



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:28 PM UTC

PDB ID : 6HZW / pdb_00006hzw
Title : THE GLIC PENTAMERIC LIGAND-GATED ION CHANNEL 2.22 resolution
Authors : Hu, H.D.; Delarue, M.
Deposited on : 2018-10-24
Resolution : 2.22 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

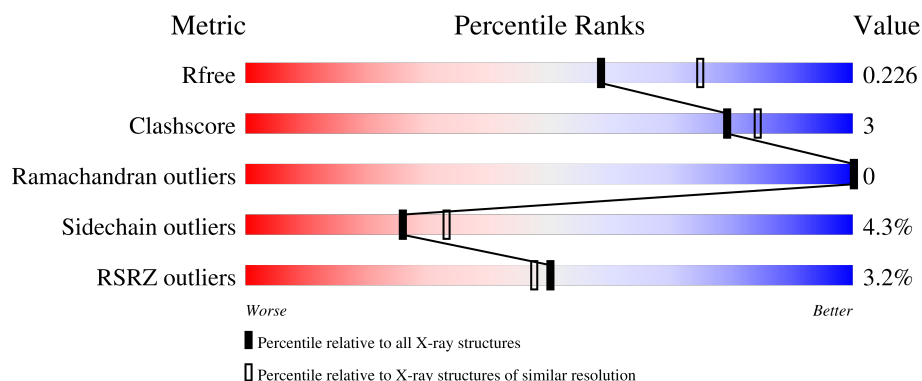
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	317	3% 89% 8% ...
1	B	317	2% 88% 8% ...
1	C	317	4% 89% 7% ...
1	D	317	3% 86% 10% ...
1	E	317	3% 89% 9% ...

2 Entry composition [i](#)

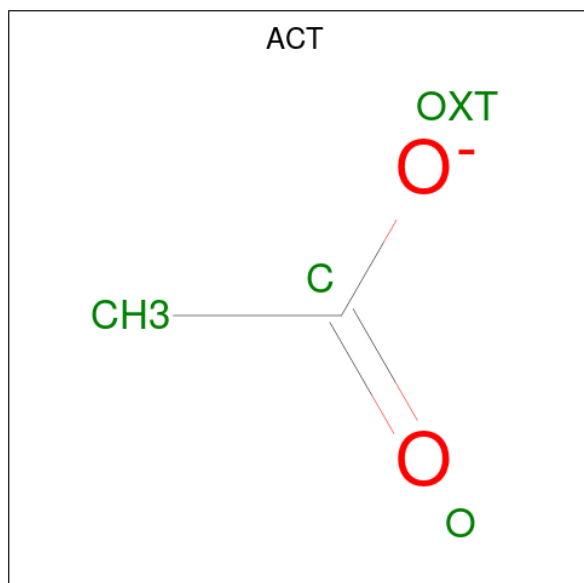
There are 7 unique types of molecules in this entry. The entry contains 13965 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Proton-gated ion channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	3	0
			2545	1677	406	458	4			
1	B	311	Total	C	N	O	S	0	3	0
			2542	1676	405	457	4			
1	C	311	Total	C	N	O	S	0	2	0
			2537	1673	405	455	4			
1	D	311	Total	C	N	O	S	0	4	0
			2548	1680	405	459	4			
1	E	311	Total	C	N	O	S	0	3	0
			2543	1678	406	455	4			

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



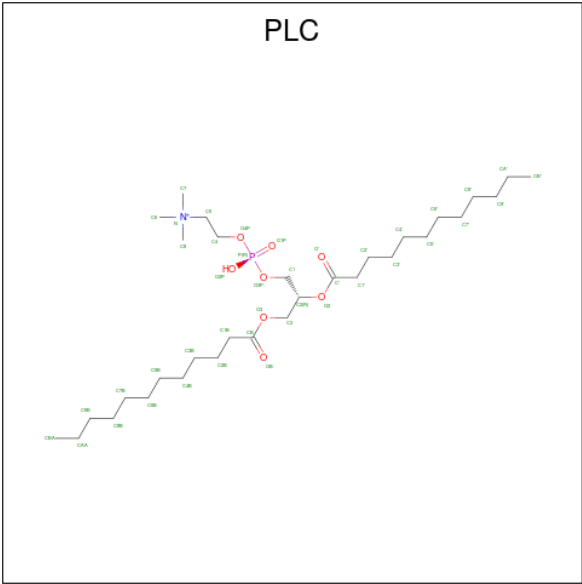
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 3 is DIUNDECYL PHOSPHATIDYL CHOLINE (CCD ID: PLC) (formula: C₃₂H₆₅NO₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	N	O	P	0	0	
			34	24	1	8	1			
3	A	1	Total		C				0	0
			12		12					

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			42	32	1	8	1		
3	B	1	Total	C	N	O	P	0	0
			42	32	1	8	1		
3	B	1	Total	C	N	O	P	0	0
			34	24	1	8	1		
3	B	1	Total	C				0	0
			12	12					
3	C	1	Total	C	N	O	P	0	0
			42	32	1	8	1		
3	C	1	Total	C	N	O	P	0	0
			34	24	1	8	1		
3	C	1	Total	C				0	0
			12	12					
3	D	1	Total	C	N	O	P	0	0
			42	32	1	8	1		
3	D	1	Total	C	N	O	P	0	0
			34	24	1	8	1		
3	D	1	Total	C				0	0
			12	12					
3	E	1	Total	C	N	O	P	0	0
			42	32	1	8	1		
3	E	1	Total	C	N	O	P	0	0
			34	24	1	8	1		
3	E	1	Total	C				0	0
			12	12					

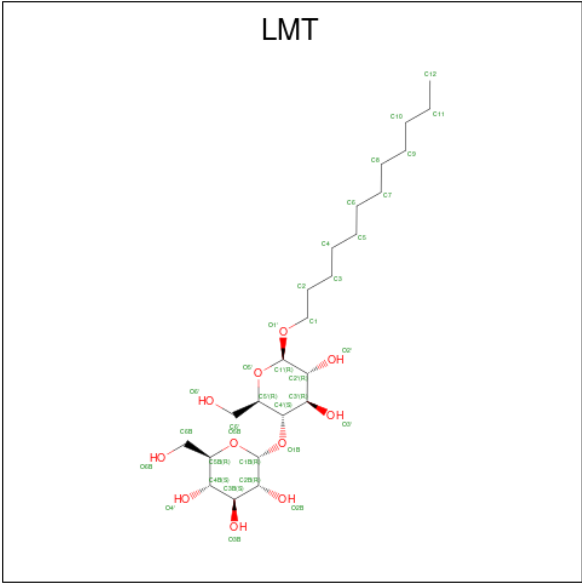
- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Cl	0	0
			3	3		
4	B	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	E	1	Total	Cl	0	0
			1	1		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Na 1 1	0	0
5	B	1	Total Na 1 1	0	0
5	C	2	Total Na 2 2	0	0
5	D	1	Total Na 1 1	0	0
5	E	1	Total Na 1 1	0	0

- Molecule 6 is DODECYL-BETA-D-MALTOSIDE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C 12 12	0	0
6	A	1	Total C 12 12	0	0
6	A	1	Total C O 25 18 7	0	0
6	B	1	Total C 12 12	0	0
6	B	1	Total C O 25 18 7	0	0
6	C	1	Total C 12 12	0	0
6	C	1	Total C O 25 19 6	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total C 12 12	0	0
6	D	1	Total C O 26 19 7	0	0
6	E	1	Total C 12 12	0	0
6	E	1	Total C O 26 19 7	0	0

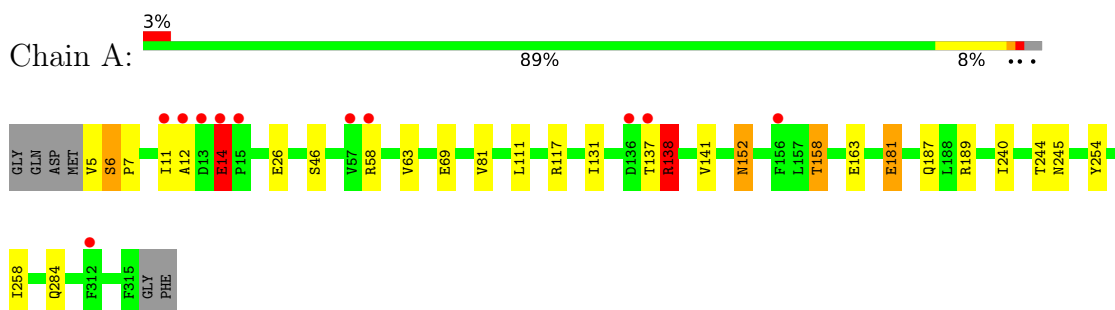
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	118	Total O 118 118	0	0
7	B	123	Total O 123 123	0	0
7	C	107	Total O 107 107	0	0
7	D	100	Total O 100 100	0	0
7	E	110	Total O 110 110	0	0

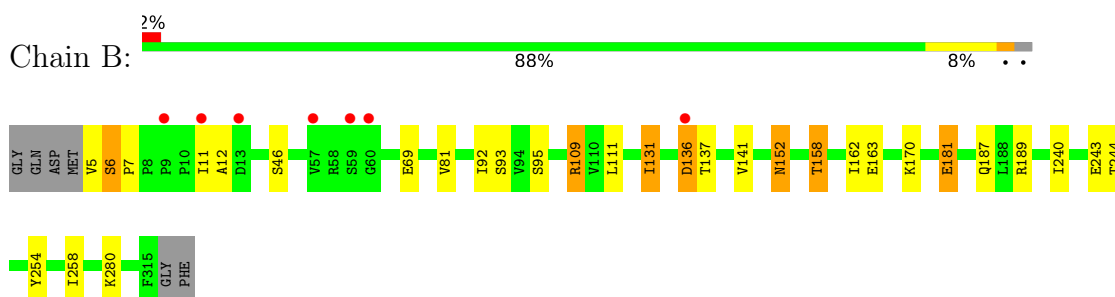
3 Residue-property plots [i](#)

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.

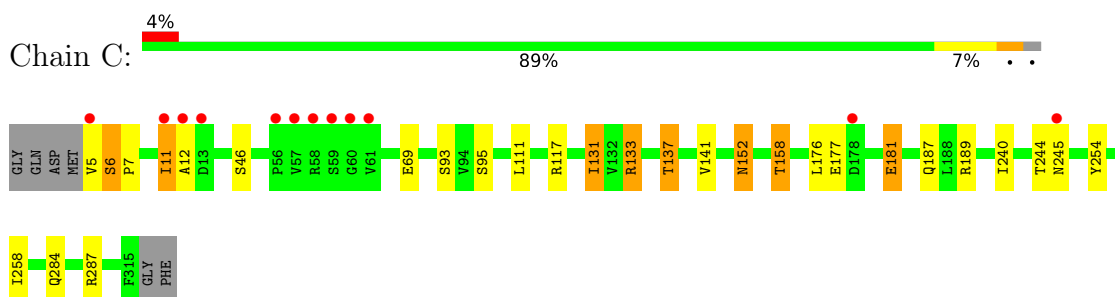
- Molecule 1: Proton-gated ion channel



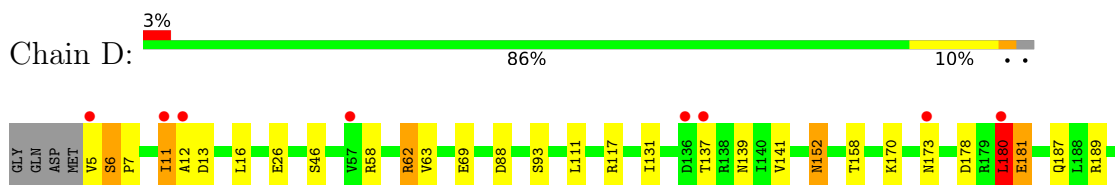
- Molecule 1: Proton-gated ion channel



- Molecule 1: Proton-gated ion channel

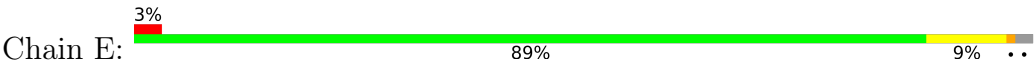


- Molecule 1: Proton-gated ion channel





- Molecule 1: Proton-gated ion channel



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	182.42Å 133.40Å 160.47Å 90.00° 102.48° 90.00°	Depositor
Resolution (Å)	20.00 – 2.22 20.00 – 2.22	Depositor EDS
% Data completeness (in resolution range)	70.0 (20.00-2.22) 70.0 (20.00-2.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 2.21Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.195 , 0.220 0.202 , 0.226	Depositor DCC
R_{free} test set	6447 reflections (3.49%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13965	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PLC, ACT, LMT, NA, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.17	1/2619 (0.0%)	1.29	5/3579 (0.1%)
1	B	1.20	4/2619 (0.2%)	1.34	8/3579 (0.2%)
1	C	1.17	1/2611 (0.0%)	1.28	8/3568 (0.2%)
1	D	1.17	0/2628	1.28	7/3591 (0.2%)
1	E	1.14	3/2620 (0.1%)	1.25	4/3579 (0.1%)
All	All	1.17	9/13097 (0.1%)	1.29	32/17896 (0.2%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	95	SER	CA-C	6.20	1.59	1.52
1	C	95	SER	CA-C	5.77	1.59	1.52
1	B	92	ILE	C-O	-5.66	1.17	1.24
1	B	162	ILE	C-O	-5.42	1.18	1.24
1	B	163	GLU	C-O	-5.24	1.18	1.24
1	A	163	GLU	C-O	-5.22	1.18	1.24
1	E	162	ILE	C-O	-5.14	1.18	1.24
1	E	149	VAL	C-O	-5.05	1.18	1.24
1	E	95	SER	CA-C	5.04	1.58	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	109	ARG	NE-CZ-NH2	18.18	135.56	119.20
1	B	109	ARG	NE-CZ-NH1	-12.35	109.15	121.50
1	B	109	ARG	CD-NE-CZ	7.87	135.42	124.40
1	D	152	ASN	CB-CA-C	7.01	122.43	109.54
1	A	152	ASN	CB-CA-C	6.88	122.20	109.54
1	A	14	GLU	CA-CB-CG	-6.84	100.42	114.10
1	C	152	ASN	CB-CA-C	6.82	122.09	109.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	6	SER	CA-C-N	-6.80	114.76	119.66
1	D	6	SER	C-N-CA	-6.80	114.76	119.66
1	B	152	ASN	CB-CA-C	6.77	122.00	109.54
1	E	152	ASN	CB-CA-C	6.65	121.78	109.54
1	E	6	SER	CA-C-N	-6.40	115.05	119.66
1	E	6	SER	C-N-CA	-6.40	115.05	119.66
1	C	133	ARG	CG-CD-NE	-6.35	98.03	112.00
1	B	109	ARG	CB-CG-CD	6.31	125.81	111.30
1	D	180	LEU	CB-CG-CD2	6.14	129.13	110.70
1	A	6	SER	CA-C-N	-6.01	115.33	119.66
1	A	6	SER	C-N-CA	-6.01	115.33	119.66
1	C	6	SER	CA-C-N	-5.81	115.48	119.66
1	C	6	SER	C-N-CA	-5.81	115.48	119.66
1	A	138	ARG	N-CA-C	5.69	117.06	108.46
1	D	178	ASP	N-CA-C	5.58	119.27	111.90
1	C	133	ARG	NE-CZ-NH1	-5.46	116.03	121.50
1	D	11	ILE	N-CA-CB	5.41	117.89	110.54
1	C	131	ILE	N-CA-C	5.31	116.01	108.42
1	E	11	ILE	N-CA-CB	5.19	117.60	110.54
1	C	158	THR	CB-CA-C	5.17	117.96	109.90
1	C	11	ILE	N-CA-CB	5.14	117.53	110.54
1	B	6	SER	CA-C-N	-5.12	115.97	119.66
1	B	6	SER	C-N-CA	-5.12	115.97	119.66
1	B	131	ILE	N-CA-C	5.07	117.02	108.81
1	D	62	ARG	CA-CB-CG	5.07	124.24	114.10

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	2545	0	2567	16	0
1	B	2542	0	2568	14	0
1	C	2537	0	2564	15	0
1	D	2548	0	2574	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2543	0	2577	14	0
2	A	8	0	6	1	0
2	B	8	0	6	1	0
2	C	8	0	6	1	0
2	D	8	0	6	1	0
2	E	8	0	6	1	0
3	A	88	0	129	1	0
3	B	88	0	129	1	0
3	C	88	0	129	1	0
3	D	88	0	129	0	0
3	E	88	0	129	1	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	A	49	0	81	0	0
6	B	37	0	58	0	0
6	C	37	0	58	0	0
6	D	38	0	58	0	0
6	E	38	0	58	0	0
7	A	118	0	0	3	1
7	B	123	0	0	4	0
7	C	107	0	0	3	0
7	D	100	0	0	7	1
7	E	110	0	0	4	0
All	All	13965	0	13838	74	1

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 3.

All (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:ARG:NH1	1:C:176:LEU:O	2.07	0.88
1:D:243[A]:GLU:OE1	7:D:501:HOH:O	1.95	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280[A]:LYS:HD3	7:B:607:HOH:O	1.91	0.70
1:D:26[B]:GLU:OE1	1:E:81:VAL:O	2.11	0.69
1:E:243:GLU:OE1	7:E:501:HOH:O	2.09	0.69
1:D:88[A]:ASP:OD1	7:D:502:HOH:O	2.11	0.68
1:D:13:ASP:HB3	7:D:576:HOH:O	1.93	0.66
1:D:117:ARG:NH2	7:D:503:HOH:O	2.28	0.66
1:D:181:GLU:OE2	2:D:402:ACT:O	2.14	0.65
1:B:181:GLU:OE2	2:B:402:ACT:O	2.19	0.61
1:A:187:GLN:OE1	1:A:189:ARG:NH2	2.33	0.61
1:B:187:GLN:OE1	1:B:189:ARG:NH2	2.33	0.60
1:E:187:GLN:OE1	1:E:189:ARG:NH2	2.34	0.60
1:C:245:ASN:ND2	7:C:501:HOH:O	2.28	0.59
1:B:11:ILE:HD12	1:B:12:ALA:HB3	1.86	0.57
1:A:181:GLU:OE2	2:A:401:ACT:O	2.22	0.57
1:C:181:GLU:OE2	2:C:403:ACT:O	2.23	0.56
1:C:187:GLN:OE1	1:C:189:ARG:NH2	2.35	0.56
1:A:11:ILE:HD12	1:A:12:ALA:HB3	1.88	0.55
1:D:187:GLN:OE1	1:D:189:ARG:NH2	2.35	0.55
1:A:14:GLU:O	1:A:138:ARG:NH1	2.40	0.55
1:E:117:ARG:NH2	7:E:502:HOH:O	2.39	0.55
1:B:280[A]:LYS:CD	7:B:607:HOH:O	2.53	0.55
1:B:240:ILE:O	1:B:244:THR:HG23	2.08	0.54
1:C:177[B]:GLU:CA	1:C:177[B]:GLU:OE1	2.56	0.54
1:E:240:ILE:O	1:E:244:THR:HG23	2.08	0.54
1:A:131:ILE:HD11	1:A:181:GLU:HG2	1.89	0.54
1:E:181:GLU:OE2	2:E:402:ACT:O	2.26	0.54
1:D:240:ILE:O	1:D:244:THR:HG23	2.08	0.53
1:C:240:ILE:O	1:C:244:THR:HG23	2.08	0.53
1:A:63:VAL:HG21	1:B:136:ASP:CB	2.39	0.52
1:A:240:ILE:O	1:A:244:THR:HG23	2.08	0.52
1:D:131:ILE:HD11	1:D:181:GLU:HG2	1.90	0.52
1:B:6:SER:HB2	1:B:7:PRO:HD2	1.93	0.51
1:B:131:ILE:HD11	1:B:181:GLU:HG2	1.92	0.51
1:C:131:ILE:HD11	1:C:181:GLU:HG2	1.94	0.50
1:C:284:GLN:HE22	3:C:402:PLC:H42	1.76	0.50
1:E:131:ILE:HD11	1:E:181:GLU:HG2	1.93	0.50
1:D:63:VAL:HG11	1:E:136:ASP:CG	2.36	0.50
4:E:405:CL:CL	7:E:578:HOH:O	2.57	0.50
1:B:158:THR:HG23	7:B:580:HOH:O	2.12	0.49
1:D:139:ASN:OD1	1:D:180:LEU:HD22	2.12	0.49
1:A:26[B]:GLU:OE1	1:B:81:VAL:O	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:GLU:OE1	7:B:501:HOH:O	2.20	0.48
1:A:158:THR:HG23	7:A:564:HOH:O	2.13	0.48
1:D:6:SER:HB2	1:D:7:PRO:HD2	1.95	0.48
3:B:401:PLC:HE'2	3:B:401:PLC:HEA2	1.94	0.48
1:D:16:LEU:HD13	7:D:507:HOH:O	2.14	0.47
1:A:81:VAL:O	1:E:26[B]:GLU:OE1	2.34	0.46
1:D:245:ASN:HB3	7:D:541:HOH:O	2.15	0.46
1:A:117:ARG:NH2	7:A:506:HOH:O	2.49	0.46
1:C:177[B]:GLU:OE1	1:C:177[B]:GLU:HA	2.16	0.46
1:D:173:ASN:ND2	7:D:504:HOH:O	2.31	0.45
1:A:6:SER:HB2	1:A:7:PRO:HD2	1.99	0.45
1:C:117:ARG:NH2	7:C:507:HOH:O	2.50	0.44
1:A:245:ASN:HB3	7:A:578:HOH:O	2.18	0.44
1:C:137:THR:C	7:C:512:HOH:O	2.60	0.44
1:A:63:VAL:HG21	1:B:136:ASP:HB2	1.98	0.44
1:E:254:TYR:CZ	1:E:258:ILE:HD11	2.53	0.43
1:E:280[B]:LYS:NZ	7:E:505:HOH:O	2.51	0.43
1:D:63:VAL:HG11	1:E:136:ASP:CB	2.48	0.43
1:D:217:TRP:CD1	3:E:401:PLC:H1'1	2.54	0.43
1:A:254:TYR:CZ	1:A:258:ILE:HD11	2.54	0.42
1:D:254:TYR:CZ	1:D:258:ILE:HD11	2.55	0.42
1:C:6:SER:HB2	1:C:7:PRO:HD2	2.01	0.42
1:B:254:TYR:CZ	1:B:258:ILE:HD11	2.54	0.42
1:D:11:ILE:HD12	1:D:12:ALA:CB	2.50	0.42
1:D:219:THR:HG22	1:D:280[A]:LYS:HE2	2.01	0.42
1:C:254:TYR:CZ	1:C:258:ILE:HD11	2.55	0.41
1:A:284:GLN:HE22	3:A:412:PLC:H42	1.85	0.41
1:C:11:ILE:HD12	1:C:12:ALA:CB	2.50	0.40
1:E:205:MET:HE3	1:E:205:MET:HB2	1.95	0.40
1:E:11:ILE:HD12	1:E:12:ALA:CB	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:502:HOH:O	7:D:576:HOH:O[4_555]	2.09	0.11

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	312/317 (98%)	304 (97%)	8 (3%)	0	100	100
1	B	312/317 (98%)	305 (98%)	7 (2%)	0	100	100
1	C	311/317 (98%)	303 (97%)	8 (3%)	0	100	100
1	D	313/317 (99%)	304 (97%)	9 (3%)	0	100	100
1	E	312/317 (98%)	303 (97%)	9 (3%)	0	100	100
All	All	1560/1585 (98%)	1519 (97%)	41 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	283/284 (100%)	271 (96%)	12 (4%)	26	34
1	B	283/284 (100%)	270 (95%)	13 (5%)	24	30
1	C	282/284 (99%)	271 (96%)	11 (4%)	28	37
1	D	284/284 (100%)	270 (95%)	14 (5%)	22	27
1	E	283/284 (100%)	273 (96%)	10 (4%)	32	41
All	All	1415/1420 (100%)	1355 (96%)	60 (4%)	26	34

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	14	GLU
1	A	46	SER
1	A	58	ARG
1	A	69	GLU
1	A	111	LEU
1	A	137	THR
1	A	138	ARG
1	A	141	VAL
1	A	152	ASN
1	A	158	THR
1	A	181	GLU
1	B	5	VAL
1	B	46	SER
1	B	69	GLU
1	B	93	SER
1	B	109	ARG
1	B	111	LEU
1	B	136	ASP
1	B	137	THR
1	B	141	VAL
1	B	152	ASN
1	B	158	THR
1	B	170	LYS
1	B	181	GLU
1	C	5	VAL
1	C	46	SER
1	C	69	GLU
1	C	93	SER
1	C	111	LEU
1	C	137	THR
1	C	141	VAL
1	C	152	ASN
1	C	158	THR
1	C	181	GLU
1	C	287	ARG
1	D	5	VAL
1	D	46	SER
1	D	58	ARG
1	D	62	ARG
1	D	69	GLU
1	D	93	SER
1	D	111	LEU

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Mol	Chain	Res	Type
1	D	137	THR
1	D	141	VAL
1	D	152	ASN
1	D	158	THR
1	D	170	LYS
1	D	180	LEU
1	D	181	GLU
1	E	5	VAL
1	E	46	SER
1	E	69	GLU
1	E	93	SER
1	E	111	LEU
1	E	137	THR
1	E	141	VAL
1	E	152	ASN
1	E	158	THR
1	E	181	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	139	ASN
1	A	277	HIS
1	A	284	GLN
1	B	200	ASN
1	B	277	HIS
1	C	277	HIS
1	C	284	GLN
1	D	277	HIS
1	E	284	GLN
1	E	307	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 49 ligands modelled in this entry, 13 are monoatomic - leaving 36 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
3	PLC	A	403	-	11,11,41	0.51	0	10,10,49	0.27	0
2	ACT	A	408	-	3,3,3	1.08	0	3,3,3	0.81	0
6	LMT	A	409	-	11,11,36	0.79	0	10,10,47	0.59	0
2	ACT	B	402	-	3,3,3	1.04	0	3,3,3	1.02	0
3	PLC	D	403	-	33,33,41	1.83	3 (9%)	39,41,49	2.37	9 (23%)
6	LMT	B	408	-	11,11,36	1.04	0	10,10,47	1.03	0
3	PLC	C	404	-	33,33,41	1.65	2 (6%)	39,41,49	1.93	7 (17%)
3	PLC	C	405	-	11,11,41	0.89	0	10,10,49	0.68	0
3	PLC	A	412	-	41,41,41	1.19	2 (4%)	47,49,49	1.07	4 (8%)
6	LMT	A	410	-	11,11,36	0.86	0	10,10,47	1.10	1 (10%)
2	ACT	D	402	-	3,3,3	0.61	0	3,3,3	1.89	1 (33%)
6	LMT	B	409	-	24,24,36	1.20	1 (4%)	29,29,47	1.45	4 (13%)
6	LMT	E	408	-	11,11,36	0.78	0	10,10,47	0.92	0
6	LMT	C	410	-	25,25,36	1.49	2 (8%)	30,30,47	1.38	5 (16%)
3	PLC	B	404	-	11,11,41	0.82	0	10,10,49	0.57	0
3	PLC	A	402	-	33,33,41	1.87	5 (15%)	39,41,49	2.28	10 (25%)
3	PLC	E	403	-	33,33,41	1.51	2 (6%)	39,41,49	1.49	5 (12%)
2	ACT	B	407	-	3,3,3	1.30	1 (33%)	3,3,3	1.33	0
2	ACT	E	402	-	3,3,3	0.79	0	3,3,3	1.36	0
6	LMT	D	408	-	11,11,36	0.90	0	10,10,47	0.93	0
2	ACT	D	407	-	3,3,3	1.30	1 (33%)	3,3,3	1.13	0
6	LMT	D	409	-	26,26,36	1.57	3 (11%)	31,31,47	2.01	7 (22%)
3	PLC	D	401	-	41,41,41	1.18	2 (4%)	47,49,49	1.32	4 (8%)
2	ACT	C	408	-	3,3,3	0.77	0	3,3,3	2.36	2 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PLC	C	402	-	41,41,41	1.17	2 (4%)	47,49,49	1.13	4 (8%)
3	PLC	B	403	-	33,33,41	1.72	4 (12%)	39,41,49	1.93	8 (20%)
3	PLC	D	404	-	11,11,41	0.81	0	10,10,49	0.37	0
2	ACT	A	401	-	3,3,3	0.78	0	3,3,3	1.36	0
6	LMT	A	411	-	24,24,36	1.13	2 (8%)	29,29,47	1.40	5 (17%)
3	PLC	E	401	-	41,41,41	1.09	2 (4%)	47,49,49	1.07	3 (6%)
6	LMT	C	409	-	11,11,36	1.00	0	10,10,47	0.98	0
2	ACT	E	407	-	3,3,3	1.14	0	3,3,3	0.87	0
3	PLC	E	404	-	11,11,41	0.66	0	10,10,49	0.22	0
6	LMT	E	409	-	26,26,36	1.36	3 (11%)	31,31,47	1.74	5 (16%)
2	ACT	C	403	-	3,3,3	1.01	0	3,3,3	0.54	0
3	PLC	B	401	-	41,41,41	1.26	2 (4%)	47,49,49	1.05	4 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLC	A	403	-	-	1/9/9/45	-
6	LMT	A	409	-	-	4/9/9/61	-
3	PLC	D	403	-	-	18/37/37/45	-
6	LMT	B	408	-	-	1/9/9/61	-
3	PLC	C	404	-	-	17/37/37/45	-
3	PLC	C	405	-	-	3/9/9/45	-
3	PLC	A	412	-	-	21/45/45/45	-
6	LMT	A	410	-	-	3/9/9/61	-
6	LMT	B	409	-	-	8/15/35/61	0/1/1/2
6	LMT	E	408	-	-	1/9/9/61	-
6	LMT	C	410	-	-	9/17/37/61	0/1/1/2
3	PLC	B	404	-	-	3/9/9/45	-
3	PLC	A	402	-	-	16/37/37/45	-
3	PLC	E	403	-	-	20/37/37/45	-
6	LMT	D	408	-	-	3/9/9/61	-
6	LMT	D	409	-	-	8/17/38/61	0/1/1/2
3	PLC	D	401	-	-	18/45/45/45	-
3	PLC	C	402	-	-	21/45/45/45	-
3	PLC	B	403	-	-	16/37/37/45	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLC	D	404	-	-	3/9/9/45	-
6	LMT	A	411	-	-	6/15/35/61	0/1/1/2
3	PLC	E	401	-	-	21/45/45/45	-
6	LMT	C	409	-	-	1/9/9/61	-
3	PLC	E	404	-	-	3/9/9/45	-
6	LMT	E	409	-	-	9/17/38/61	0/1/1/2
3	PLC	B	401	-	-	16/45/45/45	-

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	403	PLC	O2-C'	7.12	1.54	1.34
3	A	402	PLC	O2-C'	7.07	1.54	1.34
3	C	404	PLC	O2-C'	6.16	1.51	1.34
3	B	403	PLC	O2-C'	6.09	1.51	1.34
3	A	402	PLC	O3-CB	5.72	1.50	1.33
3	E	403	PLC	O2-C'	5.72	1.50	1.34
3	B	403	PLC	O3-CB	5.42	1.49	1.33
3	C	404	PLC	O3-CB	5.41	1.49	1.33
3	D	403	PLC	O3-CB	5.35	1.48	1.33
3	B	401	PLC	O3-CB	5.15	1.48	1.33
3	C	402	PLC	O3-CB	4.95	1.47	1.33
6	D	409	LMT	O1'-C1'	4.86	1.48	1.40
3	E	403	PLC	O3-CB	4.79	1.47	1.33
3	A	412	PLC	O3-CB	4.70	1.47	1.33
3	D	401	PLC	O3-CB	4.60	1.46	1.33
6	C	410	LMT	O1'-C1'	4.50	1.47	1.40
3	D	401	PLC	O2-C'	4.29	1.46	1.34
3	B	401	PLC	O2-C'	4.22	1.46	1.34
6	B	409	LMT	O1'-C1'	4.19	1.47	1.40
3	E	401	PLC	O3-CB	4.09	1.45	1.33
6	A	411	LMT	O1'-C1'	4.07	1.47	1.40
6	E	409	LMT	O1'-C1'	3.98	1.46	1.40
3	A	412	PLC	O2-C'	3.81	1.45	1.34
3	E	401	PLC	O2-C'	3.63	1.44	1.34
3	C	402	PLC	O2-C'	3.47	1.44	1.34
3	B	403	PLC	C1'-C'	2.72	1.58	1.50
6	D	409	LMT	O5'-C1'	2.67	1.48	1.41
6	C	410	LMT	O1B-C4'	2.52	1.48	1.42
6	D	409	LMT	O1B-C4'	2.41	1.47	1.43
6	E	409	LMT	O5'-C1'	2.30	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	407	ACT	OXT-C	-2.21	1.20	1.30
6	A	411	LMT	O5'-C1'	2.20	1.47	1.41
3	A	402	PLC	P-O3P	2.20	1.68	1.59
2	B	407	ACT	OXT-C	-2.19	1.20	1.30
3	A	402	PLC	O2-C2	2.13	1.51	1.46
3	B	403	PLC	C3-C2	2.08	1.57	1.50
3	D	403	PLC	C1-C2	2.08	1.57	1.50
3	A	402	PLC	C1-C2	2.03	1.57	1.50
6	E	409	LMT	O1B-C4'	2.02	1.46	1.43

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	403	PLC	O2-C'-C1'	9.69	132.44	111.48
3	A	402	PLC	O2-C'-C1'	8.54	129.96	111.48
6	D	409	LMT	C1B-O1B-C4'	6.71	125.66	114.92
3	D	403	PLC	C2-O2-C'	6.68	133.78	117.80
3	A	402	PLC	C2-O2-C'	6.60	133.60	117.80
6	E	409	LMT	C1B-O1B-C4'	6.40	125.16	114.92
3	B	403	PLC	O2-C'-C1'	6.20	124.90	111.48
3	C	404	PLC	C2-O2-C'	6.09	132.36	117.80
3	C	404	PLC	O3-CB-C1B	5.83	129.62	111.83
3	E	403	PLC	O2-C'-C1'	5.28	122.90	111.48
3	C	404	PLC	O2-C'-C1'	5.24	122.81	111.48
3	B	403	PLC	O3-CB-C1B	5.23	127.78	111.83
3	D	401	PLC	O2-C'-C1'	4.84	121.96	111.48
3	B	403	PLC	C2-O2-C'	4.76	129.19	117.80
3	C	402	PLC	O2-C'-C1'	4.29	120.76	111.48
6	B	409	LMT	C1-O1'-C1'	4.15	120.78	113.68
6	D	409	LMT	O1B-C4'-C3'	3.97	117.83	109.83
6	B	409	LMT	C4'-C3'-C2'	3.95	117.76	110.83
3	D	403	PLC	O3-CB-C1B	3.93	123.81	111.83
3	A	412	PLC	O2-C'-C1'	3.89	119.89	111.48
6	A	411	LMT	O5'-C5'-C6'	3.88	116.07	106.44
3	A	402	PLC	O3-CB-C1B	3.85	123.59	111.83
3	E	403	PLC	O3-CB-C1B	3.72	123.18	111.83
6	C	410	LMT	C1B-O1B-C4'	3.70	123.98	114.47
6	D	409	LMT	O5'-C5'-C6'	3.62	115.42	106.44
6	E	409	LMT	O1B-C4'-C3'	3.58	117.04	109.83
3	B	403	PLC	O2-C'-O'	-3.54	115.43	123.70
3	B	401	PLC	O3-CB-C1B	3.50	122.50	111.83
6	A	411	LMT	C4'-C3'-C2'	3.40	116.80	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	PLC	C3-O3-CB	3.36	129.38	117.12
3	D	403	PLC	O'-C'-C1'	-3.21	111.25	123.78
3	D	403	PLC	O2-C'-O'	-3.16	116.32	123.70
6	E	409	LMT	C2'-C3'-C4'	3.10	116.72	109.68
3	D	401	PLC	C3-C2-C1	-3.07	104.62	111.78
3	D	403	PLC	C3-O3-CB	3.04	128.24	117.12
6	D	409	LMT	O5'-C1'-O1'	3.03	117.21	110.04
3	E	401	PLC	O3-CB-OB	-3.02	116.06	123.63
2	C	408	ACT	OXT-C-CH3	3.01	127.69	115.05
3	C	404	PLC	O3-C3-C2	2.98	116.98	108.40
6	C	410	LMT	C1-O1'-C1'	2.96	118.73	113.68
3	A	402	PLC	O'-C'-C1'	-2.94	112.29	123.78
3	C	404	PLC	OB-CB-C1B	-2.91	112.39	123.78
3	B	401	PLC	C3-O3-CB	2.91	127.74	117.12
3	A	402	PLC	O2-C2-C3	2.90	118.74	108.34
3	B	401	PLC	O3-CB-OB	-2.87	116.45	123.63
3	E	403	PLC	C2-O2-C'	2.80	124.50	117.80
6	D	409	LMT	C1-O1'-C1'	2.76	118.39	113.68
2	C	408	ACT	O-C-CH3	-2.74	111.31	122.53
3	B	401	PLC	O2-C'-C1'	2.71	117.35	111.48
6	A	411	LMT	C1-O1'-C1'	2.70	118.29	113.68
6	D	409	LMT	O2'-C2'-C1'	2.65	116.40	110.08
3	C	402	PLC	O2-C'-O'	-2.65	117.52	123.70
3	A	412	PLC	O2-C'-O'	-2.63	117.55	123.70
3	B	403	PLC	O3-C3-C2	2.62	115.94	108.40
2	D	402	ACT	OXT-C-CH3	2.61	126.00	115.05
6	E	409	LMT	C1'-O5'-C5'	2.60	118.81	113.72
3	A	412	PLC	O3-CB-OB	-2.55	117.25	123.63
3	A	402	PLC	O2-C'-O'	-2.55	117.75	123.70
6	C	410	LMT	C1'-O5'-C5'	2.49	118.58	113.72
6	B	409	LMT	C1'-C2'-C3'	2.49	115.25	110.01
6	A	411	LMT	O5'-C1'-O1'	2.49	115.92	110.04
3	C	402	PLC	O3-CB-OB	-2.48	117.42	123.63
3	B	403	PLC	OB-CB-C1B	-2.47	114.11	123.78
3	E	401	PLC	O2-C'-C1'	2.47	116.83	111.48
6	B	409	LMT	O5'-C5'-C6'	2.46	112.53	106.44
3	A	412	PLC	O3-CB-C1B	2.46	119.33	111.83
3	D	403	PLC	O3-CB-OB	-2.45	117.49	123.63
3	D	401	PLC	O3-CB-C1B	2.42	119.22	111.83
6	D	409	LMT	C2'-C3'-C4'	2.41	115.16	109.68
6	E	409	LMT	O5'-C5'-C4'	2.39	114.67	109.72
3	B	403	PLC	C2'-C1'-C'	2.35	122.31	113.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	410	LMT	C12-C11-C10	2.33	129.09	113.36
3	D	403	PLC	O2-C2-C3	2.32	116.68	108.34
3	E	403	PLC	C3-O3-CB	2.31	125.55	117.12
6	C	410	LMT	C2'-C3'-C4'	2.30	114.91	109.68
3	C	404	PLC	C3-O3-CB	2.28	125.45	117.12
3	C	404	PLC	O3-CB-OB	-2.27	117.95	123.63
3	E	403	PLC	O2-C'-O'	-2.24	118.47	123.70
3	D	401	PLC	O3-CB-OB	-2.21	118.09	123.63
3	B	403	PLC	O3-CB-OB	-2.21	118.10	123.63
3	C	402	PLC	O3-CB-C1B	2.20	118.54	111.83
3	E	401	PLC	O3-CB-C1B	2.13	118.34	111.83
6	C	410	LMT	O5'-C5'-C4'	2.13	114.13	109.72
3	A	402	PLC	C2'-C1'-C'	2.10	121.39	113.69
3	A	402	PLC	O3-CB-OB	-2.09	118.40	123.63
3	A	402	PLC	O3-C3-C2	2.07	114.36	108.40
3	D	403	PLC	C2B-C1B-CB	2.06	121.26	113.69
6	A	411	LMT	O2'-C2'-C1'	2.05	114.95	110.08

There are no chirality outliers.

All (250) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	PLC	C1'-C'-O2-C2
3	A	402	PLC	O'-C'-O2-C2
3	A	402	PLC	C1-O3P-P-O1P
3	A	402	PLC	C1-O3P-P-O2P
3	A	402	PLC	C1-O3P-P-O4P
3	A	412	PLC	C1B-CB-O3-C3
3	A	412	PLC	OB-CB-O3-C3
3	A	412	PLC	C1-O3P-P-O1P
3	A	412	PLC	C4-O4P-P-O2P
3	A	412	PLC	C4-O4P-P-O3P
3	B	401	PLC	C4-O4P-P-O2P
3	B	401	PLC	C4-O4P-P-O3P
3	B	403	PLC	O4P-C4-C5-N
3	B	403	PLC	C1-O3P-P-O2P
3	B	403	PLC	C1-O3P-P-O4P
3	C	402	PLC	C1B-CB-O3-C3
3	C	402	PLC	C4-O4P-P-O1P
3	C	402	PLC	C4-O4P-P-O2P
3	C	402	PLC	C4-O4P-P-O3P
3	C	404	PLC	C4-O4P-P-O3P

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Mol	Chain	Res	Type	Atoms
3	D	401	PLC	C1B-CB-O3-C3
3	D	401	PLC	OB-CB-O3-C3
3	D	401	PLC	C1-O3P-P-O1P
3	D	401	PLC	C4-O4P-P-O2P
3	D	401	PLC	C4-O4P-P-O3P
3	D	403	PLC	C1'-C'-O2-C2
3	D	403	PLC	O'-C'-O2-C2
3	D	403	PLC	C4-O4P-P-O3P
3	E	401	PLC	C1B-CB-O3-C3
3	E	401	PLC	OB-CB-O3-C3
3	E	401	PLC	C1-O3P-P-O1P
3	E	401	PLC	C4-O4P-P-O2P
3	E	401	PLC	C4-O4P-P-O3P
3	E	403	PLC	C1'-C'-O2-C2
3	E	403	PLC	C1-O3P-P-O1P
3	E	403	PLC	C1-O3P-P-O2P
3	E	403	PLC	C1-O3P-P-O4P
3	E	403	PLC	C4-O4P-P-O2P
3	E	403	PLC	C4-O4P-P-O3P
6	A	411	LMT	C2-C1-O1'-C1'
6	D	409	LMT	C3'-C4'-O1B-C1B
6	E	409	LMT	C3'-C4'-O1B-C1B
3	B	401	PLC	OB-CB-O3-C3
3	C	402	PLC	OB-CB-O3-C3
3	B	401	PLC	C1B-CB-O3-C3
6	C	410	LMT	O5'-C5'-C6'-O6'
3	E	403	PLC	O'-C'-O2-C2
6	B	409	LMT	O5'-C5'-C6'-O6'
6	C	410	LMT	C4'-C5'-C6'-O6'
3	B	403	PLC	C1'-C'-O2-C2
6	B	409	LMT	C4'-C5'-C6'-O6'
3	E	401	PLC	C'-C1'-C2'-C3'
6	A	411	LMT	O5'-C5'-C6'-O6'
6	A	411	LMT	C4'-C5'-C6'-O6'
3	D	403	PLC	CB-C1B-C2B-C3B
3	E	401	PLC	C4-C5-N-C8
3	A	412	PLC	CB-C1B-C2B-C3B
3	E	403	PLC	C'-C1'-C2'-C3'
6	C	410	LMT	C3'-C4'-O1B-C1B
3	A	412	PLC	C'-C1'-C2'-C3'
3	C	402	PLC	CB-C1B-C2B-C3B
3	B	403	PLC	C'-C1'-C2'-C3'

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Mol	Chain	Res	Type	Atoms
3	E	403	PLC	CB-C1B-C2B-C3B
3	A	402	PLC	OB-CB-O3-C3
3	B	403	PLC	O'-C'-O2-C2
3	A	402	PLC	C1B-CB-O3-C3
3	C	402	PLC	C4-C5-N-C8
3	E	401	PLC	CB-C1B-C2B-C3B
3	A	402	PLC	C3-C2-O2-C'
3	C	404	PLC	C1-C2-O2-C'
6	A	411	LMT	C1-C2-C3-C4
3	C	402	PLC	C4-C5-N-C6
3	C	402	PLC	C4-C5-N-C7
3	C	402	PLC	C'-C1'-C2'-C3'
3	D	401	PLC	C'-C1'-C2'-C3'
3	D	401	PLC	C7'-C8'-C9'-CA'
6	E	409	LMT	C4-C5-C6-C7
3	B	401	PLC	CB-C1B-C2B-C3B
3	D	403	PLC	C1B-C2B-C3B-C4B
3	A	402	PLC	C2B-C3B-C4B-C5B
6	D	409	LMT	C1-C2-C3-C4
6	D	409	LMT	C4-C5-C6-C7
3	B	401	PLC	C'-C1'-C2'-C3'
3	B	403	PLC	C3B-C4B-C5B-C6B
3	E	401	PLC	C4-C5-N-C7
3	C	402	PLC	C1'-C2'-C3'-C4'
3	D	403	PLC	C3B-C4B-C5B-C6B
6	D	409	LMT	C3-C4-C5-C6
6	B	409	LMT	C3-C4-C5-C6
3	A	412	PLC	C1'-C2'-C3'-C4'
3	C	404	PLC	C1'-C'-O2-C2
3	A	402	PLC	C4-C5-N-C7
3	E	401	PLC	C4-C5-N-C6
3	C	402	PLC	C7'-C8'-C9'-CA'
3	D	401	PLC	C1'-C2'-C3'-C4'
3	A	412	PLC	C7'-C8'-C9'-CA'
3	E	401	PLC	C7'-C8'-C9'-CA'
3	C	404	PLC	C3B-C4B-C5B-C6B
3	B	401	PLC	C7'-C8'-C9'-CA'
3	C	404	PLC	O'-C'-O2-C2
6	B	409	LMT	C4-C5-C6-C7
3	C	404	PLC	C1B-C2B-C3B-C4B
6	B	409	LMT	C7-C8-C9-C10
3	E	403	PLC	C1B-C2B-C3B-C4B

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Mol	Chain	Res	Type	Atoms
3	B	403	PLC	C1B-C2B-C3B-C4B
3	A	402	PLC	C1-C2-C3-O3
3	B	401	PLC	C1-C2-C3-O3
3	C	402	PLC	C1-C2-C3-O3
3	D	401	PLC	C1-C2-C3-O3
3	D	403	PLC	C1-C2-C3-O3
3	E	401	PLC	C1-C2-C3-O3
3	B	401	PLC	C1'-C2'-C3'-C4'
3	A	402	PLC	C4-C5-N-C6
3	D	403	PLC	C4B-C5B-C6B-C7B
3	D	401	PLC	C1B-C2B-C3B-C4B
3	C	402	PLC	C2'-C3'-C4'-C5'
6	B	408	LMT	C1-C2-C3-C4
6	A	410	LMT	C1-C2-C3-C4
6	D	408	LMT	C2-C3-C4-C5
3	D	401	PLC	C7B-C8B-C9B-CAA
3	C	402	PLC	C6'-C7'-C8'-C9'
6	E	409	LMT	C9-C10-C11-C12
3	B	403	PLC	C4B-C5B-C6B-C7B
3	C	405	PLC	C'-C1'-C2'-C3'
3	E	404	PLC	C'-C1'-C2'-C3'
6	A	409	LMT	C9-C10-C11-C12
6	A	411	LMT	C3-C4-C5-C6
6	D	409	LMT	C9-C10-C11-C12
3	A	412	PLC	C1B-C2B-C3B-C4B
6	C	410	LMT	C1-C2-C3-C4
3	A	412	PLC	C1-C2-C3-O3
3	B	401	PLC	C2'-C3'-C4'-C5'
3	B	403	PLC	C1'-C2'-C3'-C4'
6	C	410	LMT	C4-C5-C6-C7
3	E	401	PLC	C1'-C2'-C3'-C4'
3	A	412	PLC	O2-C2-C3-O3
3	C	402	PLC	O2-C2-C3-O3
3	E	401	PLC	O2-C2-C3-O3
3	C	402	PLC	C1B-C2B-C3B-C4B
3	B	403	PLC	CB-C1B-C2B-C3B
3	C	404	PLC	C'-C1'-C2'-C3'
3	E	403	PLC	C3B-C4B-C5B-C6B
3	E	403	PLC	O3P-C1-C2-C3
3	C	402	PLC	C2B-C3B-C4B-C5B
6	A	411	LMT	C7-C8-C9-C10
6	C	410	LMT	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
6	C	410	LMT	C9-C10-C11-C12
3	A	402	PLC	C4-C5-N-C8
3	B	403	PLC	C1-C2-O2-C'
3	D	403	PLC	O3P-C1-C2-O2
6	E	408	LMT	C1-C2-C3-C4
3	B	401	PLC	C5-C4-O4P-P
3	B	401	PLC	O2-C2-C3-O3
3	D	401	PLC	O2-C2-C3-O3
6	B	409	LMT	C9-C10-C11-C12
3	A	412	PLC	C6'-C7'-C8'-C9'
3	A	412	PLC	O4P-C4-C5-N
3	B	401	PLC	O4P-C4-C5-N
3	C	402	PLC	O4P-C4-C5-N
3	C	404	PLC	O4P-C4-C5-N
3	D	401	PLC	O4P-C4-C5-N
3	D	403	PLC	O4P-C4-C5-N
3	E	401	PLC	O4P-C4-C5-N
3	E	403	PLC	O4P-C4-C5-N
3	D	404	PLC	C2'-C3'-C4'-C5'
3	A	403	PLC	C8'-C9'-CA'-CB'
6	B	409	LMT	C2-C1-O1'-C1'
3	C	405	PLC	C4'-C5'-C6'-C7'
3	A	402	PLC	CB-C1B-C2B-C3B
3	A	402	PLC	C4B-C5B-C6B-C7B
3	E	401	PLC	C1B-C2B-C3B-C4B
3	D	403	PLC	O3P-C1-C2-C3
6	C	410	LMT	C7-C8-C9-C10
3	E	403	PLC	C1'-C2'-C3'-C4'
3	C	404	PLC	CB-C1B-C2B-C3B
3	C	404	PLC	C3'-C4'-C5'-C6'
3	D	401	PLC	C2'-C3'-C4'-C5'
3	D	403	PLC	O2-C2-C3-O3
3	E	403	PLC	C1-C2-C3-O3
3	B	404	PLC	C'-C1'-C2'-C3'
3	D	403	PLC	C3'-C4'-C5'-C6'
6	D	408	LMT	C11-C10-C9-C8
6	D	409	LMT	C7-C8-C9-C10
3	A	412	PLC	C1-O3P-P-O4P
3	B	403	PLC	C1-O3P-P-O1P
3	C	404	PLC	C4-O4P-P-O1P
3	D	403	PLC	C4-O4P-P-O1P
3	E	403	PLC	C4-C5-N-C8

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Mol	Chain	Res	Type	Atoms
3	A	412	PLC	C7B-C8B-C9B-CAA
6	A	409	LMT	C2-C3-C4-C5
3	E	401	PLC	C7B-C8B-C9B-CAA
3	E	403	PLC	O3P-C1-C2-O2
3	B	401	PLC	C3B-C4B-C5B-C6B
3	E	401	PLC	C2'-C3'-C4'-C5'
3	D	403	PLC	C1'-C2'-C3'-C4'
3	C	404	PLC	OB-CB-O3-C3
6	A	410	LMT	C5-C6-C7-C8
6	C	409	LMT	C4-C5-C6-C7
6	E	409	LMT	C1-C2-C3-C4
6	C	410	LMT	C2-C1-O1'-C1'
6	D	409	LMT	C2-C1-O1'-C1'
6	E	409	LMT	C2-C1-O1'-C1'
6	D	409	LMT	O5'-C5'-C6'-O6'
3	E	404	PLC	C3'-C4'-C5'-C6'
6	A	409	LMT	C11-C10-C9-C8
3	A	412	PLC	C6B-C7B-C8B-C9B
6	E	409	LMT	C11-C10-C9-C8
3	C	404	PLC	C1'-C2'-C3'-C4'
3	D	401	PLC	C8B-C9B-CAA-CBA
6	B	409	LMT	C1-C2-C3-C4
3	C	402	PLC	C4B-C5B-C6B-C7B
3	D	404	PLC	C1'-C2'-C3'-C4'
6	D	408	LMT	C7-C8-C9-C10
3	A	412	PLC	C2'-C3'-C4'-C5'
3	B	404	PLC	C8'-C9'-CA'-CB'
3	C	405	PLC	C3'-C4'-C5'-C6'
3	B	403	PLC	OB-CB-O3-C3
6	A	410	LMT	C2-C3-C4-C5
3	B	404	PLC	C1'-C2'-C3'-C4'
3	D	401	PLC	C4B-C5B-C6B-C7B
3	C	404	PLC	C1B-CB-O3-C3
3	E	401	PLC	C6'-C7'-C8'-C9'
3	E	401	PLC	O3P-C1-C2-O2
3	A	412	PLC	C4-C5-N-C8
3	E	403	PLC	C4-C5-N-C7
6	E	409	LMT	C7-C8-C9-C10
3	C	404	PLC	C4B-C5B-C6B-C7B
3	B	403	PLC	C2'-C3'-C4'-C5'
3	E	401	PLC	O3P-C1-C2-C3
3	D	404	PLC	C3'-C4'-C5'-C6'

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Mol	Chain	Res	Type	Atoms
3	E	403	PLC	C4-C5-N-C6
6	A	409	LMT	C3-C4-C5-C6
6	E	409	LMT	O5'-C1'-O1'-C1
3	E	404	PLC	C4'-C5'-C6'-C7'
3	A	412	PLC	C8B-C9B-CAA-CBA
3	D	401	PLC	C4-C5-N-C8
3	E	403	PLC	C2B-C1B-CB-O3
3	B	403	PLC	C1B-CB-O3-C3
3	D	403	PLC	C2B-C1B-CB-O3
3	B	401	PLC	C7B-C8B-C9B-CAA
3	C	402	PLC	C7B-C8B-C9B-CAA
3	A	412	PLC	C4-C5-N-C6
3	D	401	PLC	C4-C5-N-C7
3	C	404	PLC	O2-C'-C1'-C2'
3	D	403	PLC	C2B-C1B-CB-OB
3	A	402	PLC	O2-C2-C3-O3
3	B	401	PLC	C2B-C1B-CB-O3
3	D	403	PLC	C2'-C3'-C4'-C5'
6	E	409	LMT	O5'-C5'-C6'-O6'
3	C	404	PLC	O'-C'-C1'-C2'

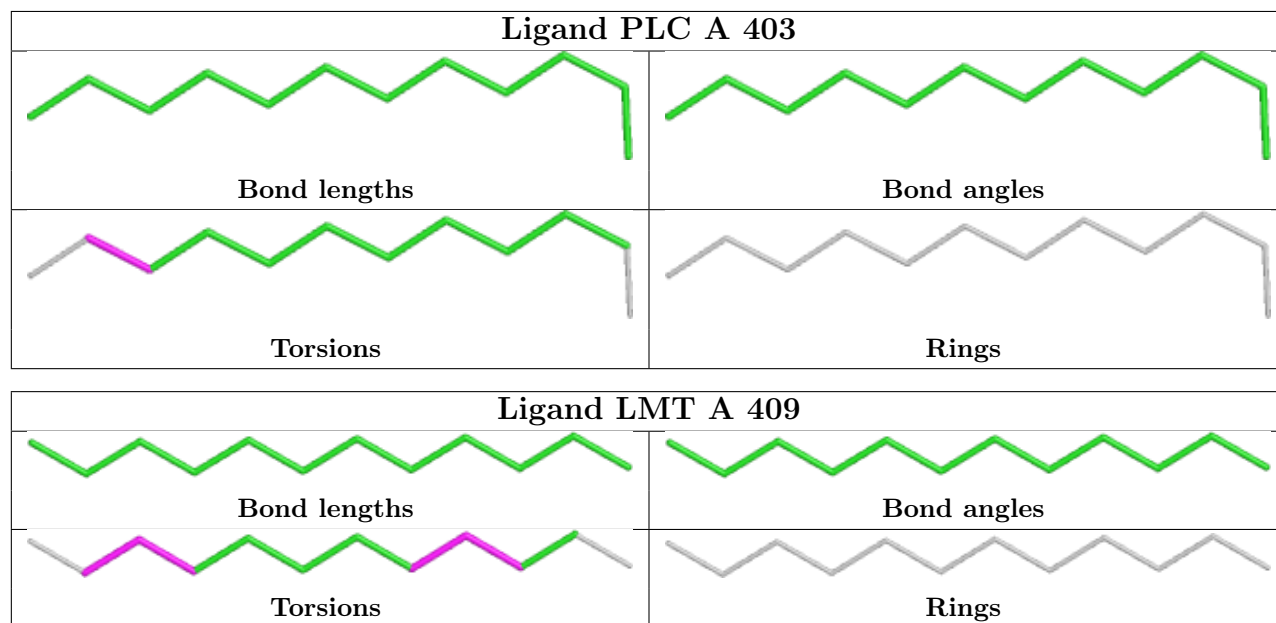
There are no ring outliers.

9 monomers are involved in 9 short contacts:

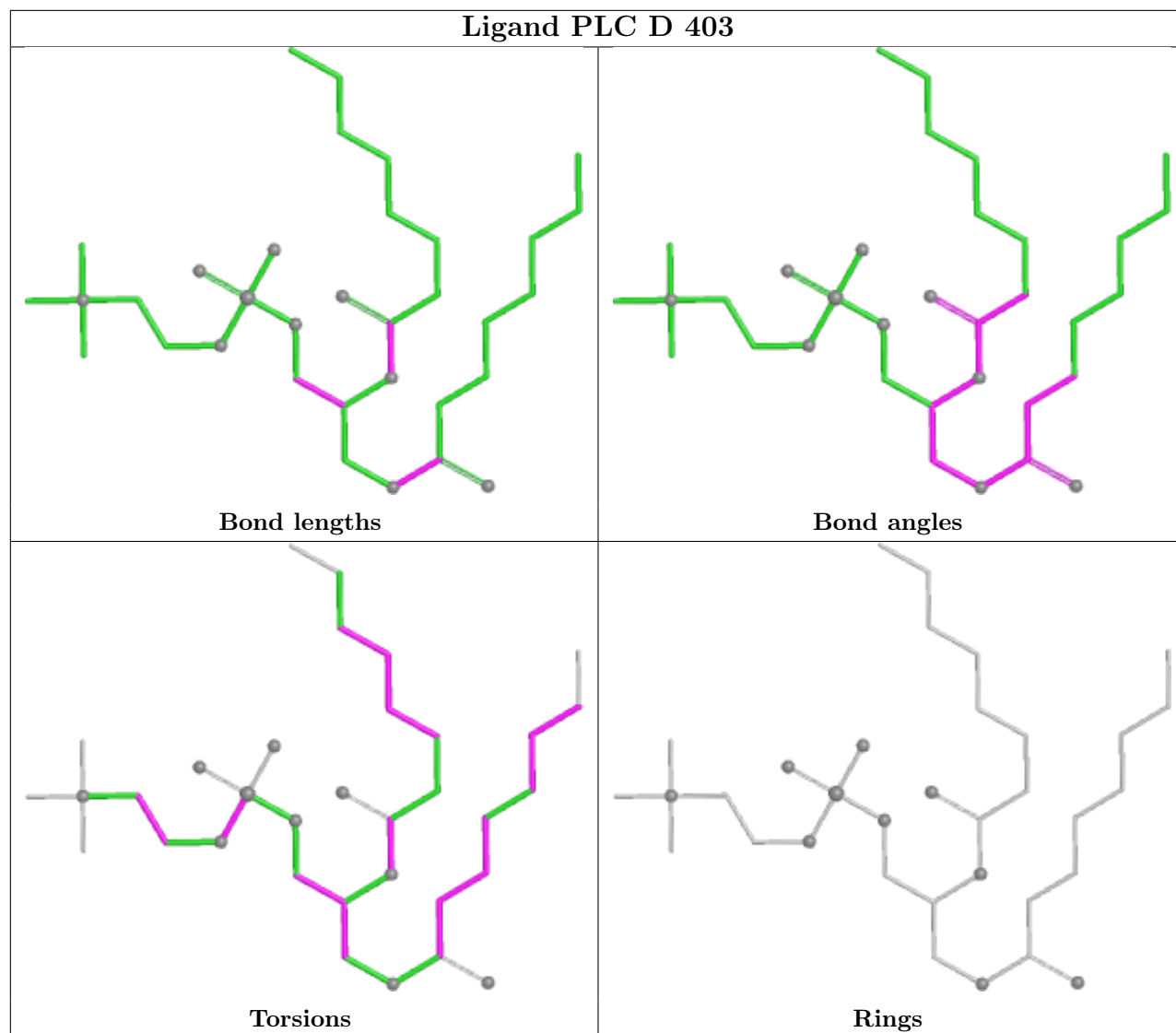
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	402	ACT	1	0
3	A	412	PLC	1	0
2	D	402	ACT	1	0
2	E	402	ACT	1	0
3	C	402	PLC	1	0
2	A	401	ACT	1	0
3	E	401	PLC	1	0
2	C	403	ACT	1	0
3	B	401	PLC	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

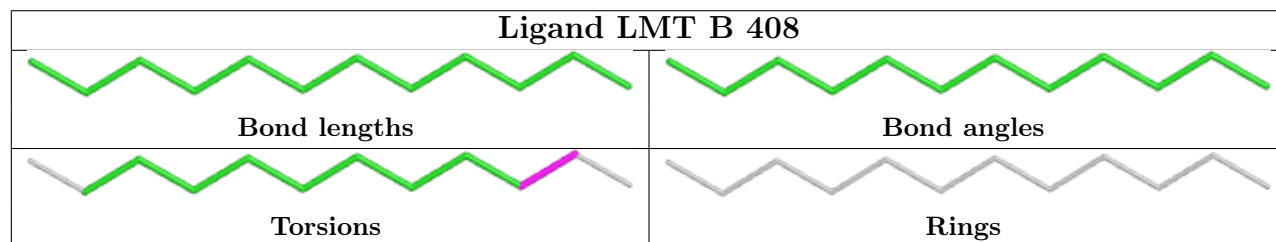
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



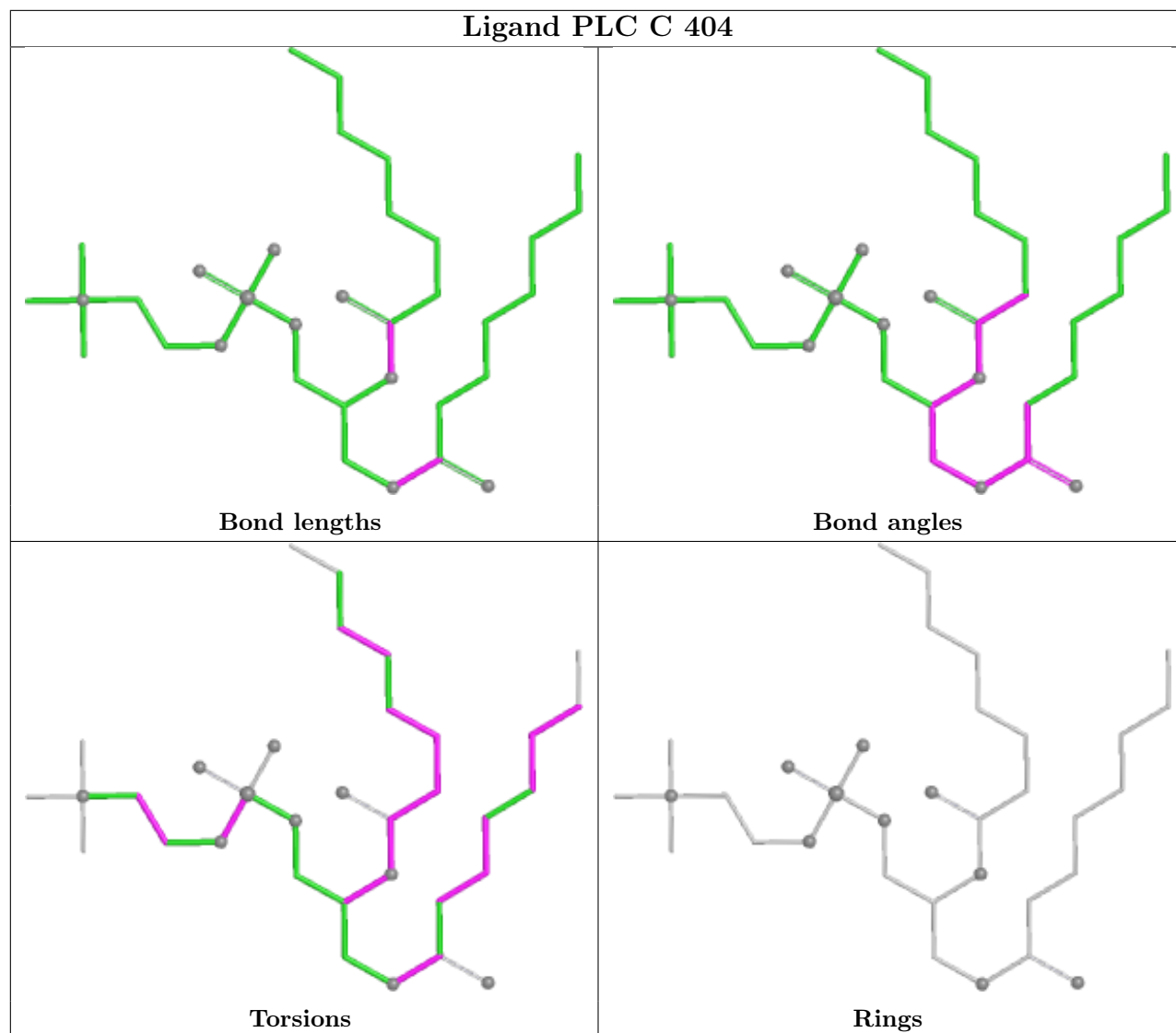
Ligand PLC D 403



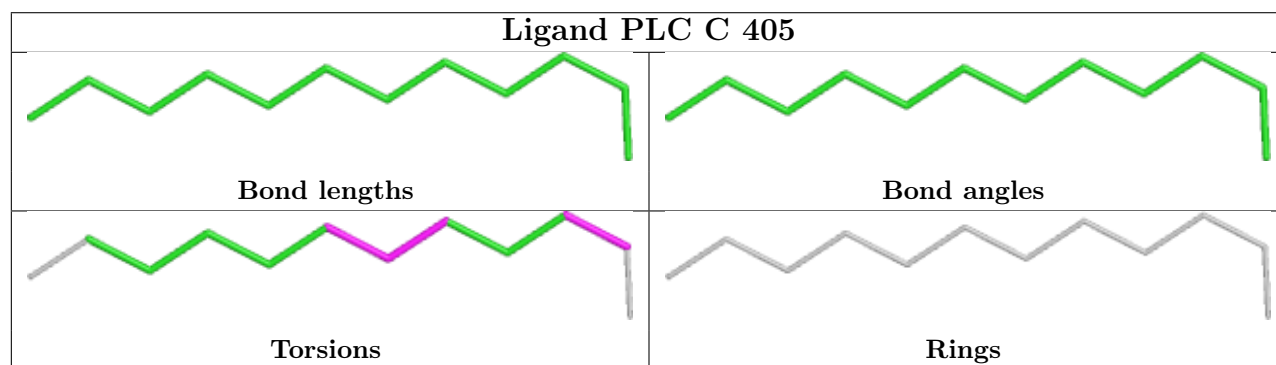
Ligand LMT B 408

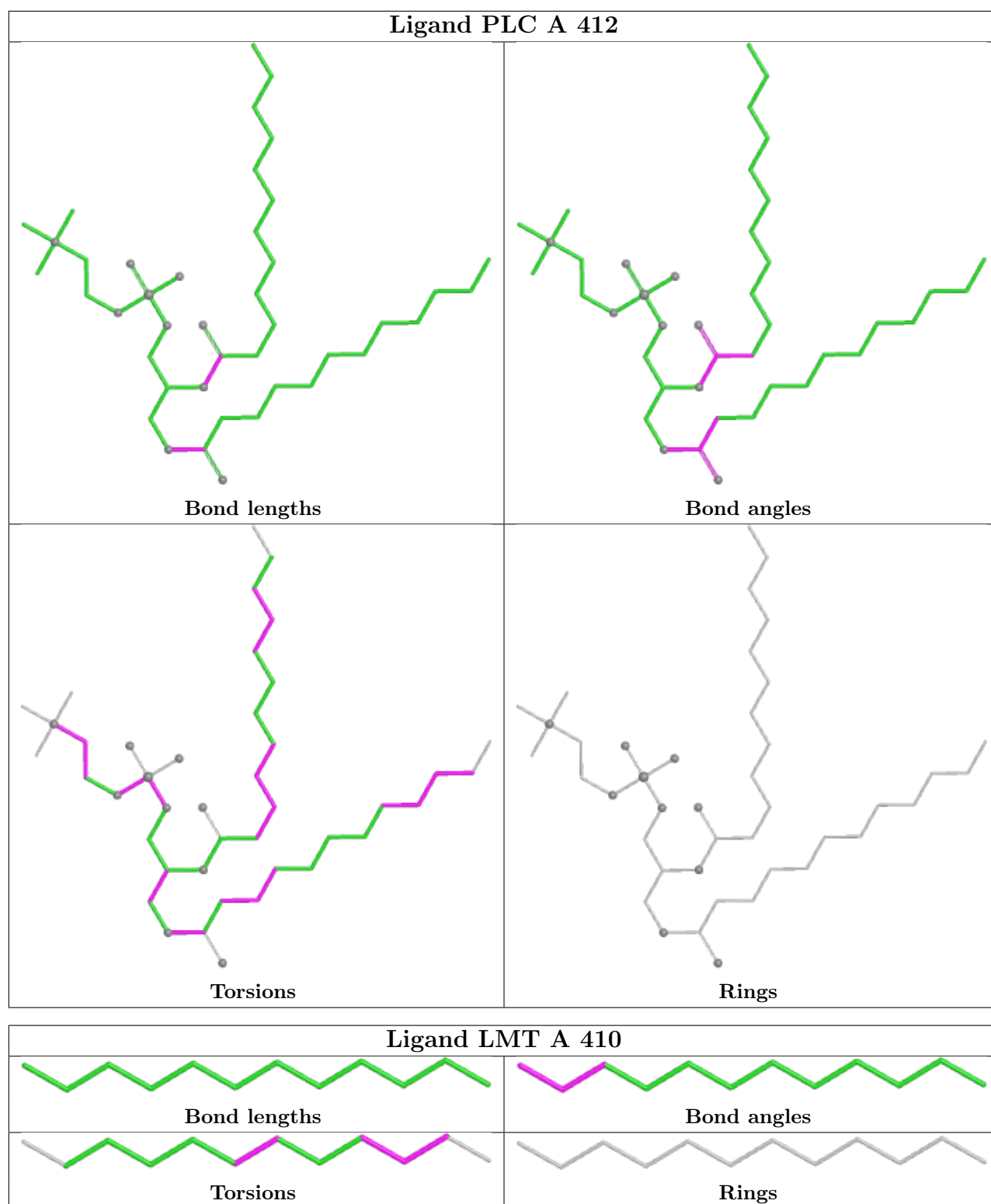


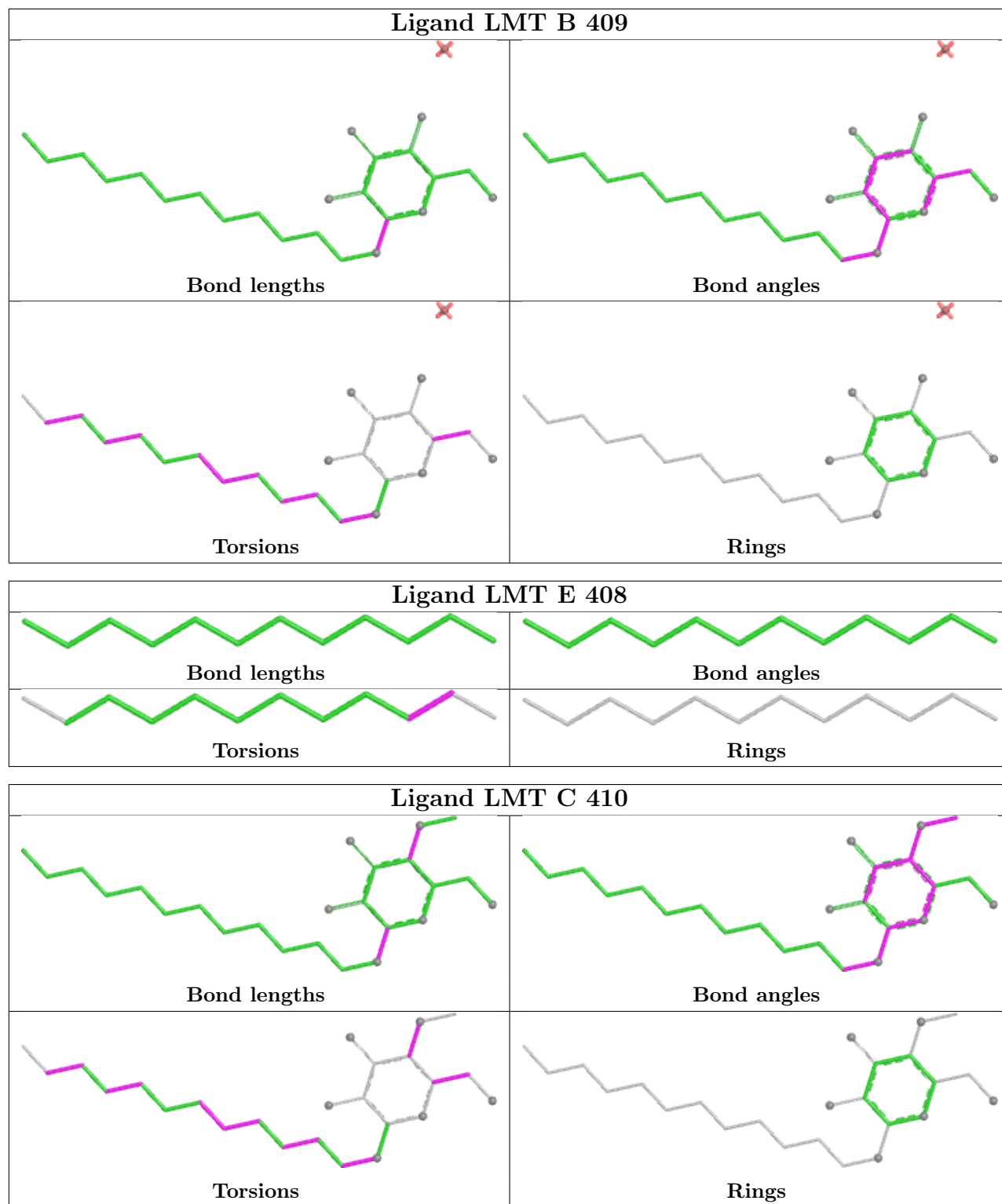
Ligand PLC C 404

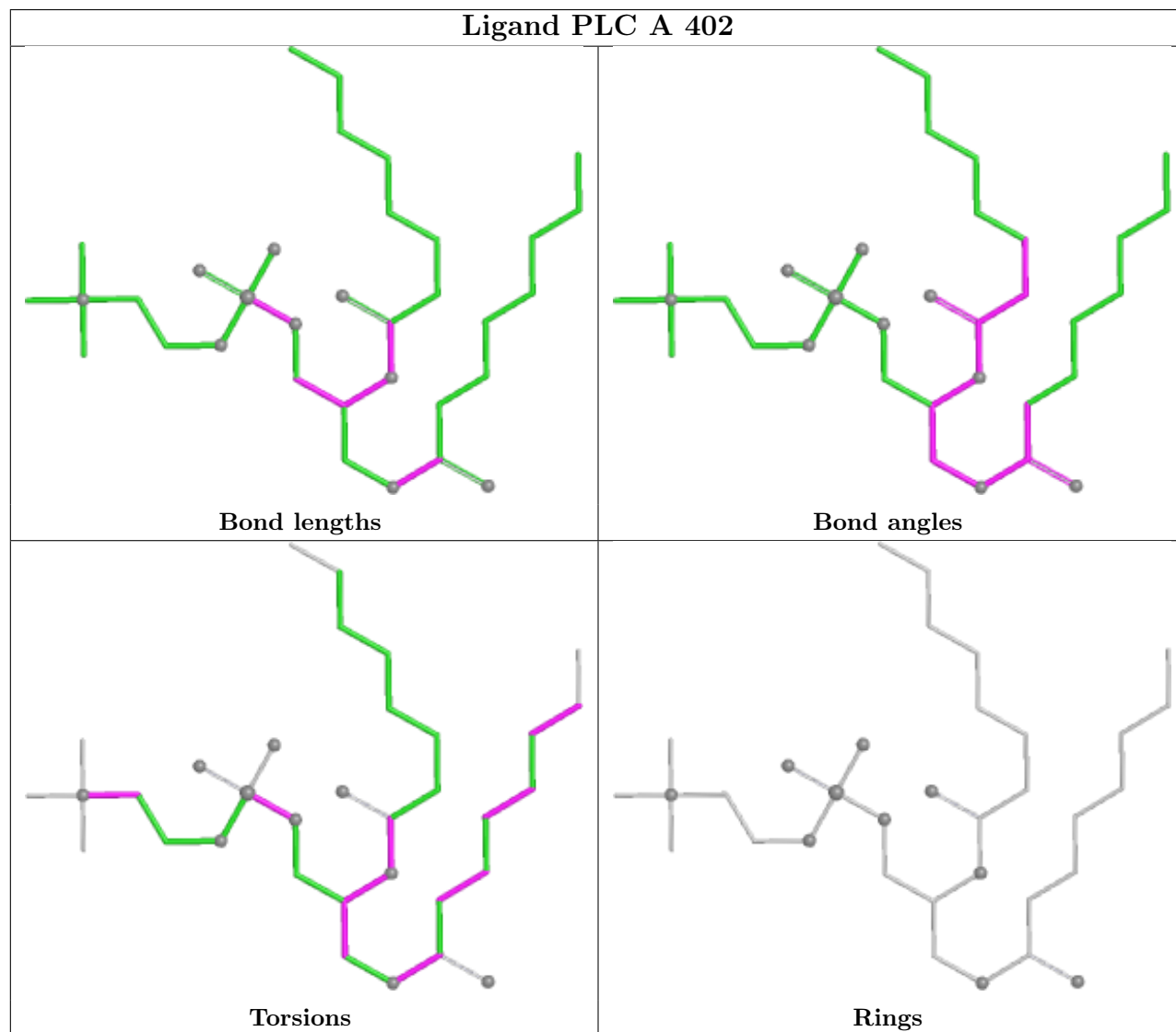
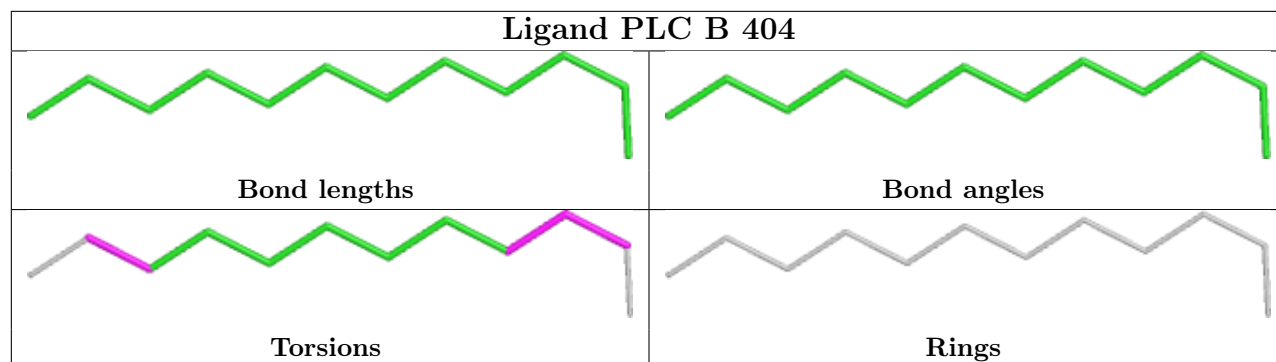


Ligand PLC C 405

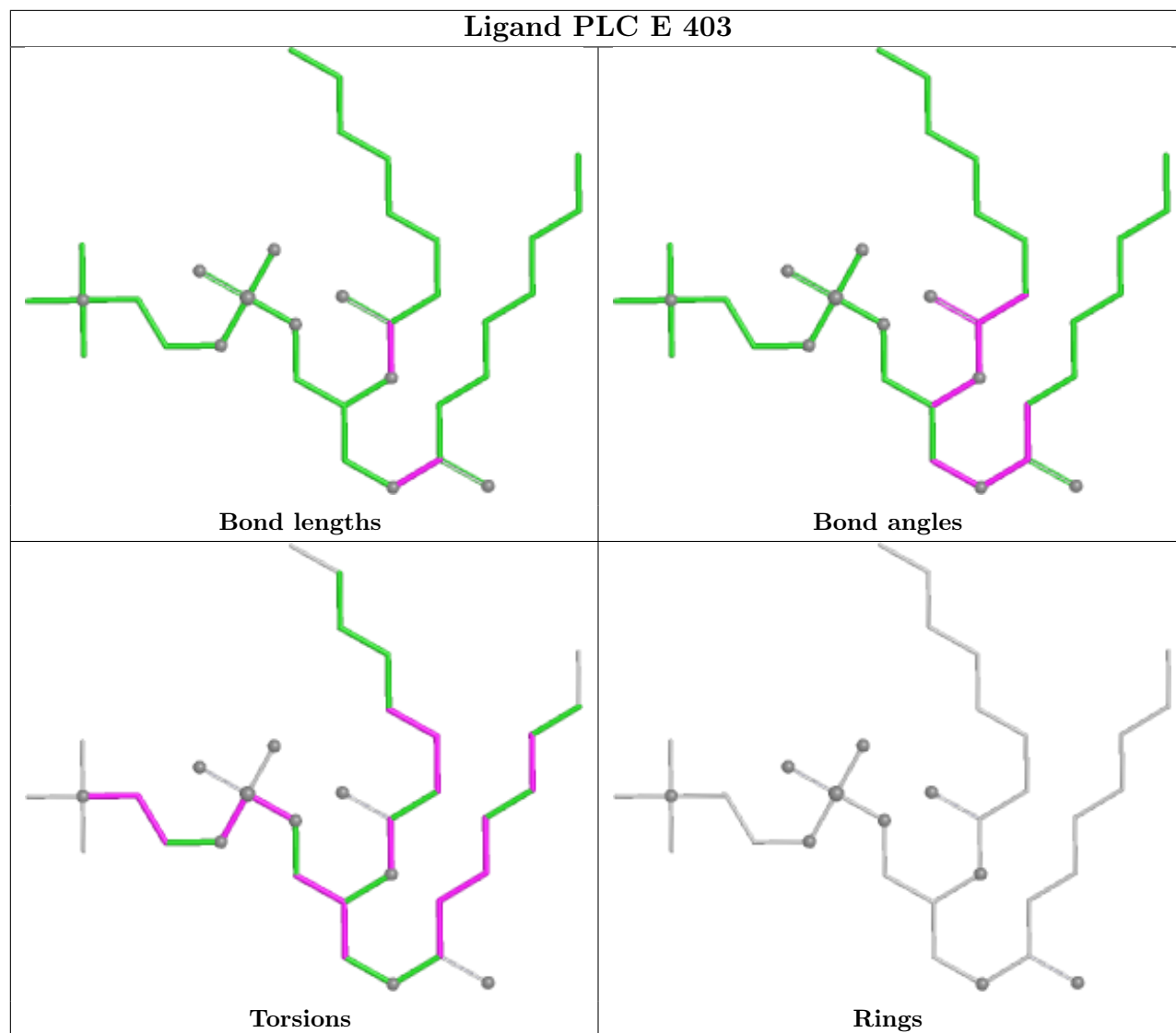




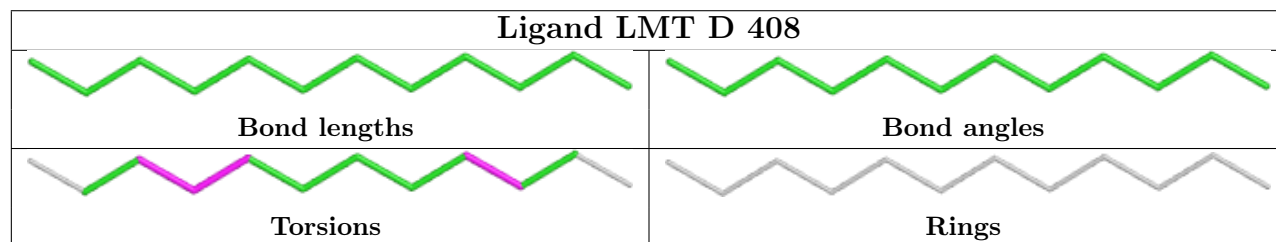


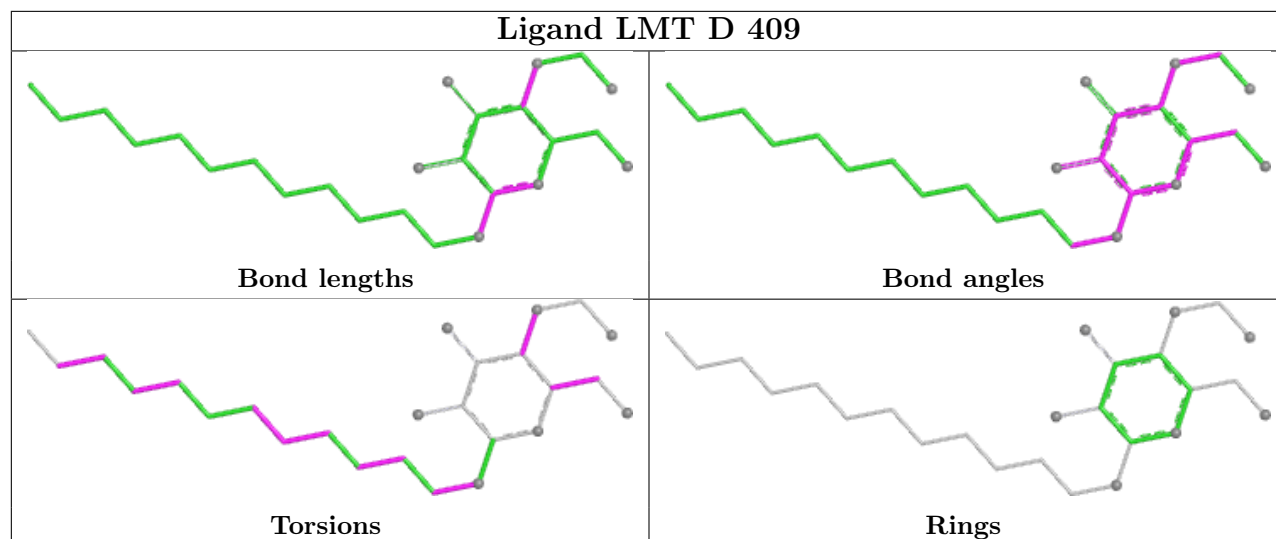


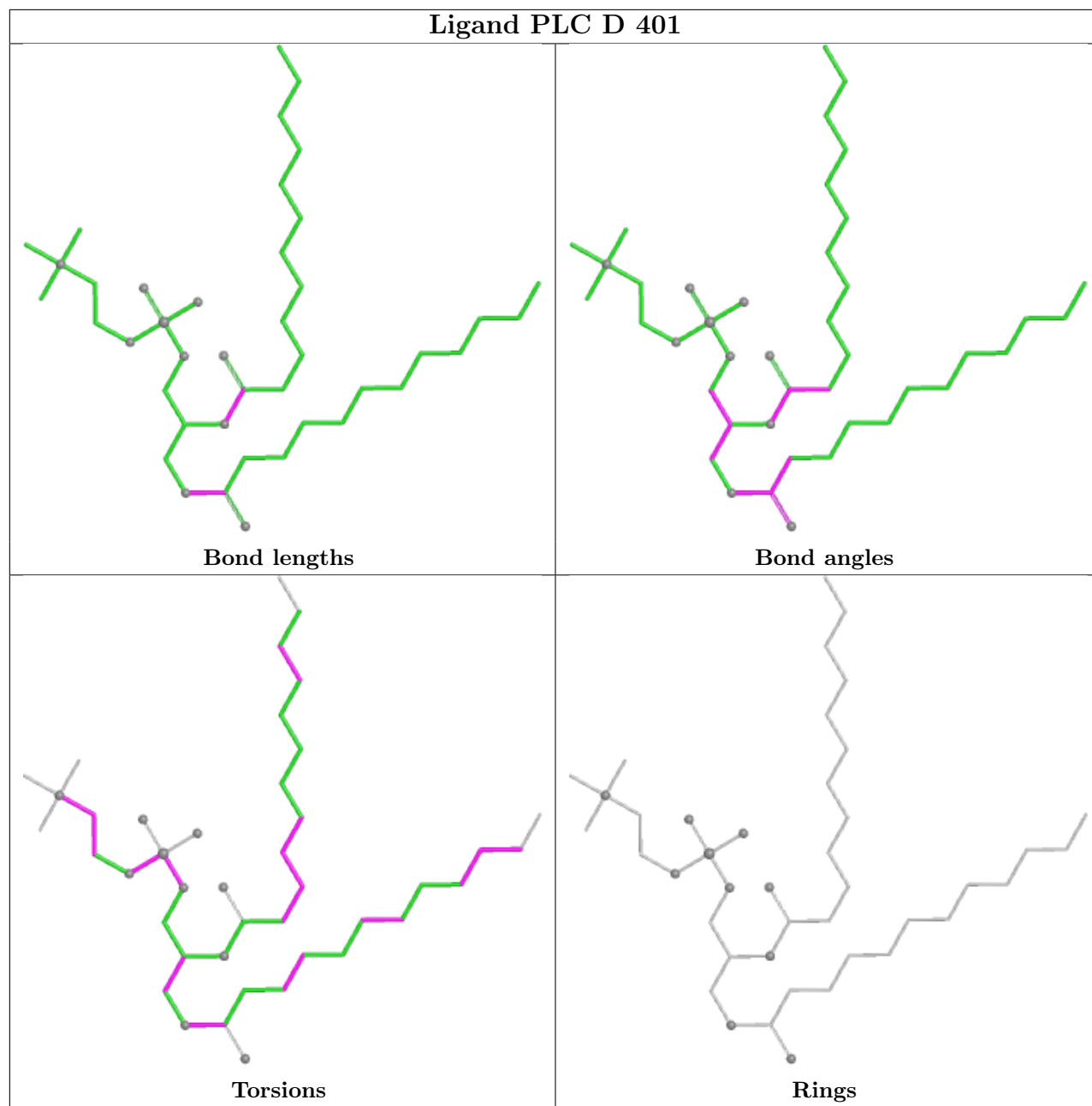
Ligand PLC E 403

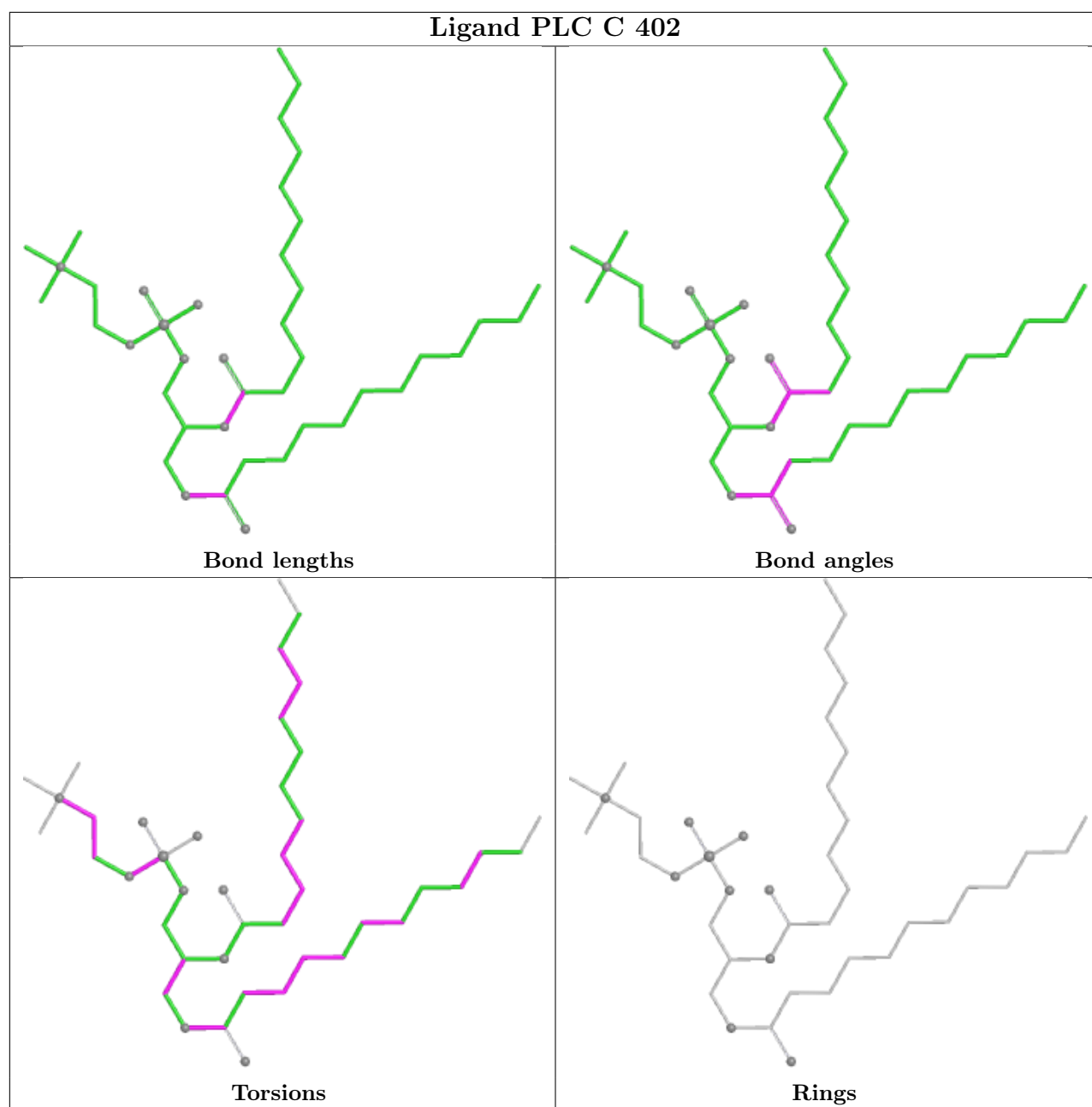


Ligand LMT D 408

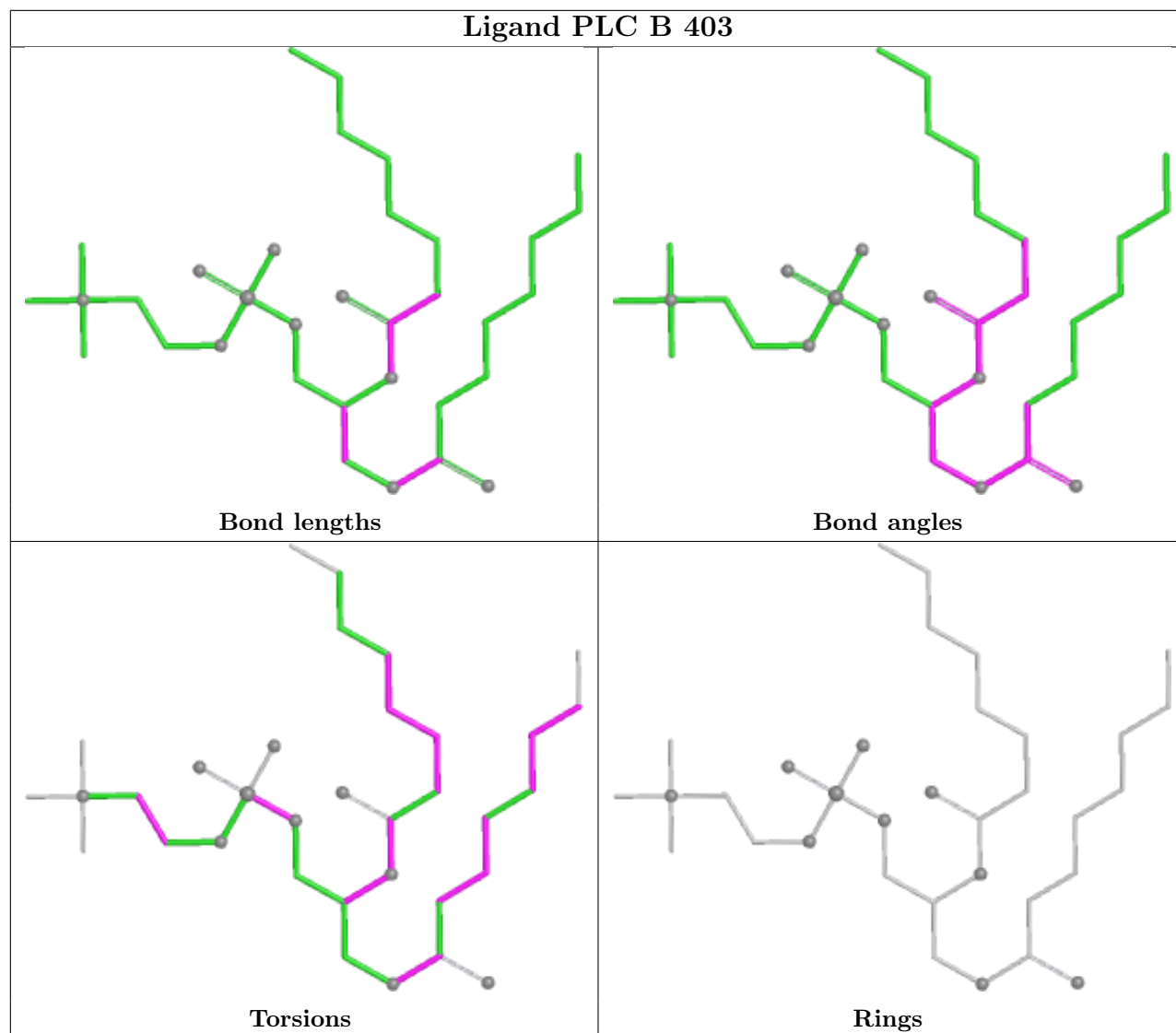




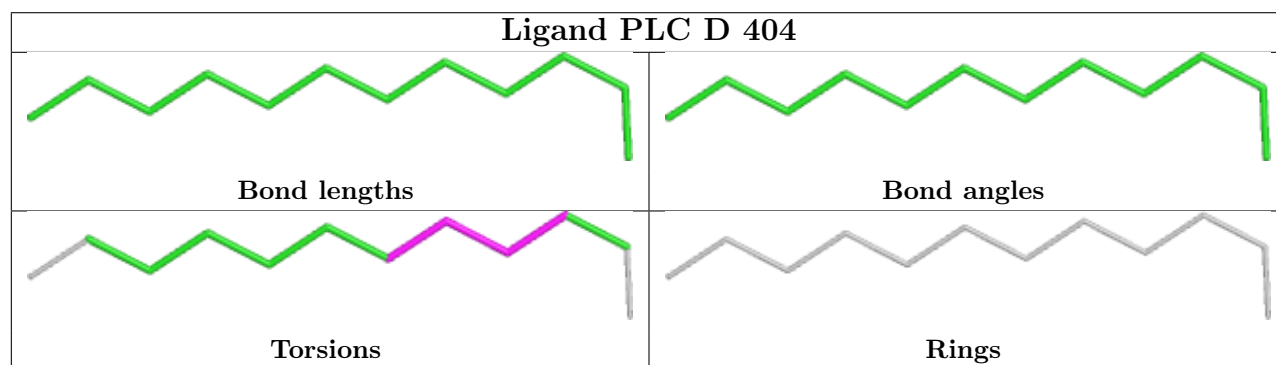


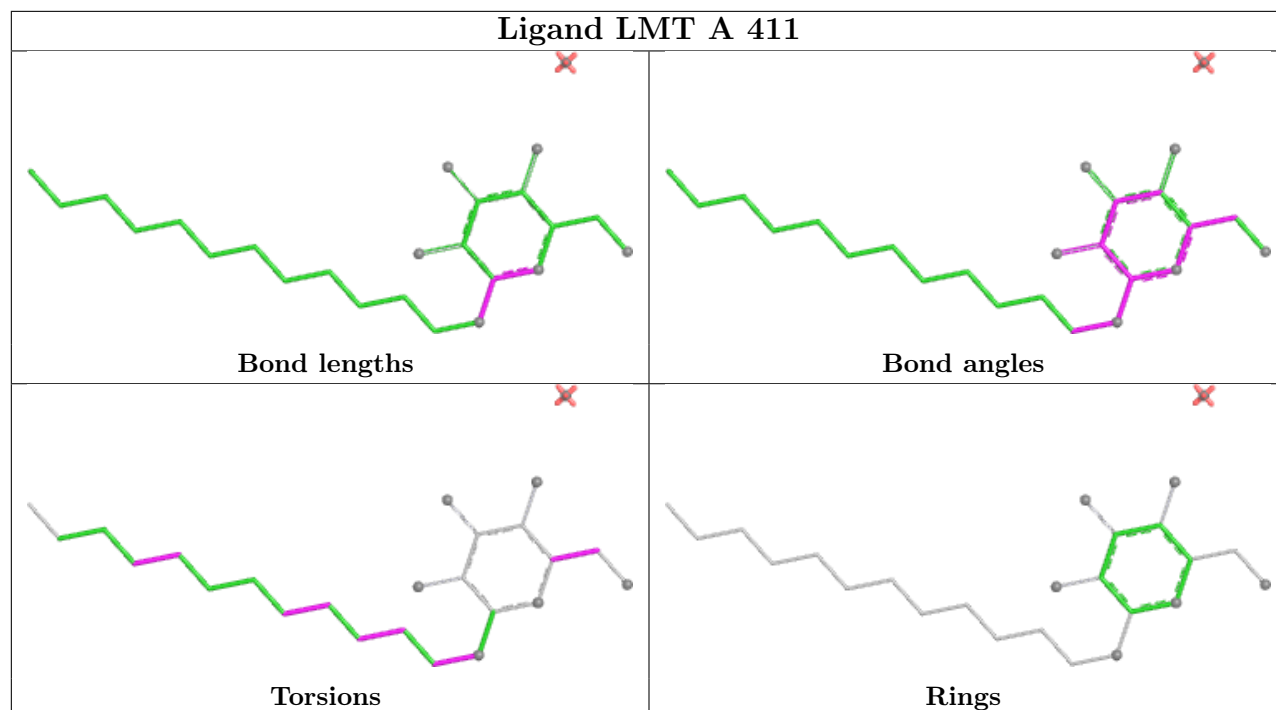


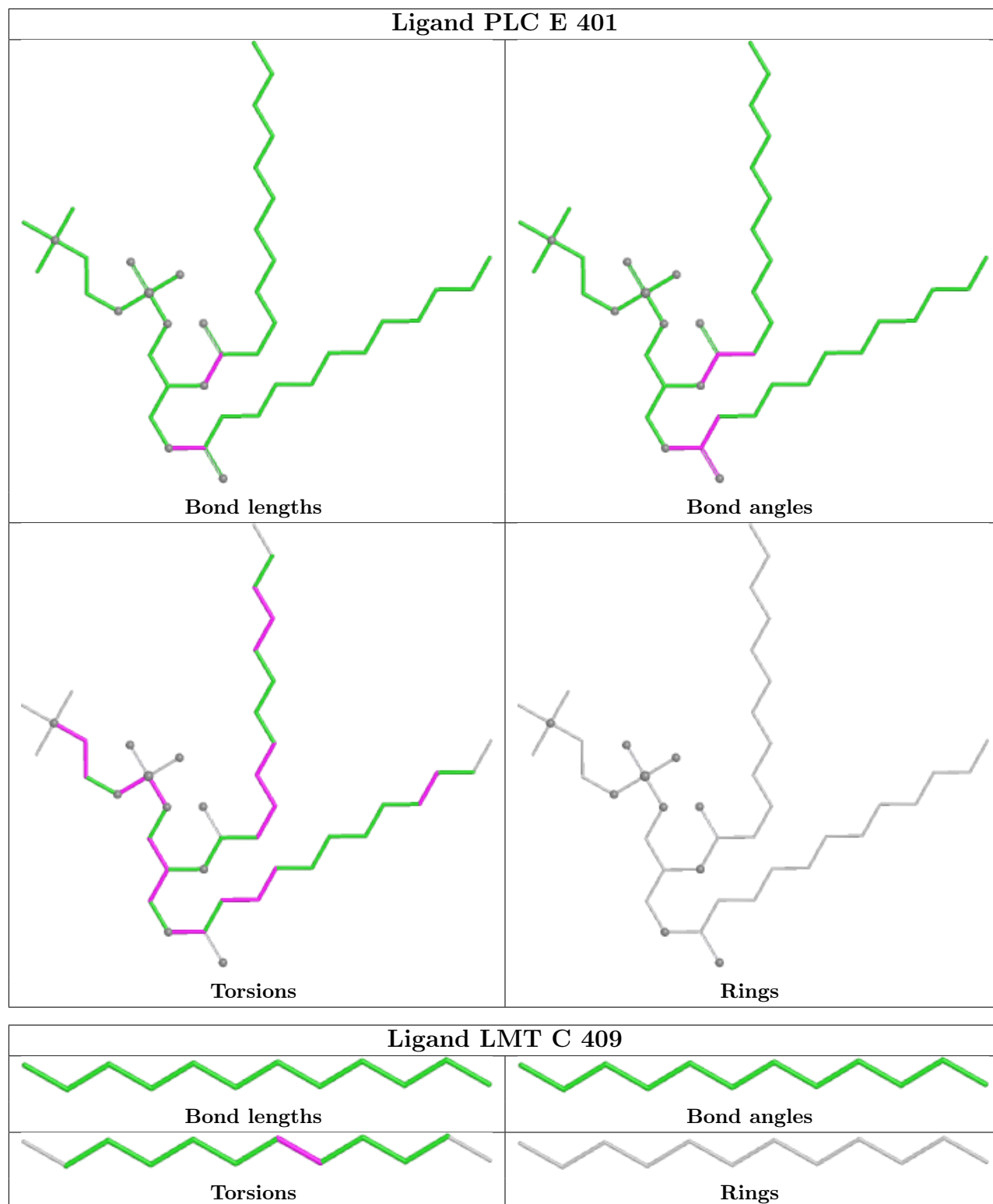
Ligand PLC B 403

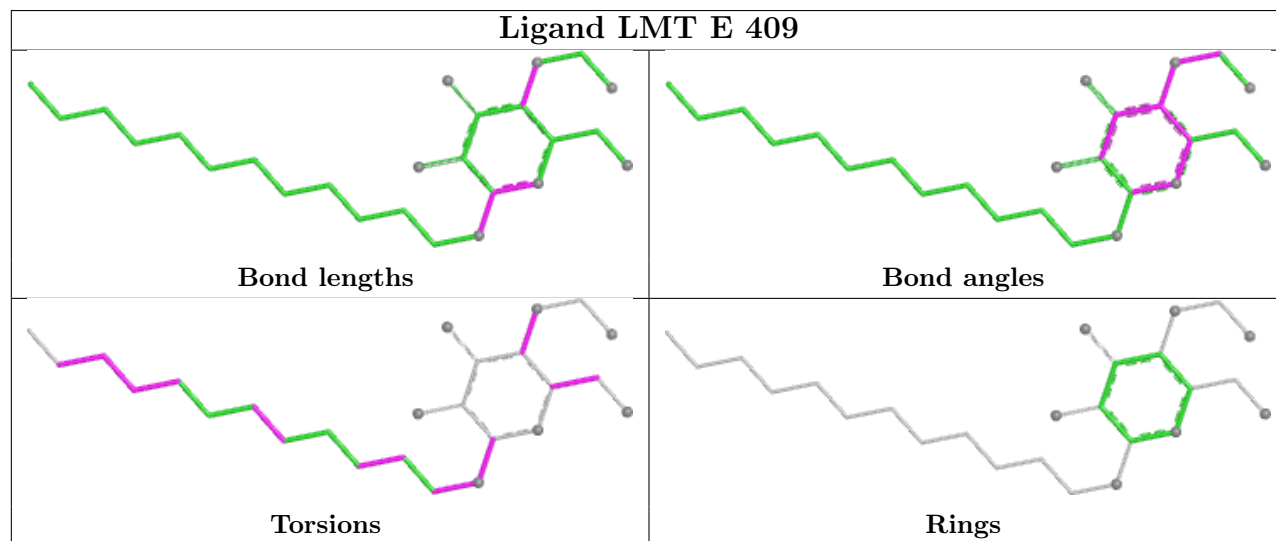
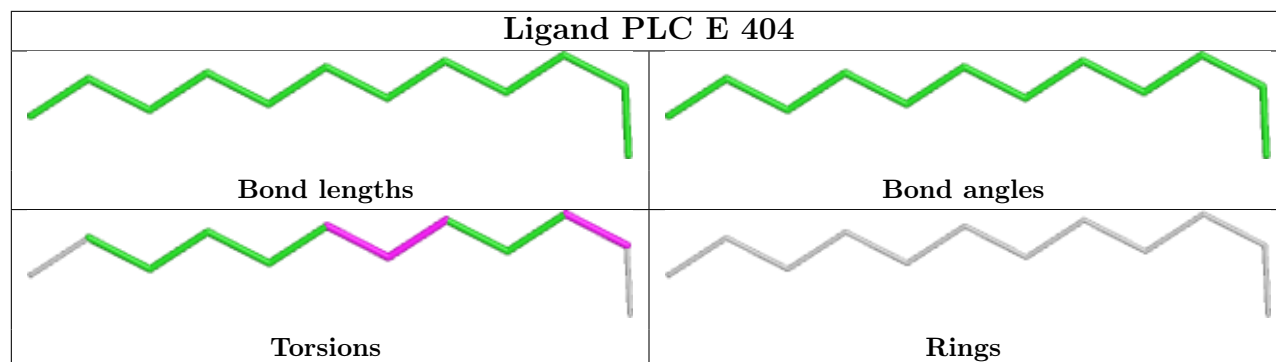


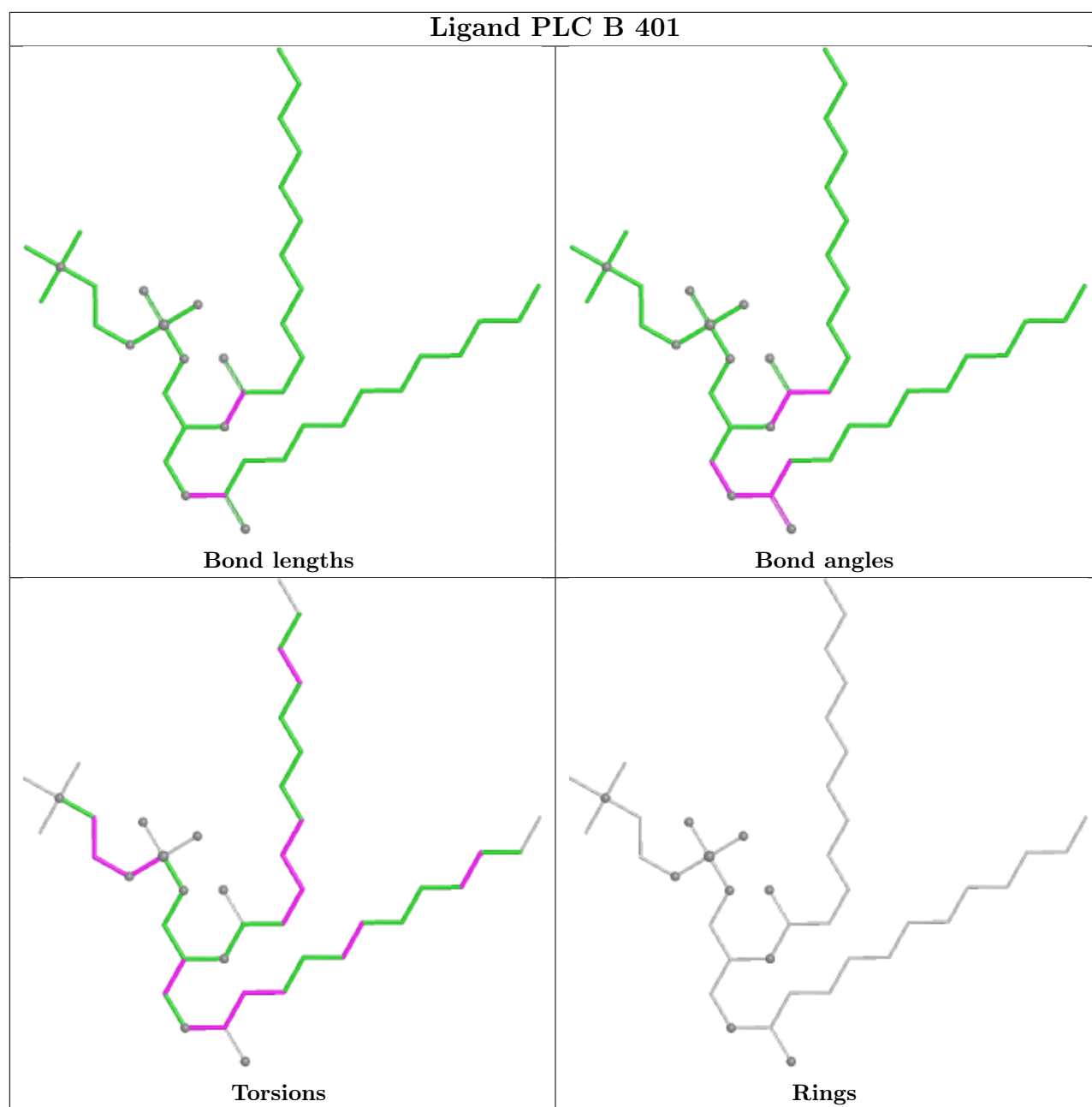
Ligand PLC D 404











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	311/317 (98%)	0.00	11 (3%) 47 44	18, 32, 69, 106	3 (0%)
1	B	311/317 (98%)	-0.07	7 (2%) 61 59	18, 31, 61, 94	3 (0%)
1	C	311/317 (98%)	0.01	12 (3%) 43 40	20, 32, 67, 104	2 (0%)
1	D	311/317 (98%)	0.02	8 (2%) 57 55	17, 32, 71, 100	4 (1%)
1	E	311/317 (98%)	0.01	11 (3%) 47 44	19, 33, 70, 102	3 (0%)
All	All	1555/1585 (98%)	-0.01	49 (3%) 50 47	17, 32, 68, 106	15 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	57	VAL	4.6
1	A	11	ILE	4.5
1	C	61	VAL	4.1
1	E	136	ASP	4.0
1	E	57	VAL	4.0
1	B	11	ILE	3.9
1	A	57	VAL	3.8
1	A	58	ARG	3.8
1	E	11	ILE	3.7
1	C	58	ARG	3.7
1	D	11	ILE	3.6
1	C	11	ILE	3.6
1	B	57	VAL	3.6
1	D	57	VAL	3.4
1	D	180	LEU	3.3
1	C	56	PRO	3.3
1	D	137	THR	3.2
1	C	13	ASP	3.2
1	E	62	ARG	3.1
1	B	136	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	312	PHE	2.9
1	E	61	VAL	2.8
1	A	13	ASP	2.8
1	C	59	SER	2.8
1	A	12	ALA	2.8
1	D	136	ASP	2.7
1	E	58	ARG	2.7
1	C	60	GLY	2.7
1	B	60	GLY	2.7
1	E	63	VAL	2.6
1	E	5	VAL	2.6
1	D	173	ASN	2.5
1	B	59	SER	2.5
1	C	5	VAL	2.4
1	A	136	ASP	2.4
1	D	5	VAL	2.4
1	E	135	VAL	2.4
1	C	245	ASN	2.3
1	B	9	PRO	2.3
1	B	13	ASP	2.3
1	A	14	GLU	2.3
1	E	55	ASP	2.2
1	C	178	ASP	2.2
1	D	12	ALA	2.2
1	C	12	ALA	2.1
1	A	156	PHE	2.1
1	E	137	THR	2.1
1	A	137	THR	2.0
1	A	15	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 oligosaccharides 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(Å ²)	Q<0.9
5	NA	A	407	1/1	0.69	0.16	59,59,59,59	0
5	NA	B	406	1/1	0.71	0.13	53,53,53,53	0
3	PLC	A	412	42/42	0.76	0.20	54,64,133,134	0
5	NA	D	406	1/1	0.76	0.19	62,62,62,62	0
3	PLC	C	402	42/42	0.77	0.20	51,75,115,127	0
3	PLC	B	403	34/42	0.78	0.21	44,85,115,123	0
3	PLC	B	401	42/42	0.78	0.22	52,73,134,145	0
3	PLC	E	403	34/42	0.78	0.20	50,90,117,127	0
3	PLC	A	402	34/42	0.79	0.17	46,76,125,137	0
3	PLC	D	403	34/42	0.79	0.19	38,71,108,130	0
5	NA	C	407	1/1	0.80	0.12	54,54,54,54	0
6	LMT	C	410	25/35	0.80	0.19	58,81,111,119	0
3	PLC	C	405	12/42	0.81	0.24	61,71,93,95	0
6	LMT	A	411	25/35	0.82	0.17	56,71,101,109	0
3	PLC	C	404	34/42	0.82	0.20	42,80,127,148	0
6	LMT	B	409	25/35	0.83	0.18	54,79,116,117	0
3	PLC	D	401	42/42	0.83	0.19	42,67,119,131	0
6	LMT	D	409	26/35	0.83	0.19	50,75,101,105	0
3	PLC	E	401	42/42	0.84	0.16	46,77,122,130	0
5	NA	E	406	1/1	0.84	0.11	55,55,55,55	0
6	LMT	E	409	26/35	0.85	0.20	60,85,114,118	0
3	PLC	E	404	12/42	0.86	0.20	64,73,79,81	0
3	PLC	B	404	12/42	0.87	0.17	57,61,77,83	0
3	PLC	A	403	12/42	0.88	0.17	65,67,73,73	0
6	LMT	B	408	12/35	0.88	0.10	29,35,50,55	0
6	LMT	A	410	12/35	0.88	0.12	29,34,51,53	0
3	PLC	D	404	12/42	0.89	0.16	58,66,78,79	0
6	LMT	E	408	12/35	0.90	0.10	26,33,39,41	0
6	LMT	A	409	12/35	0.91	0.11	33,41,70,72	0
6	LMT	C	409	12/35	0.92	0.08	28,31,42,43	0
2	ACT	E	402	4/4	0.92	0.10	39,39,40,44	0
6	LMT	D	408	12/35	0.92	0.10	28,29,38,41	0
2	ACT	B	402	4/4	0.93	0.10	36,40,40,44	0
4	CL	A	406	1/1	0.93	0.18	61,61,61,61	0
2	ACT	E	407	4/4	0.93	0.12	37,38,43,48	0
2	ACT	D	407	4/4	0.94	0.09	38,39,42,52	0
5	NA	C	401	1/1	0.95	0.30	57,57,57,57	0

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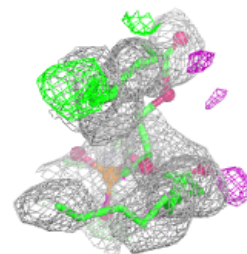
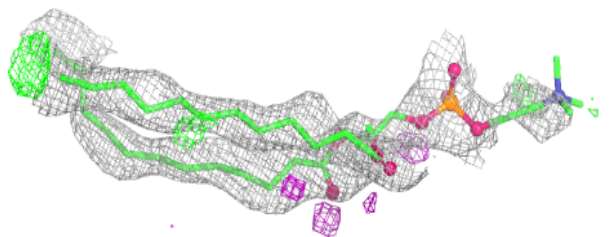
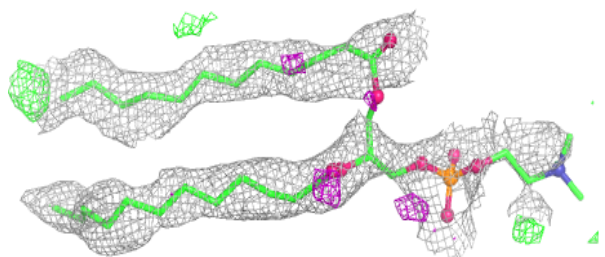
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ACT	D	402	4/4	0.95	0.09	32,35,39,47	0
2	ACT	A	401	4/4	0.95	0.10	37,38,38,39	0
2	ACT	B	407	4/4	0.96	0.09	38,40,42,45	0
2	ACT	C	403	4/4	0.96	0.12	34,37,39,40	0
2	ACT	C	408	4/4	0.96	0.08	32,33,33,43	0
2	ACT	A	408	4/4	0.96	0.07	34,36,41,43	0
4	CL	A	405	1/1	0.98	0.09	49,49,49,49	0
4	CL	C	406	1/1	0.99	0.03	33,33,33,33	0
4	CL	D	405	1/1	0.99	0.05	30,30,30,30	0
4	CL	E	405	1/1	0.99	0.04	34,34,34,34	0
4	CL	A	404	1/1	0.99	0.03	35,35,35,35	0
4	CL	B	405	1/1	0.99	0.05	32,32,32,32	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.

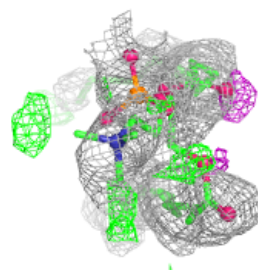
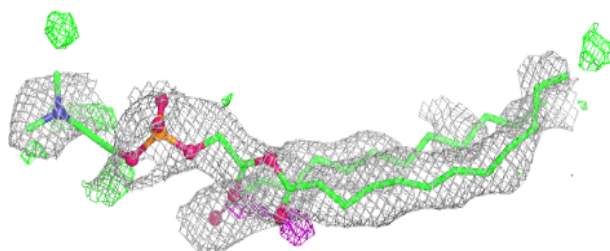
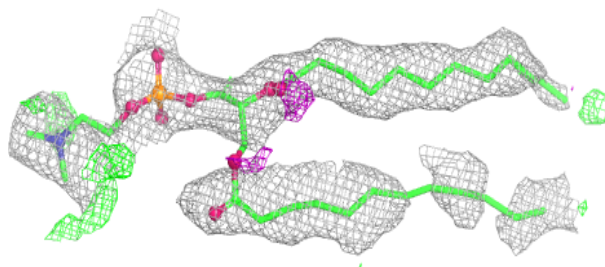
Electron density around PLC A 412:

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

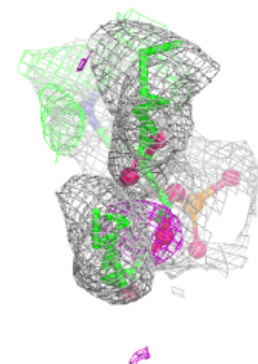
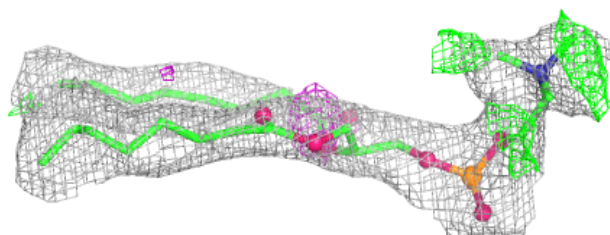
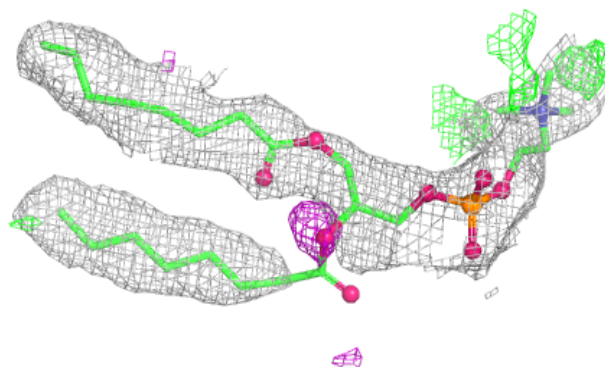


Electron density around PLC C 402:

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

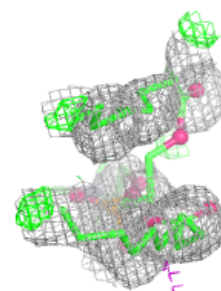
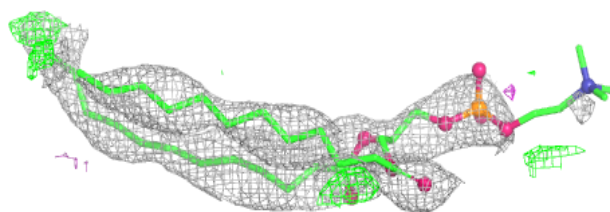
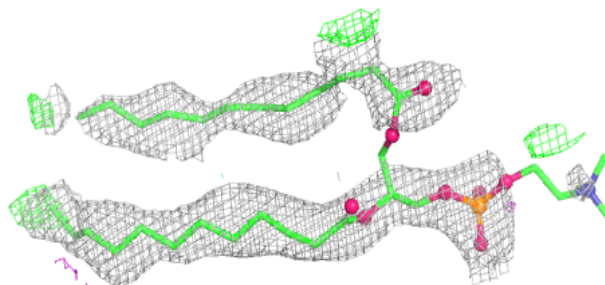
**Electron density around PLC B 403:**

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

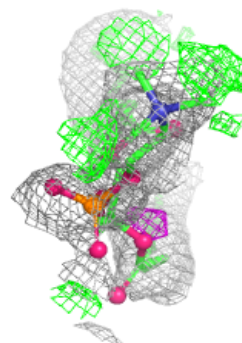
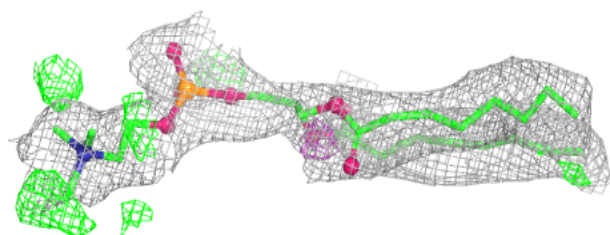
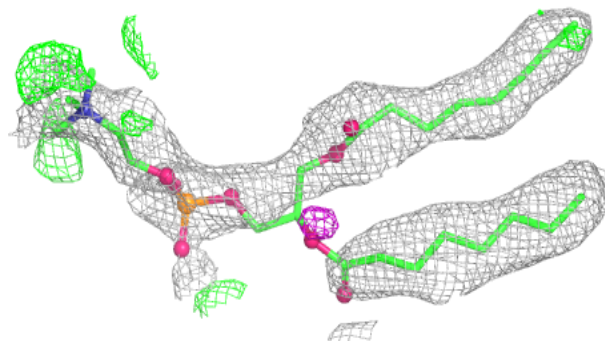


Electron density around PLC B 401:

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and green (positive)

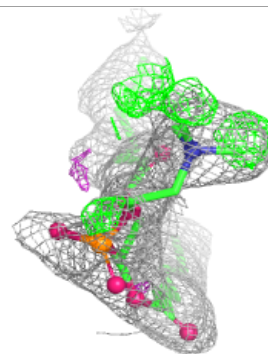
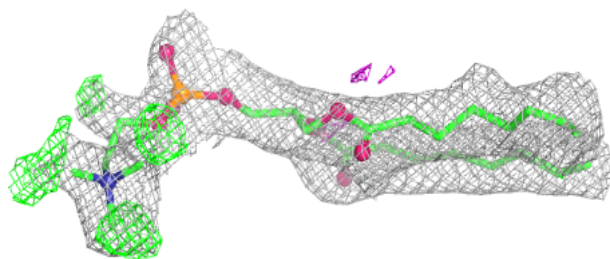
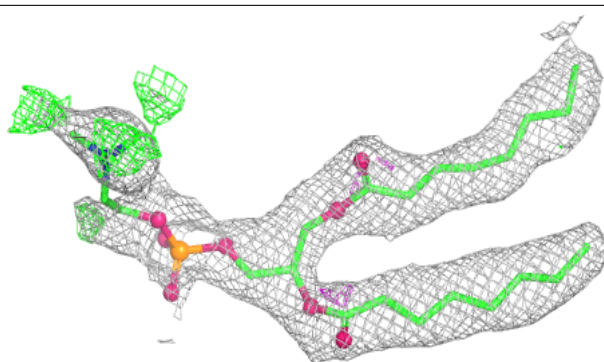
**Electron density around PLC E 403:**

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and green (positive)

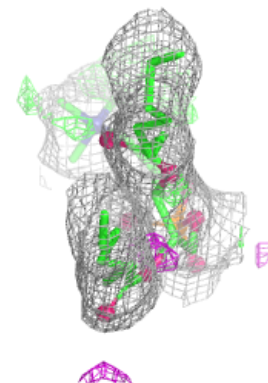
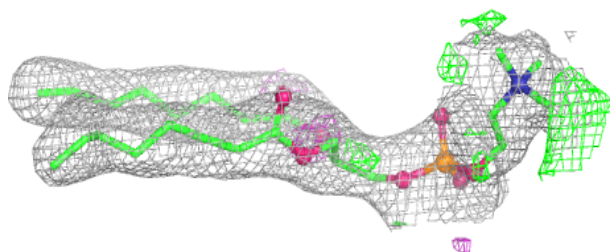
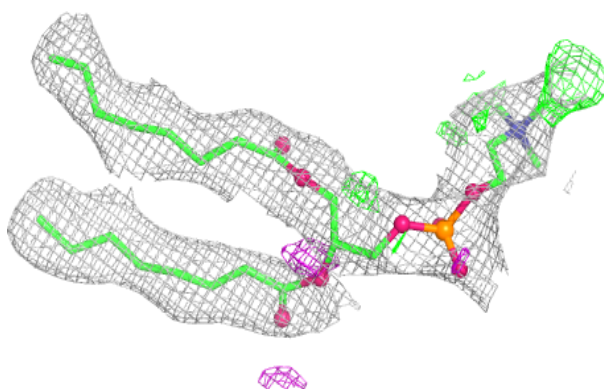


Electron density around PLC A 402:

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

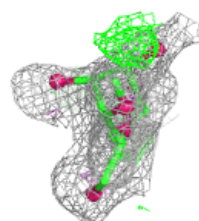
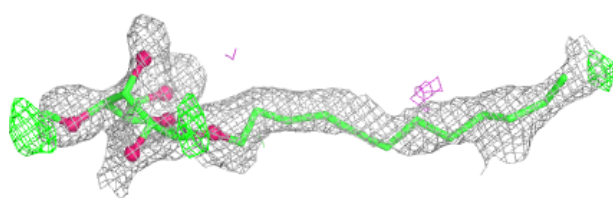
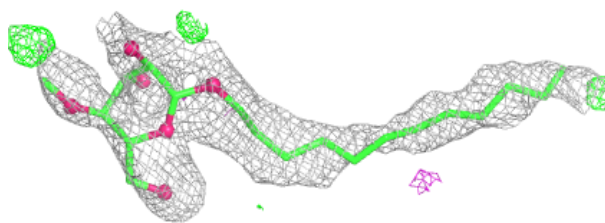
**Electron density around PLC D 403:**

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

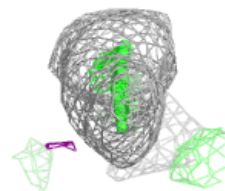
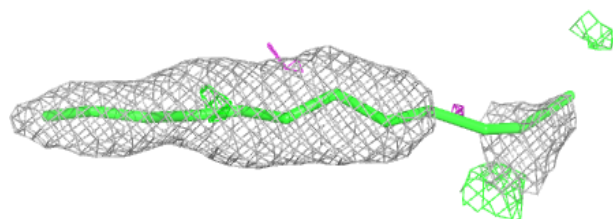
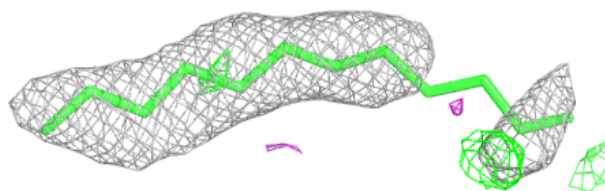


Electron density around LMT C 410:

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and green (positive)

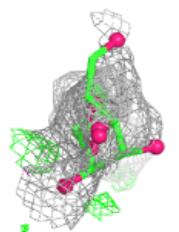
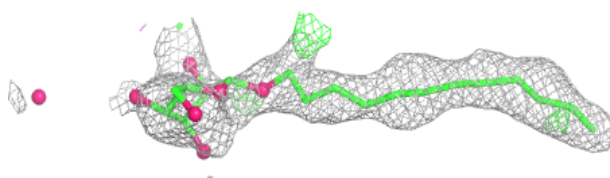
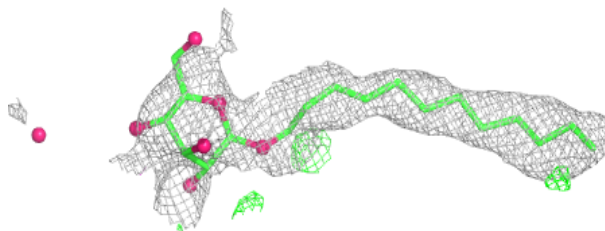
**Electron density around PLC C 405:**

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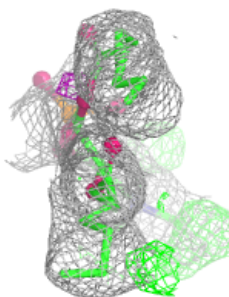
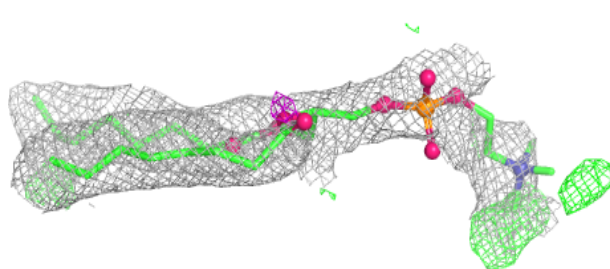
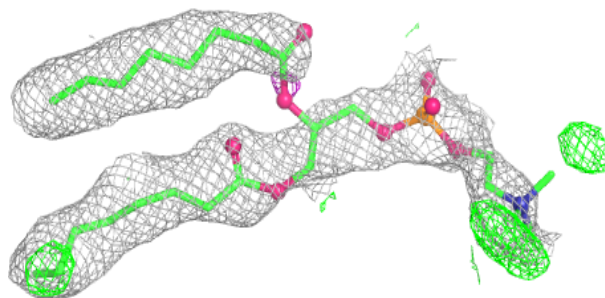


Electron density around LMT A 411:

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and green (positive)

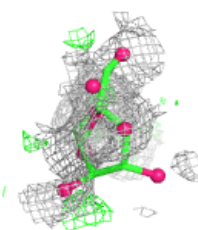
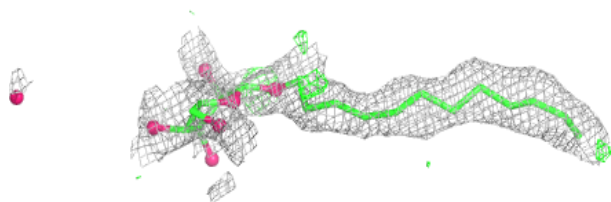
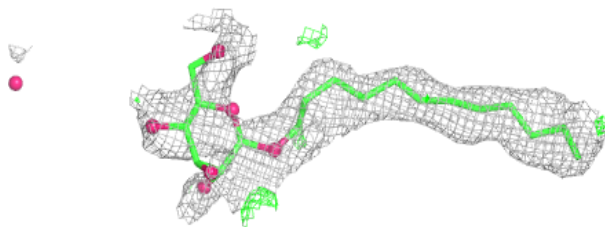
**Electron density around PLC C 404:**

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and green (positive)

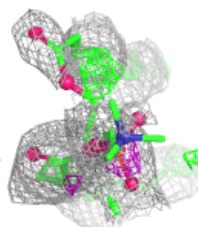
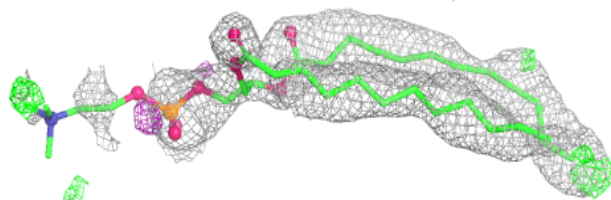
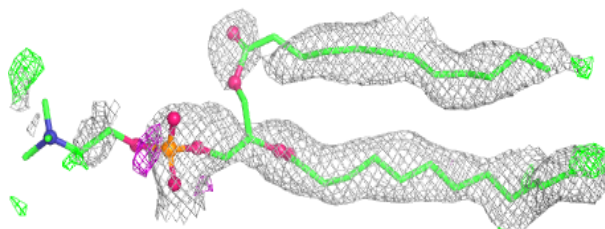


Electron density around LMT B 409:

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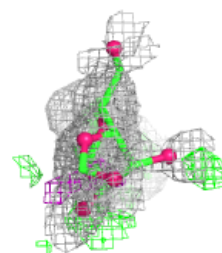
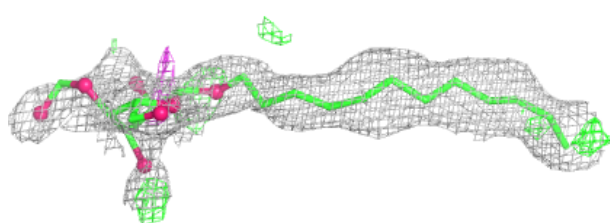
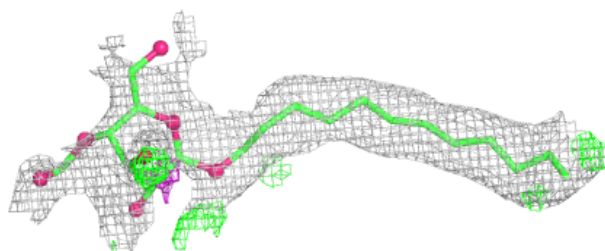
**Electron density around PLC D 401:**

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

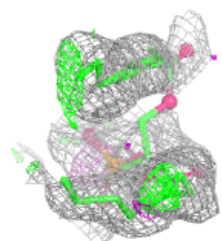
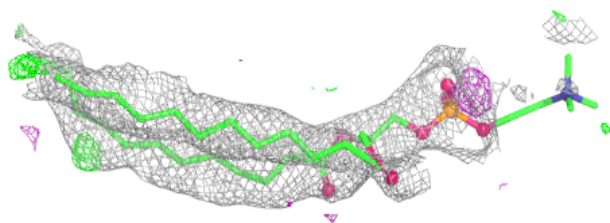
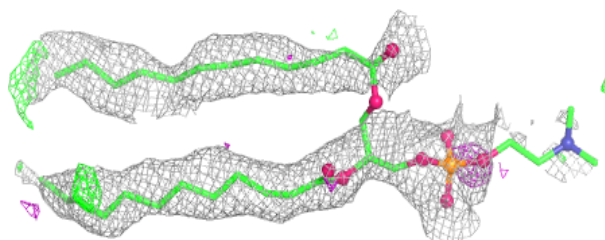


Electron density around LMT D 409:

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

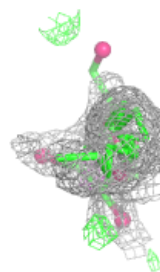
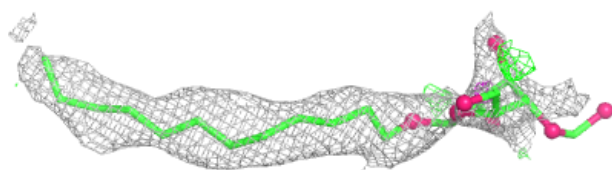
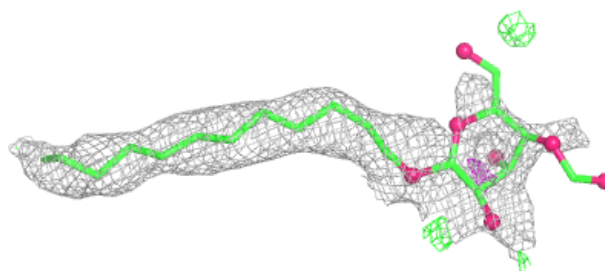
**Electron density around PLC E 401:**

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

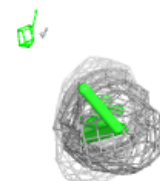
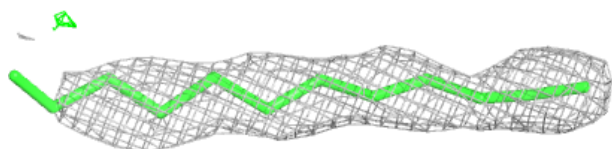
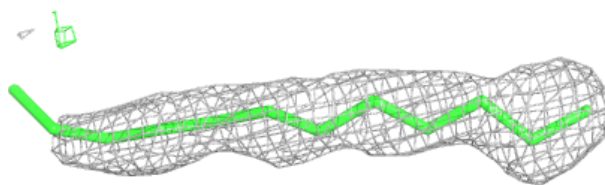


Electron density around LMT E 409:

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

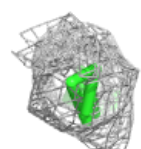
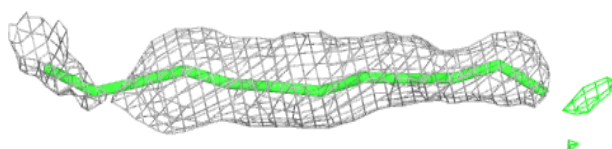
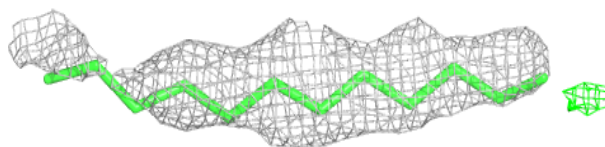
**Electron density around PLC E 404:**

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

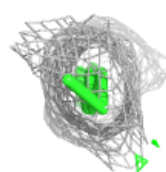
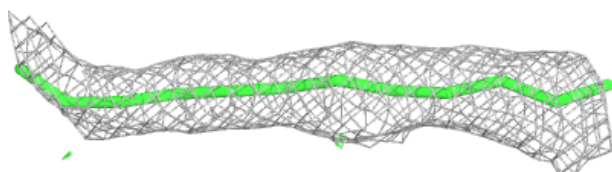
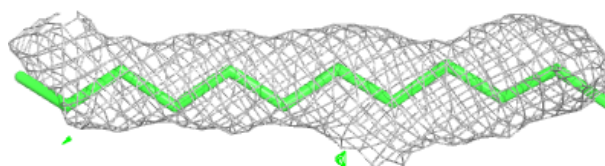


Electron density around PLC B 404:

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

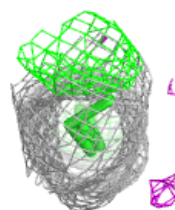
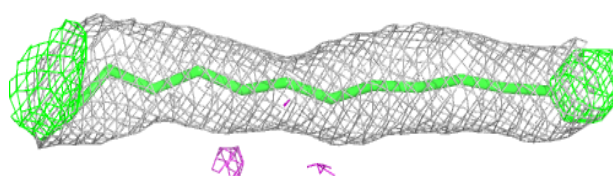
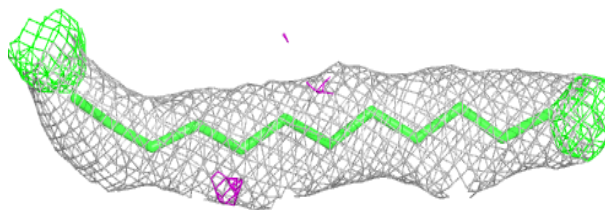
**Electron density around PLC A 403:**

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

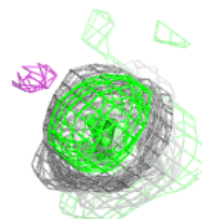
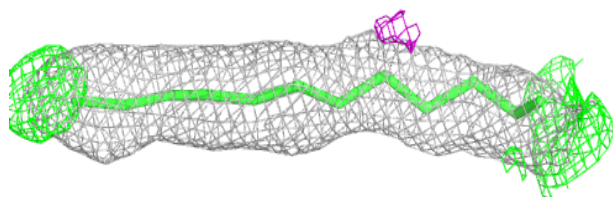
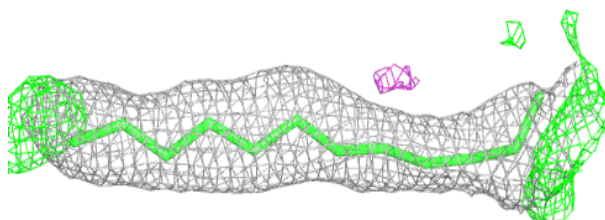


Electron density around LMT B 408:

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

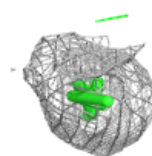
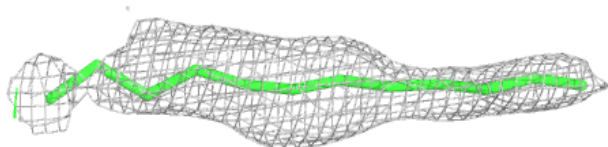
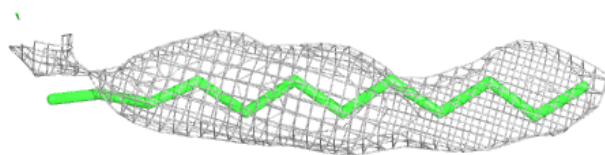
**Electron density around LMT A 410:**

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

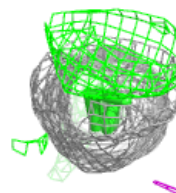
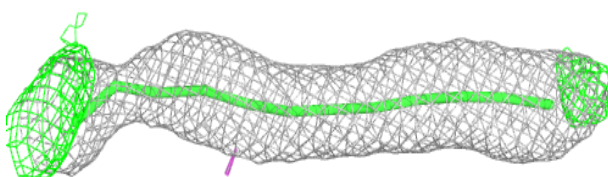
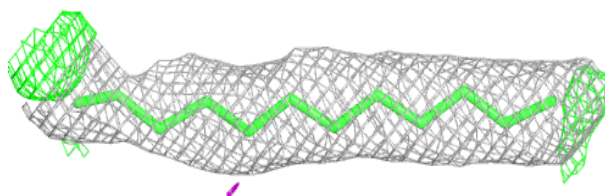


Electron density around PLC D 404:

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

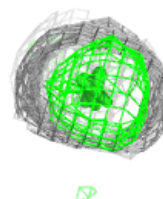
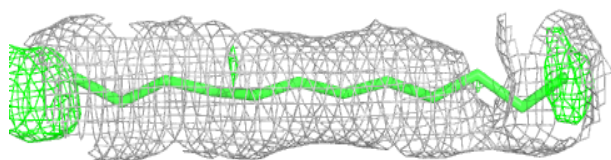
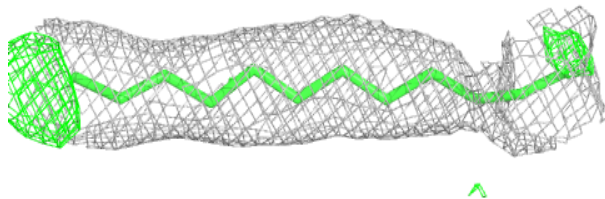
**Electron density around LMT E 408:**

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

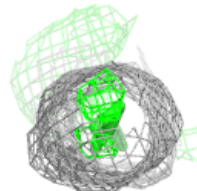
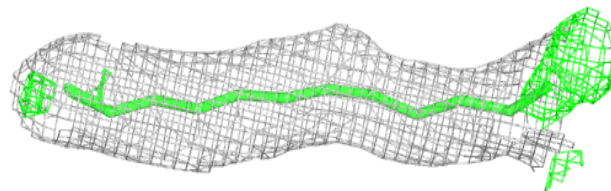
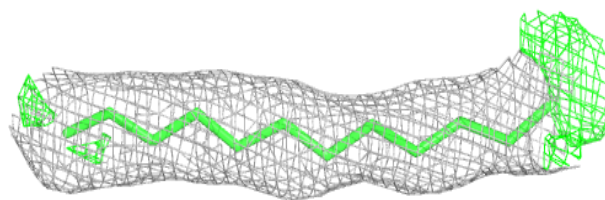


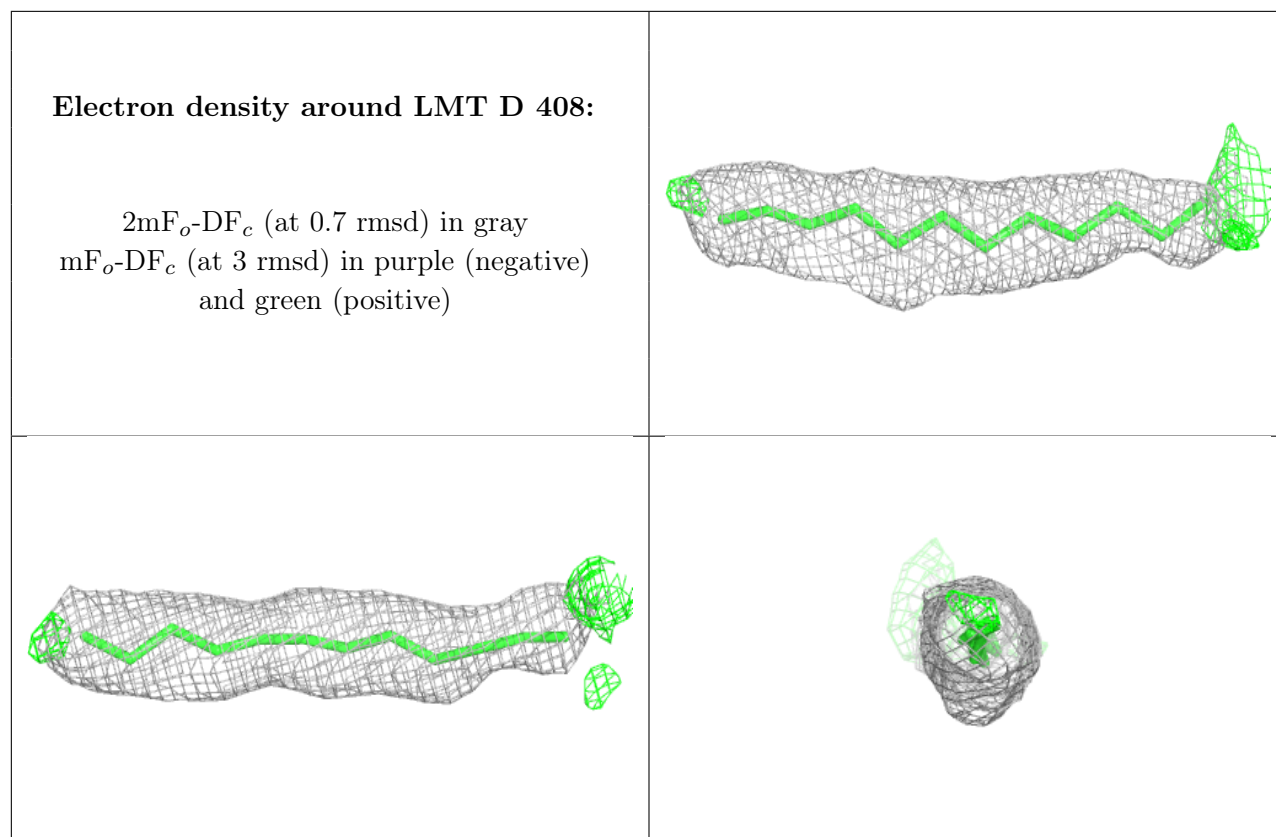
Electron density around LMT A 409:

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

**Electron density around LMT C 409:**

$2mF_o-DF_c$ (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.