



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 09:59 PM BST

PDB ID : 6HJZ  
Title : Xray structure of GLIC in complex with succinate  
Authors : Fourati, Z.; Delarue, M.  
Deposited on : 2018-09-04  
Resolution : 2.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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

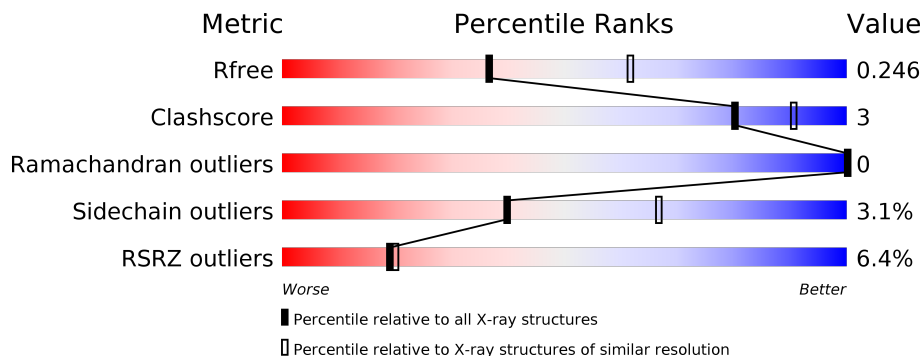
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	317	
1	B	317	
1	C	317	
1	D	317	
1	E	317	
1	F	317	

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Mol	Chain	Length	Quality of chain
1	G	317	
1	H	317	
1	I	317	
1	J	317	

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
2	PLC	A	402	-	-	-	X
2	PLC	A	403	-	-	-	X
2	PLC	B	402	-	-	-	X
2	PLC	B	403	-	-	-	X
2	PLC	B	404	-	-	-	X
2	PLC	C	402	-	-	-	X
2	PLC	C	403	-	-	-	X
2	PLC	C	404	-	-	-	X
2	PLC	D	403	-	-	-	X
2	PLC	E	403	-	-	-	X
2	PLC	F	403	-	-	-	X
2	PLC	G	402	-	-	-	X
2	PLC	H	403	-	-	-	X
2	PLC	I	403	-	-	-	X
2	PLC	J	401	-	-	-	X
2	PLC	J	403	-	-	-	X
3	CL	H	406	-	-	-	X
5	LMT	D	406	-	-	-	X
6	SIN	A	411	-	-	-	X
6	SIN	B	408	-	-	-	X
6	SIN	C	408	-	-	-	X
6	SIN	D	407	-	-	-	X
6	SIN	E	407	-	-	-	X
6	SIN	F	409	-	-	-	X
6	SIN	G	410	-	-	-	X
6	SIN	H	409	-	-	-	X
6	SIN	I	409	-	-	-	X

## 2 Entry composition [i](#)

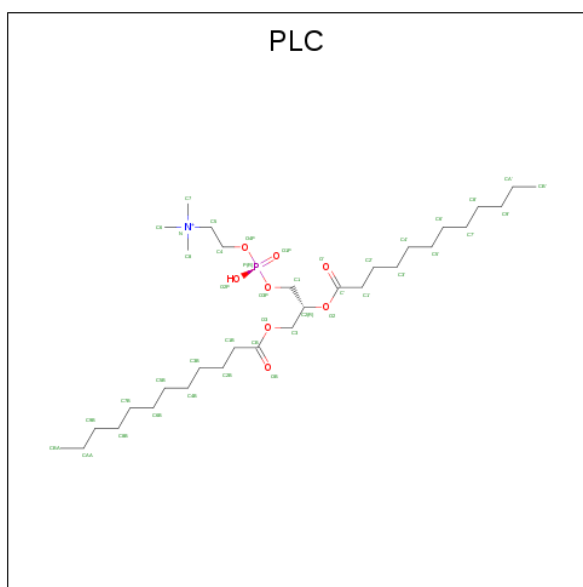
There are 7 unique types of molecules in this entry. The entry contains 26501 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	311	2525	1664	404	453	4	0	0	0
1	B	311	2525	1664	404	453	4	0	0	0
1	C	311	2525	1664	404	453	4	0	0	0
1	D	311	2525	1664	404	453	4	0	0	0
1	E	311	2525	1664	404	453	4	0	0	0
1	F	311	2533	1668	405	456	4	0	1	0
1	G	311	2525	1664	404	453	4	0	0	0
1	H	311	2525	1664	404	453	4	0	0	0
1	I	311	2525	1664	404	453	4	0	0	0
1	J	311	2525	1664	404	453	4	0	0	0

- Molecule 2 is DIUNDECYL PHOSPHATIDYL CHOLINE (three-letter code: PLC) (formula:  $C_{32}H_{65}NO_8P$ ).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	1	Total C 12 12	0	0
2	F	1	Total C N O P 34 24 1 8 1	0	0
2	F	1	Total C 24 24	0	0
2	F	1	Total C 12 12	0	0
2	G	1	Total C N O P 34 24 1 8 1	0	0
2	G	1	Total C 24 24	0	0
2	G	1	Total C 12 12	0	0
2	H	1	Total C N O P 34 24 1 8 1	0	0
2	H	1	Total C 24 24	0	0
2	H	1	Total C 12 12	0	0
2	I	1	Total C N O P 34 24 1 8 1	0	0
2	I	1	Total C 24 24	0	0
2	I	1	Total C 12 12	0	0
2	J	1	Total C N O P 34 24 1 8 1	0	0
2	J	1	Total C 24 24	0	0
2	J	1	Total C 12 12	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Cl 1 1	0	0
3	J	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0

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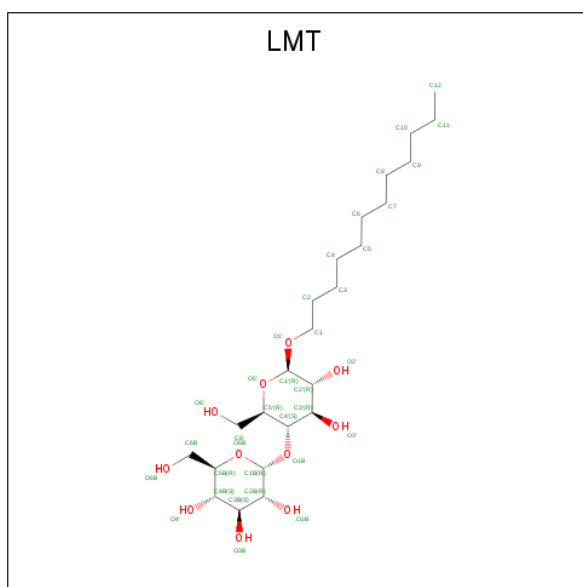
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total Cl 1 1	0	0
3	H	3	Total Cl 3 3	0	0
3	B	1	Total Cl 1 1	0	0
3	I	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	A	3	Total Cl 3 3	0	0
3	F	1	Total Cl 1 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	2	Total Na 2 2	0	0
4	J	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0
4	E	1	Total Na 1 1	0	0
4	H	1	Total Na 1 1	0	0
4	B	2	Total Na 2 2	0	0
4	I	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0
4	A	1	Total Na 1 1	0	0
4	F	1	Total Na 1 1	0	0

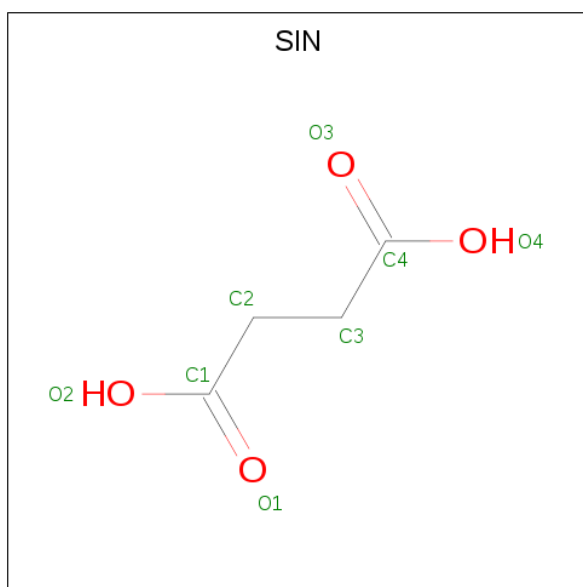
- Molecule 5 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: C<sub>24</sub>H<sub>46</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C 12 12	0	0
5	A	1	Total C 12 12	0	0
5	B	1	Total C 12 12	0	0
5	C	1	Total C 12 12	0	0
5	D	1	Total C 12 12	0	0
5	E	1	Total C 12 12	0	0
5	F	1	Total C 12 12	0	0
5	F	1	Total C 12 12	0	0
5	G	1	Total C 12 12	0	0
5	H	1	Total C 12 12	0	0
5	I	1	Total C 12 12	0	0
5	J	1	Total C 12 12	0	0

- Molecule 6 is SUCCINIC ACID (three-letter code: SIN) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>4</sub>).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			8	4	4		
6	A	1	Total	C	O	0	0
			8	4	4		
6	B	1	Total	C	O	0	0
			8	4	4		
6	B	1	Total	C	O	0	0
			8	4	4		
6	B	1	Total	C	O	0	0
			8	4	4		
6	C	1	Total	C	O	0	0
			8	4	4		
6	C	1	Total	C	O	0	0
			8	4	4		
6	D	1	Total	C	O	0	0
			8	4	4		
6	E	1	Total	C	O	0	0
			8	4	4		
6	E	1	Total	C	O	0	0
			8	4	4		
6	F	1	Total	C	O	0	0
			8	4	4		
6	F	1	Total	C	O	0	0
			8	4	4		
6	G	1	Total	C	O	0	0
			8	4	4		
6	G	1	Total	C	O	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	G	1	Total	C	O	0	0
			8	4	4		
6	H	1	Total	C	O	0	0
			8	4	4		
6	I	1	Total	C	O	0	0
			8	4	4		
6	I	1	Total	C	O	0	0
			8	4	4		
6	I	1	Total	C	O	0	0
			8	4	4		
6	J	1	Total	C	O	0	0
			8	4	4		

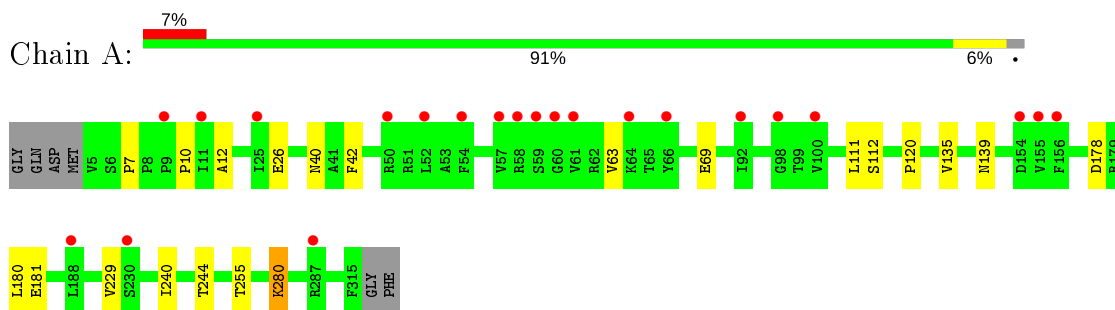
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	14	Total	O	0	0
			14	14		
7	B	22	Total	O	0	0
			22	22		
7	C	18	Total	O	0	0
			18	18		
7	D	17	Total	O	0	0
			17	17		
7	E	15	Total	O	0	0
			15	15		
7	F	21	Total	O	0	0
			21	21		
7	G	23	Total	O	0	0
			23	23		
7	H	33	Total	O	0	0
			33	33		
7	I	33	Total	O	0	0
			33	33		
7	J	17	Total	O	0	0
			17	17		

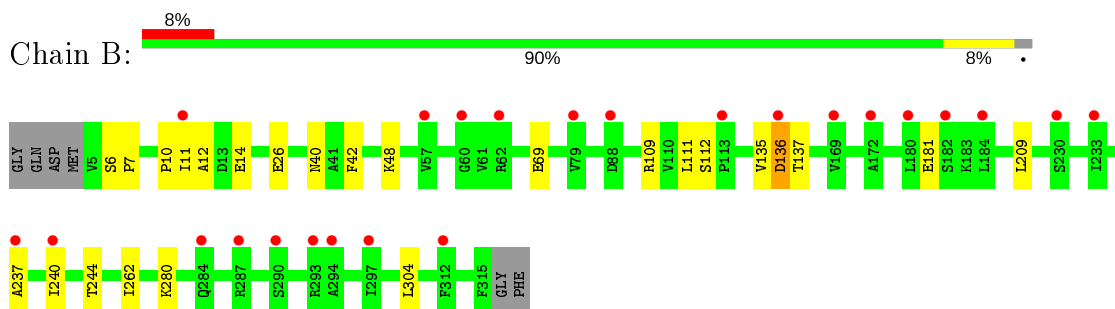
### 3 Residue-property plots [i](#)

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.

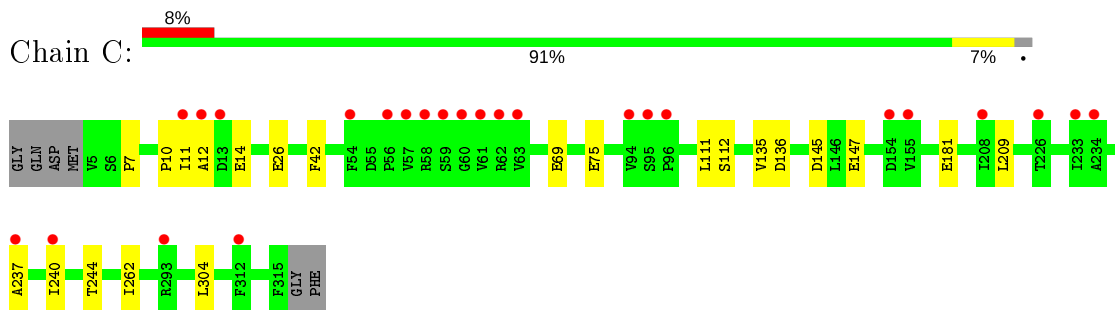
- Molecule 1: Proton-gated ion channel



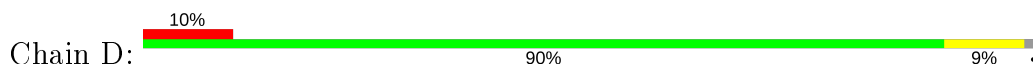
- Molecule 1: Proton-gated ion channel

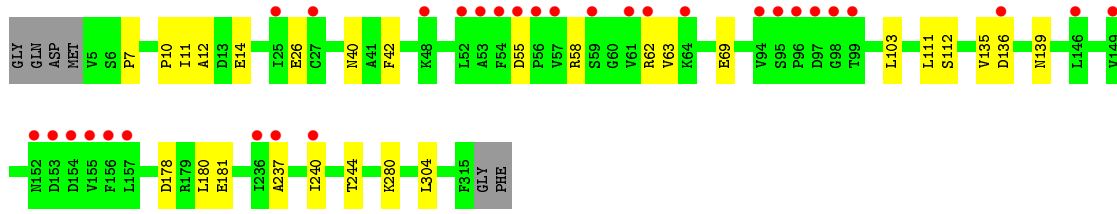


- Molecule 1: Proton-gated ion channel

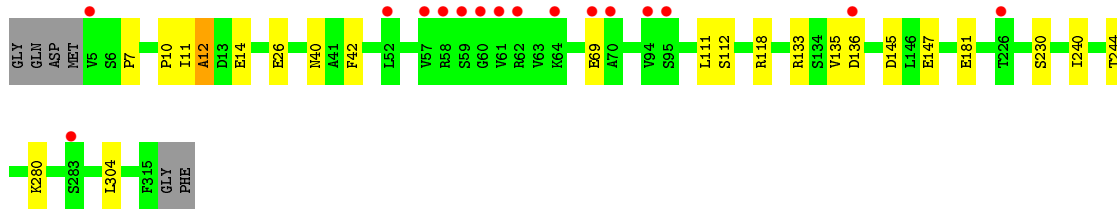
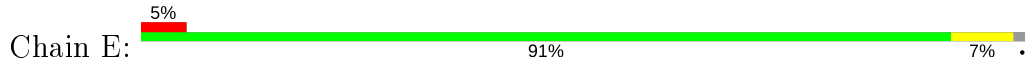


- Molecule 1: Proton-gated ion channel

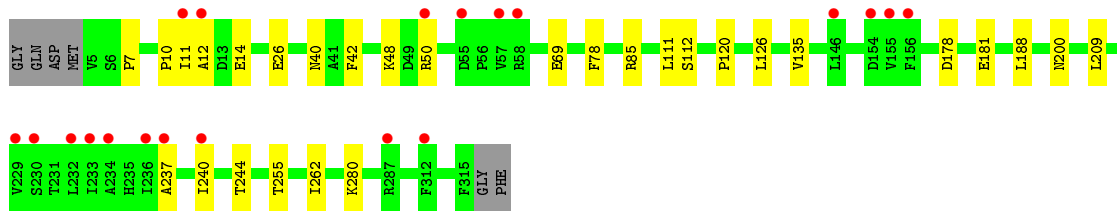
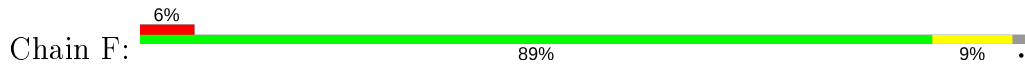




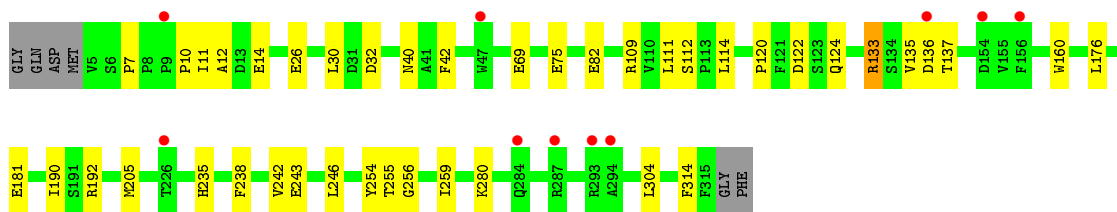
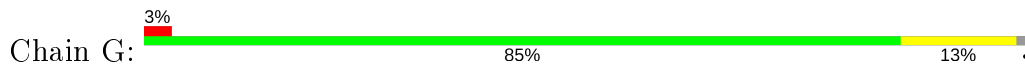
• Molecule 1: Proton-gated ion channel



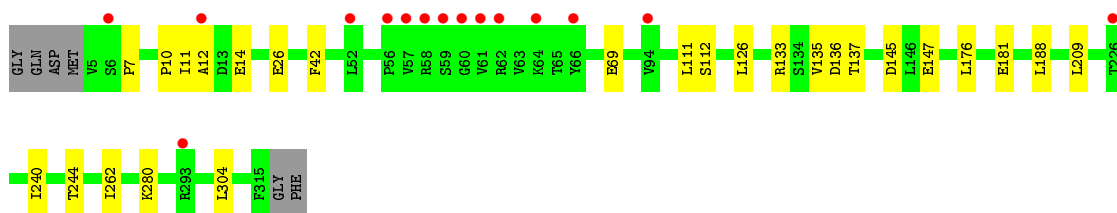
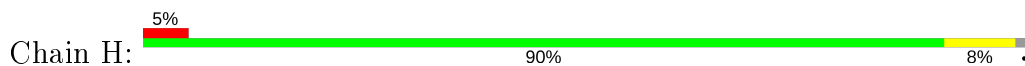
• Molecule 1: Proton-gated ion channel



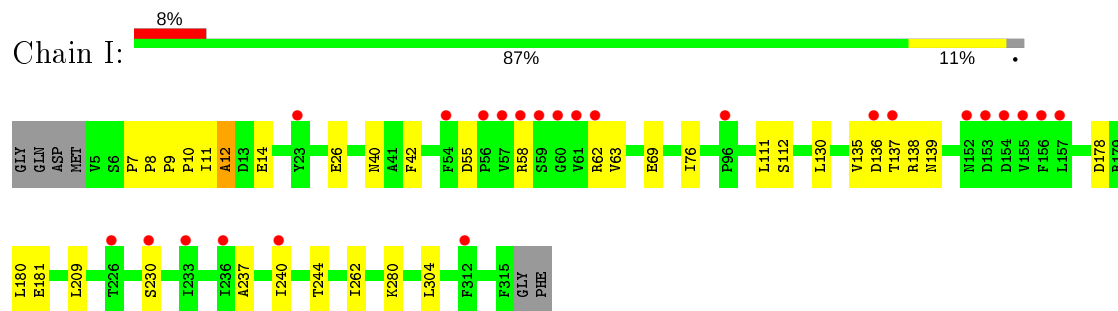
• Molecule 1: Proton-gated ion channel



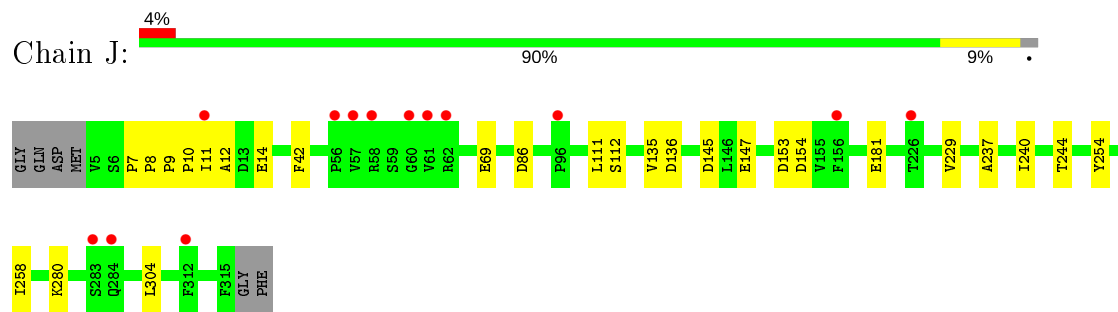
• Molecule 1: Proton-gated ion channel



- 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, $\alpha$ , $\beta$ , $\gamma$	180.71Å 132.49Å 320.56Å 90.00° 102.23° 90.00°	Depositor
Resolution (Å)	12.00 – 2.50 48.99 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (12.00-2.50) 99.7 (48.99-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.70 (at 2.51Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.217 , 0.227 0.235 , 0.246	Depositor DCC
$R_{free}$ test set	12768 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.3	Xtrriage
Anisotropy	0.211	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 63.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	26501	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.04 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6176e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: NA, LMT, PLC, SIN, 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	0.38	0/2593	0.64	0/3545
1	B	0.38	0/2593	0.64	0/3545
1	C	0.38	0/2593	0.65	0/3545
1	D	0.38	0/2593	0.64	0/3545
1	E	0.39	0/2593	0.65	1/3545 (0.0%)
1	F	0.39	0/2601	0.66	0/3556
1	G	0.45	0/2593	0.70	0/3545
1	H	0.38	0/2593	0.65	0/3545
1	I	0.39	0/2593	0.66	1/3545 (0.0%)
1	J	0.40	0/2593	0.67	1/3545 (0.0%)
All	All	0.39	0/25938	0.66	3/35461 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	153	ASP	N-CA-CB	-5.67	100.40	110.60
1	E	12	ALA	N-CA-C	-5.35	96.55	111.00
1	I	12	ALA	N-CA-C	-5.05	97.36	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2525	0	2545	10	0
1	B	2525	0	2545	10	0
1	C	2525	0	2545	11	3
1	D	2525	0	2545	17	0
1	E	2525	0	2544	15	3
1	F	2533	0	2548	21	0
1	G	2525	0	2545	29	0
1	H	2525	0	2545	11	3
1	I	2525	0	2545	17	0
1	J	2525	0	2545	10	3
2	A	70	0	111	0	0
2	B	70	0	111	0	0
2	C	70	0	111	0	0
2	D	70	0	111	0	0
2	E	70	0	111	1	0
2	F	70	0	111	0	0
2	G	70	0	111	2	0
2	H	70	0	111	0	0
2	I	70	0	111	0	0
2	J	70	0	111	0	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	3	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	2	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
5	A	24	0	46	1	0
5	B	12	0	23	1	0
5	C	12	0	23	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	12	0	23	1	0
5	E	12	0	23	1	0
5	F	24	0	46	3	0
5	G	12	0	23	2	0
5	H	12	0	23	0	0
5	I	12	0	23	1	0
5	J	12	0	23	1	0
6	A	16	0	8	0	0
6	B	24	0	12	0	0
6	C	16	0	9	1	0
6	D	8	0	4	0	0
6	E	16	0	8	0	0
6	F	16	0	8	0	0
6	G	24	0	12	1	0
6	H	8	0	4	0	0
6	I	24	0	12	0	0
6	J	8	0	4	0	0
7	A	14	0	0	0	0
7	B	22	0	0	0	0
7	C	18	0	0	0	0
7	D	17	0	0	3	0
7	E	15	0	0	0	0
7	F	21	0	0	0	0
7	G	23	0	0	6	0
7	H	33	0	0	0	0
7	I	33	0	0	4	0
7	J	17	0	0	1	0
All	All	26501	0	26919	144	6

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 (144) 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:D:103:LEU:CD2	1:E:133:ARG:NH2	1.67	1.52
1:H:26:GLU:HG3	7:I:501:HOH:O	1.22	1.23
1:F:200:ASN:HB3	1:G:243:GLU:OE2	1.45	1.13
1:C:26:GLU:HG3	7:D:501:HOH:O	1.49	1.09
1:D:103:LEU:HD22	1:E:133:ARG:NH2	1.58	1.08
1:D:103:LEU:HD23	1:E:133:ARG:NH2	1.59	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:103:LEU:HD21	1:E:133:ARG:NH2	1.72	1.02
1:C:26:GLU:CG	7:D:501:HOH:O	2.02	1.00
1:H:26:GLU:CG	7:I:501:HOH:O	1.89	0.86
1:F:11:ILE:HG13	1:F:14:GLU:OE2	1.77	0.84
1:J:11:ILE:HG13	1:J:14:GLU:OE2	1.77	0.84
1:C:11:ILE:HG13	1:C:14:GLU:OE2	1.79	0.83
1:H:11:ILE:HG13	1:H:14:GLU:OE2	1.78	0.83
1:E:11:ILE:HG13	1:E:14:GLU:OE2	1.78	0.82
1:B:11:ILE:HG13	1:B:14:GLU:OE2	1.79	0.82
1:G:11:ILE:HG13	1:G:14:GLU:OE2	1.80	0.82
1:I:11:ILE:HG13	1:I:14:GLU:OE2	1.78	0.82
1:A:10:PRO:HB2	1:A:12:ALA:O	1.78	0.82
1:F:200:ASN:CB	1:G:243:GLU:OE2	2.26	0.82
1:I:10:PRO:HB2	1:I:12:ALA:O	1.80	0.81
1:D:11:ILE:HG13	1:D:14:GLU:OE2	1.79	0.81
1:D:103:LEU:CD2	1:E:133:ARG:HH21	1.95	0.80
1:F:7:PRO:HG3	1:F:135:VAL:HG21	1.63	0.80
1:F:10:PRO:HB2	1:F:12:ALA:O	1.82	0.79
1:E:10:PRO:HB2	1:E:12:ALA:O	1.83	0.79
1:G:7:PRO:HG3	1:G:135:VAL:HG21	1.68	0.76
1:B:7:PRO:HG3	1:B:135:VAL:HG21	1.67	0.75
1:C:7:PRO:HG3	1:C:135:VAL:HG21	1.69	0.75
1:J:7:PRO:HG3	1:J:135:VAL:HG21	1.70	0.74
1:F:48:LYS:HE2	1:F:50:ARG:HG3	1.69	0.73
1:D:7:PRO:HG3	1:D:135:VAL:HG21	1.69	0.73
1:A:7:PRO:HG3	1:A:135:VAL:HG21	1.71	0.73
1:H:7:PRO:HG3	1:H:135:VAL:HG21	1.70	0.72
1:J:10:PRO:HB2	1:J:12:ALA:O	1.89	0.71
1:H:10:PRO:HB2	1:H:12:ALA:O	1.91	0.70
1:G:255:THR:HG22	1:G:259:ILE:HD11	1.74	0.70
1:C:10:PRO:HB2	1:C:12:ALA:O	1.91	0.70
1:G:255:THR:HG23	7:G:519:HOH:O	1.90	0.70
1:F:48:LYS:NZ	1:F:50:ARG:NH1	2.41	0.69
1:E:7:PRO:HG3	1:E:135:VAL:HG21	1.72	0.69
1:I:139:ASN:HB3	7:I:505:HOH:O	1.91	0.69
1:G:133:ARG:NH1	1:G:176:LEU:O	2.26	0.69
5:F:407:LMT:H41	5:G:407:LMT:H61	1.75	0.68
1:B:10:PRO:HB2	1:B:12:ALA:O	1.93	0.68
1:I:55:ASP:HB3	1:I:58:ARG:HG2	1.75	0.68
1:D:55:ASP:HB3	1:D:58:ARG:HG2	1.76	0.67
1:G:10:PRO:HB2	1:G:12:ALA:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:256:GLY:HA2	1:G:259:ILE:HD12	1.79	0.64
1:I:237:ALA:HA	5:I:406:LMT:H92	1.80	0.63
1:D:10:PRO:HB2	1:D:12:ALA:O	1.99	0.62
1:J:237:ALA:HA	5:J:406:LMT:H92	1.82	0.62
1:B:237:ALA:HA	5:B:407:LMT:H92	1.82	0.61
1:D:237:ALA:HA	5:D:406:LMT:H92	1.83	0.61
1:C:237:ALA:HA	5:C:407:LMT:H92	1.84	0.60
1:F:48:LYS:HZ1	1:F:50:ARG:HH11	1.51	0.58
1:G:242:VAL:HB	7:G:505:HOH:O	2.04	0.58
1:G:255:THR:CG2	7:G:519:HOH:O	2.50	0.58
1:F:237:ALA:HA	5:F:406:LMT:H92	1.85	0.58
2:G:402:PLC:H1A2	2:G:402:PLC:H3'1	1.86	0.57
1:G:259:ILE:CG1	7:G:519:HOH:O	2.51	0.57
1:I:7:PRO:HG3	1:I:135:VAL:HG21	1.87	0.56
1:G:75:GLU:HA	6:G:410:SIN:H21	1.88	0.56
1:G:242:VAL:CG2	7:G:505:HOH:O	2.54	0.55
1:E:12:ALA:HB3	1:E:14:GLU:OE1	2.06	0.55
1:B:12:ALA:HB3	1:B:14:GLU:OE1	2.06	0.55
1:J:12:ALA:HB3	1:J:14:GLU:OE1	2.07	0.55
1:G:12:ALA:HB3	1:G:14:GLU:OE1	2.07	0.55
1:C:75:GLU:HA	6:C:408:SIN:H32	1.89	0.55
1:C:12:ALA:HB3	1:C:14:GLU:OE1	2.07	0.55
1:I:139:ASN:HD21	1:I:180:LEU:HD13	1.71	0.54
1:D:103:LEU:HD23	1:E:133:ARG:HH21	1.64	0.54
1:H:12:ALA:HB3	1:H:14:GLU:OE1	2.07	0.53
1:G:242:VAL:O	1:G:246:LEU:HD12	2.10	0.52
1:F:209:LEU:HD13	1:F:262:ILE:HG23	1.91	0.52
1:G:120:PRO:HD3	1:G:255:THR:OG1	2.10	0.52
1:D:12:ALA:HB3	1:D:14:GLU:OE1	2.10	0.52
1:I:178:ASP:O	1:I:178:ASP:OD1	2.27	0.52
1:D:103:LEU:HD22	1:E:133:ARG:CZ	2.35	0.51
1:A:63:VAL:HG21	1:B:136:ASP:HB3	1.94	0.50
1:F:240:ILE:O	1:F:244:THR:HG23	2.12	0.50
1:F:48:LYS:NZ	1:F:50:ARG:HH11	2.07	0.50
1:F:78:PHE:CE2	1:F:85:ARG:HD3	2.47	0.50
1:D:240:ILE:O	1:D:244:THR:HG23	2.12	0.50
1:I:240:ILE:O	1:I:244:THR:HG23	2.12	0.49
1:F:48:LYS:HZ3	1:F:50:ARG:NH1	2.11	0.49
1:H:240:ILE:O	1:H:244:THR:HG23	2.12	0.49
1:A:240:ILE:O	1:A:244:THR:HG23	2.12	0.49
1:G:82:GLU:HG3	1:G:109:ARG:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:ILE:O	1:C:244:THR:HG23	2.13	0.49
1:E:240:ILE:O	1:E:244:THR:HG23	2.13	0.49
1:J:240:ILE:O	1:J:244:THR:HG23	2.12	0.49
1:B:240:ILE:O	1:B:244:THR:HG23	2.14	0.48
1:B:6:SER:OG	1:B:7:PRO:HD2	2.14	0.48
1:G:30:LEU:C	1:G:30:LEU:HD23	2.34	0.48
5:F:407:LMT:H61	5:G:407:LMT:H81	1.95	0.47
1:G:122:ASP:OD1	1:G:192:ARG:HD2	2.14	0.47
1:I:139:ASN:ND2	1:I:180:LEU:HD13	2.29	0.47
1:G:256:GLY:CA	1:G:259:ILE:HD12	2.44	0.46
1:I:12:ALA:HB3	1:I:14:GLU:OE1	2.16	0.46
1:H:26:GLU:CB	7:I:501:HOH:O	2.46	0.46
1:A:178:ASP:O	1:A:178:ASP:OD1	2.34	0.46
1:C:26:GLU:HG2	7:D:501:HOH:O	1.89	0.46
1:E:118:ARG:HH12	2:E:401:PLC:H83	1.81	0.46
1:I:135:VAL:HG23	1:I:138:ARG:H	1.82	0.45
1:A:139:ASN:HD22	1:A:180:LEU:HD22	1.82	0.44
1:F:12:ALA:HB3	1:F:14:GLU:OE1	2.18	0.44
1:H:133:ARG:NH1	1:H:176:LEU:O	2.51	0.44
1:D:178:ASP:O	1:D:178:ASP:OD1	2.35	0.44
1:G:254:TYR:HB2	1:G:314:PHE:CD1	2.53	0.43
1:D:139:ASN:HD22	1:D:180:LEU:HD22	1.84	0.43
1:G:235:HIS:O	1:G:235:HIS:CG	2.72	0.43
2:G:402:PLC:H3A2	2:G:402:PLC:H5'1	2.01	0.42
1:G:205:MET:CE	1:G:238:PHE:HB3	2.49	0.42
1:G:160:TRP:CE3	1:G:190:ILE:HD12	2.54	0.42
1:J:154:ASP:HB2	7:J:509:HOH:O	2.19	0.42
1:B:26:GLU:HB2	1:B:40:ASN:HB3	2.02	0.42
1:F:48:LYS:HE2	1:F:50:ARG:CG	2.46	0.42
1:D:26:GLU:HB2	1:D:40:ASN:HB3	2.02	0.42
1:J:8:PRO:HA	1:J:9:PRO:HD3	1.98	0.41
1:H:209:LEU:HD13	1:H:262:ILE:HG23	2.02	0.41
1:C:209:LEU:HD13	1:C:262:ILE:HG23	2.02	0.41
1:G:32:ASP:CG	1:G:192:ARG:HH22	2.24	0.41
1:A:26:GLU:HB2	1:A:40:ASN:HB3	2.03	0.41
1:G:259:ILE:HG13	7:G:519:HOH:O	2.17	0.41
1:G:26:GLU:HB2	1:G:40:ASN:HB3	2.01	0.41
1:A:229:VAL:HG11	1:E:230:SER:HB2	2.03	0.41
1:F:26:GLU:HB2	1:F:40:ASN:HB3	2.02	0.41
1:I:76:ILE:CG2	1:I:130:LEU:HD22	2.51	0.41
1:F:178:ASP:OD1	1:F:178:ASP:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:254:TYR:CZ	1:J:258:ILE:HD11	2.55	0.41
1:A:280:LYS:HG3	1:A:280:LYS:O	2.21	0.41
1:B:209:LEU:HD13	1:B:262:ILE:HG23	2.03	0.41
1:H:126:LEU:HD12	1:H:188:LEU:HD23	2.03	0.41
1:E:26:GLU:HB2	1:E:40:ASN:HB3	2.03	0.41
1:G:114:LEU:HD22	1:G:124:GLN:HG3	2.03	0.41
1:I:8:PRO:HA	1:I:9:PRO:HD3	1.98	0.41
1:F:126:LEU:HD12	1:F:188:LEU:HD23	2.04	0.40
1:I:230:SER:HB2	1:J:229:VAL:HG11	2.04	0.40
1:I:209:LEU:HD13	1:I:262:ILE:HG23	2.03	0.40
1:I:26:GLU:HB2	1:I:40:ASN:HB3	2.02	0.40
1:F:78:PHE:HE2	1:F:85:ARG:HD3	1.85	0.40
1:A:120:PRO:HD3	1:A:255:THR:OG1	2.20	0.40
5:A:408:LMT:H61	5:E:406:LMT:H92	2.02	0.40
1:F:120:PRO:HD3	1:F:255:THR:OG1	2.20	0.40

All (6) 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)
1:C:147:GLU:OE1	1:E:147:GLU:OE1[4_445]	1.61	0.59
1:C:145:ASP:OD2	1:E:147:GLU:OE2[4_445]	1.72	0.48
1:H:145:ASP:OD2	1:J:147:GLU:OE2[4_546]	1.73	0.47
1:C:147:GLU:OE2	1:E:145:ASP:OD2[4_445]	1.88	0.32
1:H:147:GLU:OE1	1:J:147:GLU:OE1[4_546]	1.89	0.31
1:H:147:GLU:OE2	1:J:145:ASP:OD2[4_546]	1.99	0.21

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	309/317 (98%)	302 (98%)	7 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	309/317 (98%)	302 (98%)	7 (2%)	0	100	100
1	C	309/317 (98%)	303 (98%)	6 (2%)	0	100	100
1	D	309/317 (98%)	303 (98%)	6 (2%)	0	100	100
1	E	309/317 (98%)	303 (98%)	6 (2%)	0	100	100
1	F	310/317 (98%)	304 (98%)	6 (2%)	0	100	100
1	G	309/317 (98%)	302 (98%)	7 (2%)	0	100	100
1	H	309/317 (98%)	302 (98%)	7 (2%)	0	100	100
1	I	309/317 (98%)	302 (98%)	7 (2%)	0	100	100
1	J	309/317 (98%)	303 (98%)	6 (2%)	0	100	100
All	All	3091/3170 (98%)	3026 (98%)	65 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	280/284 (99%)	274 (98%)	6 (2%)	53	78
1	B	280/284 (99%)	269 (96%)	11 (4%)	32	57
1	C	280/284 (99%)	273 (98%)	7 (2%)	47	73
1	D	280/284 (99%)	270 (96%)	10 (4%)	35	61
1	E	280/284 (99%)	272 (97%)	8 (3%)	42	69
1	F	281/284 (99%)	275 (98%)	6 (2%)	53	78
1	G	280/284 (99%)	270 (96%)	10 (4%)	35	61
1	H	280/284 (99%)	271 (97%)	9 (3%)	39	65
1	I	280/284 (99%)	269 (96%)	11 (4%)	32	57
1	J	280/284 (99%)	271 (97%)	9 (3%)	39	65
All	All	2801/2840 (99%)	2714 (97%)	87 (3%)	40	67

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	PHE
1	A	69	GLU
1	A	111	LEU
1	A	112	SER
1	A	181	GLU
1	A	280	LYS
1	B	42	PHE
1	B	48	LYS
1	B	69	GLU
1	B	109	ARG
1	B	111	LEU
1	B	112	SER
1	B	136	ASP
1	B	137	THR
1	B	181	GLU
1	B	280	LYS
1	B	304	LEU
1	C	42	PHE
1	C	69	GLU
1	C	111	LEU
1	C	112	SER
1	C	136	ASP
1	C	181	GLU
1	C	304	LEU
1	D	42	PHE
1	D	62	ARG
1	D	63	VAL
1	D	69	GLU
1	D	111	LEU
1	D	112	SER
1	D	136	ASP
1	D	181	GLU
1	D	280	LYS
1	D	304	LEU
1	E	42	PHE
1	E	69	GLU
1	E	111	LEU
1	E	112	SER
1	E	136	ASP
1	E	181	GLU
1	E	280	LYS
1	E	304	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	F	42	PHE
1	F	69	GLU
1	F	111	LEU
1	F	112	SER
1	F	181	GLU
1	F	280	LYS
1	G	42	PHE
1	G	69	GLU
1	G	111	LEU
1	G	112	SER
1	G	133	ARG
1	G	136	ASP
1	G	137	THR
1	G	181	GLU
1	G	280	LYS
1	G	304	LEU
1	H	42	PHE
1	H	69	GLU
1	H	111	LEU
1	H	112	SER
1	H	136	ASP
1	H	137	THR
1	H	181	GLU
1	H	280	LYS
1	H	304	LEU
1	I	42	PHE
1	I	62	ARG
1	I	63	VAL
1	I	69	GLU
1	I	111	LEU
1	I	112	SER
1	I	136	ASP
1	I	137	THR
1	I	181	GLU
1	I	280	LYS
1	I	304	LEU
1	J	42	PHE
1	J	69	GLU
1	J	86	ASP
1	J	111	LEU
1	J	112	SER
1	J	136	ASP

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Mol	Chain	Res	Type
1	J	181	GLU
1	J	280	LYS
1	J	304	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	139	ASN
1	B	139	ASN
1	B	307	ASN
1	C	307	ASN
1	D	139	ASN
1	E	139	ASN
1	E	307	ASN
1	F	307	ASN
1	G	139	ASN
1	G	307	ASN
1	H	139	ASN
1	I	139	ASN
1	J	307	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 88 ligands modelled in this entry, 26 are monoatomic - leaving 62 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SIN	D	407	-	1,7,7	0.00	0	2,8,8	1.47	1 (50%)
2	PLC	G	402	-	33,33,41	1.07	3 (9%)	39,41,49	0.85	0
2	PLC	H	401	-	33,33,41	1.12	2 (6%)	39,41,49	1.04	2 (5%)
5	LMT	D	406	-	11,11,36	0.51	0	10,10,47	0.58	0
6	SIN	E	407	-	1,7,7	0.05	0	2,8,8	1.82	1 (50%)
5	LMT	J	406	-	11,11,36	0.52	0	10,10,47	0.56	0
2	PLC	E	402	-	22,22,41	0.42	0	20,20,49	0.61	0
2	PLC	A	401	-	33,33,41	1.08	2 (6%)	39,41,49	0.93	2 (5%)
6	SIN	C	408	-	1,7,7	0.24	0	2,8,8	2.32	1 (50%)
6	SIN	E	408	-	1,7,7	0.07	0	2,8,8	1.66	1 (50%)
5	LMT	F	407	-	11,11,36	0.40	0	10,10,47	0.71	0
6	SIN	B	409	-	1,7,7	0.13	0	2,8,8	1.43	0
2	PLC	H	403	-	11,11,41	0.43	0	10,10,49	0.63	0
2	PLC	H	402	-	22,22,41	0.44	0	20,20,49	0.62	0
5	LMT	B	407	-	11,11,36	0.48	0	10,10,47	0.55	0
5	LMT	I	406	-	11,11,36	0.52	0	10,10,47	0.57	0
6	SIN	B	410	-	1,7,7	0.20	0	2,8,8	0.56	0
6	SIN	F	408	-	1,7,7	0.10	0	2,8,8	0.26	0
6	SIN	I	409	-	1,7,7	0.01	0	2,8,8	1.08	0
2	PLC	D	401	-	33,33,41	1.10	3 (9%)	39,41,49	0.99	2 (5%)
2	PLC	C	402	-	33,33,41	1.08	2 (6%)	39,41,49	0.94	2 (5%)
2	PLC	A	402	-	22,22,41	0.44	0	20,20,49	0.59	0
6	SIN	I	407	-	1,7,7	0.15	0	2,8,8	0.95	0
5	LMT	F	406	-	11,11,36	0.49	0	10,10,47	0.59	0
2	PLC	B	402	-	33,33,41	1.08	2 (6%)	39,41,49	1.00	2 (5%)
2	PLC	I	403	-	11,11,41	0.45	0	10,10,49	0.67	0
2	PLC	F	403	-	11,11,41	0.40	0	10,10,49	0.63	0
2	PLC	E	401	-	33,33,41	1.04	1 (3%)	39,41,49	0.99	2 (5%)
2	PLC	D	403	-	11,11,41	0.44	0	10,10,49	0.64	0
6	SIN	I	408	-	1,7,7	0.08	0	2,8,8	1.74	1 (50%)
6	SIN	J	407	-	1,7,7	0.03	0	2,8,8	0.87	0
6	SIN	G	401	-	1,7,7	0.11	0	2,8,8	0.28	0
6	SIN	F	409	-	1,7,7	0.03	0	2,8,8	1.85	1 (50%)
2	PLC	C	404	-	11,11,41	0.40	0	10,10,49	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	LMT	E	406	-	11,11,36	0.52	0	10,10,47	0.55	0
2	PLC	G	403	-	22,22,41	0.44	0	20,20,49	0.58	0
2	PLC	F	401	-	33,33,41	1.08	3 (9%)	39,41,49	1.00	2 (5%)
2	PLC	D	402	-	22,22,41	0.44	0	20,20,49	0.59	0
5	LMT	A	408	-	11,11,36	0.44	0	10,10,47	0.62	0
6	SIN	A	411	-	1,7,7	0.19	0	2,8,8	2.79	1 (50%)
2	PLC	B	403	-	22,22,41	0.43	0	20,20,49	0.60	0
2	PLC	J	402	-	22,22,41	0.42	0	20,20,49	0.62	0
6	SIN	G	408	-	1,7,7	0.08	0	2,8,8	0.92	0
2	PLC	J	403	-	11,11,41	0.43	0	10,10,49	0.59	0
5	LMT	G	407	-	11,11,36	0.62	0	10,10,47	0.53	0
2	PLC	G	404	-	11,11,41	0.38	0	10,10,49	0.64	0
2	PLC	B	404	-	11,11,41	0.39	0	10,10,49	0.73	0
5	LMT	A	409	-	11,11,36	0.49	0	10,10,47	0.59	0
6	SIN	B	408	-	1,7,7	0.30	0	2,8,8	2.44	1 (50%)
2	PLC	E	403	-	11,11,41	0.45	0	10,10,49	0.58	0
2	PLC	C	403	-	22,22,41	0.44	0	20,20,49	0.59	0
2	PLC	A	403	-	11,11,41	0.39	0	10,10,49	0.65	0
6	SIN	A	410	-	1,7,7	0.11	0	2,8,8	0.51	0
2	PLC	F	402	-	22,22,41	0.41	0	20,20,49	0.61	0
5	LMT	H	408	-	11,11,36	0.50	0	10,10,47	0.59	0
2	PLC	I	402	-	22,22,41	0.43	0	20,20,49	0.61	0
6	SIN	G	410	-	1,7,7	0.02	0	2,8,8	1.82	1 (50%)
2	PLC	J	401	-	33,33,41	1.07	1 (3%)	39,41,49	0.79	1 (2%)
2	PLC	I	401	-	33,33,41	1.14	2 (6%)	39,41,49	0.83	1 (2%)
6	SIN	C	401	-	1,7,7	0.20	0	2,8,8	1.19	0
5	LMT	C	407	-	11,11,36	0.51	0	10,10,47	0.55	0
6	SIN	H	409	-	1,7,7	0.02	0	2,8,8	3.36	1 (50%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SIN	D	407	-	-	0/1/5/5	-
2	PLC	G	402	-	-	10/37/37/45	-
2	PLC	H	401	-	-	15/37/37/45	-
5	LMT	D	406	-	-	0/9/9/61	-
6	SIN	E	407	-	-	0/1/5/5	-
5	LMT	J	406	-	-	0/9/9/61	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLC	E	402	-	-	3/18/18/45	-
2	PLC	A	401	-	-	13/37/37/45	-
6	SIN	C	408	-	-	0/1/5/5	-
6	SIN	E	408	-	-	0/1/5/5	-
5	LMT	F	407	-	-	0/9/9/61	-
6	SIN	B	409	-	-	0/1/5/5	-
2	PLC	H	403	-	-	3/9/9/45	-
2	PLC	H	402	-	-	3/18/18/45	-
5	LMT	B	407	-	-	0/9/9/61	-
5	LMT	I	406	-	-	0/9/9/61	-
6	SIN	B	410	-	-	0/1/5/5	-
6	SIN	F	408	-	-	0/1/5/5	-
6	SIN	I	409	-	-	0/1/5/5	-
2	PLC	D	401	-	-	15/37/37/45	-
2	PLC	C	402	-	-	17/37/37/45	-
2	PLC	A	402	-	-	3/18/18/45	-
6	SIN	I	407	-	-	0/1/5/5	-
5	LMT	F	406	-	-	0/9/9/61	-
2	PLC	B	402	-	-	18/37/37/45	-
2	PLC	I	403	-	-	1/9/9/45	-
2	PLC	F	403	-	-	0/9/9/45	-
2	PLC	E	401	-	-	16/37/37/45	-
2	PLC	D	403	-	-	3/9/9/45	-
6	SIN	I	408	-	-	0/1/5/5	-
6	SIN	J	407	-	-	0/1/5/5	-
6	SIN	G	401	-	-	0/1/5/5	-
6	SIN	F	409	-	-	1/1/5/5	-
2	PLC	C	404	-	-	0/9/9/45	-
5	LMT	E	406	-	-	0/9/9/61	-
2	PLC	G	403	-	-	3/18/18/45	-
2	PLC	F	401	-	-	17/37/37/45	-
2	PLC	D	402	-	-	3/18/18/45	-
5	LMT	A	408	-	-	0/9/9/61	-
6	SIN	A	411	-	-	0/1/5/5	-
2	PLC	B	403	-	-	3/18/18/45	-
2	PLC	J	402	-	-	3/18/18/45	-
6	SIN	G	408	-	-	0/1/5/5	-
2	PLC	J	403	-	-	0/9/9/45	-
5	LMT	G	407	-	-	0/9/9/61	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLC	G	404	-	-	3/9/9/45	-
2	PLC	B	404	-	-	0/9/9/45	-
5	LMT	A	409	-	-	1/9/9/61	-
6	SIN	B	408	-	-	0/1/5/5	-
2	PLC	E	403	-	-	0/9/9/45	-
2	PLC	C	403	-	-	3/18/18/45	-
2	PLC	A	403	-	-	0/9/9/45	-
6	SIN	A	410	-	-	0/1/5/5	-
2	PLC	F	402	-	-	4/18/18/45	-
5	LMT	H	408	-	-	2/9/9/61	-
2	PLC	I	402	-	-	3/18/18/45	-
6	SIN	G	410	-	-	0/1/5/5	-
2	PLC	J	401	-	-	14/37/37/45	-
2	PLC	I	401	-	-	14/37/37/45	-
6	SIN	C	401	-	-	0/1/5/5	-
5	LMT	C	407	-	-	0/9/9/61	-
6	SIN	H	409	-	-	0/1/5/5	-

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	PLC	O2-C'	2.68	1.41	1.34
2	D	401	PLC	O2-C'	2.63	1.41	1.34
2	E	401	PLC	O2-C'	2.60	1.41	1.34
2	C	402	PLC	O2-C'	2.55	1.41	1.34
2	B	402	PLC	O2-C'	2.51	1.41	1.34
2	H	401	PLC	O3-CB	2.47	1.40	1.33
2	I	401	PLC	O3-CB	2.41	1.40	1.33
2	I	401	PLC	O2-C'	2.35	1.40	1.34
2	F	401	PLC	O3-CB	2.30	1.40	1.33
2	J	401	PLC	O2-C'	2.30	1.40	1.34
2	G	402	PLC	O2-C'	2.21	1.40	1.34
2	F	401	PLC	O2-C'	2.16	1.40	1.34
2	B	402	PLC	O3-CB	2.13	1.39	1.33
2	F	401	PLC	C5-N	2.11	1.58	1.51
2	A	401	PLC	O3-CB	2.09	1.39	1.33
2	D	401	PLC	C5-N	2.07	1.58	1.51
2	H	401	PLC	O2-C'	2.05	1.40	1.34
2	G	402	PLC	O3-CB	2.04	1.39	1.33
2	D	401	PLC	O3-CB	2.04	1.39	1.33
2	C	402	PLC	C5-N	2.02	1.58	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	402	PLC	C5-N	2.01	1.58	1.51

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	409	SIN	C3-C2-C1	-4.73	104.74	112.67
2	B	402	PLC	C2-O2-C'	3.63	126.73	117.79
2	A	401	PLC	C2-O2-C'	3.46	126.31	117.79
6	A	411	SIN	C3-C2-C1	-3.42	106.94	112.67
2	D	401	PLC	C2-O2-C'	3.36	126.07	117.79
2	E	401	PLC	C2-O2-C'	3.32	125.97	117.79
2	C	402	PLC	C2-O2-C'	3.04	125.27	117.79
2	H	401	PLC	O3-CB-OB	-3.02	115.98	123.59
2	F	401	PLC	O3-CB-OB	-2.95	116.15	123.59
2	H	401	PLC	C3-C2-C1	2.91	118.67	111.79
6	C	408	SIN	C3-C2-C1	-2.90	107.80	112.67
6	B	408	SIN	C3-C2-C1	-2.83	107.92	112.67
2	C	402	PLC	C3-C2-C1	2.74	118.27	111.79
2	E	401	PLC	C3-C2-C1	2.65	118.06	111.79
2	B	402	PLC	C3-C2-C1	2.63	118.01	111.79
6	G	410	SIN	C2-C3-C4	-2.57	108.36	112.67
2	D	401	PLC	C3-C2-C1	2.55	117.81	111.79
6	E	407	SIN	C2-C3-C4	-2.52	108.44	112.67
6	F	409	SIN	C2-C3-C4	-2.43	108.59	112.67
2	I	401	PLC	C3-C2-C1	2.42	117.51	111.79
6	E	408	SIN	C2-C3-C4	-2.26	108.88	112.67
2	A	401	PLC	C3-C2-C1	2.20	116.98	111.79
6	I	408	SIN	C2-C3-C4	2.16	116.29	112.67
6	D	407	SIN	C2-C3-C4	-2.08	109.18	112.67
2	F	401	PLC	C3-C2-C1	2.06	116.66	111.79
2	J	401	PLC	C3-C2-C1	2.01	116.54	111.79

There are no chirality outliers.

All (194) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	401	PLC	C1B-CB-O3-C3
2	H	401	PLC	OB-CB-O3-C3
2	H	401	PLC	C4-O4P-P-O1P
2	H	401	PLC	C4-O4P-P-O2P
2	H	401	PLC	C4-O4P-P-O3P
2	G	402	PLC	C1'-C'-O2-C2

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Mol	Chain	Res	Type	Atoms
2	G	402	PLC	C1-O3P-P-O1P
2	G	402	PLC	C1-O3P-P-O2P
2	G	402	PLC	C4-O4P-P-O1P
2	G	402	PLC	C4-O4P-P-O3P
2	D	401	PLC	O4P-C4-C5-N
2	D	401	PLC	C1'-C'-O2-C2
2	D	401	PLC	C1-O3P-P-O1P
2	D	401	PLC	C1-O3P-P-O4P
2	D	401	PLC	C4-O4P-P-O1P
2	D	401	PLC	C4-O4P-P-O3P
2	C	402	PLC	C1'-C'-O2-C2
2	C	402	PLC	C1-O3P-P-O1P
2	C	402	PLC	C1-O3P-P-O4P
2	C	402	PLC	C4-O4P-P-O1P
2	C	402	PLC	C4-O4P-P-O3P
2	F	401	PLC	C1B-CB-O3-C3
2	F	401	PLC	OB-CB-O3-C3
2	F	401	PLC	C1-O3P-P-O1P
2	B	402	PLC	C1'-C'-O2-C2
2	B	402	PLC	C1-O3P-P-O2P
2	B	402	PLC	C4-O4P-P-O1P
2	B	402	PLC	C4-O4P-P-O3P
2	J	401	PLC	C1'-C'-O2-C2
2	J	401	PLC	C1-O3P-P-O1P
2	J	401	PLC	C4-O4P-P-O1P
2	I	401	PLC	C1-O3P-P-O1P
2	I	401	PLC	C1-O3P-P-O2P
2	I	401	PLC	C4-O4P-P-O1P
2	I	401	PLC	C4-O4P-P-O3P
2	A	401	PLC	O4P-C4-C5-N
2	E	401	PLC	C1'-C'-O2-C2
2	E	401	PLC	C1-O3P-P-O1P
2	E	401	PLC	C4-O4P-P-O1P
2	E	401	PLC	C4-O4P-P-O3P
2	G	402	PLC	O'-C'-O2-C2
2	D	401	PLC	O'-C'-O2-C2
2	C	402	PLC	O'-C'-O2-C2
2	B	402	PLC	O'-C'-O2-C2
2	E	401	PLC	O'-C'-O2-C2
2	J	401	PLC	O'-C'-O2-C2
2	D	401	PLC	C'-C1'-C2'-C3'
2	C	402	PLC	CB-C1B-C2B-C3B

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Mol	Chain	Res	Type	Atoms
2	J	401	PLC	C <sup>1</sup> -C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup>
2	G	402	PLC	C <sup>1</sup> -C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup>
2	B	402	PLC	C <sup>1</sup> -C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup>
2	B	402	PLC	CB-C1B-C2B-C3B
2	J	401	PLC	CB-C1B-C2B-C3B
2	A	401	PLC	CB-C1B-C2B-C3B
2	E	401	PLC	C <sup>1</sup> -C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup>
2	E	401	PLC	CB-C1B-C2B-C3B
2	D	401	PLC	CB-C1B-C2B-C3B
2	C	402	PLC	C <sup>1</sup> -C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup>
2	G	402	PLC	C1-O3P-P-O4P
2	F	401	PLC	C1-O3P-P-O4P
2	B	402	PLC	C1-O3P-P-O4P
2	J	401	PLC	C1-O3P-P-O4P
2	J	401	PLC	C4-O4P-P-O3P
2	I	401	PLC	C1-O3P-P-O4P
2	G	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	B	402	PLC	C3B-C4B-C5B-C6B
2	F	401	PLC	C1B-C2B-C3B-C4B
2	G	404	PLC	C5 <sup>1</sup> -C6 <sup>1</sup> -C7 <sup>1</sup> -C8 <sup>1</sup>
2	A	401	PLC	O <sup>1</sup> -C <sup>1</sup> -O2-C2
2	H	401	PLC	C3 <sup>1</sup> -C4 <sup>1</sup> -C5 <sup>1</sup> -C6 <sup>1</sup>
2	A	401	PLC	C3B-C4B-C5B-C6B
2	G	404	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	C	402	PLC	C3B-C4B-C5B-C6B
2	F	401	PLC	O <sup>1</sup> -C <sup>1</sup> -O2-C2
2	E	401	PLC	C3B-C4B-C5B-C6B
2	F	401	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	I	401	PLC	C1B-C2B-C3B-C4B
2	E	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	C	403	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	G	403	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	A	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	I	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	D	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	B	403	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	H	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	F	402	PLC	C1 <sup>1</sup> -C2 <sup>1</sup> -C3 <sup>1</sup> -C4 <sup>1</sup>
2	I	401	PLC	CB-C1B-C2B-C3B
2	H	401	PLC	C1 <sup>1</sup> -C <sup>1</sup> -O2-C2
2	A	401	PLC	C1 <sup>1</sup> -C <sup>1</sup> -O2-C2
2	J	401	PLC	C3B-C4B-C5B-C6B

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Mol	Chain	Res	Type	Atoms
2	J	402	PLC	C1'-C2'-C3'-C4'
2	H	401	PLC	O'-C'-O2-C2
2	H	401	PLC	C1'-C2'-C3'-C4'
2	F	401	PLC	C1'-C'-O2-C2
2	I	401	PLC	O'-C'-O2-C2
2	I	401	PLC	C2B-C3B-C4B-C5B
2	E	401	PLC	C1'-C2'-C3'-C4'
2	H	401	PLC	C2B-C3B-C4B-C5B
2	I	401	PLC	C3B-C4B-C5B-C6B
2	H	403	PLC	C2'-C3'-C4'-C5'
2	I	401	PLC	C1'-C'-O2-C2
2	H	401	PLC	C2'-C3'-C4'-C5'
2	J	401	PLC	C1'-C2'-C3'-C4'
2	E	401	PLC	C1-O3P-P-O4P
2	B	402	PLC	C1'-C2'-C3'-C4'
2	C	402	PLC	C1B-C2B-C3B-C4B
2	A	401	PLC	C3-C2-O2-C'
2	D	401	PLC	C4B-C5B-C6B-C7B
2	H	401	PLC	C1B-C2B-C3B-C4B
2	E	401	PLC	C1B-C2B-C3B-C4B
2	B	402	PLC	C1B-C2B-C3B-C4B
2	G	403	PLC	C8'-C9'-CA'-CB'
2	E	402	PLC	C8'-C9'-CA'-CB'
2	B	403	PLC	C8'-C9'-CA'-CB'
2	F	402	PLC	C8'-C9'-CA'-CB'
2	H	403	PLC	C'-C1'-C2'-C3'
2	D	401	PLC	C1B-C2B-C3B-C4B
2	I	402	PLC	C8'-C9'-CA'-CB'
2	D	402	PLC	C8'-C9'-CA'-CB'
2	C	403	PLC	C8'-C9'-CA'-CB'
2	J	401	PLC	C1B-C2B-C3B-C4B
2	A	402	PLC	C8'-C9'-CA'-CB'
2	J	402	PLC	C8'-C9'-CA'-CB'
2	F	401	PLC	C3B-C4B-C5B-C6B
2	F	401	PLC	O3P-C1-C2-O2
2	H	402	PLC	C8'-C9'-CA'-CB'
2	D	401	PLC	C1'-C2'-C3'-C4'
2	A	401	PLC	C1B-C2B-C3B-C4B
2	J	401	PLC	C3'-C4'-C5'-C6'
2	B	403	PLC	C2'-C3'-C4'-C5'
2	E	402	PLC	C2'-C3'-C4'-C5'
2	H	403	PLC	C1'-C2'-C3'-C4'

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Mol	Chain	Res	Type	Atoms
2	I	402	PLC	C2'-C3'-C4'-C5'
2	A	401	PLC	C4-O4P-P-O3P
2	C	403	PLC	C2'-C3'-C4'-C5'
2	A	402	PLC	C2'-C3'-C4'-C5'
2	B	402	PLC	C1-O3P-P-O1P
2	H	402	PLC	C2'-C3'-C4'-C5'
2	I	403	PLC	C2'-C3'-C4'-C5'
2	F	401	PLC	O3P-C1-C2-C3
2	J	402	PLC	C2'-C3'-C4'-C5'
2	F	402	PLC	C2'-C3'-C4'-C5'
2	G	403	PLC	C2'-C3'-C4'-C5'
2	D	402	PLC	C2'-C3'-C4'-C5'
2	D	403	PLC	C'-C1'-C2'-C3'
2	C	402	PLC	C1'-C2'-C3'-C4'
2	H	401	PLC	O4P-C4-C5-N
2	G	402	PLC	O4P-C4-C5-N
2	C	402	PLC	O4P-C4-C5-N
2	F	401	PLC	O4P-C4-C5-N
2	B	402	PLC	O4P-C4-C5-N
2	J	401	PLC	O4P-C4-C5-N
2	I	401	PLC	O4P-C4-C5-N
2	E	401	PLC	O4P-C4-C5-N
2	F	401	PLC	C2B-C3B-C4B-C5B
2	H	401	PLC	C4B-C5B-C6B-C7B
2	F	401	PLC	C4B-C5B-C6B-C7B
2	J	401	PLC	C2B-C3B-C4B-C5B
2	A	401	PLC	C1-O3P-P-O4P
2	D	401	PLC	C3B-C4B-C5B-C6B
5	A	409	LMT	C1-C2-C3-C4
2	D	403	PLC	C1'-C2'-C3'-C4'
2	G	404	PLC	C6'-C7'-C8'-C9'
2	D	403	PLC	C2'-C3'-C4'-C5'
2	F	401	PLC	C2-C1-O3P-P
2	C	402	PLC	C3-C2-O2-C'
2	B	402	PLC	C3-C2-O2-C'
5	H	408	LMT	C1-C2-C3-C4
2	I	401	PLC	O2-C'-C1'-C2'
2	E	401	PLC	C2B-C1B-CB-O3
2	A	401	PLC	C2B-C1B-CB-O3
2	B	402	PLC	C2B-C1B-CB-O3
2	C	402	PLC	C2B-C1B-CB-O3
2	C	402	PLC	C2B-C3B-C4B-C5B

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Mol	Chain	Res	Type	Atoms
2	I	401	PLC	O'-C'-C1'-C2'
2	E	401	PLC	C2B-C1B-CB-OB
2	F	401	PLC	O2-C'-C1'-C2'
2	B	402	PLC	C2B-C1B-CB-OB
2	A	401	PLC	C1-O3P-P-O1P
2	A	401	PLC	C4-O4P-P-O1P
2	A	401	PLC	C2B-C1B-CB-OB
2	B	402	PLC	O2-C'-C1'-C2'
2	F	402	PLC	C2B-C3B-C4B-C5B
2	E	401	PLC	C3-C2-O2-C'
2	C	402	PLC	C2B-C1B-CB-OB
5	H	408	LMT	C11-C10-C9-C8
2	E	401	PLC	O2-C'-C1'-C2'
2	D	401	PLC	C2B-C1B-CB-O3
2	C	402	PLC	O2-C'-C1'-C2'
2	F	401	PLC	O'-C'-C1'-C2'
2	D	401	PLC	C2B-C1B-CB-OB
6	F	409	SIN	C1-C2-C3-C4
2	B	402	PLC	O'-C'-C1'-C2'
2	H	401	PLC	O2-C'-C1'-C2'

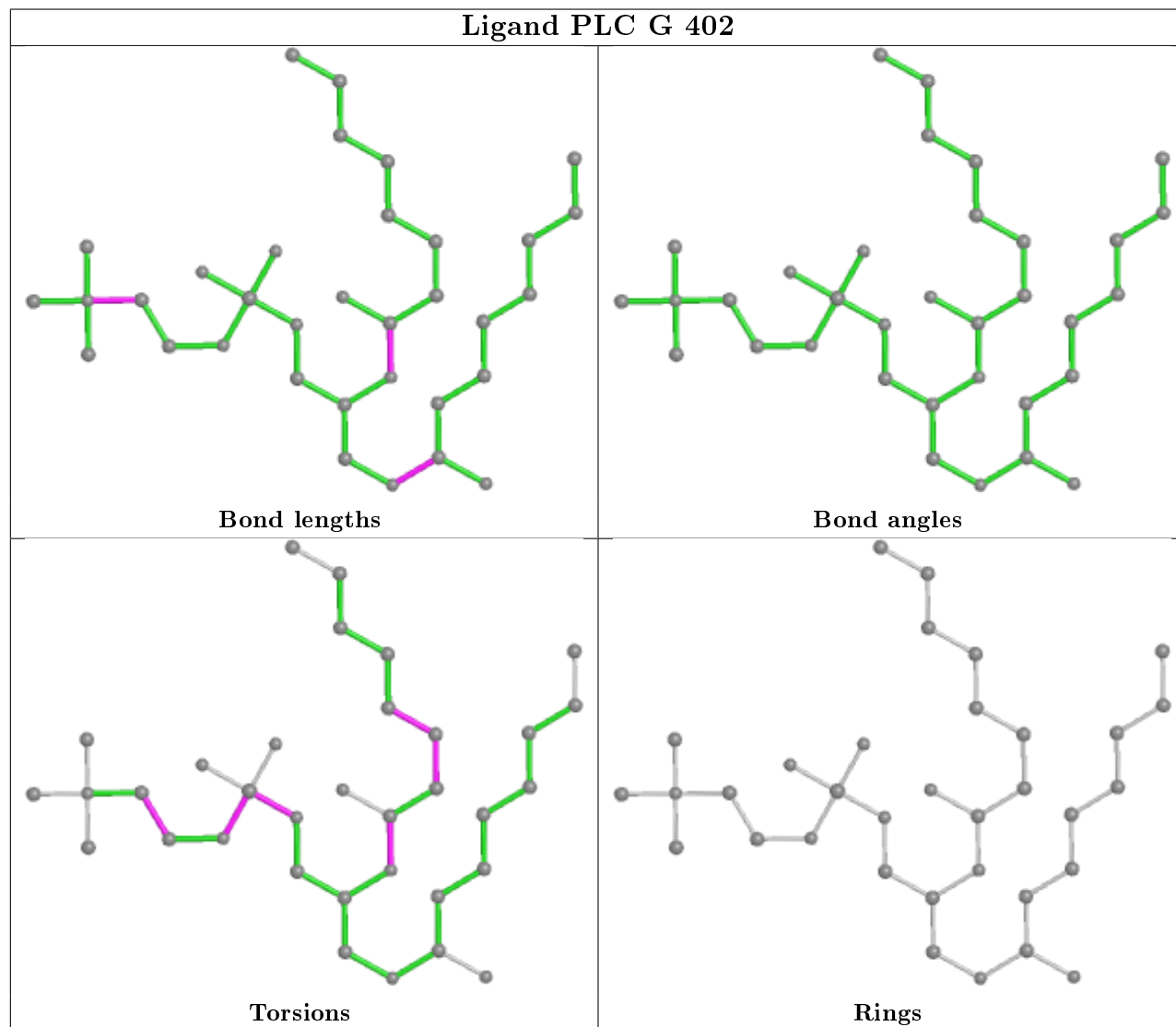
There are no ring outliers.

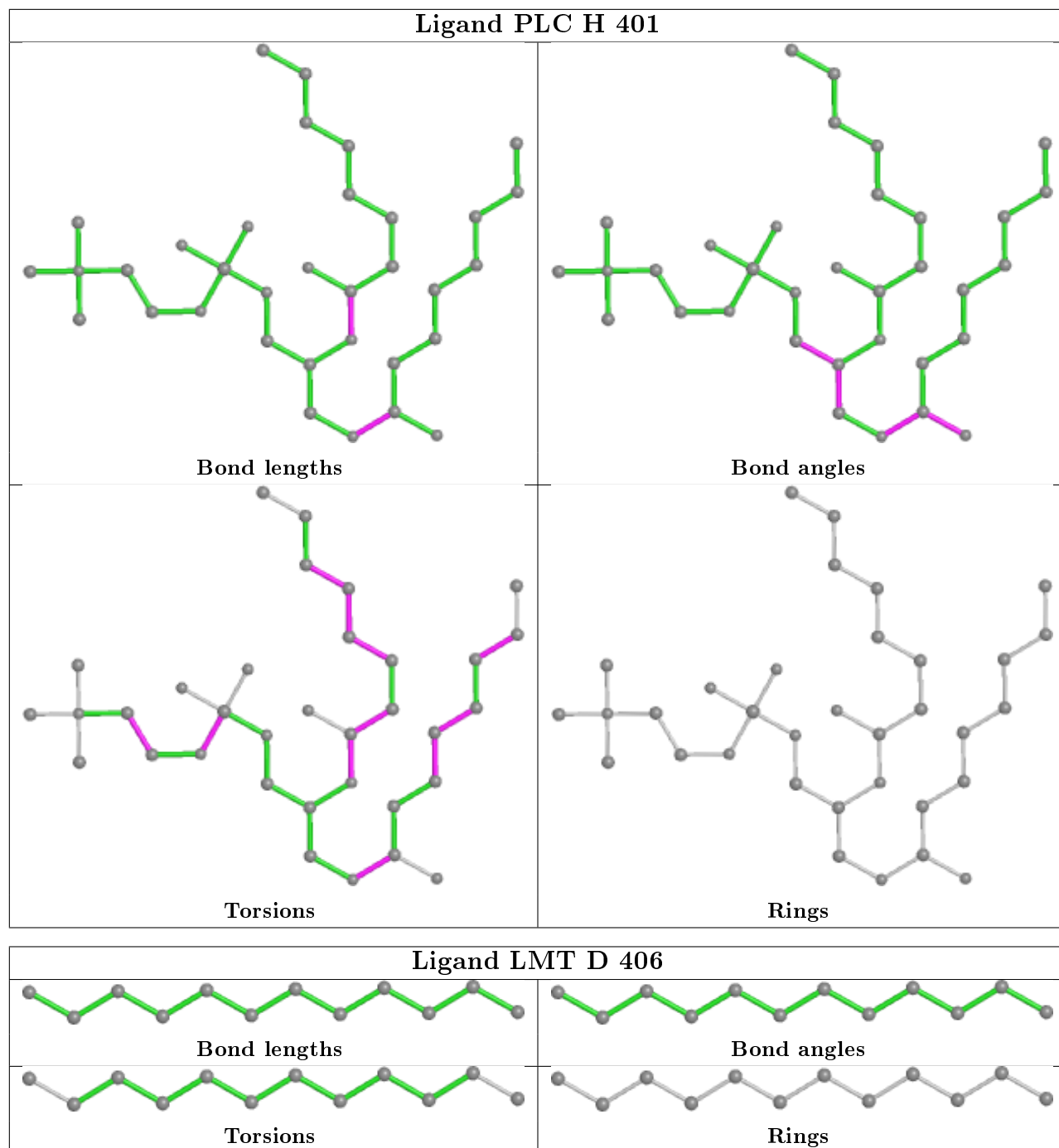
14 monomers are involved in 14 short contacts:

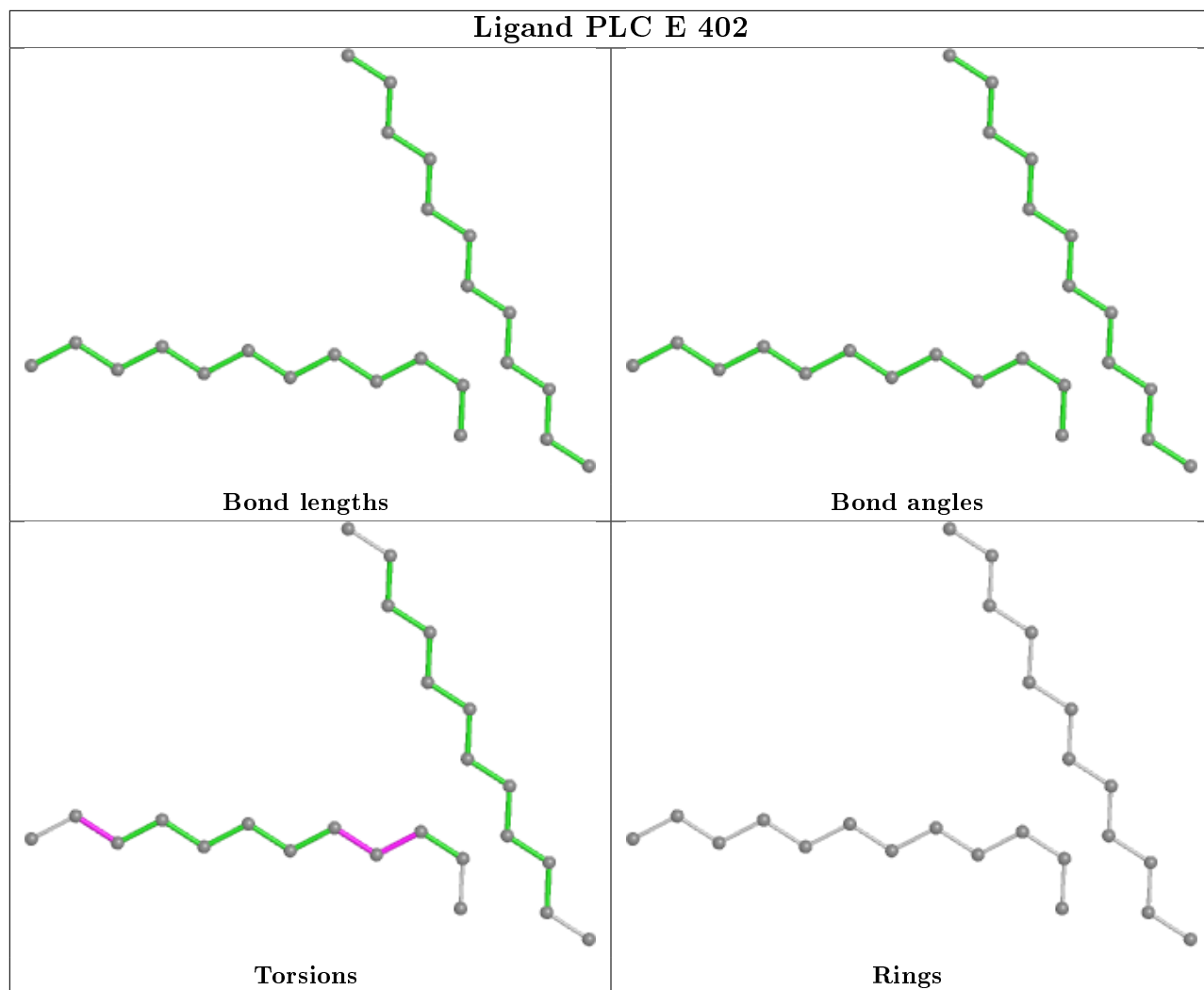
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	402	PLC	2	0
5	D	406	LMT	1	0
5	J	406	LMT	1	0
6	C	408	SIN	1	0
5	F	407	LMT	2	0
5	B	407	LMT	1	0
5	I	406	LMT	1	0
5	F	406	LMT	1	0
2	E	401	PLC	1	0
5	E	406	LMT	1	0
5	A	408	LMT	1	0
5	G	407	LMT	2	0
6	G	410	SIN	1	0
5	C	407	LMT	1	0

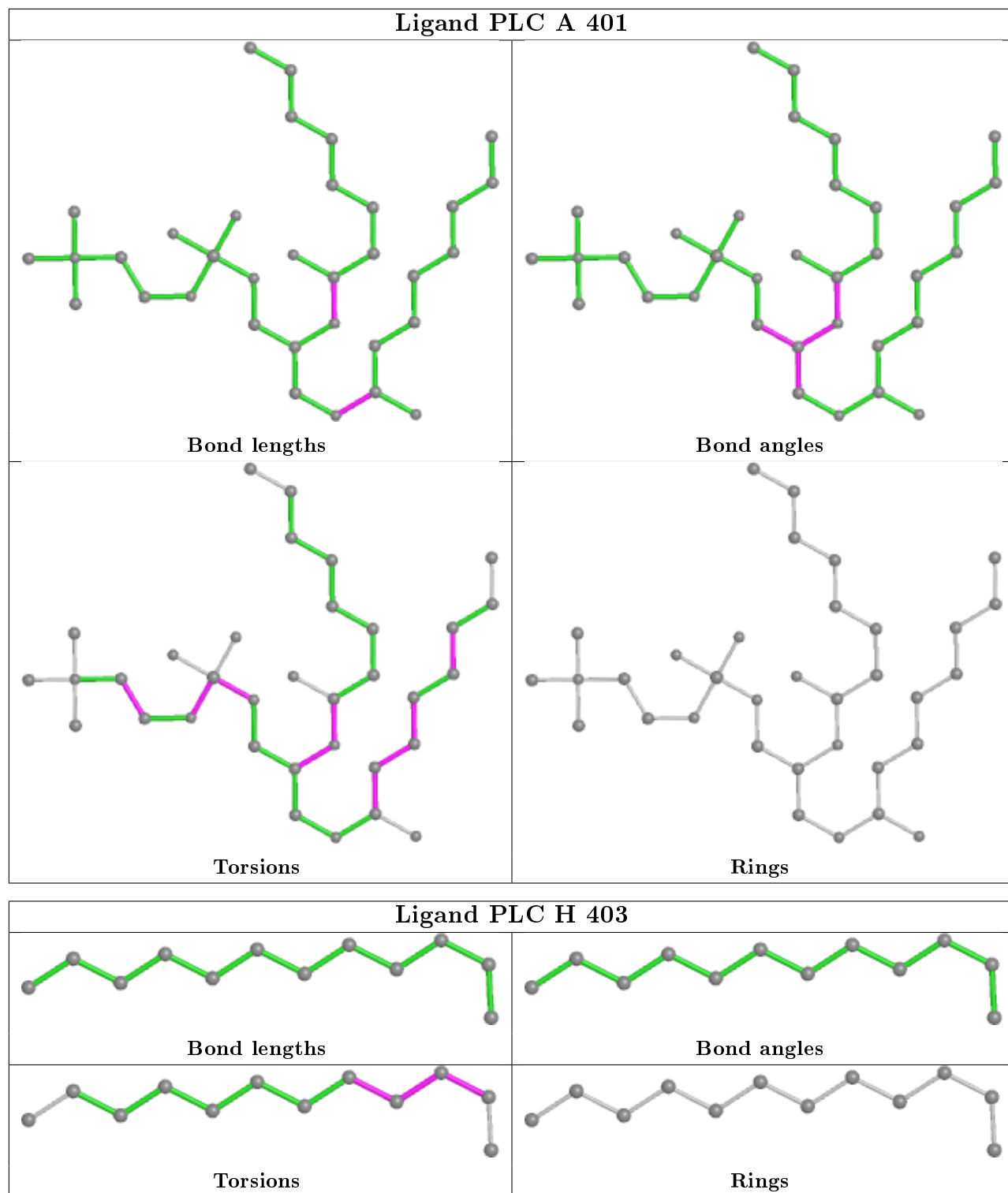
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

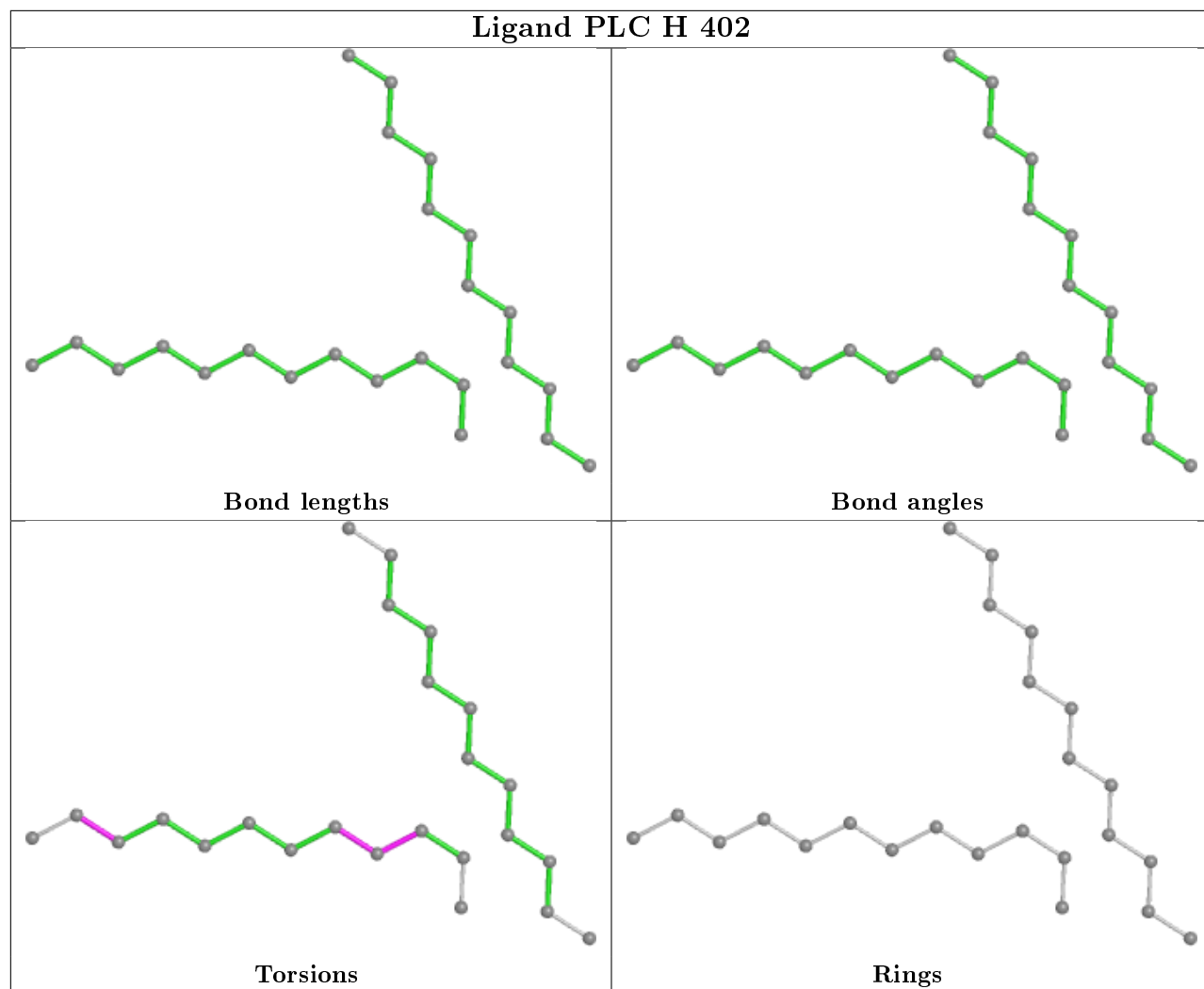
addition, ligands with molecular weight  $> 250$  and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.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



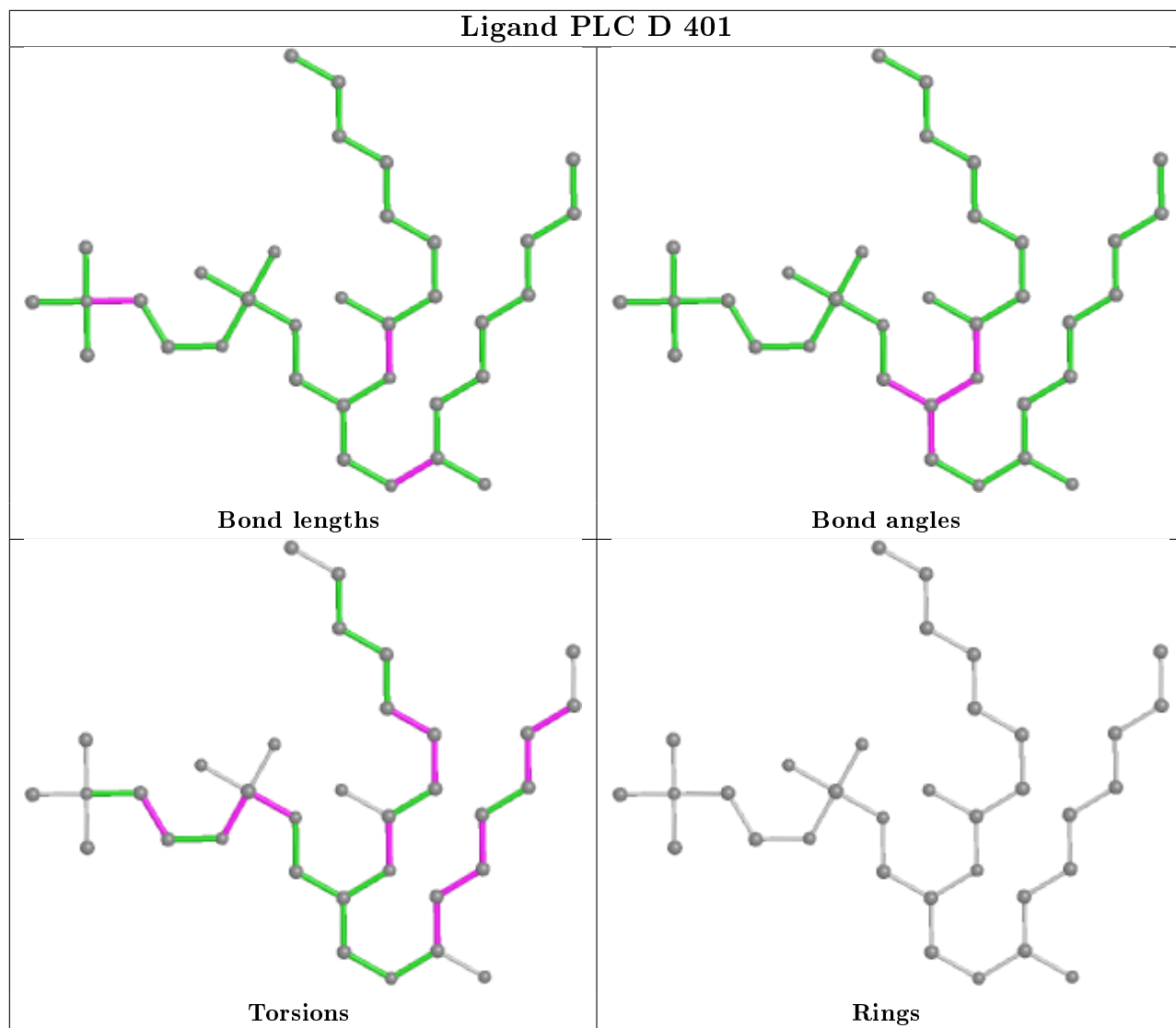


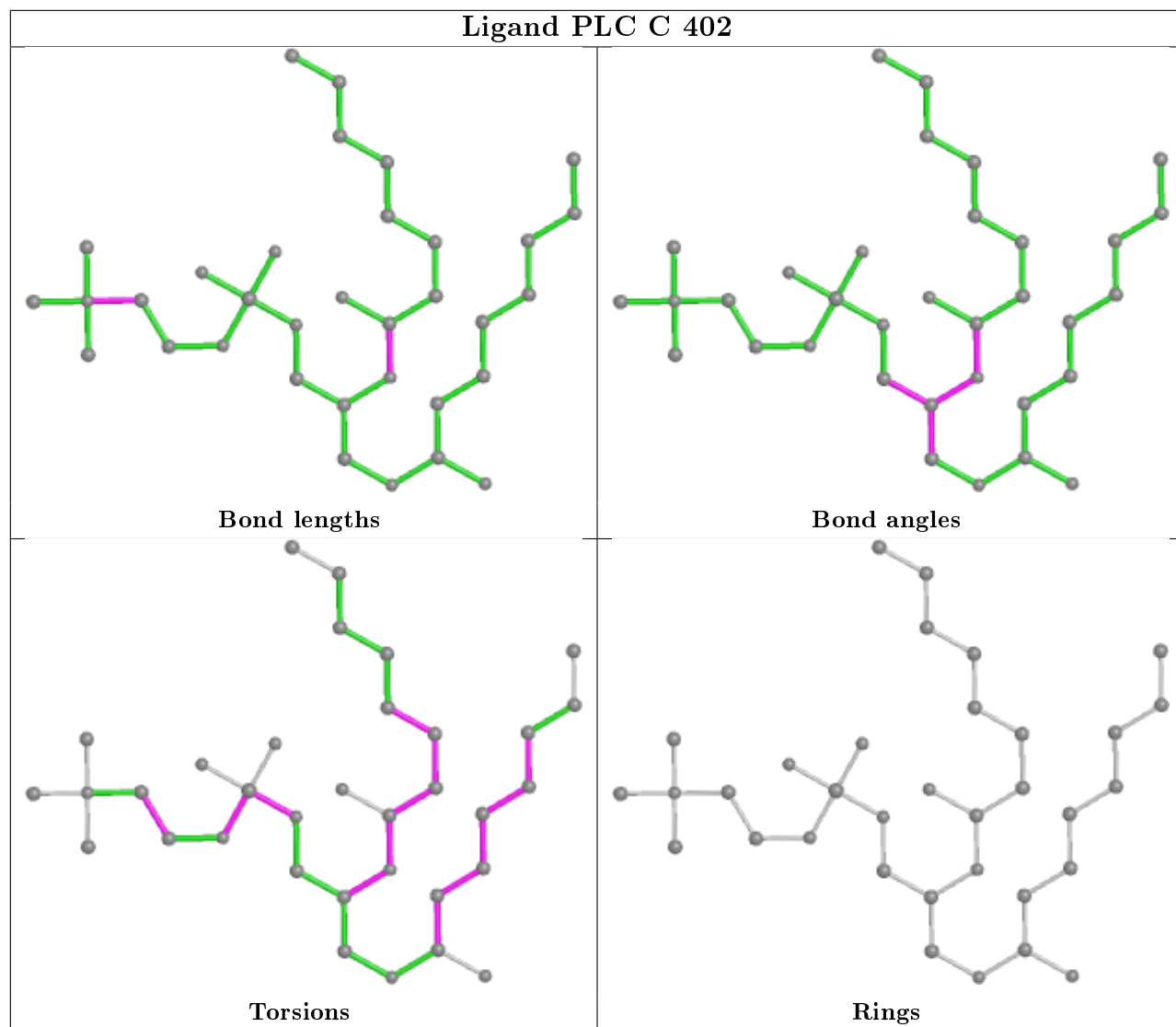


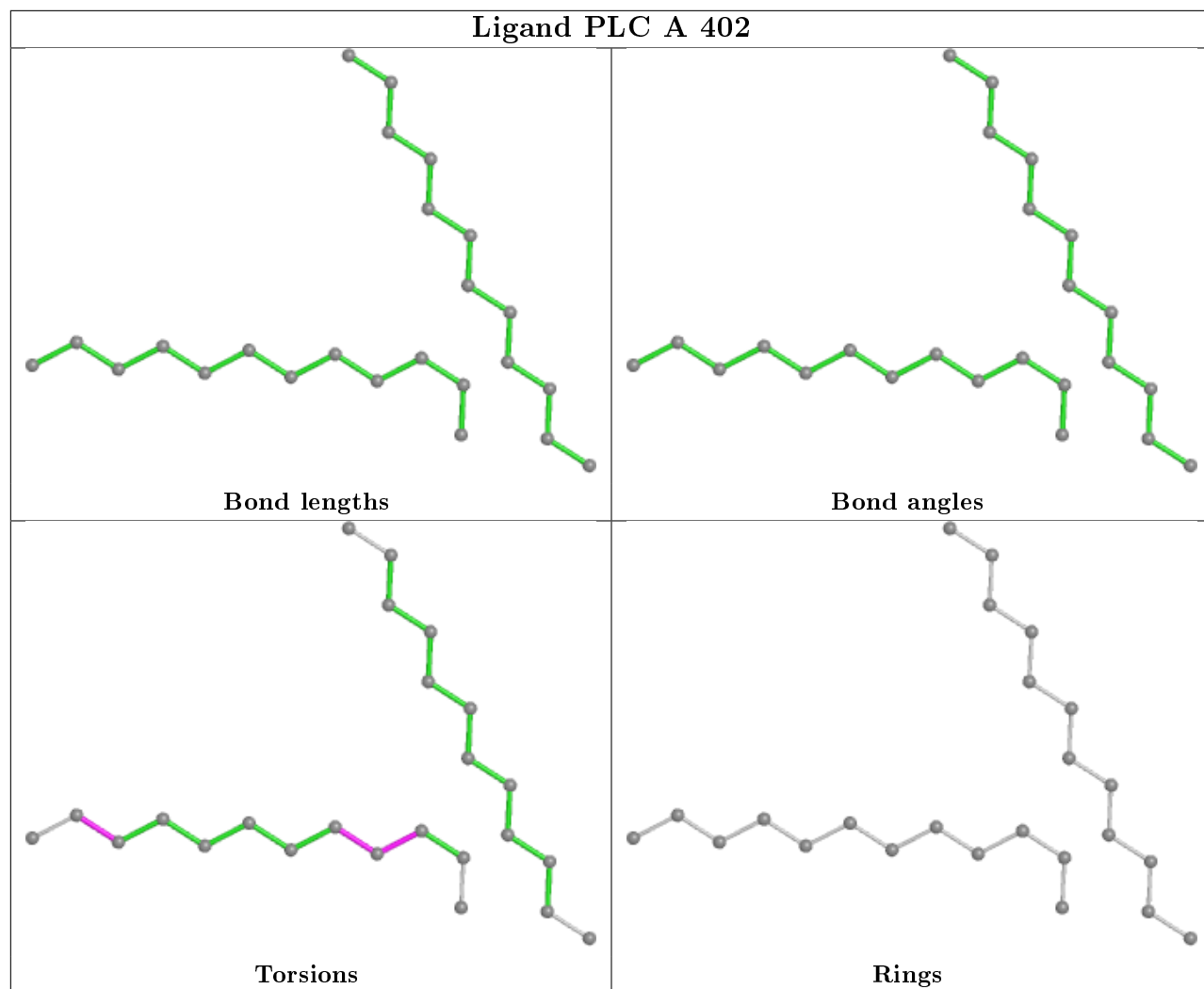


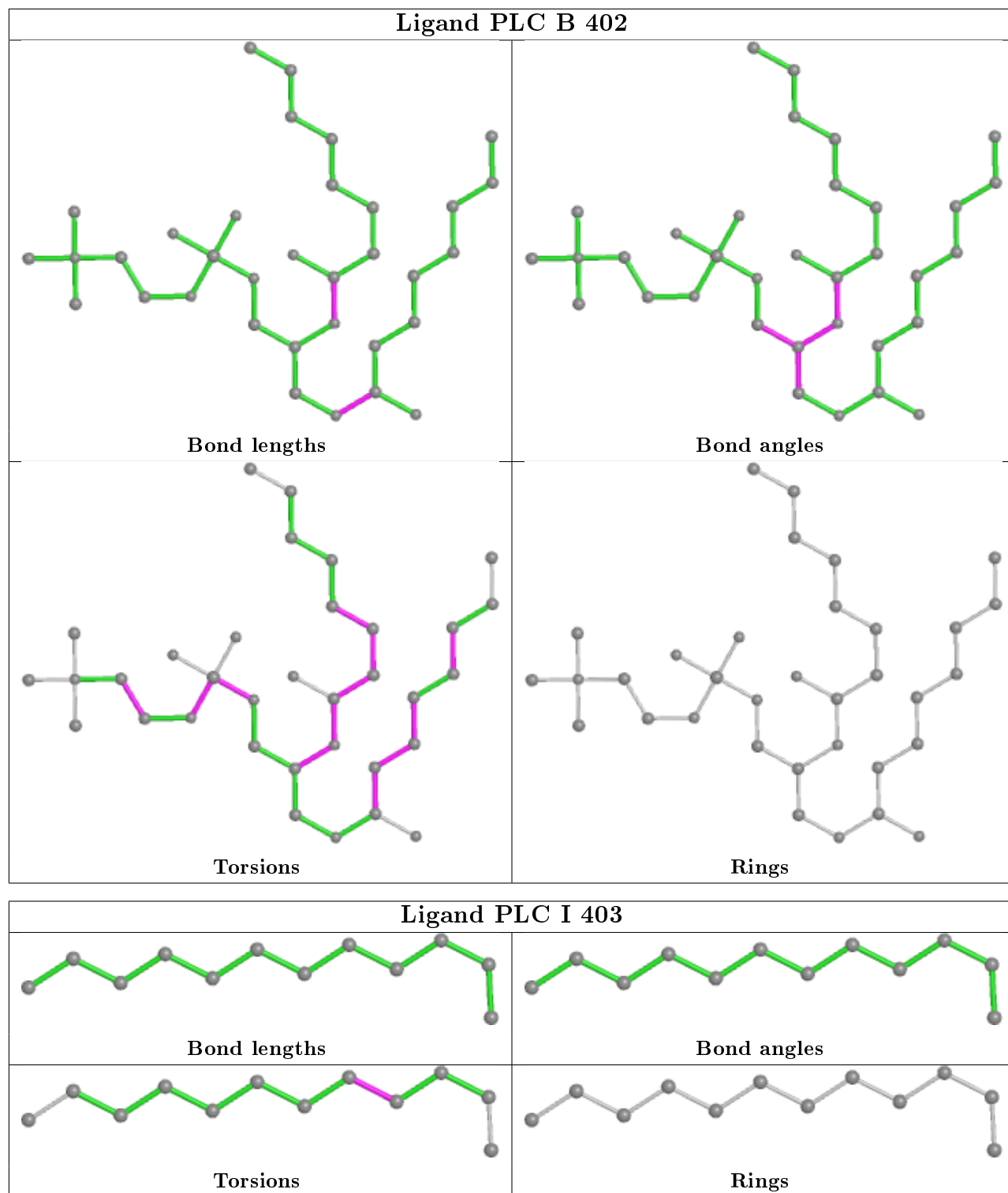


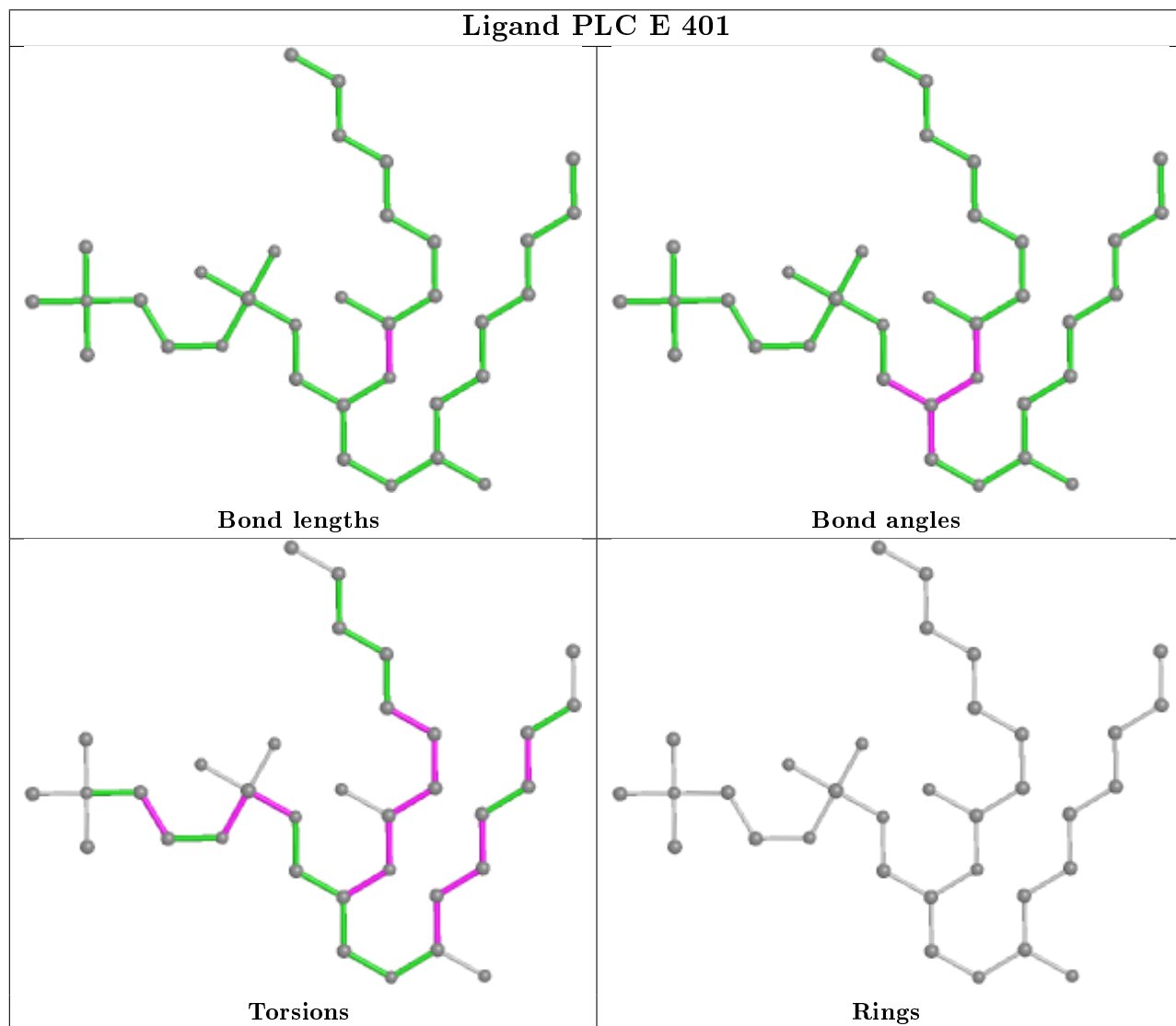
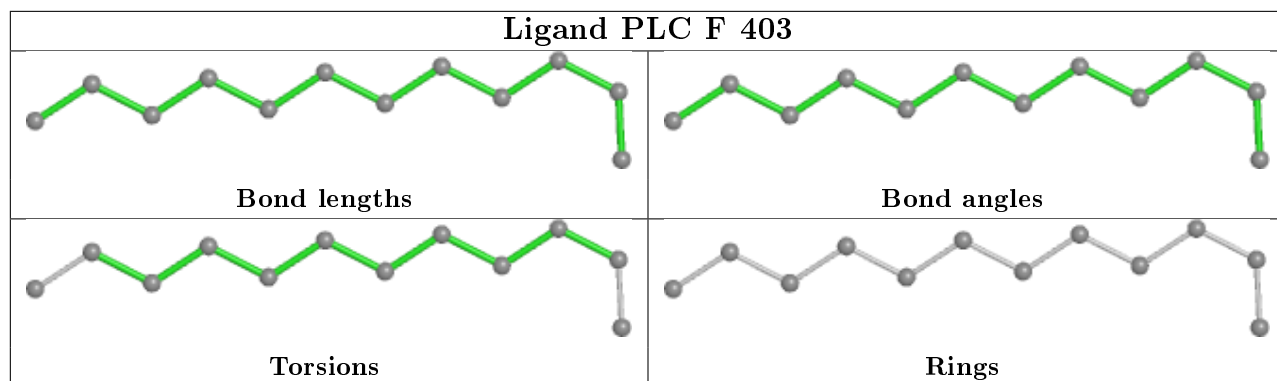


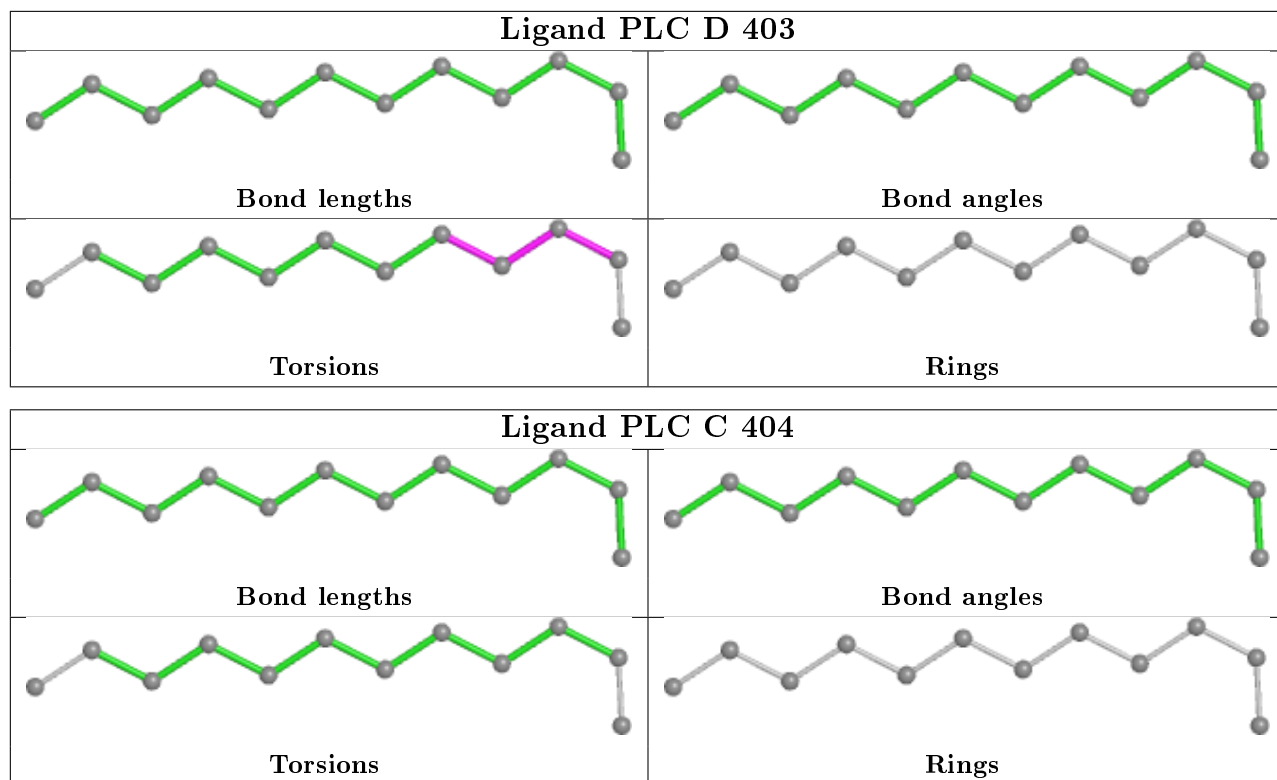


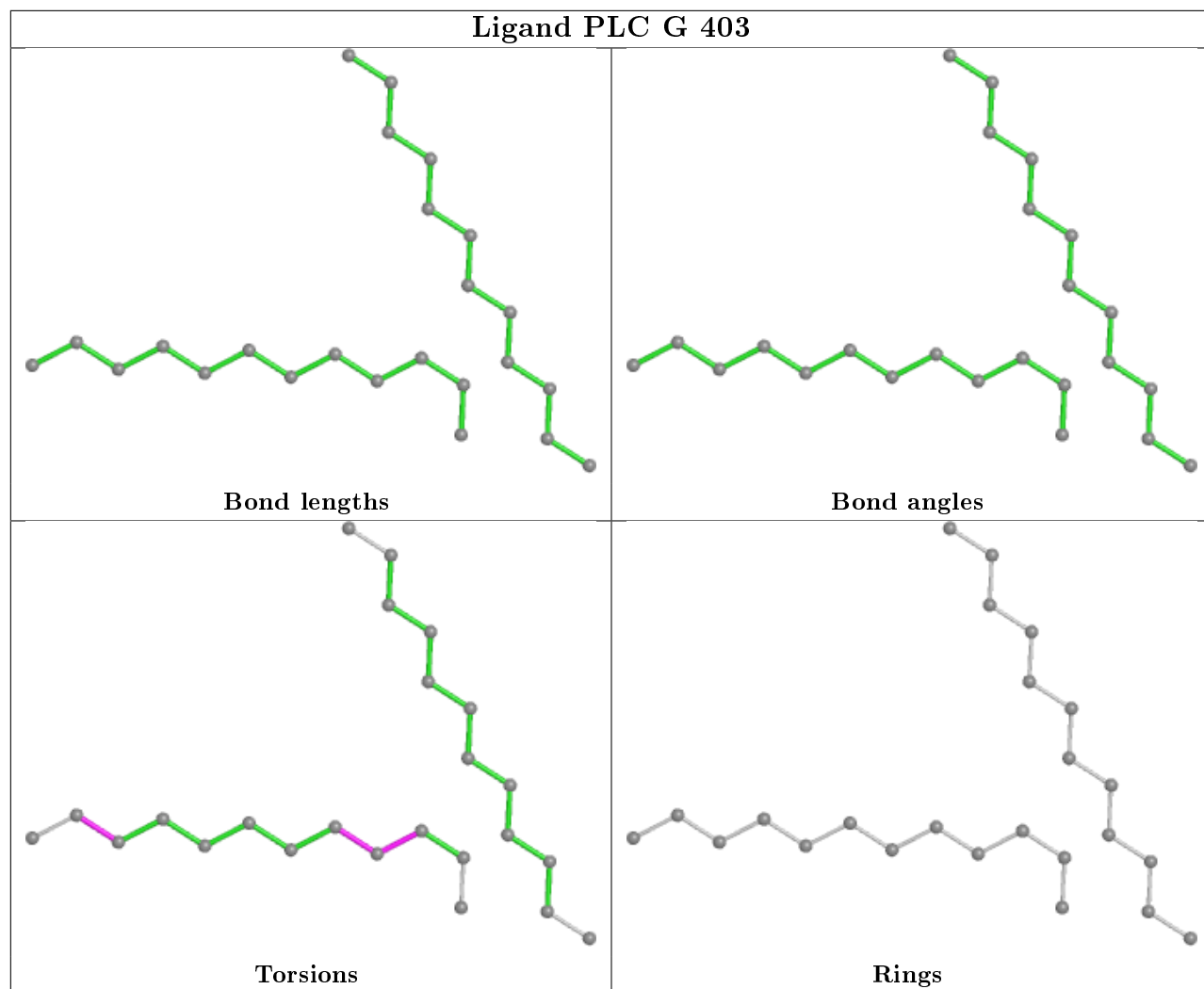


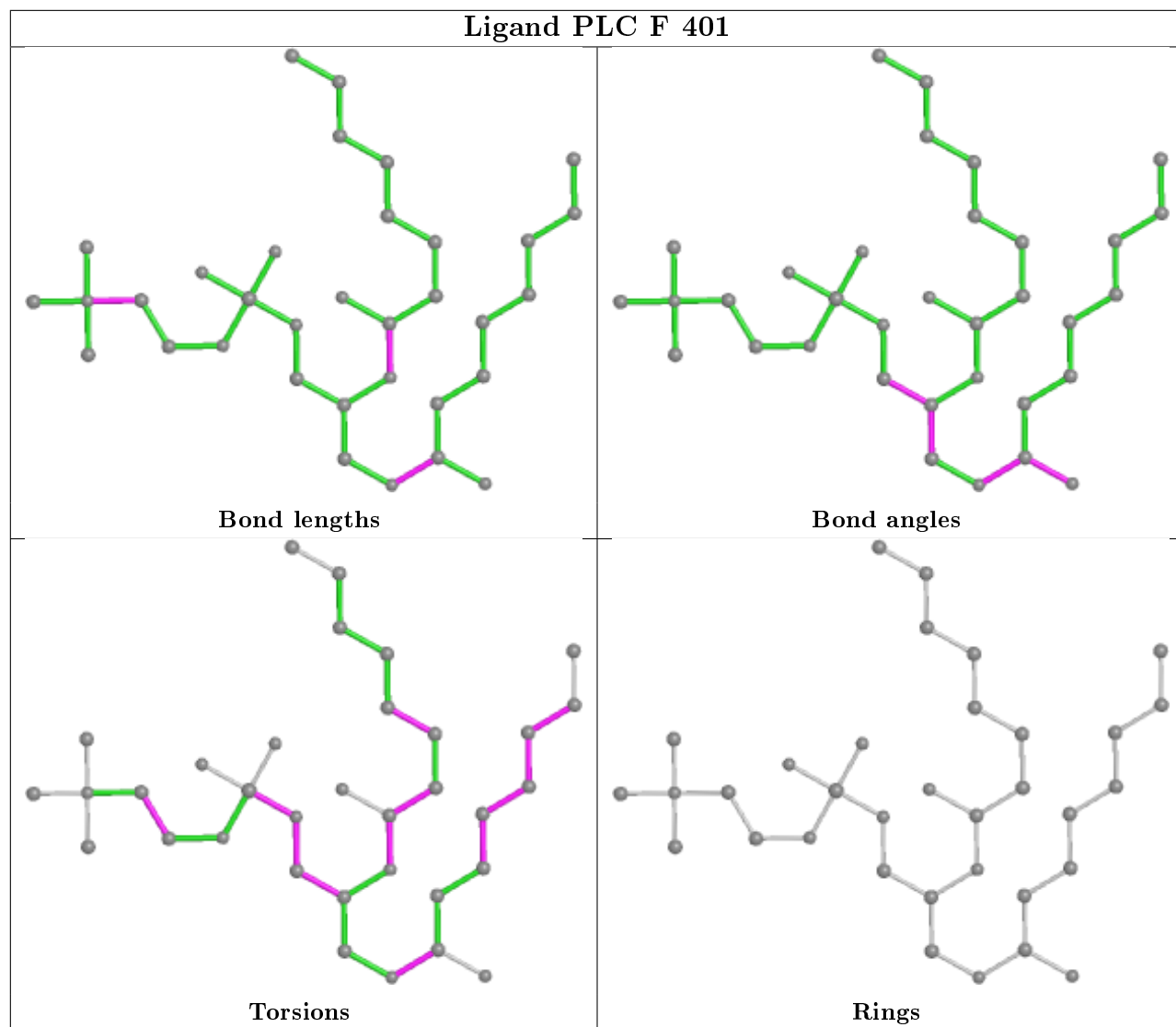




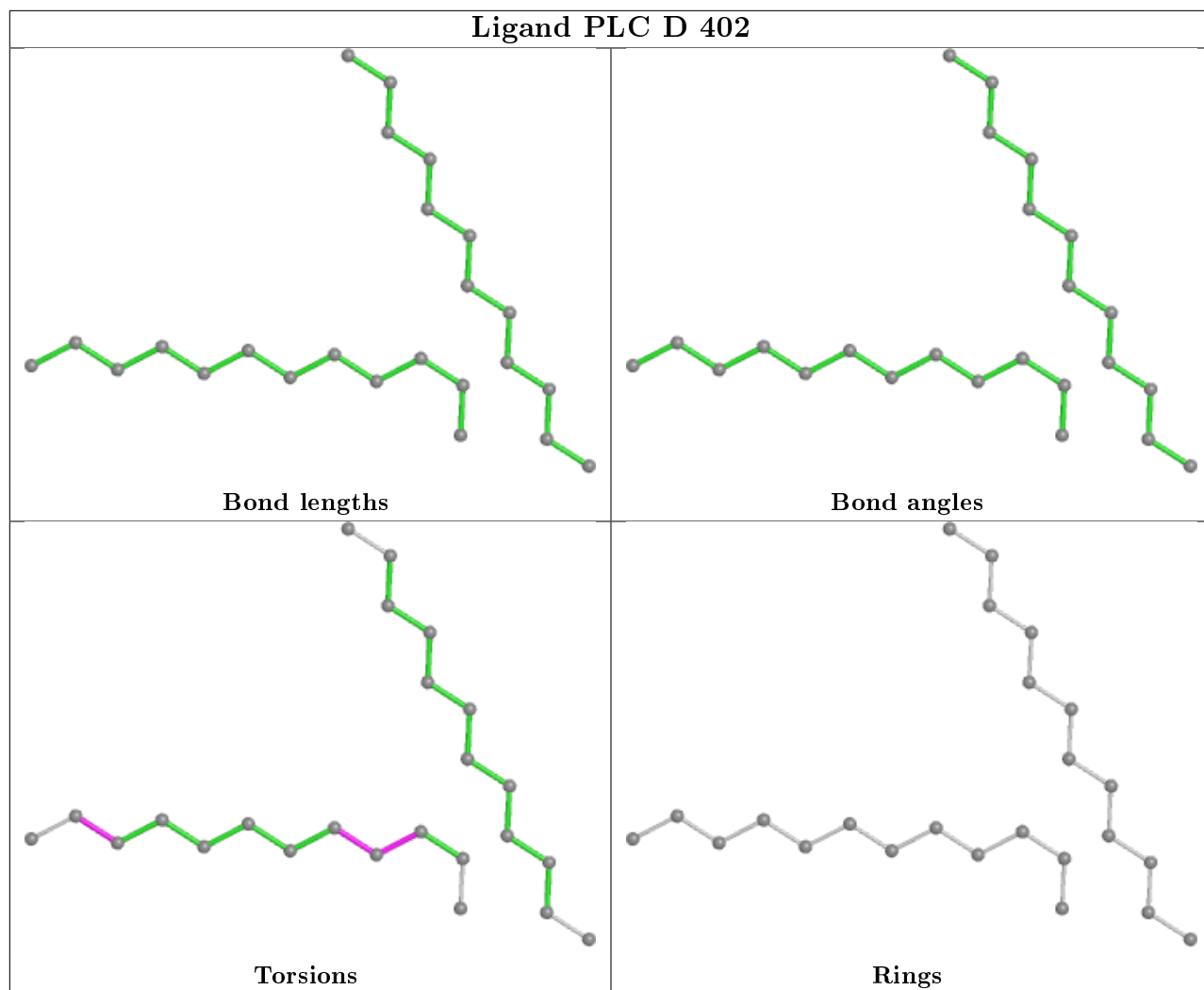


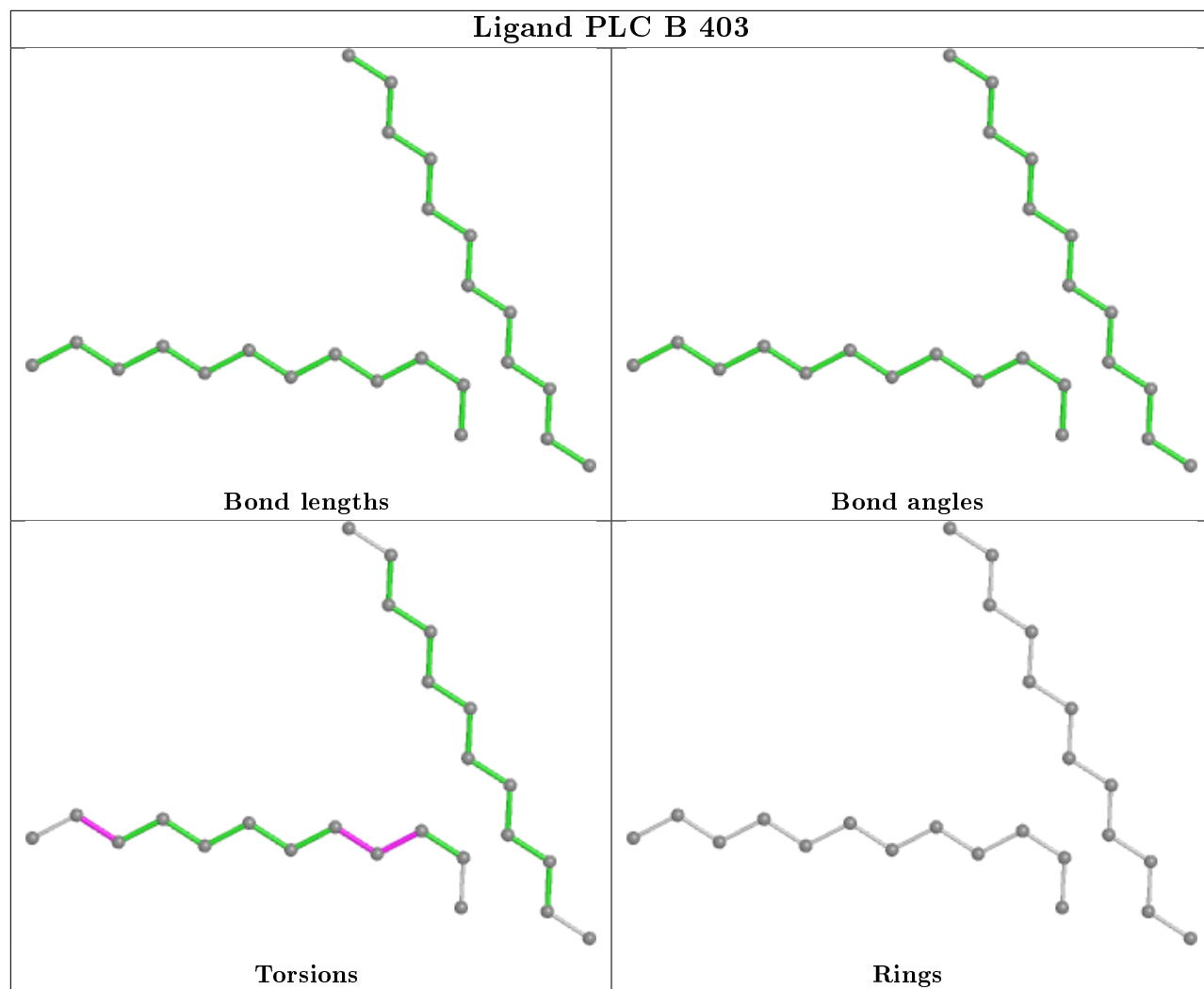


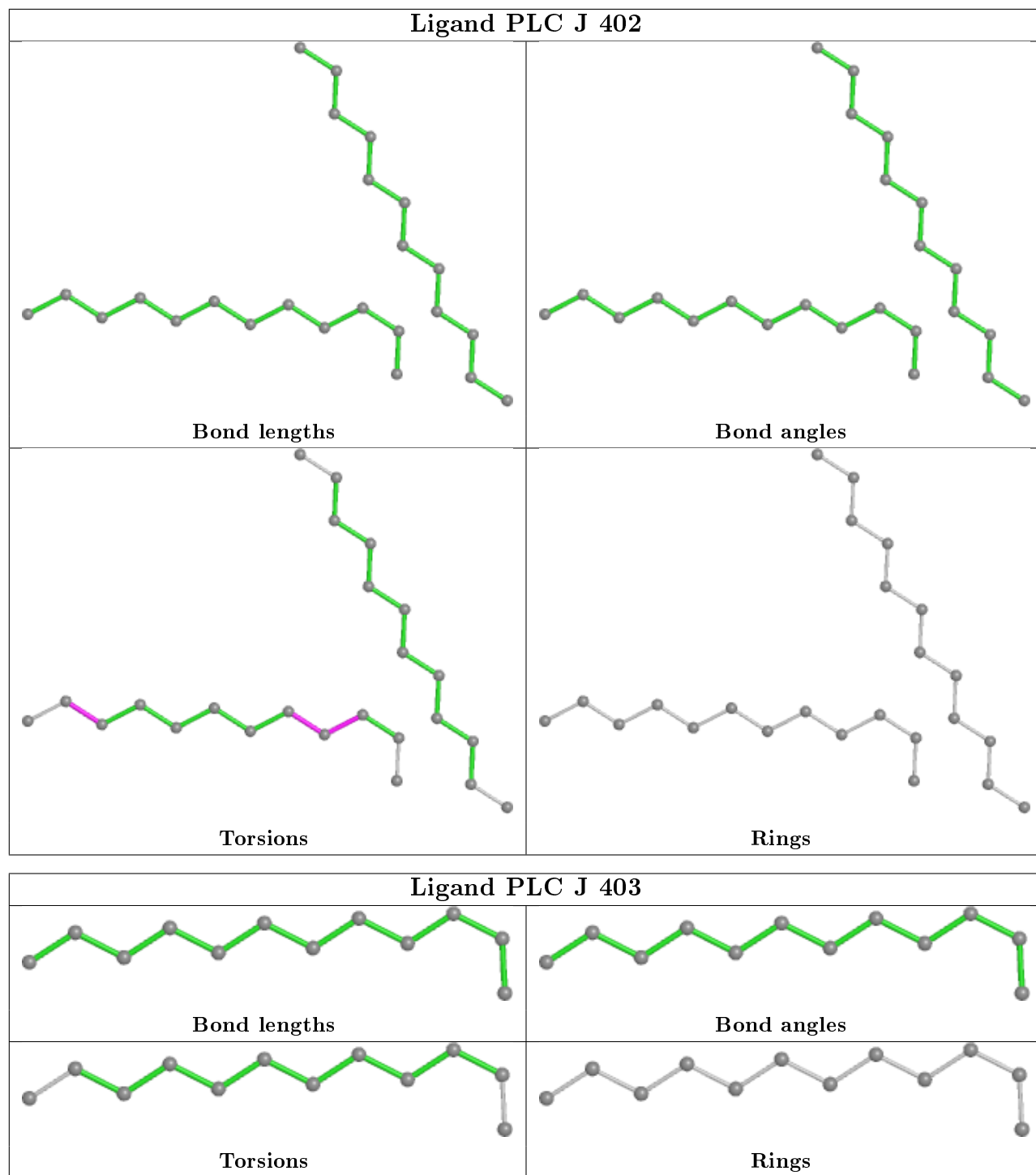


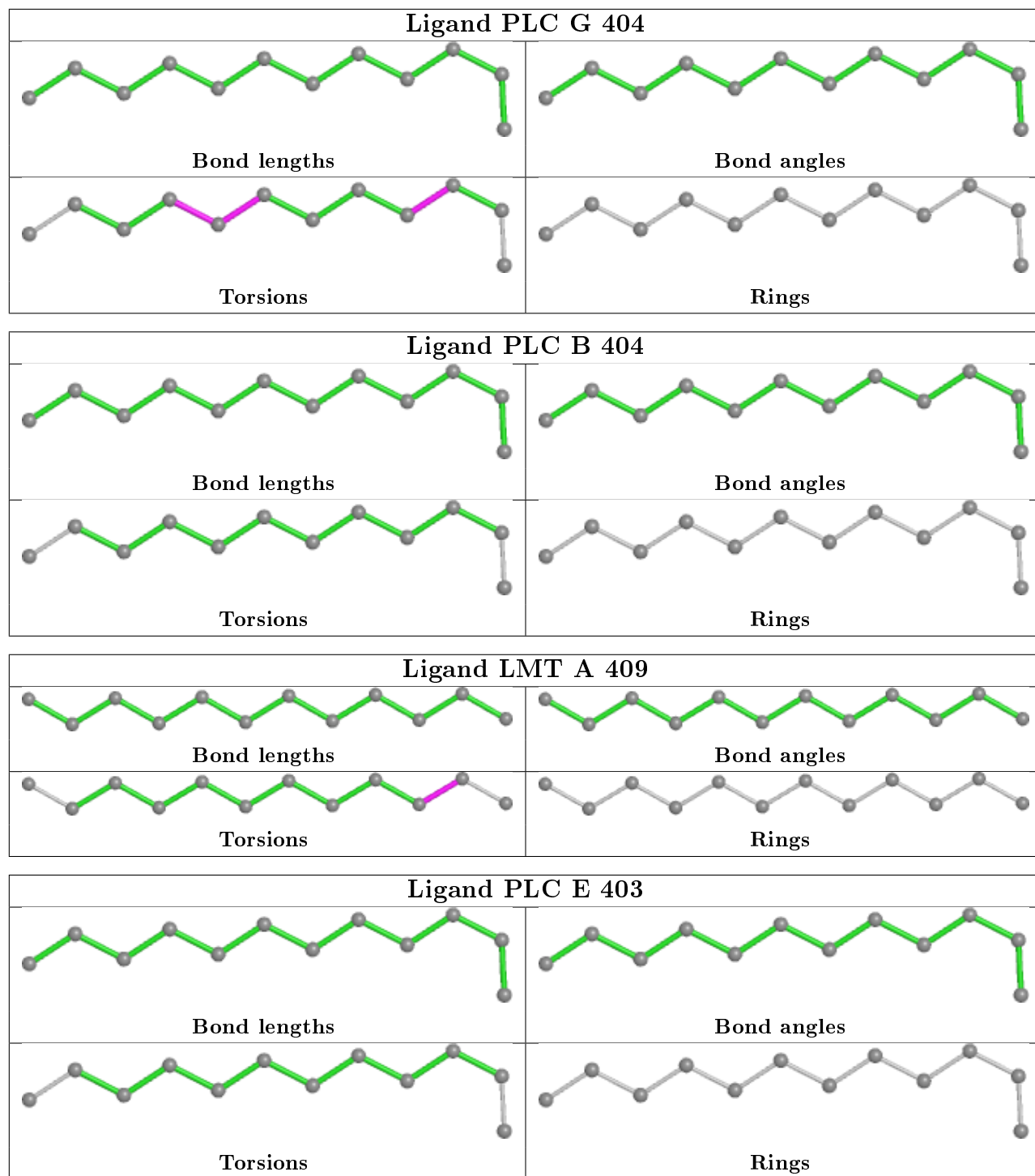


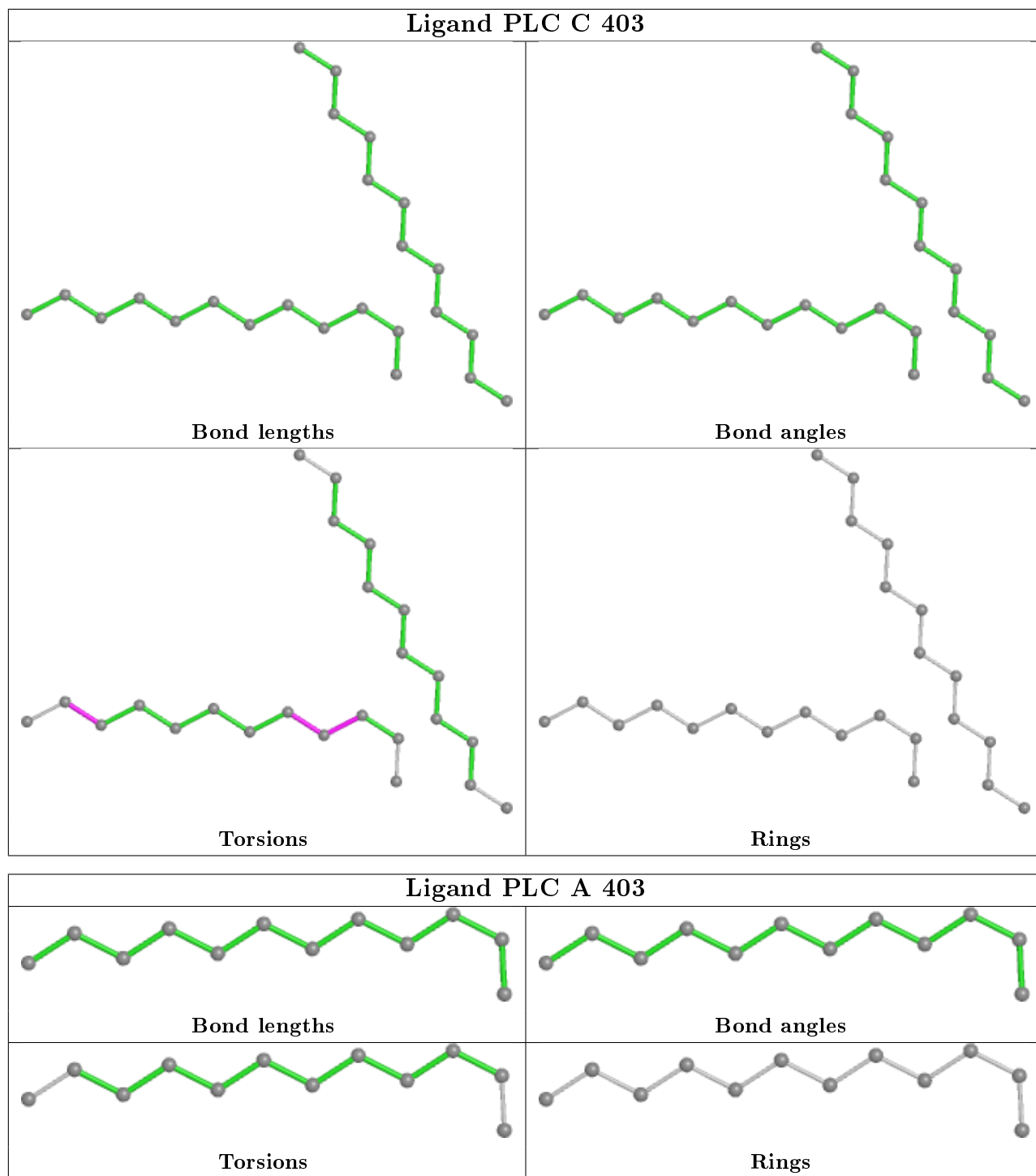


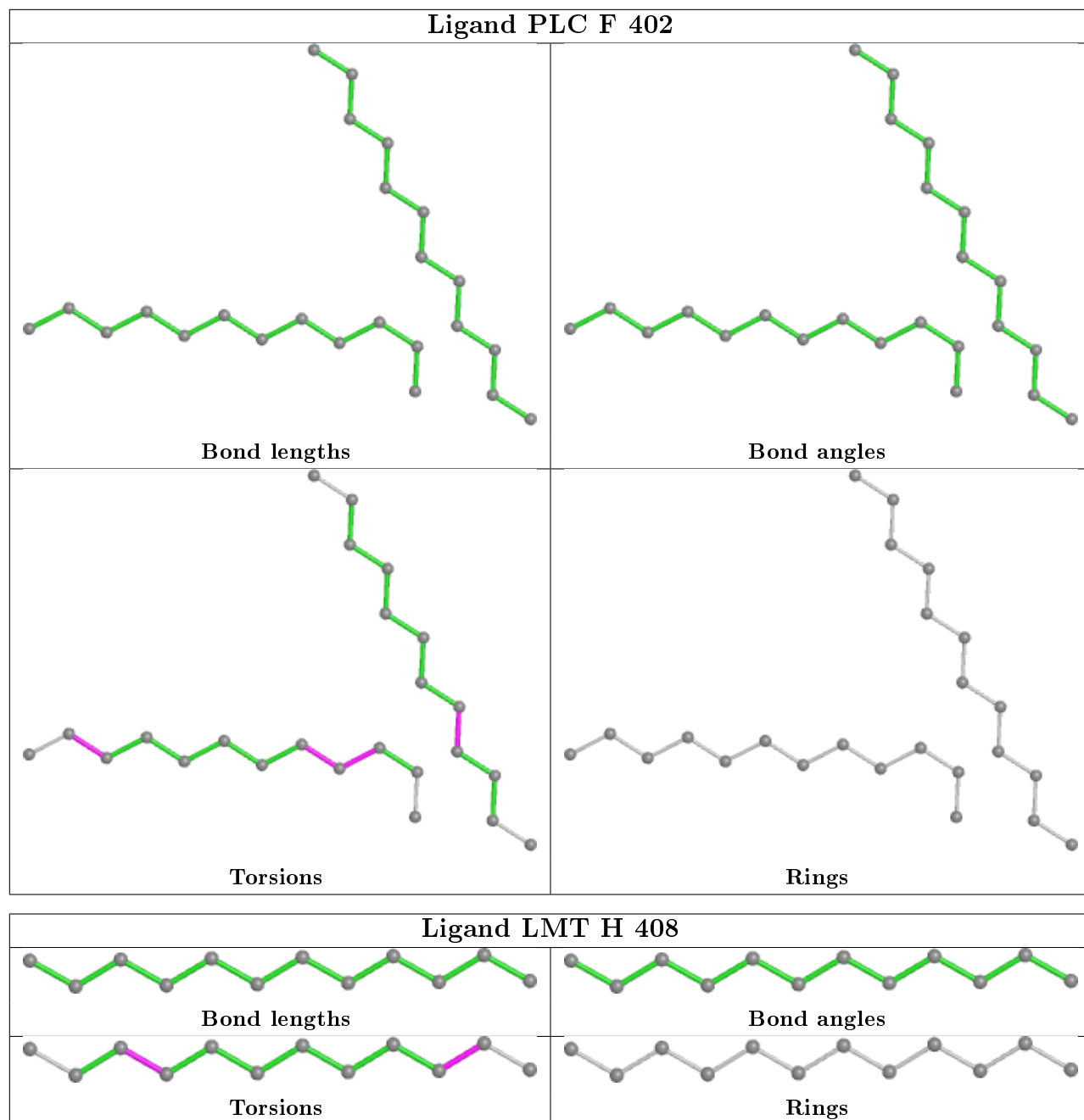


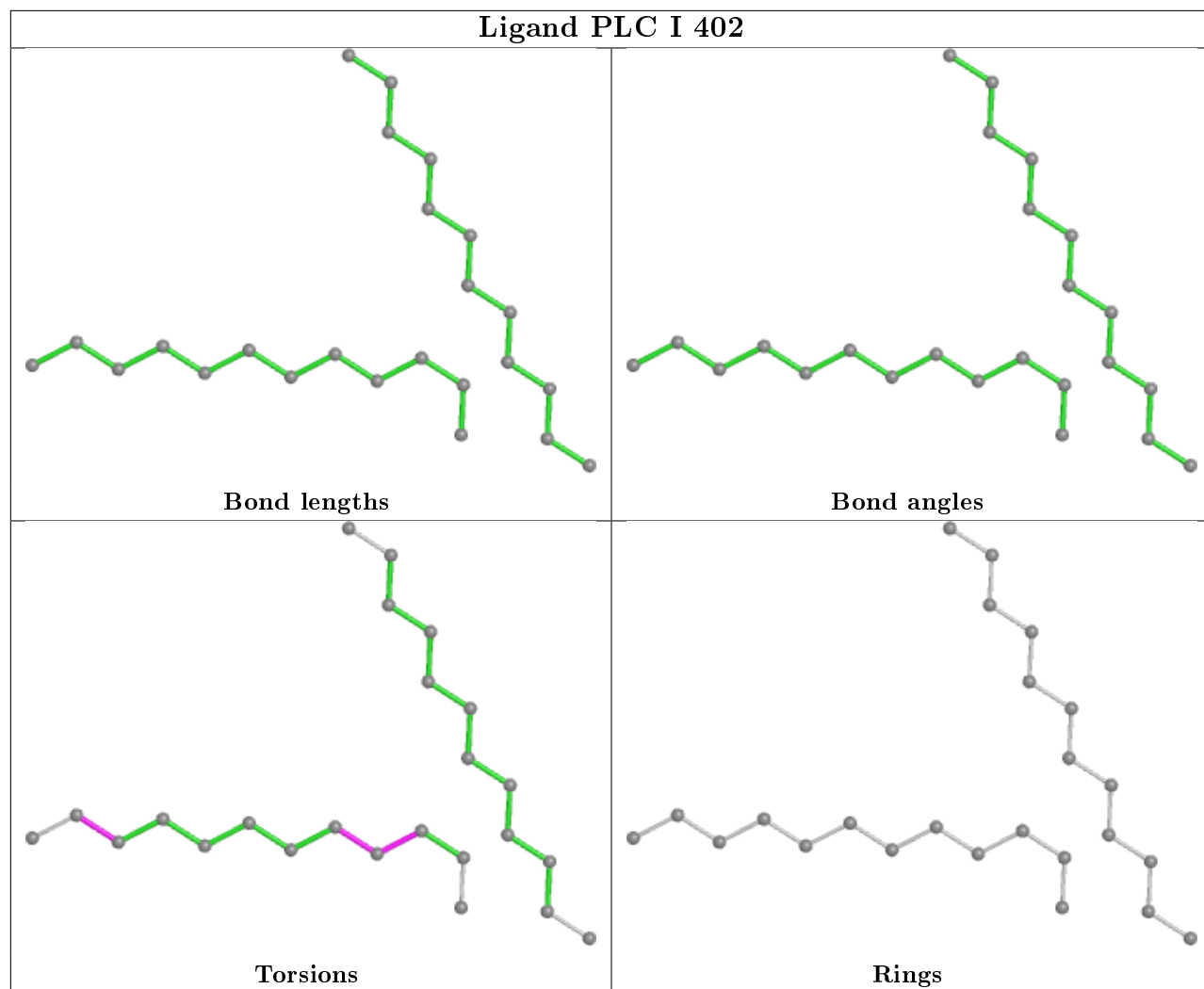


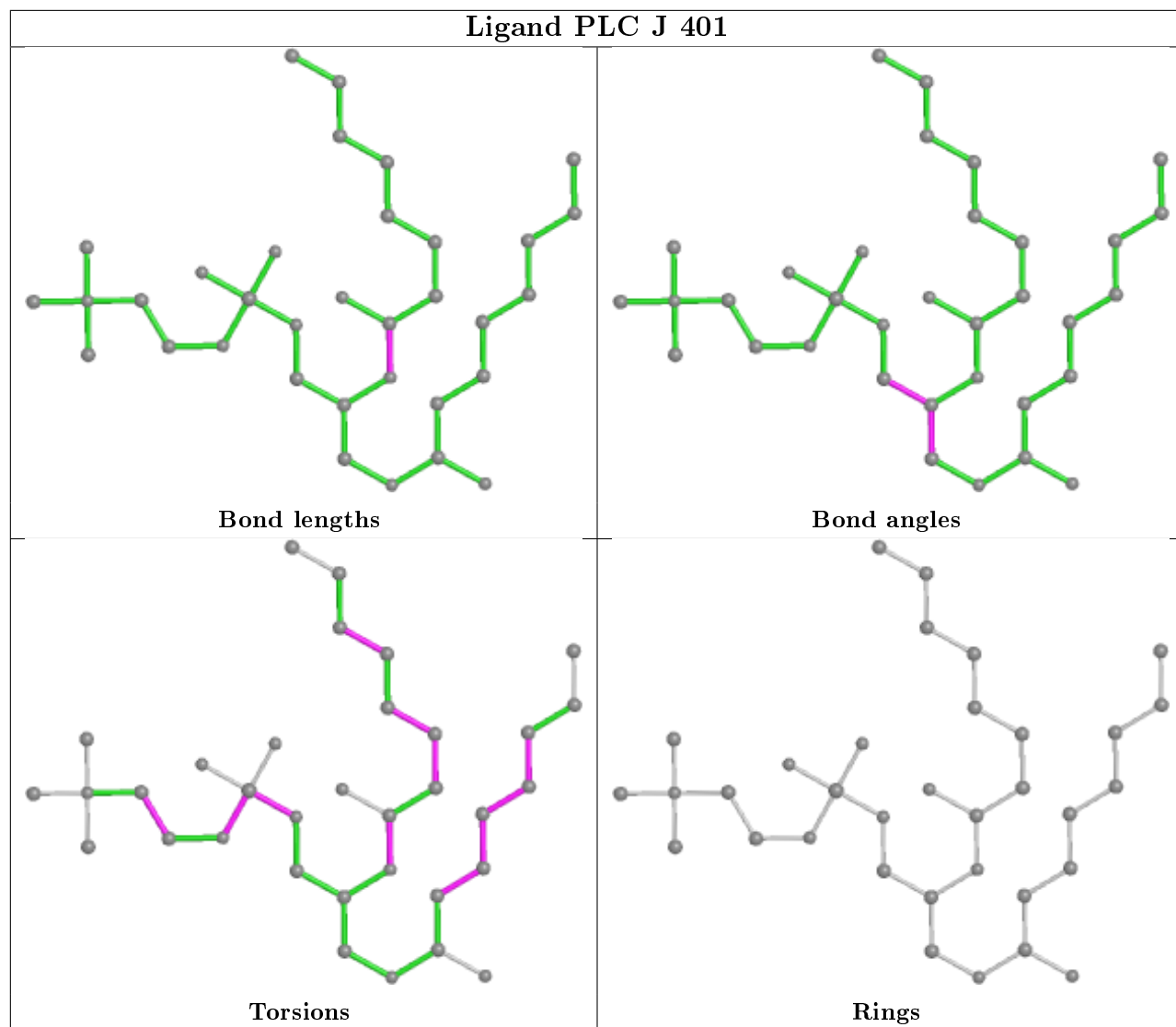




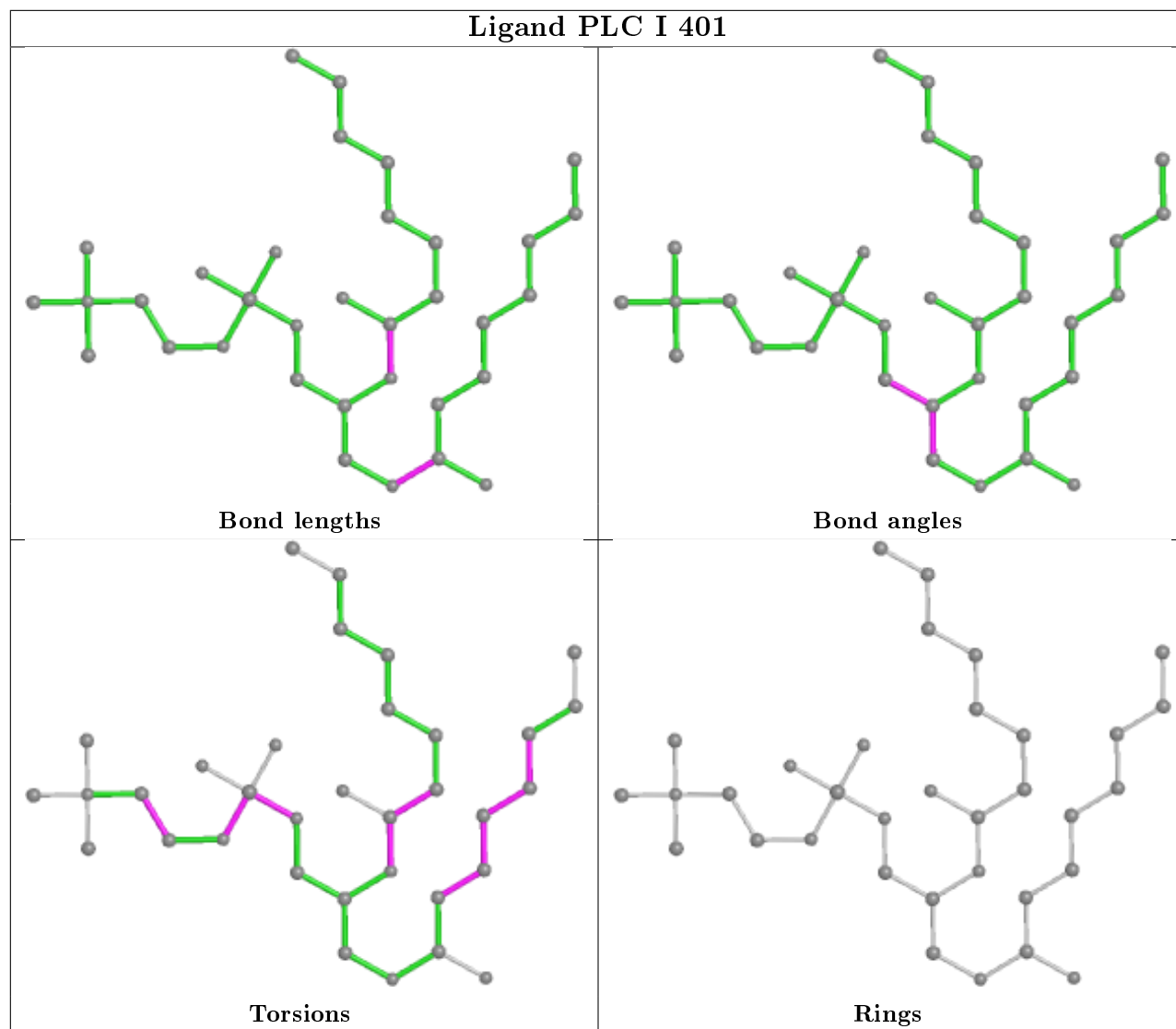












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	311/317 (98%)	0.34	22 (7%) 16 16	59, 75, 124, 179	0
1	B	311/317 (98%)	0.39	24 (7%) 13 13	61, 74, 104, 129	0
1	C	311/317 (98%)	0.35	25 (8%) 12 12	61, 75, 118, 159	0
1	D	311/317 (98%)	0.37	31 (9%) 7 6	59, 74, 124, 167	0
1	E	311/317 (98%)	0.29	16 (5%) 28 29	59, 76, 123, 159	0
1	F	311/317 (98%)	0.20	20 (6%) 19 20	53, 66, 94, 140	0
1	G	311/317 (98%)	0.11	10 (3%) 47 51	28, 63, 100, 127	0
1	H	311/317 (98%)	0.23	15 (4%) 30 32	53, 67, 104, 145	0
1	I	311/317 (98%)	0.28	24 (7%) 13 13	52, 66, 102, 154	0
1	J	311/317 (98%)	0.16	13 (4%) 36 39	52, 67, 102, 133	0
All	All	3110/3170 (98%)	0.27	200 (6%) 19 20	28, 71, 112, 179	0

All (200) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	156	PHE	8.1
1	C	61	VAL	6.1
1	A	52	LEU	6.1
1	E	58	ARG	5.9
1	D	155	VAL	5.8
1	C	62	ARG	5.8
1	J	58	ARG	5.6
1	H	57	VAL	5.6
1	J	62	ARG	5.1
1	A	156	PHE	5.1
1	A	64	LYS	5.0
1	I	57	VAL	5.0
1	C	56	PRO	4.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	11	ILE	4.6
1	D	154	ASP	4.6
1	D	57	VAL	4.6
1	D	54	PHE	4.6
1	D	157	LEU	4.6
1	B	57	VAL	4.5
1	B	312	PHE	4.5
1	C	58	ARG	4.4
1	F	57	VAL	4.4
1	I	54	PHE	4.4
1	A	155	VAL	4.3
1	H	62	ARG	4.3
1	C	312	PHE	4.3
1	I	156	PHE	4.3
1	D	56	PRO	4.2
1	F	156	PHE	4.2
1	E	60	GLY	4.2
1	I	59	SER	4.2
1	E	61	VAL	4.1
1	E	5	VAL	4.1
1	I	61	VAL	4.1
1	I	154	ASP	4.0
1	J	61	VAL	4.0
1	H	58	ARG	4.0
1	F	155	VAL	4.0
1	D	136	ASP	3.9
1	A	154	ASP	3.9
1	H	60	GLY	3.9
1	B	136	ASP	3.8
1	H	12	ALA	3.8
1	A	98	GLY	3.8
1	H	94	VAL	3.8
1	D	98	GLY	3.7
1	E	94	VAL	3.7
1	F	12	ALA	3.7
1	A	11	ILE	3.7
1	C	293	ARG	3.6
1	C	12	ALA	3.6
1	H	59	SER	3.6
1	D	96	PRO	3.6
1	J	11	ILE	3.5
1	C	13	ASP	3.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	152	ASN	3.5
1	A	59	SER	3.5
1	J	56	PRO	3.5
1	B	11	ILE	3.5
1	D	53	ALA	3.5
1	G	9	PRO	3.5
1	F	154	ASP	3.4
1	G	287	ARG	3.4
1	D	97	ASP	3.4
1	I	60	GLY	3.3
1	F	11	ILE	3.3
1	B	184	LEU	3.3
1	C	94	VAL	3.3
1	E	57	VAL	3.3
1	C	63	VAL	3.2
1	J	57	VAL	3.2
1	E	62	ARG	3.2
1	D	99	THR	3.1
1	E	59	SER	3.1
1	B	297	ILE	3.1
1	G	284	GLN	3.0
1	A	54	PHE	3.0
1	I	58	ARG	3.0
1	C	96	PRO	3.0
1	D	62	ARG	3.0
1	F	50	ARG	3.0
1	F	230	SER	3.0
1	E	69	GLU	2.9
1	J	96	PRO	2.9
1	G	136	ASP	2.9
1	I	155	VAL	2.9
1	A	58	ARG	2.9
1	G	293	ARG	2.9
1	E	64	LYS	2.9
1	H	64	LYS	2.9
1	A	57	VAL	2.9
1	B	60	GLY	2.8
1	F	312	PHE	2.8
1	I	226	THR	2.8
1	B	294	ALA	2.8
1	D	146	LEU	2.8
1	I	96	PRO	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	233	ILE	2.8
1	I	62	ARG	2.8
1	C	95	SER	2.7
1	A	61	VAL	2.7
1	A	60	GLY	2.7
1	I	152	ASN	2.7
1	B	182	SER	2.7
1	E	226	THR	2.7
1	B	284	GLN	2.6
1	B	180	LEU	2.6
1	A	287	ARG	2.6
1	E	283	SER	2.6
1	E	95	SER	2.6
1	J	284	GLN	2.6
1	F	236	ILE	2.6
1	I	23	TYR	2.6
1	D	59	SER	2.5
1	H	66	TYR	2.5
1	D	61	VAL	2.5
1	G	154	ASP	2.5
1	J	226	THR	2.5
1	B	293	ARG	2.5
1	D	153	ASP	2.5
1	D	94	VAL	2.5
1	B	290	SER	2.5
1	J	60	GLY	2.5
1	C	154	ASP	2.4
1	C	59	SER	2.4
1	C	155	VAL	2.4
1	D	48	LYS	2.4
1	B	230	SER	2.4
1	H	61	VAL	2.4
1	I	153	ASP	2.4
1	I	157	LEU	2.4
1	A	100	VAL	2.4
1	A	66	TYR	2.4
1	E	70	ALA	2.4
1	F	287	ARG	2.4
1	C	57	VAL	2.3
1	A	9	PRO	2.3
1	C	237	ALA	2.3
1	H	226	THR	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	I	312	PHE	2.3
1	F	234	ALA	2.3
1	A	50	ARG	2.3
1	B	88	ASP	2.3
1	J	156	PHE	2.3
1	D	240	ILE	2.3
1	A	230	SER	2.3
1	B	240	ILE	2.3
1	F	233	ILE	2.3
1	D	237	ALA	2.3
1	H	52	LEU	2.3
1	D	64	LYS	2.2
1	C	234	ALA	2.2
1	H	56	PRO	2.2
1	E	136	ASP	2.2
1	B	79	VAL	2.2
1	C	233	ILE	2.2
1	C	240	ILE	2.2
1	I	240	ILE	2.2
1	F	146	LEU	2.2
1	I	230	SER	2.2
1	B	172	ALA	2.2
1	B	113	PRO	2.2
1	F	55	ASP	2.2
1	B	287	ARG	2.2
1	G	47	TRP	2.2
1	H	293	ARG	2.2
1	D	149	VAL	2.2
1	B	169	VAL	2.1
1	D	236	ILE	2.1
1	G	226	THR	2.1
1	C	54	PHE	2.1
1	D	95	SER	2.1
1	G	294	ALA	2.1
1	A	25	ILE	2.1
1	A	188	LEU	2.1
1	J	283	SER	2.1
1	D	27	CYS	2.1
1	F	240	ILE	2.1
1	D	52	LEU	2.1
1	J	312	PHE	2.1
1	C	208	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	55	ASP	2.1
1	I	233	ILE	2.1
1	C	226	THR	2.1
1	I	136	ASP	2.1
1	I	236	ILE	2.1
1	F	232	LEU	2.1
1	C	60	GLY	2.1
1	F	229	VAL	2.0
1	I	137	THR	2.0
1	D	25	ILE	2.0
1	E	52	LEU	2.0
1	F	58	ARG	2.0
1	B	237	ALA	2.0
1	F	237	ALA	2.0
1	H	6	SER	2.0
1	A	92	ILE	2.0
1	B	62	ARG	2.0
1	I	56	PRO	2.0
1	G	156	PHE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	NA	E	405	1/1	0.29	0.21	95,95,95,95	0
6	SIN	C	408	8/8	0.32	1.08	137,139,141,141	0
4	NA	D	405	1/1	0.37	0.38	109,109,109,109	0
2	PLC	E	403	12/42	0.38	0.74	101,102,103,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	SIN	B	408	8/8	0.49	0.54	134,136,139,139	0
2	PLC	H	403	12/42	0.52	0.68	97,98,101,101	0
2	PLC	F	403	12/42	0.53	0.49	99,100,101,101	0
2	PLC	C	402	34/42	0.54	0.48	97,113,141,142	0
2	PLC	B	402	34/42	0.55	0.63	101,114,139,139	0
2	PLC	F	401	34/42	0.56	0.37	98,117,137,137	0
2	PLC	G	402	34/42	0.56	0.45	96,112,140,142	0
2	PLC	J	401	34/42	0.56	0.45	99,112,138,139	0
4	NA	B	406	1/1	0.57	0.23	96,96,96,96	0
2	PLC	E	401	34/42	0.59	0.39	100,113,139,141	0
2	PLC	C	404	12/42	0.59	0.78	94,95,97,97	0
6	SIN	D	407	8/8	0.60	0.46	77,78,78,79	8
2	PLC	B	404	12/42	0.61	0.82	97,98,99,99	0
2	PLC	A	401	34/42	0.61	0.35	94,109,138,139	0
6	SIN	H	409	8/8	0.62	0.58	64,65,67,67	8
2	PLC	J	403	12/42	0.64	0.60	98,100,101,101	0
4	NA	A	407	1/1	0.65	0.18	90,90,90,90	0
2	PLC	H	401	34/42	0.65	0.34	101,115,142,143	0
4	NA	C	406	1/1	0.66	0.15	86,86,86,86	0
2	PLC	D	403	12/42	0.66	0.63	94,94,95,95	0
6	SIN	G	410	8/8	0.67	0.65	101,103,104,105	0
4	NA	F	405	1/1	0.67	0.18	83,83,83,83	0
2	PLC	D	401	34/42	0.67	0.31	98,112,135,136	0
6	SIN	A	411	8/8	0.67	0.75	120,122,124,125	0
2	PLC	I	403	12/42	0.70	0.60	88,90,93,94	0
6	SIN	J	407	8/8	0.70	0.38	109,110,111,112	0
2	PLC	F	402	24/42	0.70	0.39	84,87,93,95	0
6	SIN	F	409	8/8	0.70	0.44	59,59,60,61	8
2	PLC	J	402	24/42	0.71	0.31	75,81,93,96	0
4	NA	G	406	1/1	0.71	0.18	86,86,86,86	0
2	PLC	A	402	24/42	0.71	0.43	79,81,96,96	0
2	PLC	G	403	24/42	0.71	0.40	78,93,118,122	0
2	PLC	B	403	24/42	0.72	0.42	74,79,98,100	0
6	SIN	E	407	8/8	0.73	0.44	133,134,135,135	0
2	PLC	A	403	12/42	0.73	0.43	98,99,101,101	0
2	PLC	E	402	24/42	0.73	0.27	72,76,93,94	0
2	PLC	C	403	24/42	0.73	0.41	75,78,86,88	0
2	PLC	I	401	34/42	0.74	0.28	82,100,126,127	0
4	NA	I	405	1/1	0.74	0.15	95,95,95,95	0
6	SIN	I	409	8/8	0.76	0.80	114,115,116,116	0
3	CL	H	406	1/1	0.76	0.55	119,119,119,119	0

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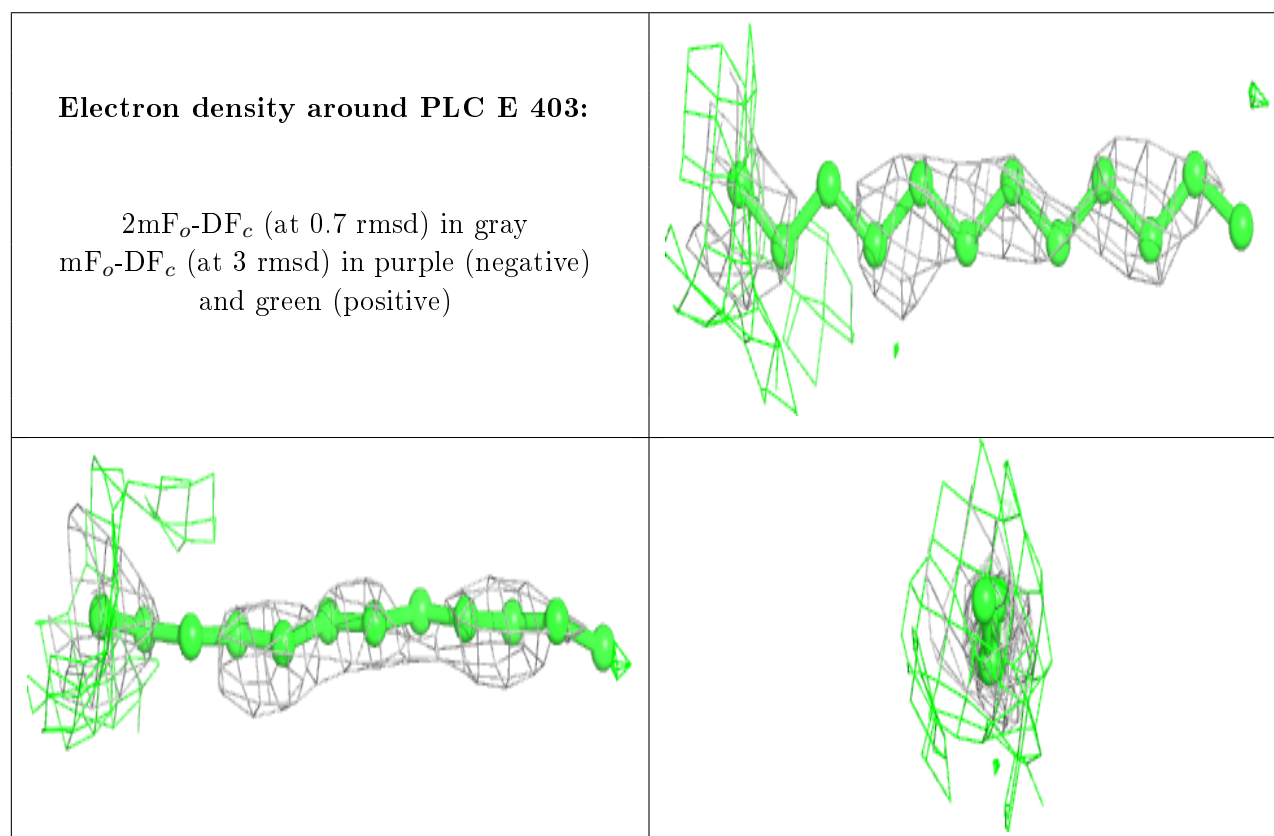
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	PLC	I	402	24/42	0.76	0.29	75,79,93,95	0
5	LMT	D	406	12/35	0.79	0.50	49,54,62,62	0
2	PLC	D	402	24/42	0.79	0.37	70,75,98,99	0
2	PLC	H	402	24/42	0.80	0.35	76,78,90,91	0
5	LMT	J	406	12/35	0.81	0.50	51,57,64,65	0
2	PLC	G	404	12/42	0.82	0.66	96,98,100,101	0
5	LMT	B	407	12/35	0.82	0.50	53,54,61,61	0
4	NA	B	401	1/1	0.82	1.96	110,110,110,110	0
4	NA	H	407	1/1	0.83	0.12	84,84,84,84	0
4	NA	G	409	1/1	0.83	2.50	117,117,117,117	0
4	NA	J	405	1/1	0.83	0.17	81,81,81,81	0
5	LMT	C	407	12/35	0.83	0.46	46,51,59,59	0
5	LMT	F	406	12/35	0.86	0.47	52,54,62,63	0
5	LMT	E	406	12/35	0.86	0.44	48,56,64,65	0
5	LMT	I	406	12/35	0.87	0.39	48,50,54,54	0
5	LMT	A	408	12/35	0.87	0.54	48,51,56,58	0
5	LMT	A	409	12/35	0.87	0.43	60,64,71,71	0
5	LMT	F	407	12/35	0.88	0.61	53,55,63,64	0
5	LMT	G	407	12/35	0.90	0.20	16,20,23,27	0
6	SIN	B	410	8/8	0.90	0.38	91,91,92,92	0
6	SIN	I	408	8/8	0.91	0.27	86,89,93,93	0
5	LMT	H	408	12/35	0.91	0.41	44,51,61,61	0
3	CL	H	405	1/1	0.91	0.30	94,94,94,94	0
3	CL	B	405	1/1	0.92	0.11	68,68,68,68	0
6	SIN	E	408	8/8	0.92	0.31	84,85,88,89	0
3	CL	H	404	1/1	0.92	0.13	66,66,66,66	0
6	SIN	G	408	8/8	0.92	0.21	73,75,78,79	0
3	CL	A	406	1/1	0.92	0.10	88,88,88,88	0
6	SIN	G	401	8/8	0.93	0.24	85,87,90,93	0
3	CL	I	404	1/1	0.93	0.18	58,58,58,58	0
6	SIN	C	401	8/8	0.93	0.24	103,106,108,111	0
6	SIN	A	410	8/8	0.94	0.20	82,83,85,87	0
3	CL	C	405	1/1	0.94	0.10	67,67,67,67	0
3	CL	E	404	1/1	0.94	0.10	75,75,75,75	0
3	CL	F	404	1/1	0.95	0.17	61,61,61,61	0
3	CL	D	404	1/1	0.95	0.10	67,67,67,67	0
6	SIN	B	409	8/8	0.95	0.31	78,79,80,81	0
6	SIN	F	408	8/8	0.95	0.23	79,82,86,87	0
3	CL	A	405	1/1	0.96	0.25	99,99,99,99	0
6	SIN	I	407	8/8	0.96	0.21	71,71,75,78	0
3	CL	A	404	1/1	0.96	0.18	71,71,71,71	0
3	CL	G	405	1/1	0.98	0.10	53,53,53,53	0

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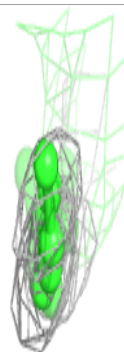
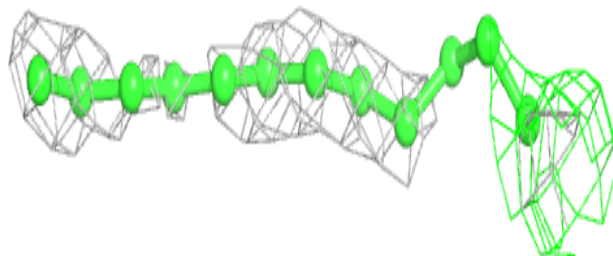
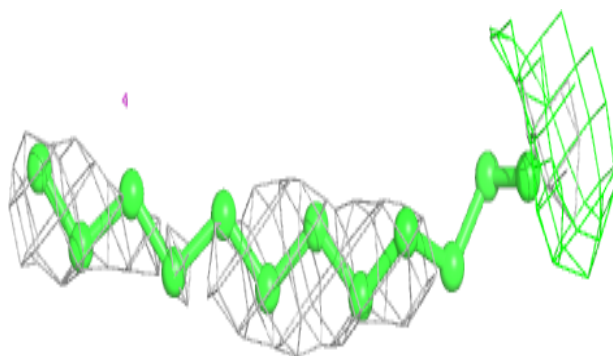
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	J	404	1/1	0.98	0.10	59,59,59,59	0

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.

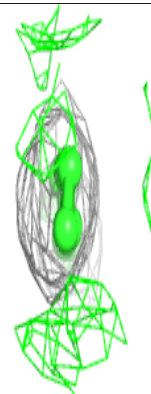
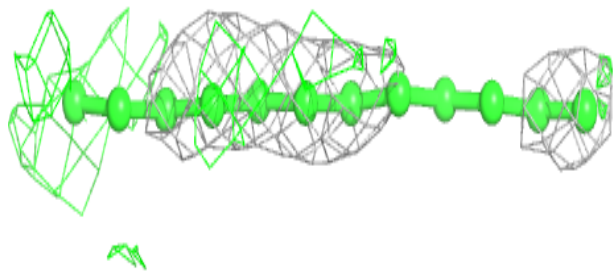
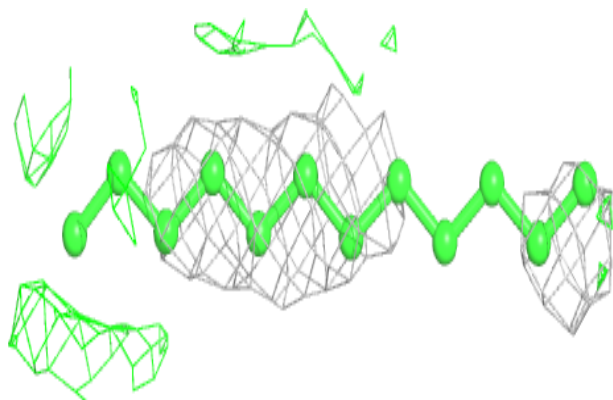


**Electron density around PLC H 403:**

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

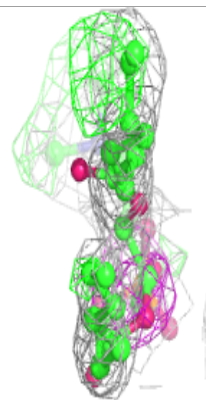
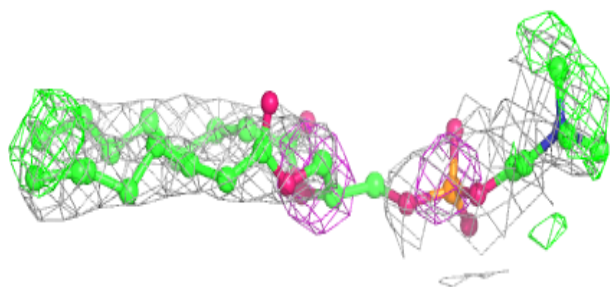
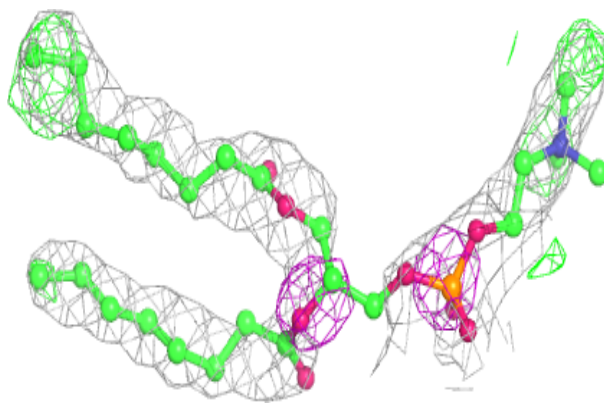
**Electron density around PLC F 403:**

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

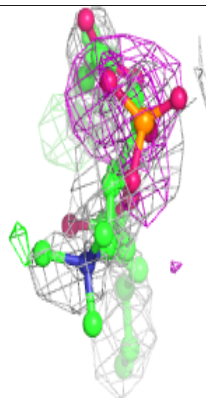
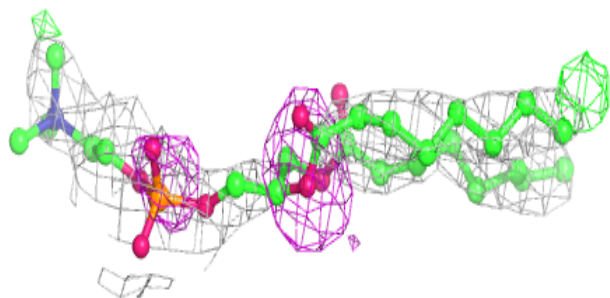
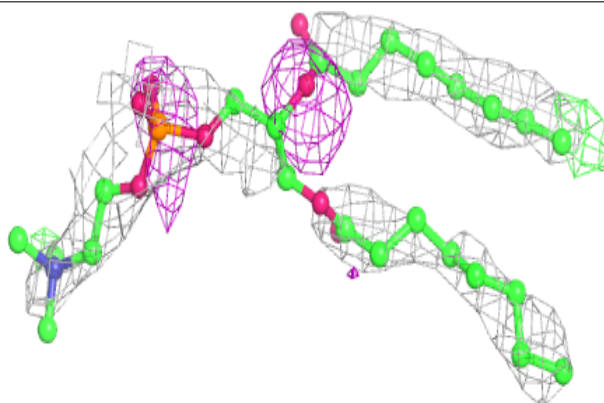


**Electron density around PLC C 402:**

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

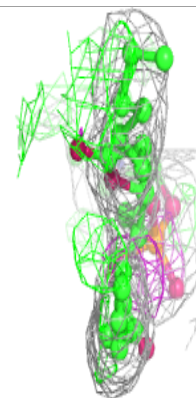
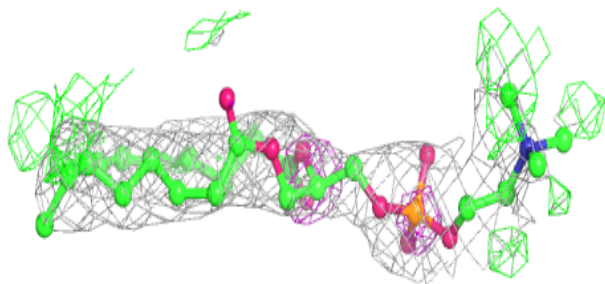
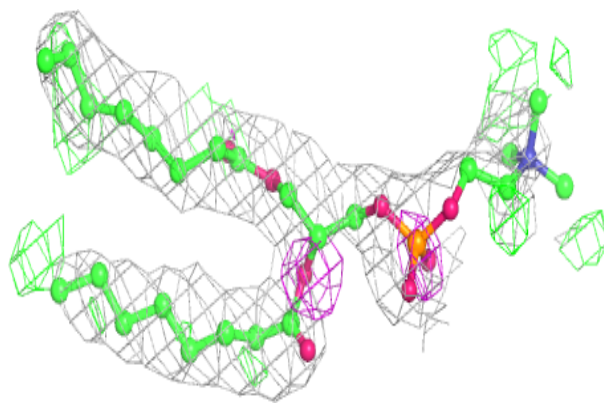
**Electron density around PLC B 402:**

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

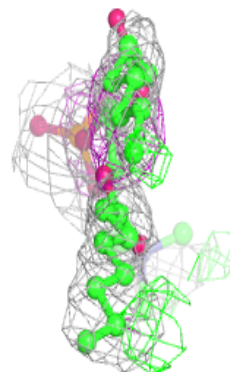
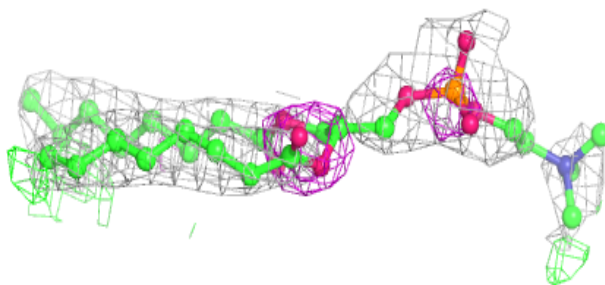
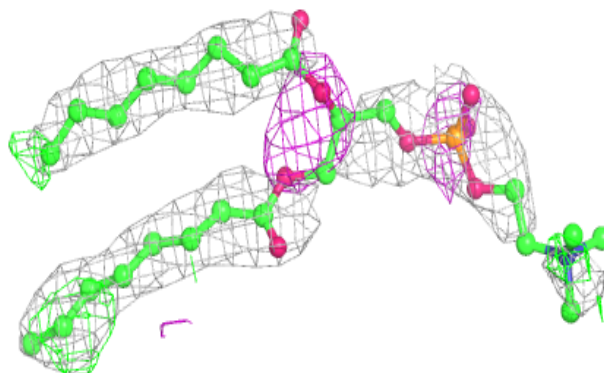


**Electron density around PLC F 401:**

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

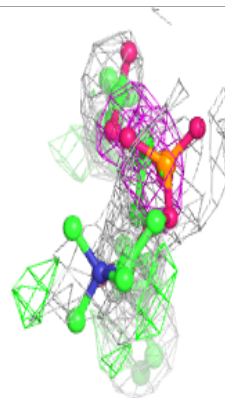
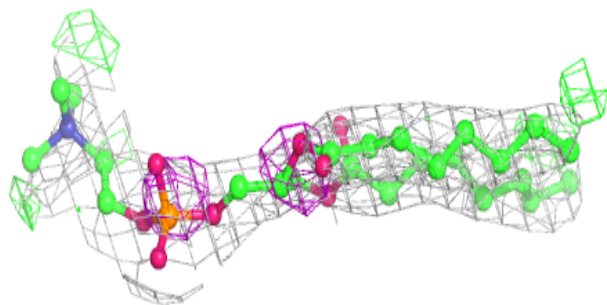
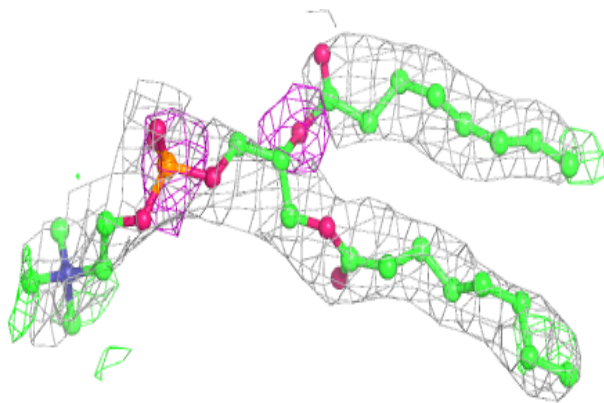
**Electron density around PLC G 402:**

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

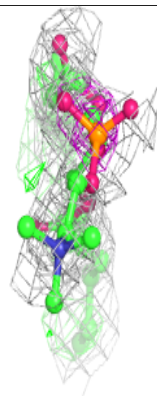
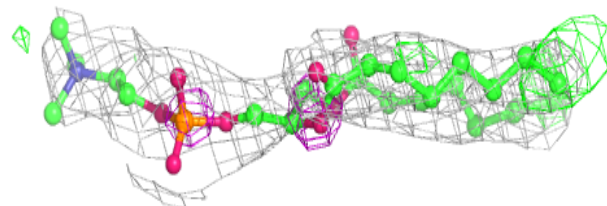
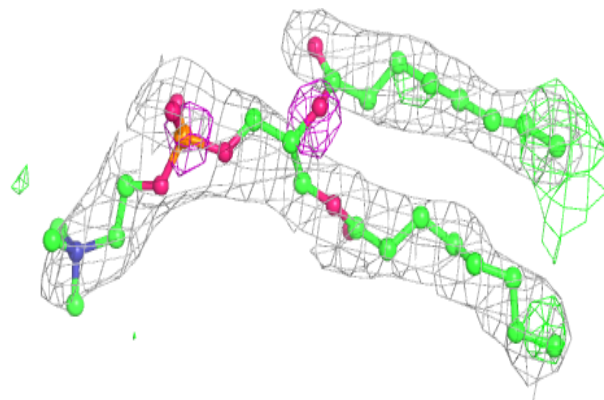


**Electron density around PLC J 401:**

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

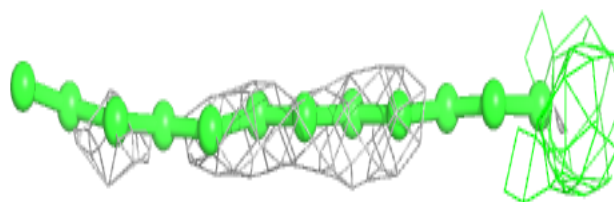
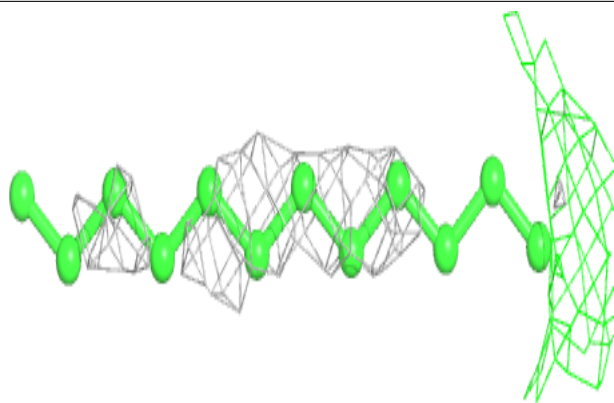
**Electron density around PLC E 401:**

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

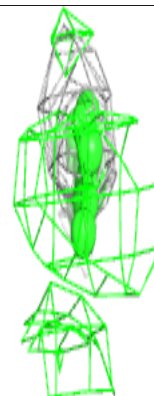
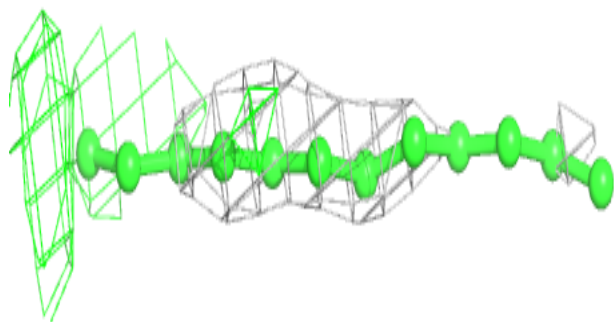
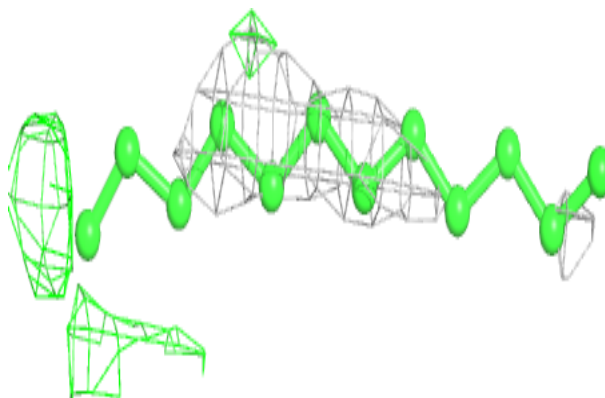


**Electron density around PLC C 404:**

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

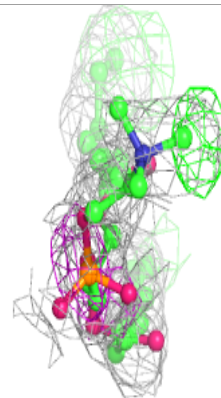
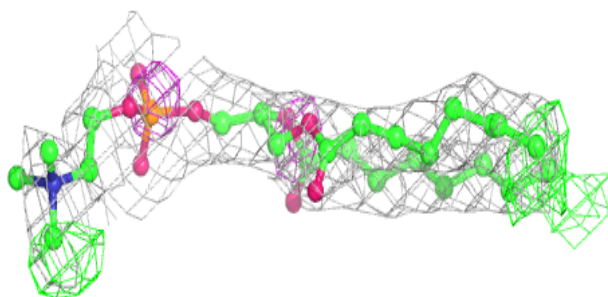
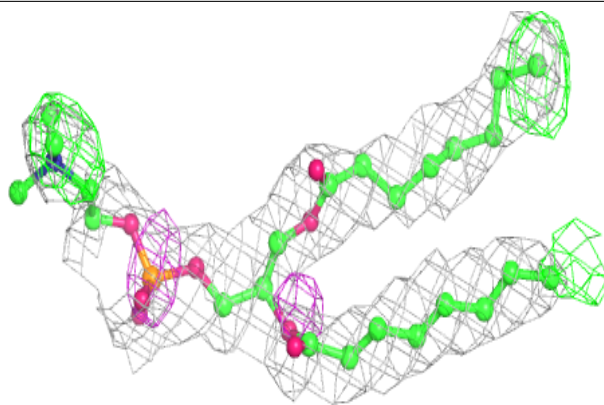
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

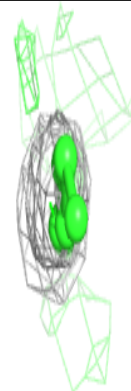
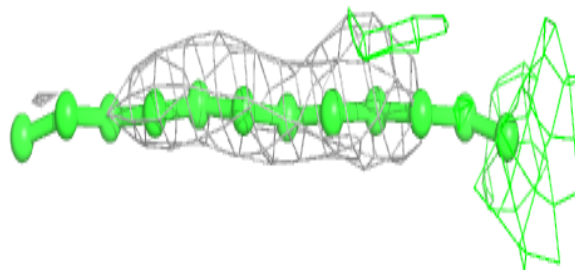
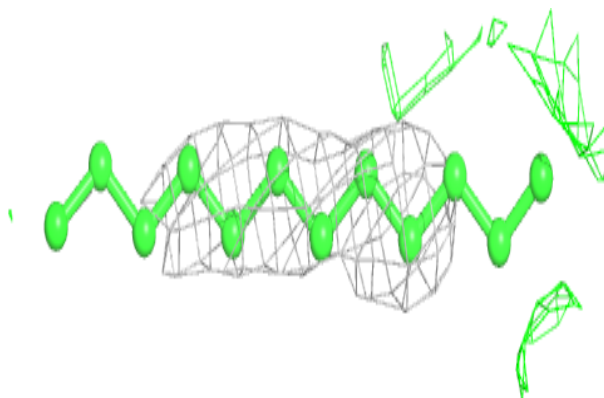


**Electron density around PLC A 401:**

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and green (positive)

**Electron density around PLC J 403:**

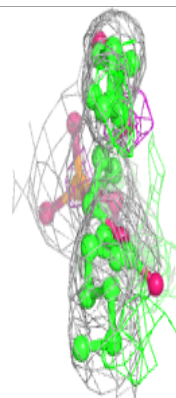
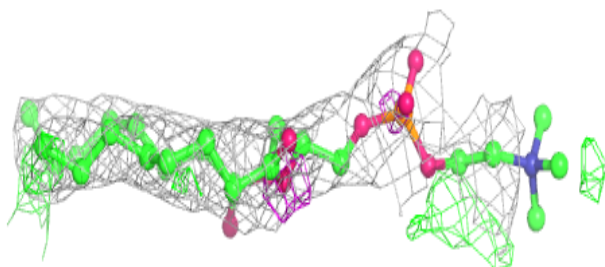
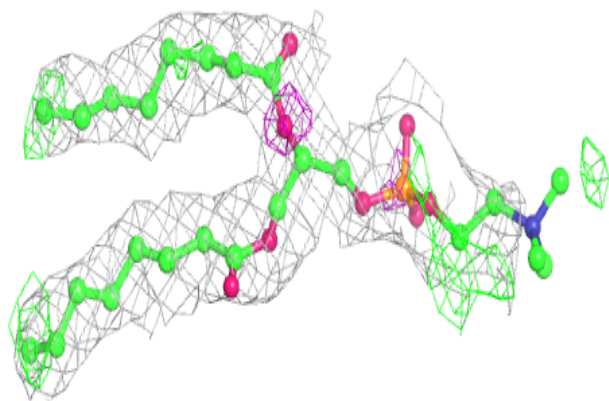
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



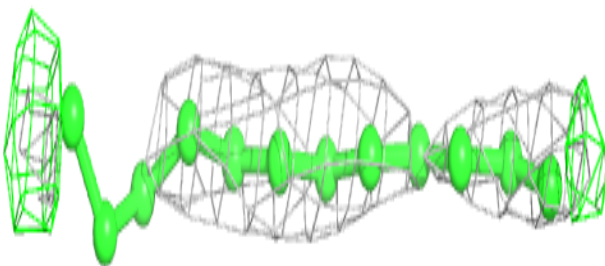
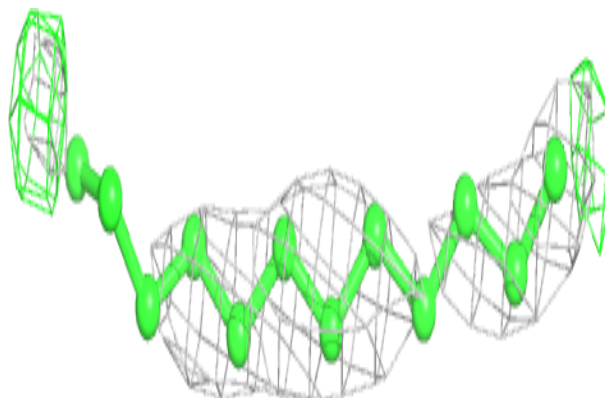


**Electron density around PLC H 401:**

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

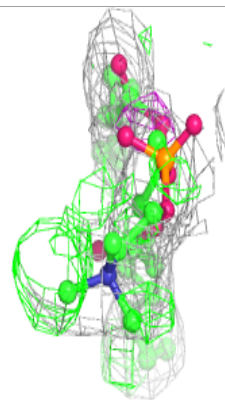
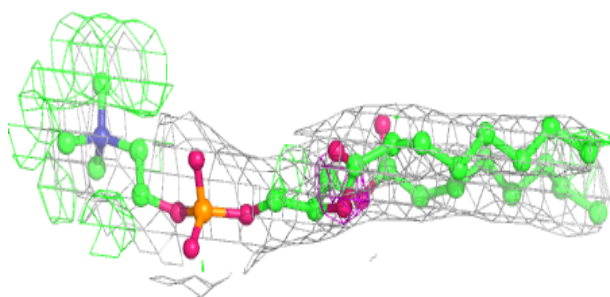
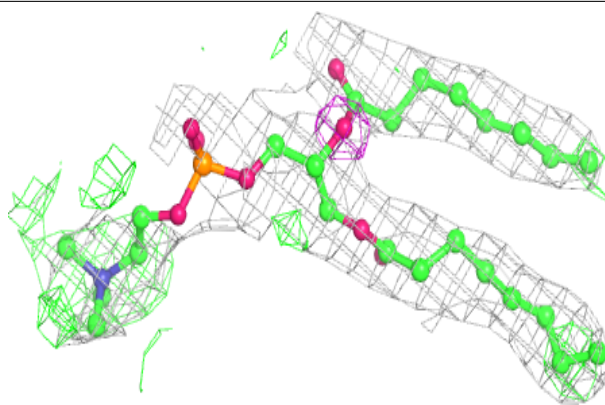
**Electron density around PLC D 403:**

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

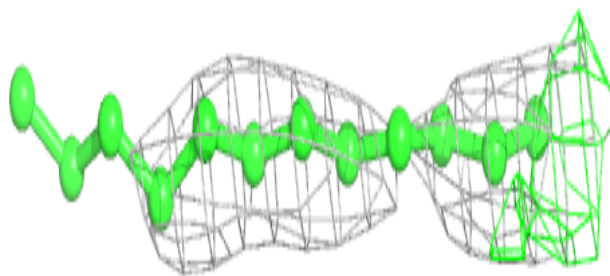
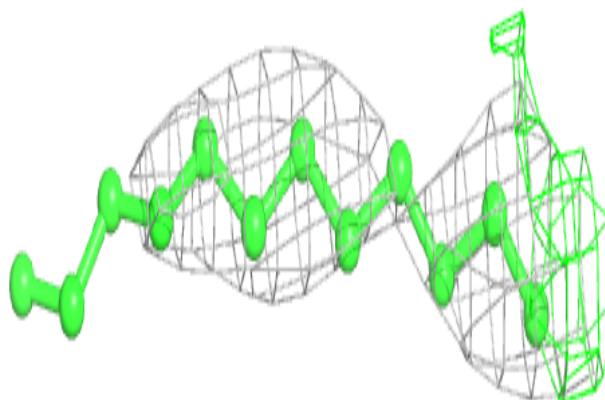


**Electron density around PLC D 401:**

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

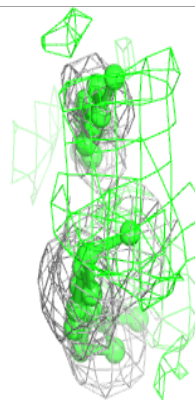
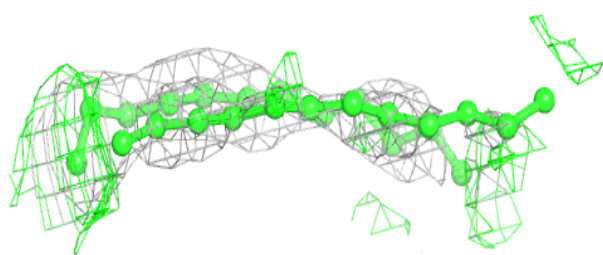
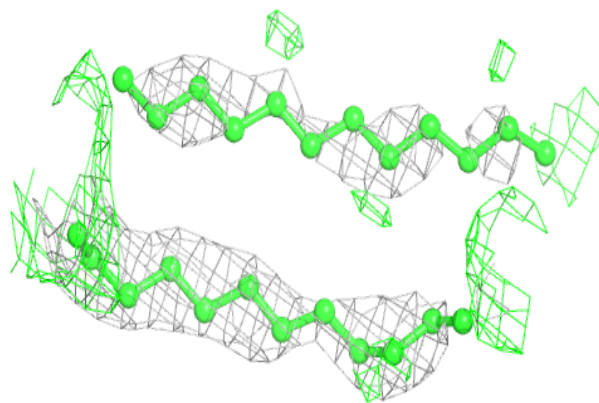
**Electron density around PLC I 403:**

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

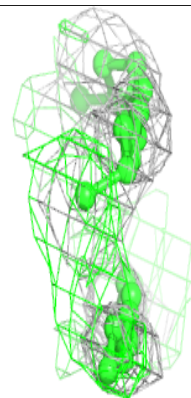
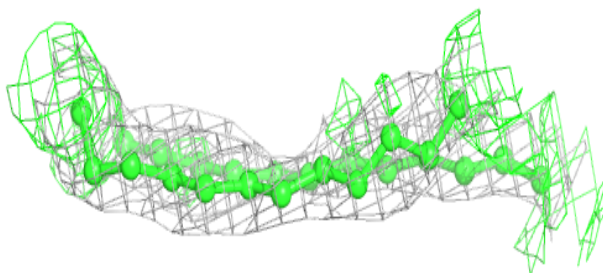
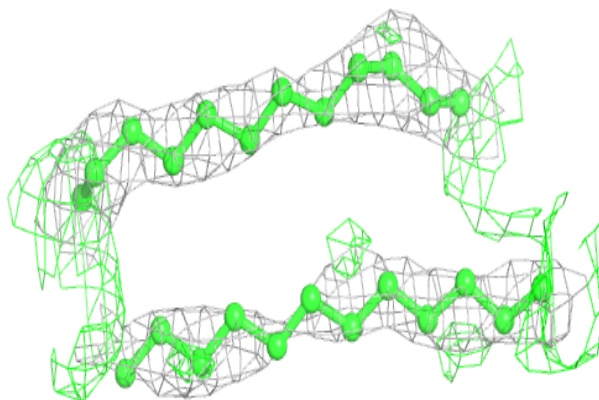


**Electron density around PLC F 402:**

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

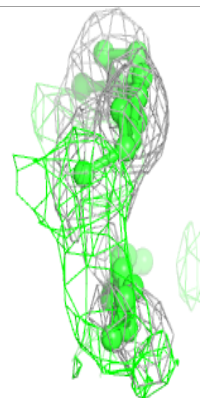
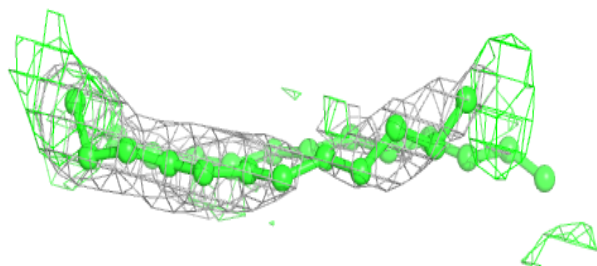
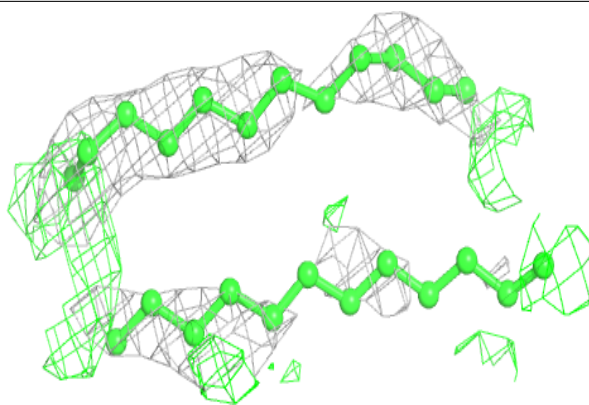
**Electron density around PLC J 402:**

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

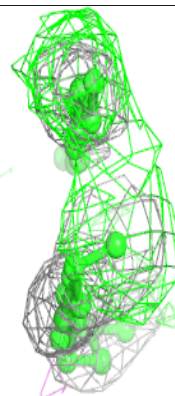
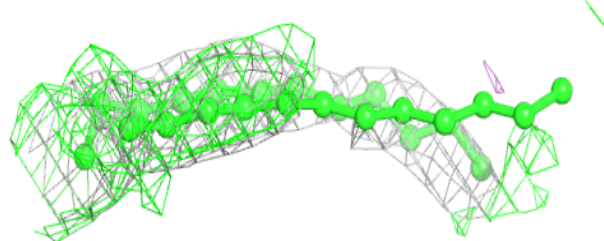
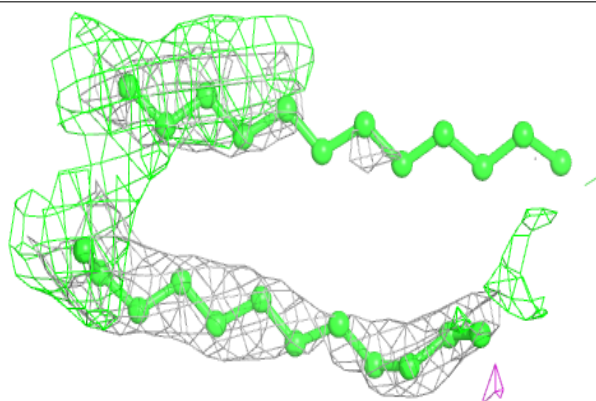


**Electron density around PLC A 402:**

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

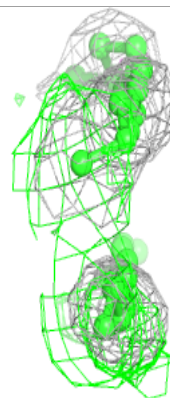
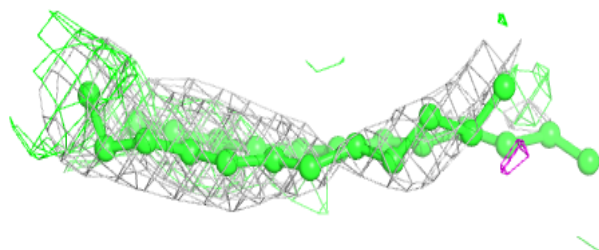
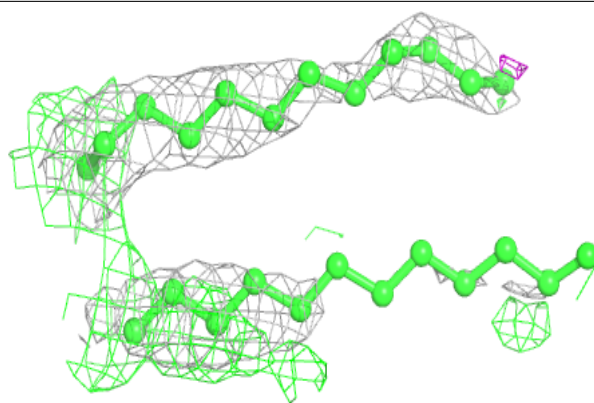
**Electron density around PLC G 403:**

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

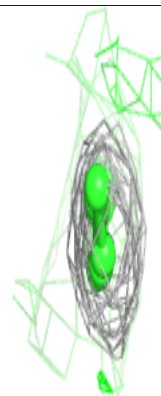
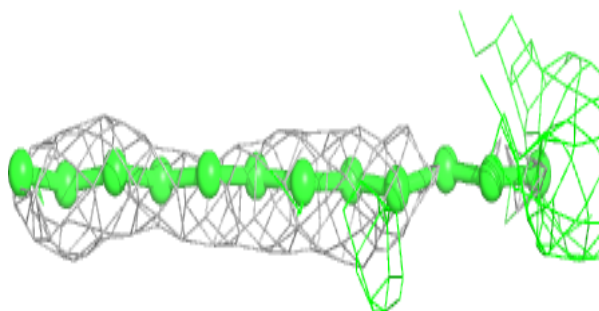
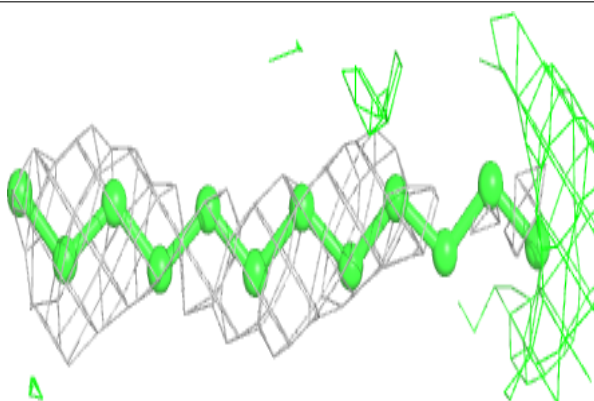


**Electron density around PLC B 403:**

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

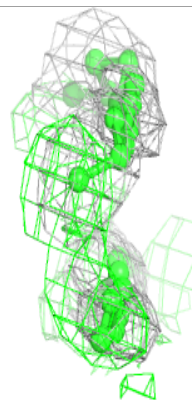
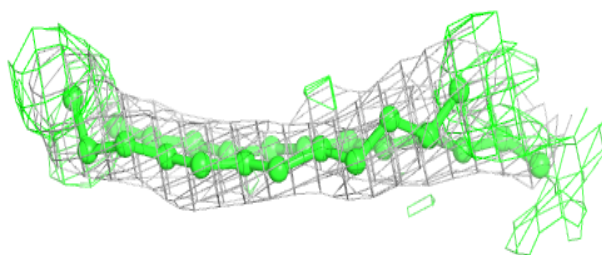
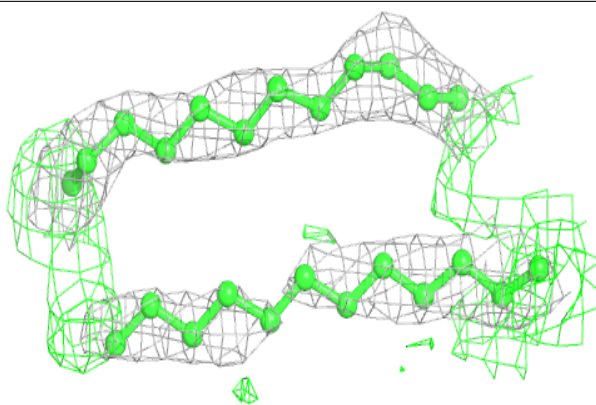
**Electron density around PLC A 403:**

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

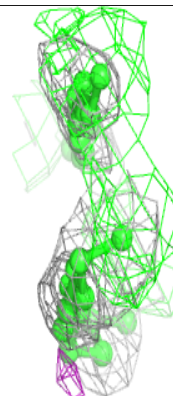
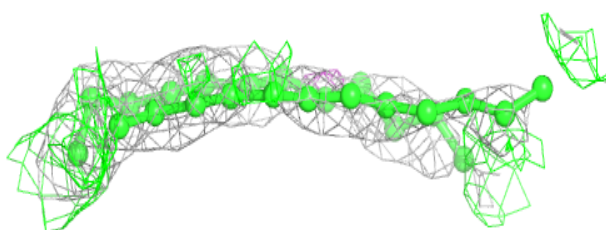
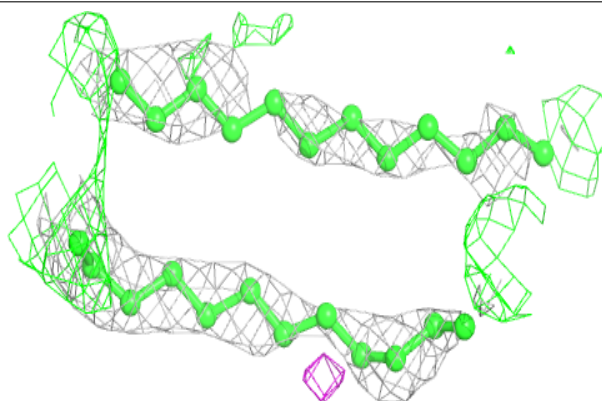


**Electron density around PLC E 402:**

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

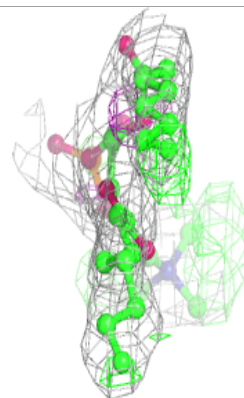
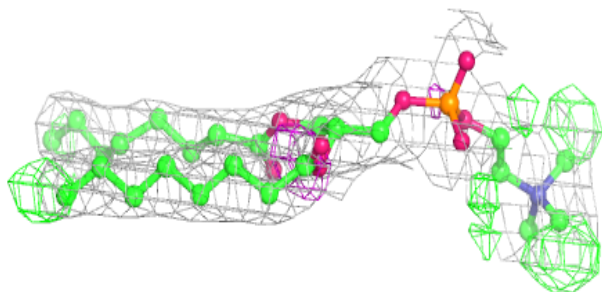
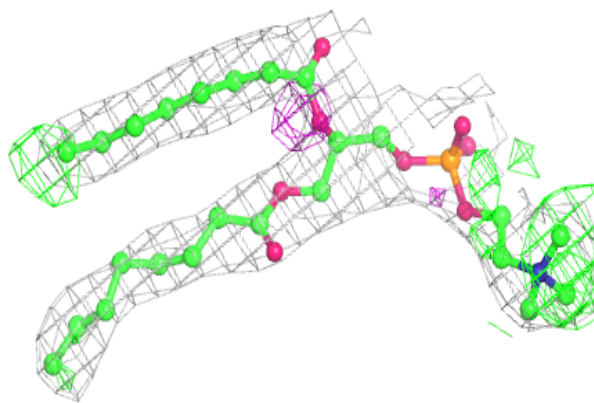
**Electron density around PLC C 403:**

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

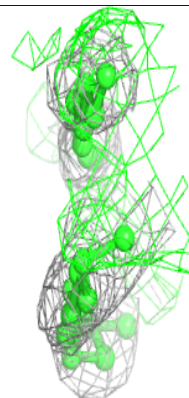
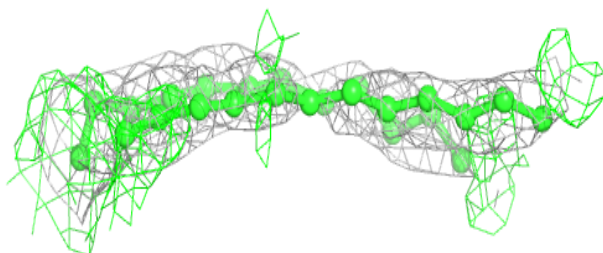
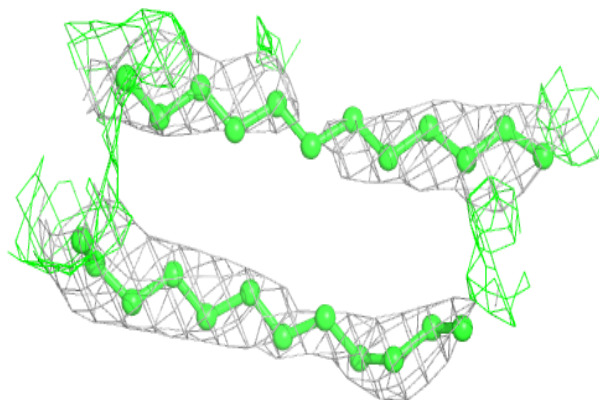


**Electron density around PLC I 401:**

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

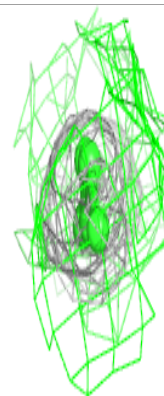
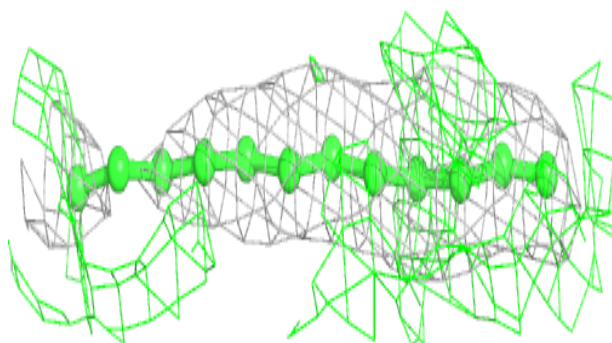
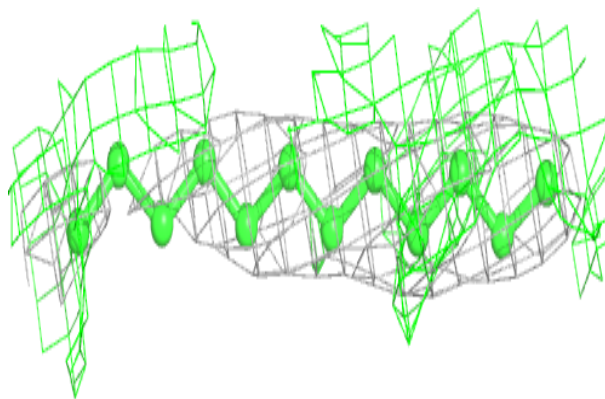
**Electron density around PLC I 402:**

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

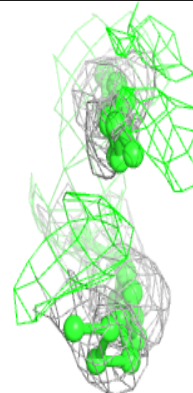
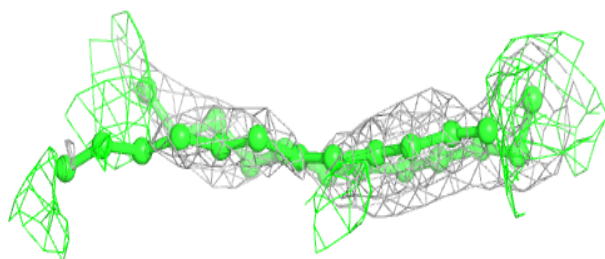
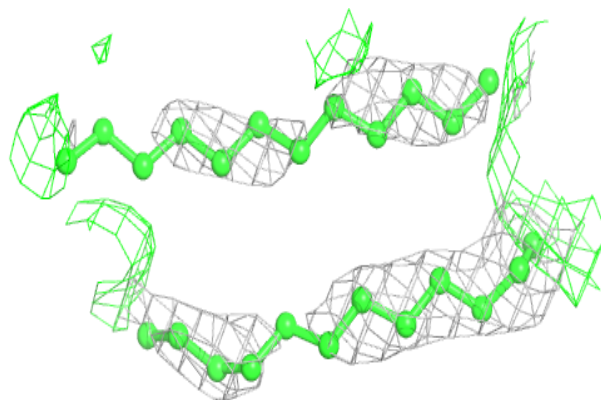


**Electron density around LMT D 406:**

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

**Electron density around PLC D 402:**

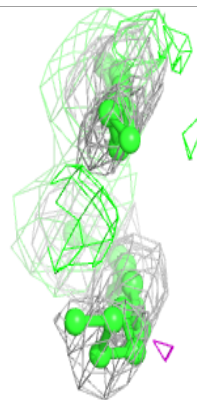
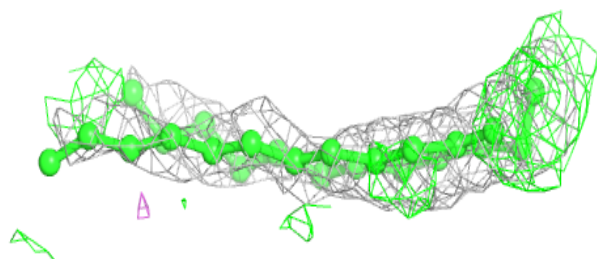
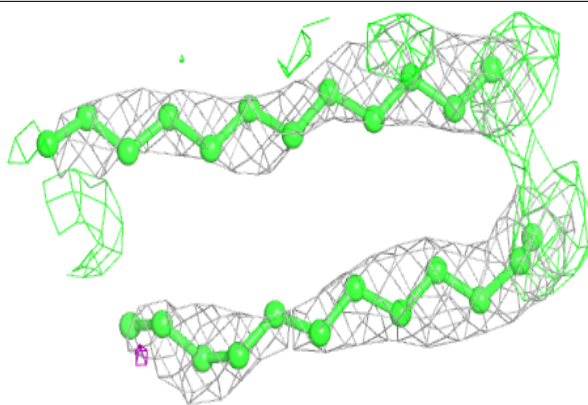
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



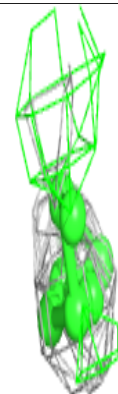
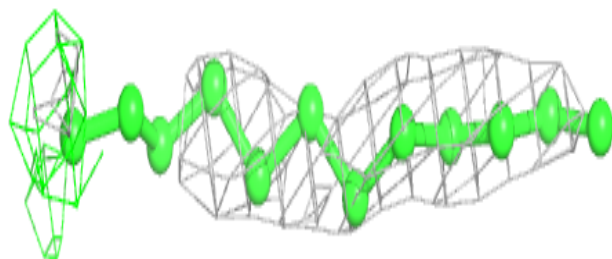
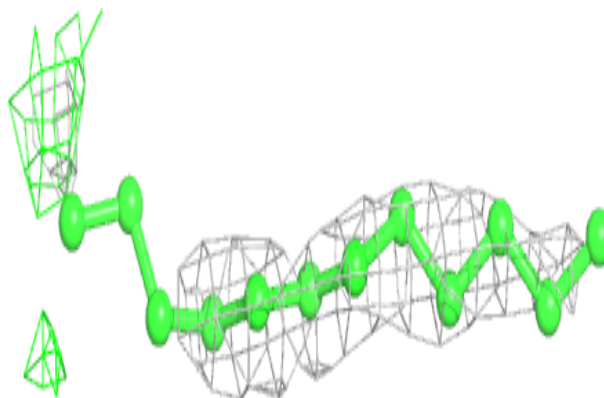


**Electron density around PLC H 402:**

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

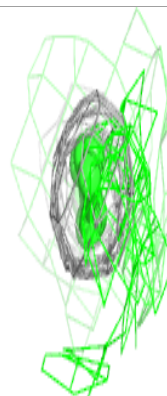
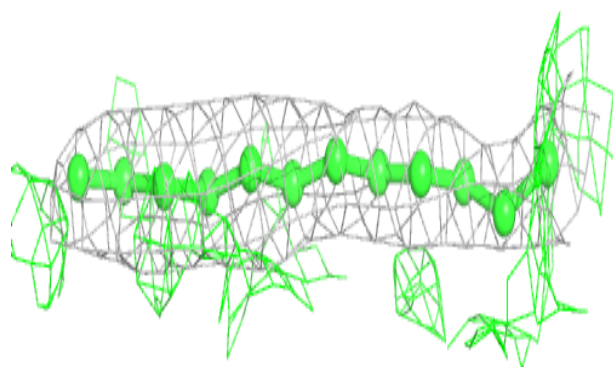
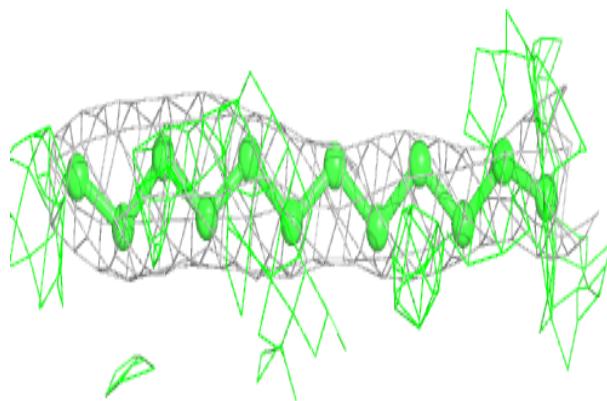
**Electron density around PLC G 404:**

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

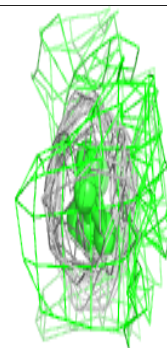
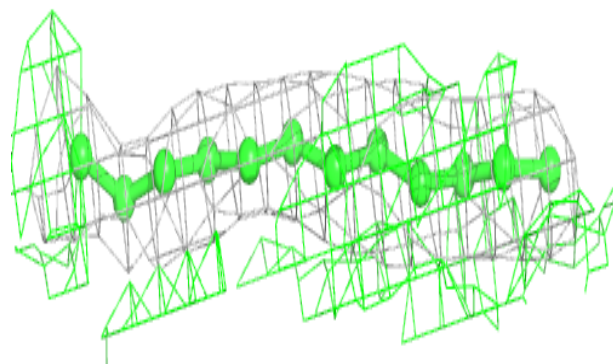
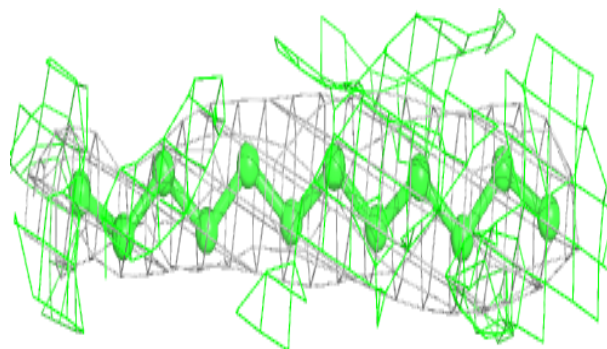


**Electron density around LMT A 409:**

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

**Electron density around LMT H 408:**

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



## 6.5 Other polymers

There are no such residues in this entry.