMU:H30	1.97	0.44
3:U:92:DMU:O55	3:U:92:DMU:C10	2.65	0.44
1:A:9:ILE:HD13	3:B:92:DMU:H10	1.99	0.44
1:T:34:TYR:CD2	1:U:34:TYR:HA	2.53	0.44
4:C:1091:LMT:H52	4:C:1091:LMT:H82	1.81	0.44
5:R:1090:TAM:H62	5:R:1090:TAM:H22	1.85	0.44
1:E:9:ILE:HG12	3:E:92:DMU:H13	1.98	0.44
1:F:87:LYS:NZ	6:F:2021:HOH:O	2.51	0.44
1:N:9:ILE:HD13	3:O:92:DMU:H10	1.98	0.44
1:R:50:ARG:HH12	5:R:1090:TAM:HN1	1.66	0.44
3:F:92:DMU:H30	3:G:92:DMU:H38	1.82	0.44
1:C:67:THR:HA	1:C:70:TYR:CD2	2.53	0.44
3:I:92:DMU:O3	3:J:92:DMU:H2	2.16	0.44
1:N:3:LEU:HD13	1:N:89:GLY:HA3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:92:DMU:H36	3:E:92:DMU:H4	1.62	0.44
3:K:92:DMU:H40	3:K:92:DMU:H36	1.56	0.44
3:R:92:DMU:H36	3:R:92:DMU:H41	1.70	0.44
3:C:92:DMU:C2	3:D:92:DMU:H27	2.30	0.43
1:O:9:ILE:HG12	3:O:92:DMU:H15	2.00	0.43
3:Q:92:DMU:O49	3:R:92:DMU:H10	2.18	0.43
1:M:34:TYR:O	1:M:38:LYS:HG2	2.18	0.43
3:P:92:DMU:O7	3:Q:92:DMU:O6	2.36	0.43
4:C:1090:LMT:H21	4:C:1090:LMT:H52	1.75	0.43
1:E:50:ARG:O	1:E:54:ILE:HG12	2.18	0.43
1:M:67:THR:HA	1:M:70:TYR:CD2	2.53	0.43
3:N:92:DMU:H36	3:N:92:DMU:O55	2.17	0.43
5:M:1090:TAM:H62	5:M:1090:TAM:H22	1.68	0.43
1:M:76:LEU:HD12	1:M:76:LEU:HA	1.83	0.43
3:A:92:DMU:O55	3:A:92:DMU:H36	2.18	0.43
3:D:92:DMU:O3	3:D:92:DMU:O2	2.04	0.43
1:Q:34:TYR:O	1:Q:38:LYS:HG2	2.18	0.43
1:N:1:MET:HB2	3:O:92:DMU:H29	2.00	0.43
1:A:34:TYR:HA	1:K:34:TYR:CD2	2.54	0.43
3:I:92:DMU:H40	3:I:92:DMU:H36	1.62	0.42
3:A:92:DMU:O49	3:A:92:DMU:H7	2.19	0.42
1:H:42:SER:O	1:H:46:GLN:HG2	2.19	0.42
1:A:53:ILE:HG23	1:B:40:VAL:HG13	1.99	0.42
5:R:1090:TAM:H21	5:R:1090:TAM:H41	1.52	0.42
1:U:34:TYR:CD2	1:V:34:TYR:HA	2.55	0.42
3:M:92:DMU:O4	3:M:92:DMU:O6	2.26	0.42
1:D:34:TYR:O	1:D:38:LYS:HG2	2.20	0.42
1:T:2:ASP:OD1	1:T:5:THR:OG1	2.30	0.42
3:K:92:DMU:H2	3:K:92:DMU:H36	1.89	0.42
1:L:9:ILE:HG12	3:L:92:DMU:H15	2.02	0.42
3:S:92:DMU:H40	3:S:92:DMU:H36	1.76	0.42
1:R:1:MET:O	1:S:4:LEU:HD23	2.20	0.42
1:G:10:VAL:HG21	1:G:88:LEU:HD11	2.00	0.42
3:L:92:DMU:H9	3:L:92:DMU:H5	1.42	0.42
1:R:9:ILE:HD13	3:S:92:DMU:H15	2.00	0.42
3:F:92:DMU:H36	3:F:92:DMU:H41	1.39	0.41
3:S:92:DMU:H36	3:S:92:DMU:H2	1.99	0.41
1:E:5:THR:HG21	3:E:92:DMU:C57	2.50	0.41
1:L:67:THR:HA	1:L:70:TYR:CD2	2.55	0.41
1:T:53:ILE:HG23	1:U:40:VAL:HG13	2.02	0.41
3:B:92:DMU:H2	3:C:92:DMU:O61	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:67:THR:HA	1:I:70:TYR:CD2	2.55	0.41
1:F:7:LYS:NZ	6:F:2004:HOH:O	2.53	0.41
1:G:18:ALA:O	1:G:22:MET:HG2	2.21	0.41
1:N:67:THR:HA	1:N:70:TYR:CD2	2.55	0.41
1:A:67:THR:HA	1:A:70:TYR:CD2	2.55	0.41
1:O:9:ILE:HG12	3:O:92:DMU:H11	2.03	0.41
1:V:34:TYR:O	1:V:38:LYS:HG2	2.21	0.41
1:B:73:VAL:HG21	4:C:1090:LMT:H121	2.03	0.41
1:P:82:ASN:HA	1:P:83:PRO:HD3	1.72	0.41
1:R:75:ALA:O	1:R:79:LEU:HG	2.20	0.41
1:L:83:PRO:HG3	1:M:79:LEU:HB3	2.03	0.41
1:B:34:TYR:OH	1:B:38:LYS:HE3	2.21	0.41
1:F:67:THR:HA	1:F:70:TYR:CD2	2.56	0.40
3:Q:92:DMU:O2	3:Q:92:DMU:O3	2.06	0.40
1:S:53:ILE:HG23	1:T:40:VAL:HG13	2.01	0.40
1:V:88:LEU:HD12	1:V:88:LEU:HA	1.89	0.40
1:S:66:SER:OG	1:T:65:GLU:OE2	2.39	0.40
1:K:67:THR:HA	1:K:70:TYR:CD2	2.56	0.40
1:I:38:LYS:HD3	1:I:38:LYS:HA	1.89	0.40
1:R:38:LYS:HA	1:R:38:LYS:HD3	1.88	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	87/89 (98%)	87 (100%)	0	0	100	100
1	B	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	C	87/89 (98%)	87 (100%)	0	0	100	100
1	D	87/89 (98%)	87 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	87/89 (98%)	87 (100%)	0	0	100	100
1	F	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	G	87/89 (98%)	87 (100%)	0	0	100	100
1	H	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	I	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	J	87/89 (98%)	87 (100%)	0	0	100	100
1	K	87/89 (98%)	87 (100%)	0	0	100	100
1	L	87/89 (98%)	87 (100%)	0	0	100	100
1	M	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	N	87/89 (98%)	86 (99%)	0	1 (1%)	14	12
1	O	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	P	87/89 (98%)	87 (100%)	0	0	100	100
1	Q	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	R	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	S	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	T	87/89 (98%)	87 (100%)	0	0	100	100
1	U	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	V	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
All	All	1914/1958 (98%)	1898 (99%)	15 (1%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	88	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	B	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	C	62/62 (100%)	59 (95%)	3 (5%)	25	32
1	D	62/62 (100%)	59 (95%)	3 (5%)	25	32
1	E	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	F	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	G	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	H	62/62 (100%)	56 (90%)	6 (10%)	8	7
1	I	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	J	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	K	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	L	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	M	62/62 (100%)	58 (94%)	4 (6%)	17	19
1	N	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	O	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	P	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	Q	62/62 (100%)	61 (98%)	1 (2%)	62	76
1	R	62/62 (100%)	59 (95%)	3 (5%)	25	32
1	S	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	T	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	U	62/62 (100%)	60 (97%)	2 (3%)	39	50
1	V	62/62 (100%)	61 (98%)	1 (2%)	62	76
All	All	1364/1364 (100%)	1319 (97%)	45 (3%)	38	49

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	59	LEU
1	B	3	LEU
1	B	59	LEU
1	C	3	LEU
1	C	46	GLN
1	C	48	GLU
1	D	3	LEU

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Mol	Chain	Res	Type
1	D	50	ARG
1	D	59	LEU
1	E	50	ARG
1	F	59	LEU
1	F	87	LYS
1	G	48	GLU
1	H	3	LEU
1	H	46	GLN
1	H	48	GLU
1	H	50	ARG
1	H	59	LEU
1	H	76	LEU
1	I	11	LEU
1	I	46	GLN
1	J	76	LEU
1	K	48	GLU
1	L	59	LEU
1	M	3	LEU
1	M	45	ARG
1	M	46	GLN
1	M	76	LEU
1	N	43	VAL
1	N	88	LEU
1	O	3	LEU
1	O	87	LYS
1	P	87	LYS
1	Q	48	GLU
1	R	4	LEU
1	R	10	VAL
1	R	50	ARG
1	S	3	LEU
1	S	46	GLN
1	T	46	GLN
1	T	50	ARG
1	U	46	GLN
1	U	87	LYS
1	V	88	LEU

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

Mol	Chain	Res	Type
1	M	46	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 ⓘ

Of 49 ligands modelled in this entry, 22 are monoatomic - leaving 27 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$
4	LMT	C	1091	-	36,36,36	0.40	0	47,47,47	0.75	0
3	DMU	P	92	-	34,34,34	2.43	7 (20%)	45,45,45	6.21	17 (37%)
5	TAM	M	1090	-	7,10,10	0.50	0	9,12,12	0.66	0
3	DMU	U	92	-	34,34,34	2.31	6 (17%)	45,45,45	5.05	12 (26%)
3	DMU	H	92	-	34,34,34	0.68	0	45,45,45	1.15	4 (8%)
3	DMU	O	92	-	34,34,34	3.82	6 (17%)	45,45,45	4.32	13 (28%)
3	DMU	I	92	-	34,34,34	3.46	8 (23%)	45,45,45	4.38	18 (40%)
3	DMU	L	92	-	34,34,34	3.79	8 (23%)	45,45,45	4.51	17 (37%)
3	DMU	S	92	-	34,34,34	3.14	6 (17%)	45,45,45	4.47	13 (28%)
3	DMU	N	92	-	34,34,34	0.88	2 (5%)	45,45,45	1.52	6 (13%)
3	DMU	M	92	-	34,34,34	3.27	6 (17%)	45,45,45	4.42	16 (35%)
3	DMU	B	92	-	34,34,34	3.30	6 (17%)	45,45,45	4.23	15 (33%)
3	DMU	D	92	-	34,34,34	4.02	9 (26%)	45,45,45	4.50	14 (31%)
3	DMU	R	92	-	34,34,34	3.46	9 (26%)	45,45,45	5.98	22 (48%)
3	DMU	T	92	-	34,34,34	2.84	7 (20%)	45,45,45	4.71	15 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	LMT	B	1090	-	36,36,36	0.41	0	47,47,47	0.77	1 (2%)
3	DMU	J	92	-	34,34,34	2.26	6 (17%)	45,45,45	5.18	12 (26%)
3	DMU	G	92	-	34,34,34	0.96	1 (2%)	45,45,45	1.57	7 (15%)
3	DMU	F	92	-	34,34,34	3.00	6 (17%)	45,45,45	4.42	10 (22%)
3	DMU	E	92	-	34,34,34	3.01	6 (17%)	45,45,45	4.77	16 (35%)
3	DMU	C	92	-	34,34,34	0.86	1 (2%)	45,45,45	1.38	6 (13%)
3	DMU	V	92	-	34,34,34	2.28	8 (23%)	45,45,45	4.10	16 (35%)
4	LMT	C	1090	-	36,36,36	0.41	0	47,47,47	0.81	1 (2%)
5	TAM	R	1090	-	7,10,10	0.49	0	9,12,12	0.97	0
3	DMU	A	92	-	34,34,34	0.83	1 (2%)	45,45,45	1.33	6 (13%)
3	DMU	Q	92	-	34,34,34	3.79	7 (20%)	45,45,45	4.30	13 (28%)
3	DMU	K	92	-	34,34,34	3.13	6 (17%)	45,45,45	4.31	15 (33%)

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
4	LMT	C	1091	-	-	6/21/61/61	0/2/2/2
3	DMU	P	92	-	-	3/19/59/59	0/2/2/2
5	TAM	M	1090	-	-	6/12/12/12	-
3	DMU	U	92	-	-	4/19/59/59	0/2/2/2
3	DMU	H	92	-	-	6/19/59/59	0/2/2/2
3	DMU	O	92	-	-	4/19/59/59	0/2/2/2
3	DMU	I	92	-	-	6/19/59/59	0/2/2/2
3	DMU	L	92	-	-	5/19/59/59	0/2/2/2
3	DMU	S	92	-	-	1/19/59/59	0/2/2/2
3	DMU	N	92	-	-	6/19/59/59	0/2/2/2
3	DMU	M	92	-	-	4/19/59/59	0/2/2/2
3	DMU	B	92	-	-	1/19/59/59	0/2/2/2
3	DMU	D	92	-	-	7/19/59/59	0/2/2/2
3	DMU	R	92	-	-	8/19/59/59	0/2/2/2
3	DMU	T	92	-	-	5/19/59/59	0/2/2/2
4	LMT	B	1090	-	-	4/21/61/61	0/2/2/2
3	DMU	J	92	-	-	4/19/59/59	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMU	G	92	-	-	8/19/59/59	0/2/2/2
3	DMU	F	92	-	-	7/19/59/59	0/2/2/2
3	DMU	E	92	-	-	4/19/59/59	0/2/2/2
3	DMU	C	92	-	-	4/19/59/59	0/2/2/2
3	DMU	V	92	-	-	5/19/59/59	0/2/2/2
4	LMT	C	1090	-	-	8/21/61/61	0/2/2/2
5	TAM	R	1090	-	-	9/12/12/12	-
3	DMU	A	92	-	-	6/19/59/59	0/2/2/2
3	DMU	Q	92	-	-	4/19/59/59	0/2/2/2
3	DMU	K	92	-	-	1/19/59/59	0/2/2/2

All (122) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	92	DMU	O1-C10	15.04	1.80	1.41
3	Q	92	DMU	O1-C10	14.72	1.79	1.41
3	O	92	DMU	O1-C10	13.99	1.77	1.41
3	L	92	DMU	O1-C10	13.28	1.75	1.41
3	B	92	DMU	O1-C10	-10.99	1.13	1.41
3	Q	92	DMU	C7-C5	-10.57	1.25	1.52
3	M	92	DMU	C7-C5	10.52	1.79	1.52
3	D	92	DMU	C7-C5	-10.51	1.25	1.52
3	I	92	DMU	O1-C10	-10.34	1.15	1.41
3	M	92	DMU	O1-C10	-10.29	1.15	1.41
3	O	92	DMU	C7-C5	-10.07	1.26	1.52
3	R	92	DMU	O1-C10	-10.07	1.16	1.41
3	L	92	DMU	C7-C5	-9.86	1.27	1.52
3	K	92	DMU	O1-C10	-9.72	1.17	1.41
3	S	92	DMU	O1-C10	-9.69	1.17	1.41
3	P	92	DMU	O5-C6	9.60	1.66	1.41
3	T	92	DMU	C8-C9	-9.43	1.33	1.53
3	E	92	DMU	O1-C10	-9.25	1.18	1.41
3	O	92	DMU	O1-C9	-9.16	1.22	1.44
3	D	92	DMU	O1-C9	-9.04	1.22	1.44
3	F	92	DMU	O1-C10	-8.92	1.19	1.41
3	E	92	DMU	C7-C5	8.76	1.74	1.52
3	B	92	DMU	C7-C5	8.68	1.74	1.52
3	L	92	DMU	O1-C9	-8.57	1.23	1.44
3	Q	92	DMU	O1-C9	-8.56	1.23	1.44
3	S	92	DMU	C7-C5	8.31	1.73	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	92	DMU	C8-C7	8.21	1.73	1.52
3	I	92	DMU	C7-C5	8.12	1.73	1.52
3	R	92	DMU	C7-C5	8.09	1.72	1.52
3	K	92	DMU	C7-C5	8.05	1.72	1.52
3	B	92	DMU	C8-C7	-7.92	1.32	1.52
3	U	92	DMU	C2-C3	7.92	1.73	1.52
3	K	92	DMU	C8-C7	-7.89	1.32	1.52
3	F	92	DMU	C7-C5	7.72	1.72	1.52
3	T	92	DMU	C10-C5	-7.59	1.30	1.52
3	S	92	DMU	C8-C9	7.50	1.68	1.53
3	I	92	DMU	C10-C5	7.49	1.74	1.52
3	I	92	DMU	C8-C7	-7.36	1.33	1.52
3	F	92	DMU	C10-C5	7.33	1.73	1.52
3	M	92	DMU	C10-C5	7.32	1.73	1.52
3	E	92	DMU	C10-C5	7.31	1.73	1.52
3	V	92	DMU	O5-C6	7.25	1.60	1.41
3	K	92	DMU	C10-C5	7.23	1.73	1.52
3	P	92	DMU	C2-C1	-7.20	1.34	1.52
3	R	92	DMU	C8-C7	-7.19	1.34	1.52
3	R	92	DMU	C10-C5	7.17	1.73	1.52
3	S	92	DMU	C8-C7	-7.11	1.34	1.52
3	F	92	DMU	C8-C7	-7.06	1.34	1.52
3	J	92	DMU	O5-C6	7.04	1.59	1.41
3	L	92	DMU	C10-C5	7.00	1.72	1.52
3	S	92	DMU	C10-C5	6.94	1.72	1.52
3	B	92	DMU	C10-C5	6.88	1.72	1.52
3	B	92	DMU	C8-C9	6.84	1.67	1.53
3	K	92	DMU	C8-C9	6.79	1.67	1.53
3	I	92	DMU	C8-C9	6.78	1.67	1.53
3	I	92	DMU	O16-C6	6.77	1.51	1.40
3	R	92	DMU	C8-C9	6.75	1.67	1.53
3	D	92	DMU	C8-C9	6.71	1.67	1.53
3	Q	92	DMU	C10-C5	6.67	1.71	1.52
3	U	92	DMU	O5-C4	-6.51	1.28	1.44
3	O	92	DMU	C8-C9	6.28	1.66	1.53
3	F	92	DMU	C8-C9	6.27	1.66	1.53
3	J	92	DMU	C2-C1	-6.23	1.36	1.52
3	O	92	DMU	C10-C5	6.21	1.70	1.52
3	J	92	DMU	O16-C6	6.20	1.50	1.40
3	M	92	DMU	C8-C7	-6.19	1.36	1.52
3	V	92	DMU	O5-C4	6.04	1.59	1.44
3	M	92	DMU	C8-C9	6.03	1.65	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	92	DMU	C8-C9	6.02	1.65	1.53
3	U	92	DMU	C2-C1	-5.88	1.37	1.52
3	E	92	DMU	C8-C9	5.58	1.64	1.53
3	L	92	DMU	O16-C6	5.55	1.49	1.40
3	E	92	DMU	C8-C7	-5.48	1.38	1.52
3	V	92	DMU	C3-C4	-5.34	1.38	1.52
3	R	92	DMU	O5-C4	5.31	1.57	1.44
3	D	92	DMU	C10-C5	4.93	1.66	1.52
3	T	92	DMU	C7-C5	4.71	1.64	1.52
3	Q	92	DMU	C8-C9	4.67	1.62	1.53
3	R	92	DMU	O16-C6	4.54	1.47	1.40
3	D	92	DMU	O7-C3	4.39	1.55	1.43
3	P	92	DMU	O5-C4	4.31	1.54	1.44
3	D	92	DMU	O16-C6	4.17	1.47	1.40
3	O	92	DMU	O16-C6	4.12	1.47	1.40
3	R	92	DMU	C3-C4	4.06	1.63	1.52
3	V	92	DMU	C2-C1	4.06	1.62	1.52
3	T	92	DMU	O1-C9	3.81	1.53	1.44
3	G	92	DMU	O16-C6	3.78	1.46	1.40
3	F	92	DMU	O16-C6	3.72	1.46	1.40
3	E	92	DMU	O16-C6	3.68	1.46	1.40
3	J	92	DMU	C3-C4	3.63	1.62	1.52
3	U	92	DMU	O5-C6	3.60	1.51	1.41
3	V	92	DMU	O16-C6	3.28	1.45	1.40
3	V	92	DMU	C6-C1	-3.25	1.43	1.52
3	J	92	DMU	O5-C4	-3.21	1.36	1.44
3	N	92	DMU	O16-C6	3.15	1.45	1.40
3	U	92	DMU	O16-C6	2.93	1.45	1.40
3	D	92	DMU	O7-C10	2.92	1.50	1.41
3	P	92	DMU	O16-C6	2.86	1.45	1.40
3	A	92	DMU	O16-C6	2.84	1.45	1.40
3	P	92	DMU	C2-C3	-2.77	1.44	1.52
3	C	92	DMU	O7-C3	2.75	1.51	1.43
3	P	92	DMU	C3-C4	2.73	1.60	1.52
3	V	92	DMU	O49-C1	2.61	1.49	1.43
3	U	92	DMU	C6-C1	2.60	1.60	1.52
3	L	92	DMU	C6-C1	2.60	1.60	1.52
3	I	92	DMU	O5-C6	2.58	1.48	1.41
3	T	92	DMU	O16-C6	2.51	1.44	1.40
3	K	92	DMU	O16-C6	2.49	1.44	1.40
3	V	92	DMU	C2-C3	2.47	1.59	1.52
3	R	92	DMU	O1-C9	2.46	1.50	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	92	DMU	O16-C6	2.40	1.44	1.40
3	Q	92	DMU	O4-C7	2.28	1.48	1.43
3	T	92	DMU	O7-C10	2.27	1.48	1.41
3	S	92	DMU	O16-C6	2.27	1.44	1.40
3	I	92	DMU	C6-C1	2.25	1.59	1.52
3	Q	92	DMU	O16-C6	2.20	1.43	1.40
3	L	92	DMU	O4-C7	2.16	1.48	1.43
3	D	92	DMU	O4-C7	2.15	1.48	1.43
3	P	92	DMU	C6-C1	2.15	1.58	1.52
3	B	92	DMU	O16-C6	2.10	1.43	1.40
3	N	92	DMU	O7-C3	2.10	1.49	1.43
3	J	92	DMU	C6-C1	2.02	1.58	1.52

All (285) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	92	DMU	O16-C6-C1	21.75	142.25	108.30
3	U	92	DMU	O16-C6-C1	-20.78	75.87	108.30
3	P	92	DMU	C18-O16-C6	-19.57	81.39	113.84
3	P	92	DMU	O7-C3-C2	17.77	154.55	107.28
3	O	92	DMU	C10-O1-C9	-17.76	78.83	113.69
3	D	92	DMU	C10-O1-C9	-17.52	79.30	113.69
3	L	92	DMU	C10-O1-C9	-17.40	79.53	113.69
3	P	92	DMU	O5-C6-O16	16.95	150.12	109.97
3	P	92	DMU	O16-C6-C1	-16.88	81.95	108.30
3	U	92	DMU	O5-C6-O16	16.85	149.89	109.97
3	Q	92	DMU	C10-O1-C9	-16.62	81.06	113.69
3	J	92	DMU	O5-C6-O16	-16.33	71.30	109.97
3	E	92	DMU	O1-C10-C5	-16.02	76.43	110.35
3	R	92	DMU	O5-C6-O16	15.71	147.18	109.97
3	S	92	DMU	O1-C10-C5	-15.59	77.34	110.35
3	K	92	DMU	O1-C10-C5	-15.12	78.35	110.35
3	I	92	DMU	O1-C10-C5	-14.84	78.94	110.35
3	F	92	DMU	O1-C10-C5	-14.75	79.13	110.35
3	M	92	DMU	O1-C10-C5	-14.70	79.23	110.35
3	R	92	DMU	O1-C10-C5	-14.59	79.46	110.35
3	B	92	DMU	O1-C10-C5	-14.48	79.70	110.35
3	F	92	DMU	C8-C7-C5	-14.14	86.14	110.82
3	R	92	DMU	C8-C7-C5	-13.97	86.43	110.82
3	M	92	DMU	C8-C7-C5	-13.79	86.74	110.82
3	L	92	DMU	C10-C5-C7	-13.73	81.39	110.00
3	F	92	DMU	C10-O1-C9	-13.73	86.74	113.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	O	92	DMU	C10-C5-C7	-13.58	81.71	110.00
3	E	92	DMU	C8-C7-C5	-13.55	87.16	110.82
3	J	92	DMU	O7-C3-C2	13.42	142.98	107.28
3	I	92	DMU	C8-C7-C5	-13.40	87.43	110.82
3	B	92	DMU	C8-C7-C5	-13.29	87.62	110.82
3	K	92	DMU	C8-C7-C5	-13.25	87.70	110.82
3	Q	92	DMU	C10-C5-C7	-13.23	82.44	110.00
3	T	92	DMU	C7-C8-C9	-12.88	87.27	110.24
3	T	92	DMU	C10-O1-C9	12.85	138.92	113.69
3	D	92	DMU	C10-C5-C7	-12.78	83.38	110.00
3	S	92	DMU	C8-C7-C5	-12.61	88.81	110.82
3	T	92	DMU	O1-C9-C8	-12.38	87.22	109.69
3	P	92	DMU	C1-C2-C3	12.30	137.77	109.68
3	V	92	DMU	O5-C6-C1	-12.19	84.55	110.35
3	K	92	DMU	C10-O1-C9	-11.85	90.43	113.69
3	T	92	DMU	C8-C7-C5	11.79	131.41	110.82
3	S	92	DMU	C10-O1-C9	-11.58	90.95	113.69
3	E	92	DMU	O3-C5-C10	-11.57	81.95	110.05
3	U	92	DMU	O7-C3-C4	11.36	140.59	109.45
3	V	92	DMU	O7-C3-C4	11.24	140.25	109.45
3	R	92	DMU	C10-O1-C9	-11.07	91.96	113.69
3	R	92	DMU	C18-O16-C6	11.05	132.16	113.84
3	J	92	DMU	O7-C3-C4	-10.94	79.47	109.45
3	R	92	DMU	C2-C3-C4	-10.86	86.02	110.93
3	T	92	DMU	C10-C5-C7	-10.76	87.58	110.00
3	I	92	DMU	C10-O1-C9	-10.66	92.76	113.69
3	D	92	DMU	O1-C9-C8	-10.37	90.87	109.69
3	E	92	DMU	C10-C5-C7	10.36	131.57	110.00
3	P	92	DMU	C6-O5-C4	-10.30	93.48	113.69
3	U	92	DMU	O7-C3-C2	-10.28	79.94	107.28
3	E	92	DMU	O7-C10-C5	10.24	134.63	108.10
3	B	92	DMU	C10-O1-C9	-10.00	94.05	113.69
3	O	92	DMU	O1-C10-C5	9.83	131.16	110.35
3	M	92	DMU	O3-C5-C10	-9.68	86.53	110.05
3	M	92	DMU	O7-C10-C5	9.49	132.70	108.10
3	R	92	DMU	O7-C10-O1	9.49	137.19	110.67
3	S	92	DMU	C7-C8-C9	-9.41	93.45	110.24
3	L	92	DMU	O1-C10-C5	9.39	130.22	110.35
3	T	92	DMU	O3-C5-C10	-9.17	87.76	110.05
3	M	92	DMU	C10-C5-C7	9.03	128.81	110.00
3	V	92	DMU	O16-C6-C1	-8.85	94.48	108.30
3	V	92	DMU	O5-C6-O16	8.81	130.85	109.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	V	92	DMU	O5-C4-C3	-8.80	91.20	109.75
3	S	92	DMU	C18-O16-C6	-8.78	99.28	113.84
3	I	92	DMU	O7-C10-O1	8.67	134.88	110.67
3	B	92	DMU	C7-C8-C9	-8.64	94.82	110.24
3	D	92	DMU	O1-C10-C5	8.44	128.21	110.35
3	R	92	DMU	O5-C6-C1	-8.41	92.54	110.35
3	B	92	DMU	O7-C10-O1	8.30	133.87	110.67
3	F	92	DMU	C7-C8-C9	-8.29	95.46	110.24
3	F	92	DMU	O7-C10-O1	8.13	133.40	110.67
3	O	92	DMU	O1-C9-C8	-8.09	95.00	109.69
3	I	92	DMU	C7-C8-C9	-8.07	95.84	110.24
3	P	92	DMU	C2-C3-C4	-8.01	92.57	110.93
3	K	92	DMU	C7-C8-C9	-7.95	96.06	110.24
3	K	92	DMU	O7-C10-O1	7.94	132.86	110.67
3	R	92	DMU	O7-C3-C4	7.91	131.12	109.45
3	Q	92	DMU	O1-C10-C5	7.85	126.97	110.35
3	R	92	DMU	O16-C6-C1	-7.83	96.07	108.30
3	E	92	DMU	C18-O16-C6	7.71	126.62	113.84
3	S	92	DMU	O7-C10-O1	7.70	132.18	110.67
3	Q	92	DMU	O3-C5-C10	7.68	128.71	110.05
3	Q	92	DMU	O1-C9-C8	-7.67	95.77	109.69
3	R	92	DMU	C7-C8-C9	-7.62	96.65	110.24
3	V	92	DMU	C6-O5-C4	7.60	128.62	113.69
3	L	92	DMU	O3-C5-C10	7.60	128.50	110.05
3	D	92	DMU	C8-C7-C5	-7.32	98.04	110.82
3	L	92	DMU	C18-O16-C6	-7.19	101.92	113.84
3	Q	92	DMU	C8-C7-C5	-7.12	98.39	110.82
3	L	92	DMU	O1-C9-C8	-7.09	96.81	109.69
3	V	92	DMU	C2-C3-C4	-7.08	94.70	110.93
3	R	92	DMU	O7-C3-C2	-7.06	88.52	107.28
3	L	92	DMU	C8-C7-C5	-6.96	98.67	110.82
3	T	92	DMU	O7-C10-C5	6.87	125.90	108.10
3	U	92	DMU	O55-C2-C1	-6.86	94.50	110.35
3	J	92	DMU	C10-O7-C3	-6.67	101.45	117.96
3	T	92	DMU	C10-O7-C3	6.62	134.36	117.96
3	O	92	DMU	O3-C5-C10	6.60	126.09	110.05
3	D	92	DMU	O3-C5-C10	6.58	126.04	110.05
3	D	92	DMU	C7-C8-C9	6.58	121.98	110.24
3	Q	92	DMU	C7-C8-C9	6.38	121.63	110.24
3	Q	92	DMU	O7-C10-C5	-6.37	91.58	108.10
3	B	92	DMU	C10-O7-C3	-6.32	102.33	117.96
3	K	92	DMU	O3-C5-C10	6.31	125.38	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	92	DMU	O4-C7-C8	6.28	124.88	110.35
3	J	92	DMU	C18-O16-C6	-6.28	103.42	113.84
3	U	92	DMU	C10-O7-C3	6.24	133.40	117.96
3	F	92	DMU	O1-C9-C8	6.17	120.90	109.69
3	S	92	DMU	O3-C5-C10	6.15	124.98	110.05
3	P	92	DMU	C6-C1-C2	-6.13	97.23	110.00
3	O	92	DMU	C8-C7-C5	-6.11	100.16	110.82
3	M	92	DMU	C7-C8-C9	-6.02	99.50	110.24
3	G	92	DMU	C18-O16-C6	-5.62	104.53	113.84
3	O	92	DMU	C7-C8-C9	5.57	120.18	110.24
3	I	92	DMU	O3-C5-C10	5.55	123.53	110.05
3	R	92	DMU	C6-O5-C4	-5.55	102.80	113.69
3	N	92	DMU	O1-C9-C11	5.55	120.22	106.44
3	D	92	DMU	C10-O7-C3	5.52	131.63	117.96
3	B	92	DMU	O1-C9-C8	5.45	119.59	109.69
3	R	92	DMU	C10-C5-C7	5.44	121.33	110.00
3	B	92	DMU	O3-C5-C10	5.33	123.00	110.05
3	V	92	DMU	O49-C1-C2	5.28	122.56	110.35
3	L	92	DMU	C7-C8-C9	5.26	119.62	110.24
3	U	92	DMU	C18-O16-C6	-5.08	105.42	113.84
3	M	92	DMU	O5-C4-C57	5.07	119.04	106.44
3	B	92	DMU	C10-C5-C7	5.05	120.51	110.00
3	I	92	DMU	O1-C9-C8	5.05	118.86	109.69
3	E	92	DMU	O7-C10-O1	-5.03	96.61	110.67
3	I	92	DMU	C10-O7-C3	5.02	130.38	117.96
3	S	92	DMU	O1-C9-C8	4.99	118.76	109.69
3	R	92	DMU	O1-C9-C8	4.98	118.73	109.69
3	F	92	DMU	O3-C5-C10	4.96	122.09	110.05
3	M	92	DMU	O7-C10-O1	-4.93	96.91	110.67
3	I	92	DMU	C18-O16-C6	-4.92	105.67	113.84
3	I	92	DMU	C10-C5-C7	4.91	120.23	110.00
3	K	92	DMU	O1-C9-C8	4.86	118.51	109.69
3	L	92	DMU	O7-C10-C5	-4.82	95.61	108.10
3	R	92	DMU	O5-C4-C3	4.74	119.74	109.75
3	M	92	DMU	C18-O16-C6	-4.73	105.99	113.84
3	E	92	DMU	C7-C8-C9	-4.64	101.97	110.24
3	C	92	DMU	O55-C2-C1	-4.56	99.81	110.35
3	E	92	DMU	C10-O1-C9	4.49	122.50	113.69
3	D	92	DMU	O7-C3-C2	4.41	119.02	107.28
3	V	92	DMU	C6-C1-C2	-4.37	100.89	110.00
3	U	92	DMU	O5-C4-C3	4.27	118.76	109.75
3	F	92	DMU	C10-C5-C7	4.25	118.84	110.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	R	92	DMU	O3-C5-C10	4.23	120.31	110.05
3	R	92	DMU	C10-O7-C3	-4.13	107.74	117.96
3	T	92	DMU	O3-C5-C7	4.08	119.79	110.35
3	K	92	DMU	C10-C5-C7	4.05	118.44	110.00
3	Q	92	DMU	C11-C9-C8	-4.05	103.51	113.00
3	K	92	DMU	C18-O16-C6	-4.03	107.15	113.84
3	O	92	DMU	O7-C10-C5	-4.02	97.68	108.10
3	P	92	DMU	O5-C4-C3	4.01	118.20	109.75
3	S	92	DMU	C10-C5-C7	3.98	118.28	110.00
3	M	92	DMU	O1-C9-C11	3.96	116.29	106.44
3	S	92	DMU	C10-O7-C3	3.95	127.74	117.96
3	I	92	DMU	O16-C6-C1	3.92	114.42	108.30
3	U	92	DMU	O5-C4-C57	3.84	115.99	106.44
3	J	92	DMU	O1-C9-C11	3.84	115.98	106.44
3	M	92	DMU	O4-C7-C8	3.81	119.16	110.35
3	P	92	DMU	O16-C18-C19	3.75	122.70	109.56
3	V	92	DMU	O7-C3-C2	-3.72	97.40	107.28
3	N	92	DMU	C18-O16-C6	3.69	119.96	113.84
3	U	92	DMU	C2-C3-C4	-3.69	102.47	110.93
3	K	92	DMU	O5-C4-C57	3.67	115.57	106.44
3	D	92	DMU	O5-C6-C1	-3.65	102.63	110.35
3	P	92	DMU	C10-O7-C3	-3.63	108.98	117.96
3	C	92	DMU	O5-C4-C57	3.60	115.39	106.44
3	T	92	DMU	C57-C4-C3	-3.57	102.93	113.33
3	M	92	DMU	O1-C9-C8	3.54	116.13	109.69
3	I	92	DMU	O49-C1-C2	-3.50	102.25	110.35
3	U	92	DMU	O55-C2-C3	3.49	119.18	109.94
3	V	92	DMU	C8-C7-C5	-3.44	104.82	110.82
3	F	92	DMU	O49-C1-C2	-3.34	102.64	110.35
3	R	92	DMU	O5-C4-C57	3.26	114.55	106.44
3	E	92	DMU	C31-C28-C25	-3.24	97.98	114.42
3	T	92	DMU	O1-C10-C5	-3.22	103.54	110.35
3	P	92	DMU	O55-C2-C1	-3.20	102.95	110.35
3	P	92	DMU	C22-C19-C18	-3.20	99.31	113.49
3	G	92	DMU	O49-C1-C2	-3.16	103.04	110.35
4	B	1090	LMT	C1B-O1B-C4'	-3.13	110.21	117.96
3	G	92	DMU	O5-C4-C57	3.11	114.17	106.44
3	A	92	DMU	O55-C2-C1	-3.10	103.19	110.35
3	J	92	DMU	C1-C2-C3	3.09	116.73	109.68
3	K	92	DMU	C57-C4-C3	-3.06	104.42	113.33
3	V	92	DMU	C11-C9-C8	-3.06	105.85	113.00
3	J	92	DMU	C57-C4-C3	-3.04	104.49	113.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	92	DMU	O55-C2-C1	-3.03	103.34	110.35
3	D	92	DMU	C11-C9-C8	-3.02	105.92	113.00
3	R	92	DMU	O1-C9-C11	3.01	113.92	106.44
3	V	92	DMU	O49-C1-C6	2.99	117.32	110.05
3	H	92	DMU	C57-C4-C3	-2.96	104.70	113.33
3	L	92	DMU	O49-C1-C6	2.90	117.08	110.05
3	H	92	DMU	O7-C3-C2	2.89	114.98	107.28
3	L	92	DMU	O16-C6-C1	2.88	112.81	108.30
3	P	92	DMU	O1-C9-C11	2.88	113.60	106.44
3	V	92	DMU	O7-C10-O1	2.86	118.65	110.67
4	C	1090	LMT	C1B-O1B-C4'	-2.80	111.03	117.96
3	K	92	DMU	C10-O7-C3	2.80	124.89	117.96
3	A	92	DMU	C11-C9-C8	-2.75	106.57	113.00
3	Q	92	DMU	O5-C4-C57	2.70	113.15	106.44
3	P	92	DMU	O7-C10-O1	-2.69	103.16	110.67
3	M	92	DMU	O2-C8-C7	2.66	116.51	110.35
3	J	92	DMU	C37-C34-C31	-2.66	100.93	114.42
3	E	92	DMU	O1-C9-C11	2.64	112.99	106.44
3	A	92	DMU	O5-C4-C57	2.63	112.98	106.44
3	V	92	DMU	O3-C5-C10	-2.61	103.70	110.05
3	L	92	DMU	O49-C1-C2	-2.60	104.33	110.35
3	N	92	DMU	C31-C28-C25	-2.60	101.24	114.42
3	F	92	DMU	C10-O7-C3	-2.59	111.57	117.96
3	E	92	DMU	O2-C8-C9	2.57	115.68	109.30
3	N	92	DMU	O7-C3-C2	2.57	114.12	107.28
3	C	92	DMU	C57-C4-C3	-2.57	105.84	113.33
3	B	92	DMU	O5-C4-C57	2.57	112.82	106.44
3	M	92	DMU	C10-O7-C3	2.56	124.30	117.96
3	S	92	DMU	C57-C4-C3	-2.55	105.90	113.33
3	B	92	DMU	C11-C9-C8	-2.50	107.14	113.00
3	K	92	DMU	C22-C19-C18	-2.50	102.42	113.49
3	L	92	DMU	O4-C7-C5	2.48	116.07	110.35
3	I	92	DMU	O49-C1-C6	2.47	116.05	110.05
3	C	92	DMU	O7-C3-C2	2.47	113.86	107.28
3	T	92	DMU	C28-C25-C22	-2.45	101.97	114.42
3	J	92	DMU	C6-O5-C4	-2.43	108.91	113.69
3	M	92	DMU	O2-C8-C9	2.43	115.33	109.30
3	O	92	DMU	C2-C3-C4	-2.42	105.37	110.93
3	K	92	DMU	O7-C3-C2	2.41	113.70	107.28
3	S	92	DMU	O1-C9-C11	2.40	112.41	106.44
3	O	92	DMU	O55-C2-C1	-2.40	104.81	110.35
3	C	92	DMU	C10-O7-C3	-2.40	112.04	117.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	92	DMU	O3-C5-C7	-2.39	104.81	110.35
3	A	92	DMU	C8-C7-C5	-2.39	106.65	110.82
3	R	92	DMU	O55-C2-C3	2.37	116.22	109.94
3	A	92	DMU	O49-C1-C2	-2.37	104.88	110.35
3	P	92	DMU	O7-C3-C4	-2.37	102.96	109.45
3	K	92	DMU	C31-C28-C25	-2.36	102.46	114.42
3	N	92	DMU	C10-O7-C3	-2.36	112.13	117.96
3	B	92	DMU	O7-C3-C2	2.35	113.54	107.28
3	V	92	DMU	C1-C2-C3	2.35	115.05	109.68
3	T	92	DMU	C18-O16-C6	-2.34	109.96	113.84
3	O	92	DMU	C18-O16-C6	2.32	117.69	113.84
3	O	92	DMU	O3-C5-C7	-2.30	105.03	110.35
3	H	92	DMU	C18-O16-C6	2.30	117.65	113.84
3	U	92	DMU	C22-C19-C18	-2.28	103.41	113.49
3	I	92	DMU	O5-C4-C57	-2.26	100.81	106.44
3	Q	92	DMU	C57-C4-C3	-2.23	106.83	113.33
3	P	92	DMU	O5-C4-C57	2.23	111.98	106.44
3	Q	92	DMU	O4-C7-C5	2.22	115.48	110.35
3	L	92	DMU	O55-C2-C1	-2.21	105.23	110.35
3	G	92	DMU	O16-C18-C19	2.21	117.30	109.56
3	L	92	DMU	C25-C22-C19	2.20	125.60	114.42
3	T	92	DMU	O7-C3-C2	2.19	113.11	107.28
3	E	92	DMU	O55-C2-C1	-2.19	105.29	110.35
3	G	92	DMU	O7-C3-C2	2.18	113.08	107.28
3	J	92	DMU	C34-C31-C28	2.14	125.28	114.42
3	I	92	DMU	C11-C9-C8	-2.14	108.00	113.00
3	A	92	DMU	C18-O16-C6	-2.13	110.30	113.84
3	G	92	DMU	C10-O7-C3	2.13	123.24	117.96
3	I	92	DMU	O1-C9-C11	2.13	111.73	106.44
3	G	92	DMU	C10-O1-C9	-2.13	109.51	113.69
3	I	92	DMU	O5-C4-C3	2.12	114.22	109.75
3	T	92	DMU	O16-C18-C19	-2.12	102.14	109.56
3	M	92	DMU	O55-C2-C1	-2.10	105.50	110.35
3	B	92	DMU	C57-C4-C3	-2.10	107.22	113.33
3	I	92	DMU	C2-C3-C4	-2.09	106.12	110.93
3	S	92	DMU	O7-C3-C2	2.09	112.85	107.28
3	R	92	DMU	C11-C9-C8	-2.09	108.11	113.00
3	E	92	DMU	O2-C8-C7	2.08	115.17	110.35
3	H	92	DMU	O5-C4-C57	2.08	111.61	106.44
3	B	92	DMU	O1-C9-C11	2.08	111.61	106.44
3	Q	92	DMU	C10-O7-C3	2.07	123.10	117.96
3	E	92	DMU	O55-C2-C3	-2.07	104.45	109.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	92	DMU	O3-C5-C7	-2.06	105.59	110.35
3	O	92	DMU	O4-C7-C5	2.05	115.09	110.35
3	L	92	DMU	C31-C28-C25	-2.05	104.02	114.42
3	N	92	DMU	C57-C4-C3	-2.04	107.40	113.33
3	C	92	DMU	C11-C9-C8	2.04	117.78	113.00
3	B	92	DMU	O3-C5-C7	-2.00	105.71	110.35
3	D	92	DMU	C31-C28-C25	-2.00	104.27	114.42

There are no chirality outliers.

All (136) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	V	92	DMU	C1-C6-O16-C18
3	V	92	DMU	O5-C6-O16-C18
3	H	92	DMU	C19-C18-O16-C6
3	I	92	DMU	O5-C6-O16-C18
3	I	92	DMU	C19-C18-O16-C6
3	L	92	DMU	O5-C6-O16-C18
3	N	92	DMU	O5-C6-O16-C18
3	D	92	DMU	O5-C6-O16-C18
3	R	92	DMU	O5-C6-O16-C18
3	F	92	DMU	O5-C6-O16-C18
3	F	92	DMU	C19-C18-O16-C6
3	E	92	DMU	O5-C6-O16-C18
5	M	1090	TAM	C1-C-C3-C6
5	M	1090	TAM	N-C-C3-C6
3	G	92	DMU	O5-C6-O16-C18
5	R	1090	TAM	C2-C-C1-C4
5	R	1090	TAM	C3-C-C1-C4
5	R	1090	TAM	N-C-C1-C4
5	R	1090	TAM	C1-C-C2-C5
5	R	1090	TAM	C3-C-C2-C5
5	R	1090	TAM	N-C-C2-C5
5	R	1090	TAM	C2-C-C3-C6
5	R	1090	TAM	N-C-C3-C6
3	A	92	DMU	O5-C6-O16-C18
3	P	92	DMU	C2-C3-O7-C10
3	S	92	DMU	C2-C3-O7-C10
3	K	92	DMU	C2-C3-O7-C10
3	R	92	DMU	O1-C10-O7-C3
3	D	92	DMU	C5-C10-O7-C3
3	O	92	DMU	C5-C10-O7-C3

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Mol	Chain	Res	Type	Atoms
3	R	92	DMU	C5-C10-O7-C3
3	E	92	DMU	C4-C3-O7-C10
3	U	92	DMU	O1-C10-O7-C3
3	F	92	DMU	C2-C3-O7-C10
3	D	92	DMU	O1-C10-O7-C3
3	C	92	DMU	C2-C3-O7-C10
4	C	1090	LMT	O5'-C5'-C6'-O6'
4	C	1090	LMT	C4'-C5'-C6'-O6'
3	N	92	DMU	C1-C6-O16-C18
3	D	92	DMU	C1-C6-O16-C18
3	R	92	DMU	C1-C6-O16-C18
3	F	92	DMU	C1-C6-O16-C18
3	G	92	DMU	C1-C6-O16-C18
3	A	92	DMU	C1-C6-O16-C18
3	O	92	DMU	O1-C10-O7-C3
3	I	92	DMU	C2-C3-O7-C10
3	G	92	DMU	C4-C3-O7-C10
3	A	92	DMU	C4-C3-O7-C10
3	P	92	DMU	O5-C6-O16-C18
3	L	92	DMU	C4-C3-O7-C10
3	M	92	DMU	C2-C3-O7-C10
3	C	92	DMU	O1-C10-O7-C3
3	M	92	DMU	C4-C3-O7-C10
3	Q	92	DMU	C4-C3-O7-C10
3	A	92	DMU	C2-C3-O7-C10
3	I	92	DMU	C4-C3-O7-C10
3	G	92	DMU	C2-C3-O7-C10
3	R	92	DMU	C2-C3-O7-C10
4	B	1090	LMT	O5'-C5'-C6'-O6'
3	L	92	DMU	C19-C18-O16-C6
3	L	92	DMU	C2-C3-O7-C10
3	T	92	DMU	C4-C3-O7-C10
3	U	92	DMU	C4-C3-O7-C10
4	B	1090	LMT	C1-C2-C3-C4
3	H	92	DMU	C4-C3-O7-C10
3	T	92	DMU	O1-C10-O7-C3
3	H	92	DMU	C2-C3-O7-C10
3	J	92	DMU	C2-C3-O7-C10
3	J	92	DMU	C4-C3-O7-C10
3	Q	92	DMU	C2-C3-O7-C10
3	I	92	DMU	C1-C6-O16-C18
3	L	92	DMU	C1-C6-O16-C18

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Mol	Chain	Res	Type	Atoms
3	R	92	DMU	O6-C11-C9-O1
3	J	92	DMU	O6-C11-C9-O1
4	C	1091	LMT	C2B-C1B-O1B-C4'
3	U	92	DMU	O5-C4-C57-O61
3	R	92	DMU	O5-C4-C57-O61
3	G	92	DMU	O5-C4-C57-O61
3	G	92	DMU	O6-C11-C9-O1
3	A	92	DMU	O5-C4-C57-O61
4	C	1091	LMT	C11-C10-C9-C8
3	B	92	DMU	O5-C4-C57-O61
3	P	92	DMU	O5-C4-C57-O61
3	V	92	DMU	O6-C11-C9-O1
3	H	92	DMU	O5-C4-C57-O61
3	N	92	DMU	O5-C4-C57-O61
3	A	92	DMU	O6-C11-C9-O1
3	Q	92	DMU	O5-C4-C57-O61
3	O	92	DMU	O5-C4-C57-O61
3	T	92	DMU	C2-C3-O7-C10
4	B	1090	LMT	O5B-C5B-C6B-O6B
3	C	92	DMU	C4-C3-O7-C10
4	C	1090	LMT	C4B-C5B-C6B-O6B
5	M	1090	TAM	C2-C-C3-C6
5	R	1090	TAM	C1-C-C3-C6
4	C	1091	LMT	O5B-C1B-O1B-C4'
3	F	92	DMU	O6-C11-C9-O1
3	M	92	DMU	O6-C11-C9-C8
3	N	92	DMU	C2-C3-O7-C10
3	D	92	DMU	C2-C3-O7-C10
3	E	92	DMU	C1-C6-O16-C18
3	T	92	DMU	O6-C11-C9-C8
4	C	1090	LMT	C4-C5-C6-C7
3	U	92	DMU	C2-C3-O7-C10
3	O	92	DMU	C19-C18-O16-C6
3	R	92	DMU	C19-C18-O16-C6
3	J	92	DMU	C19-C18-O16-C6
3	N	92	DMU	C4-C3-O7-C10
4	C	1090	LMT	C2-C3-C4-C5
4	C	1091	LMT	C1-C2-C3-C4
3	N	92	DMU	C19-C18-O16-C6
3	G	92	DMU	O1-C10-O7-C3
3	G	92	DMU	C5-C10-O7-C3
3	Q	92	DMU	O1-C10-O7-C3

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Mol	Chain	Res	Type	Atoms
3	D	92	DMU	C4-C3-O7-C10
3	F	92	DMU	C4-C3-O7-C10
3	E	92	DMU	C2-C3-O7-C10
4	C	1090	LMT	O5B-C5B-C6B-O6B
3	D	92	DMU	O6-C11-C9-C8
3	T	92	DMU	C5-C10-O7-C3
4	C	1091	LMT	C6-C7-C8-C9
3	M	92	DMU	C5-C10-O7-C3
3	I	92	DMU	C5-C10-O7-C3
3	F	92	DMU	C5-C10-O7-C3
4	C	1090	LMT	C3-C4-C5-C6
3	C	92	DMU	C19-C18-O16-C6
5	M	1090	TAM	N-C-C2-C5
3	H	92	DMU	O1-C10-O7-C3
3	H	92	DMU	C5-C10-O7-C3
4	B	1090	LMT	C4-C5-C6-C7
4	C	1090	LMT	C7-C8-C9-C10
4	C	1091	LMT	C7-C8-C9-C10
3	V	92	DMU	C2-C3-O7-C10
5	M	1090	TAM	C1-C-C2-C5
5	M	1090	TAM	C3-C-C2-C5
3	V	92	DMU	C3-C4-C57-O61

There are no ring outliers.

26 monomers are involved in 135 short contacts:

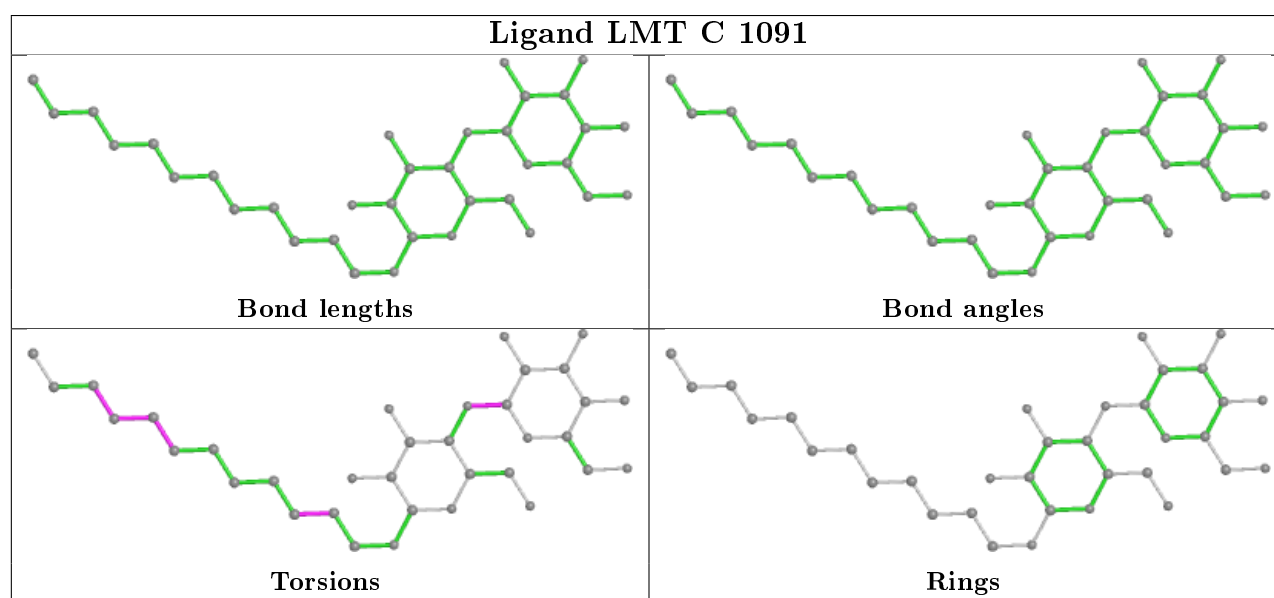
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1091	LMT	3	0
3	P	92	DMU	12	0
5	M	1090	TAM	2	0
3	U	92	DMU	5	0
3	H	92	DMU	3	0
3	O	92	DMU	13	0
3	I	92	DMU	6	0
3	L	92	DMU	10	0
3	S	92	DMU	7	0
3	N	92	DMU	4	0
3	M	92	DMU	12	0
3	B	92	DMU	5	0
3	D	92	DMU	8	0
3	R	92	DMU	7	0
3	T	92	DMU	2	0

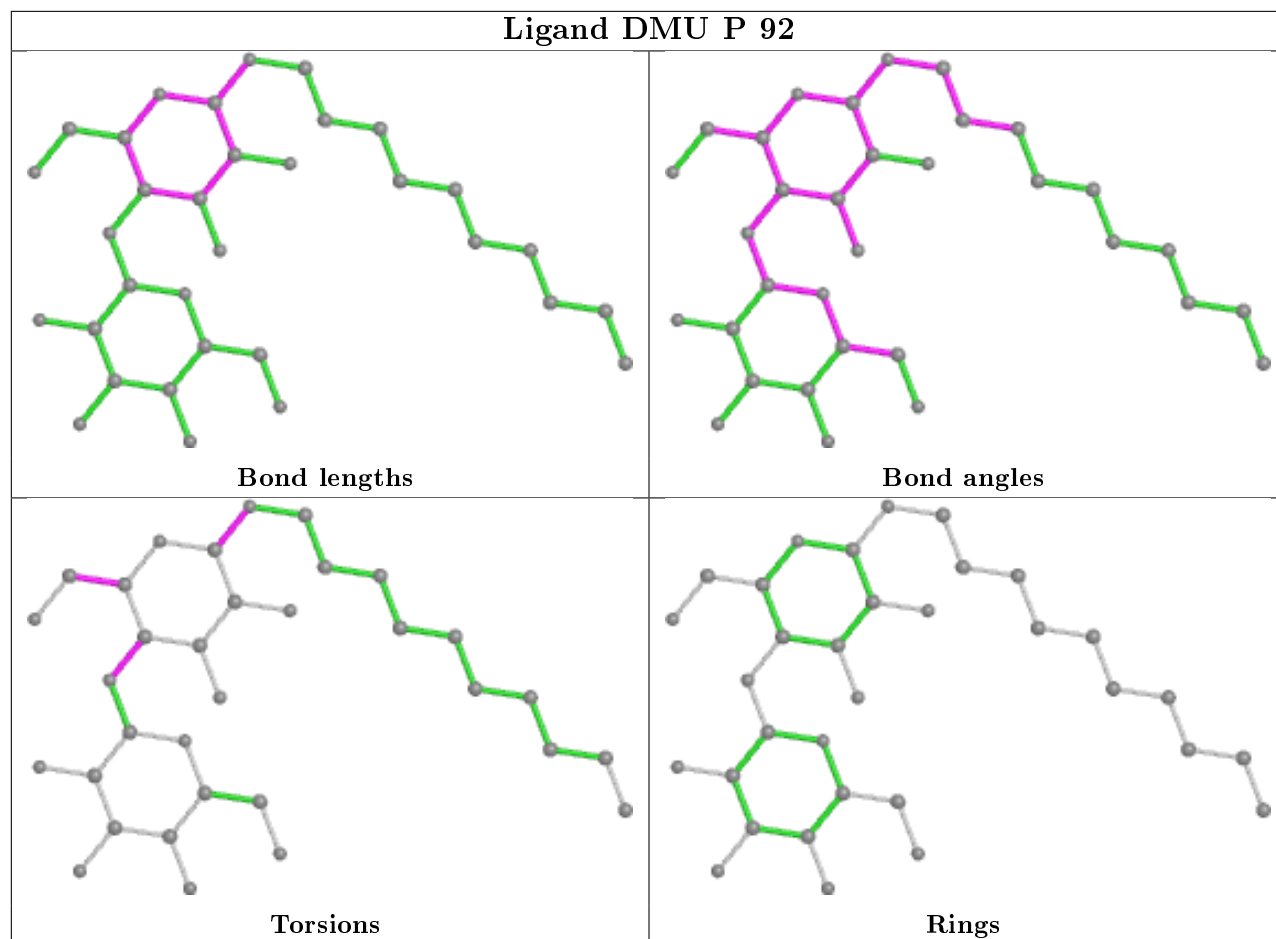
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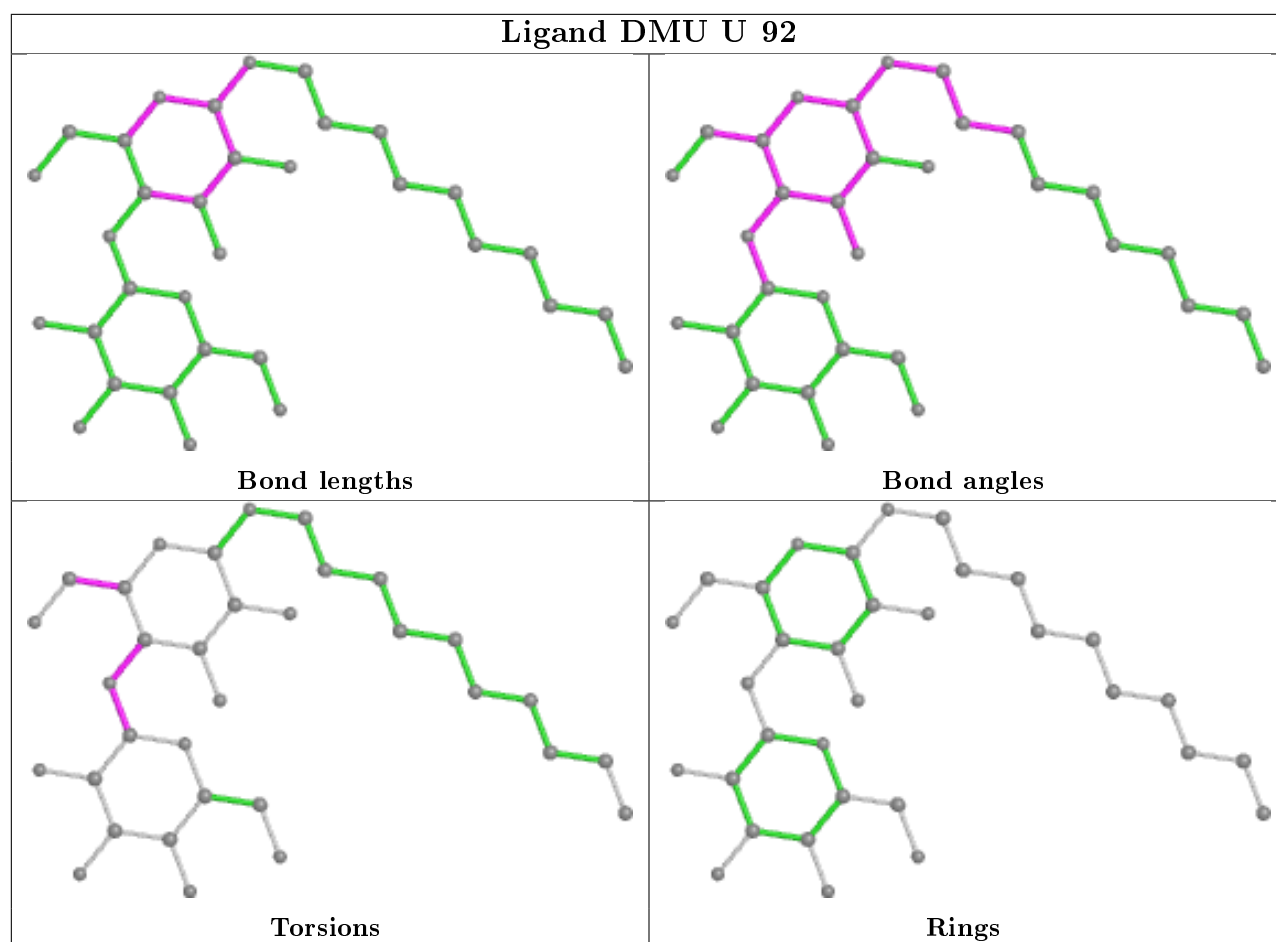
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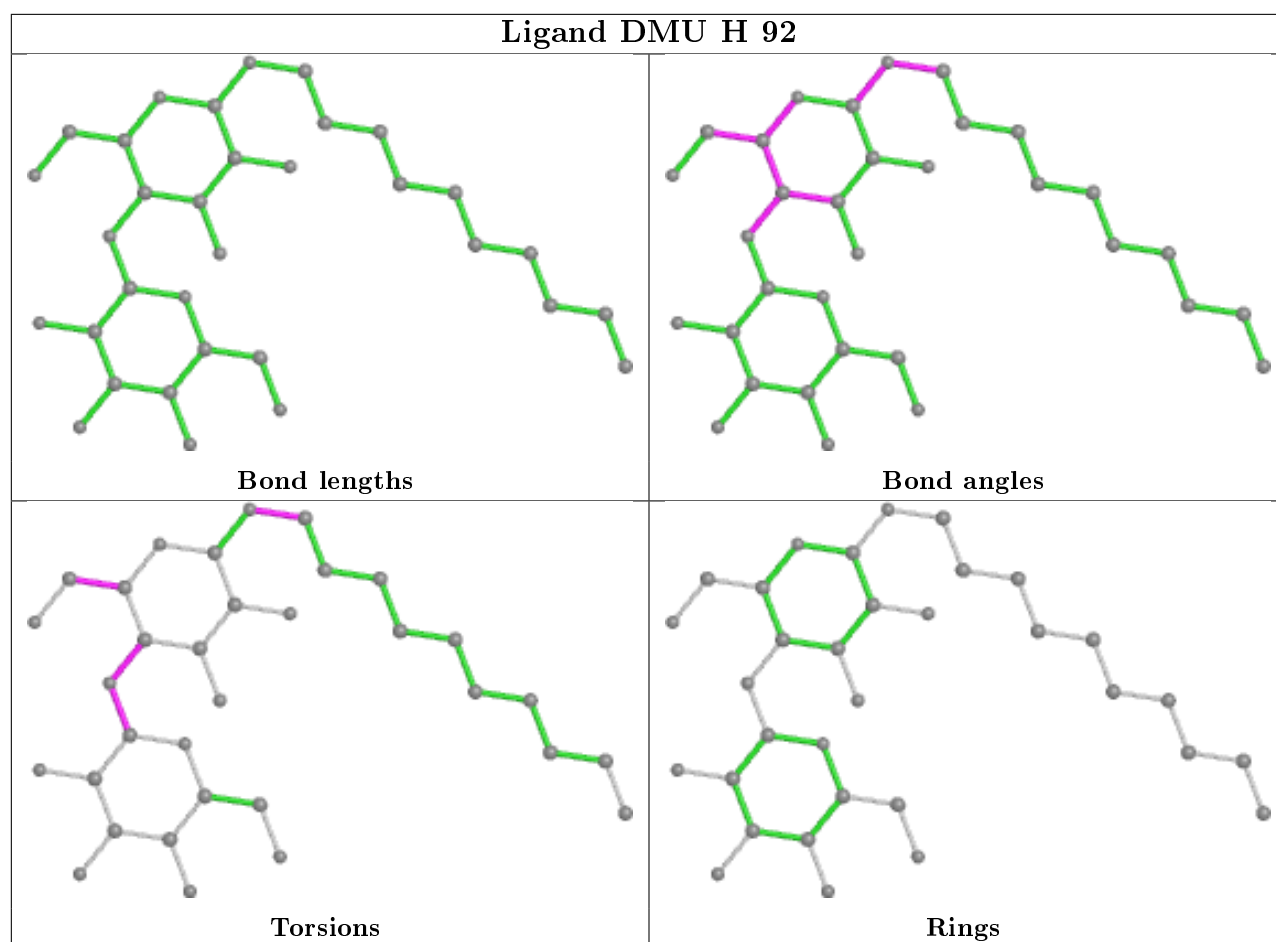
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	92	DMU	4	0
3	G	92	DMU	7	0
3	F	92	DMU	5	0
3	E	92	DMU	13	0
3	C	92	DMU	3	0
3	V	92	DMU	1	0
4	C	1090	LMT	3	0
5	R	1090	TAM	5	0
3	A	92	DMU	6	0
3	Q	92	DMU	10	0
3	K	92	DMU	4	0

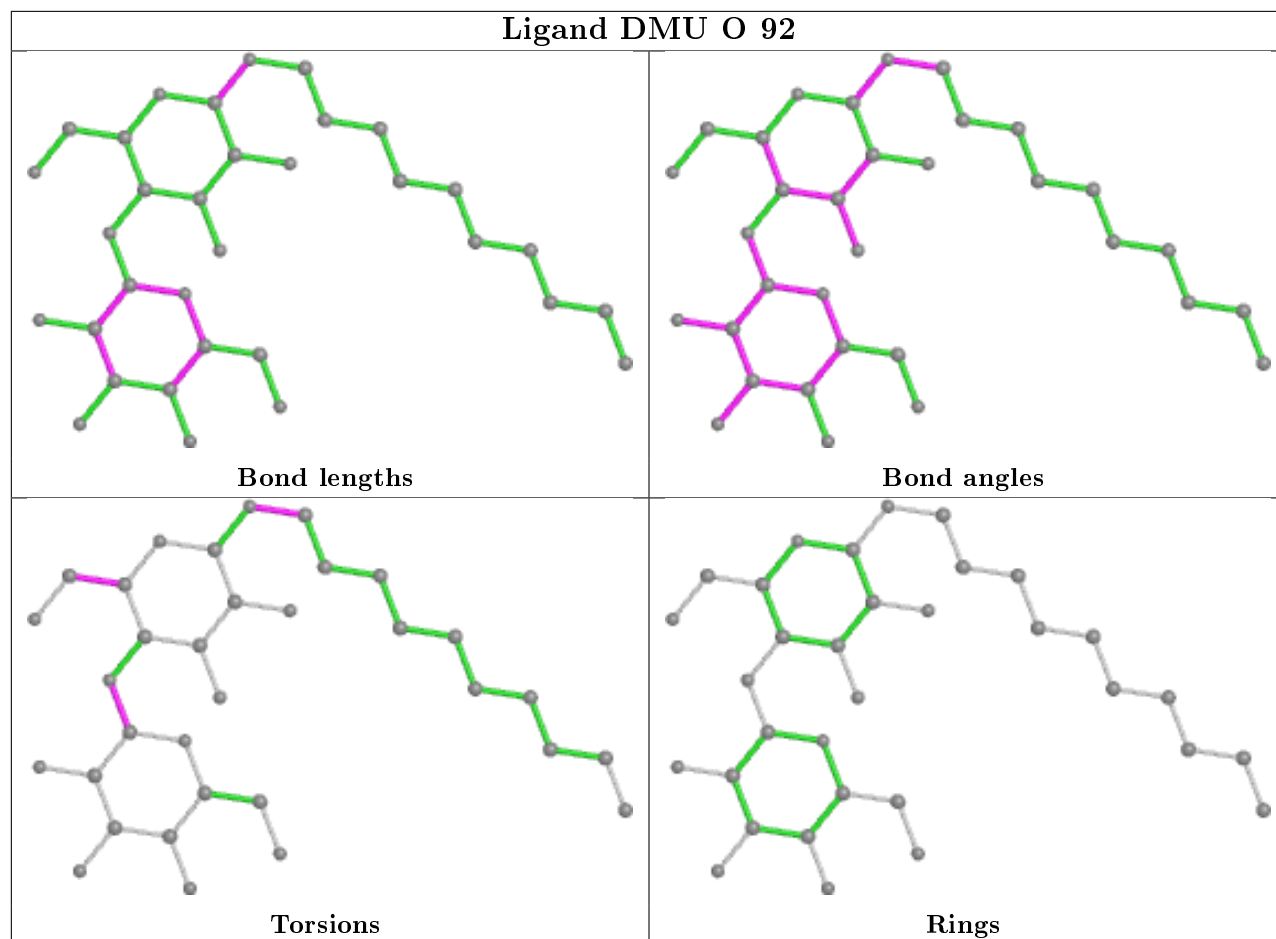
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

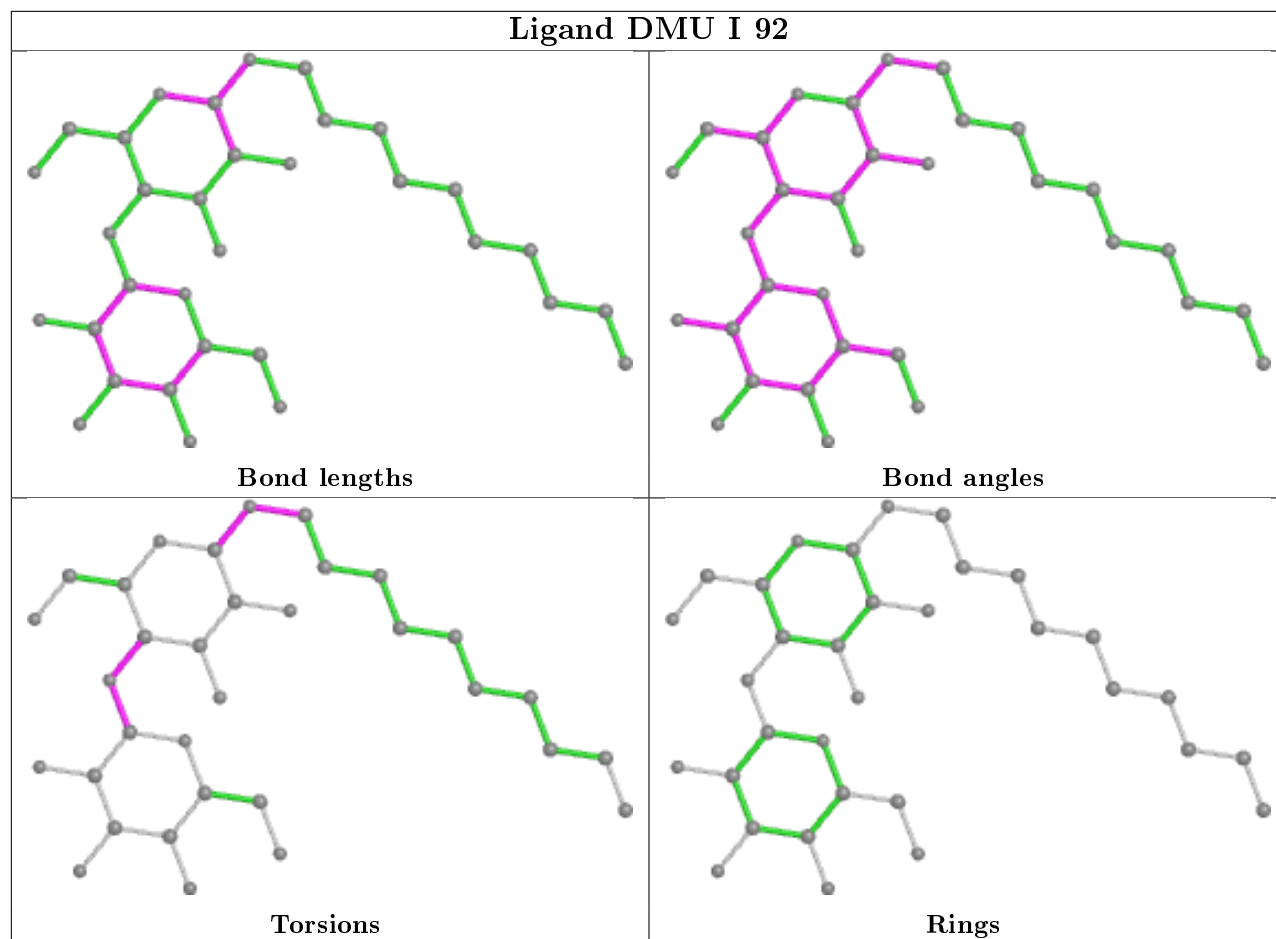


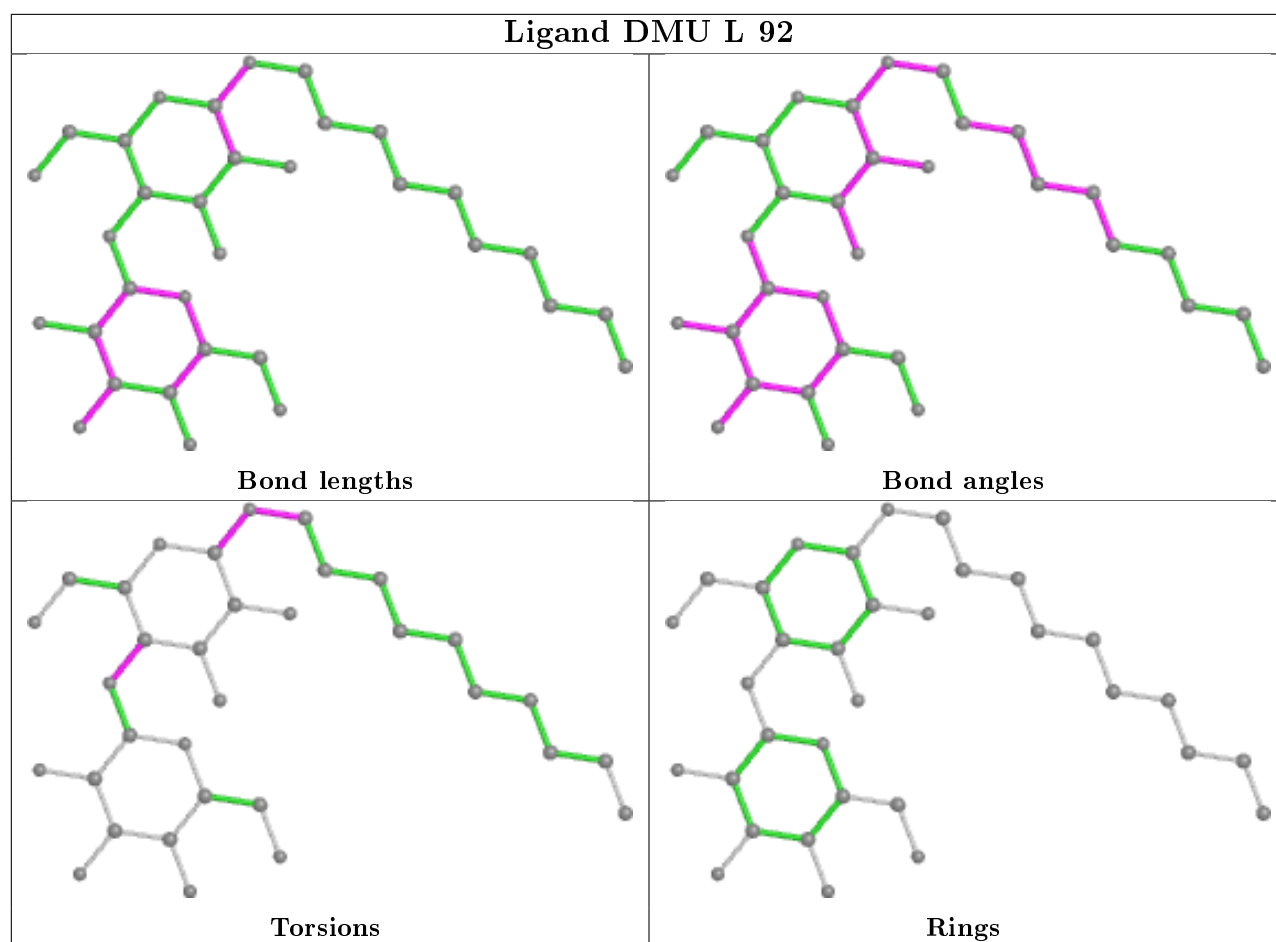


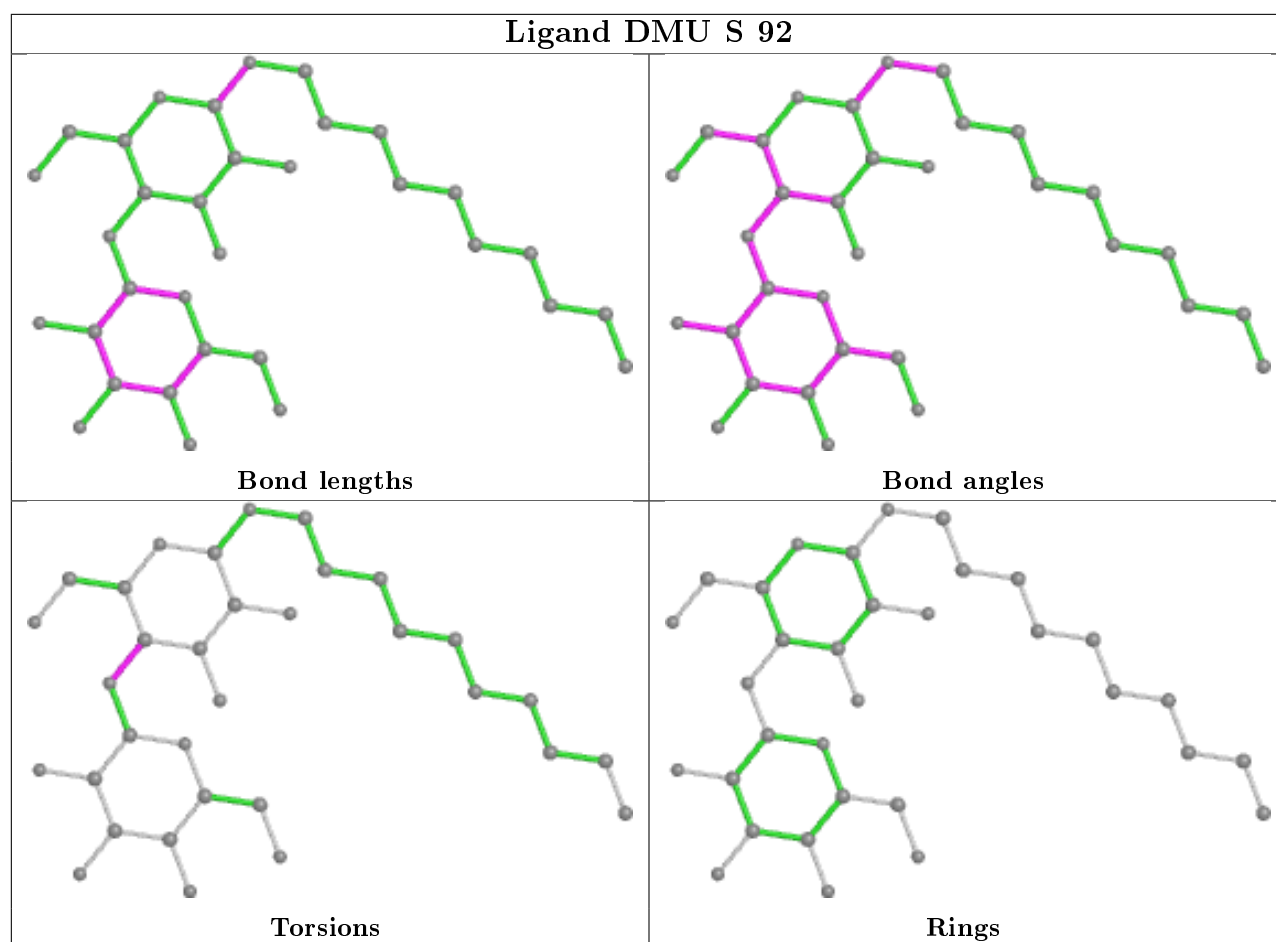


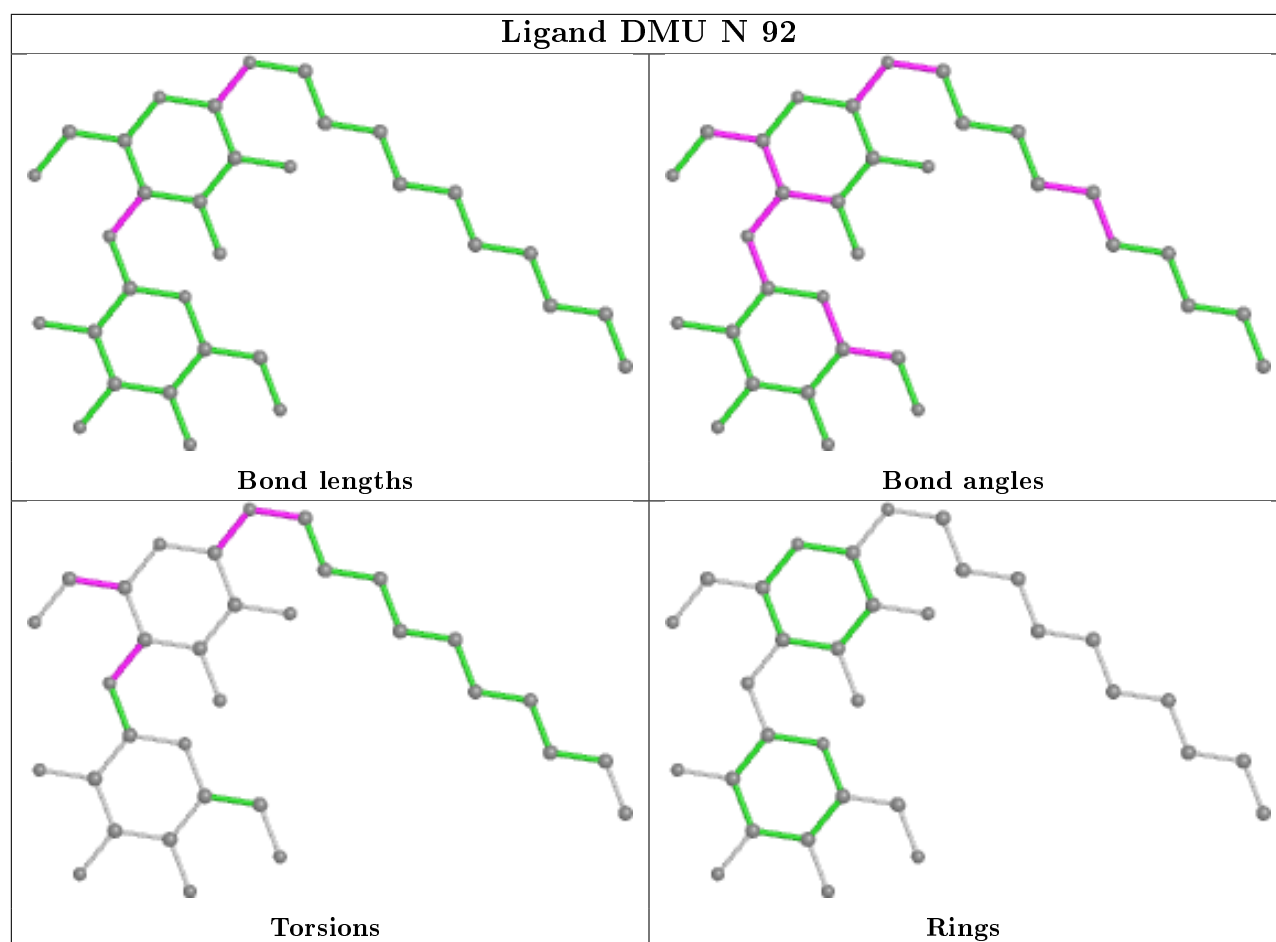


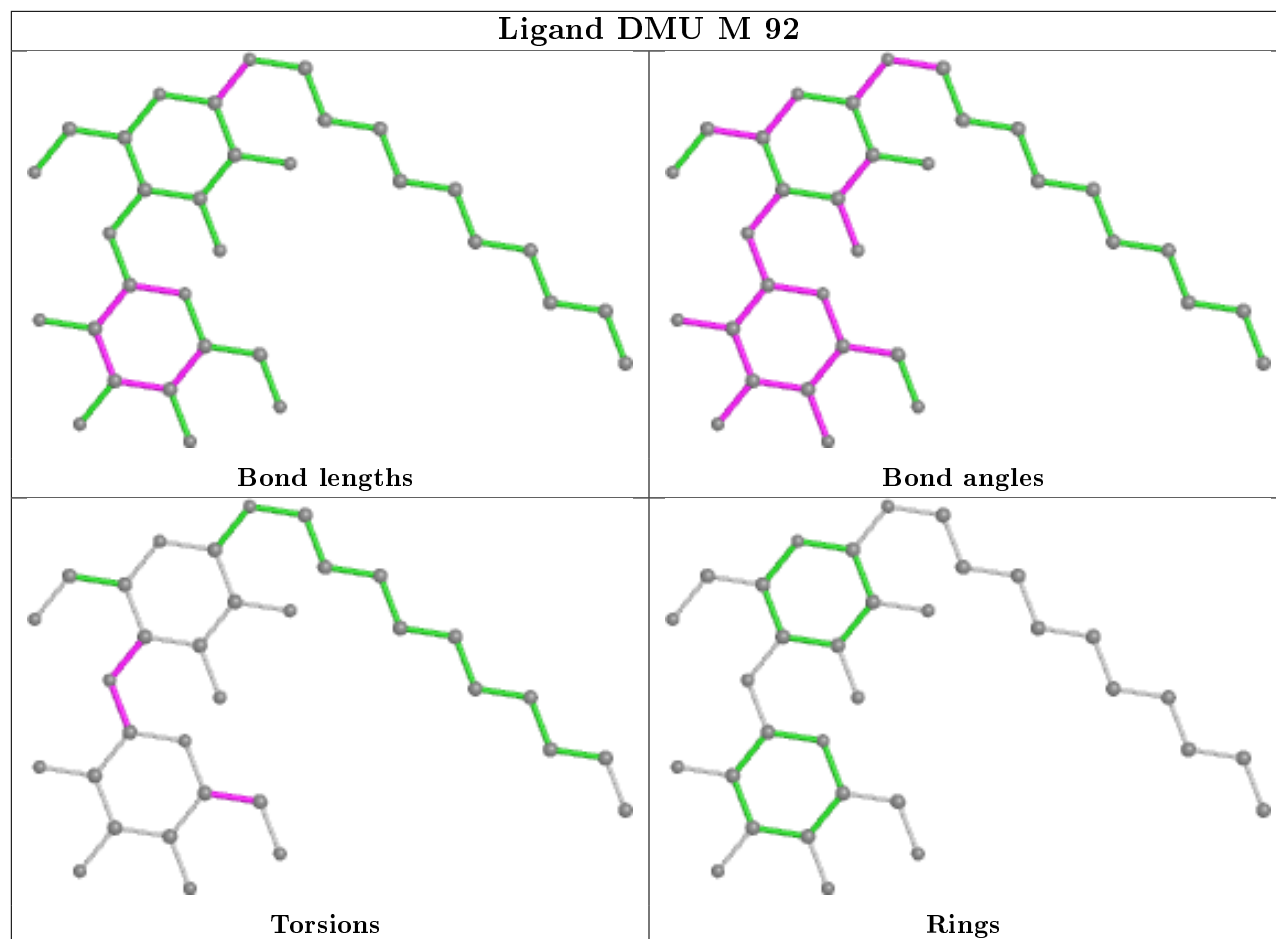


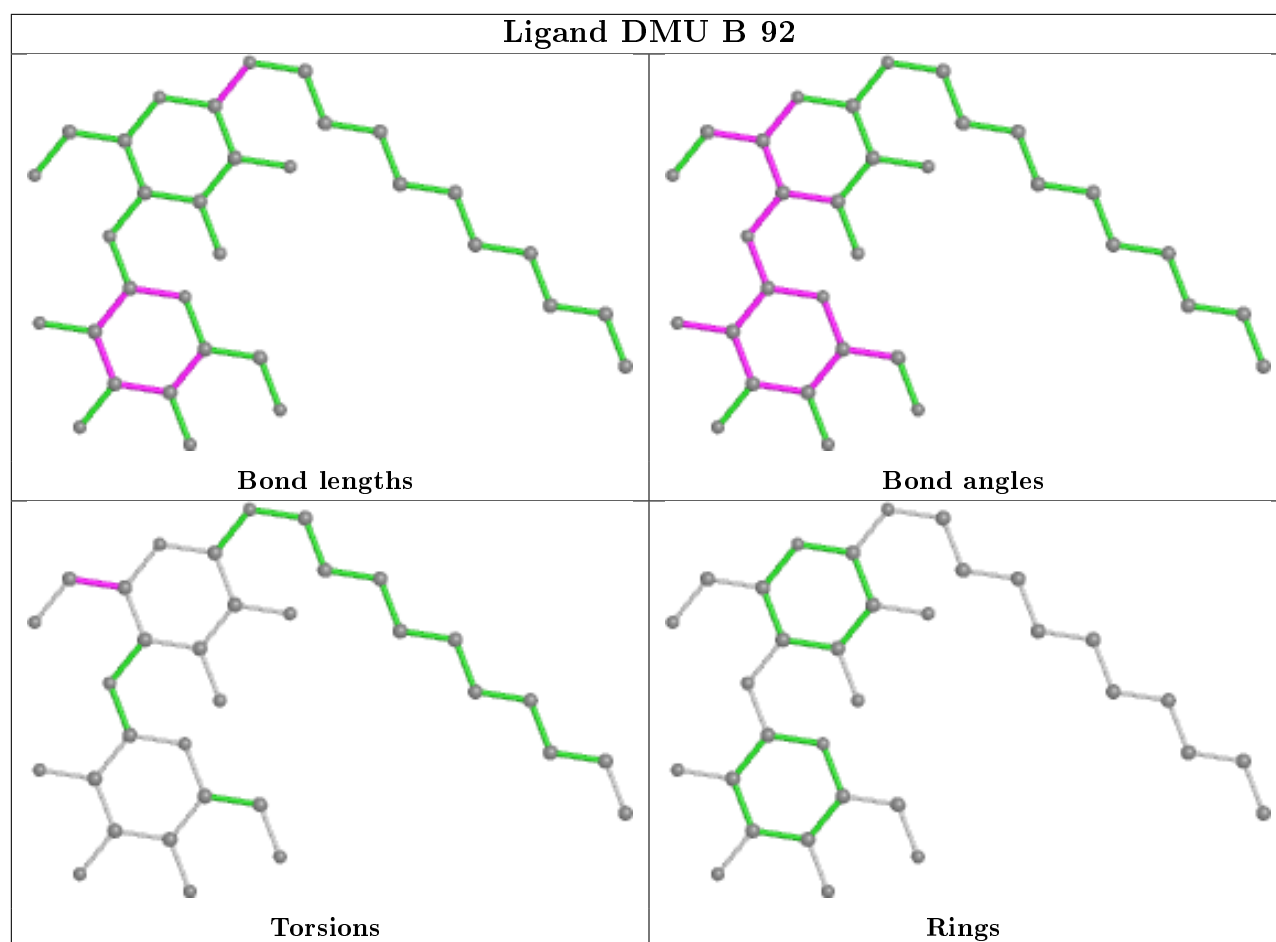


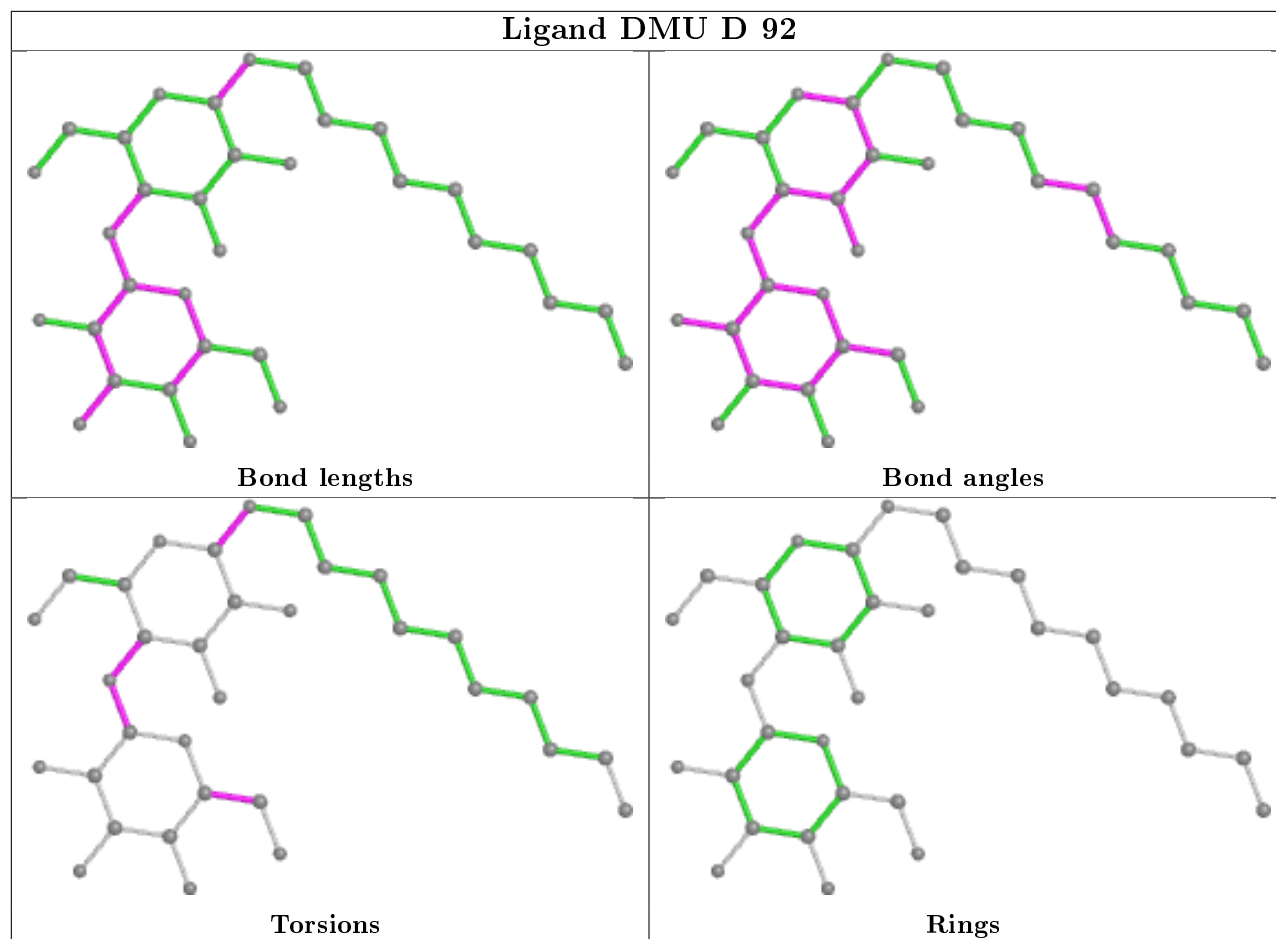


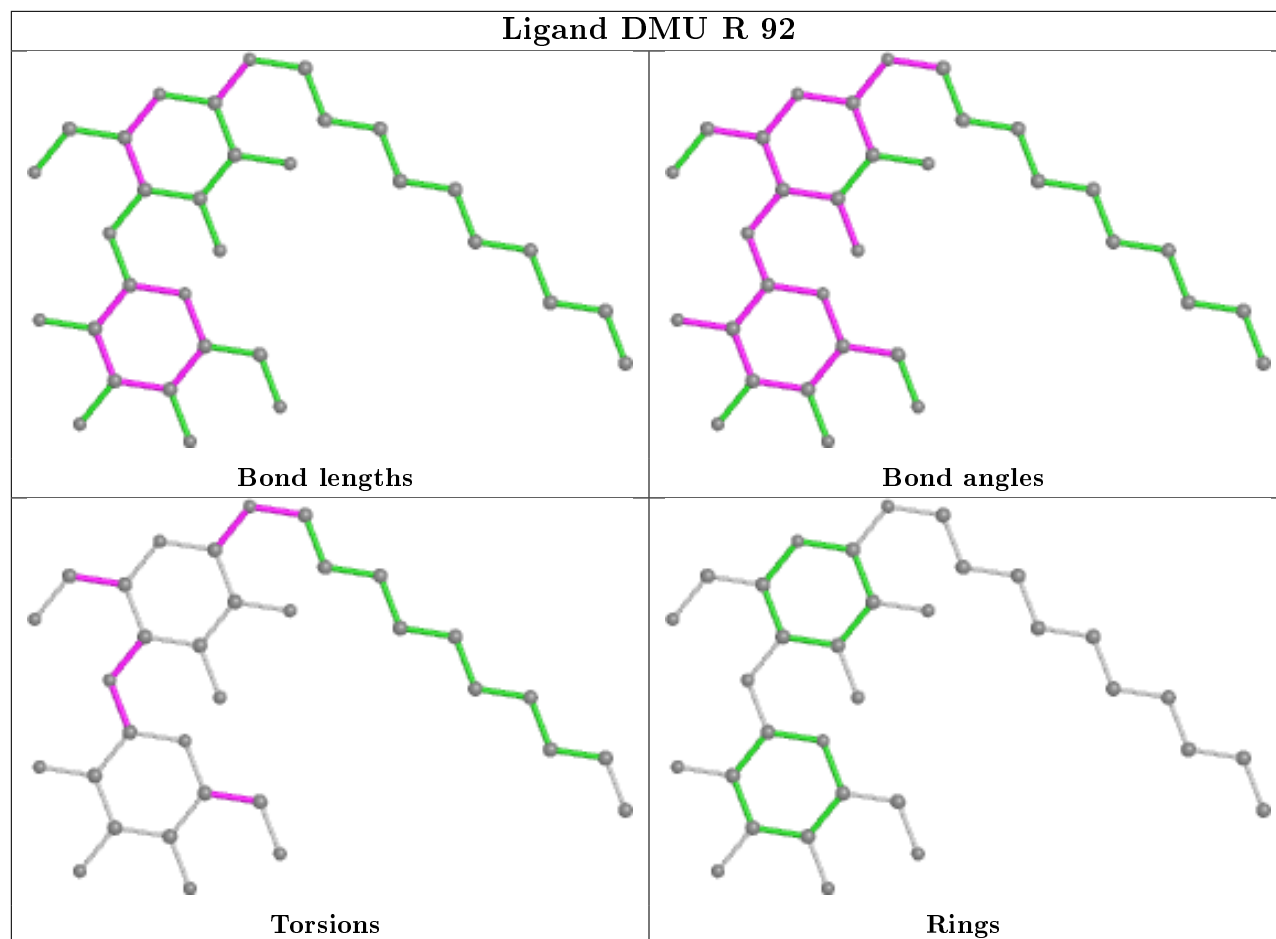




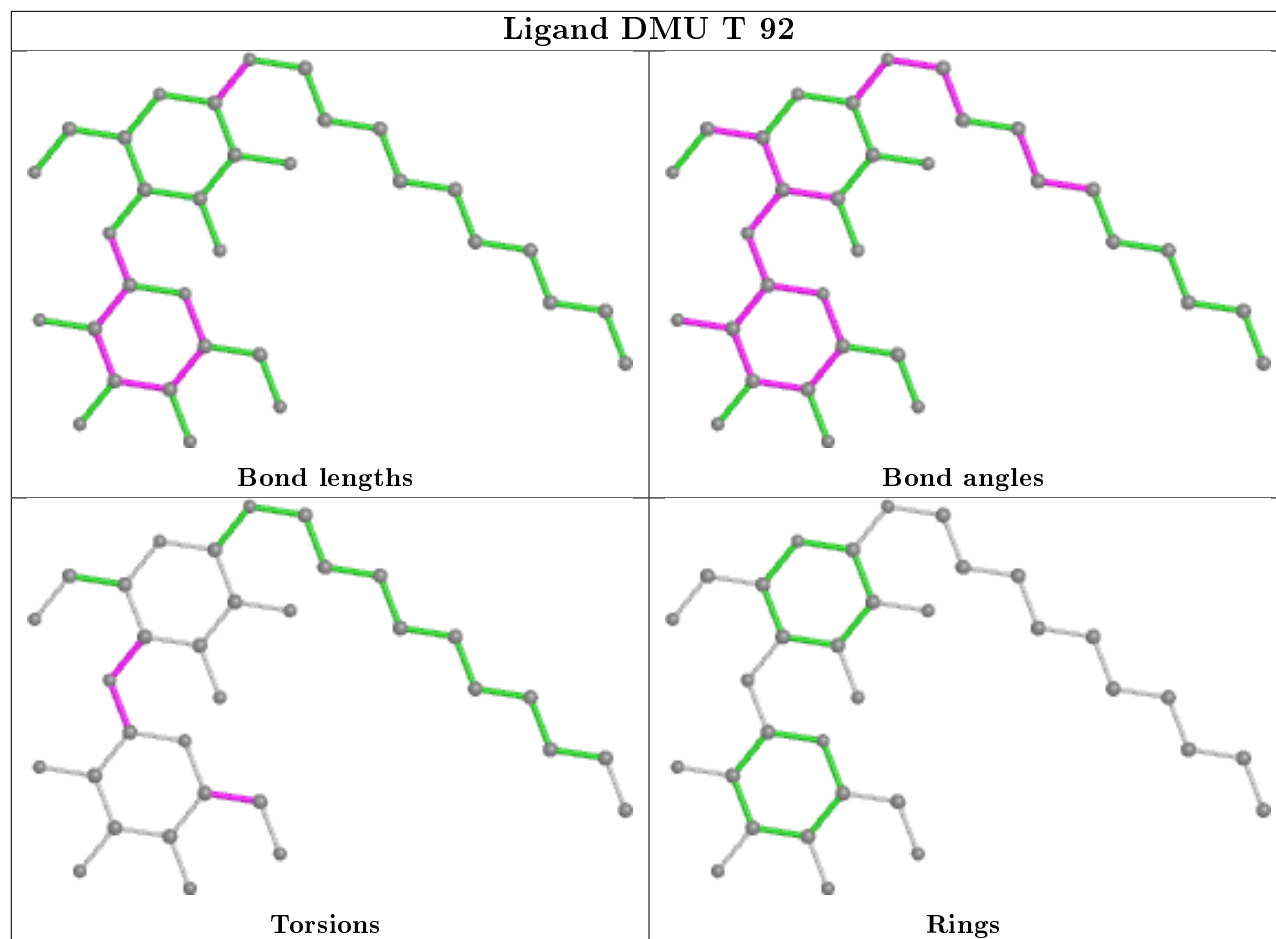




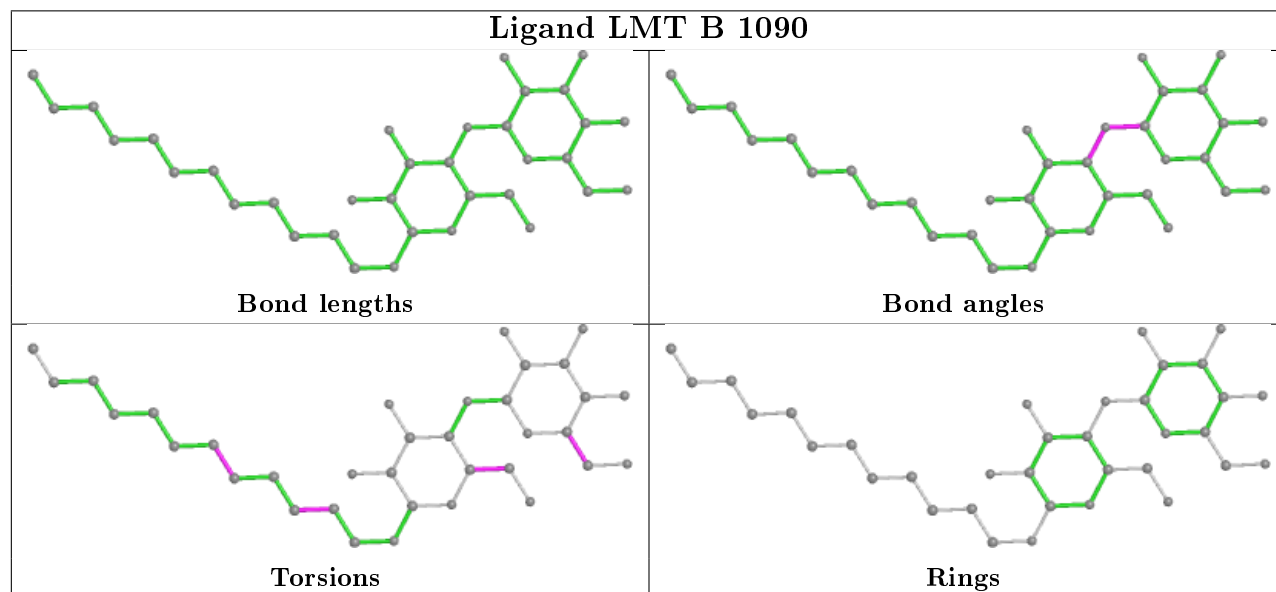




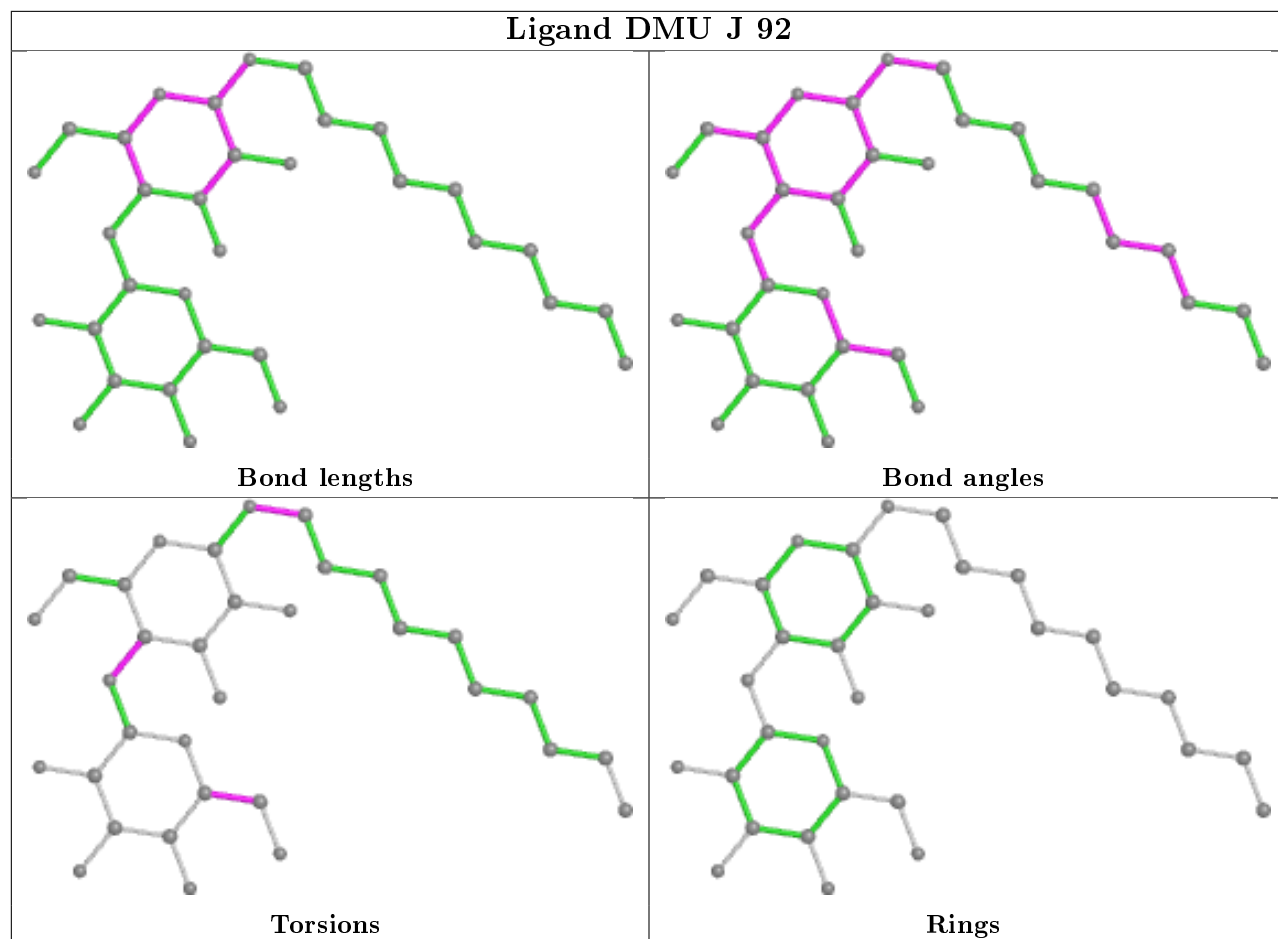
Ligand DMU T 92

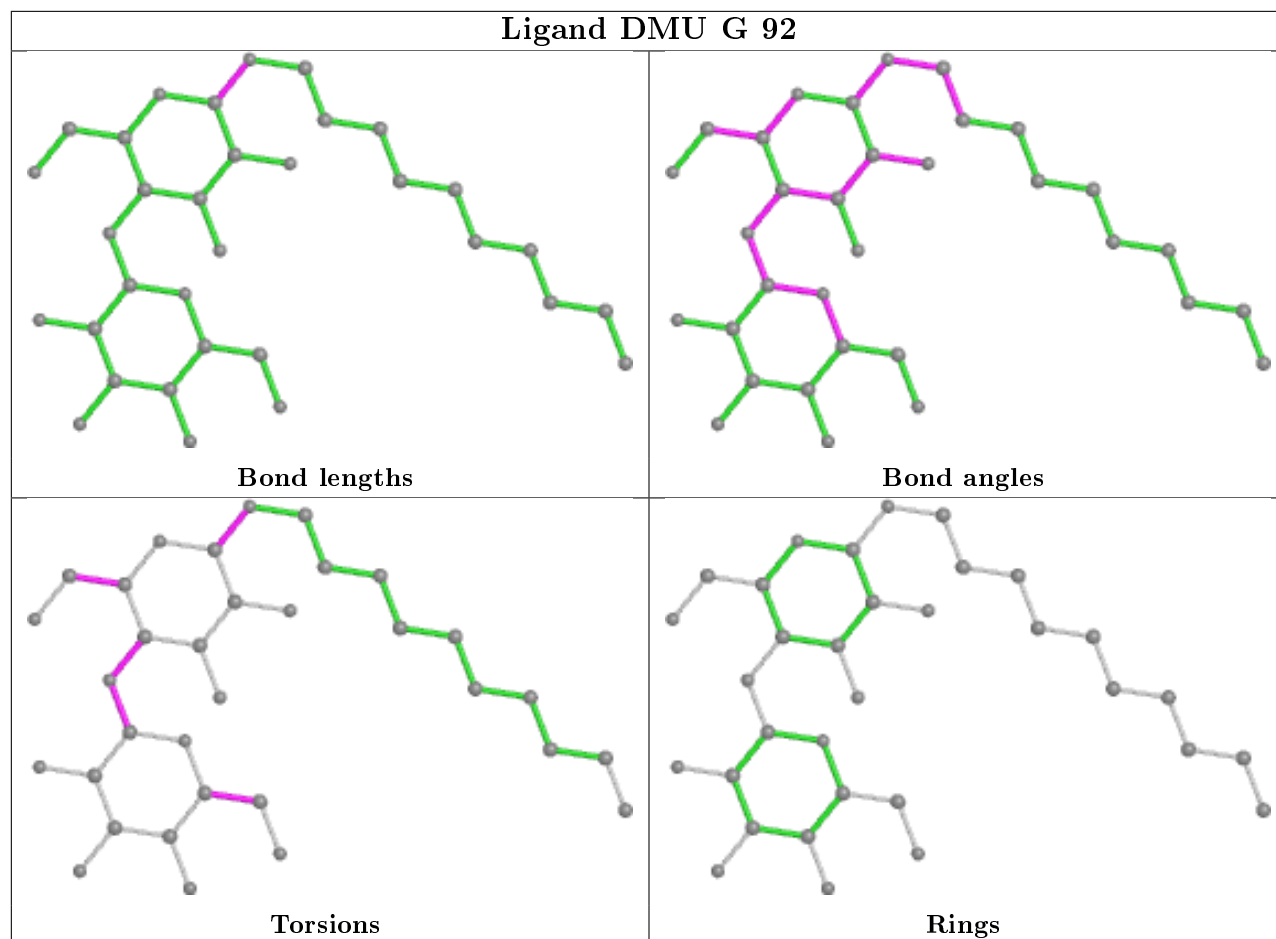


Ligand LMT B 1090

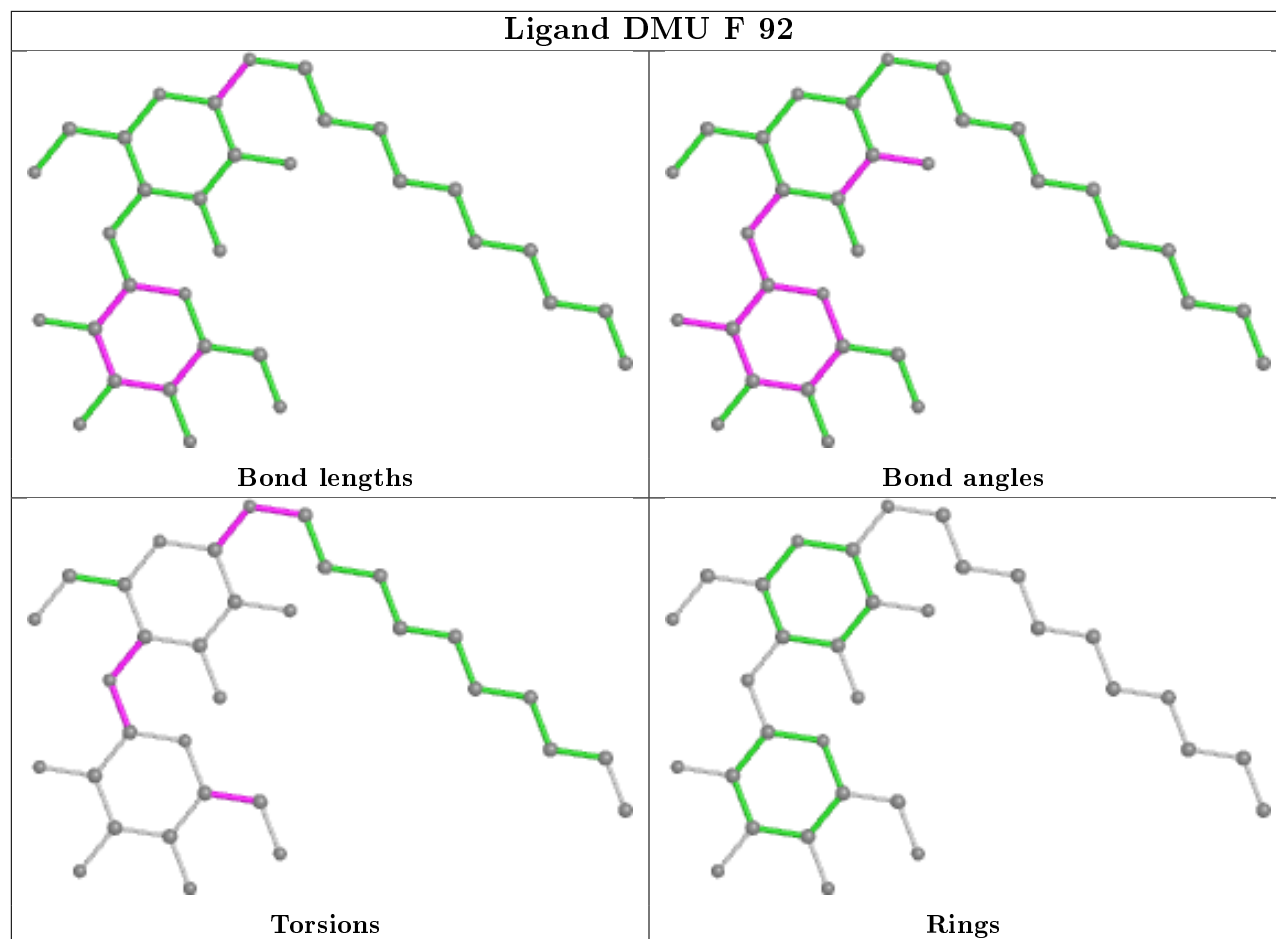


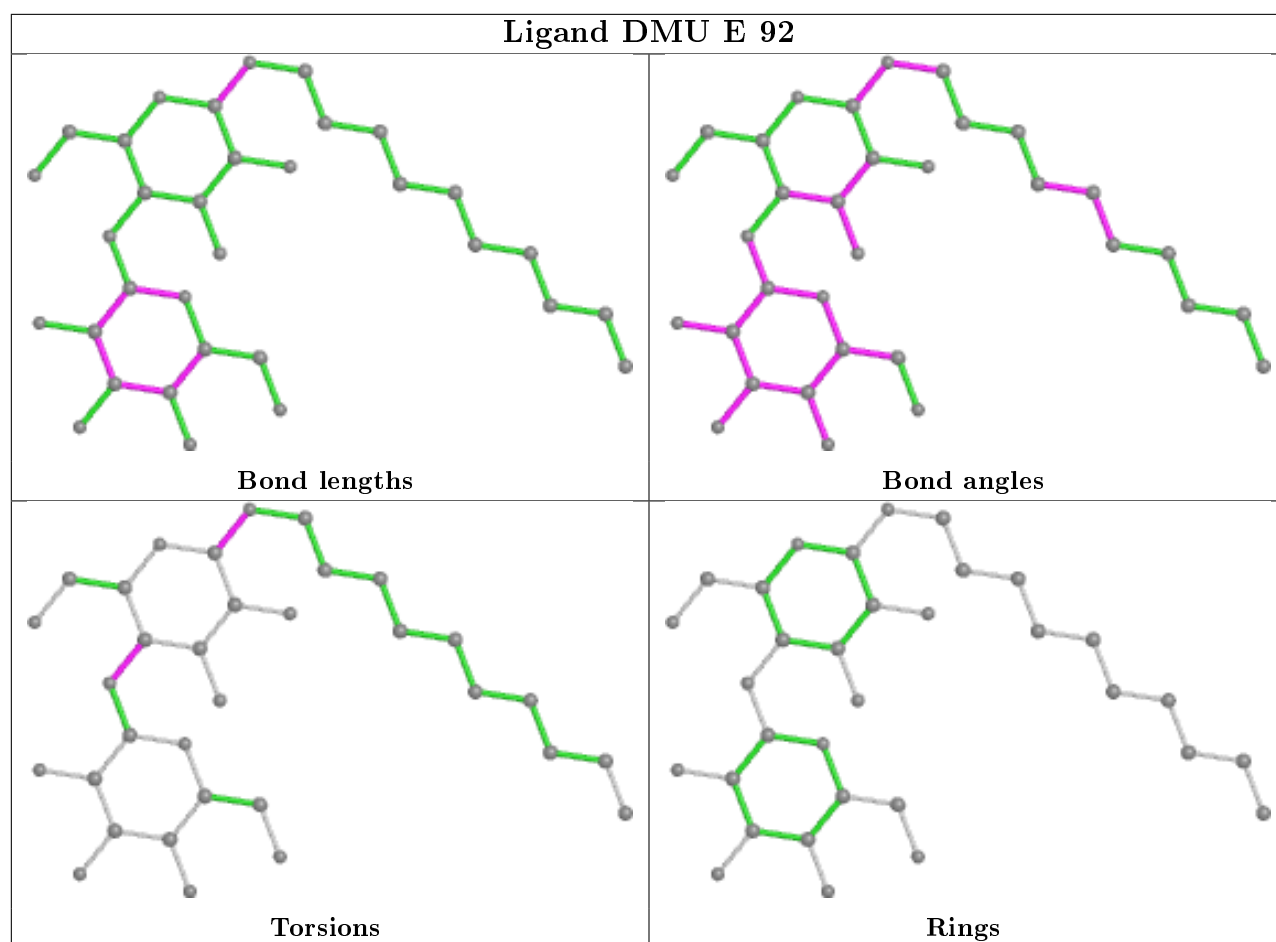
Ligand DMU J 92

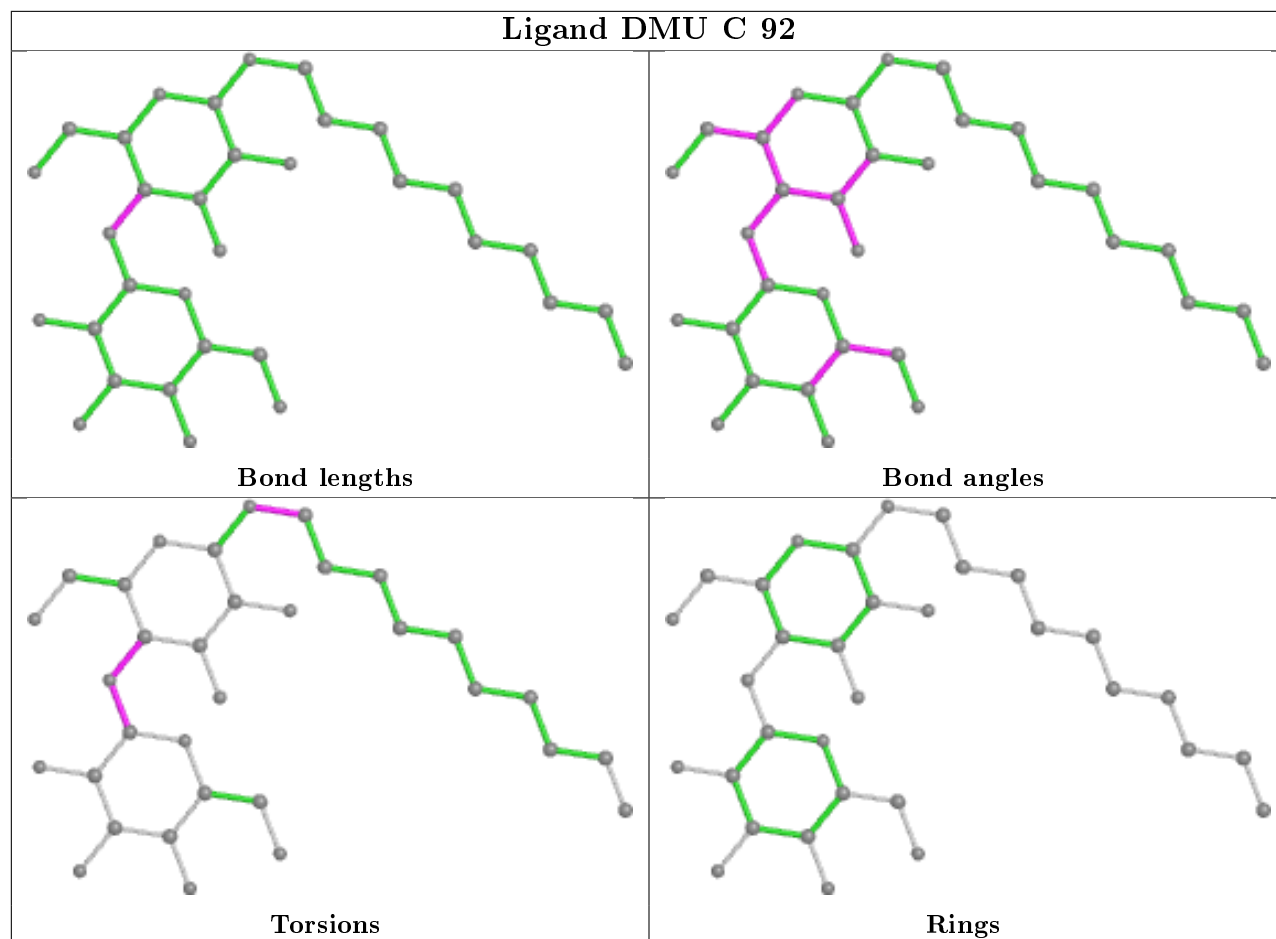




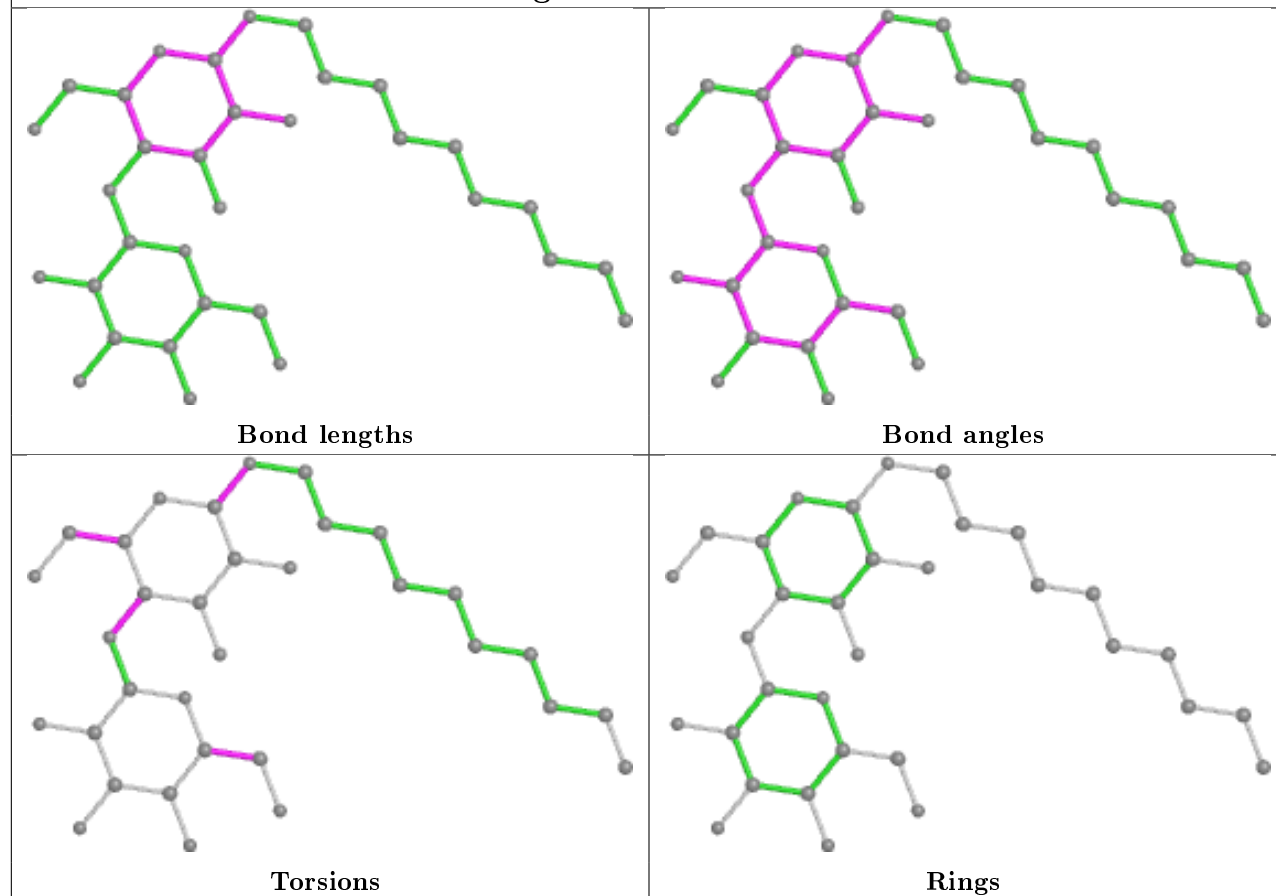
Ligand DMU F 92



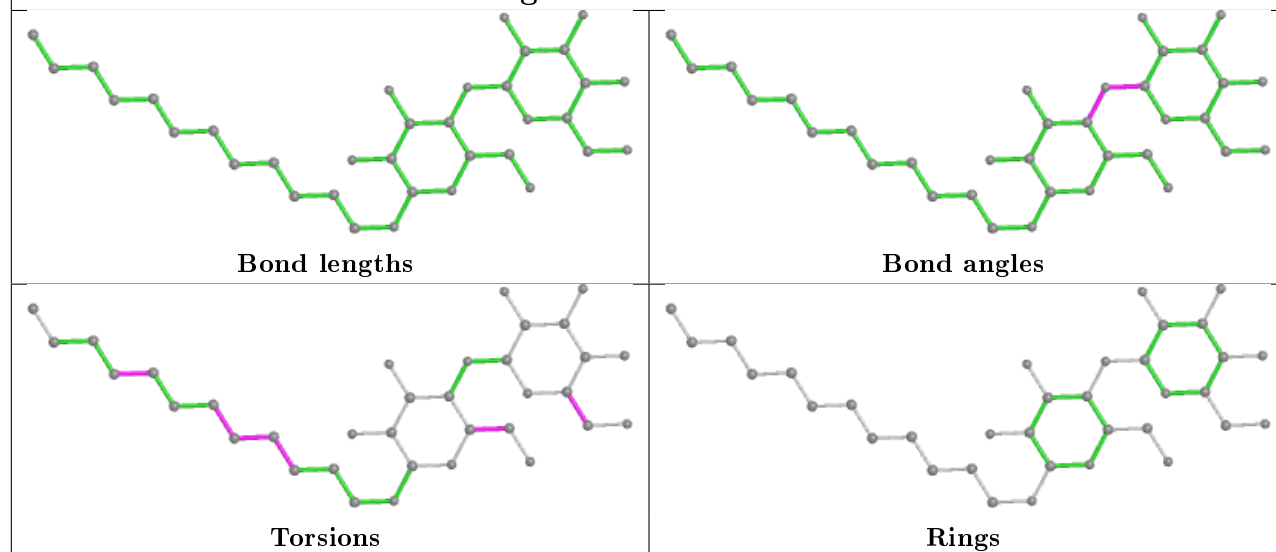


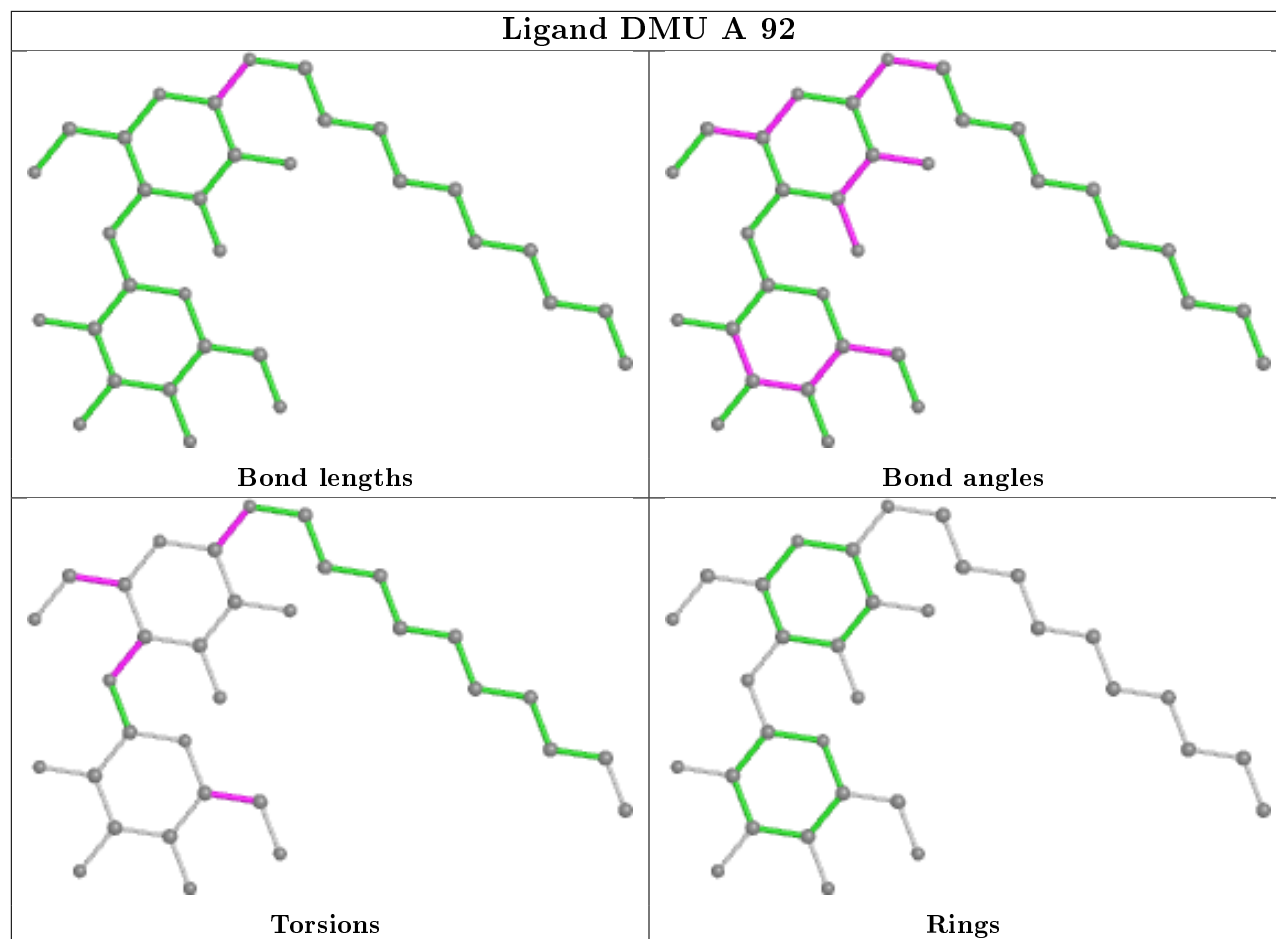


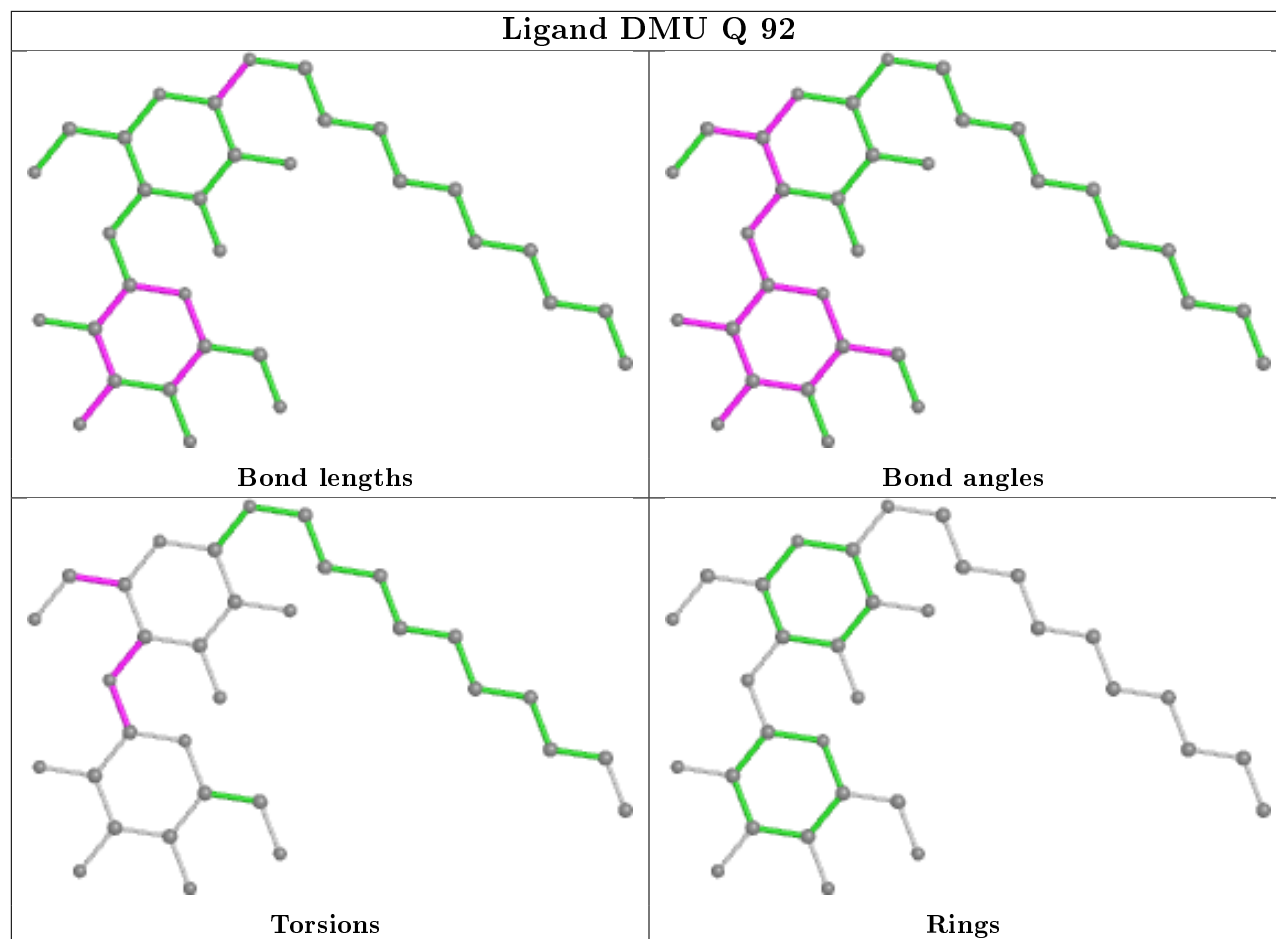
Ligand DMU V 92

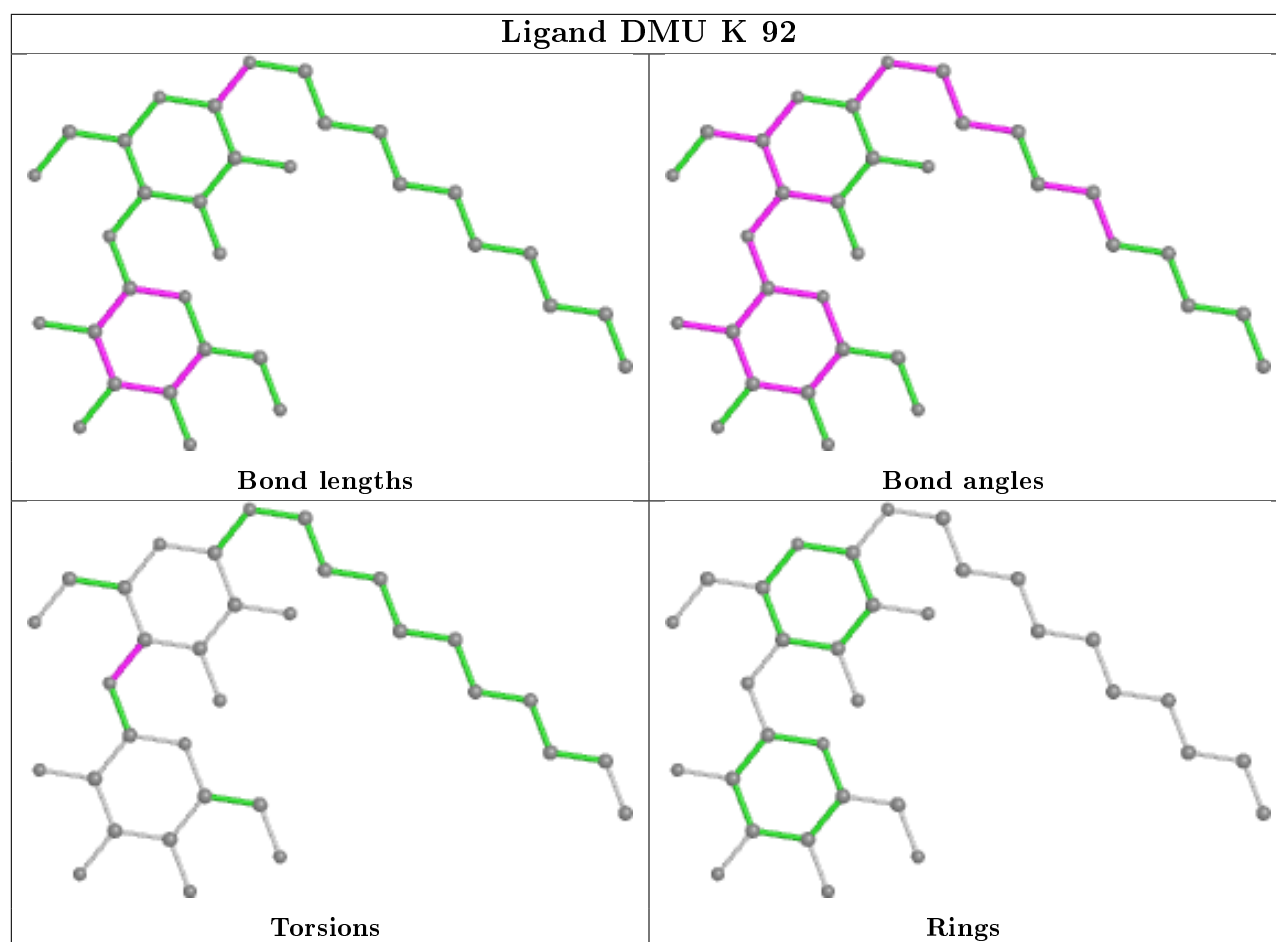


Ligand LMT C 1090









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, 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	89/89 (100%)	-0.39	0 100 100	18, 29, 54, 73	0
1	B	89/89 (100%)	-0.42	2 (2%) 62 59	18, 31, 55, 79	0
1	C	89/89 (100%)	-0.46	2 (2%) 62 59	20, 31, 57, 73	0
1	D	89/89 (100%)	-0.25	4 (4%) 33 32	19, 32, 60, 76	0
1	E	89/89 (100%)	-0.45	1 (1%) 80 79	20, 31, 66, 78	0
1	F	89/89 (100%)	-0.32	3 (3%) 45 43	19, 30, 52, 85	0
1	G	89/89 (100%)	-0.37	0 100 100	19, 29, 55, 64	0
1	H	89/89 (100%)	-0.40	2 (2%) 62 59	18, 28, 60, 79	0
1	I	89/89 (100%)	-0.48	2 (2%) 62 59	15, 28, 61, 80	0
1	J	89/89 (100%)	-0.49	1 (1%) 80 79	18, 27, 49, 83	0
1	K	89/89 (100%)	-0.43	3 (3%) 45 43	18, 27, 57, 80	0
1	L	89/89 (100%)	-0.10	6 (6%) 17 16	25, 40, 80, 100	0
1	M	89/89 (100%)	-0.24	4 (4%) 33 32	22, 36, 76, 87	0
1	N	89/89 (100%)	-0.34	3 (3%) 45 43	20, 31, 66, 83	0
1	O	89/89 (100%)	-0.48	1 (1%) 80 79	21, 31, 55, 79	0
1	P	89/89 (100%)	-0.46	0 100 100	21, 31, 54, 69	0
1	Q	89/89 (100%)	-0.25	1 (1%) 80 79	22, 34, 68, 86	0
1	R	89/89 (100%)	-0.15	3 (3%) 45 43	25, 40, 70, 87	0
1	S	89/89 (100%)	-0.12	4 (4%) 33 32	25, 41, 74, 85	0
1	T	89/89 (100%)	-0.06	2 (2%) 62 59	27, 42, 74, 96	0
1	U	89/89 (100%)	-0.17	0 100 100	29, 44, 87, 96	0
1	V	89/89 (100%)	-0.11	3 (3%) 45 43	26, 44, 79, 95	0
All	All	1958/1958 (100%)	-0.32	47 (2%) 59 56	15, 34, 68, 100	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	89	GLY	7.7
1	S	48	GLU	7.2
1	S	89	GLY	7.1
1	E	89	GLY	6.3
1	R	89	GLY	6.3
1	F	89	GLY	5.7
1	L	48	GLU	5.4
1	K	89	GLY	4.6
1	S	49	ALA	4.1
1	B	89	GLY	3.8
1	N	48	GLU	3.4
1	L	49	ALA	3.1
1	L	54	ILE	3.0
1	D	48	GLU	3.0
1	L	51	GLY	2.9
1	I	89	GLY	2.8
1	R	48	GLU	2.8
1	C	47	PRO	2.8
1	V	81	ALA	2.7
1	L	47	PRO	2.6
1	R	86	SER	2.6
1	O	89	GLY	2.6
1	J	89	GLY	2.6
1	N	89	GLY	2.5
1	S	47	PRO	2.4
1	V	52	SER	2.4
1	M	89	GLY	2.4
1	T	47	PRO	2.3
1	D	46	GLN	2.3
1	H	48	GLU	2.3
1	B	1	MET	2.3
1	H	52	SER	2.3
1	M	47	PRO	2.3
1	K	46	GLN	2.2
1	L	50	ARG	2.2
1	T	52	SER	2.2
1	M	52	SER	2.1
1	C	48	GLU	2.1
1	D	89	GLY	2.1
1	M	48	GLU	2.1
1	I	46	GLN	2.1
1	F	50	ARG	2.1
1	V	49	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	51	GLY	2.1
1	K	48	GLU	2.0
1	D	50	ARG	2.0
1	N	47	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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(\AA^2)	Q<0.9
3	DMU	I	92	33/33	0.16	0.52	73,101,128,153	0
3	DMU	M	92	33/33	0.16	0.48	63,122,141,151	0
3	DMU	E	92	33/33	0.22	0.60	82,118,160,164	0
3	DMU	S	92	33/33	0.25	0.50	81,128,141,160	0
3	DMU	O	92	33/33	0.29	0.62	89,119,161,161	0
3	DMU	R	92	33/33	0.33	0.36	80,143,153,156	0
3	DMU	J	92	33/33	0.34	0.54	65,111,146,147	0
3	DMU	F	92	33/33	0.34	0.46	78,126,145,145	0
3	DMU	L	92	33/33	0.37	0.40	71,125,139,139	0
3	DMU	K	92	33/33	0.37	0.46	63,123,158,158	0
3	DMU	P	92	33/33	0.38	0.42	69,136,149,150	0
3	DMU	G	92	33/33	0.40	0.40	69,116,127,128	0
5	TAM	M	1090	11/11	0.42	0.35	85,88,90,90	0
3	DMU	D	92	33/33	0.42	0.63	70,110,141,142	0
3	DMU	V	92	33/33	0.45	0.39	81,150,167,173	0
3	DMU	T	92	33/33	0.46	0.52	76,113,128,136	0
3	DMU	U	92	33/33	0.48	0.70	63,121,151,152	0
3	DMU	H	92	33/33	0.51	0.39	53,113,126,128	0
3	DMU	Q	92	33/33	0.51	0.34	81,120,157,157	0

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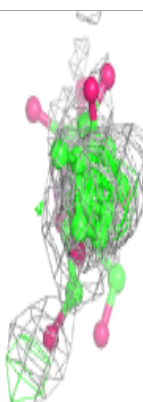
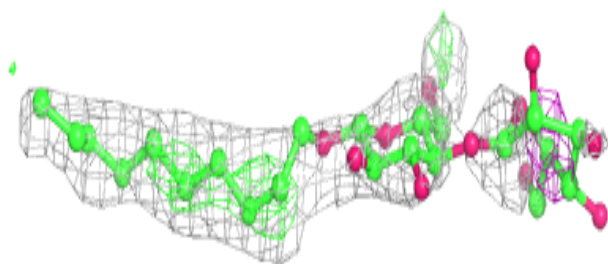
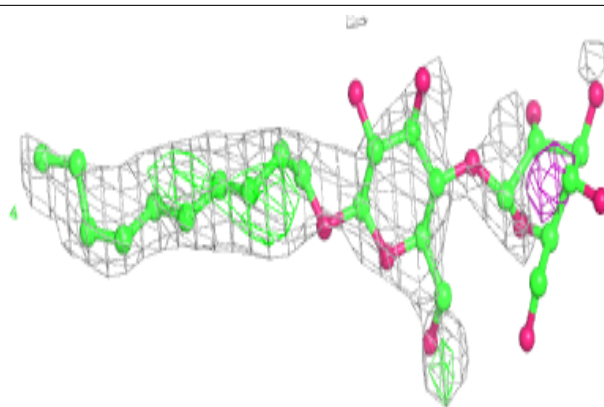
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	DMU	B	92	33/33	0.51	0.43	64,120,157,158	0
3	DMU	N	92	33/33	0.51	0.41	64,101,118,119	0
4	LMT	C	1090	35/35	0.54	0.35	85,116,131,131	0
3	DMU	C	92	33/33	0.56	0.44	61,94,112,112	0
3	DMU	A	92	33/33	0.61	0.31	64,118,146,148	0
4	LMT	C	1091	35/35	0.67	0.57	106,124,126,126	0
4	LMT	B	1090	35/35	0.67	0.42	89,99,116,116	0
5	TAM	R	1090	11/11	0.70	0.27	87,92,92,93	0
2	NA	F	90	1/1	0.92	0.06	32,32,32,32	0
2	NA	G	90	1/1	0.93	0.11	36,36,36,36	0
2	NA	V	90	1/1	0.95	0.13	53,53,53,53	0
2	NA	E	90	1/1	0.95	0.11	31,31,31,31	0
2	NA	T	90	1/1	0.96	0.09	43,43,43,43	0
2	NA	C	90	1/1	0.96	0.06	26,26,26,26	0
2	NA	J	90	1/1	0.96	0.11	26,26,26,26	0
2	NA	M	90	1/1	0.96	0.05	40,40,40,40	0
2	NA	D	90	1/1	0.97	0.06	32,32,32,32	0
2	NA	L	90	1/1	0.97	0.05	39,39,39,39	0
2	NA	P	90	1/1	0.97	0.04	30,30,30,30	0
2	NA	S	90	1/1	0.97	0.09	48,48,48,48	0
2	NA	R	90	1/1	0.98	0.07	32,32,32,32	0
2	NA	Q	90	1/1	0.98	0.14	34,34,34,34	0
2	NA	H	90	1/1	0.98	0.07	31,31,31,31	0
2	NA	N	90	1/1	0.99	0.06	36,36,36,36	0
2	NA	K	90	1/1	0.99	0.05	29,29,29,29	0
2	NA	B	90	1/1	0.99	0.05	31,31,31,31	0
2	NA	O	90	1/1	0.99	0.06	26,26,26,26	0
2	NA	U	90	1/1	0.99	0.13	44,44,44,44	0
2	NA	A	90	1/1	0.99	0.06	29,29,29,29	0
2	NA	I	90	1/1	0.99	0.05	28,28,28,28	0

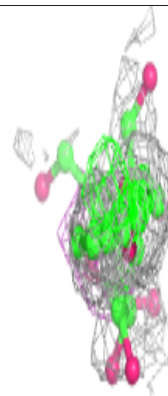
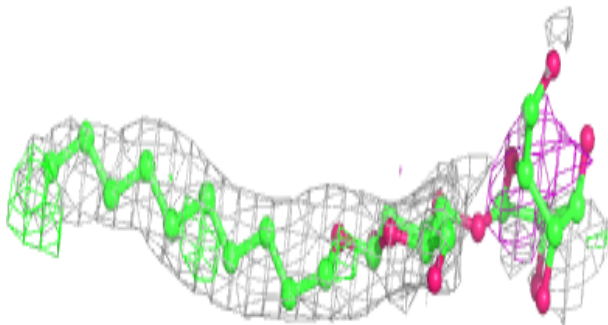
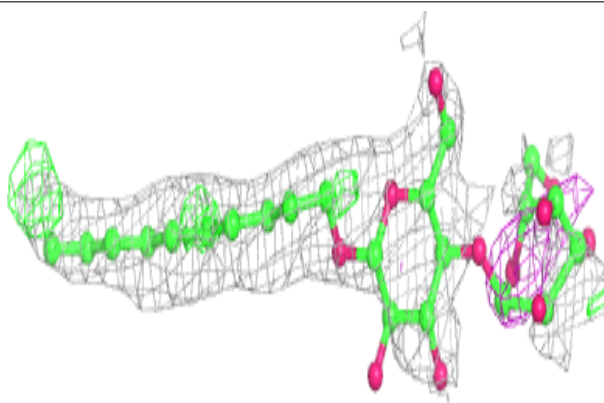
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DMU I 92:

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

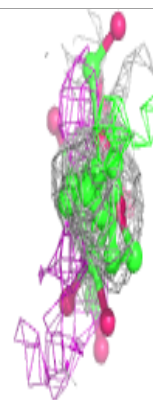
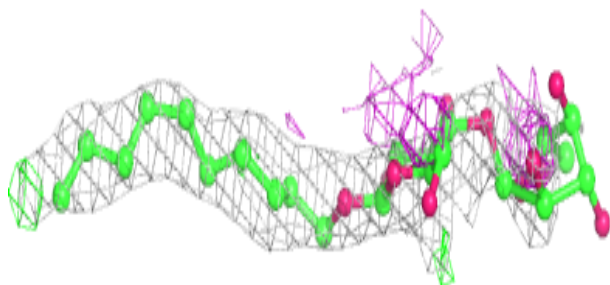
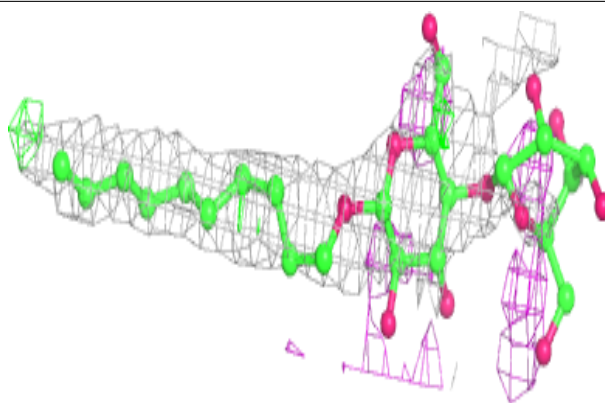
**Electron density around DMU M 92:**

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

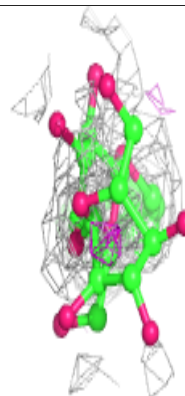
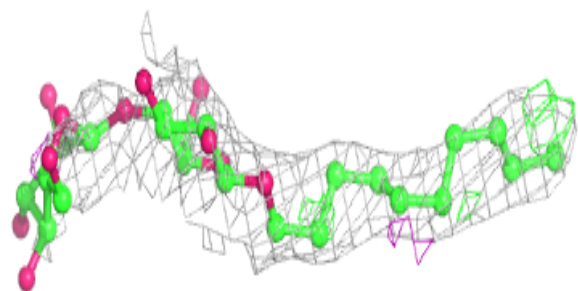
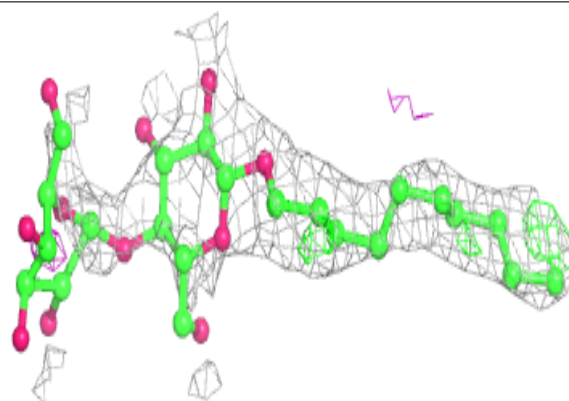


Electron density around DMU E 92:

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

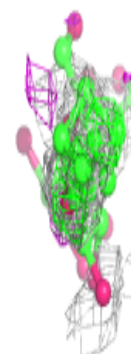
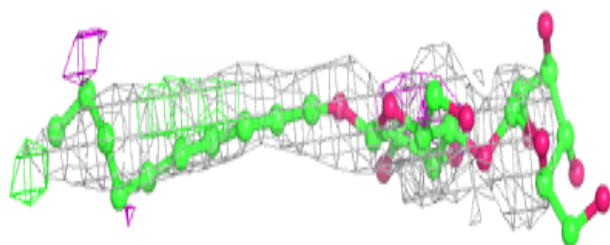
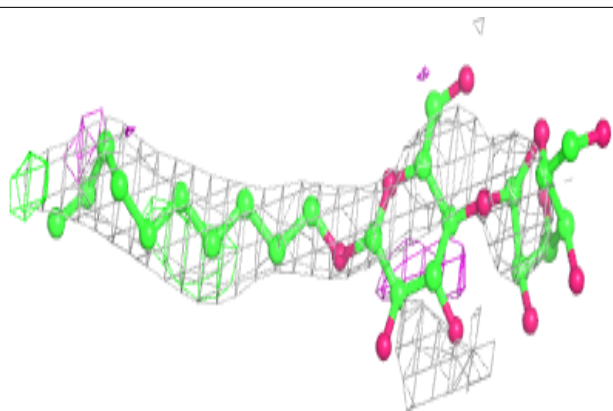
**Electron density around DMU S 92:**

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

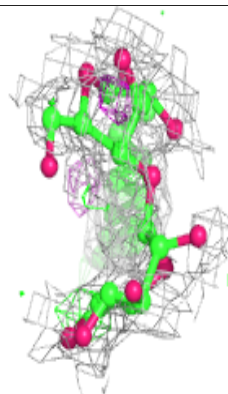
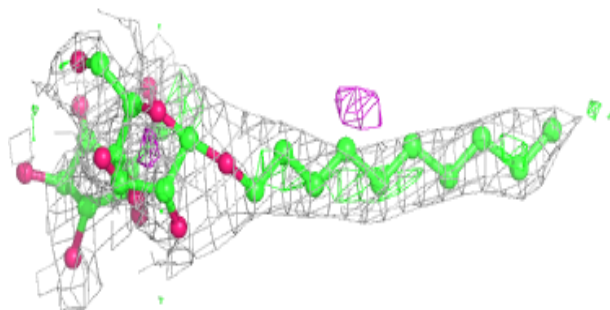
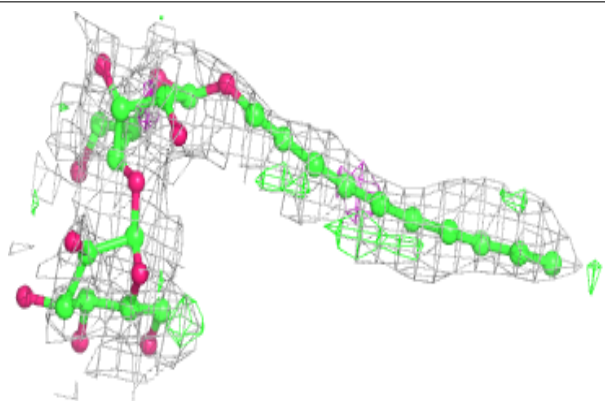


Electron density around DMU O 92:

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

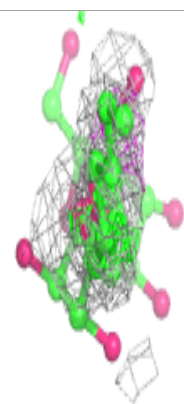
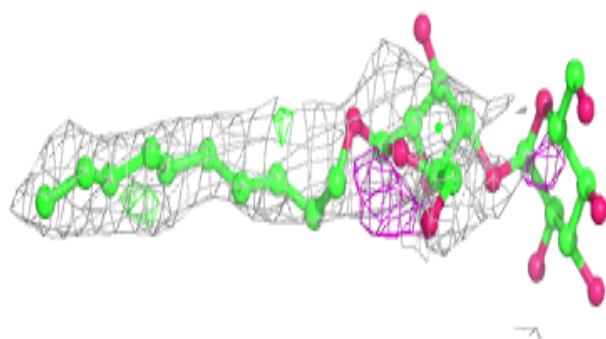
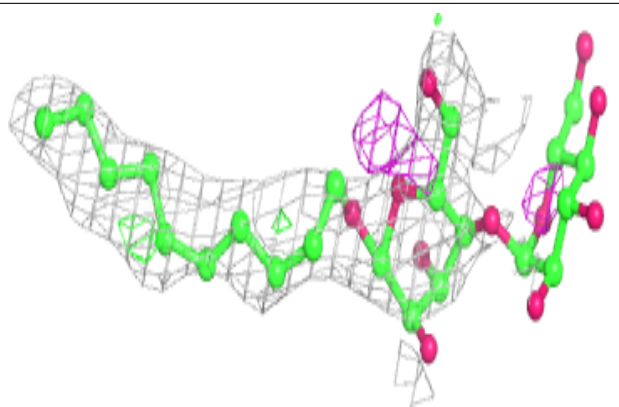
**Electron density around DMU R 92:**

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and green (positive)

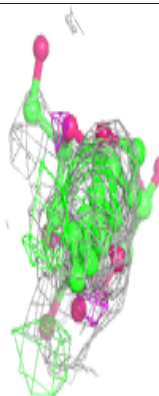
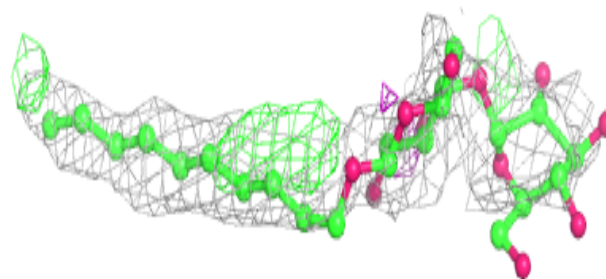
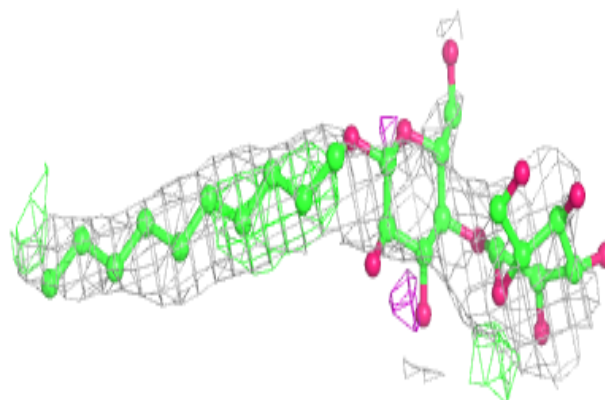


Electron density around DMU J 92:

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

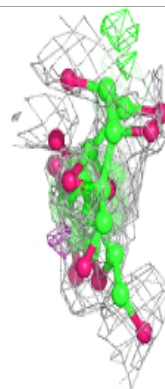
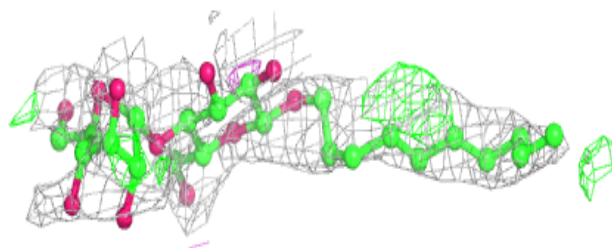
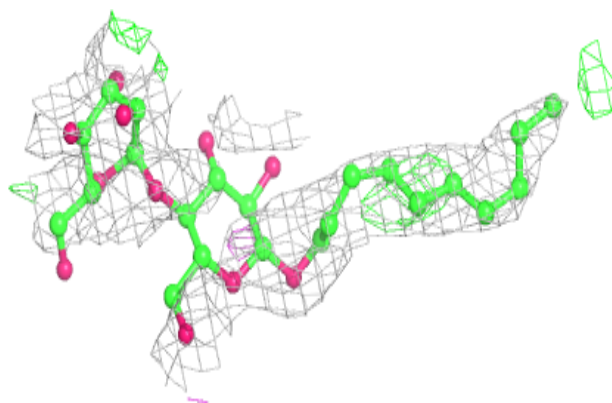
**Electron density around DMU F 92:**

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

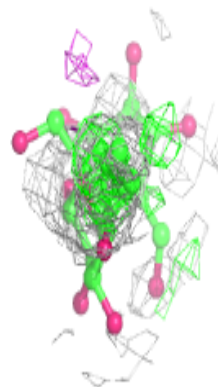
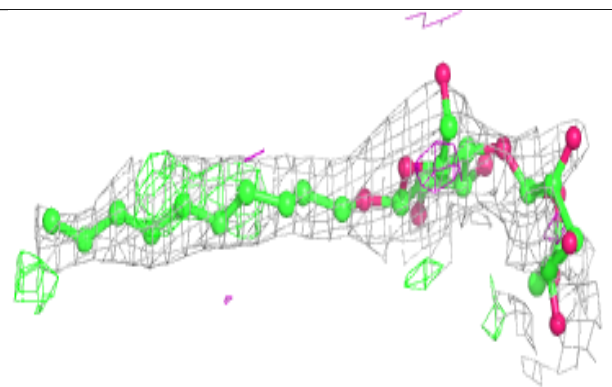
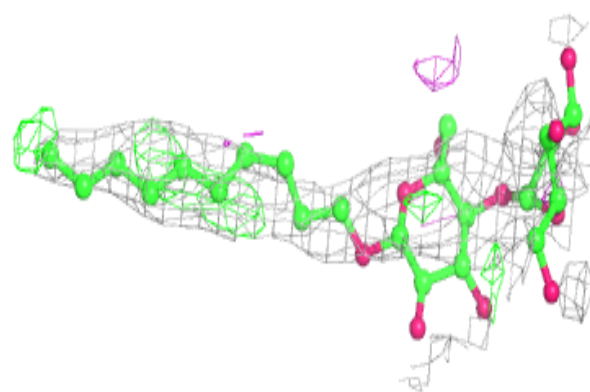


Electron density around DMU L 92:

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

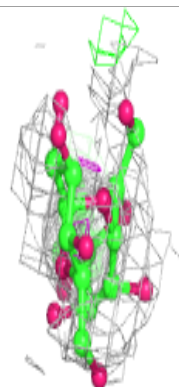
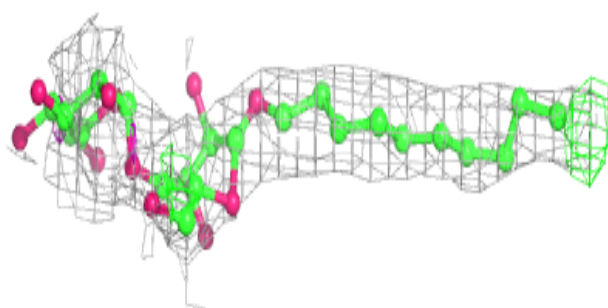
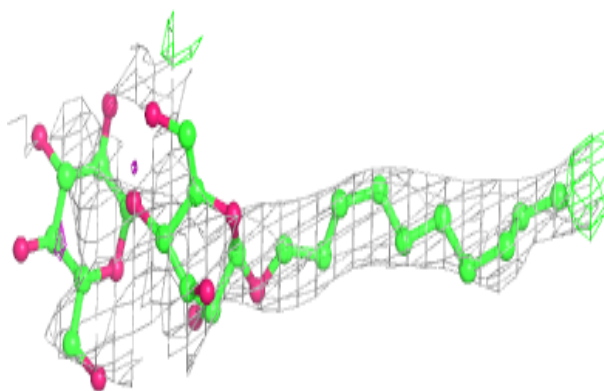
**Electron density around DMU K 92:**

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

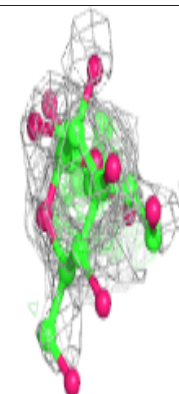
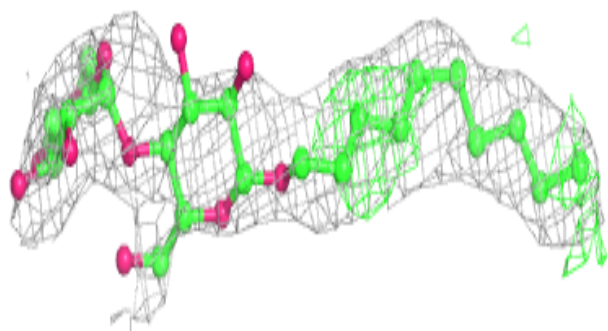
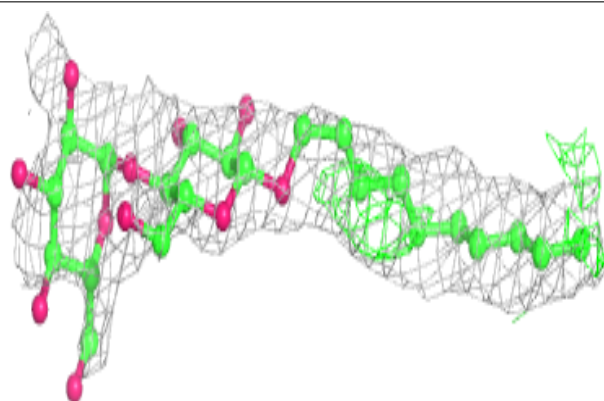


Electron density around DMU P 92:

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

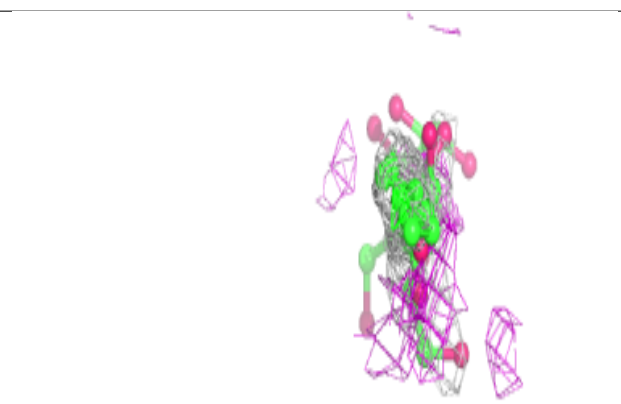
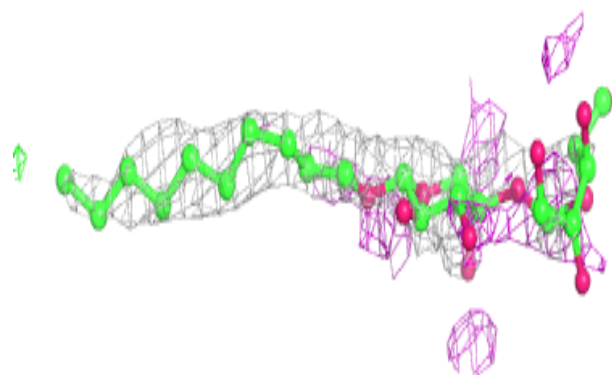
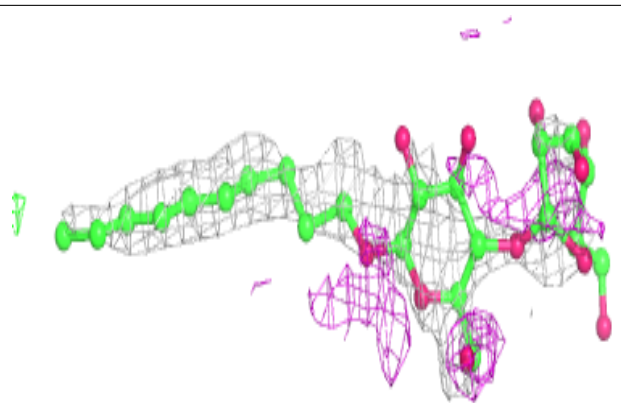
**Electron density around DMU G 92:**

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

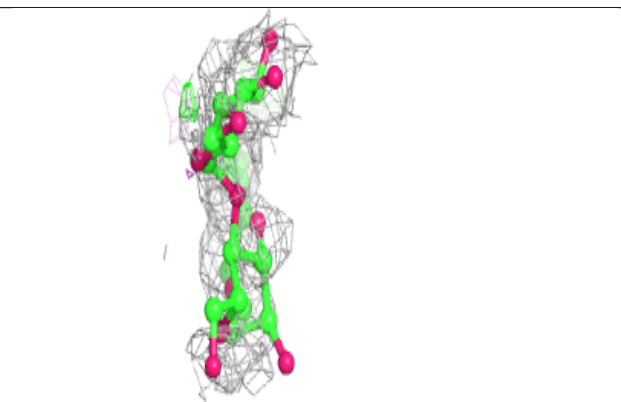
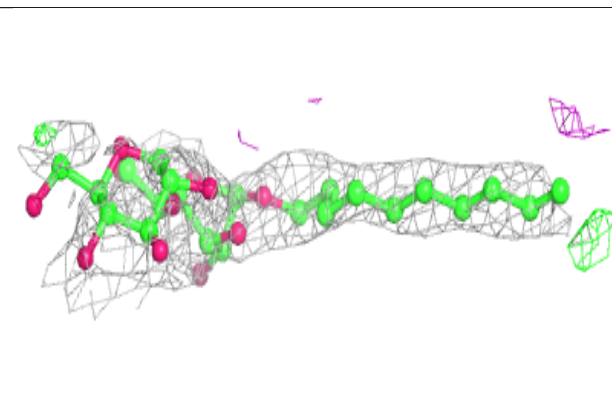
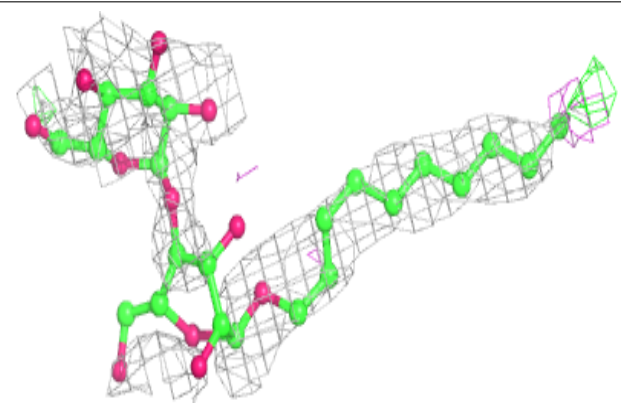


Electron density around DMU D 92:

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

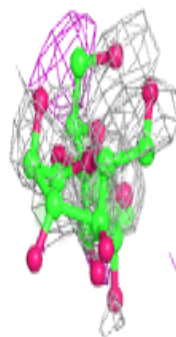
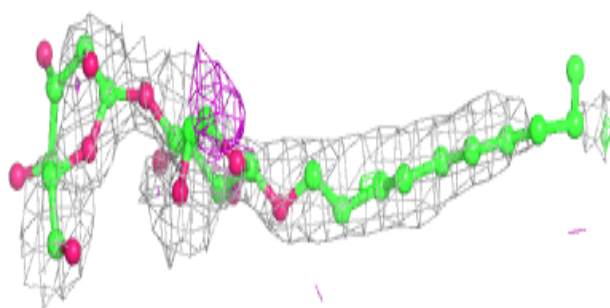
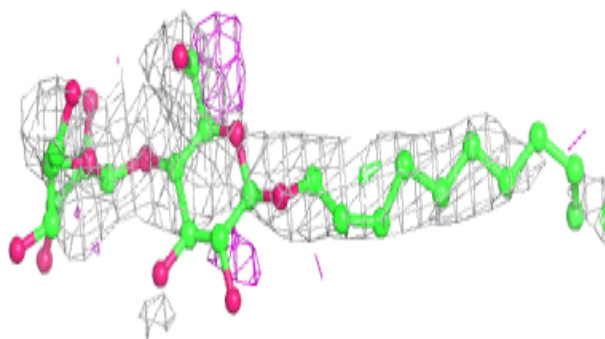
**Electron density around DMU V 92:**

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

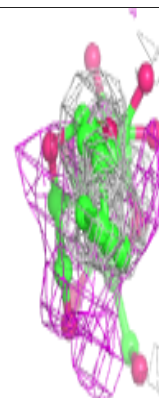
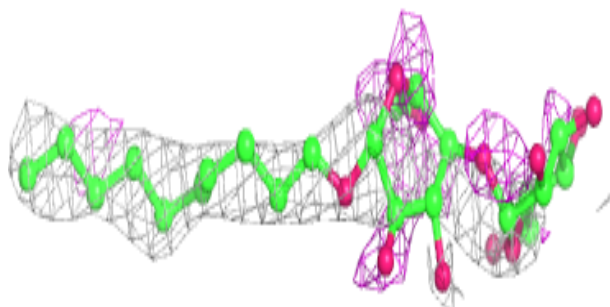
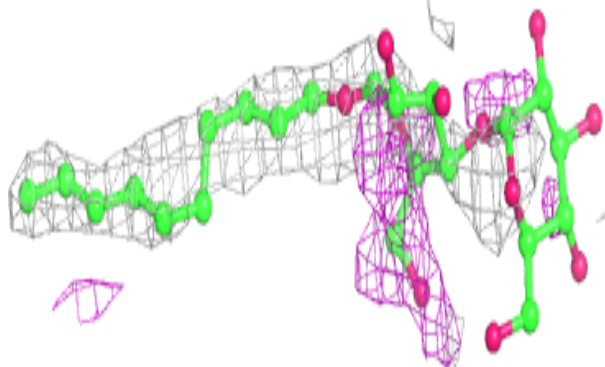


Electron density around DMU T 92:

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

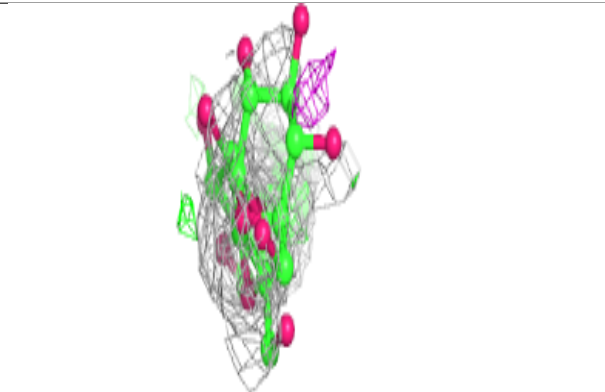
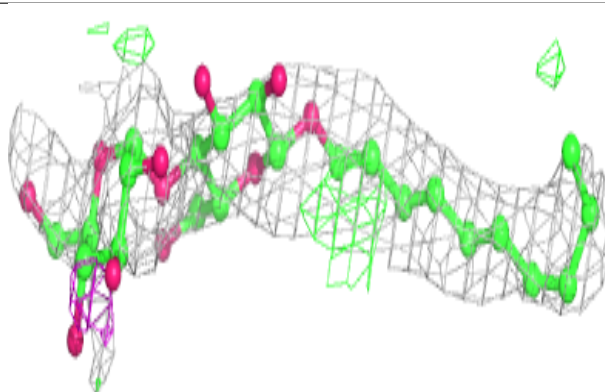
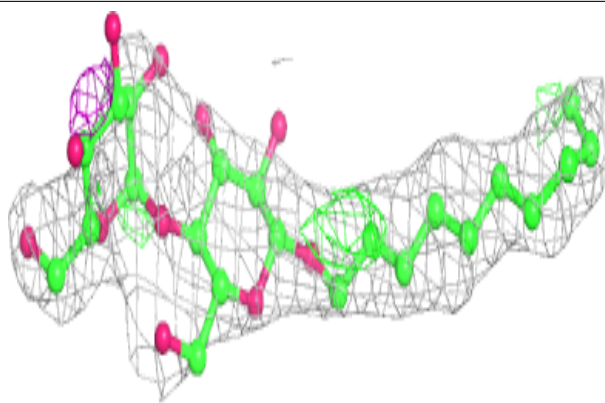
**Electron density around DMU U 92:**

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

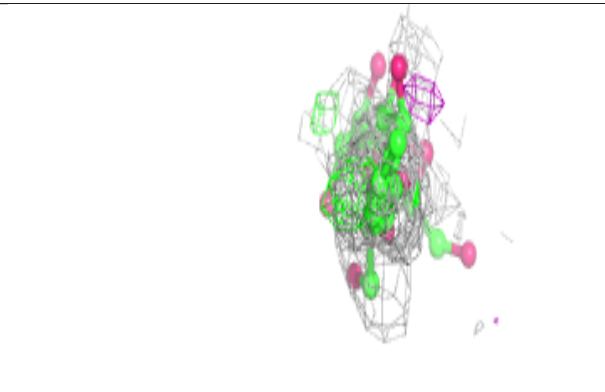
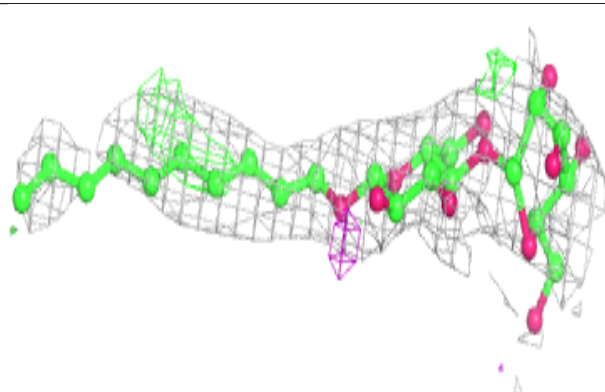
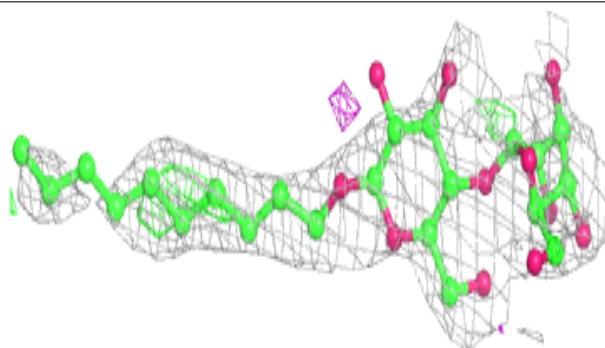


Electron density around DMU H 92:

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

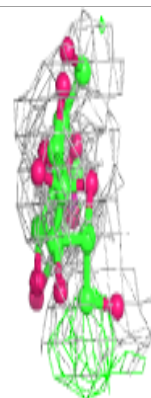
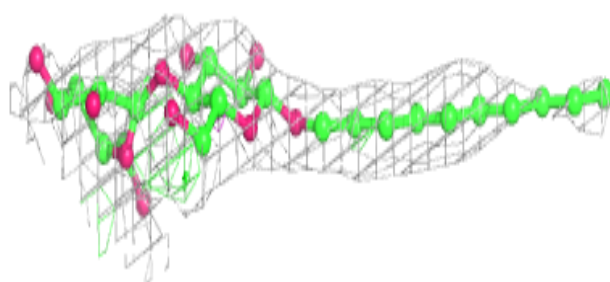
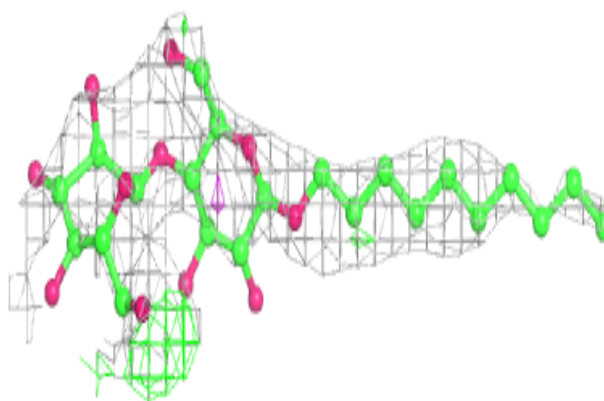
**Electron density around DMU Q 92:**

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

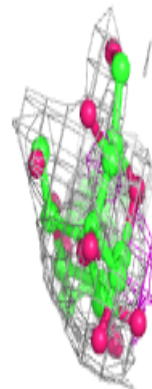
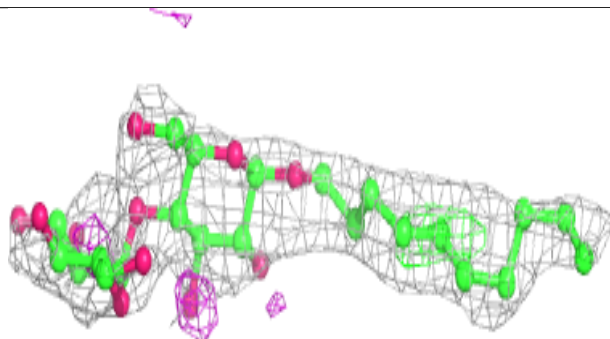
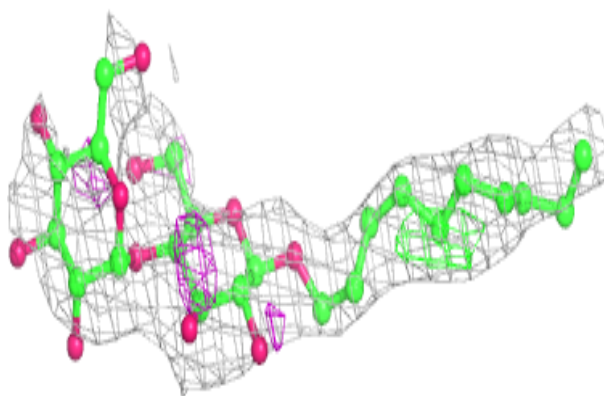


Electron density around DMU B 92:

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

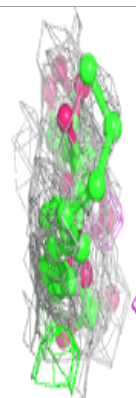
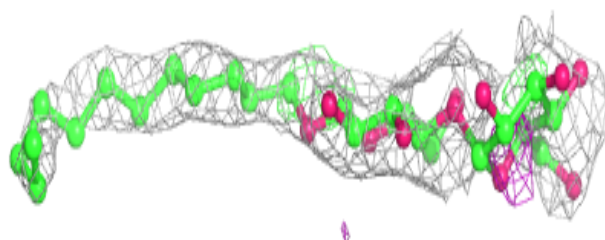
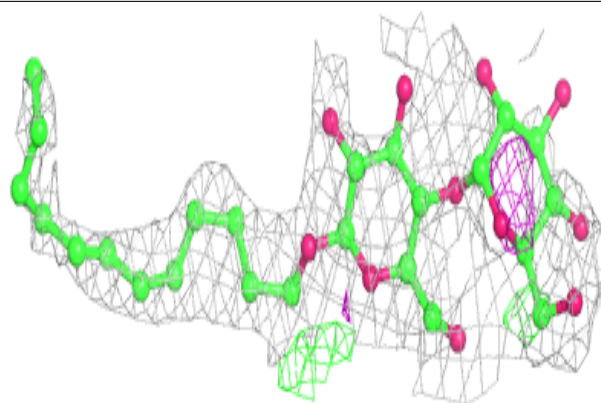
**Electron density around DMU N 92:**

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

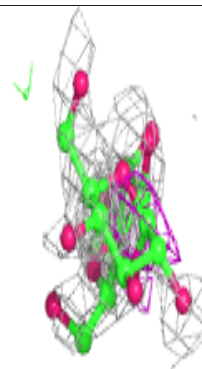
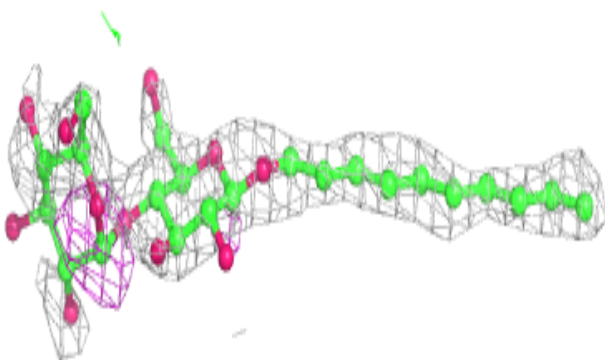
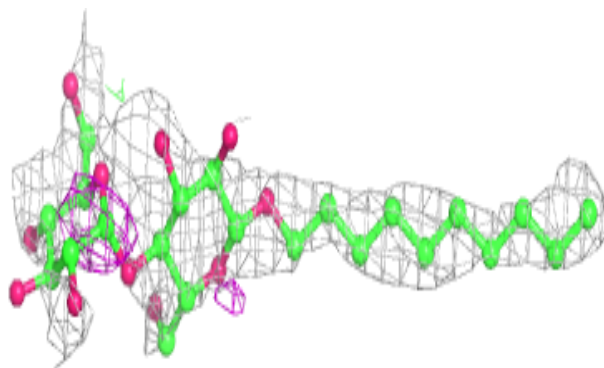


Electron density around LMT C 1090:

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

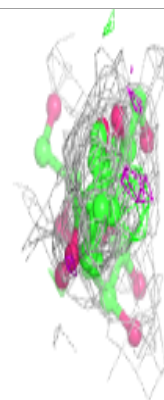
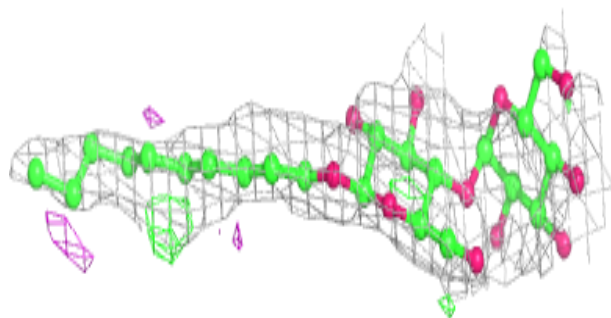
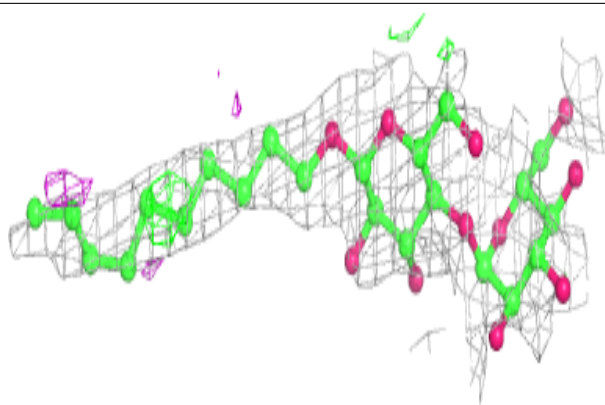
**Electron density around DMU C 92:**

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

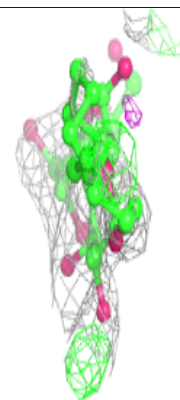
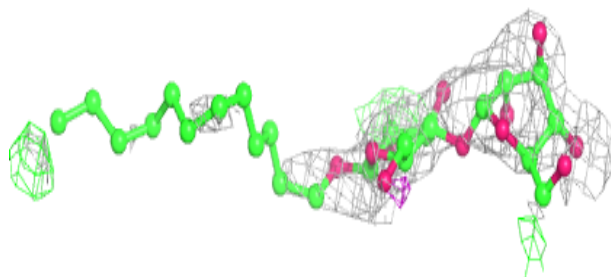
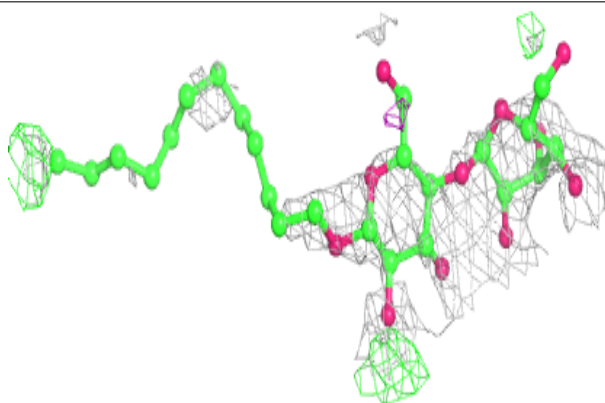


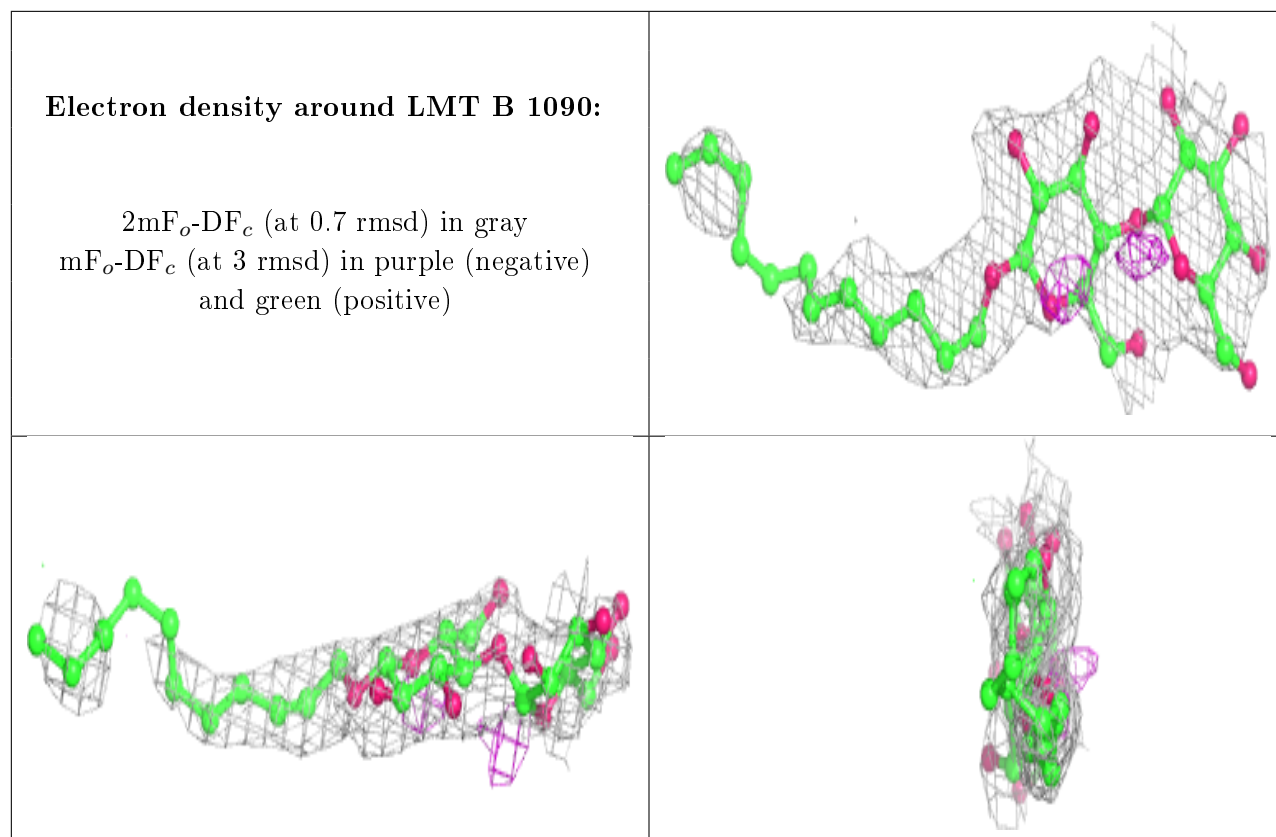
Electron density around DMU A 92:

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

**Electron density around LMT C 1091:**

$2mF_o-DF_c$ (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.