



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 28, 2025 – 08:47 PM JST

PDB ID : 7W1C / pdb_00007w1c
Title : Crystal structure of Klebsiella pneumoniae K1 capsule-specific polysaccharide lyase in a P1 crystal form
Authors : Tu, I.F.; Huang, K.F.; Wu, S.H.
Deposited on : 2021-11-19
Resolution : 1.48 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

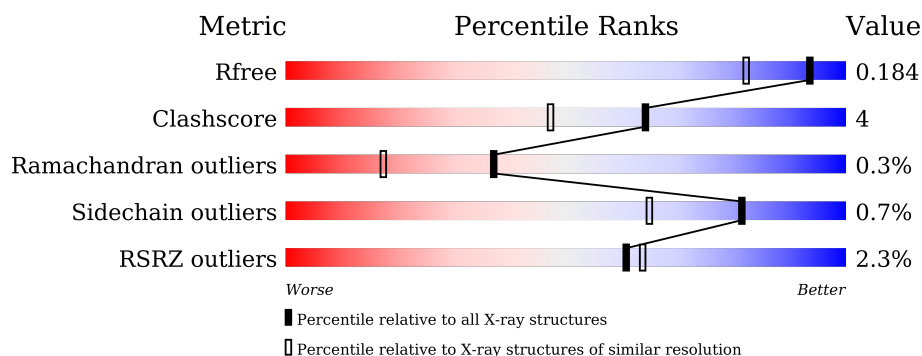
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.48 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}	164625	6131 (1.50-1.46)
Clashscore	180529	6623 (1.50-1.46)
Ramachandran outliers	177936	6521 (1.50-1.46)
Sidechain outliers	177891	6518 (1.50-1.46)
RSRZ outliers	164620	6132 (1.50-1.46)

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	671	
1	B	671	
1	C	671	
1	D	671	
1	E	671	
1	F	671	

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	LMR	A	801	-	X	-	-
2	LMR	B	703	-	X	-	-
2	LMR	E	707	-	X	-	-
2	LMR	F	707	-	-	X	-
2	LMR	F	708	-	-	X	-
3	IMD	E	704	-	-	X	-
3	IMD	F	709	-	-	X	-
4	GOL	A	803	-	X	-	-
4	GOL	B	707	-	-	X	-
4	GOL	D	704	-	X	-	-
4	GOL	F	702	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 33294 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 K1 LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	642	Total	C	N	O	S	0	2	0
			4872	3064	842	947	19			
1	B	634	Total	C	N	O	S	0	0	0
			4793	3014	829	931	19			
1	C	640	Total	C	N	O	S	0	2	0
			4852	3054	837	942	19			
1	D	622	Total	C	N	O	S	0	0	0
			4696	2952	814	912	18			
1	E	644	Total	C	N	O	S	0	1	0
			4876	3066	843	948	19			
1	F	642	Total	C	N	O	S	0	3	0
			4878	3065	844	950	19			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A068Q5Q5
A	-18	GLY	-	expression tag	UNP A0A068Q5Q5
A	-17	SER	-	expression tag	UNP A0A068Q5Q5
A	-16	SER	-	expression tag	UNP A0A068Q5Q5
A	-15	HIS	-	expression tag	UNP A0A068Q5Q5
A	-14	HIS	-	expression tag	UNP A0A068Q5Q5
A	-13	HIS	-	expression tag	UNP A0A068Q5Q5
A	-12	HIS	-	expression tag	UNP A0A068Q5Q5
A	-11	HIS	-	expression tag	UNP A0A068Q5Q5
A	-10	HIS	-	expression tag	UNP A0A068Q5Q5
A	-9	SER	-	expression tag	UNP A0A068Q5Q5
A	-8	SER	-	expression tag	UNP A0A068Q5Q5
A	-7	GLY	-	expression tag	UNP A0A068Q5Q5
A	-6	LEU	-	expression tag	UNP A0A068Q5Q5
A	-5	VAL	-	expression tag	UNP A0A068Q5Q5
A	-4	PRO	-	expression tag	UNP A0A068Q5Q5
A	-3	ARG	-	expression tag	UNP A0A068Q5Q5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A0A068Q5Q5
A	-1	SER	-	expression tag	UNP A0A068Q5Q5
A	0	HIS	-	expression tag	UNP A0A068Q5Q5
A	213	THR	ALA	conflict	UNP A0A068Q5Q5
A	256	ILE	SER	conflict	UNP A0A068Q5Q5
A	391	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
A	392	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
B	-19	MET	-	initiating methionine	UNP A0A068Q5Q5
B	-18	GLY	-	expression tag	UNP A0A068Q5Q5
B	-17	SER	-	expression tag	UNP A0A068Q5Q5
B	-16	SER	-	expression tag	UNP A0A068Q5Q5
B	-15	HIS	-	expression tag	UNP A0A068Q5Q5
B	-14	HIS	-	expression tag	UNP A0A068Q5Q5
B	-13	HIS	-	expression tag	UNP A0A068Q5Q5
B	-12	HIS	-	expression tag	UNP A0A068Q5Q5
B	-11	HIS	-	expression tag	UNP A0A068Q5Q5
B	-10	HIS	-	expression tag	UNP A0A068Q5Q5
B	-9	SER	-	expression tag	UNP A0A068Q5Q5
B	-8	SER	-	expression tag	UNP A0A068Q5Q5
B	-7	GLY	-	expression tag	UNP A0A068Q5Q5
B	-6	LEU	-	expression tag	UNP A0A068Q5Q5
B	-5	VAL	-	expression tag	UNP A0A068Q5Q5
B	-4	PRO	-	expression tag	UNP A0A068Q5Q5
B	-3	ARG	-	expression tag	UNP A0A068Q5Q5
B	-2	GLY	-	expression tag	UNP A0A068Q5Q5
B	-1	SER	-	expression tag	UNP A0A068Q5Q5
B	0	HIS	-	expression tag	UNP A0A068Q5Q5
B	213	THR	ALA	conflict	UNP A0A068Q5Q5
B	256	ILE	SER	conflict	UNP A0A068Q5Q5
B	391	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
B	392	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
C	-19	MET	-	initiating methionine	UNP A0A068Q5Q5
C	-18	GLY	-	expression tag	UNP A0A068Q5Q5
C	-17	SER	-	expression tag	UNP A0A068Q5Q5
C	-16	SER	-	expression tag	UNP A0A068Q5Q5
C	-15	HIS	-	expression tag	UNP A0A068Q5Q5
C	-14	HIS	-	expression tag	UNP A0A068Q5Q5
C	-13	HIS	-	expression tag	UNP A0A068Q5Q5
C	-12	HIS	-	expression tag	UNP A0A068Q5Q5
C	-11	HIS	-	expression tag	UNP A0A068Q5Q5
C	-10	HIS	-	expression tag	UNP A0A068Q5Q5
C	-9	SER	-	expression tag	UNP A0A068Q5Q5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	SER	-	expression tag	UNP A0A068Q5Q5
C	-7	GLY	-	expression tag	UNP A0A068Q5Q5
C	-6	LEU	-	expression tag	UNP A0A068Q5Q5
C	-5	VAL	-	expression tag	UNP A0A068Q5Q5
C	-4	PRO	-	expression tag	UNP A0A068Q5Q5
C	-3	ARG	-	expression tag	UNP A0A068Q5Q5
C	-2	GLY	-	expression tag	UNP A0A068Q5Q5
C	-1	SER	-	expression tag	UNP A0A068Q5Q5
C	0	HIS	-	expression tag	UNP A0A068Q5Q5
C	213	THR	ALA	conflict	UNP A0A068Q5Q5
C	256	ILE	SER	conflict	UNP A0A068Q5Q5
C	391	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
C	392	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
D	-19	MET	-	initiating methionine	UNP A0A068Q5Q5
D	-18	GLY	-	expression tag	UNP A0A068Q5Q5
D	-17	SER	-	expression tag	UNP A0A068Q5Q5
D	-16	SER	-	expression tag	UNP A0A068Q5Q5
D	-15	HIS	-	expression tag	UNP A0A068Q5Q5
D	-14	HIS	-	expression tag	UNP A0A068Q5Q5
D	-13	HIS	-	expression tag	UNP A0A068Q5Q5
D	-12	HIS	-	expression tag	UNP A0A068Q5Q5
D	-11	HIS	-	expression tag	UNP A0A068Q5Q5
D	-10	HIS	-	expression tag	UNP A0A068Q5Q5
D	-9	SER	-	expression tag	UNP A0A068Q5Q5
D	-8	SER	-	expression tag	UNP A0A068Q5Q5
D	-7	GLY	-	expression tag	UNP A0A068Q5Q5
D	-6	LEU	-	expression tag	UNP A0A068Q5Q5
D	-5	VAL	-	expression tag	UNP A0A068Q5Q5
D	-4	PRO	-	expression tag	UNP A0A068Q5Q5
D	-3	ARG	-	expression tag	UNP A0A068Q5Q5
D	-2	GLY	-	expression tag	UNP A0A068Q5Q5
D	-1	SER	-	expression tag	UNP A0A068Q5Q5
D	0	HIS	-	expression tag	UNP A0A068Q5Q5
D	213	THR	ALA	conflict	UNP A0A068Q5Q5
D	256	ILE	SER	conflict	UNP A0A068Q5Q5
D	391	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
D	392	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
E	-19	MET	-	initiating methionine	UNP A0A068Q5Q5
E	-18	GLY	-	expression tag	UNP A0A068Q5Q5
E	-17	SER	-	expression tag	UNP A0A068Q5Q5
E	-16	SER	-	expression tag	UNP A0A068Q5Q5
E	-15	HIS	-	expression tag	UNP A0A068Q5Q5

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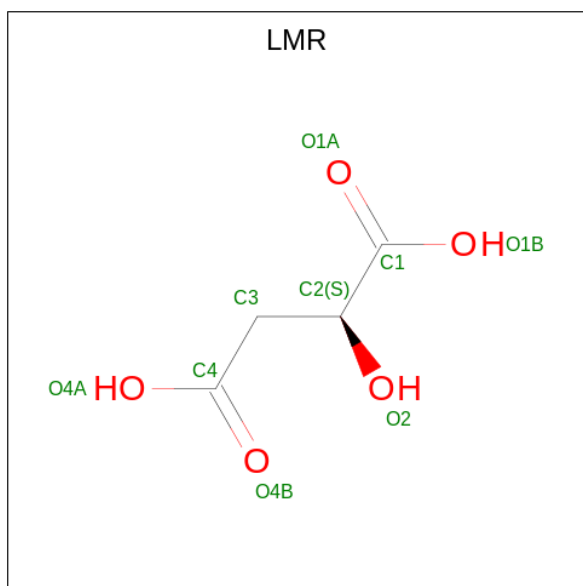
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E	-14	HIS	-	expression tag	UNP A0A068Q5Q5
E	-13	HIS	-	expression tag	UNP A0A068Q5Q5
E	-12	HIS	-	expression tag	UNP A0A068Q5Q5
E	-11	HIS	-	expression tag	UNP A0A068Q5Q5
E	-10	HIS	-	expression tag	UNP A0A068Q5Q5
E	-9	SER	-	expression tag	UNP A0A068Q5Q5
E	-8	SER	-	expression tag	UNP A0A068Q5Q5
E	-7	GLY	-	expression tag	UNP A0A068Q5Q5
E	-6	LEU	-	expression tag	UNP A0A068Q5Q5
E	-5	VAL	-	expression tag	UNP A0A068Q5Q5
E	-4	PRO	-	expression tag	UNP A0A068Q5Q5
E	-3	ARG	-	expression tag	UNP A0A068Q5Q5
E	-2	GLY	-	expression tag	UNP A0A068Q5Q5
E	-1	SER	-	expression tag	UNP A0A068Q5Q5
E	0	HIS	-	expression tag	UNP A0A068Q5Q5
E	213	THR	ALA	conflict	UNP A0A068Q5Q5
E	256	ILE	SER	conflict	UNP A0A068Q5Q5
E	391	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
E	392	ALA	ASP	engineered mutation	UNP A0A068Q5Q5
F	-19	MET	-	initiating methionine	UNP A0A068Q5Q5
F	-18	GLY	-	expression tag	UNP A0A068Q5Q5
F	-17	SER	-	expression tag	UNP A0A068Q5Q5
F	-16	SER	-	expression tag	UNP A0A068Q5Q5
F	-15	HIS	-	expression tag	UNP A0A068Q5Q5
F	-14	HIS	-	expression tag	UNP A0A068Q5Q5
F	-13	HIS	-	expression tag	UNP A0A068Q5Q5
F	-12	HIS	-	expression tag	UNP A0A068Q5Q5
F	-11	HIS	-	expression tag	UNP A0A068Q5Q5
F	-10	HIS	-	expression tag	UNP A0A068Q5Q5
F	-9	SER	-	expression tag	UNP A0A068Q5Q5
F	-8	SER	-	expression tag	UNP A0A068Q5Q5
F	-7	GLY	-	expression tag	UNP A0A068Q5Q5
F	-6	LEU	-	expression tag	UNP A0A068Q5Q5
F	-5	VAL	-	expression tag	UNP A0A068Q5Q5
F	-4	PRO	-	expression tag	UNP A0A068Q5Q5
F	-3	ARG	-	expression tag	UNP A0A068Q5Q5
F	-2	GLY	-	expression tag	UNP A0A068Q5Q5
F	-1	SER	-	expression tag	UNP A0A068Q5Q5
F	0	HIS	-	expression tag	UNP A0A068Q5Q5
F	213	THR	ALA	conflict	UNP A0A068Q5Q5
F	256	ILE	SER	conflict	UNP A0A068Q5Q5
F	391	ALA	ASP	engineered mutation	UNP A0A068Q5Q5

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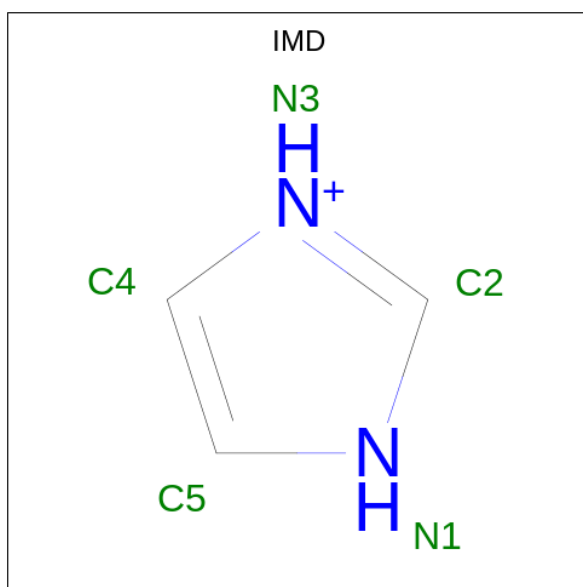
Chain	Residue	Modelled	Actual	Comment	Reference
F	392	ALA	ASP	engineered mutation	UNP A0A068Q5Q5

- Molecule 2 is (2S)-2-hydroxybutanedioic acid (CCD ID: LMR) (formula: $C_4H_6O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 9 4 5	0	0
2	B	1	Total C O 9 4 5	0	0
2	C	1	Total C O 9 4 5	0	0
2	D	1	Total C O 9 4 5	0	0
2	E	1	Total C O 9 4 5	0	0
2	F	1	Total C O 9 4 5	0	0
2	F	1	Total C O 9 4 5	0	0

- Molecule 3 is IMIDAZOLE (CCD ID: IMD) (formula: $C_3H_5N_2$) (labeled as "Ligand of Interest" by depositor).



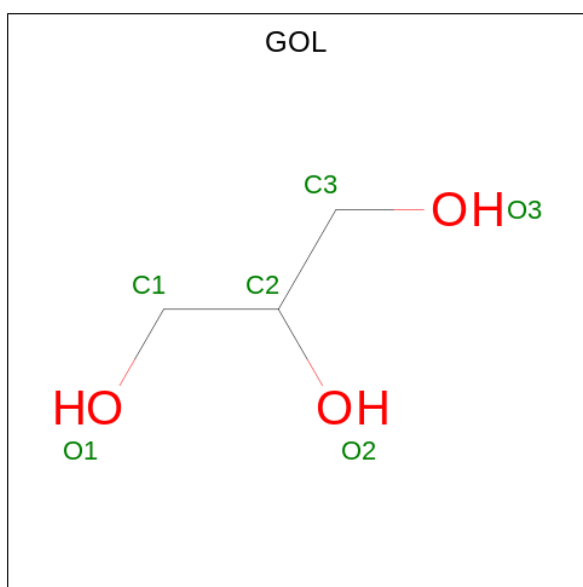
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			5	3	2		
3	A	1	Total	C	N	0	0
			5	3	2		
3	A	1	Total	C	N	0	0
			5	3	2		
3	B	1	Total	C	N	0	0
			5	3	2		
3	B	1	Total	C	N	0	0
			5	3	2		
3	B	1	Total	C	N	0	0
			5	3	2		
3	B	1	Total	C	N	0	0
			5	3	2		
3	C	1	Total	C	N	0	0
			5	3	2		
3	C	1	Total	C	N	0	0
			5	3	2		
3	C	1	Total	C	N	0	0
			5	3	2		
3	C	1	Total	C	N	0	0
			5	3	2		
3	D	1	Total	C	N	0	0
			5	3	2		
3	D	1	Total	C	N	0	0
			5	3	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	N	0	0
			5	3	2		
3	E	1	Total	C	N	0	0
			5	3	2		
3	E	1	Total	C	N	0	0
			5	3	2		
3	E	1	Total	C	N	0	0
			5	3	2		
3	E	1	Total	C	N	0	0
			5	3	2		
3	F	1	Total	C	N	0	0
			5	3	2		
3	F	1	Total	C	N	0	0
			5	3	2		
3	F	1	Total	C	N	0	0
			5	3	2		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	F	1	Total C O 6 3 3	0	0
4	F	1	Total C O 6 3 3	0	0
4	F	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	663	Total O 663 663	0	0
5	B	629	Total O 629 629	0	0
5	C	586	Total O 586 586	0	0

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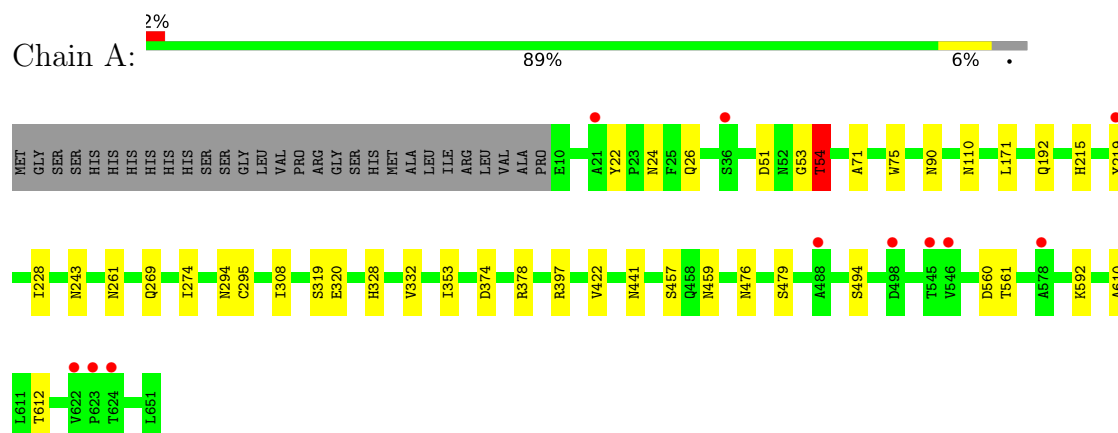
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	722	Total 722	O 722	0	0
5	E	728	Total 728	O 728	0	0
5	F	713	Total 713	O 713	0	0

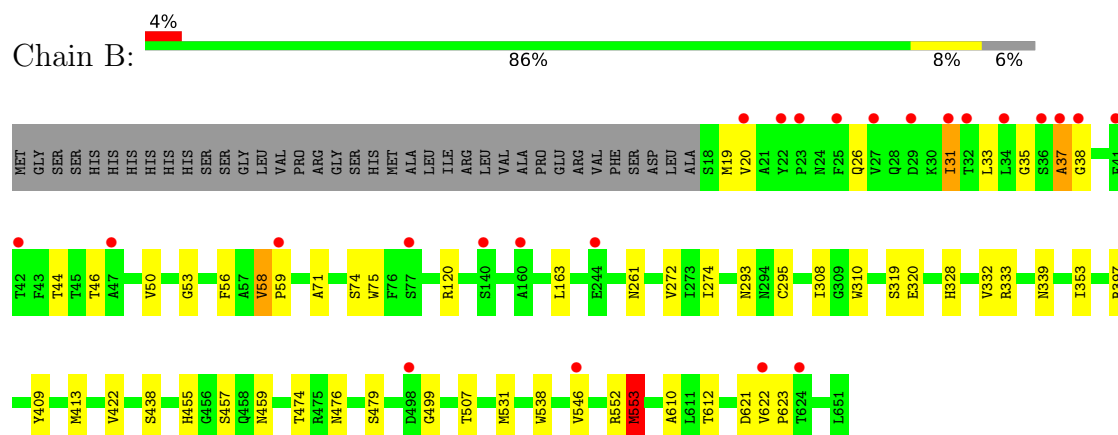
3 Residue-property plots [i](#)

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.

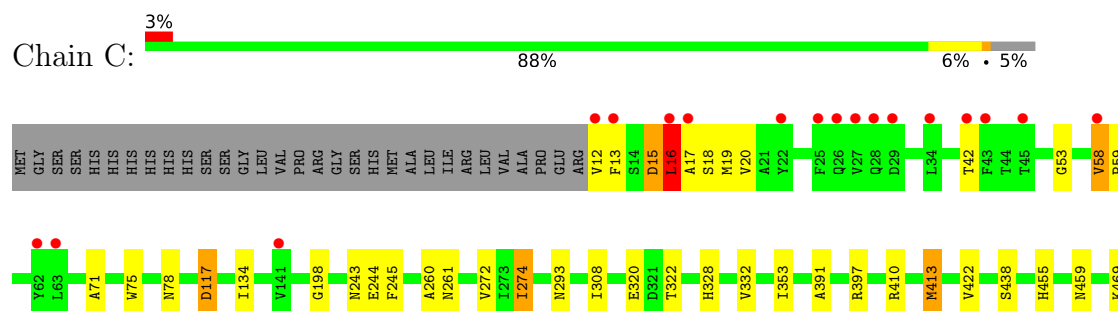
• Molecule 1: K1 LYASE

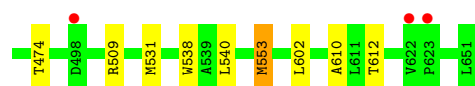


• Molecule 1: K1 LYASE

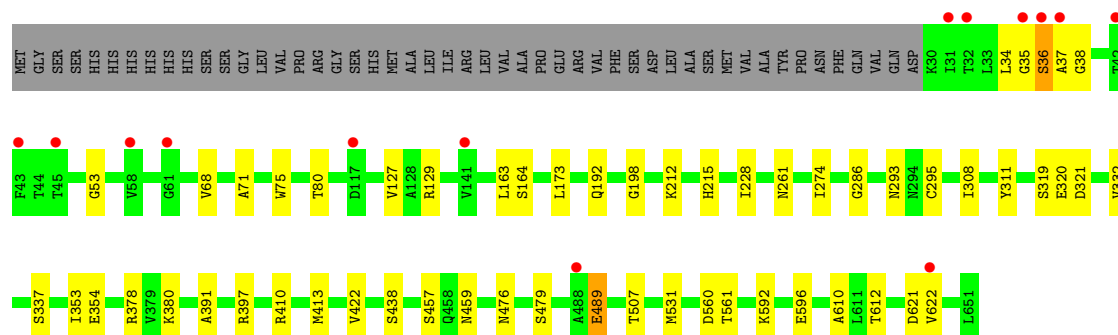
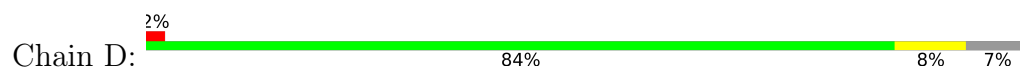


• Molecule 1: K1 LYASE

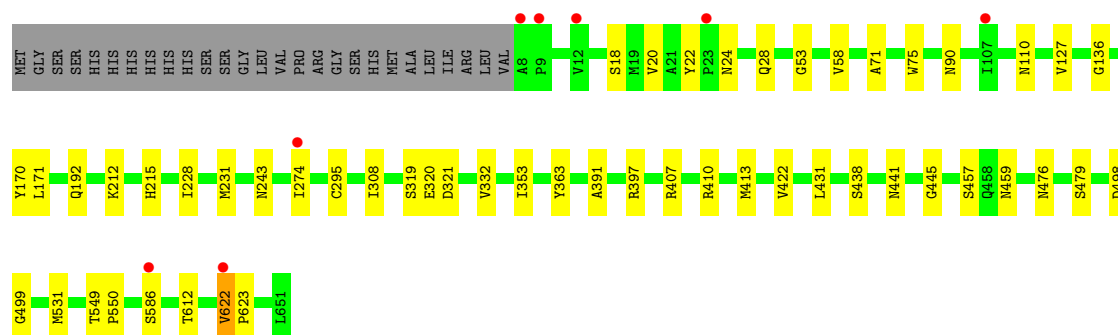
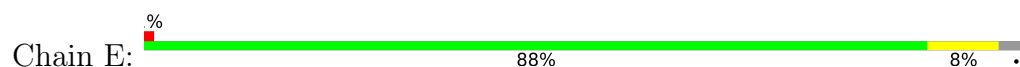




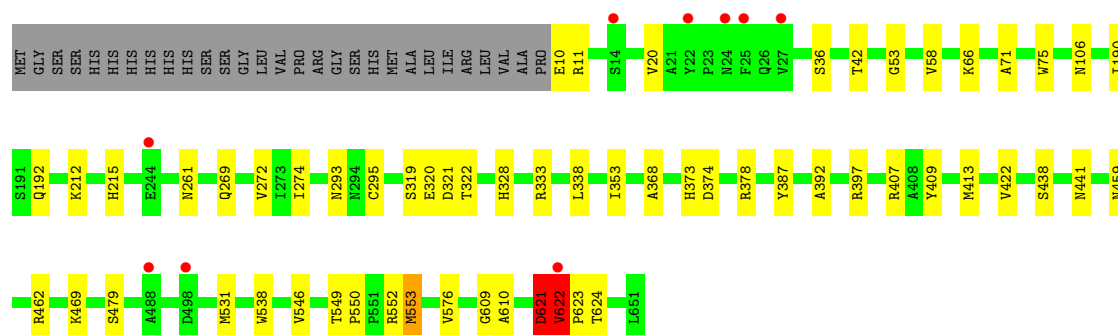
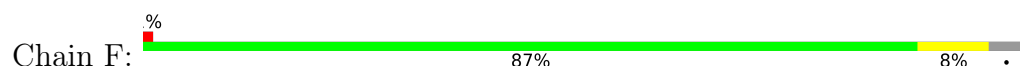
● Molecule 1: K1 LYASE



● Molecule 1: K1 LYASE



● Molecule 1: K1 LYASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	90.28Å 100.57Å 125.03Å 80.50° 70.32° 83.43°	Depositor
Resolution (Å)	30.00 – 1.48 30.00 – 1.48	Depositor EDS
% Data completeness (in resolution range)	96.8 (30.00-1.48) 96.8 (30.00-1.48)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 1.48Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.137 , 0.184 0.137 , 0.184	Depositor DCC
R_{free} test set	34007 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	15.8	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33294	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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: GOL, LMR, IMD

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	1.10	2/4976 (0.0%)	0.94	2/6774 (0.0%)
1	B	1.12	5/4896 (0.1%)	1.00	6/6666 (0.1%)
1	C	1.11	6/4959 (0.1%)	0.99	7/6752 (0.1%)
1	D	1.12	5/4796 (0.1%)	0.95	3/6529 (0.0%)
1	E	1.12	2/4981 (0.0%)	0.94	1/6782 (0.0%)
1	F	1.17	8/4982 (0.2%)	0.99	8/6782 (0.1%)
All	All	1.12	28/29590 (0.1%)	0.97	27/40285 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
1	F	0	1
All	All	0	3

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	413	MET	CA-C	6.82	1.55	1.52
1	B	38	GLY	CA-C	6.81	1.61	1.51
1	B	56	PHE	CA-C	6.32	1.60	1.52
1	C	42	THR	N-CA	6.29	1.53	1.45
1	F	609	GLY	C-O	-6.14	1.16	1.23

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	17	ALA	N-CA-C	-14.35	91.37	112.04
1	F	553	MET	CG-SD-CE	-10.83	77.08	100.90
1	E	531	MET	CG-SD-CE	-10.21	78.44	100.90
1	C	553	MET	CG-SD-CE	-9.46	80.09	100.90
1	B	553	MET	CG-SD-CE	-7.81	83.72	100.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	621	ASP	Peptide
1	D	274	ILE	Peptide
1	F	621	ASP	Peptide

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	4872	0	4726	30	0
1	B	4793	0	4650	38	0
1	C	4852	0	4711	33	0
1	D	4696	0	4562	37	0
1	E	4876	0	4728	37	0
1	F	4878	0	4725	48	0
2	A	9	0	4	0	0
2	B	9	0	4	1	0
2	C	9	0	4	0	0
2	D	9	0	4	0	0
2	E	9	0	4	0	0
2	F	18	0	8	8	0
3	A	15	0	15	0	0
3	B	20	0	20	5	0
3	C	25	0	25	2	0
3	D	15	0	15	0	0
3	E	20	0	20	10	0
3	F	20	0	20	7	0
4	A	12	0	16	0	0
4	B	18	0	23	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	24	0	32	1	0
4	D	18	0	24	2	0
4	E	18	0	24	0	0
4	F	18	0	24	0	0
5	A	663	0	0	6	0
5	B	629	0	0	5	1
5	C	586	0	0	5	0
5	D	722	0	0	4	0
5	E	728	0	0	6	0
5	F	713	0	0	6	1
All	All	33294	0	28388	218	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 4.

The worst 5 of 218 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)
2:F:707:LMR:C2	2:F:708:LMR:O2	1.69	1.40
2:F:707:LMR:H2	2:F:708:LMR:O2	1.21	1.34
2:F:707:LMR:C2	2:F:708:LMR:HO2	1.66	0.83
1:C:16:LEU:O	1:C:20:VAL:HG22	1.82	0.80
2:F:707:LMR:O2	2:F:708:LMR:O2	1.85	0.79

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)
5:B:900:HOH:O	5:F:1443:HOH:O[1_664]	1.93	0.27

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	642/671 (96%)	618 (96%)	23 (4%)	1 (0%)	44	22
1	B	632/671 (94%)	605 (96%)	25 (4%)	2 (0%)	37	17
1	C	640/671 (95%)	612 (96%)	26 (4%)	2 (0%)	37	17
1	D	620/671 (92%)	594 (96%)	23 (4%)	3 (0%)	25	8
1	E	643/671 (96%)	617 (96%)	24 (4%)	2 (0%)	37	17
1	F	643/671 (96%)	619 (96%)	22 (3%)	2 (0%)	37	17
All	All	3820/4026 (95%)	3665 (96%)	143 (4%)	12 (0%)	37	17

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	622	VAL
1	D	36	SER
1	B	623	PRO
1	D	37	ALA
1	E	53	GLY

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	522/544 (96%)	520 (100%)	2 (0%)	89	79
1	B	513/544 (94%)	507 (99%)	6 (1%)	67	42
1	C	520/544 (96%)	516 (99%)	4 (1%)	79	61
1	D	502/544 (92%)	497 (99%)	5 (1%)	73	50
1	E	522/544 (96%)	518 (99%)	4 (1%)	79	61
1	F	523/544 (96%)	520 (99%)	3 (1%)	84	69
All	All	3102/3264 (95%)	3078 (99%)	24 (1%)	81	61

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	164	SER

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Mol	Chain	Res	Type
1	E	18	SER
1	D	592	LYS
1	E	28	GLN
1	B	553	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	293	ASN
1	F	133	ASN
1	E	307	ASN
1	E	476	ASN
1	F	215	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

48 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	IMD	D	706	-	3,5,5	0.61	0	4,5,5	0.72	0
4	GOL	C	801	-	5,5,5	0.99	0	5,5,5	0.72	0
3	IMD	C	805	-	3,5,5	0.73	0	4,5,5	0.52	0
3	IMD	C	804	-	3,5,5	0.65	0	4,5,5	0.77	0
3	IMD	C	810	-	3,5,5	0.57	0	4,5,5	0.22	0
3	IMD	B	706	-	3,5,5	1.00	0	4,5,5	0.52	0
2	LMR	F	708	-	8,8,8	1.31	0	10,10,10	1.74	4 (40%)
4	GOL	D	705	-	5,5,5	2.80	4 (80%)	5,5,5	1.32	1 (20%)
2	LMR	F	707	-	8,8,8	1.20	0	10,10,10	2.36	5 (50%)
4	GOL	C	802	-	5,5,5	2.08	1 (20%)	5,5,5	1.35	1 (20%)
4	GOL	E	703	-	5,5,5	2.08	2 (40%)	5,5,5	1.77	1 (20%)
4	GOL	D	707	-	5,5,5	0.40	0	5,5,5	0.44	0
2	LMR	A	801	-	8,8,8	1.65	1 (12%)	10,10,10	2.67	3 (30%)
3	IMD	B	704	-	3,5,5	0.70	0	4,5,5	0.46	0
4	GOL	A	806	-	5,5,5	0.22	0	5,5,5	0.78	0
3	IMD	E	708	-	3,5,5	0.77	0	4,5,5	0.83	0
3	IMD	F	703	-	3,5,5	0.42	0	4,5,5	0.45	0
3	IMD	C	806	-	3,5,5	0.51	0	4,5,5	0.93	0
4	GOL	D	704	-	5,5,5	0.67	0	5,5,5	1.70	2 (40%)
2	LMR	B	703	-	8,8,8	2.32	5 (62%)	10,10,10	1.93	4 (40%)
3	IMD	B	708	-	3,5,5	0.53	0	4,5,5	0.63	0
3	IMD	E	705	-	3,5,5	0.57	0	4,5,5	0.72	0
4	GOL	F	706	-	5,5,5	1.75	1 (20%)	5,5,5	1.20	0
4	GOL	B	701	-	5,5,5	0.24	0	5,5,5	0.63	0
3	IMD	A	805	-	3,5,5	0.61	0	4,5,5	0.70	0
4	GOL	B	702	-	5,5,5	1.17	0	5,5,5	1.00	0
4	GOL	C	807	-	5,5,5	0.40	0	5,5,5	1.06	0
3	IMD	A	804	-	3,5,5	0.56	0	4,5,5	0.32	0
3	IMD	B	705	-	3,5,5	0.56	0	4,5,5	0.85	0
3	IMD	A	802	-	3,5,5	0.53	0	4,5,5	0.48	0
3	IMD	E	704	-	3,5,5	0.91	0	4,5,5	0.97	0
3	IMD	F	709	-	3,5,5	0.66	0	4,5,5	0.45	0
4	GOL	A	803	-	5,5,5	1.08	0	5,5,5	1.80	2 (40%)
2	LMR	D	702	-	8,8,8	2.13	3 (37%)	10,10,10	1.06	0
3	IMD	C	808	-	3,5,5	0.72	0	4,5,5	0.35	0
3	IMD	F	705	-	3,5,5	0.90	0	4,5,5	0.65	0
4	GOL	C	803	-	5,5,5	0.53	0	5,5,5	0.87	0
4	GOL	E	706	-	5,5,5	0.93	0	5,5,5	0.72	0
3	IMD	D	701	-	3,5,5	0.55	0	4,5,5	0.26	0
4	GOL	F	701	-	5,5,5	0.75	0	5,5,5	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	IMD	E	702	-	3,5,5	0.59	0	4,5,5	0.54	0
4	GOL	B	707	-	5,5,5	1.28	0	5,5,5	1.42	1 (20%)
2	LMR	E	707	-	8,8,8	2.02	3 (37%)	10,10,10	1.44	1 (10%)
3	IMD	D	703	-	3,5,5	0.80	0	4,5,5	0.47	0
4	GOL	E	701	-	5,5,5	0.54	0	5,5,5	0.20	0
4	GOL	F	702	-	5,5,5	1.41	1 (20%)	5,5,5	1.71	2 (40%)
2	LMR	C	809	-	8,8,8	2.35	1 (12%)	10,10,10	2.52	4 (40%)
3	IMD	F	704	-	3,5,5	0.74	0	4,5,5	0.68	0

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	IMD	D	706	-	-	-	0/1/1/1
4	GOL	C	801	-	-	2/4/4/4	-
3	IMD	C	805	-	-	-	0/1/1/1
3	IMD	C	804	-	-	-	0/1/1/1
3	IMD	C	810	-	-	-	0/1/1/1
3	IMD	B	706	-	-	-	0/1/1/1
2	LMR	F	708	-	-	1/8/8/8	-
4	GOL	D	705	-	-	0/4/4/4	-
2	LMR	F	707	-	-	4/8/8/8	-
4	GOL	C	802	-	-	2/4/4/4	-
4	GOL	E	703	-	-	2/4/4/4	-
4	GOL	D	707	-	-	0/4/4/4	-
2	LMR	A	801	-	-	7/8/8/8	-
3	IMD	B	704	-	-	-	0/1/1/1
4	GOL	A	806	-	-	2/4/4/4	-
3	IMD	E	708	-	-	-	0/1/1/1
3	IMD	F	703	-	-	-	0/1/1/1
3	IMD	C	806	-	-	-	0/1/1/1
4	GOL	D	704	-	-	4/4/4/4	-
2	LMR	B	703	-	-	4/8/8/8	-
3	IMD	B	708	-	-	-	0/1/1/1
3	IMD	E	705	-	-	-	0/1/1/1
4	GOL	F	706	-	-	2/4/4/4	-
4	GOL	B	701	-	-	0/4/4/4	-
3	IMD	A	805	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	702	-	-	2/4/4/4	-
4	GOL	C	807	-	-	0/4/4/4	-
3	IMD	A	804	-	-	-	0/1/1/1
3	IMD	A	802	-	-	-	0/1/1/1
3	IMD	B	705	-	-	-	0/1/1/1
3	IMD	E	704	-	-	-	0/1/1/1
3	IMD	F	709	-	-	-	0/1/1/1
4	GOL	A	803	-	-	4/4/4/4	-
2	LMR	D	702	-	-	6/8/8/8	-
4	GOL	F	701	-	-	2/4/4/4	-
3	IMD	C	808	-	-	-	0/1/1/1
4	GOL	E	706	-	-	0/4/4/4	-
3	IMD	F	705	-	-	-	0/1/1/1
3	IMD	D	701	-	-	-	0/1/1/1
2	LMR	C	809	-	-	5/8/8/8	-
3	IMD	E	702	-	-	-	0/1/1/1
4	GOL	B	707	-	-	2/4/4/4	-
2	LMR	E	707	-	-	7/8/8/8	-
4	GOL	E	701	-	-	2/4/4/4	-
3	IMD	D	703	-	-	-	0/1/1/1
4	GOL	F	702	-	-	4/4/4/4	-
4	GOL	C	803	-	-	0/4/4/4	-
3	IMD	F	704	-	-	-	0/1/1/1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	809	LMR	C2-C1	5.67	1.60	1.52
2	D	702	LMR	C2-C1	4.39	1.58	1.52
2	E	707	LMR	C2-C1	4.10	1.58	1.52
2	A	801	LMR	C2-C1	4.04	1.58	1.52
4	C	802	GOL	O2-C2	3.76	1.54	1.43

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	LMR	O1A-C1-C2	-5.57	111.65	122.54
2	C	809	LMR	O1B-C1-C2	5.19	124.12	112.72
2	A	801	LMR	O1B-C1-C2	4.90	123.47	112.72
2	C	809	LMR	O1A-C1-C2	-4.53	113.69	122.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	707	LMR	C3-C2-C1	4.00	119.79	110.33

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	LMR	O1A-C1-C2-O2
2	A	801	LMR	O1A-C1-C2-C3
2	A	801	LMR	O1B-C1-C2-O2
2	A	801	LMR	O1B-C1-C2-C3
2	B	703	LMR	O1A-C1-C2-O2

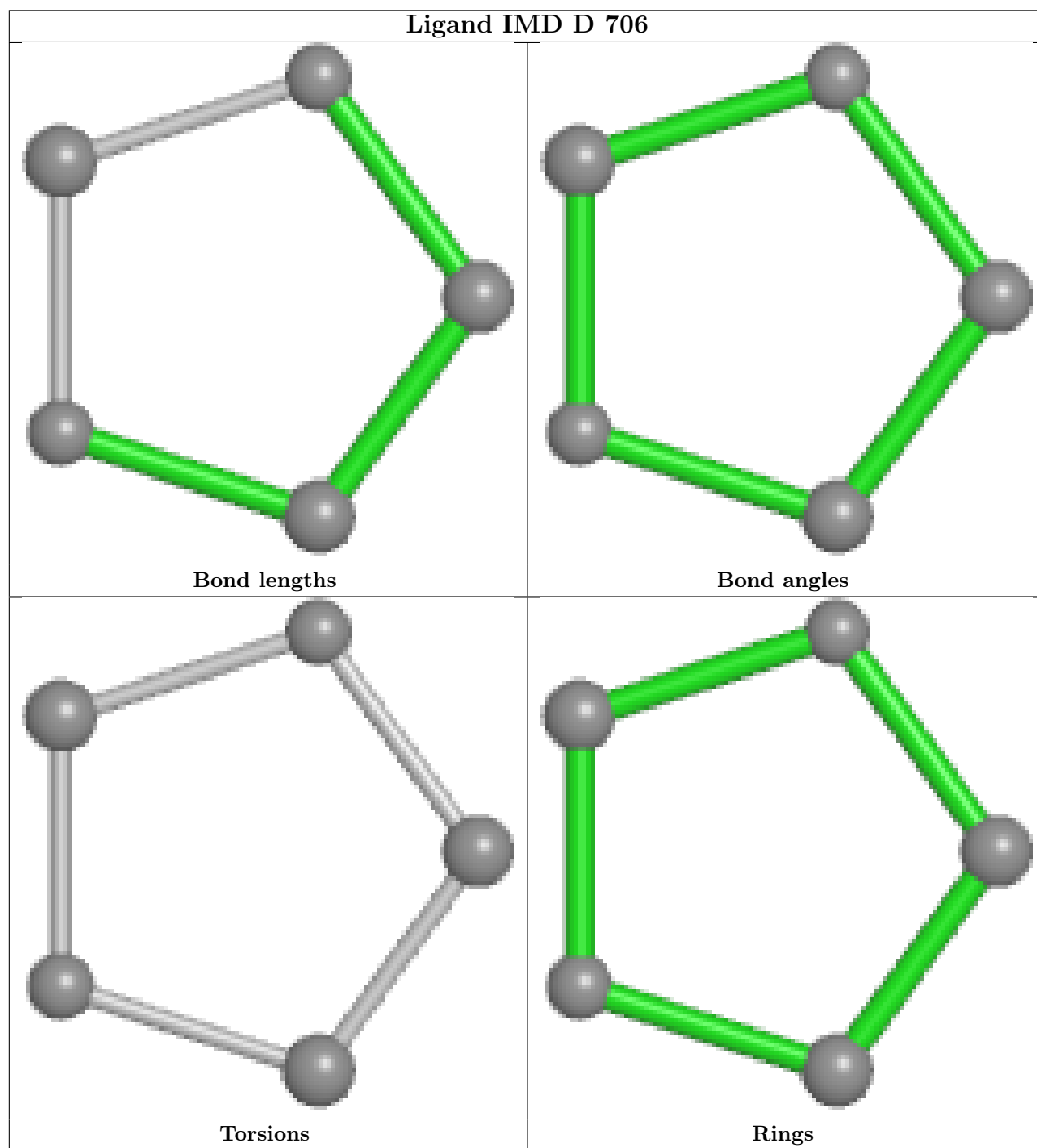
There are no ring outliers.

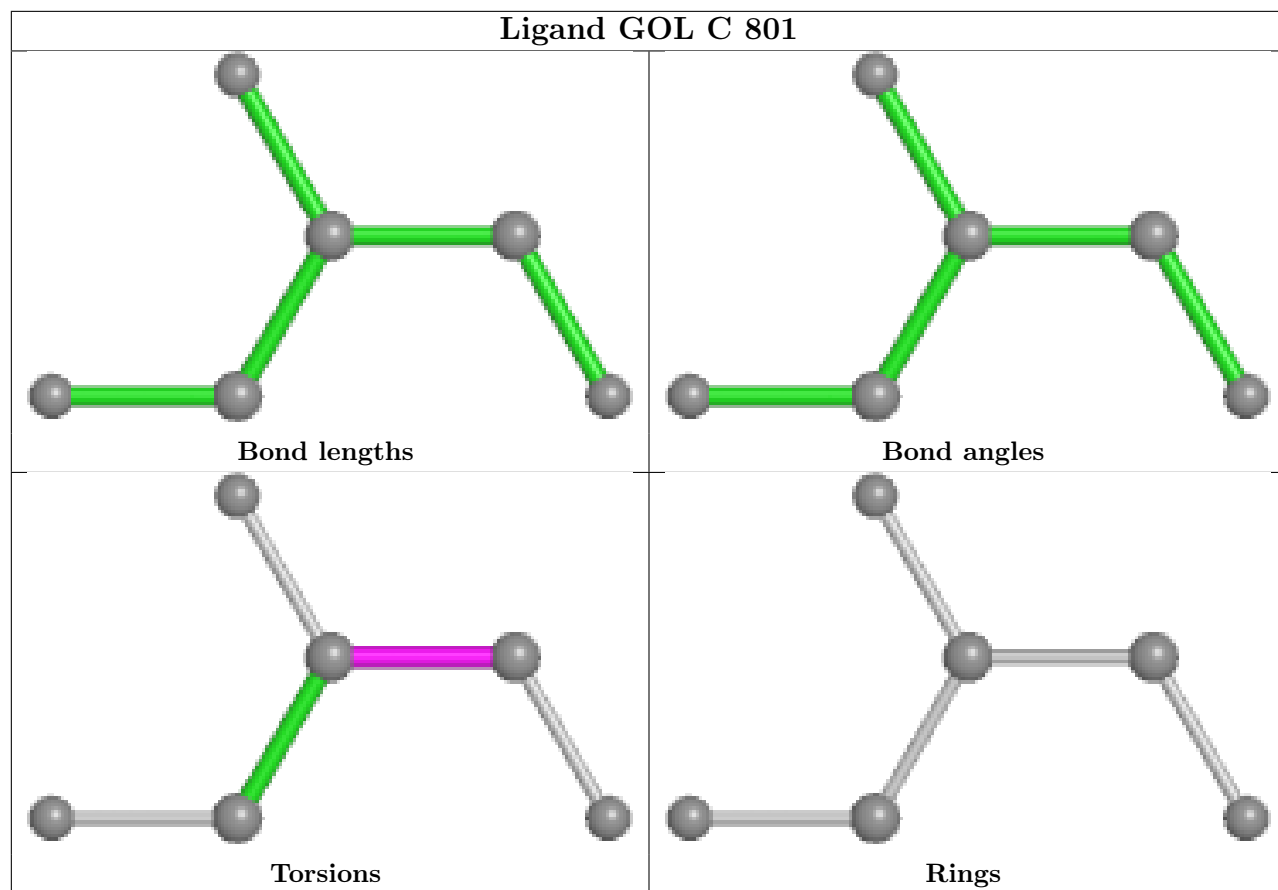
15 monomers are involved in 41 short contacts:

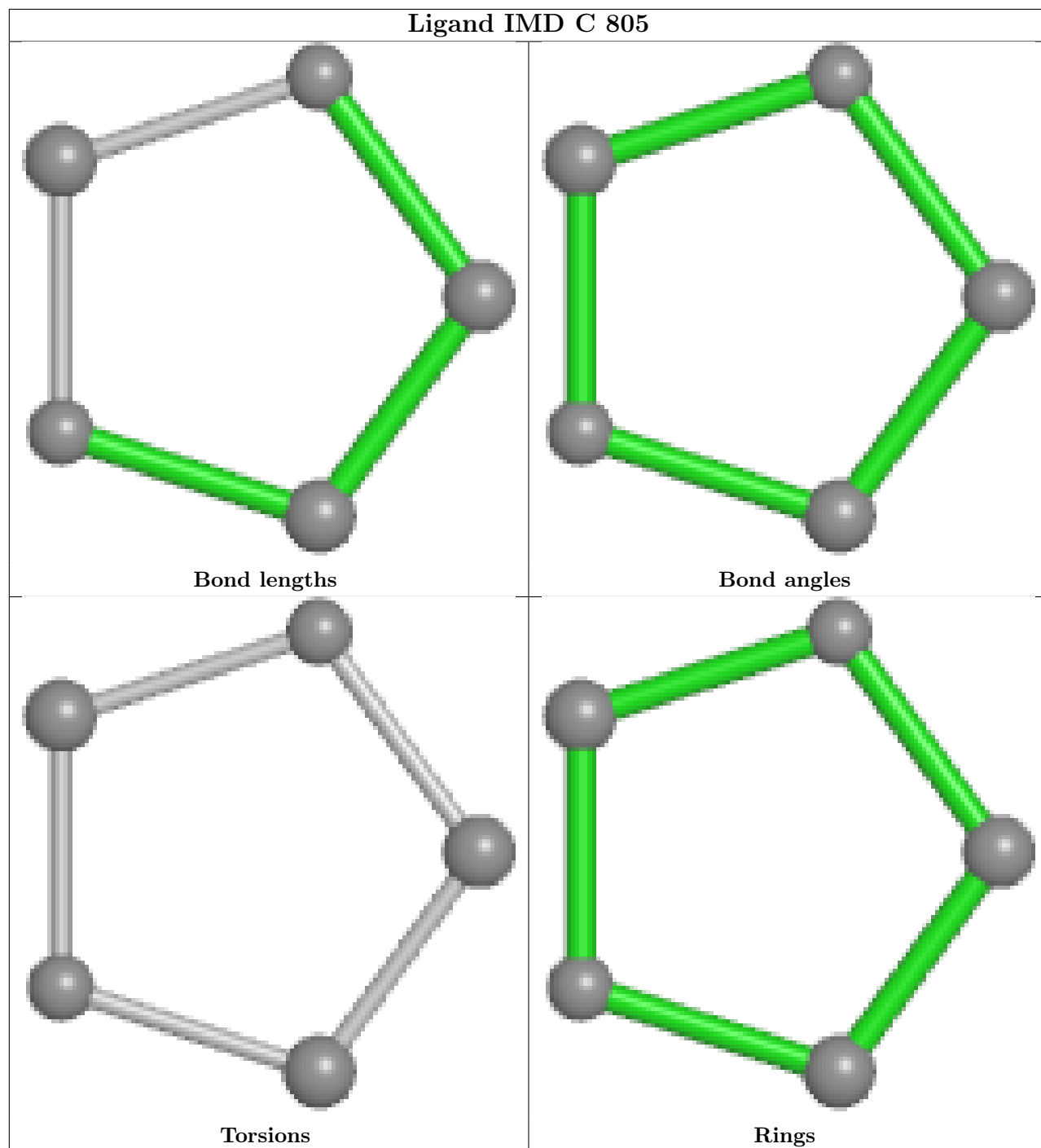
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	805	IMD	1	0
3	C	804	IMD	1	0
3	B	706	IMD	1	0
2	F	708	LMR	7	0
4	D	705	GOL	2	0
2	F	707	LMR	7	0
4	C	802	GOL	1	0
3	B	704	IMD	1	0
3	F	703	IMD	1	0
2	B	703	LMR	1	0
3	B	708	IMD	3	0
3	E	704	IMD	10	0
3	F	709	IMD	5	0
3	F	705	IMD	1	0
4	B	707	GOL	5	0

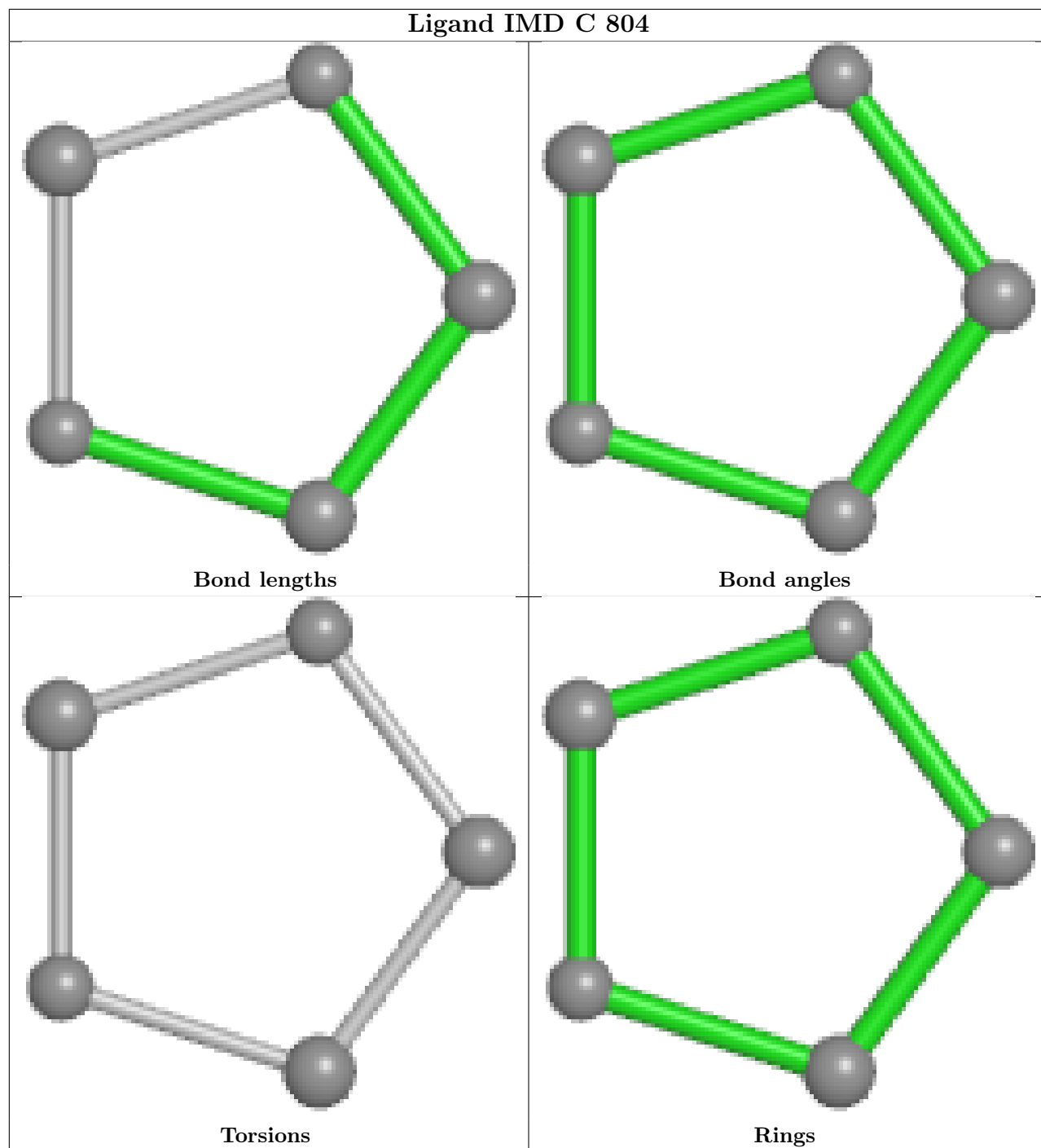
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

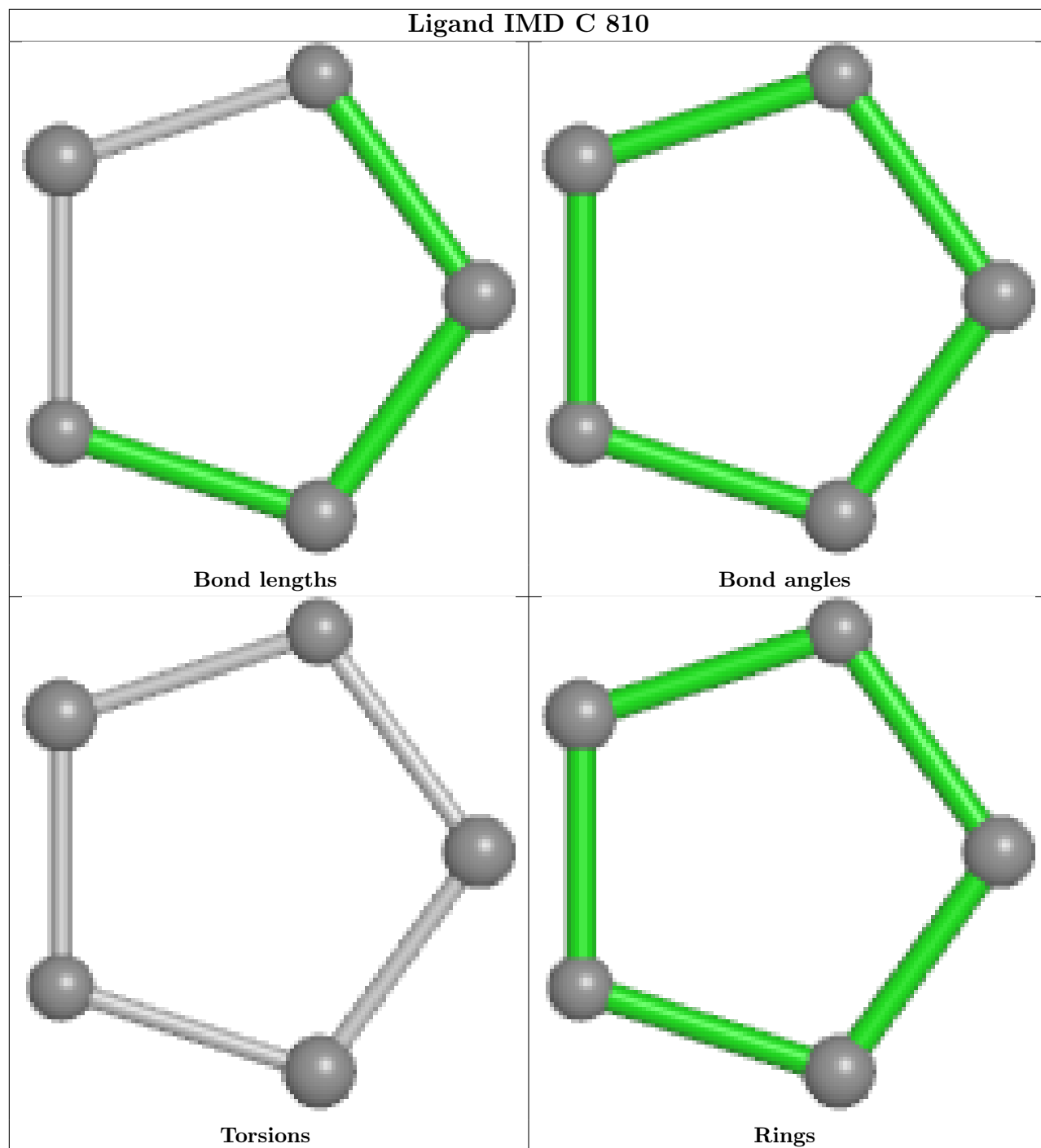
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

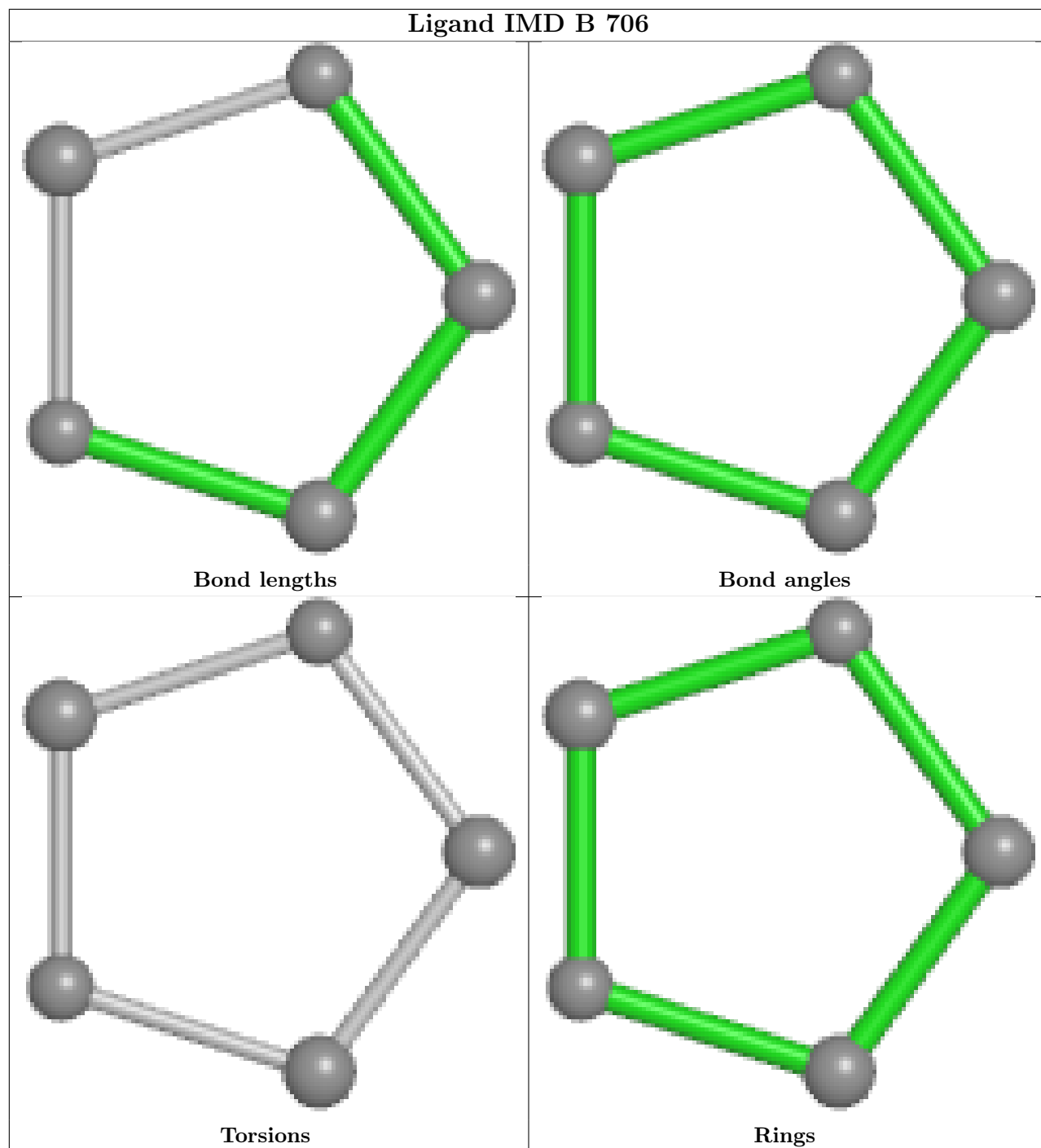


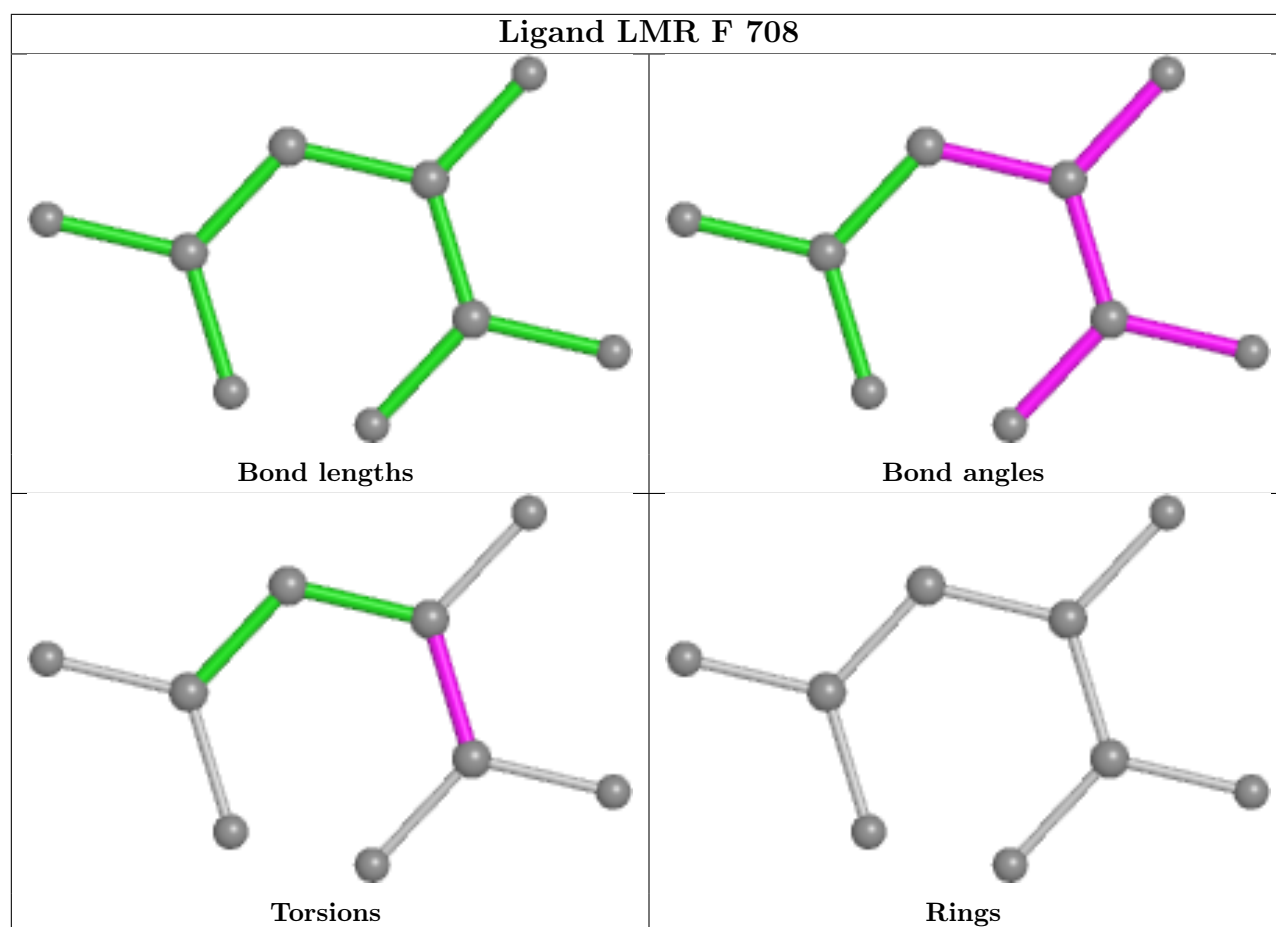


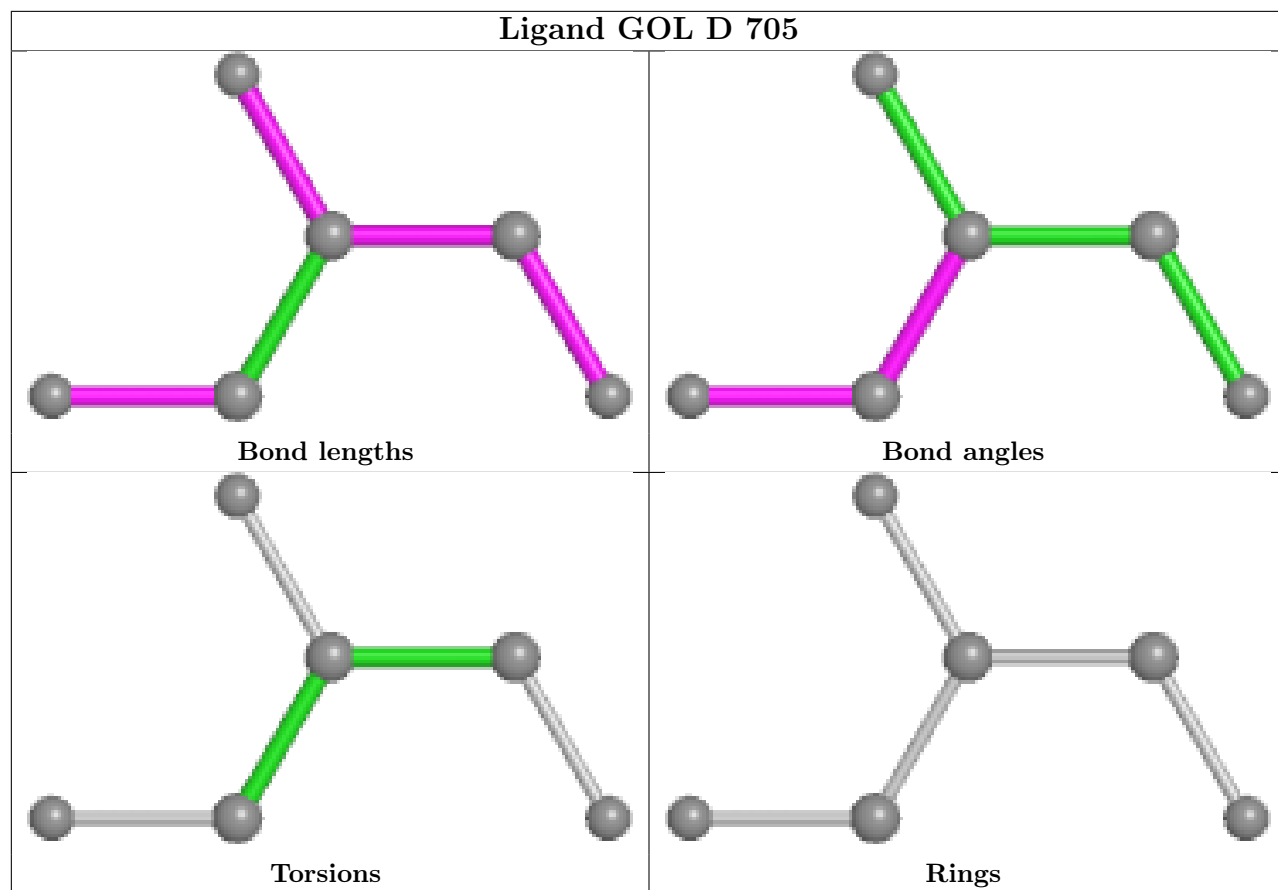


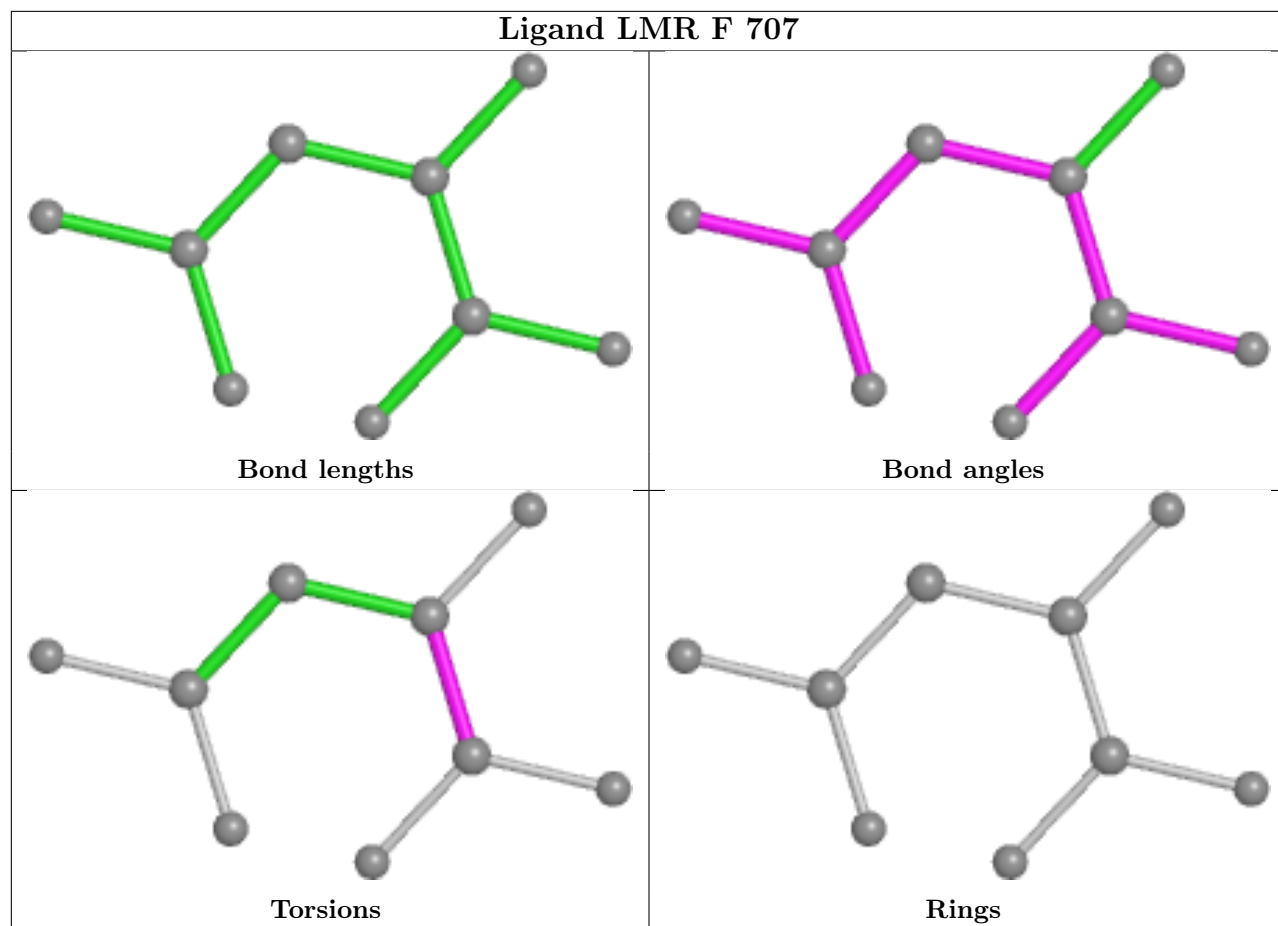


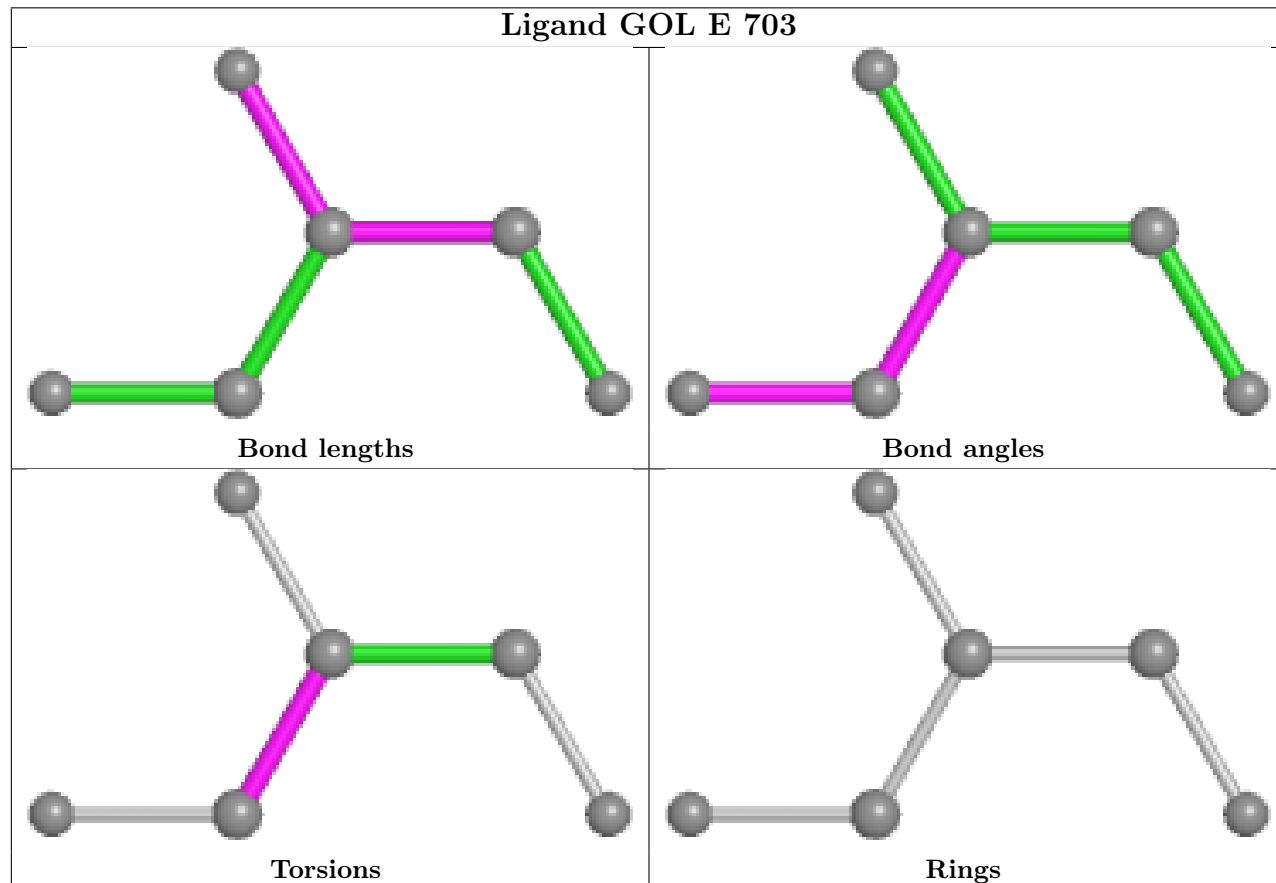
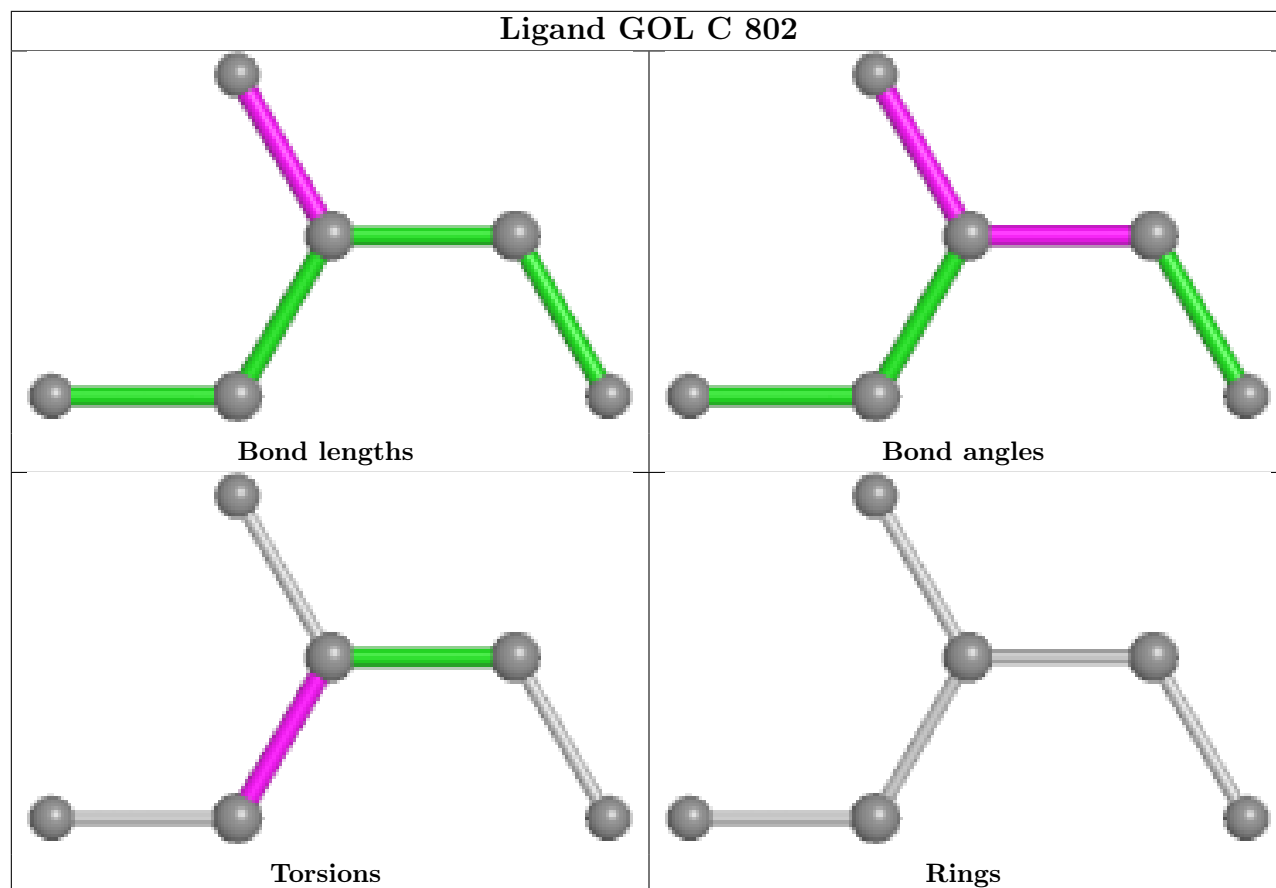


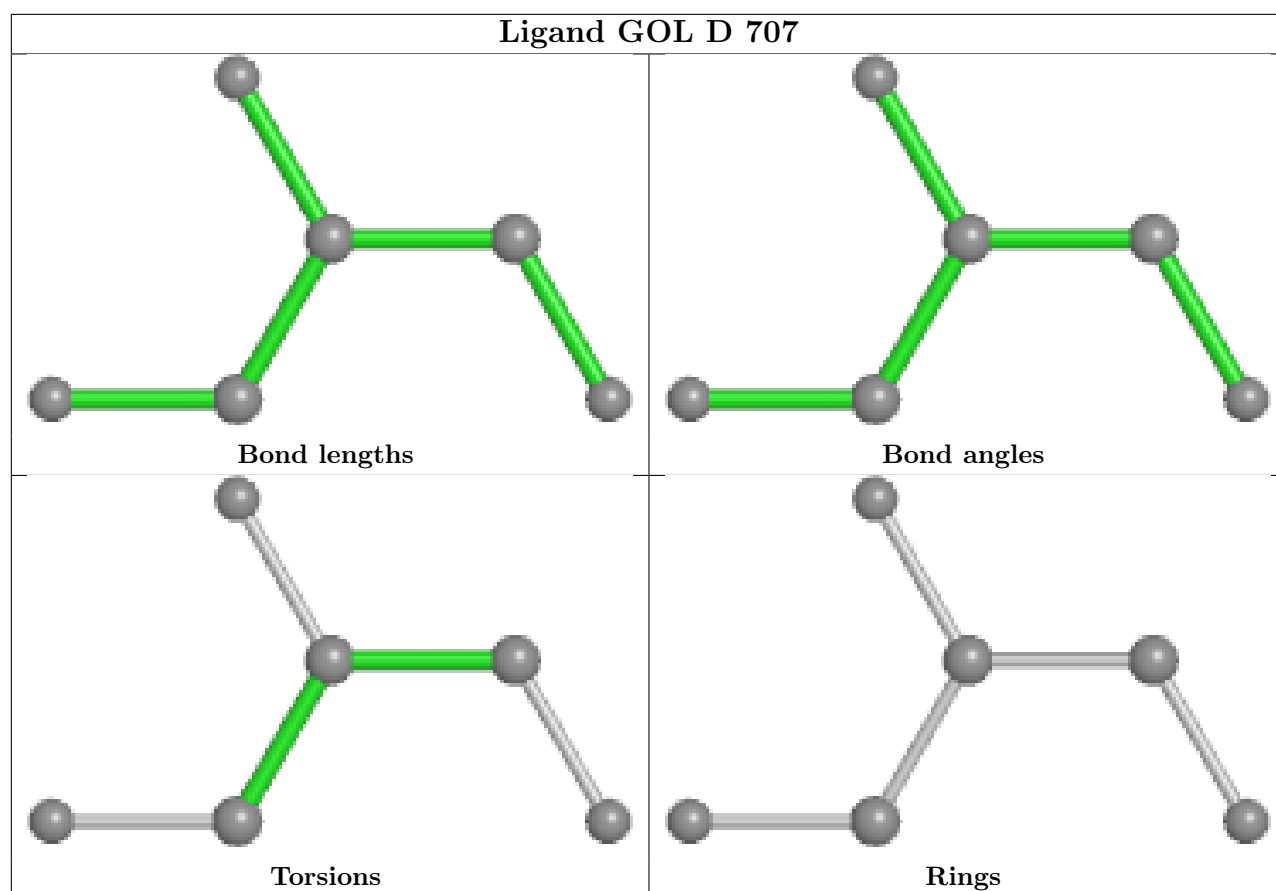


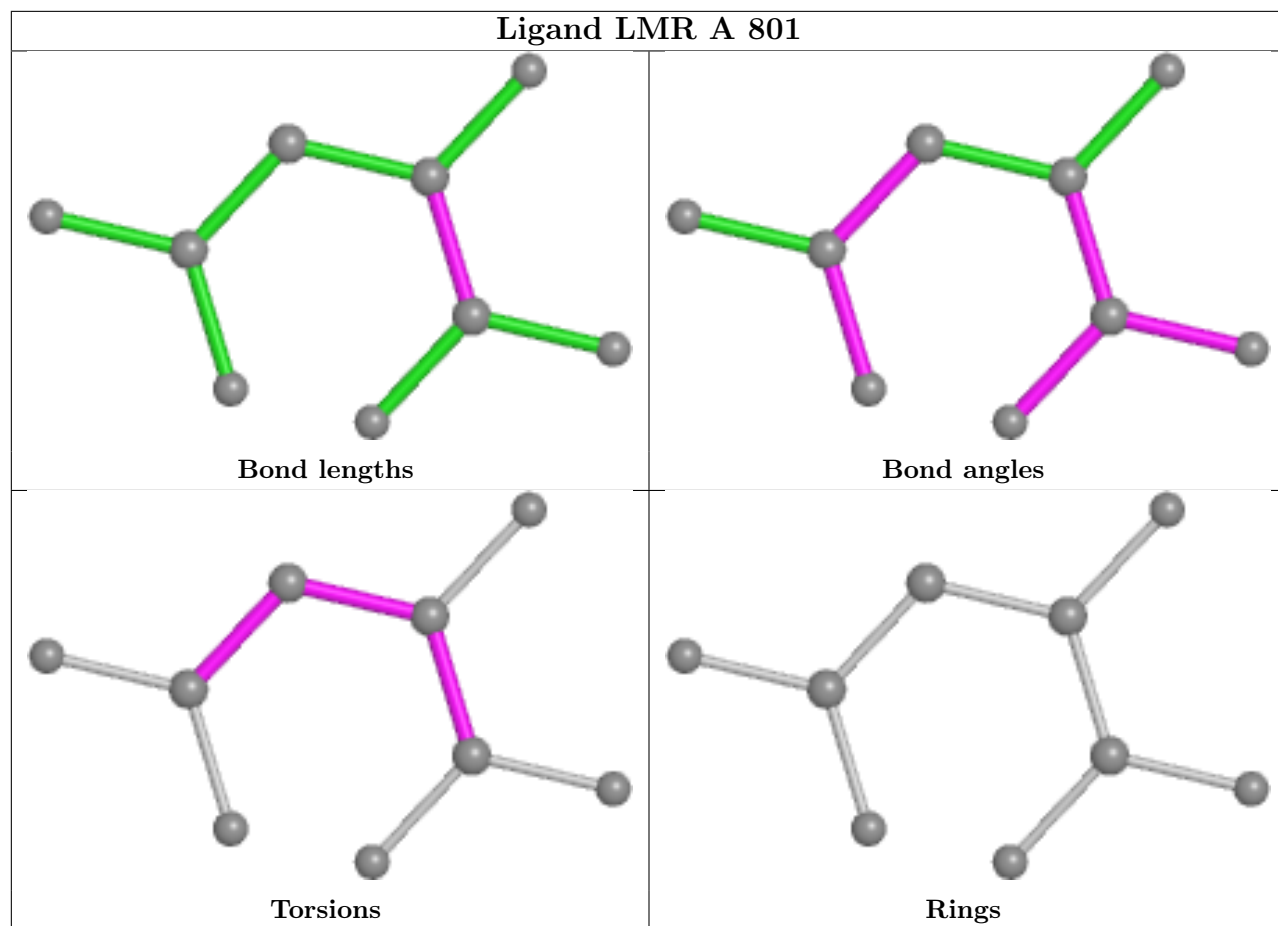


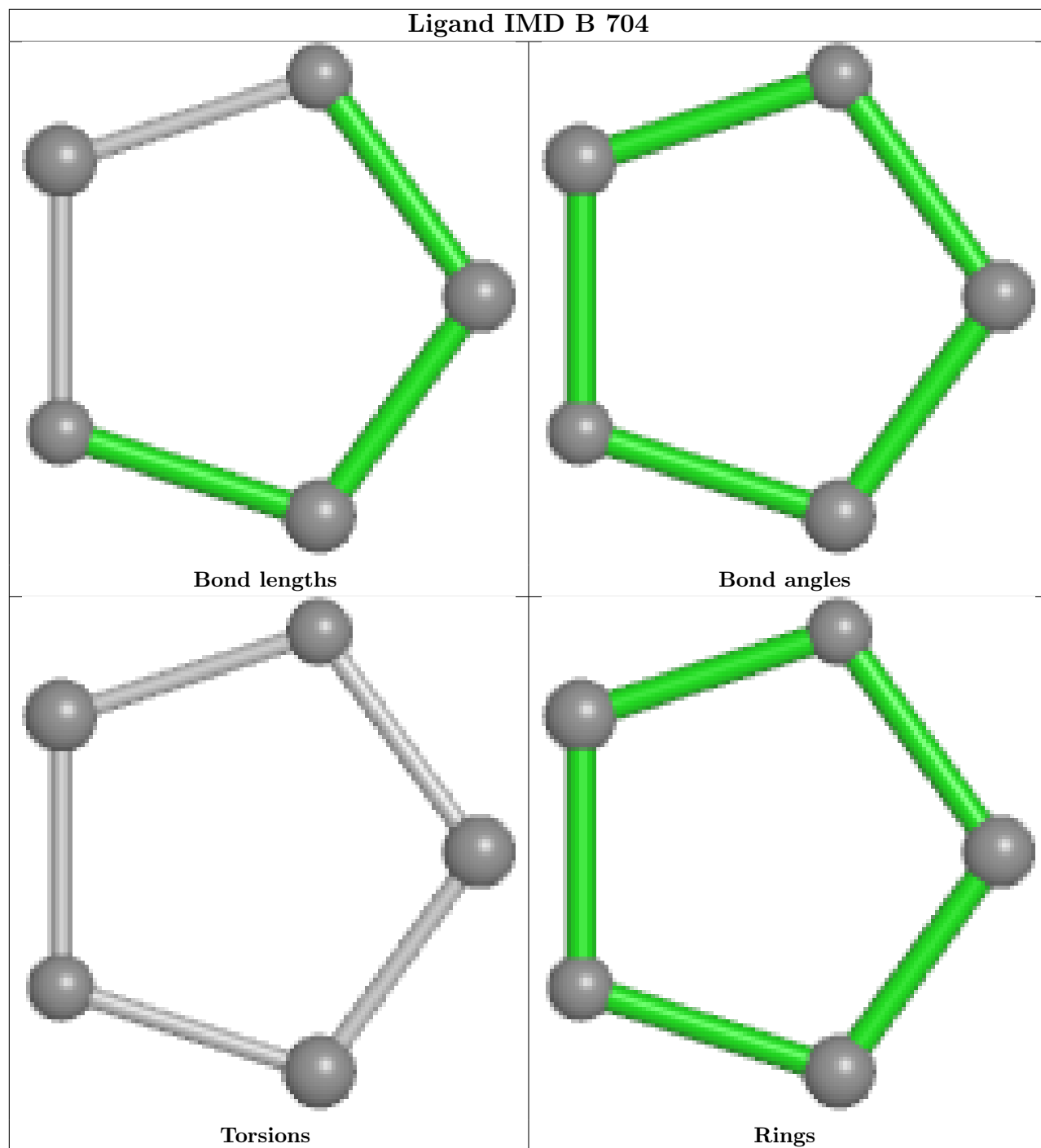


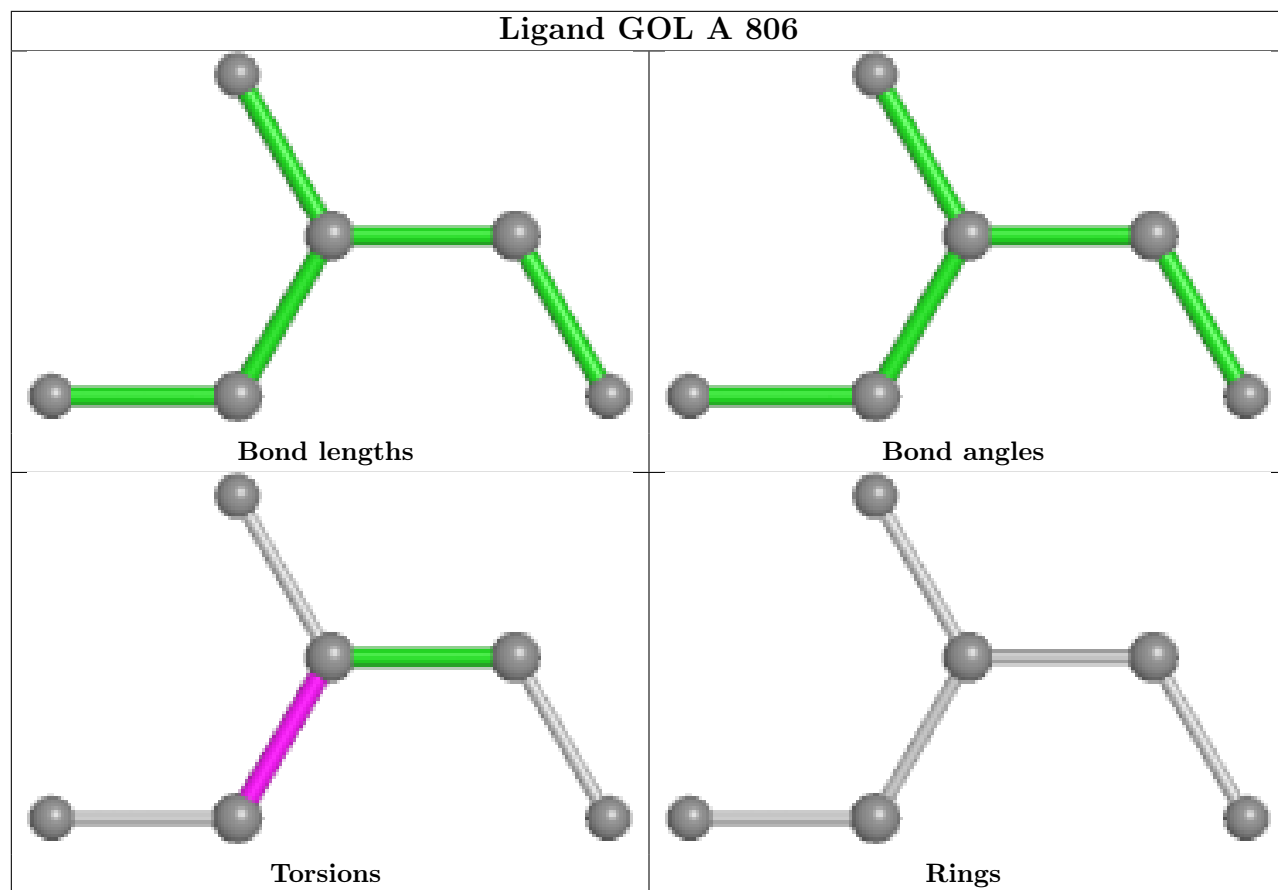


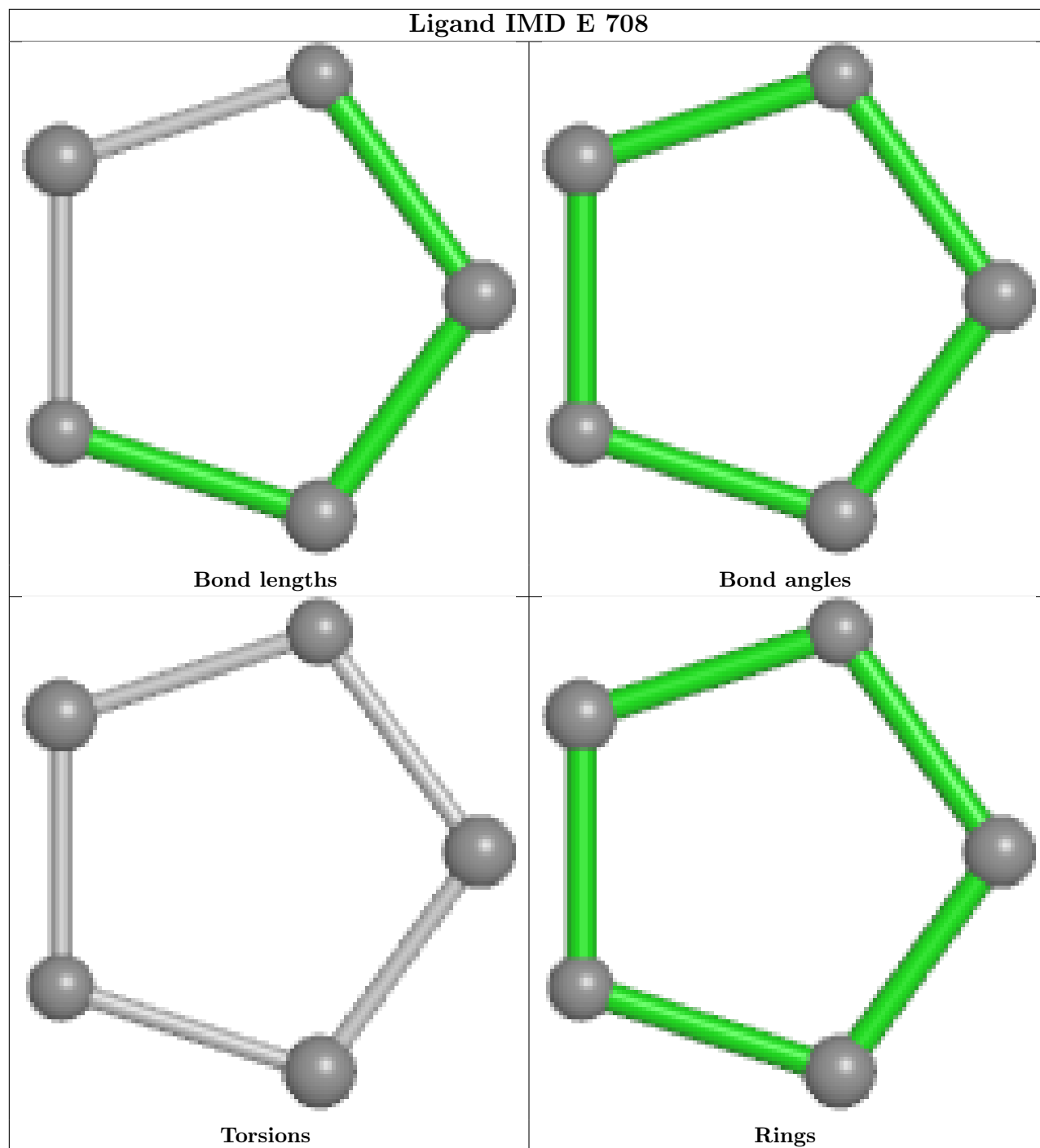


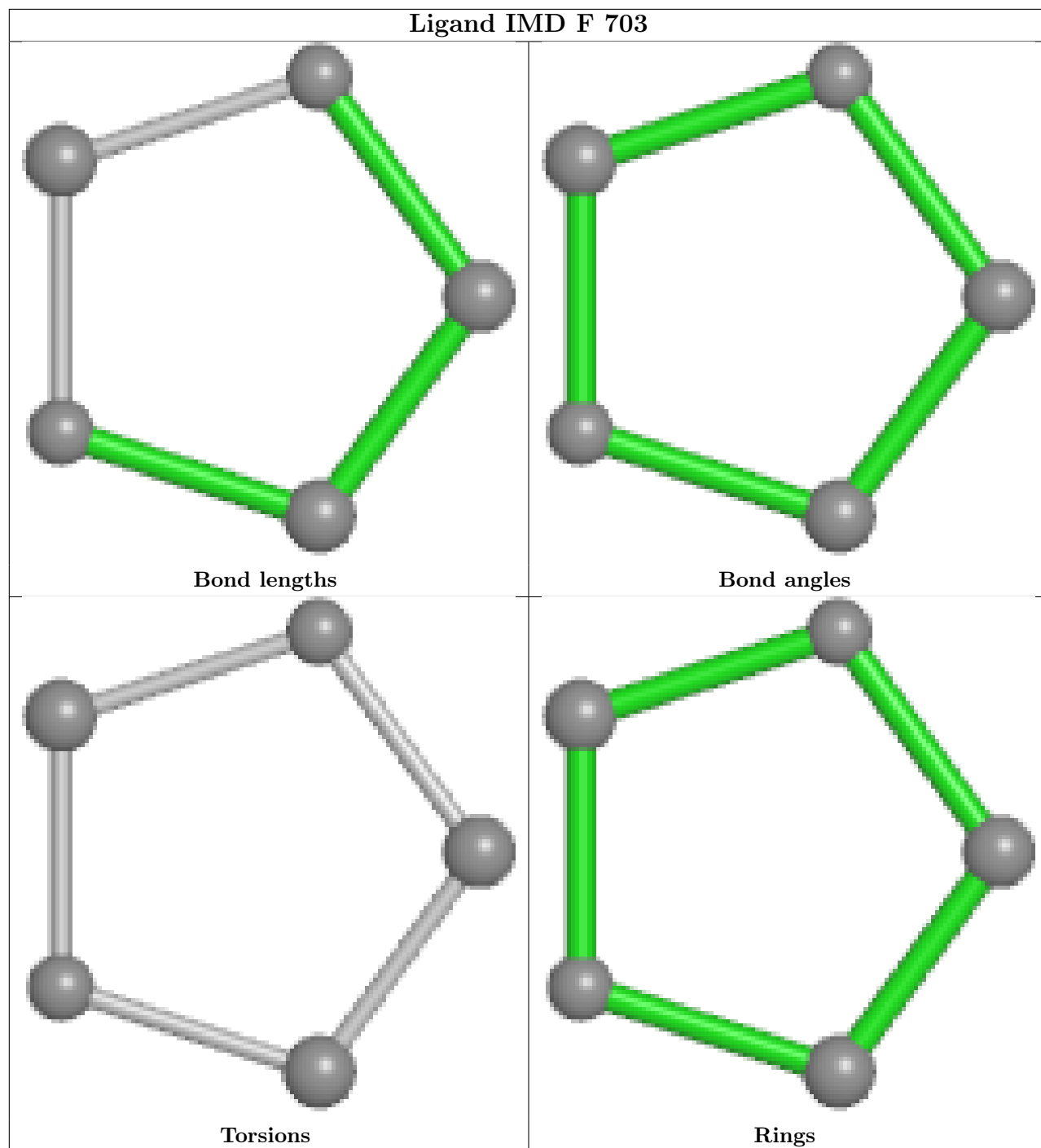


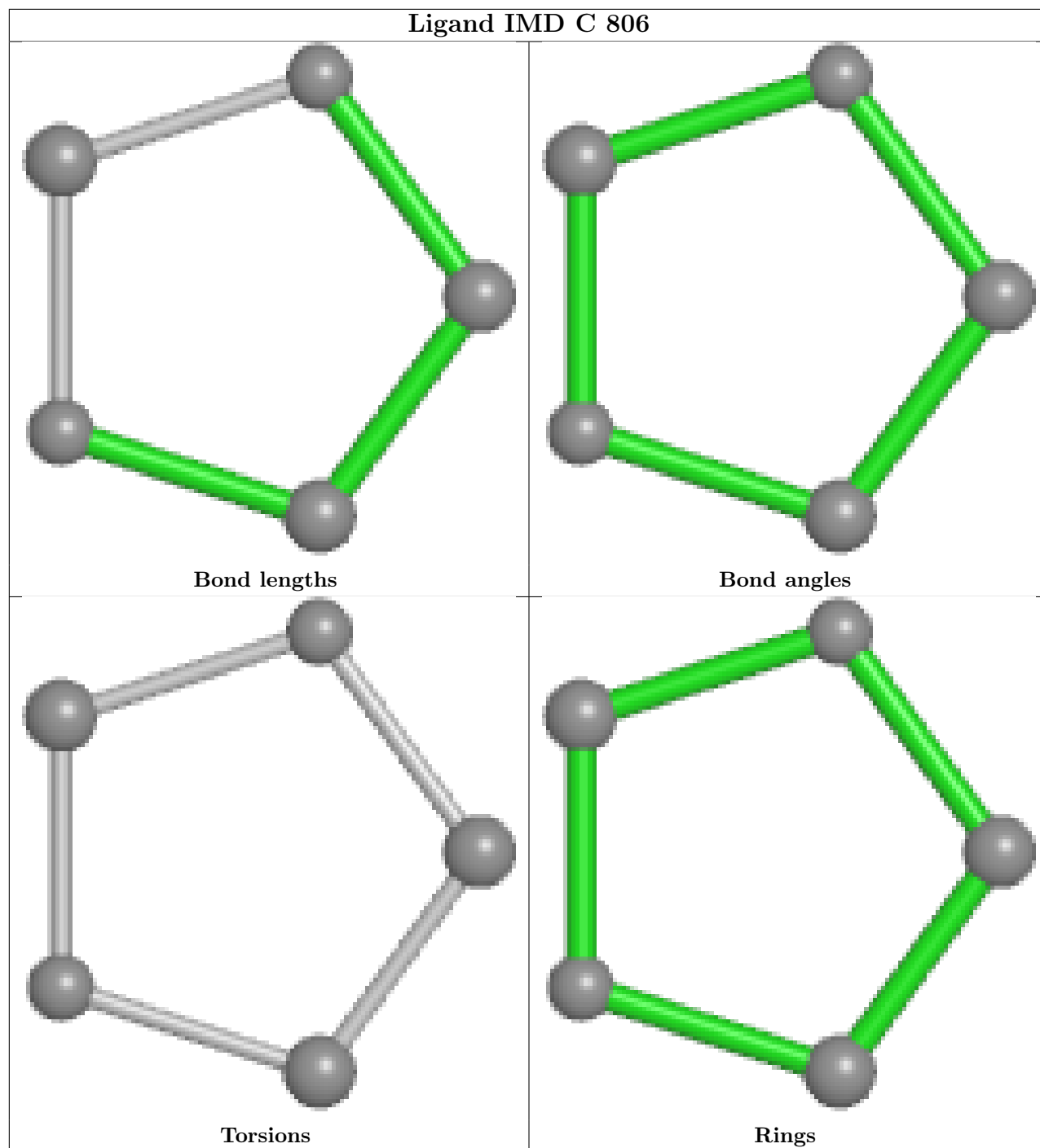


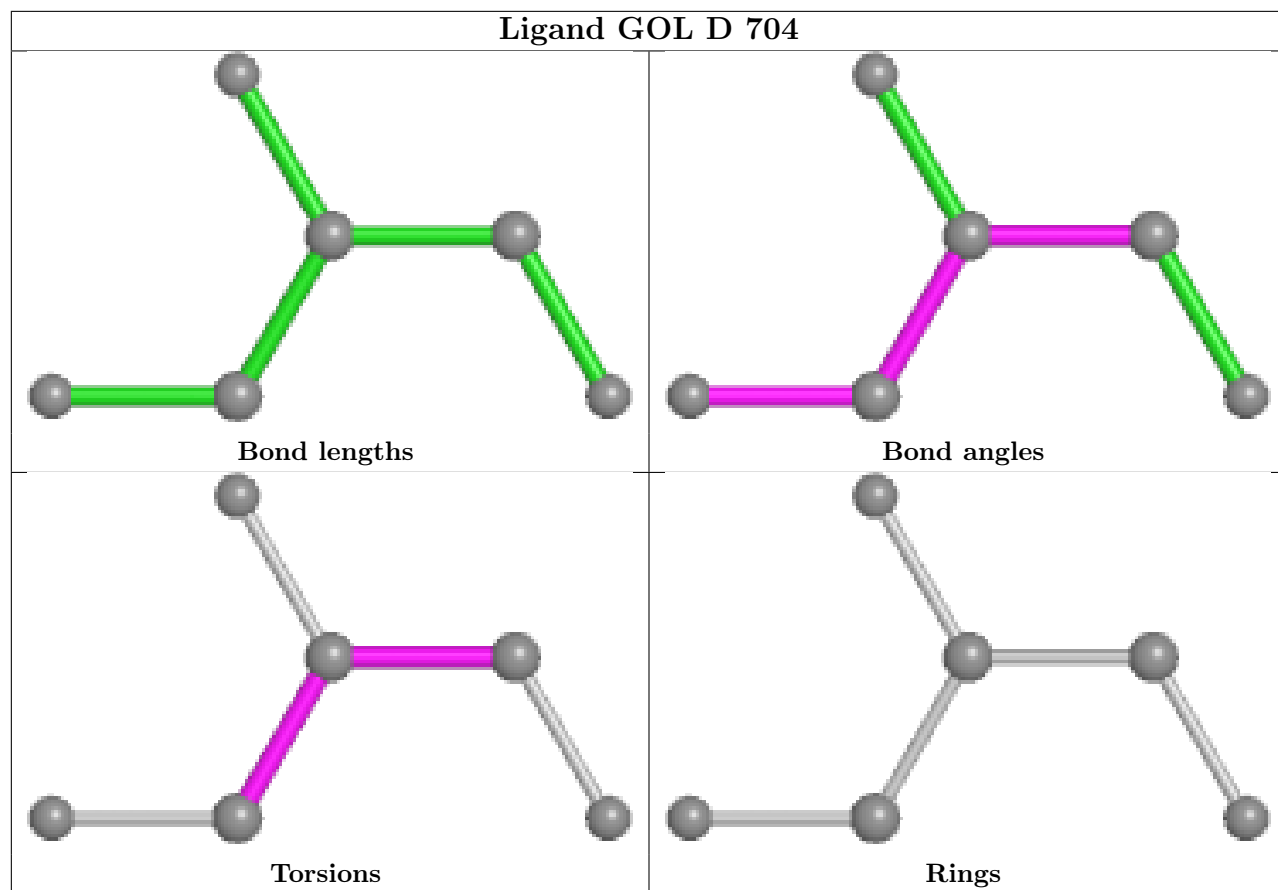


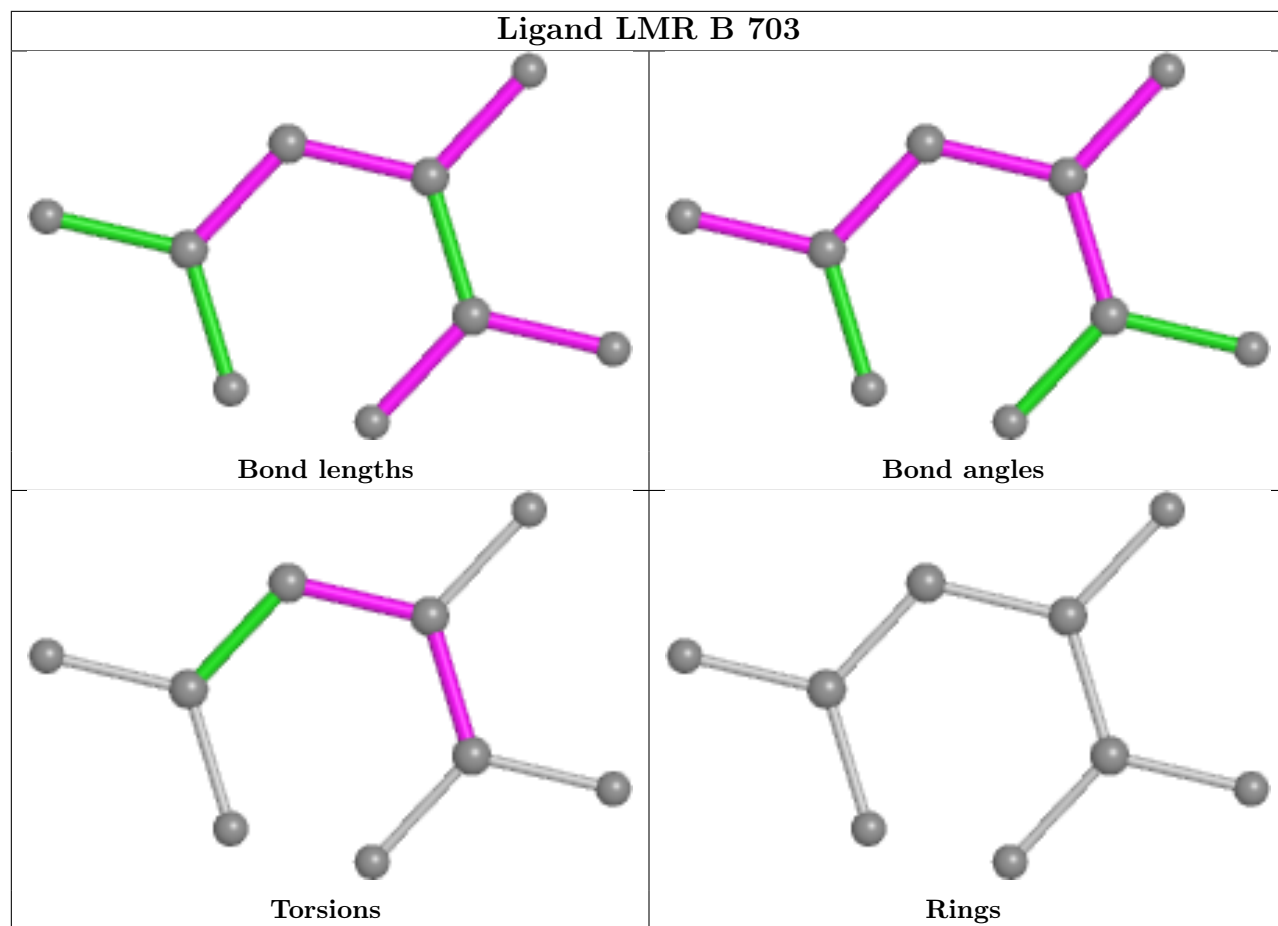


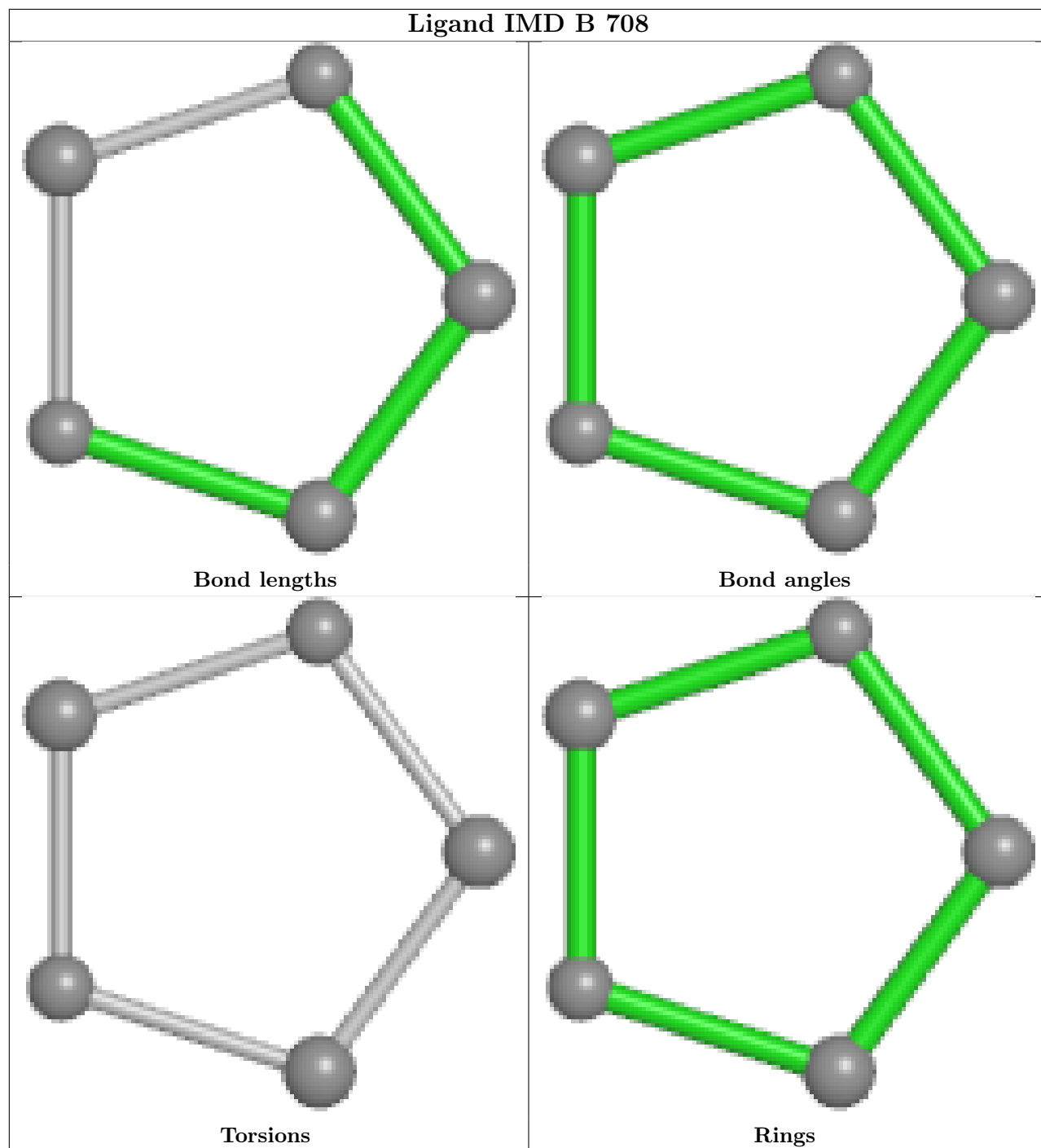


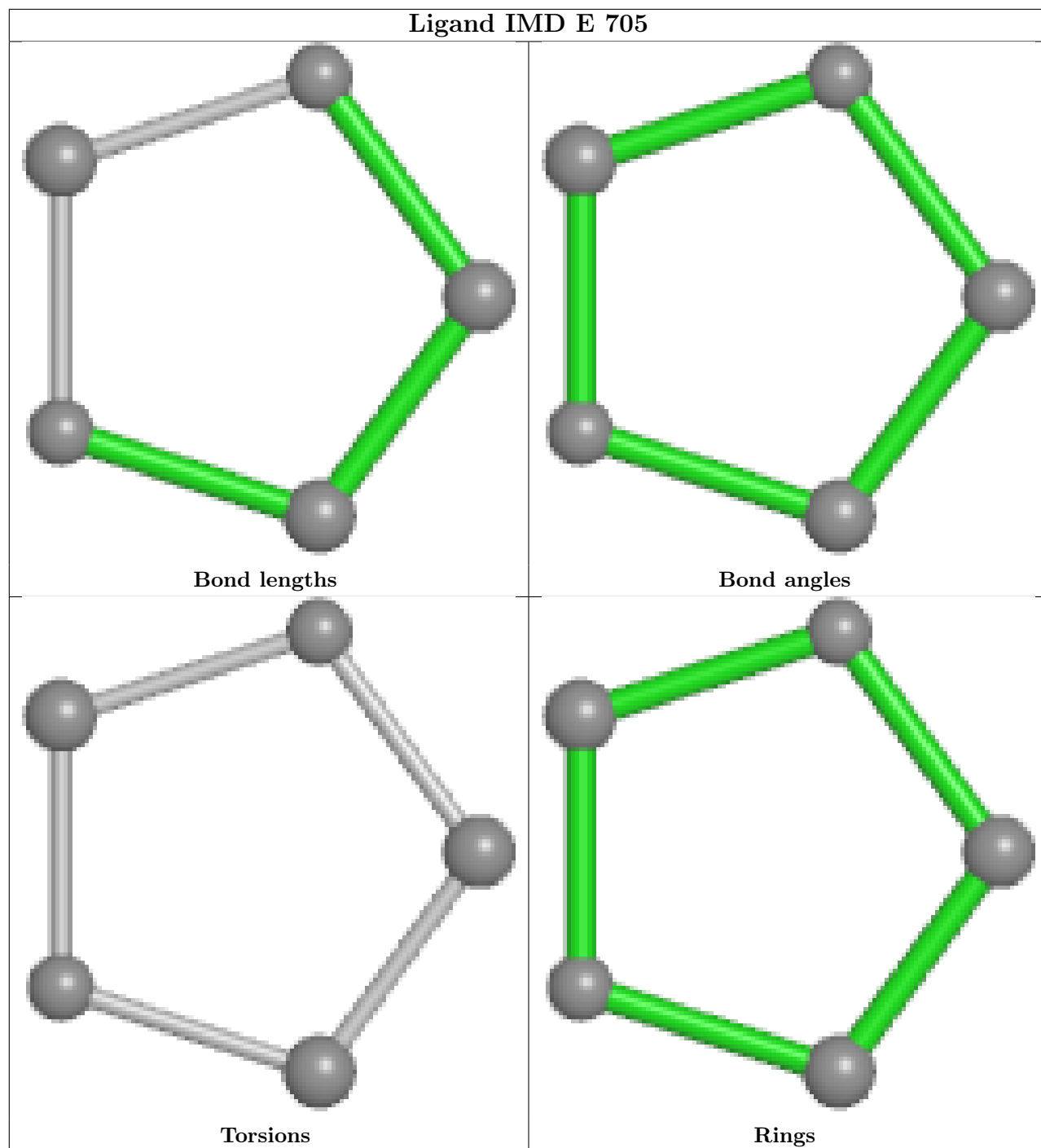


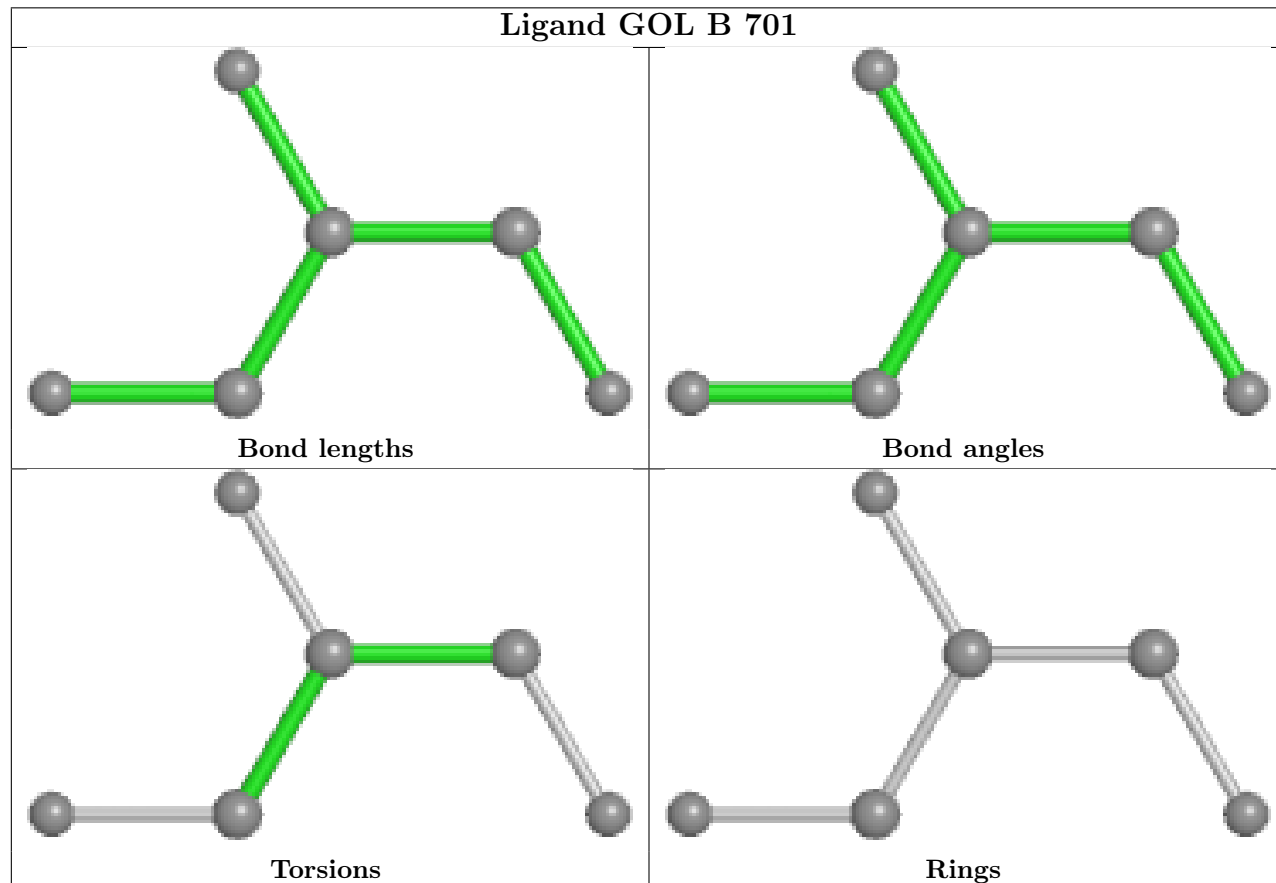
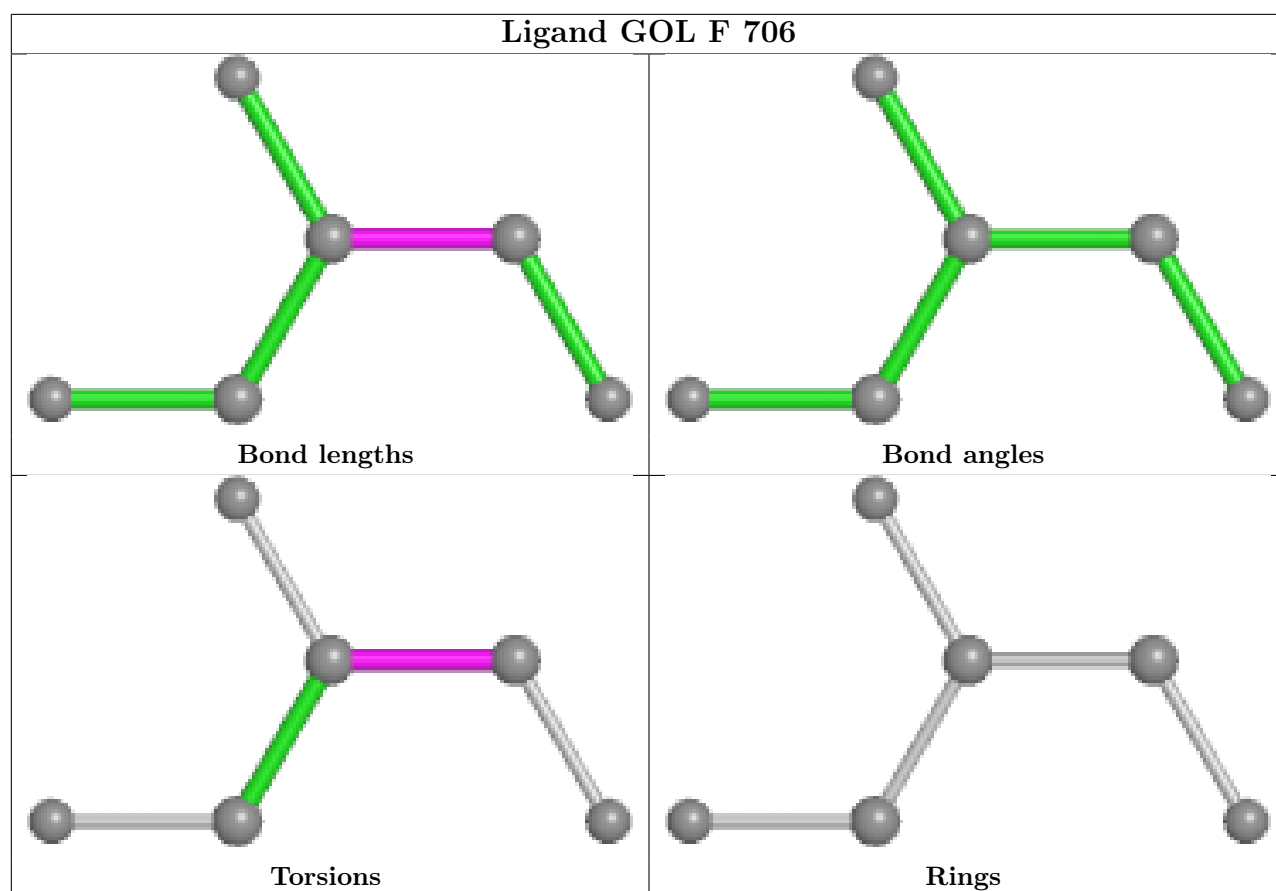


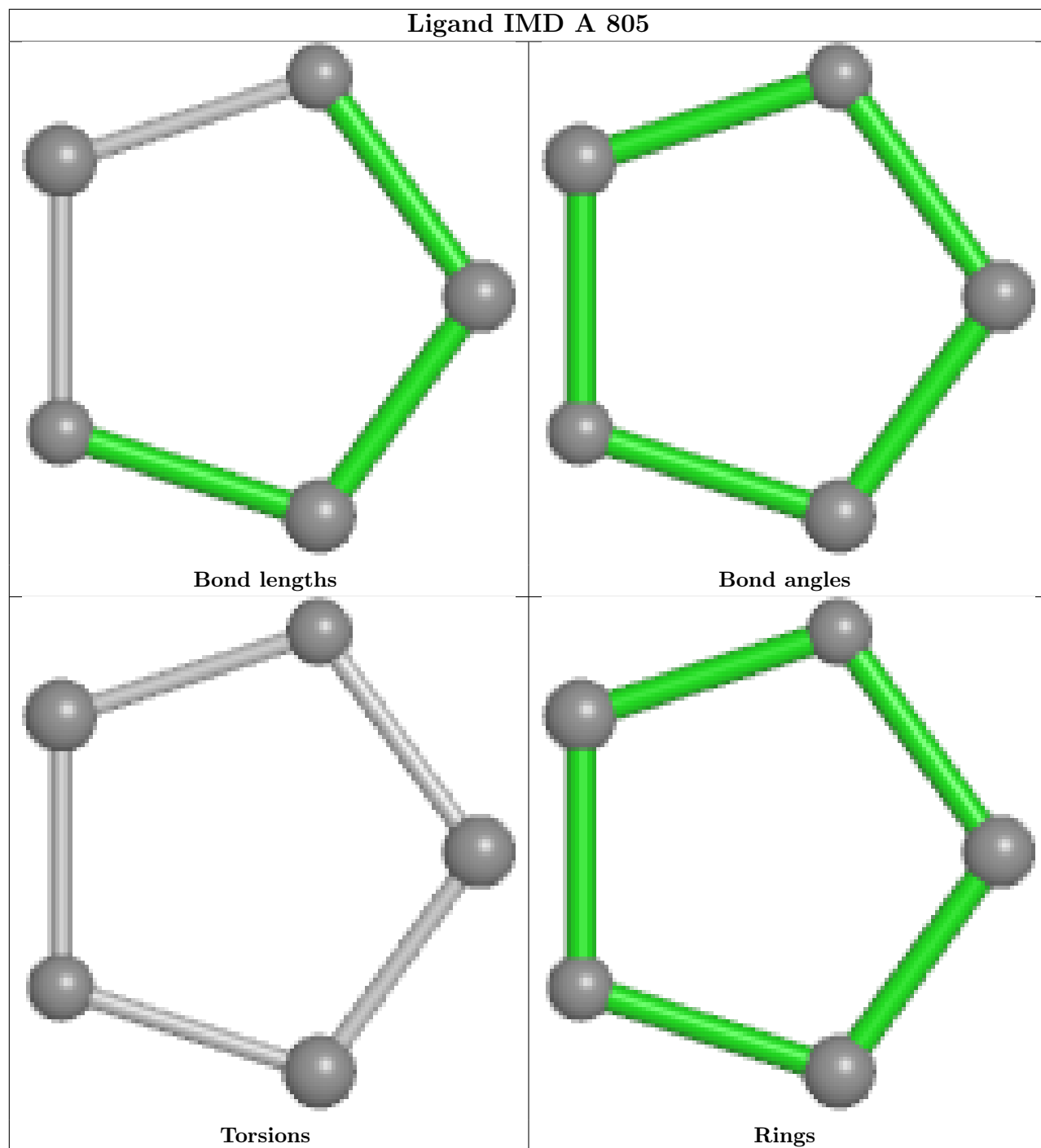


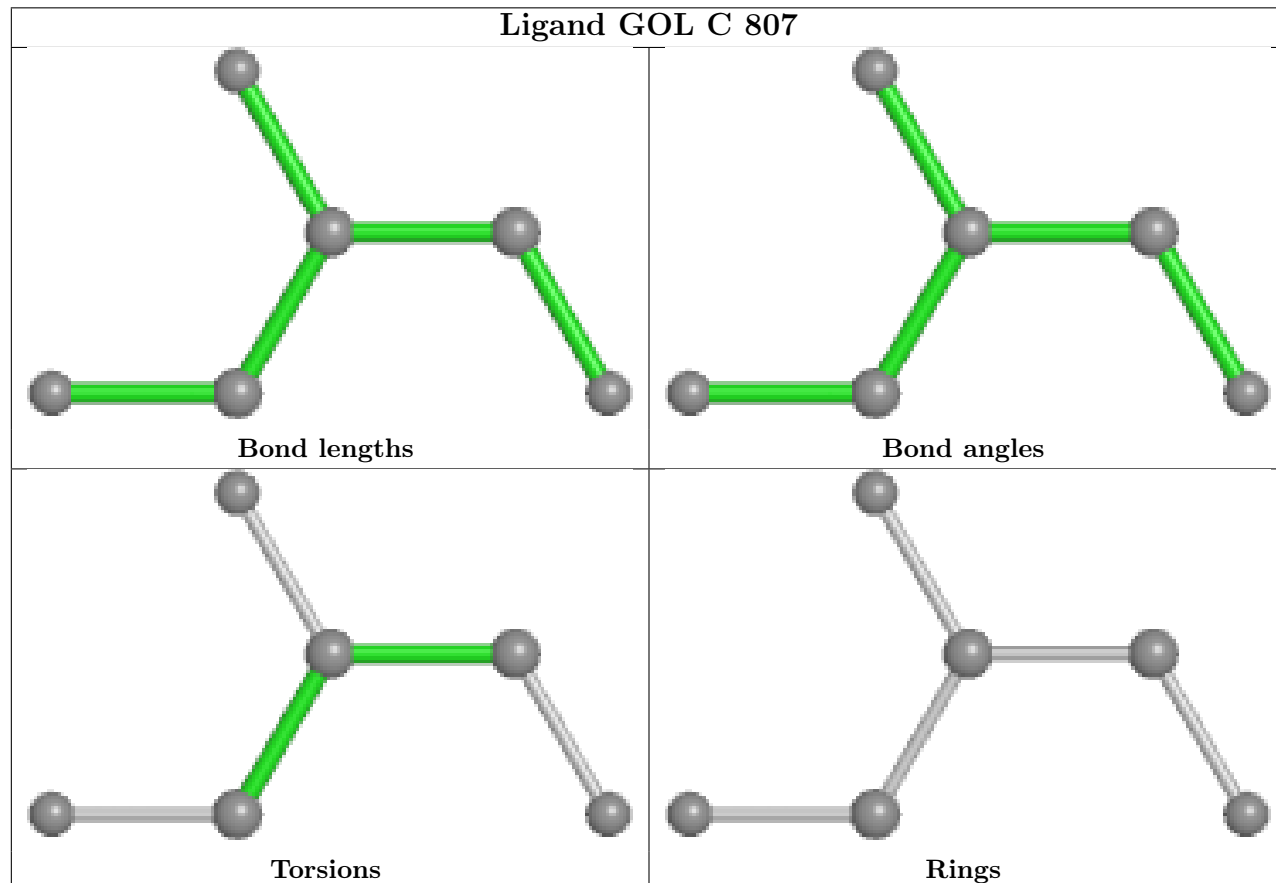
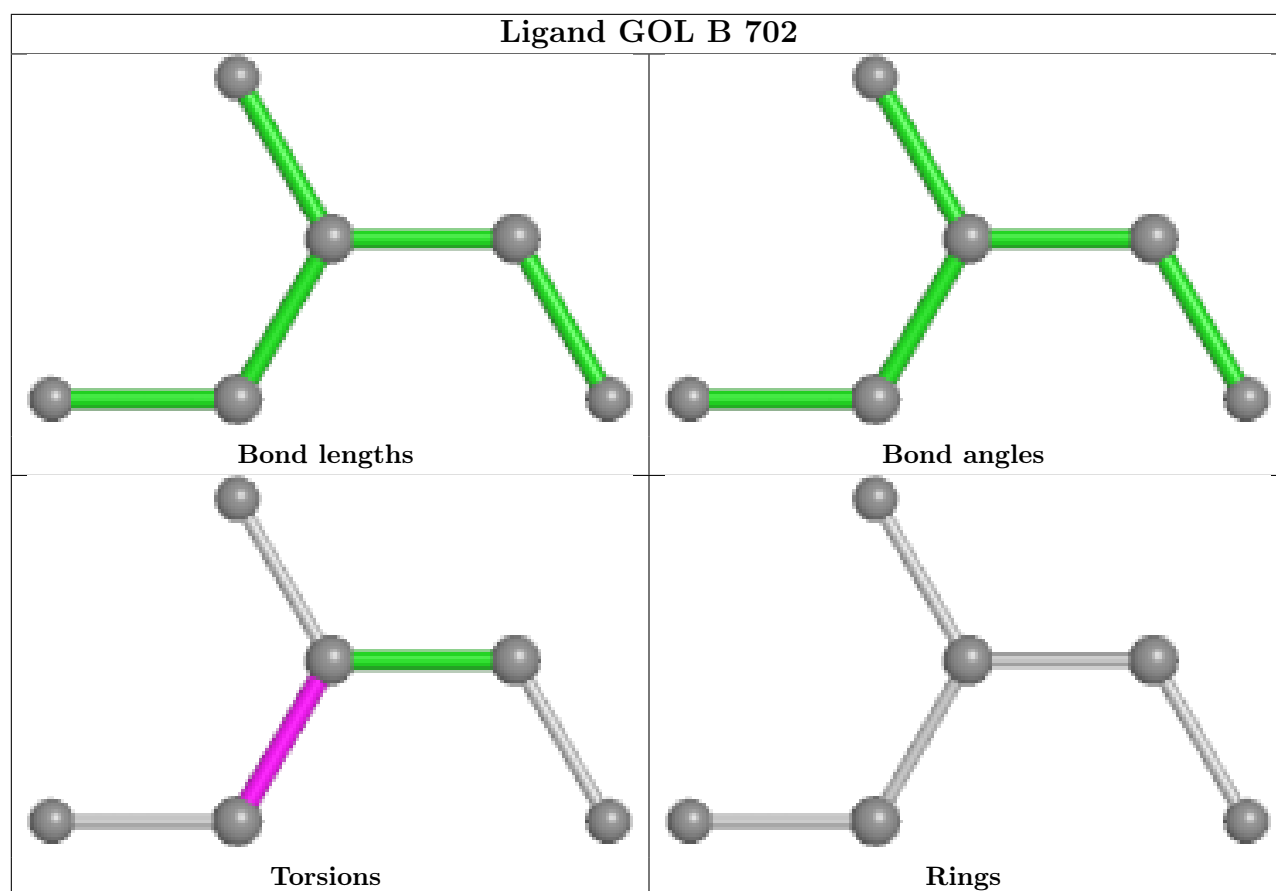


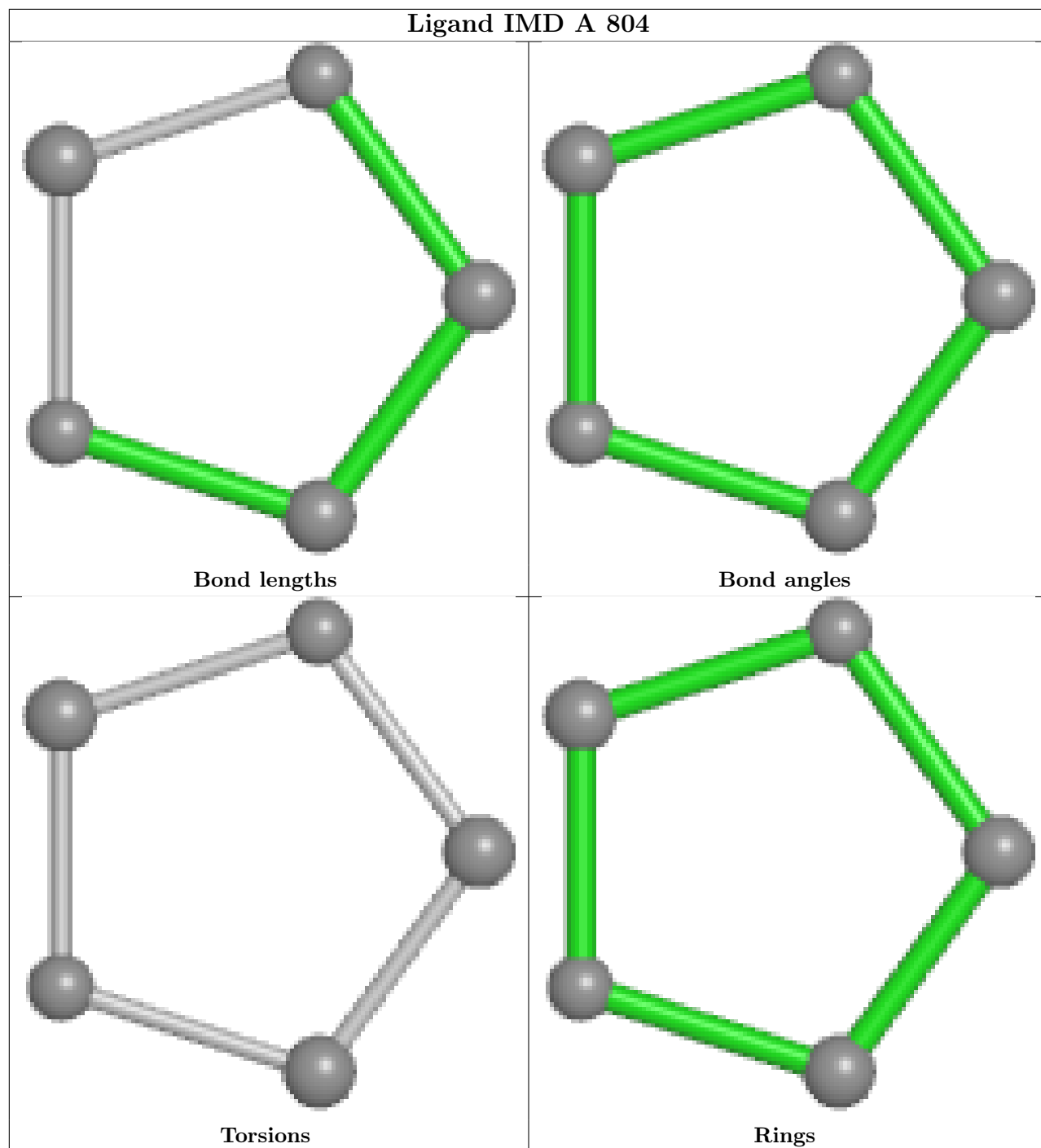


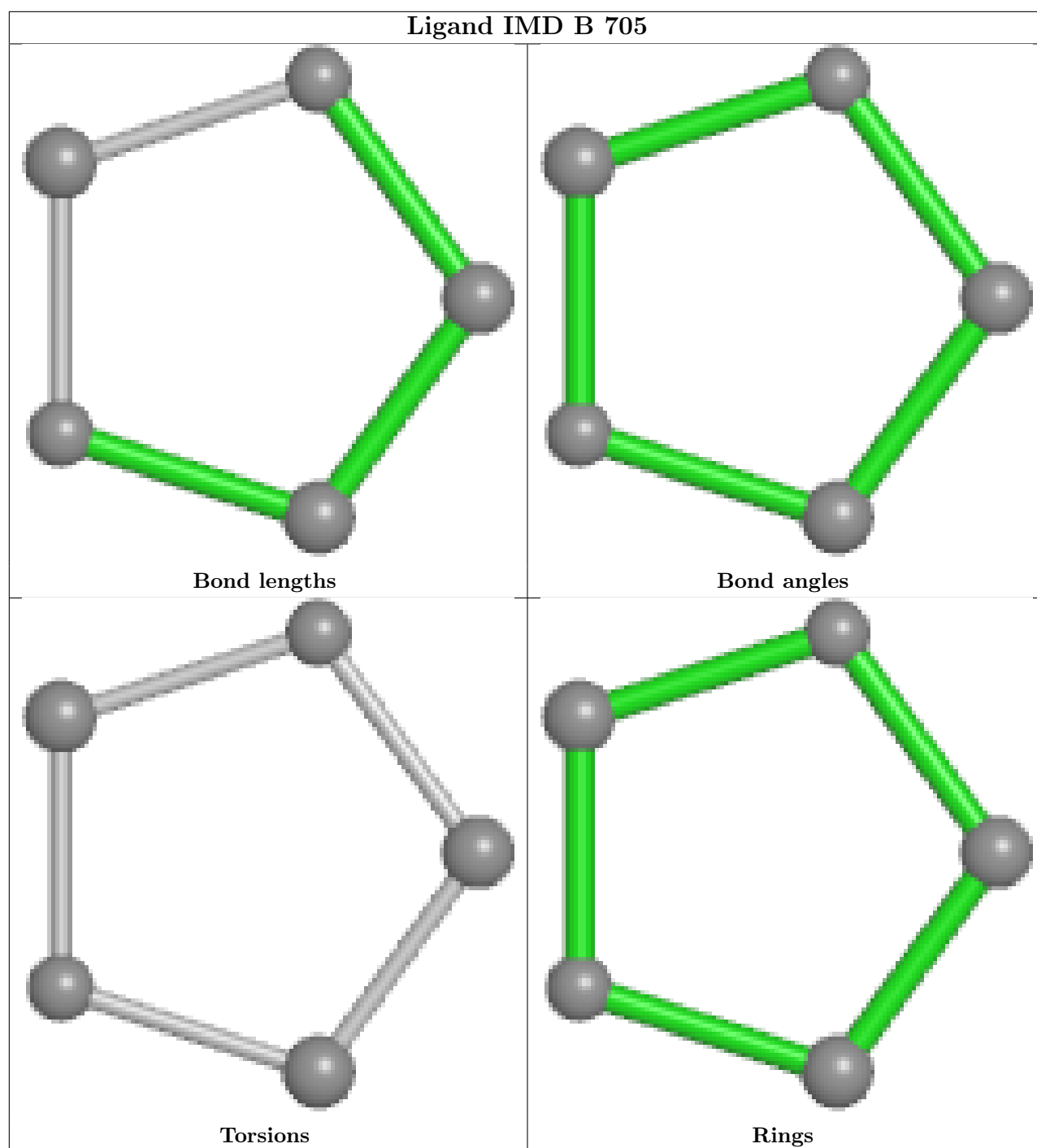


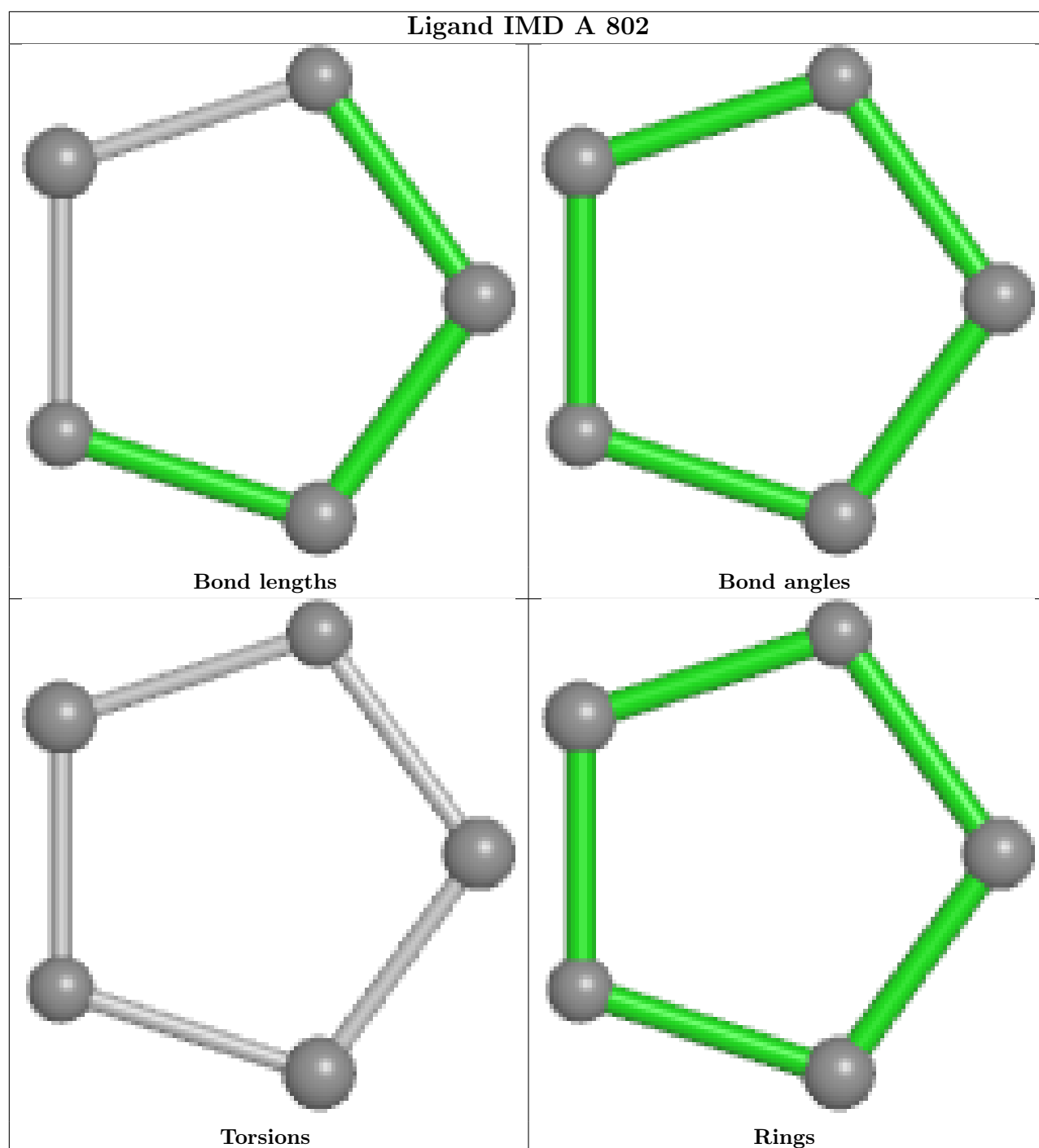


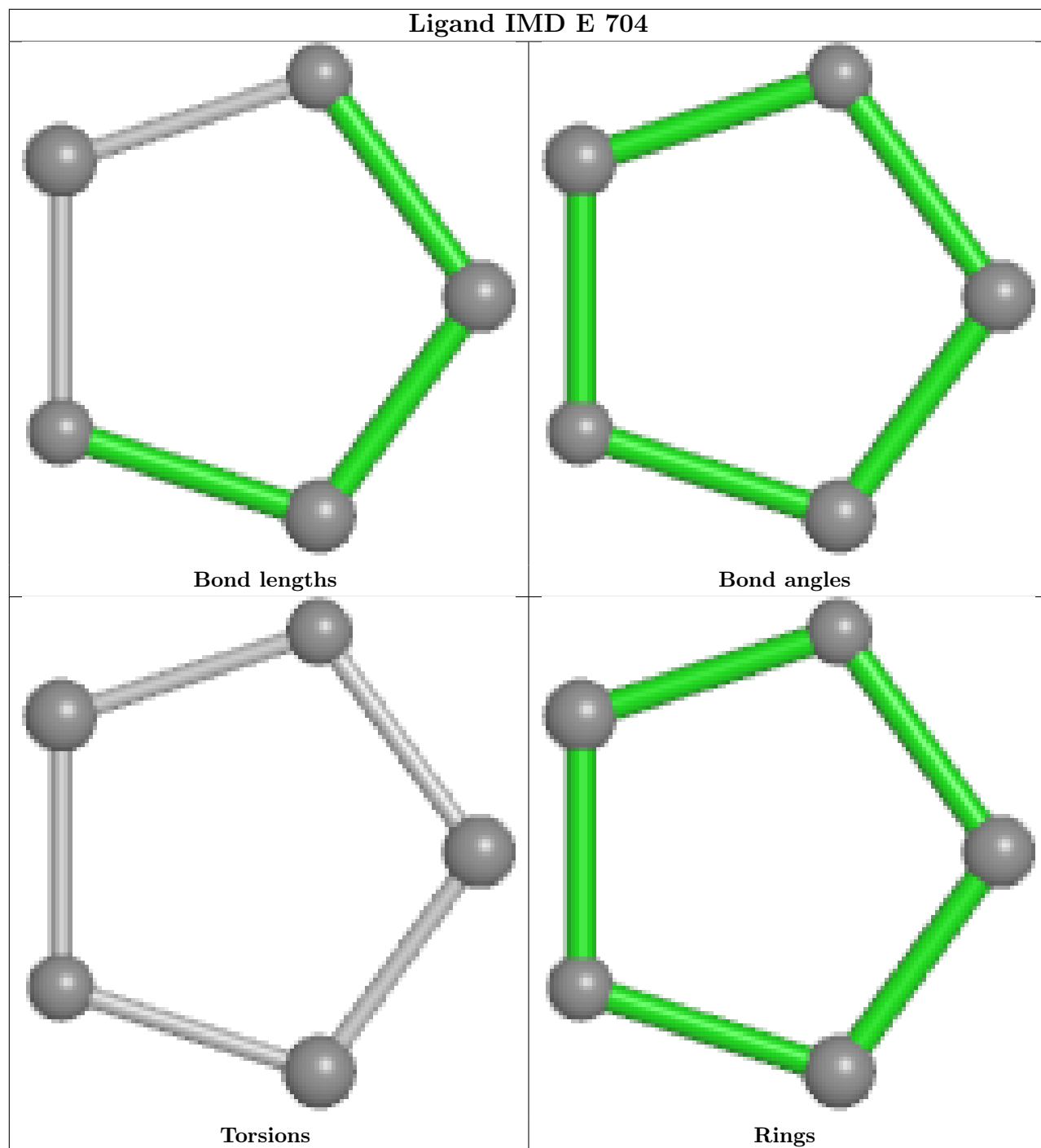


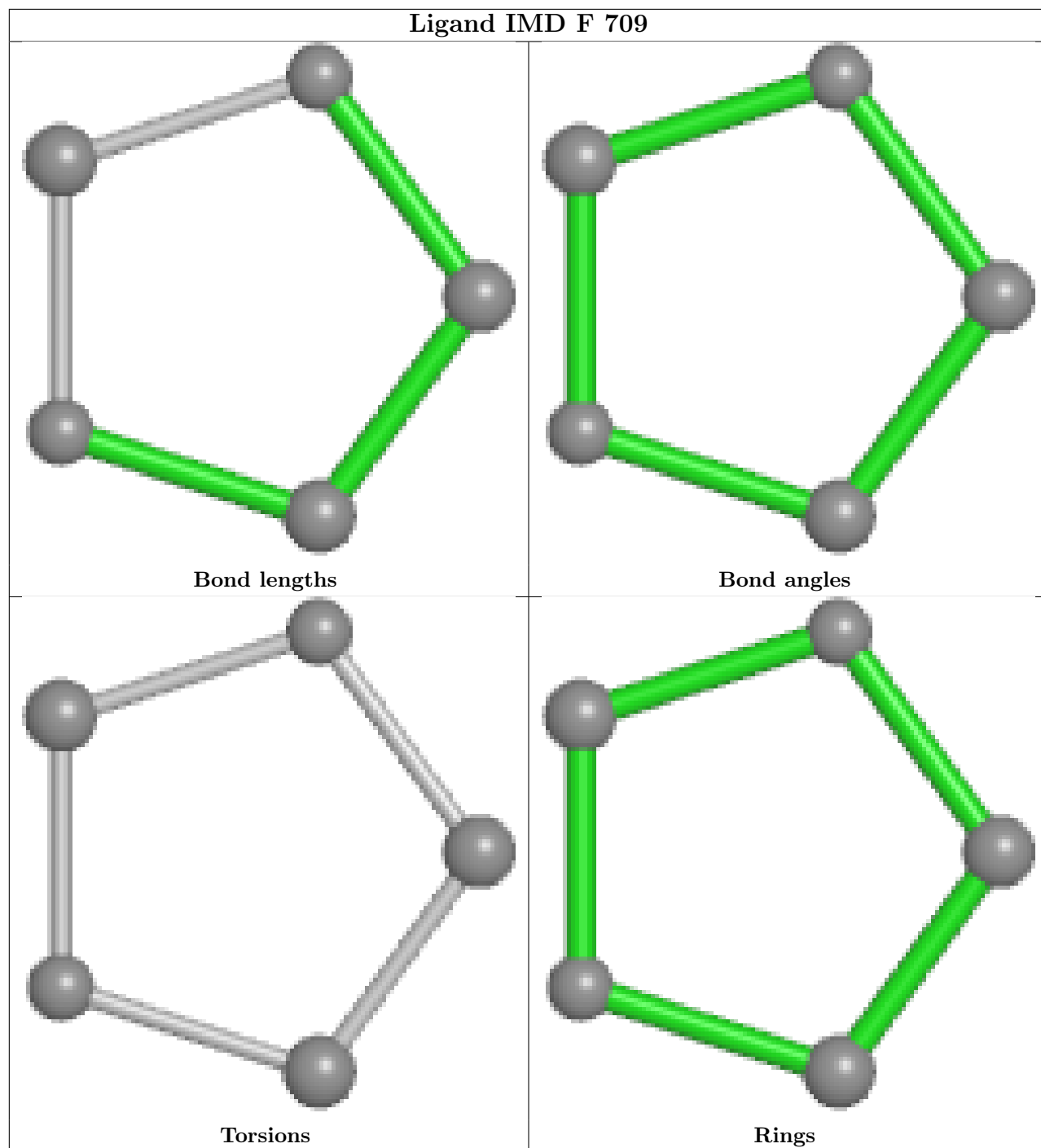


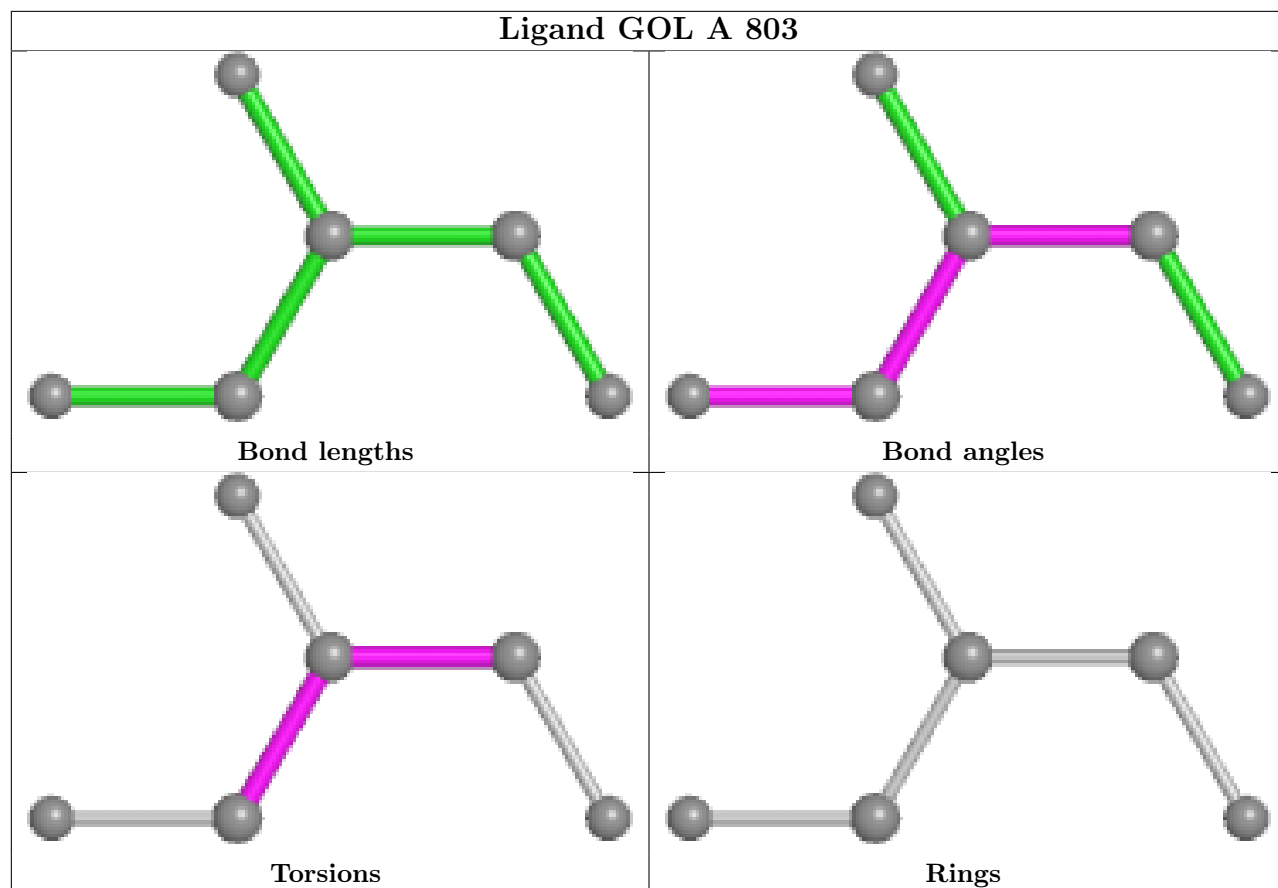


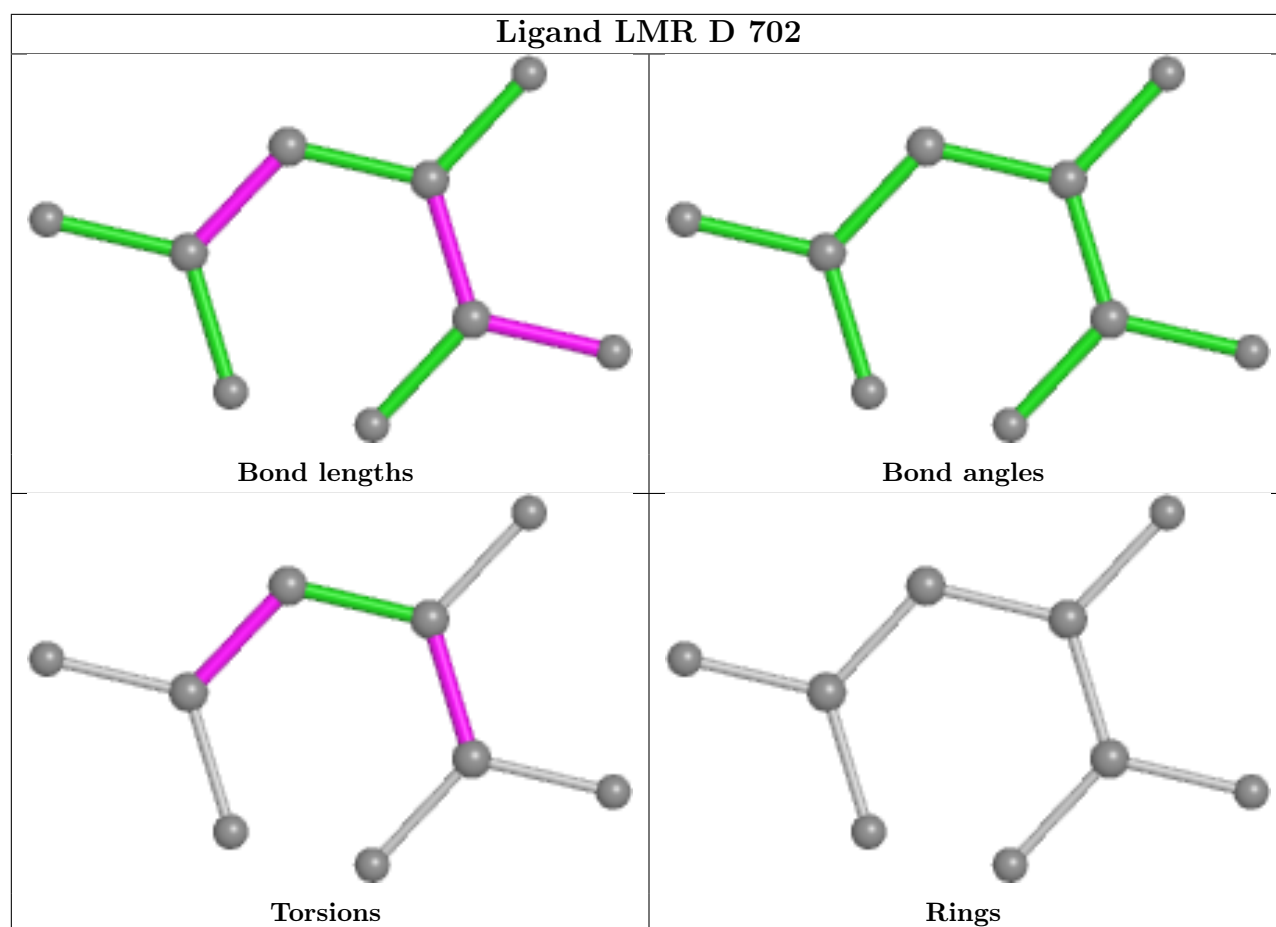


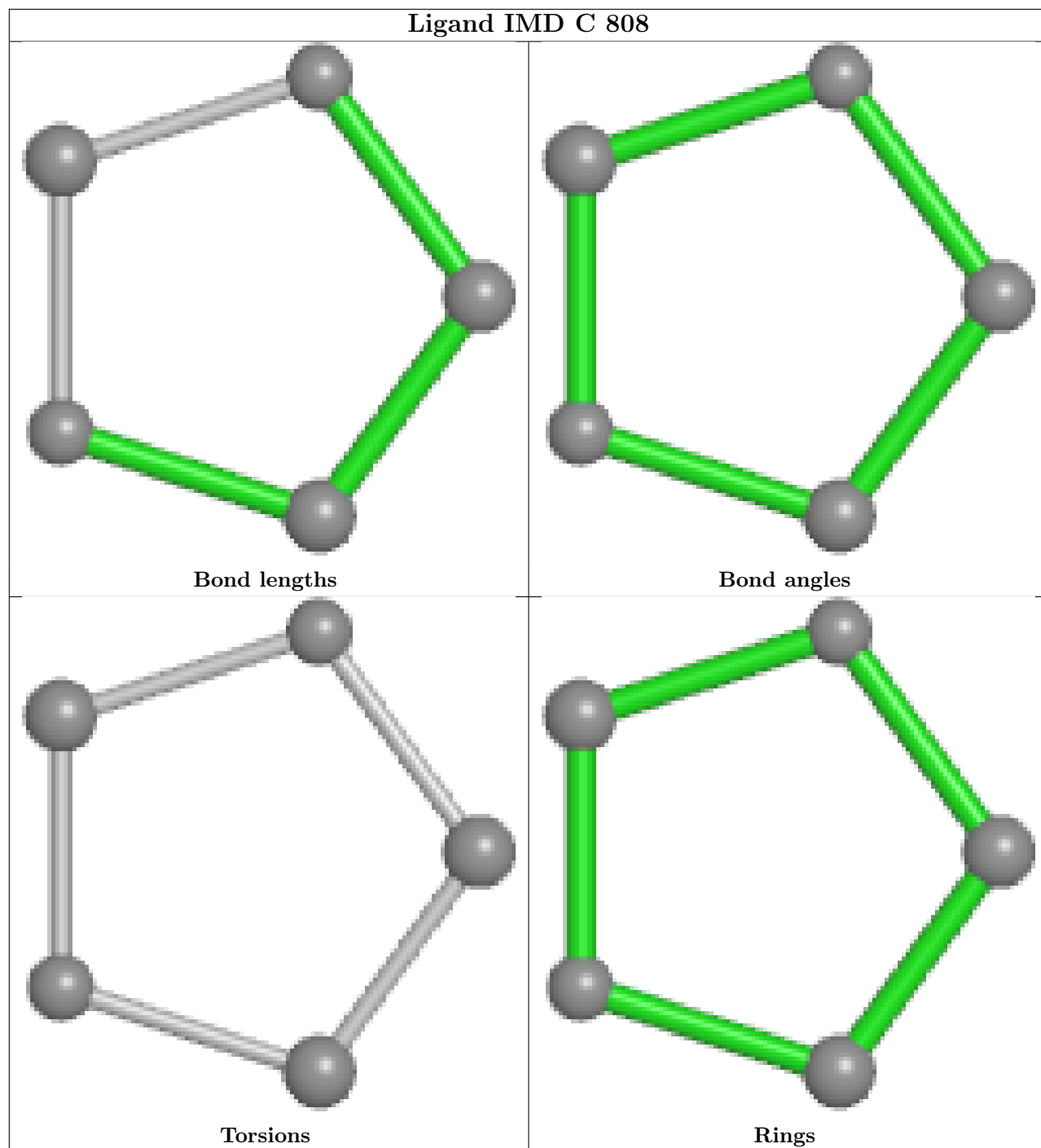


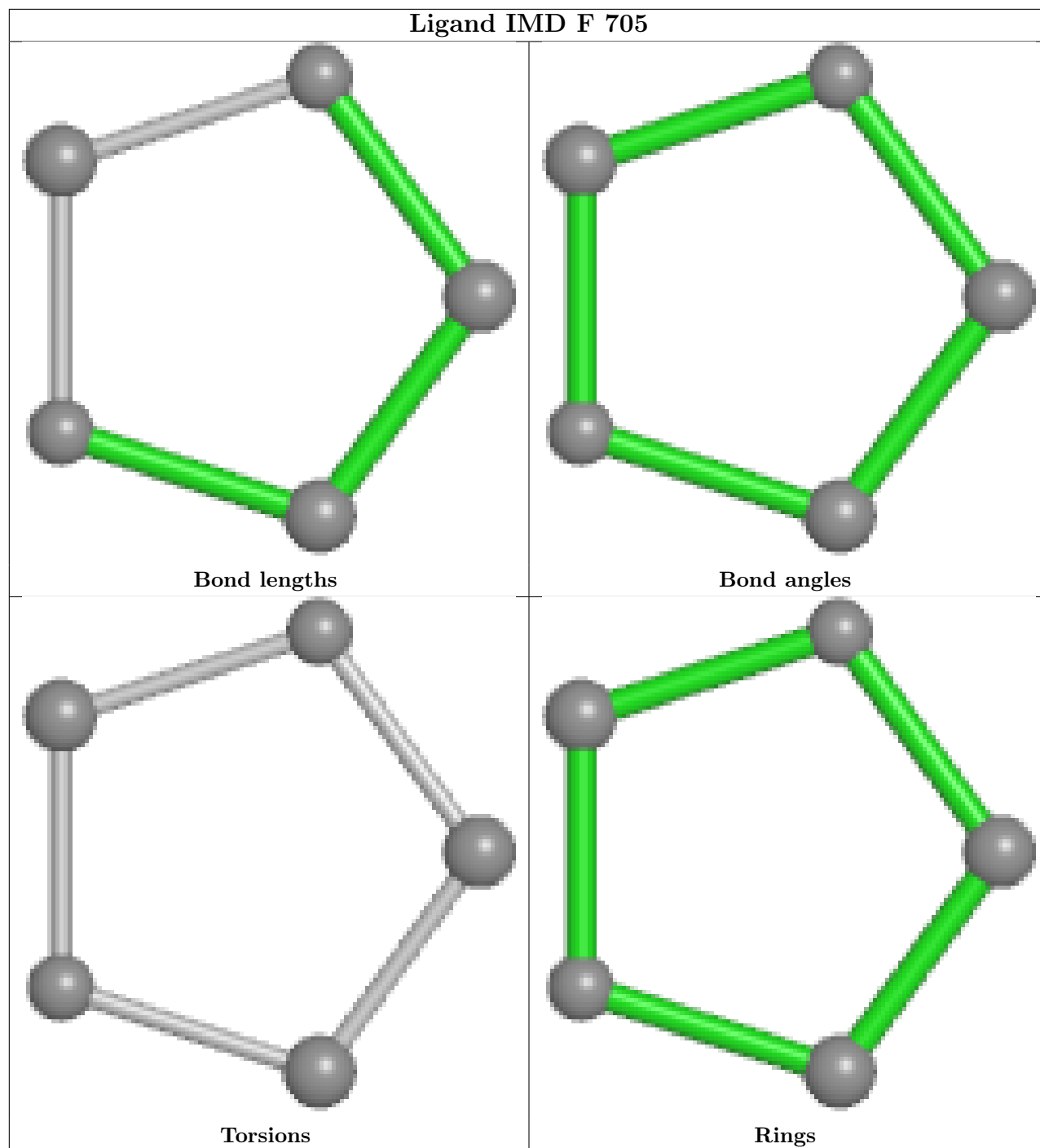


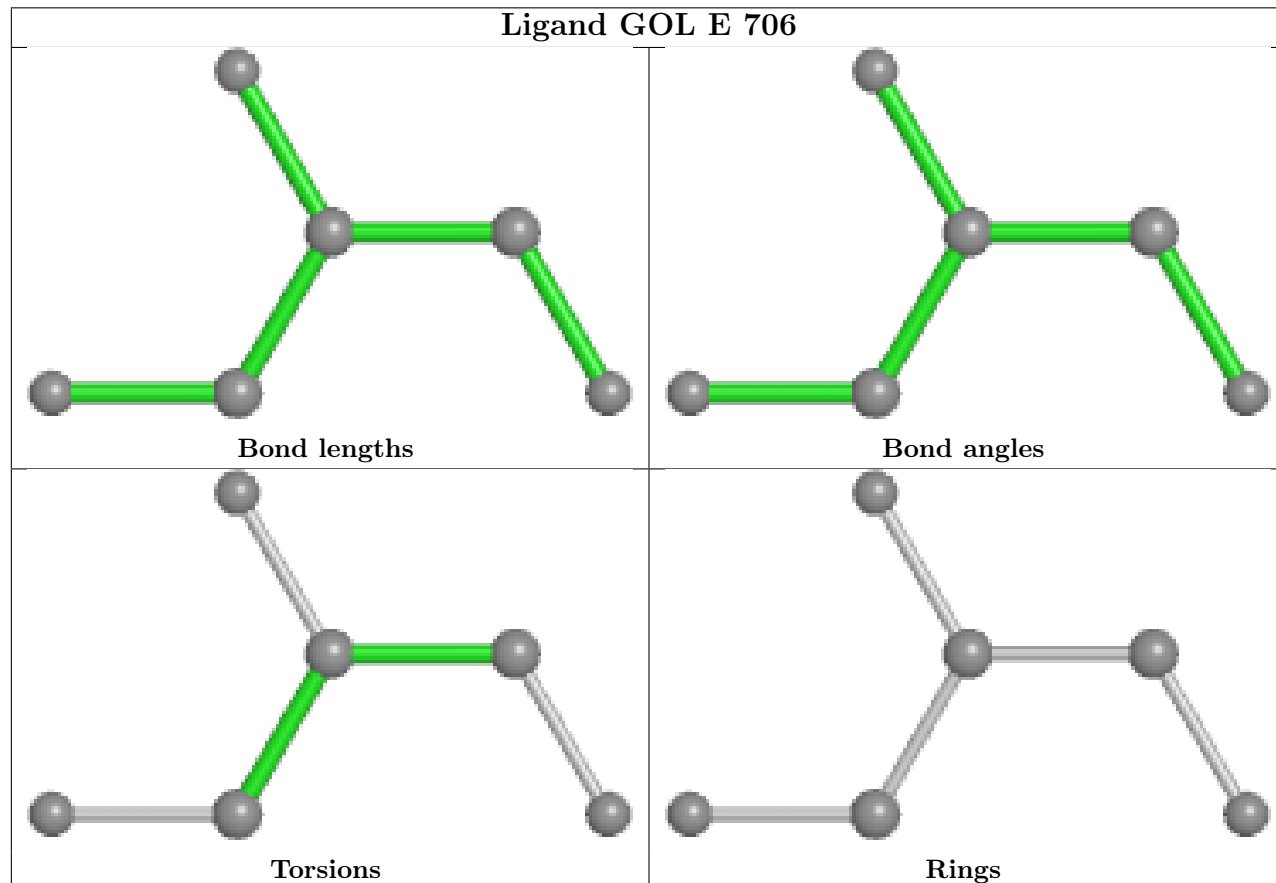
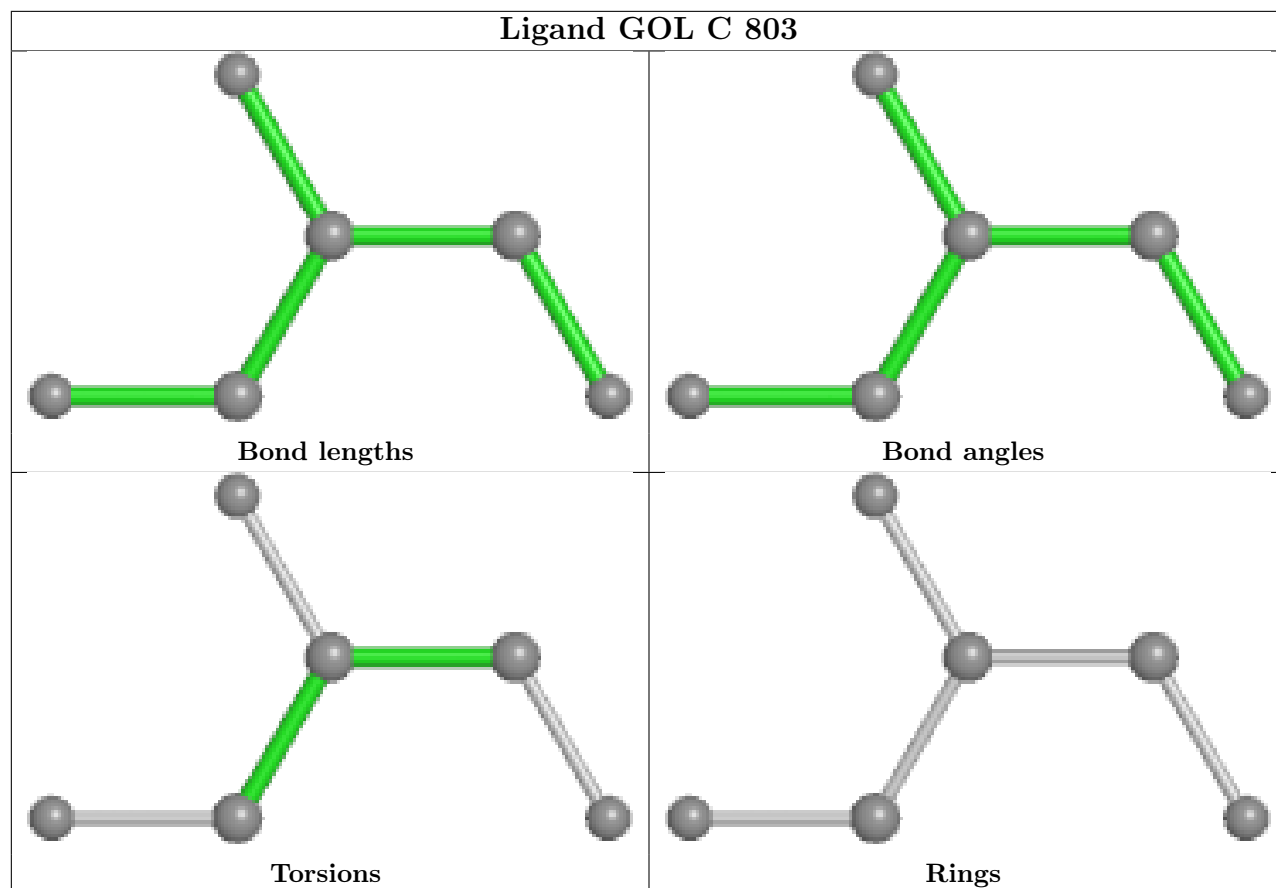


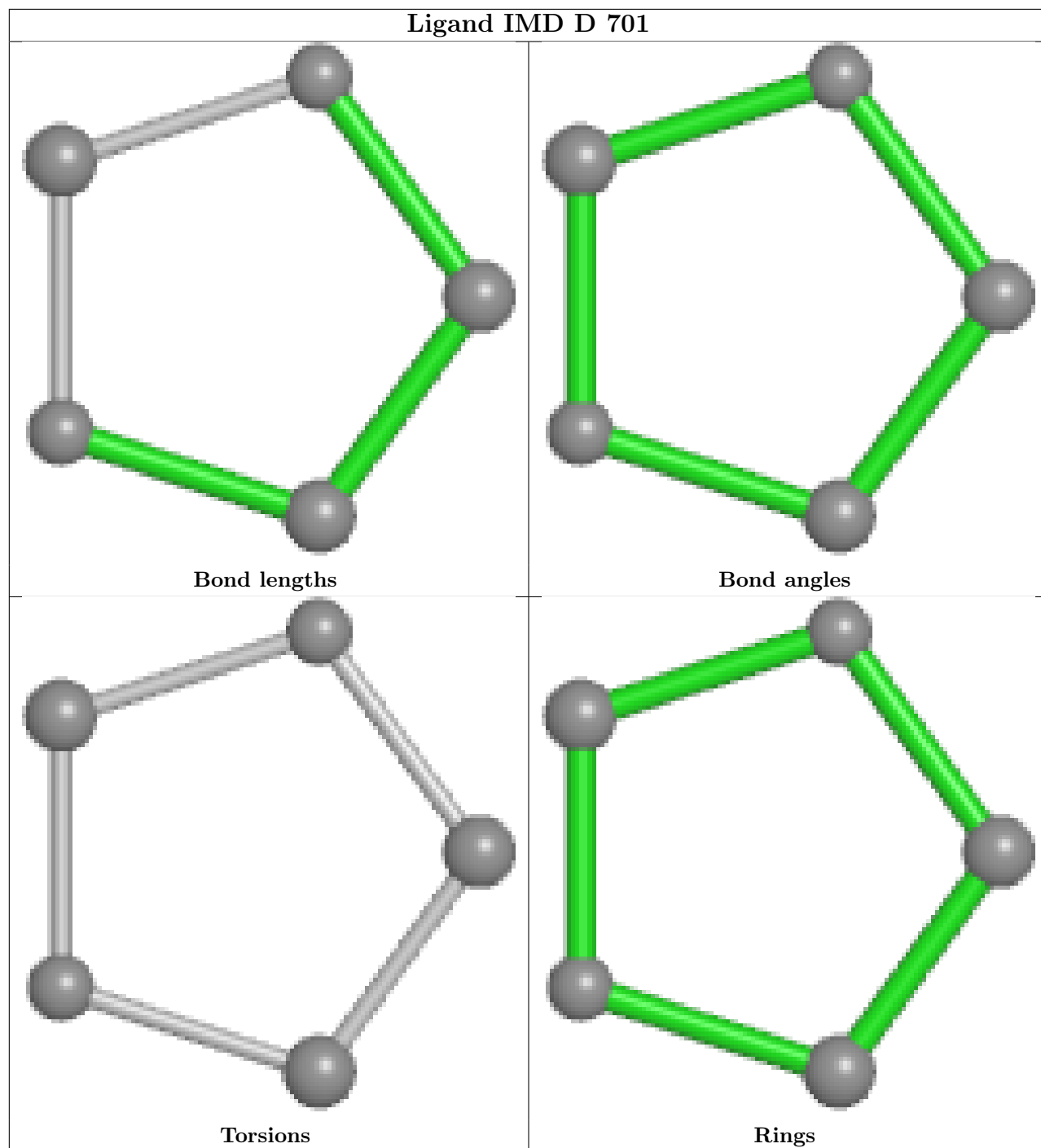


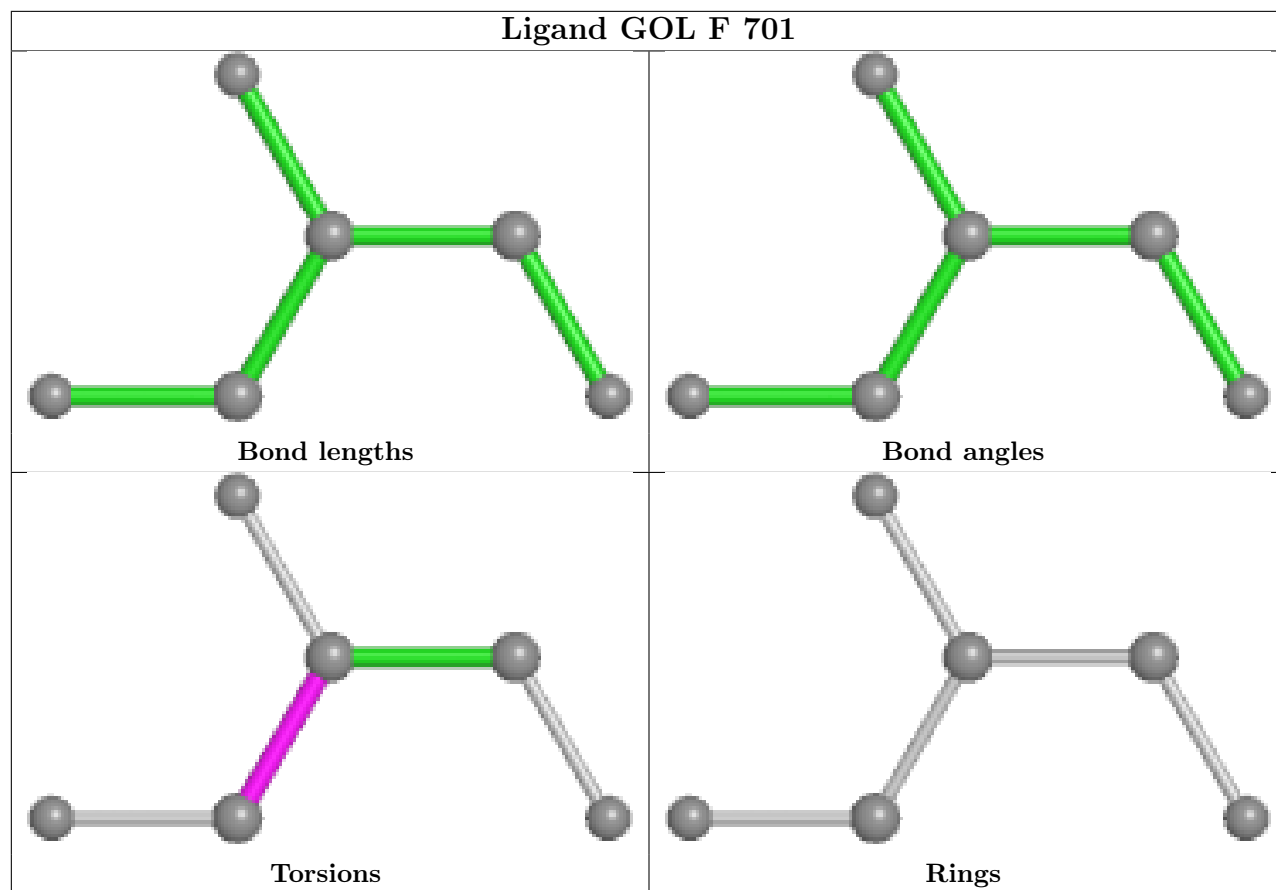


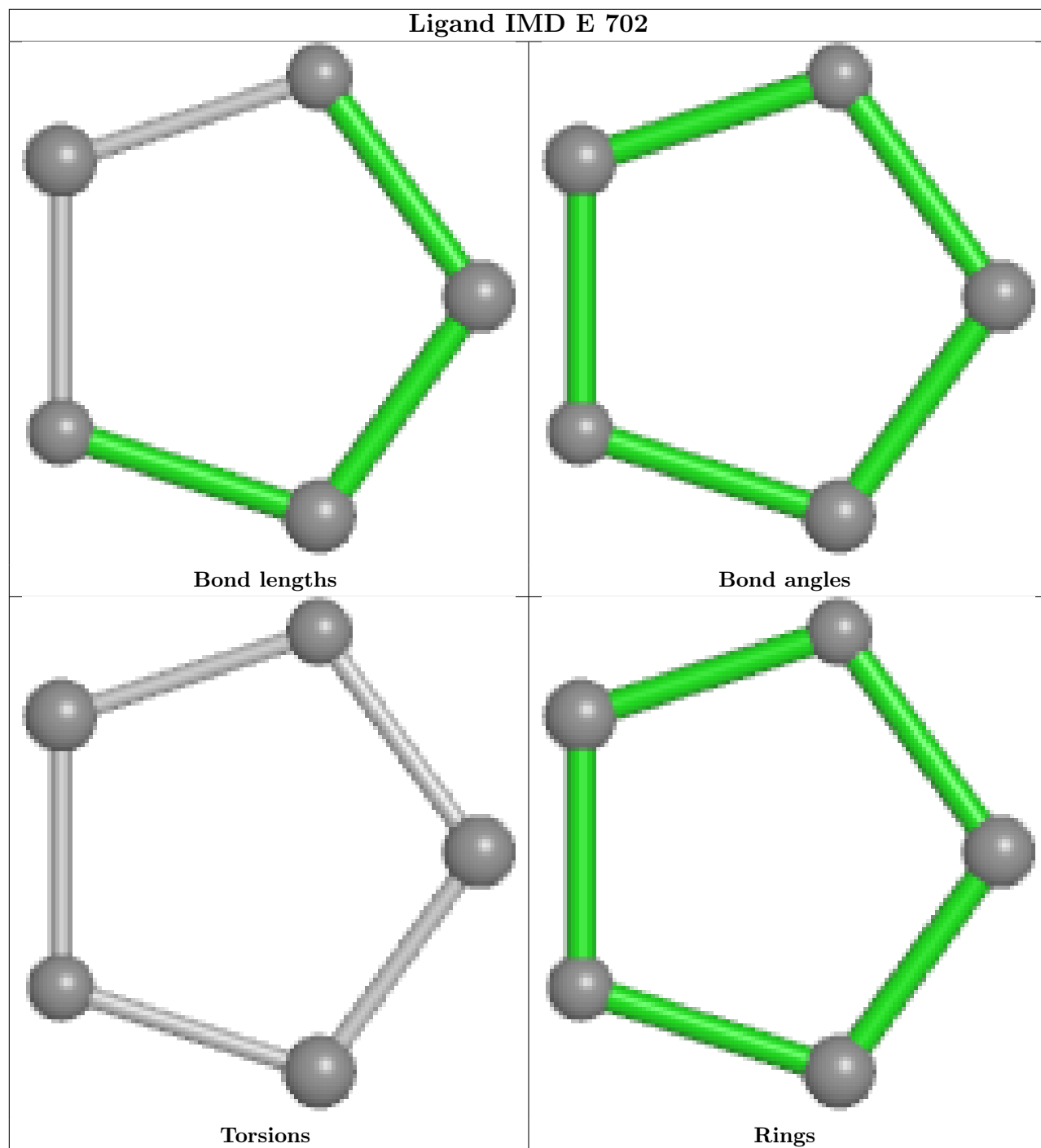


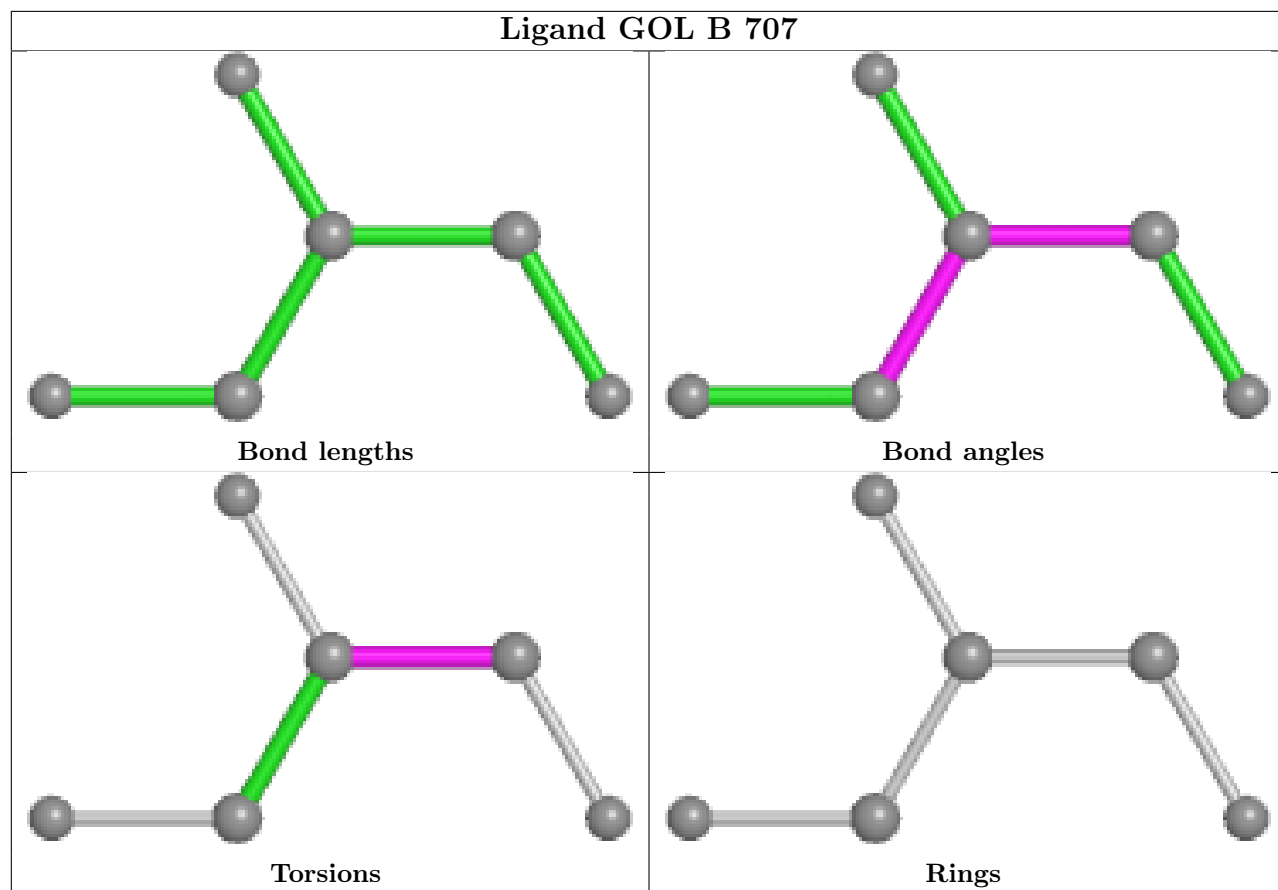


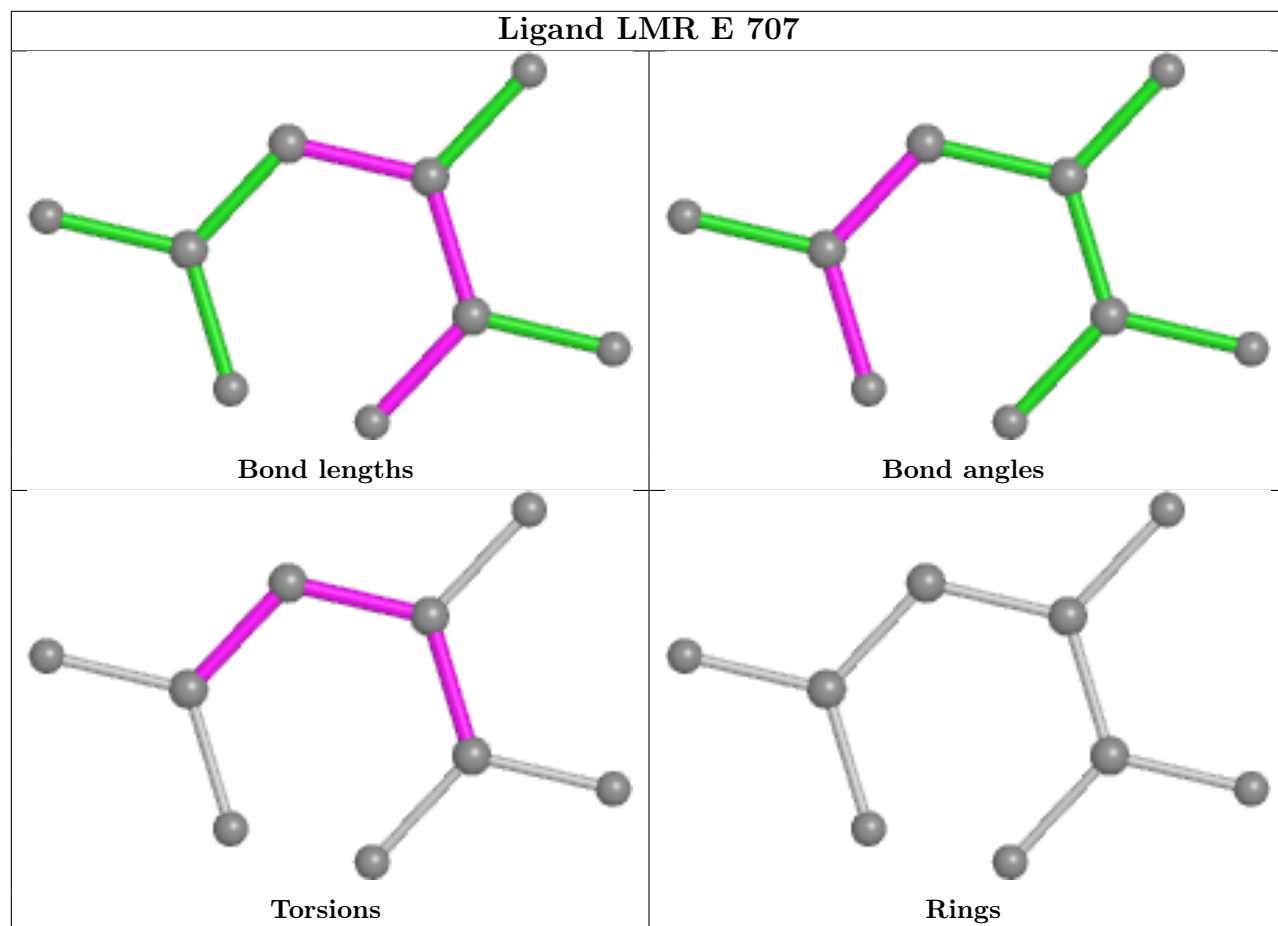


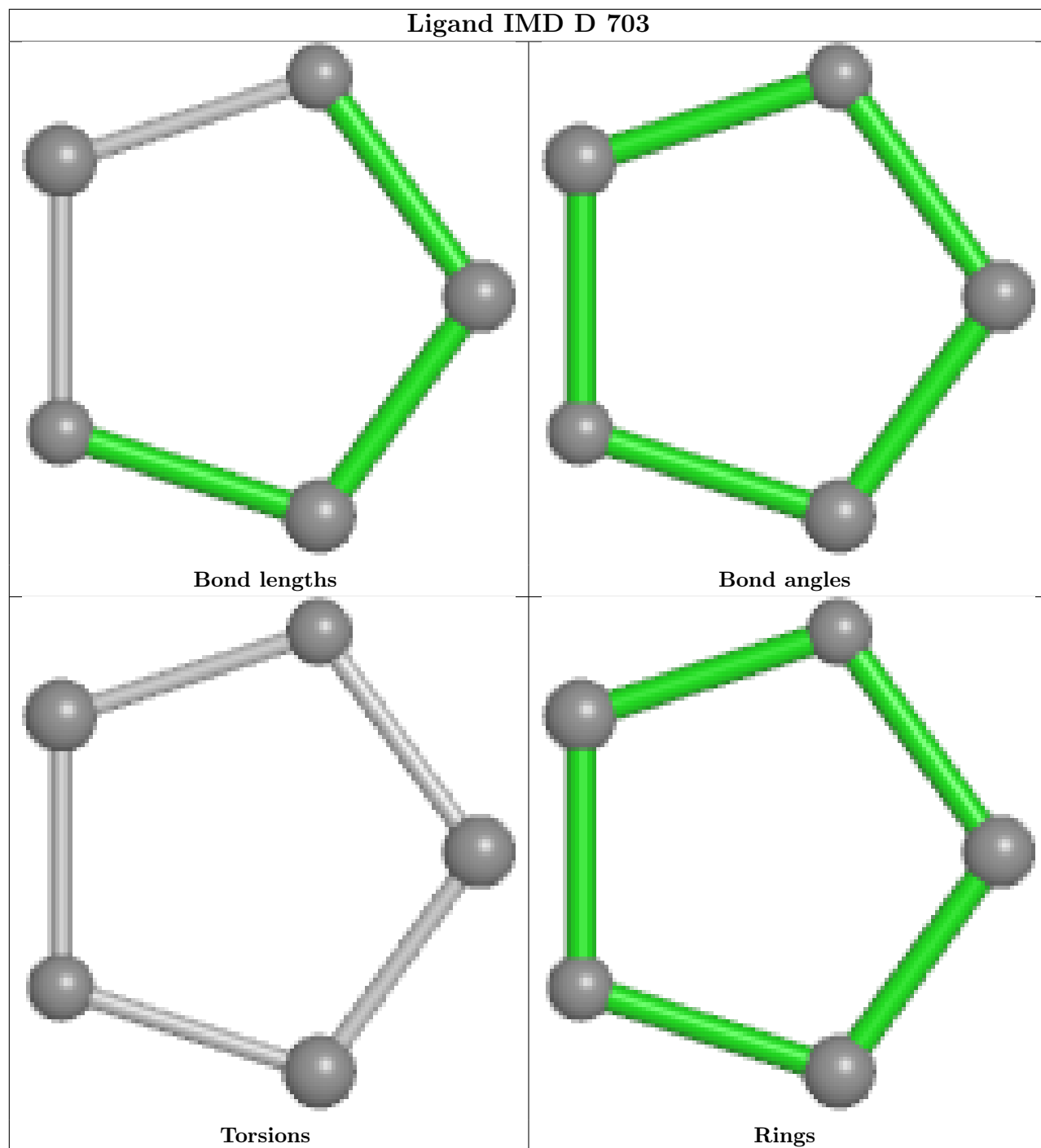


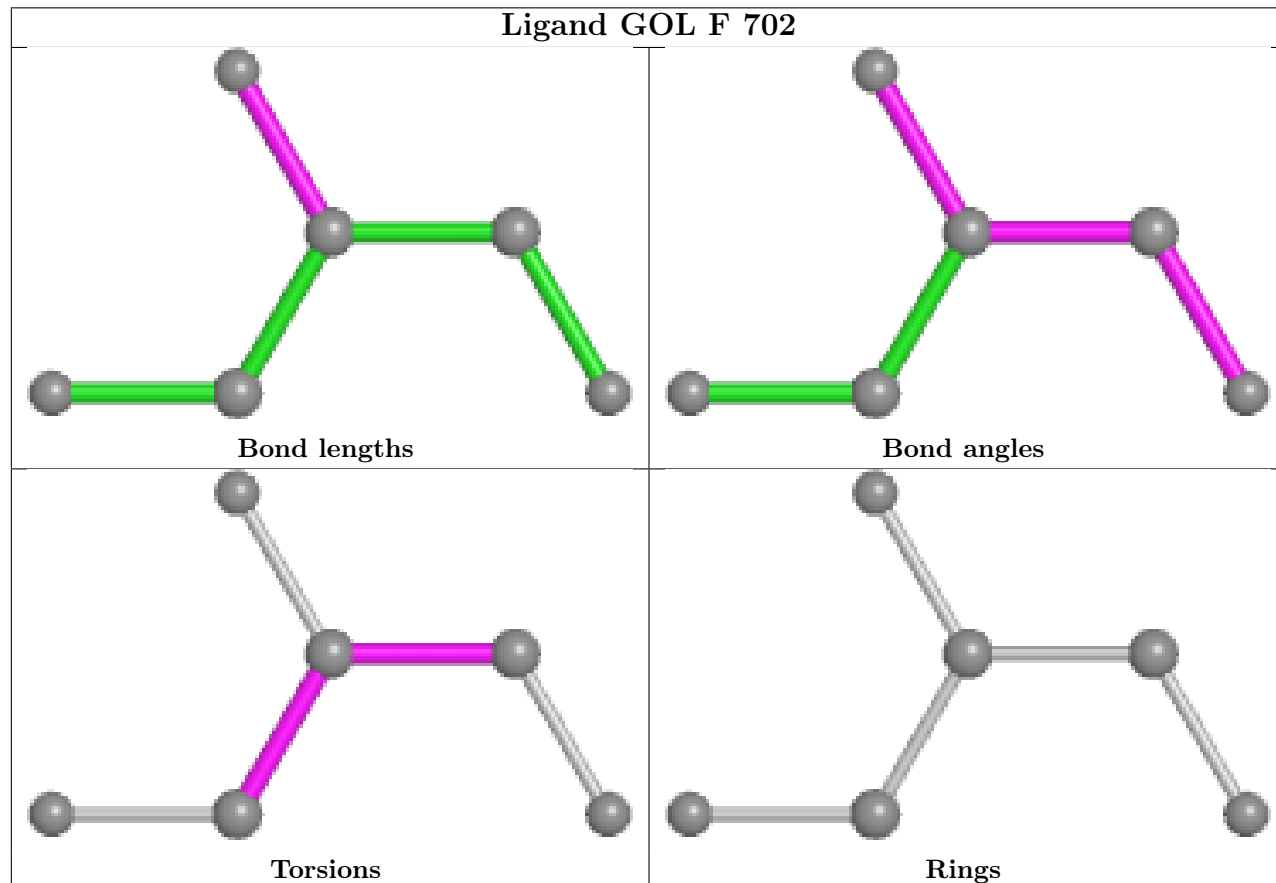
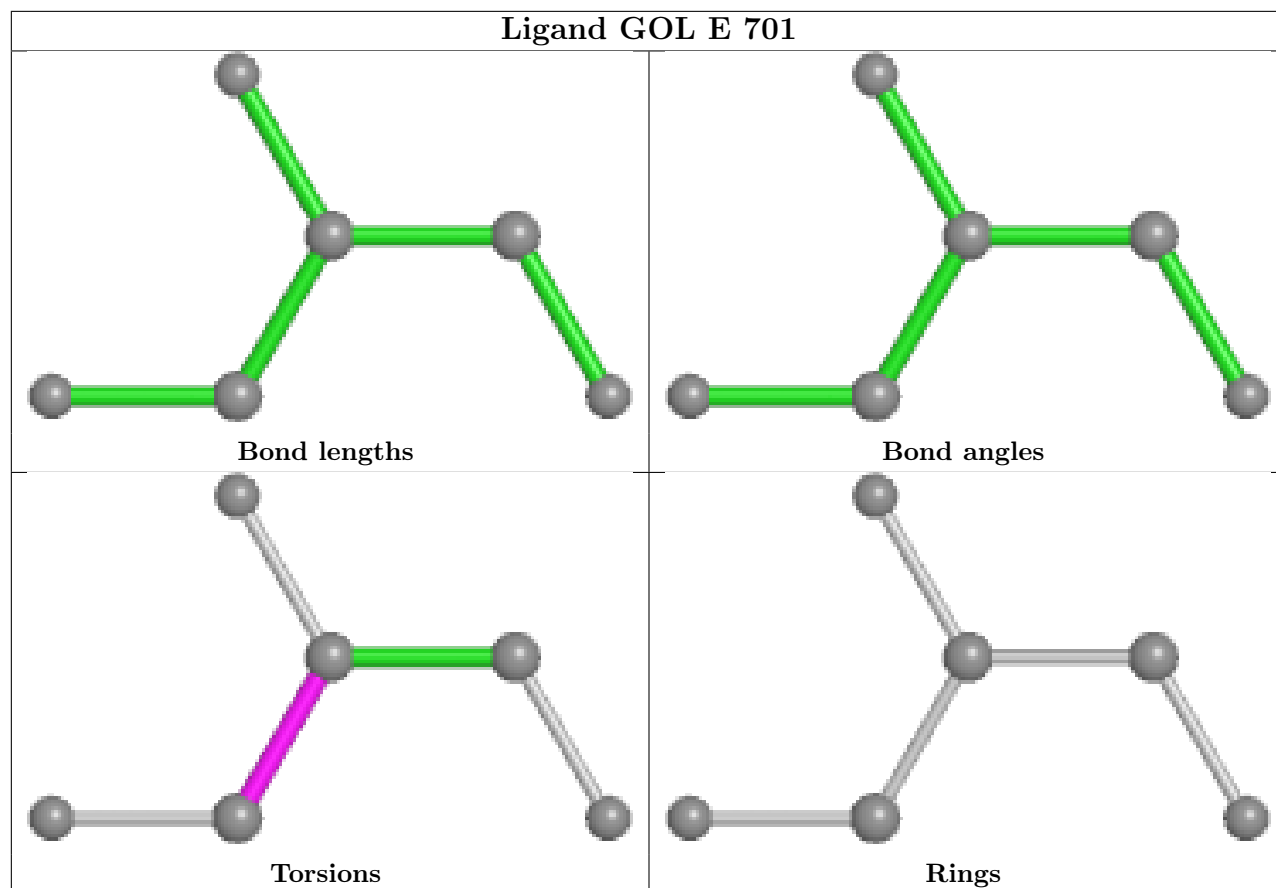


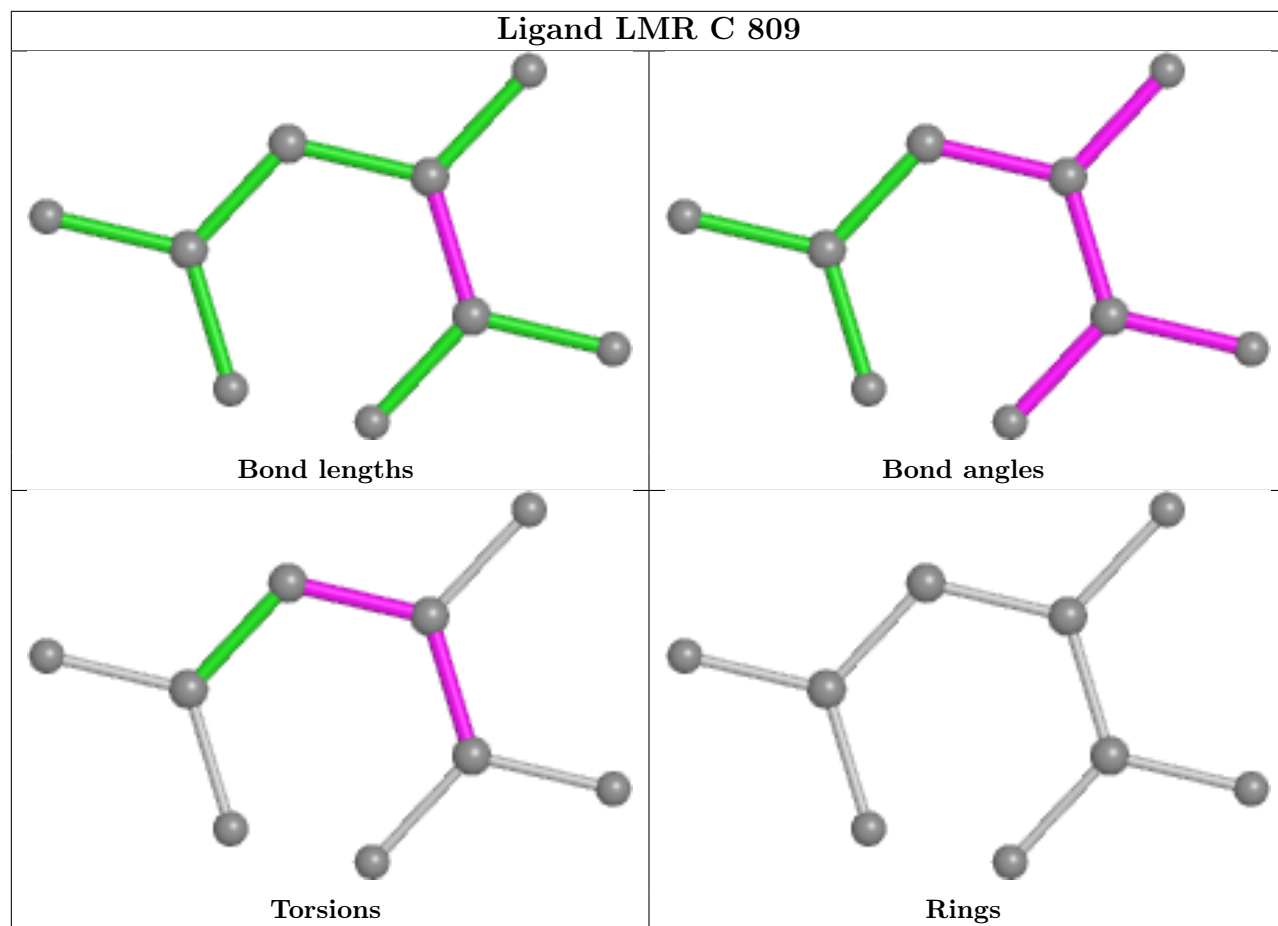


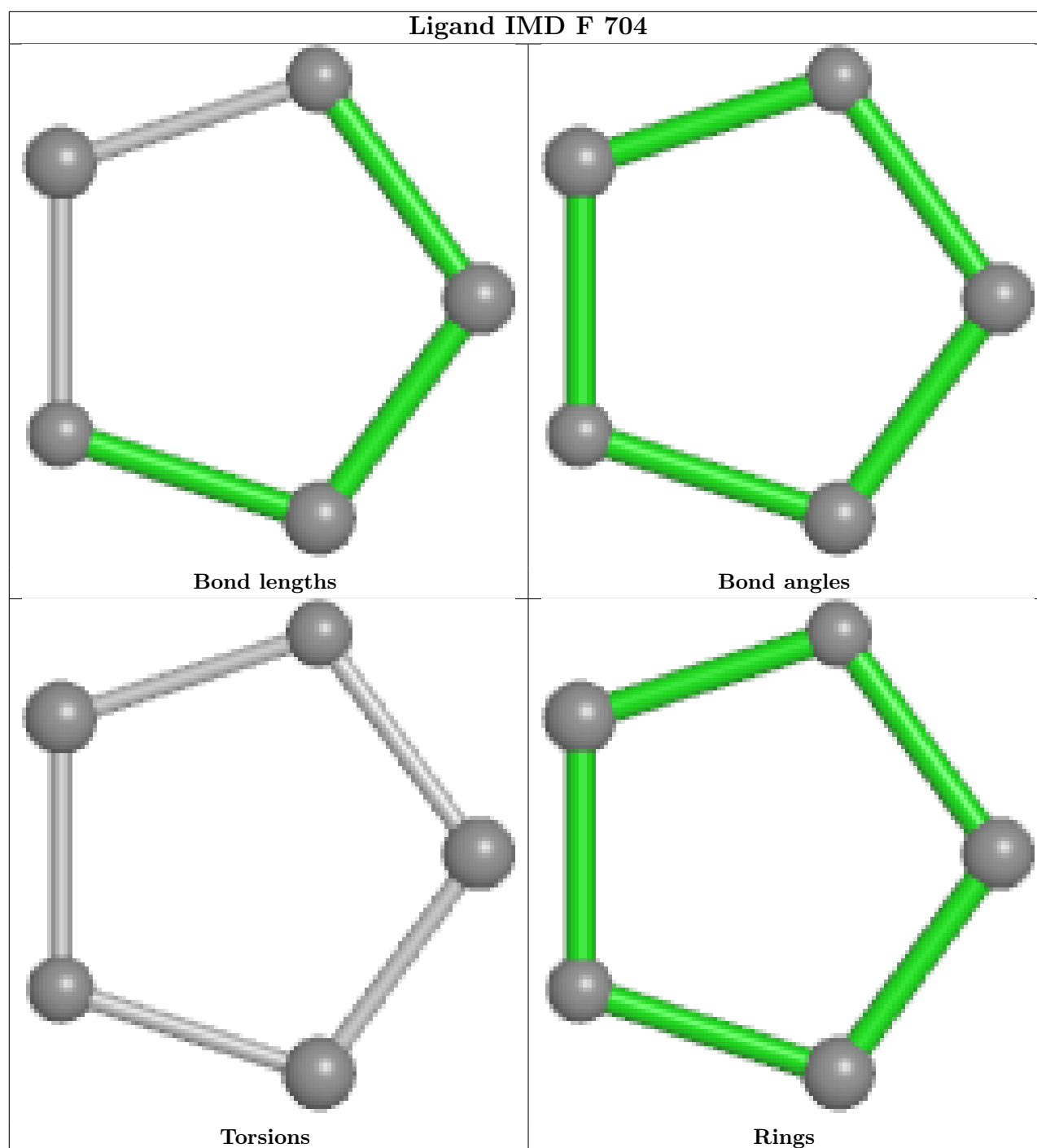












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	642/671 (95%)	0.04	11 (1%) 69 71	6, 20, 34, 68	5 (0%)
1	B	634/671 (94%)	0.08	24 (3%) 44 48	8, 20, 45, 102	3 (0%)
1	C	640/671 (95%)	0.16	21 (3%) 49 52	8, 21, 49, 79	2 (0%)
1	D	622/671 (92%)	-0.13	14 (2%) 61 64	8, 16, 33, 74	2 (0%)
1	E	644/671 (95%)	-0.08	8 (1%) 76 79	5, 17, 33, 76	4 (0%)
1	F	642/671 (95%)	-0.12	9 (1%) 73 76	7, 17, 41, 80	4 (0%)
All	All	3824/4026 (94%)	-0.01	87 (2%) 61 64	5, 18, 40, 102	20 (0%)

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	16	LEU	7.8
1	E	274	ILE	6.6
1	F	622	VAL	5.9
1	B	37	ALA	5.3
1	C	27	VAL	5.2

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands

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

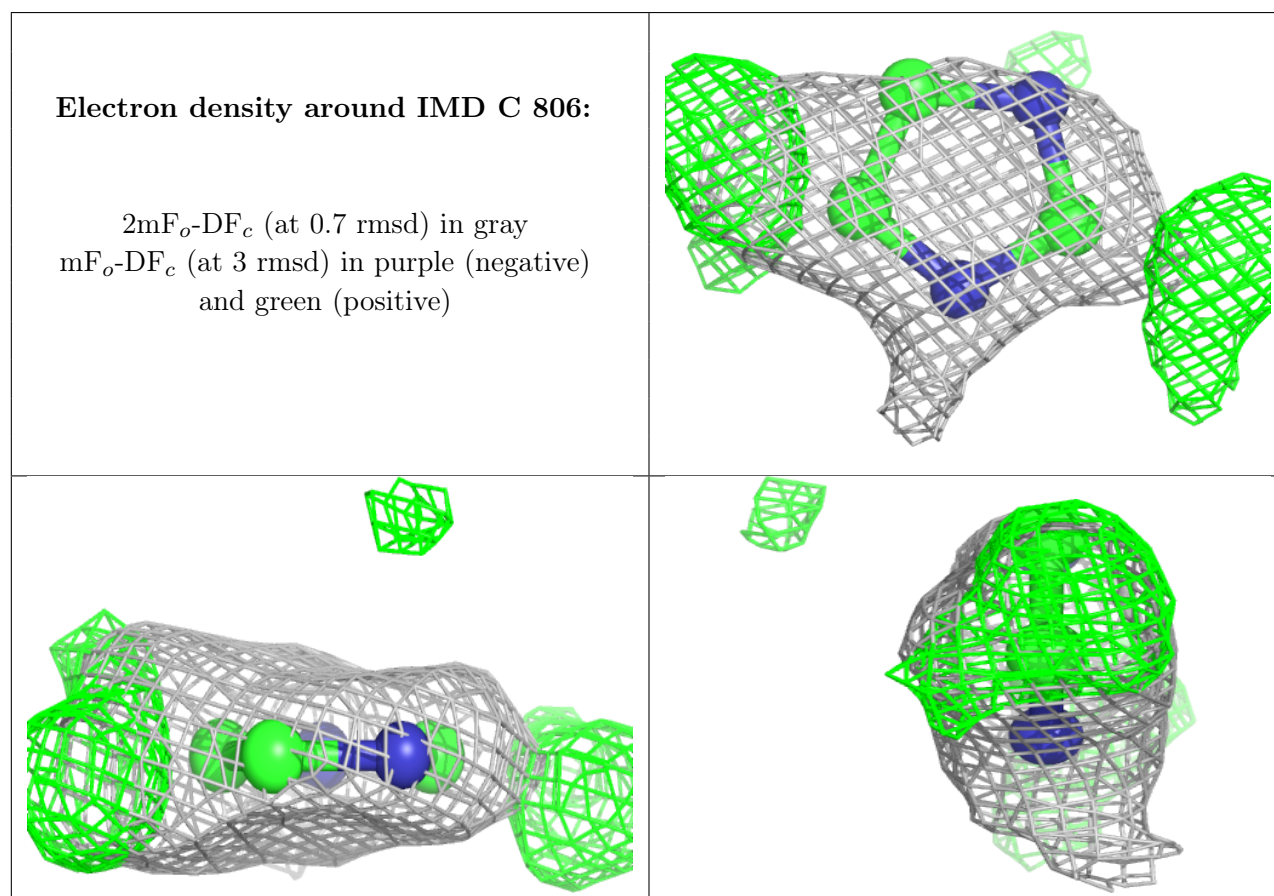
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	IMD	C	806	5/5	0.60	0.20	41,44,49,56	0
3	IMD	E	708	5/5	0.60	0.20	47,49,53,54	0
3	IMD	F	709	5/5	0.68	0.19	25,34,40,44	0
3	IMD	B	708	5/5	0.74	0.20	26,27,45,47	0
3	IMD	B	705	5/5	0.74	0.14	35,42,44,45	0
3	IMD	A	804	5/5	0.78	0.14	37,44,45,46	0
3	IMD	C	805	5/5	0.80	0.14	28,33,40,41	0
3	IMD	A	802	5/5	0.81	0.17	44,47,66,73	0
3	IMD	F	704	5/5	0.81	0.14	37,41,45,53	0
3	IMD	D	706	5/5	0.81	0.16	39,42,45,47	0
3	IMD	E	704	5/5	0.83	0.13	21,26,44,45	0
3	IMD	F	703	5/5	0.84	0.11	33,33,39,42	0
3	IMD	F	705	5/5	0.86	0.12	23,33,43,44	0
3	IMD	C	804	5/5	0.86	0.11	31,36,38,40	0
3	IMD	B	704	5/5	0.87	0.12	35,41,45,47	0
4	GOL	C	802	6/6	0.87	0.14	24,36,50,57	0
4	GOL	B	707	6/6	0.88	0.11	23,29,35,50	0
3	IMD	B	706	5/5	0.88	0.12	26,31,40,48	0
4	GOL	D	705	6/6	0.88	0.14	26,32,34,37	0
4	GOL	F	701	6/6	0.88	0.12	19,28,30,31	0
4	GOL	E	703	6/6	0.89	0.11	20,27,40,44	0
4	GOL	F	702	6/6	0.89	0.12	25,29,40,45	0
3	IMD	C	808	5/5	0.90	0.12	47,50,54,56	0
4	GOL	A	806	6/6	0.90	0.09	23,35,39,49	0
3	IMD	C	810	5/5	0.90	0.10	28,31,40,43	0
3	IMD	D	703	5/5	0.90	0.10	31,34,35,38	0
4	GOL	A	803	6/6	0.91	0.11	25,29,33,35	0
2	LMR	E	707	9/9	0.91	0.11	20,30,41,46	0
2	LMR	F	708	9/9	0.91	0.09	22,26,29,30	0
2	LMR	B	703	9/9	0.91	0.11	19,25,48,56	0
3	IMD	E	702	5/5	0.92	0.09	26,30,33,36	0
3	IMD	A	805	5/5	0.92	0.10	23,29,43,47	0
4	GOL	E	701	6/6	0.92	0.10	22,30,34,42	0
4	GOL	F	706	6/6	0.92	0.12	21,27,30,35	0
3	IMD	E	705	5/5	0.93	0.12	22,29,45,45	0
4	GOL	C	807	6/6	0.93	0.09	28,36,40,47	0
2	LMR	D	702	9/9	0.93	0.09	23,30,43,44	0

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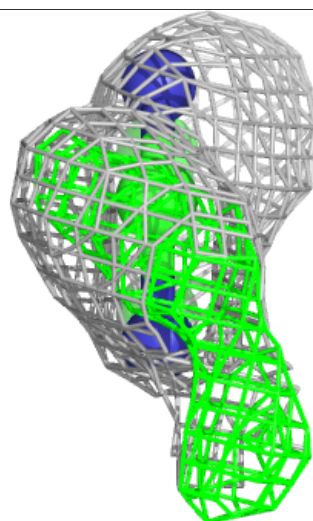
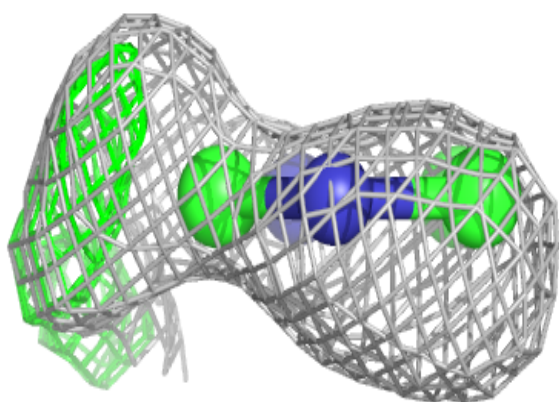
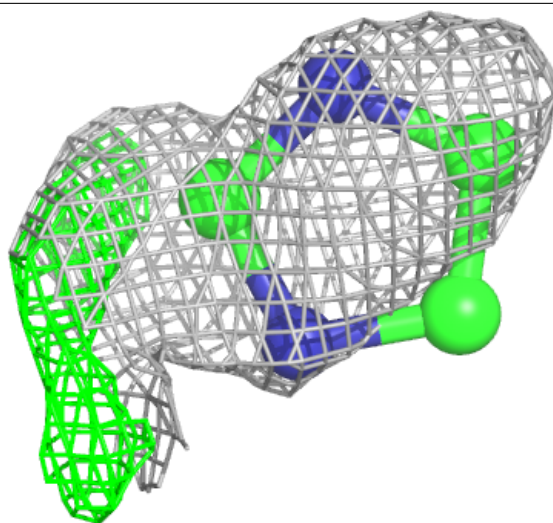
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IMD	D	701	5/5	0.93	0.09	23,28,37,43	0
4	GOL	B	701	6/6	0.94	0.09	25,28,31,41	0
4	GOL	D	704	6/6	0.94	0.09	19,20,24,30	0
2	LMR	A	801	9/9	0.94	0.08	25,31,45,50	0
2	LMR	C	809	9/9	0.94	0.08	26,30,45,51	0
4	GOL	D	707	6/6	0.95	0.09	18,26,28,45	0
4	GOL	C	803	6/6	0.95	0.08	21,23,24,26	0
4	GOL	C	801	6/6	0.95	0.07	24,29,37,46	0
4	GOL	B	702	6/6	0.96	0.08	24,28,31,36	0
2	LMR	F	707	9/9	0.97	0.06	19,26,36,54	0
4	GOL	E	706	6/6	0.98	0.05	17,18,21,22	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.



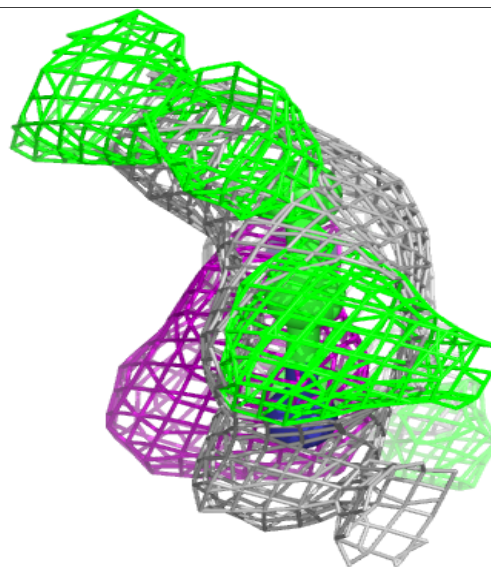
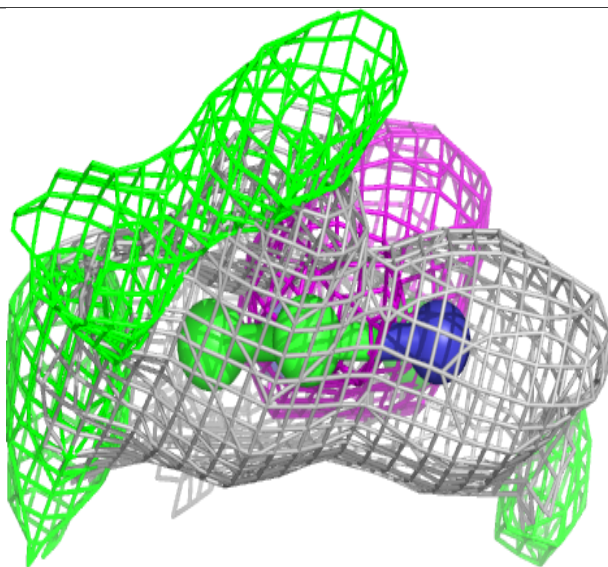
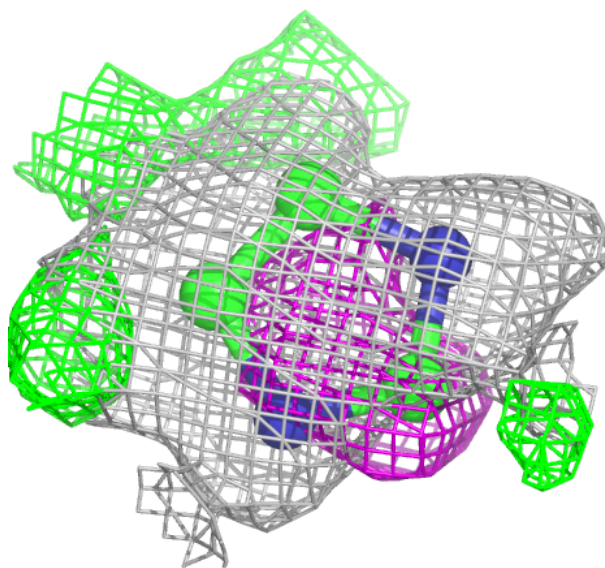
Electron density around IMD E 708:

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



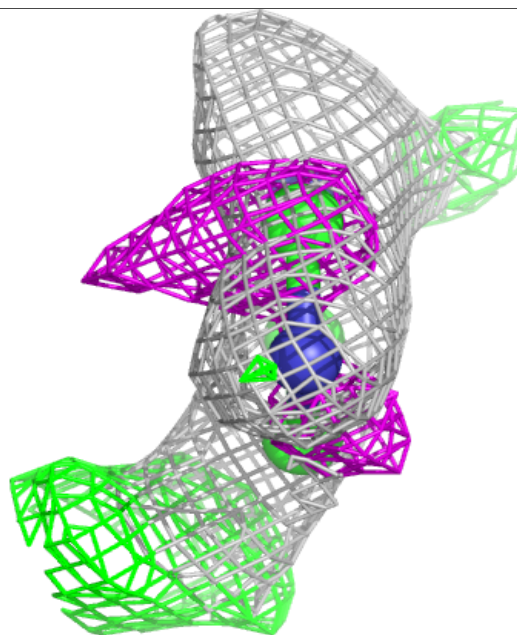
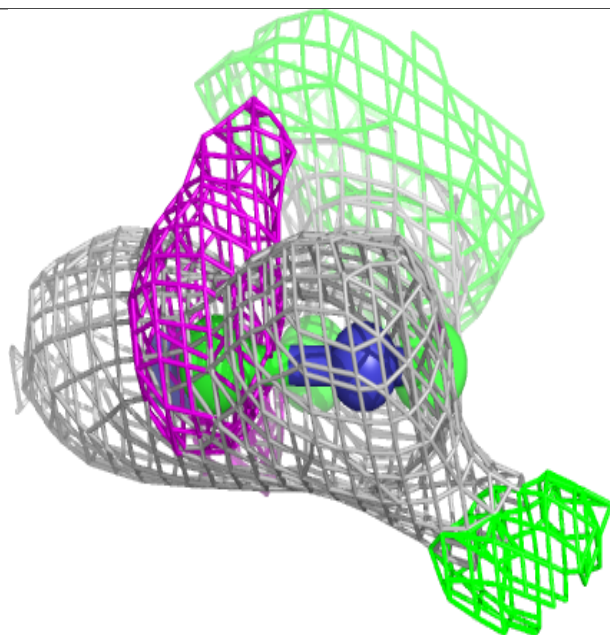
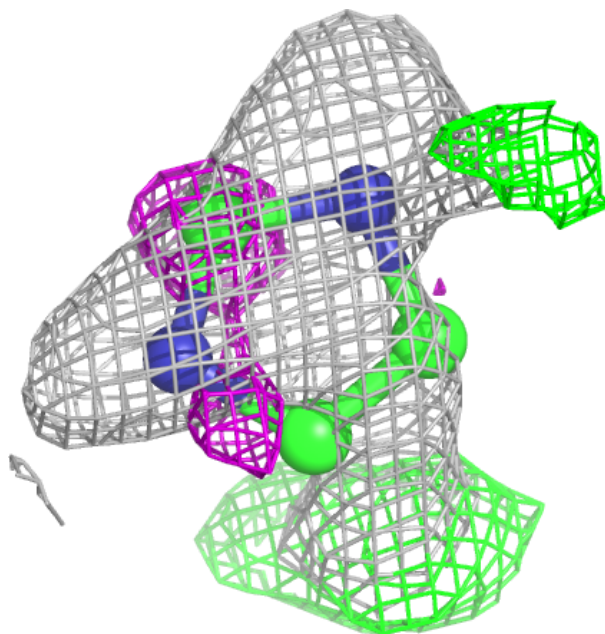
Electron density around IMD F 709:

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



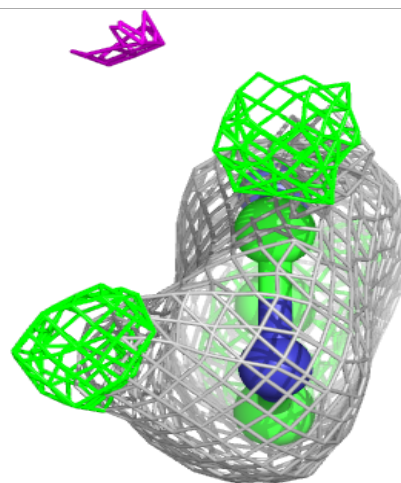
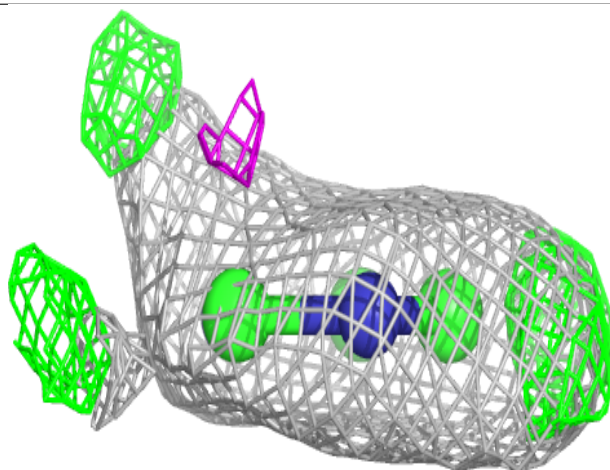
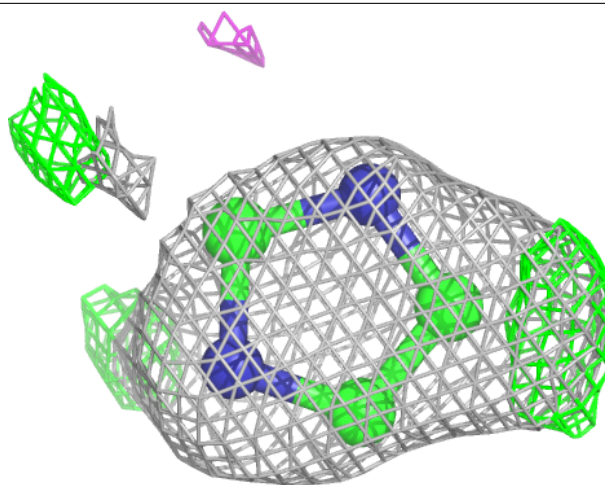
Electron density around IMD B 708:

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



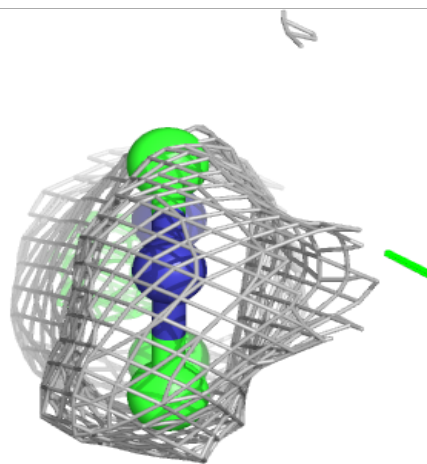
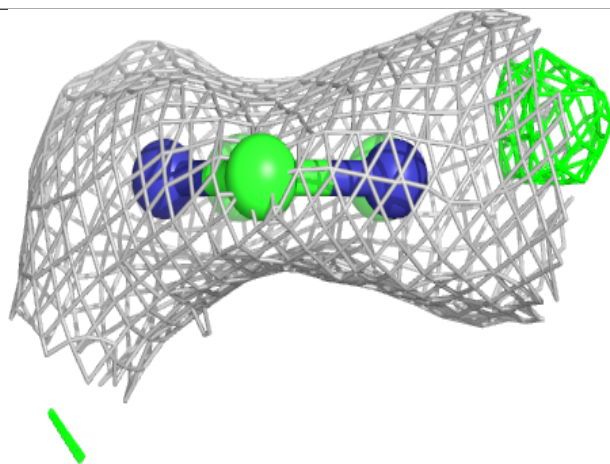
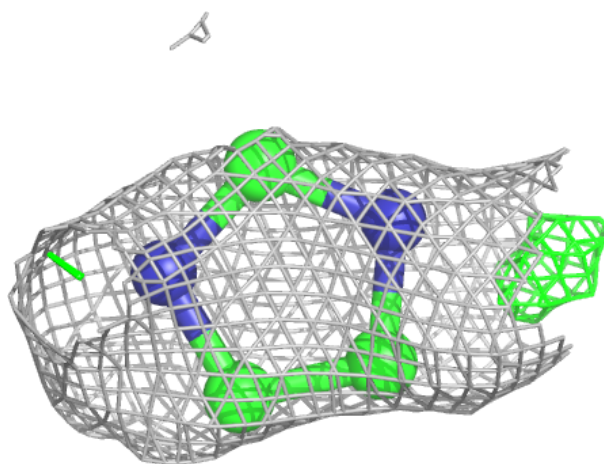
Electron density around IMD B 705:

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



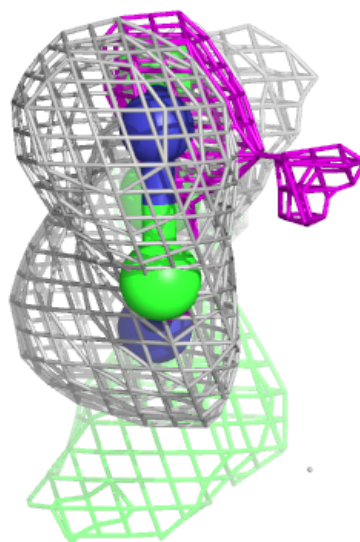
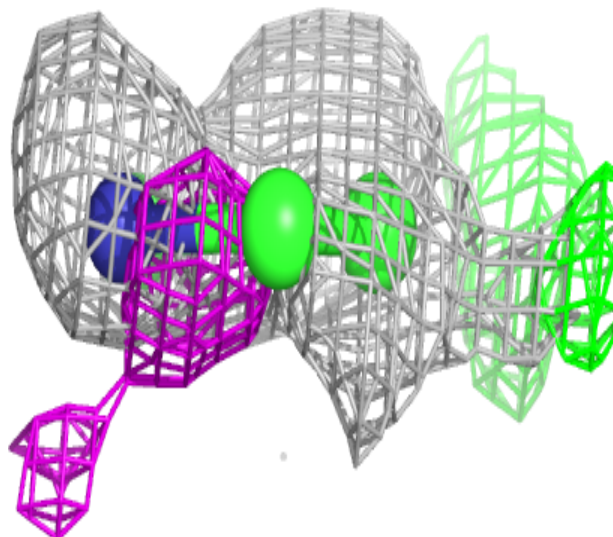
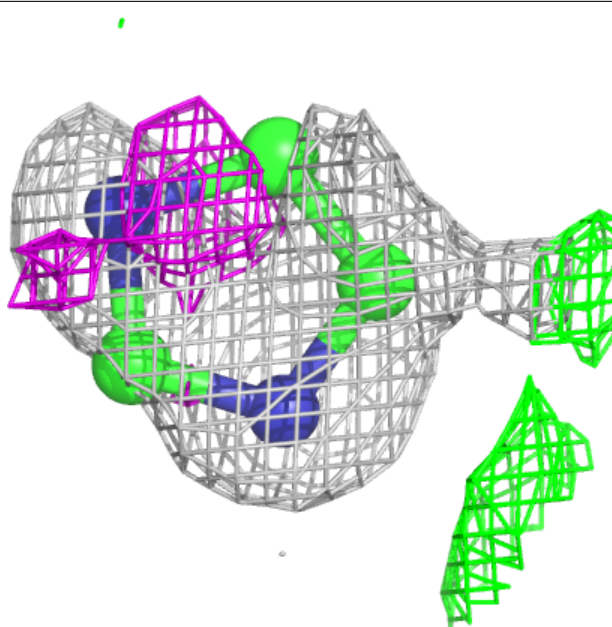
Electron density around IMD A 804:

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



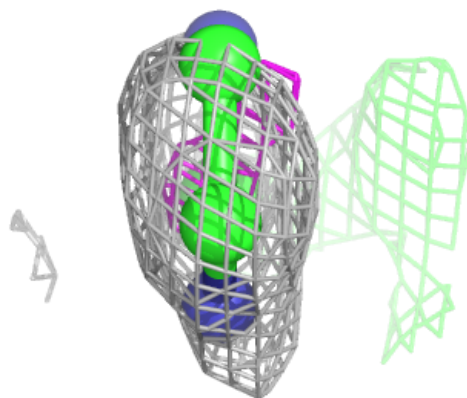
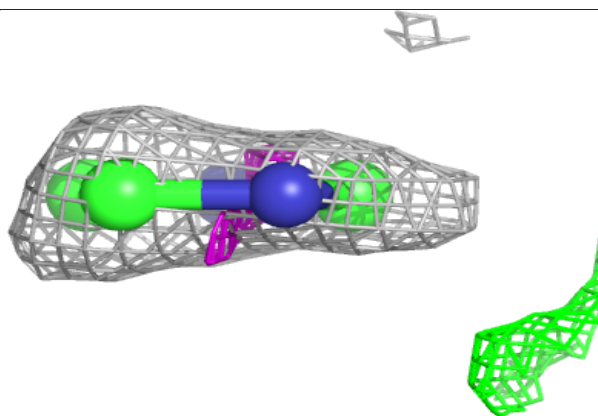
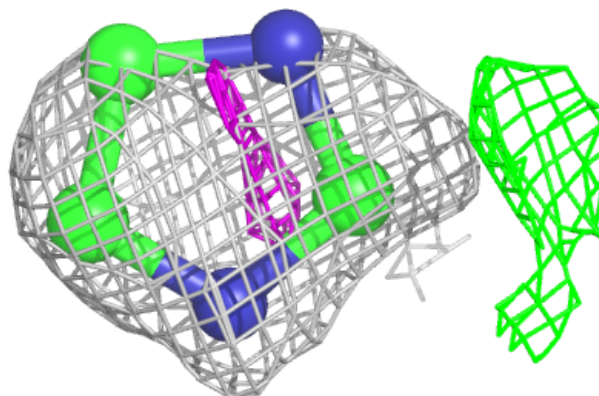
Electron density around IMD C 805:

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



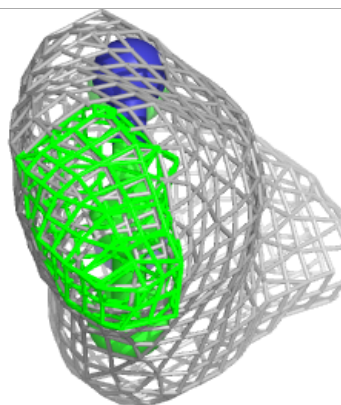
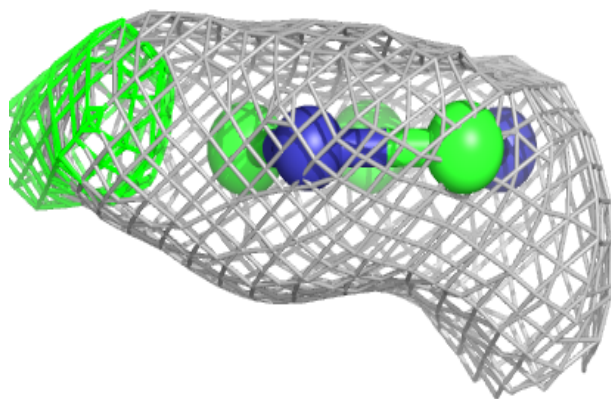
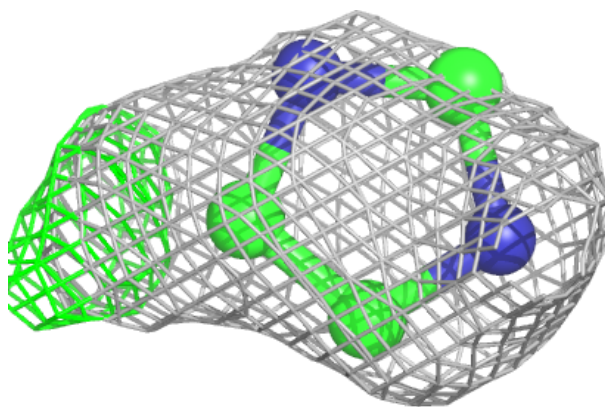
Electron density around IMD A 802:

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



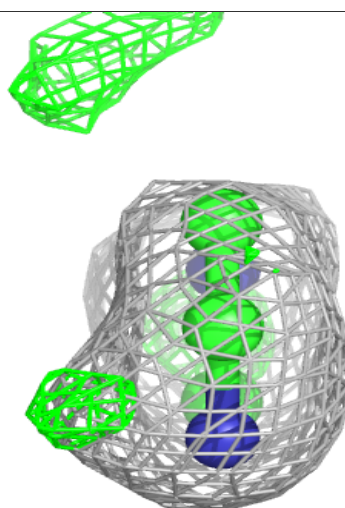
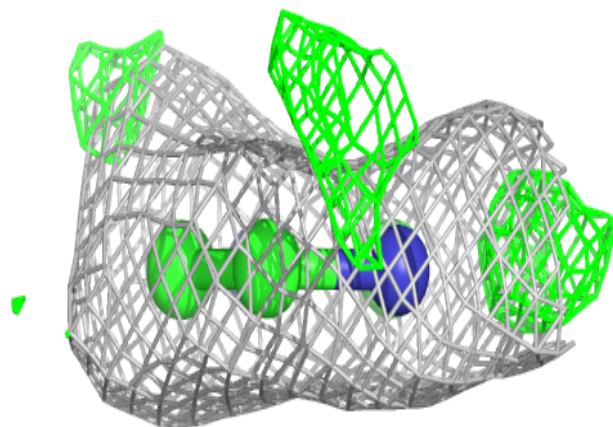
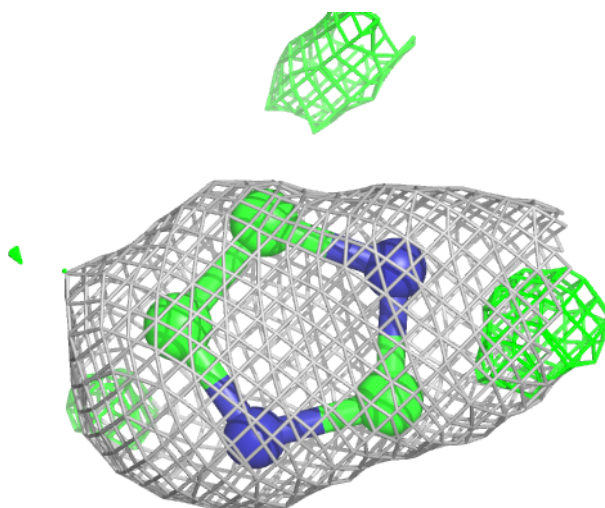
Electron density around IMD F 704:

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



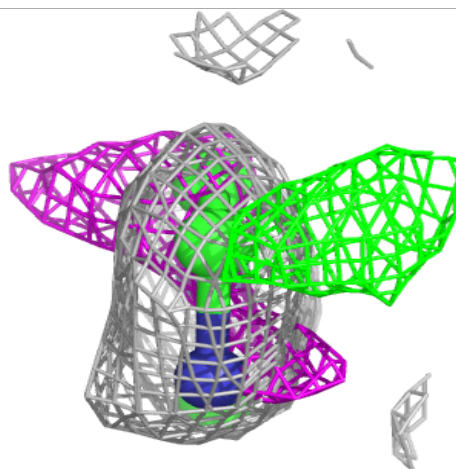
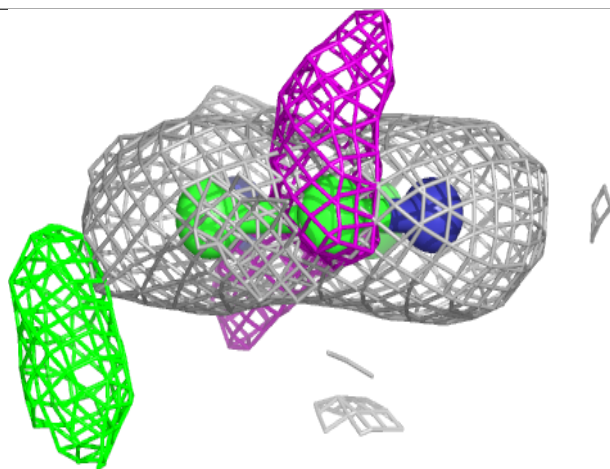
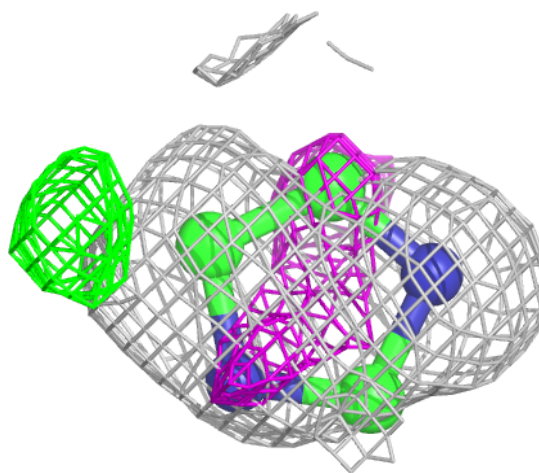
Electron density around IMD D 706:

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



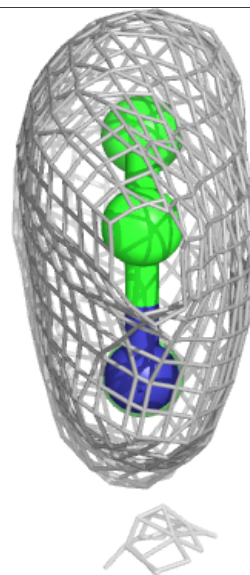
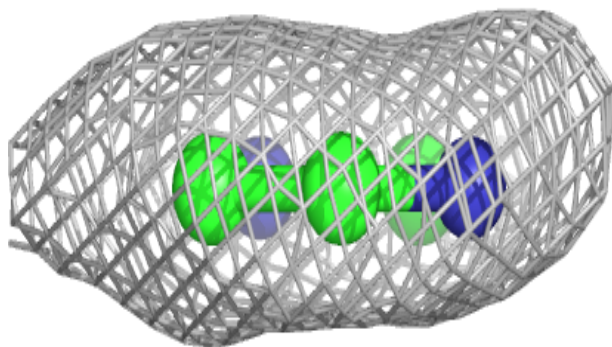
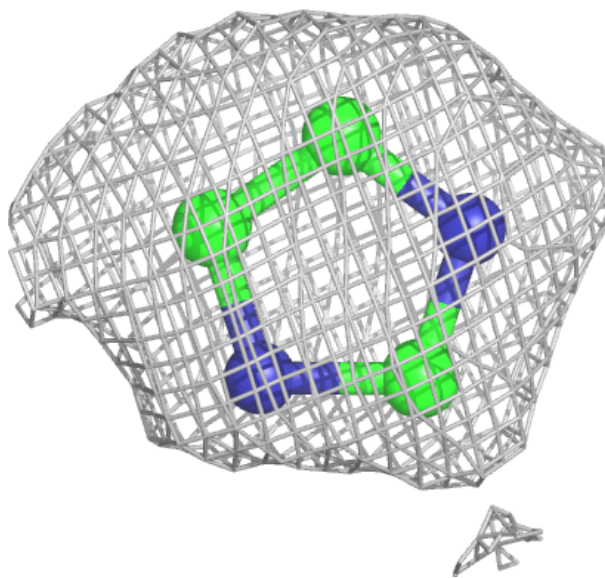
Electron density around IMD E 704:

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



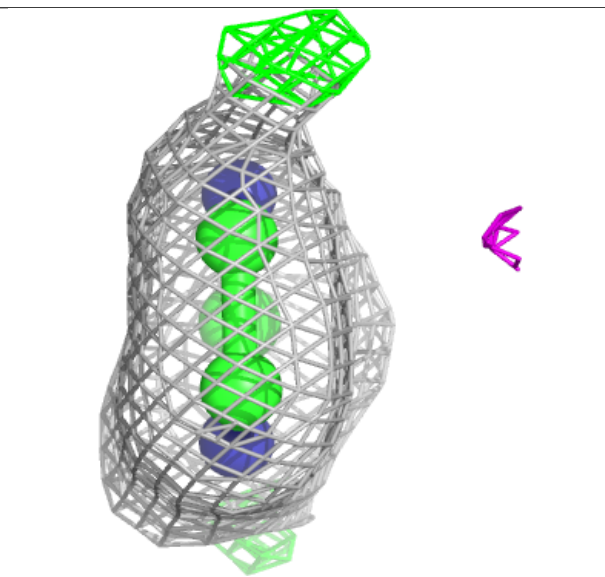
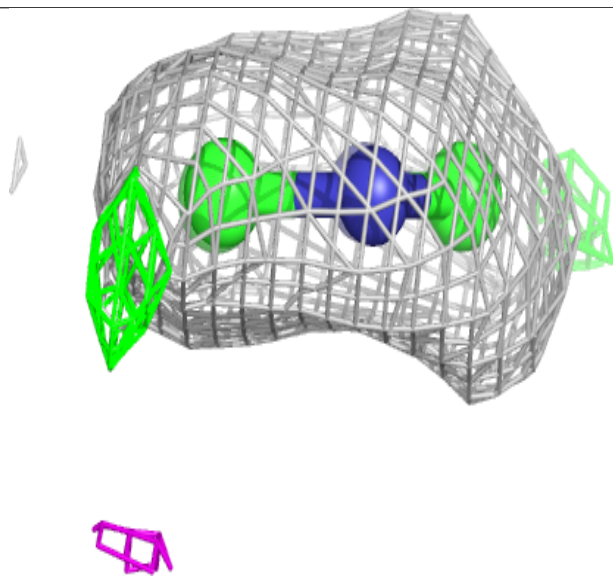
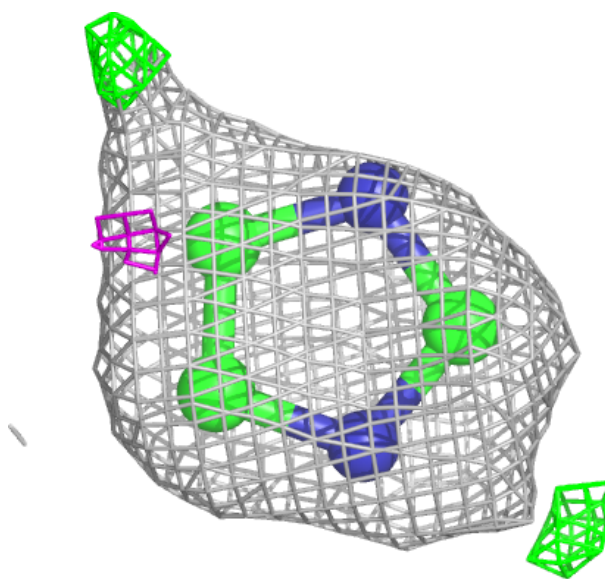
Electron density around IMD F 703:

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



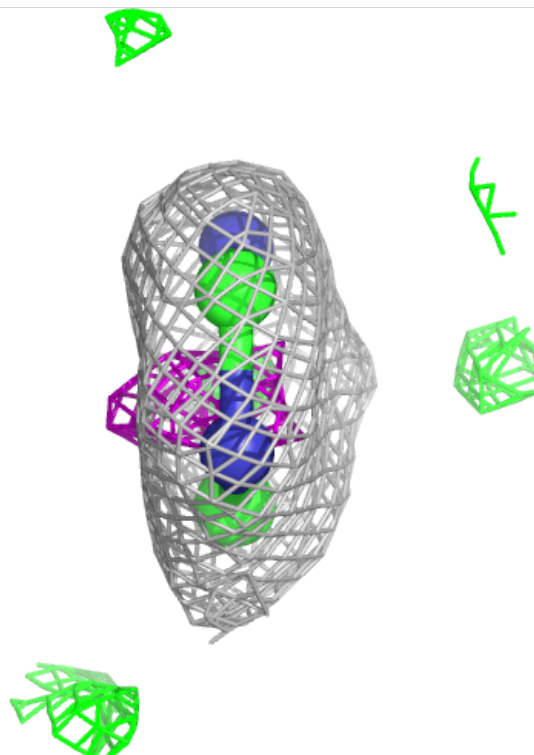
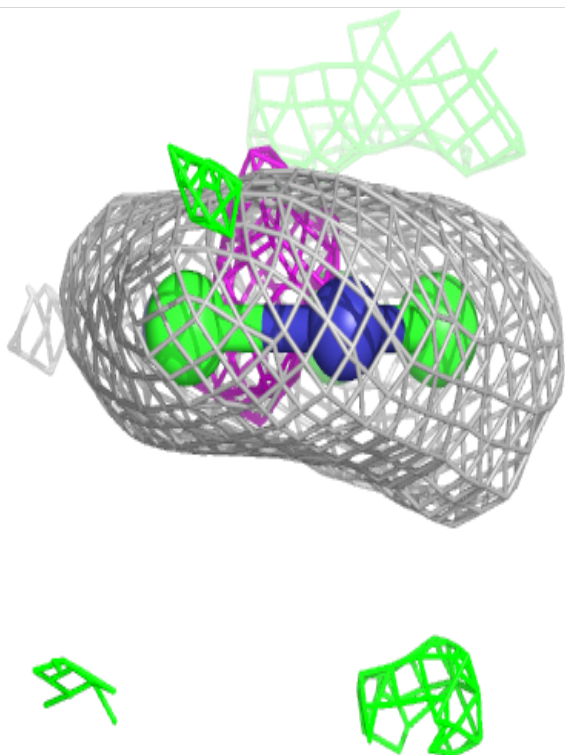
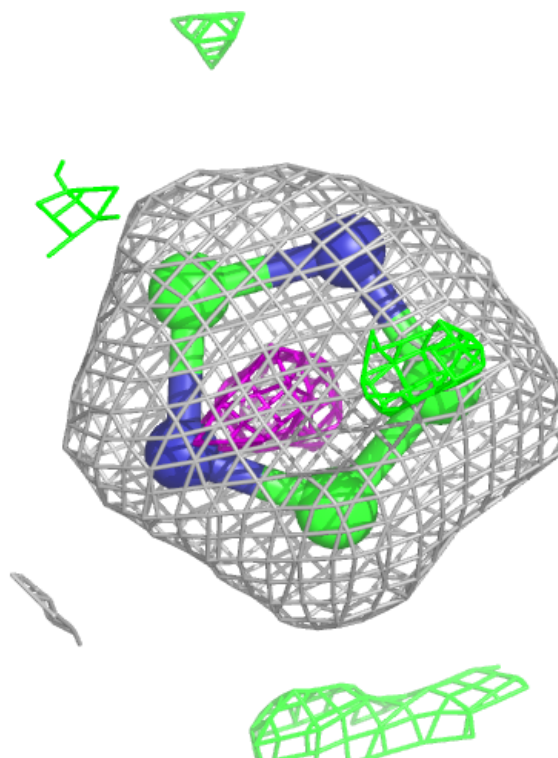
Electron density around IMD F 705:

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



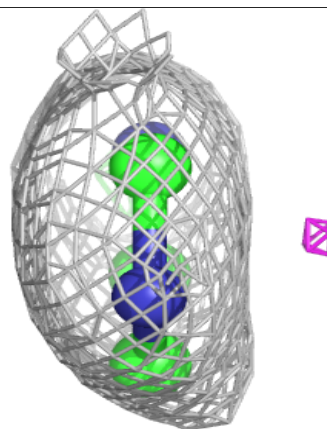
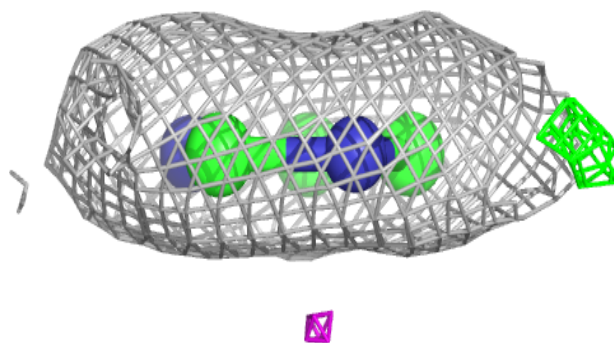
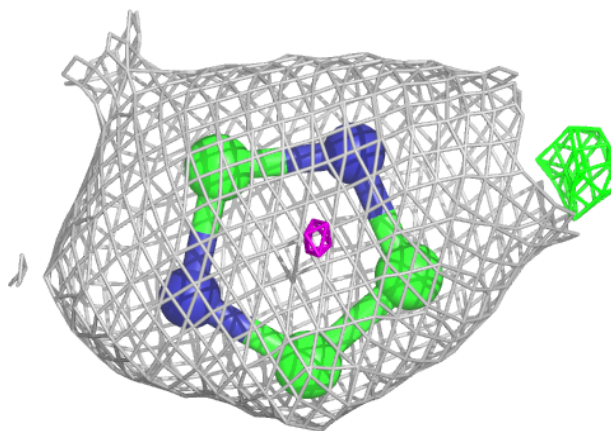
Electron density around IMD C 804:

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



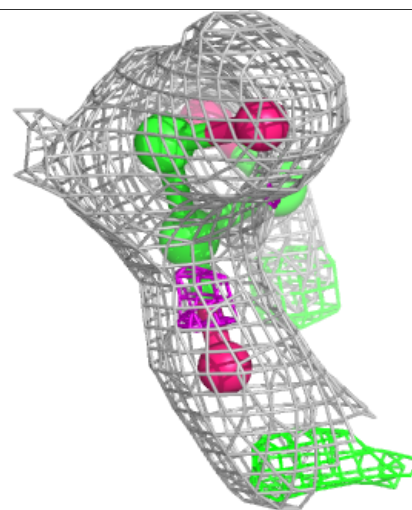
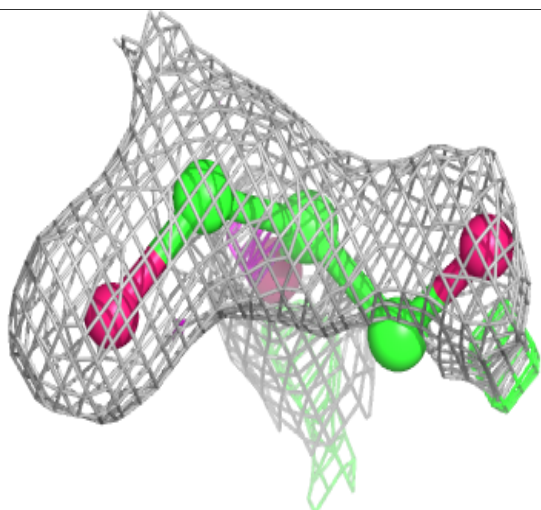
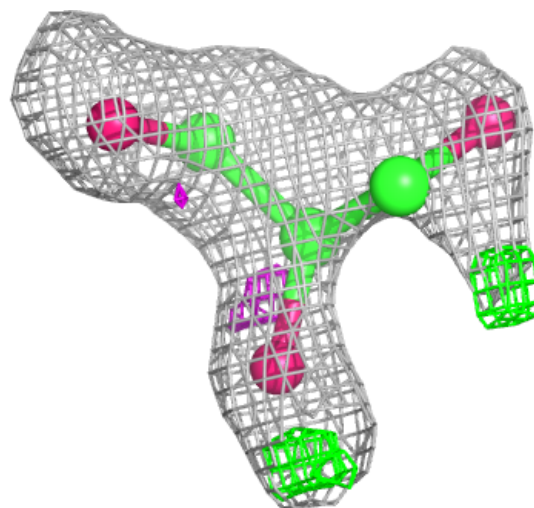
Electron density around IMD B 704:

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



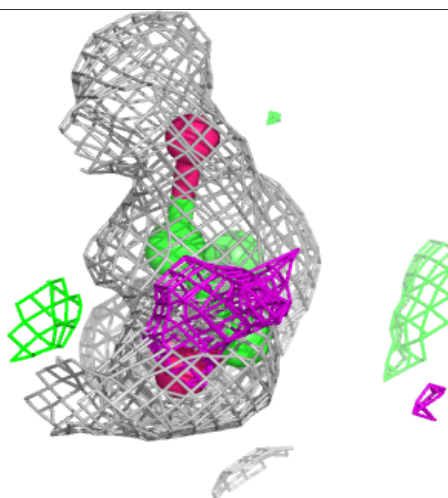
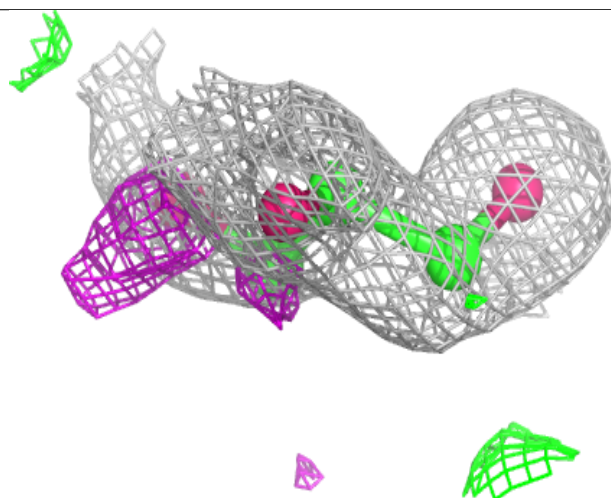
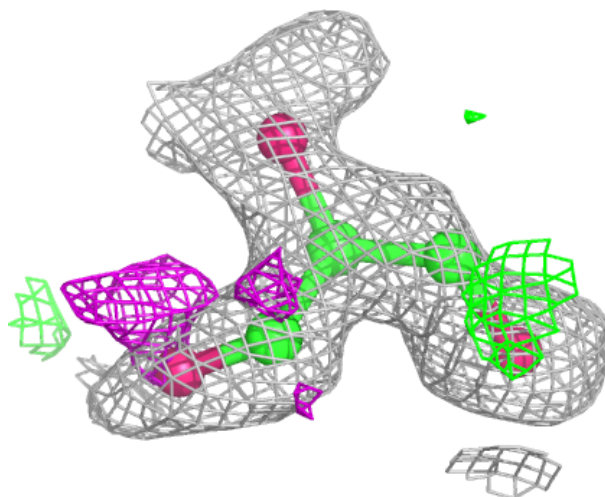
Electron density around GOL C 802:

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



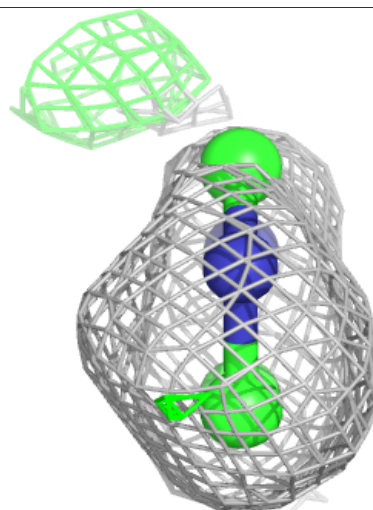
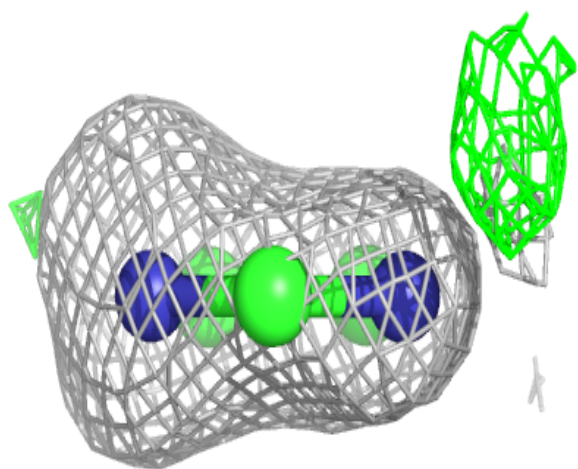
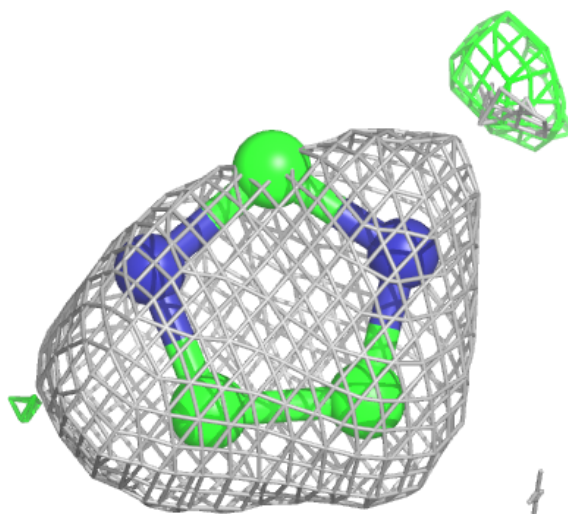
Electron density around GOL B 707:

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



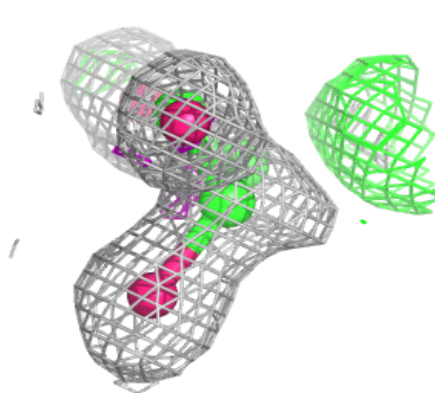
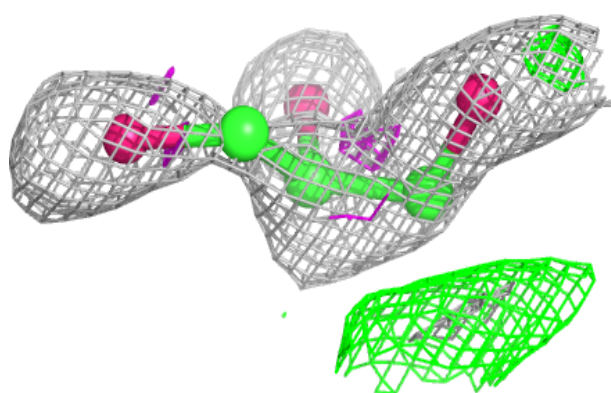
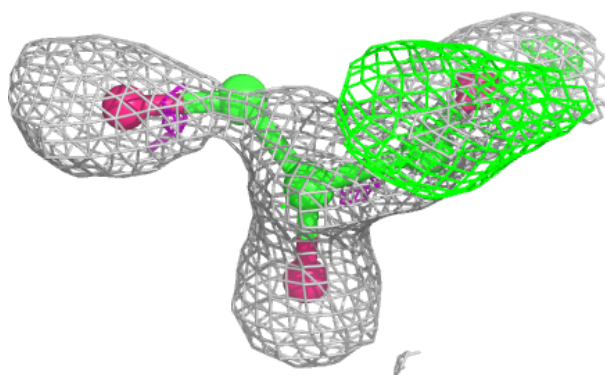
Electron density around IMD B 706:

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

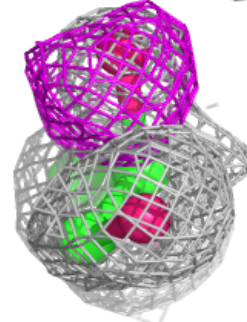
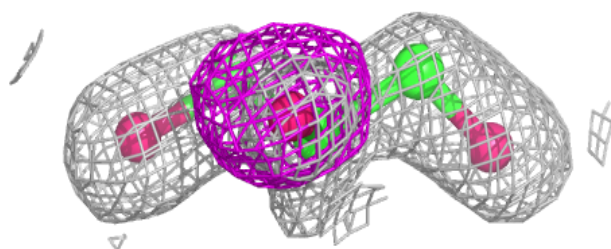
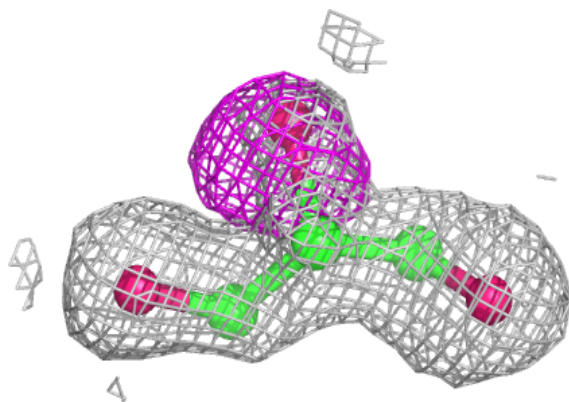


Electron density around GOL D 705:

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

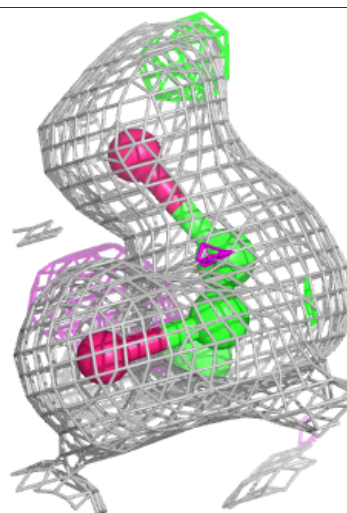
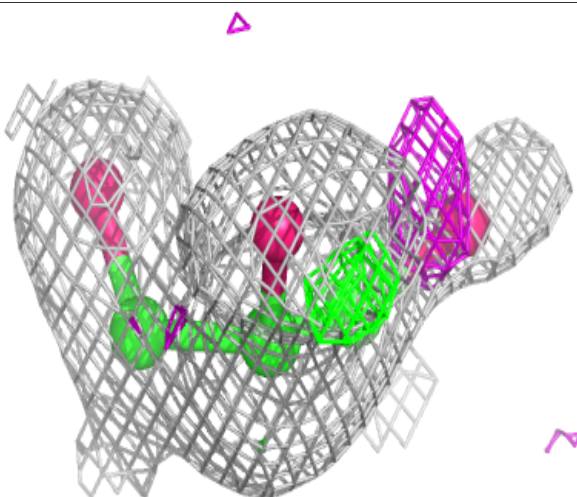
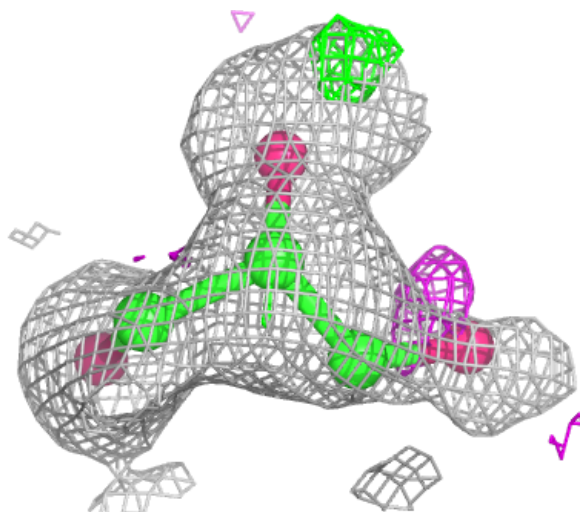
**Electron density around GOL F 701:**

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



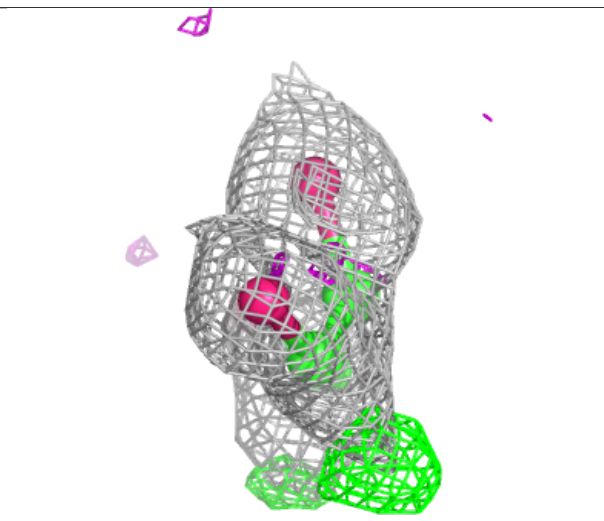
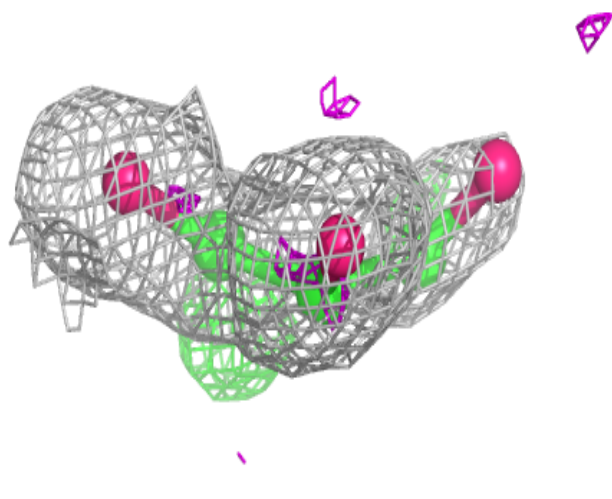
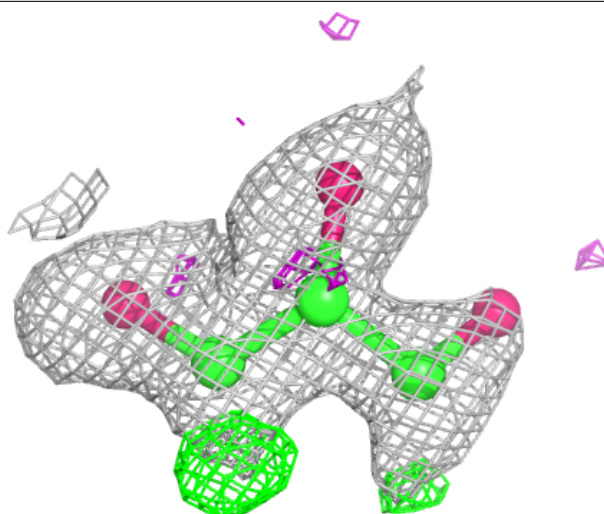
Electron density around GOL E 703:

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



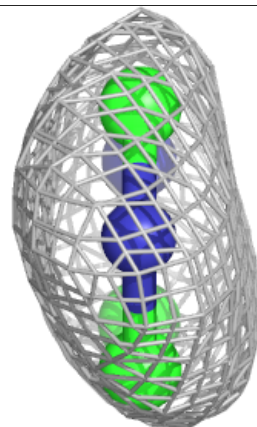
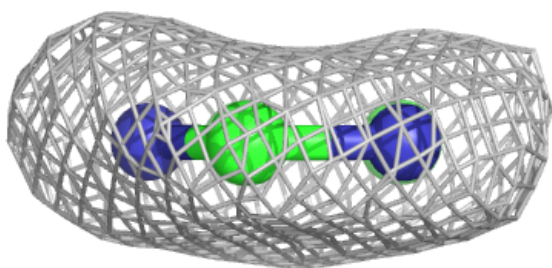
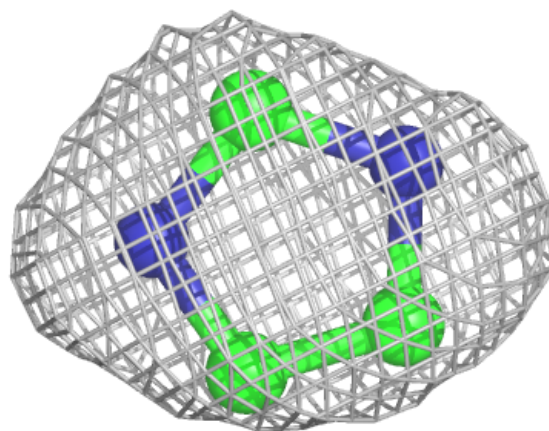
Electron density around GOL F 702:

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

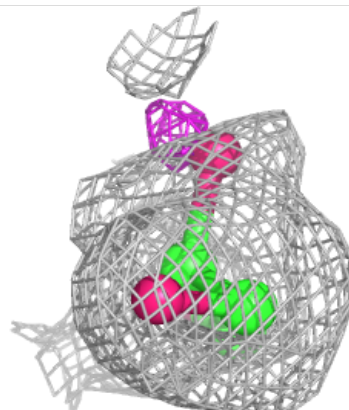
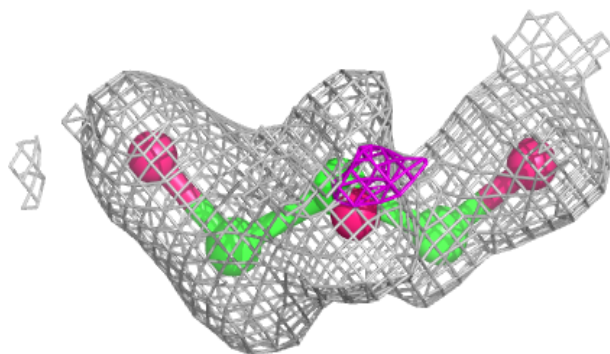
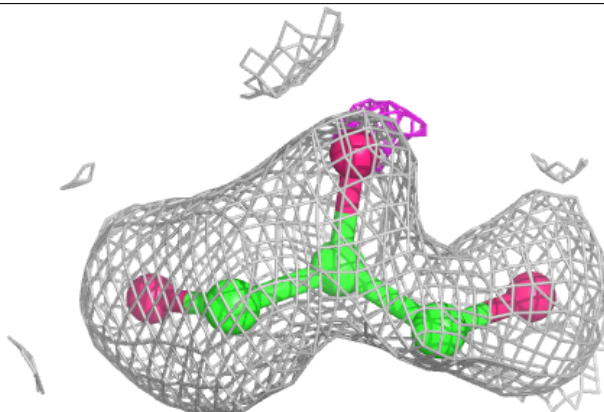


Electron density around IMD C 808:

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

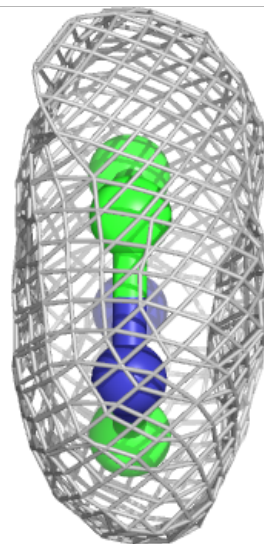
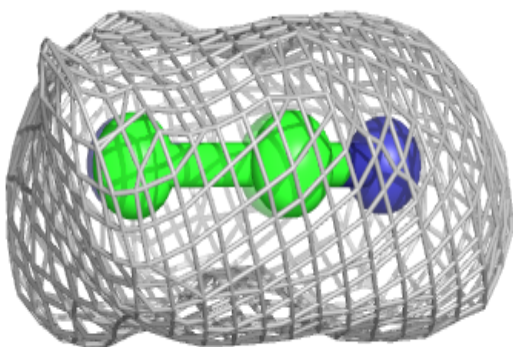
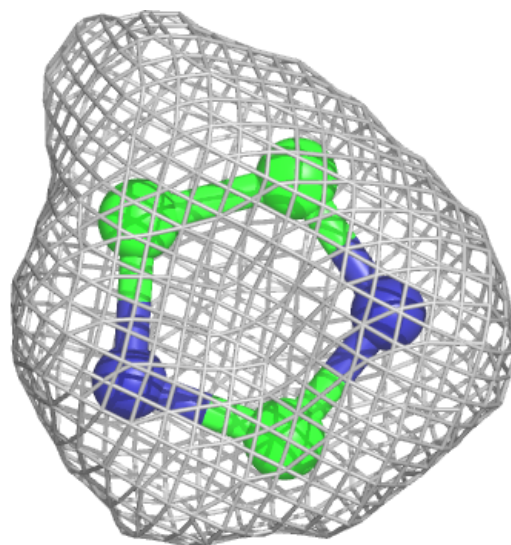
**Electron density around GOL A 806:**

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



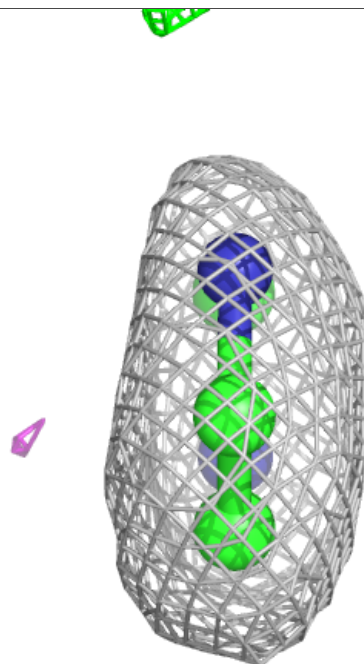
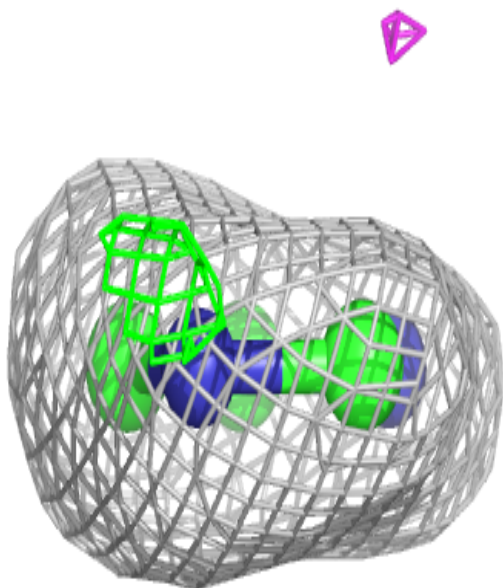
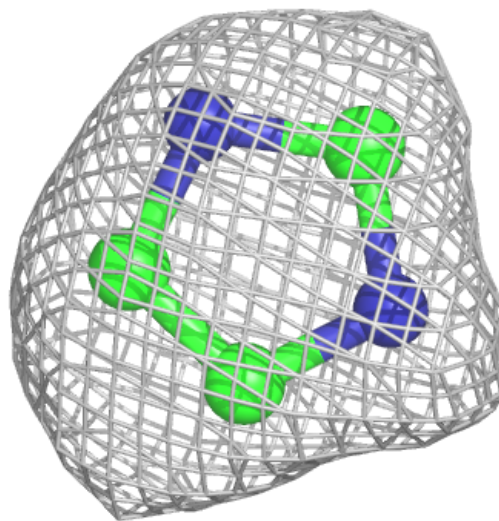
Electron density around IMD C 810:

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



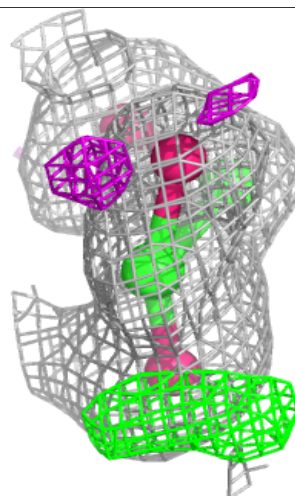
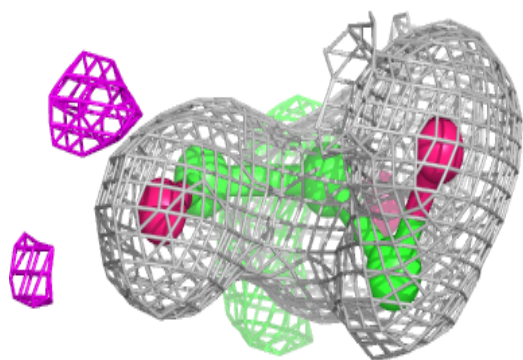
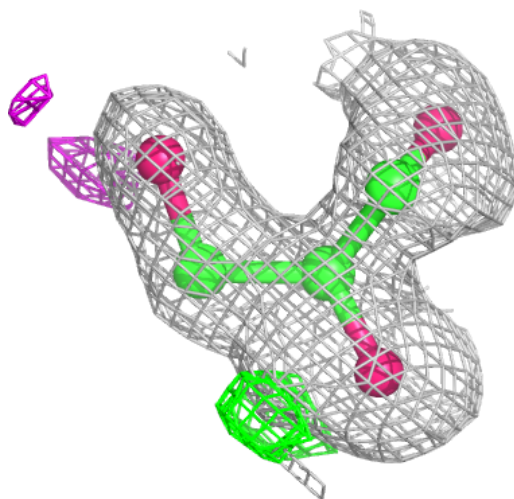
Electron density around IMD D 703:

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



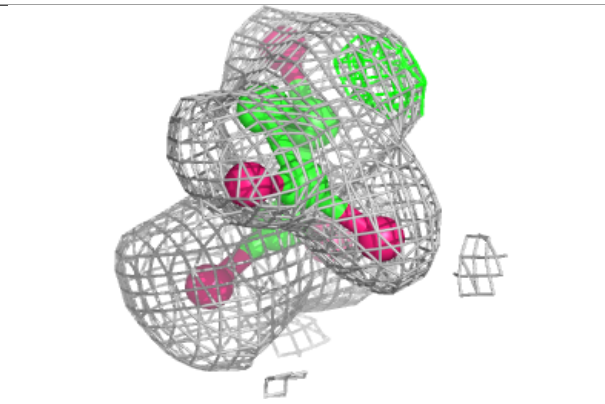
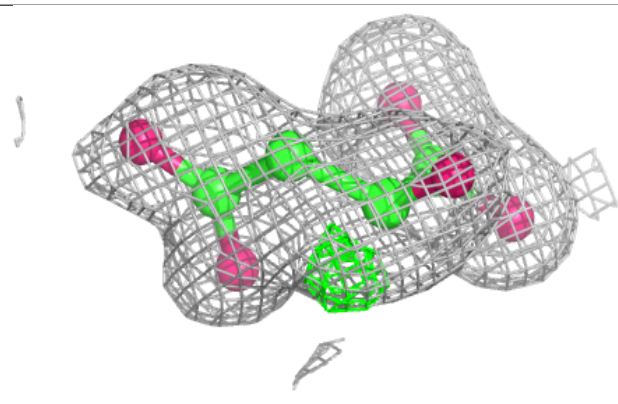
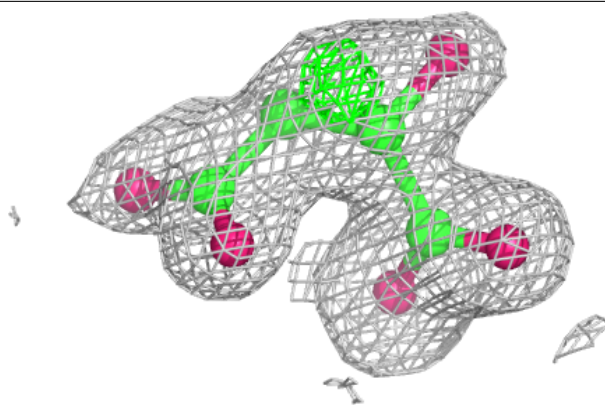
Electron density around GOL A 803:

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



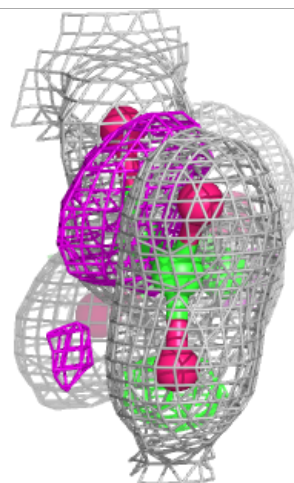
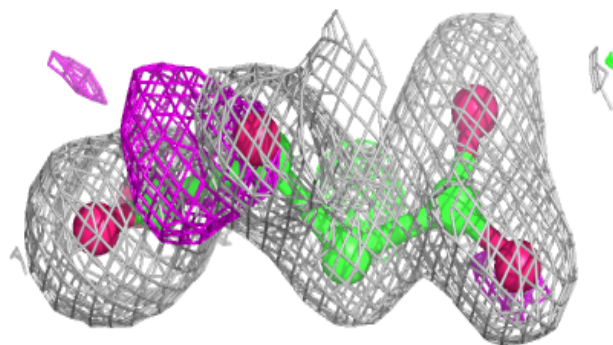
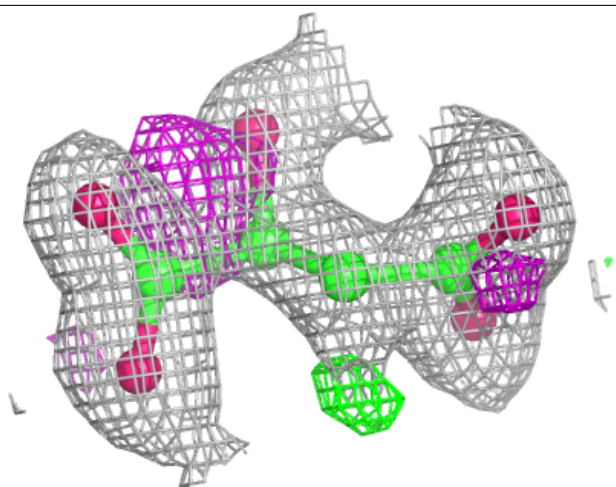
Electron density around LMR E 707:

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



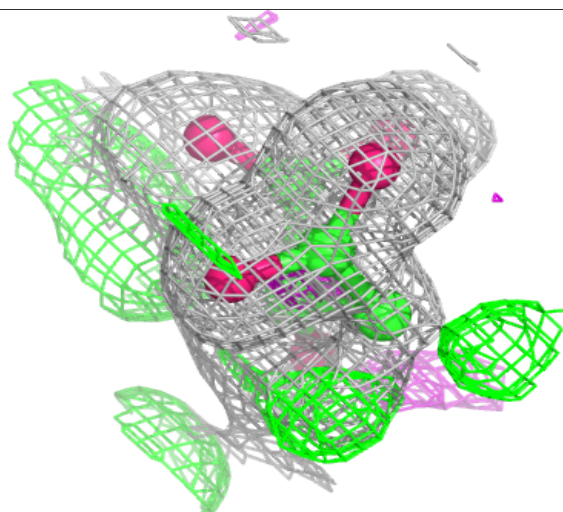
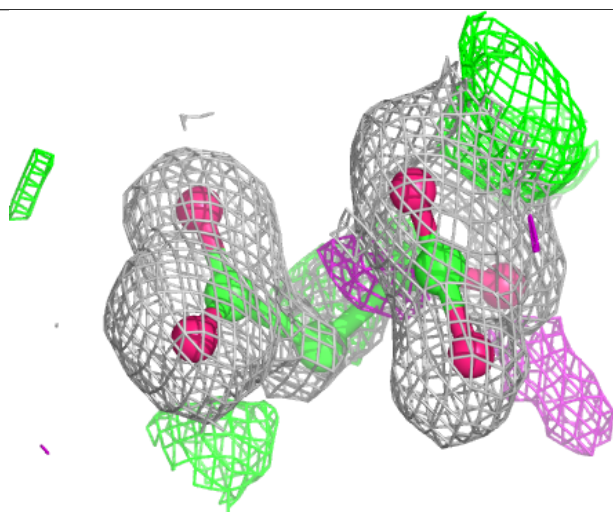
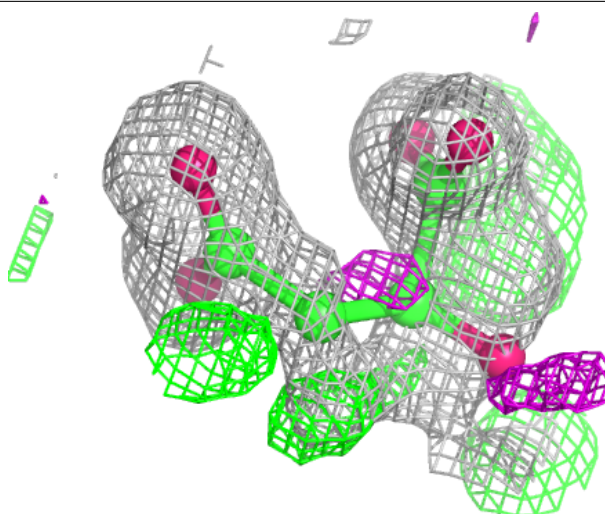
Electron density around LMR F 708:

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



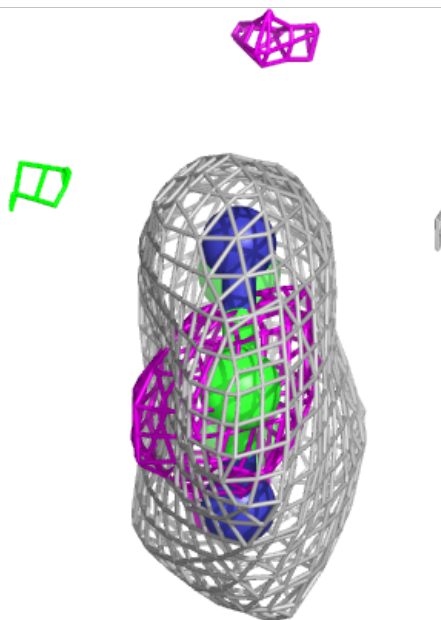
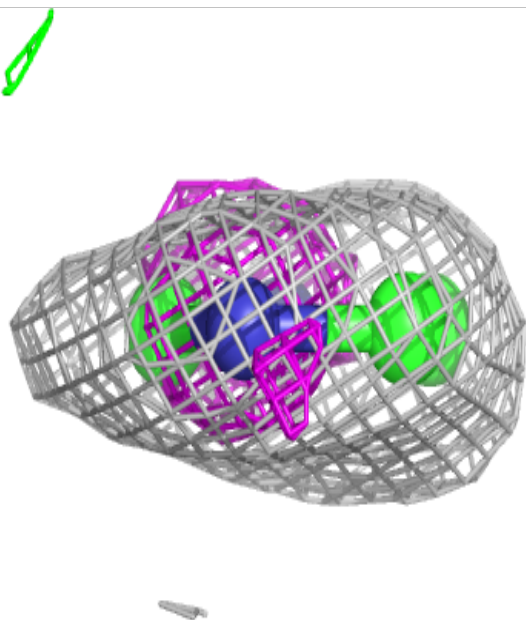
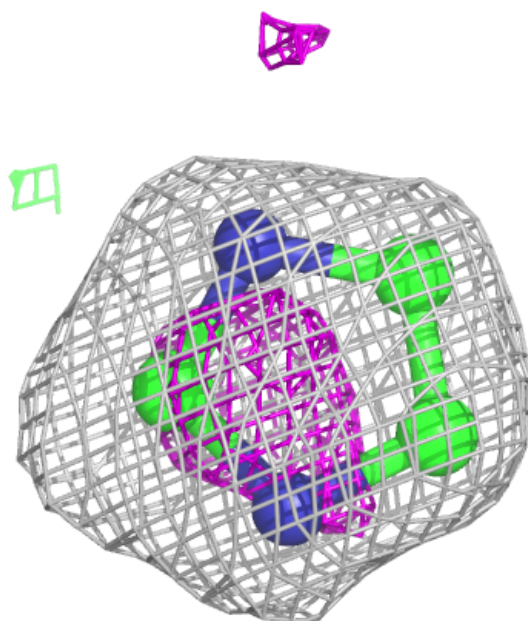
Electron density around LMR B 703:

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



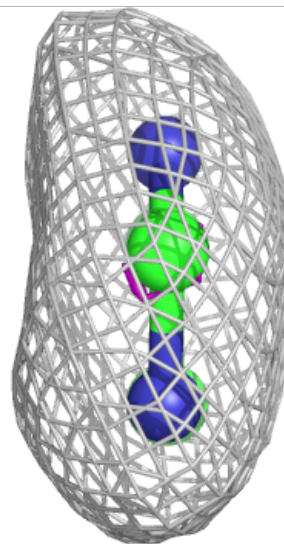
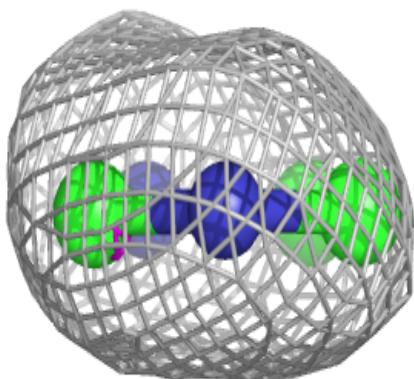
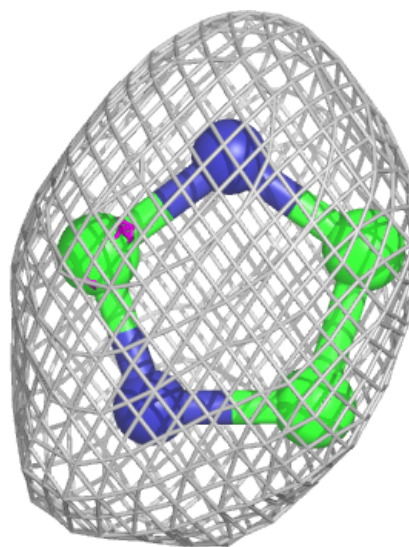
Electron density around IMD E 702:

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



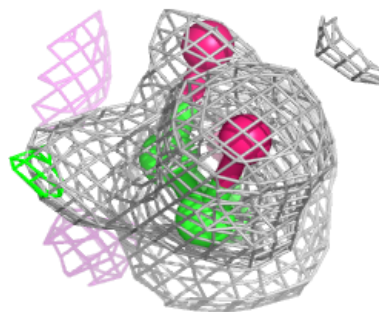
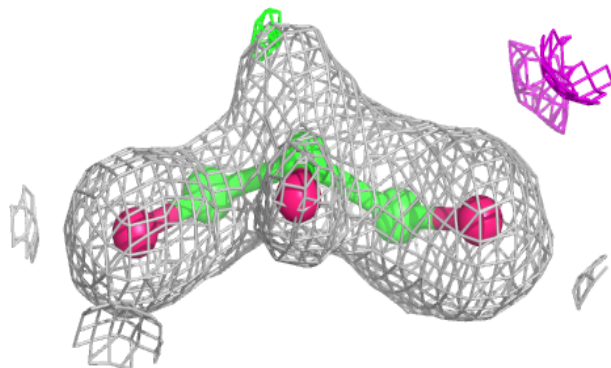
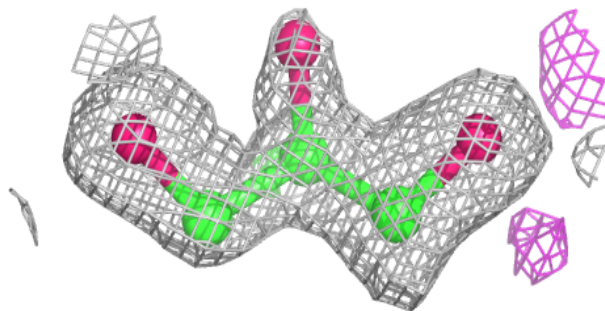
Electron density around IMD A 805:

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



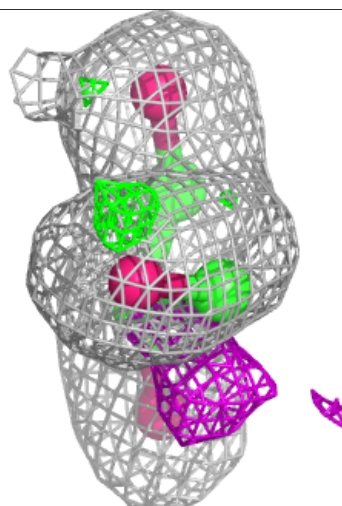
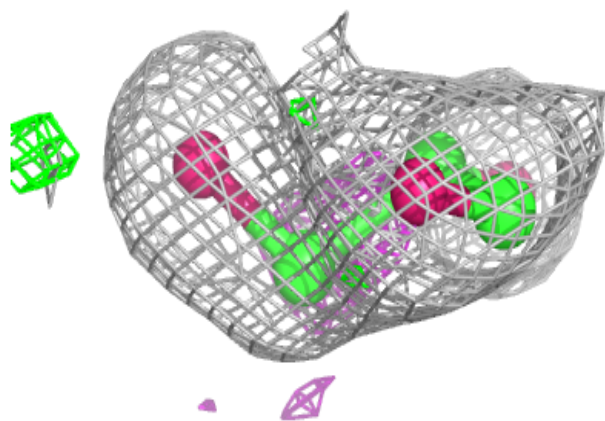
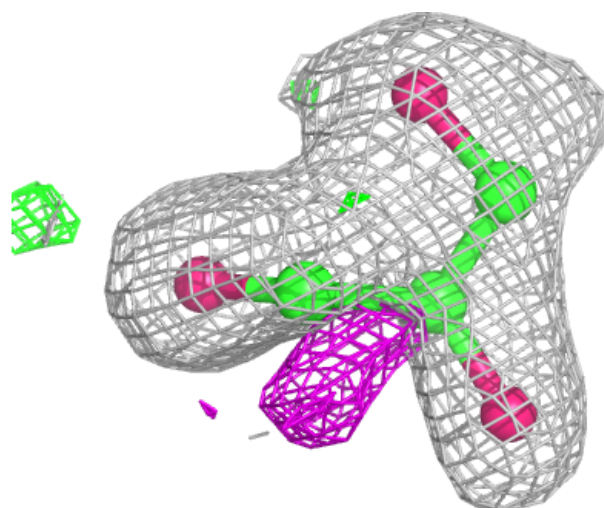
Electron density around GOL E 701:

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



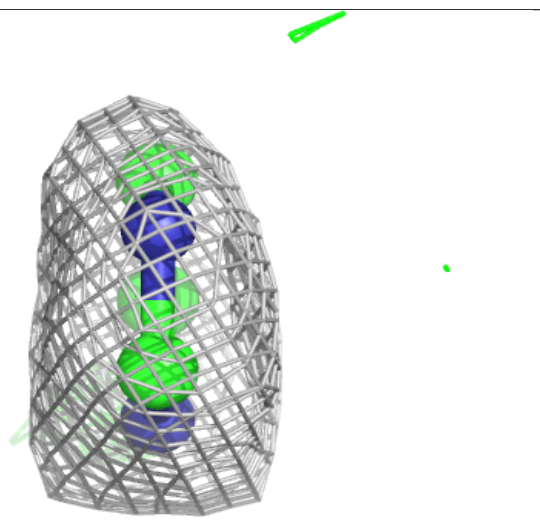
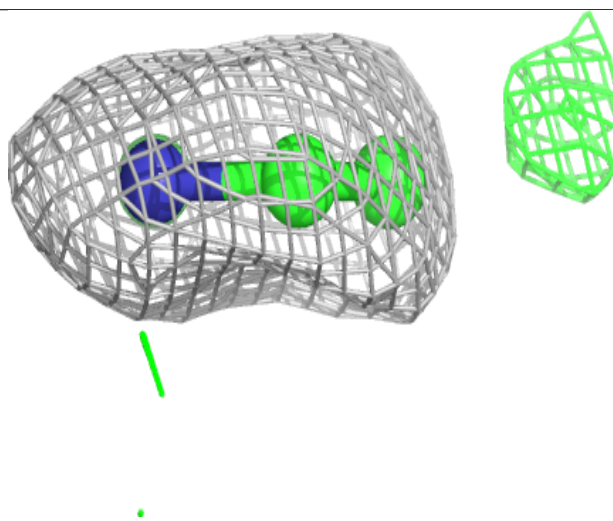
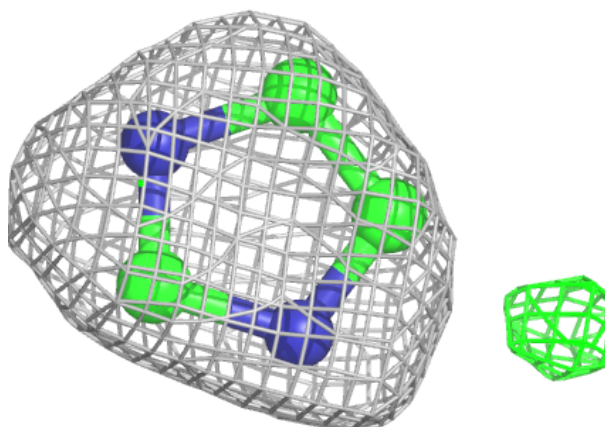
Electron density around GOL F 706:

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



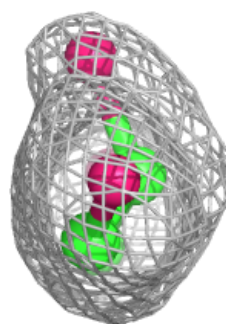
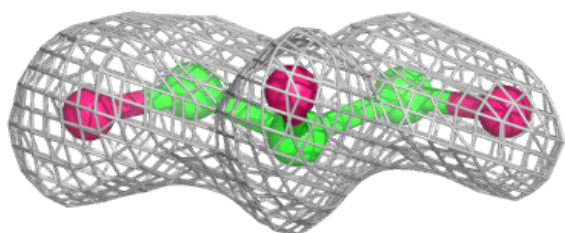
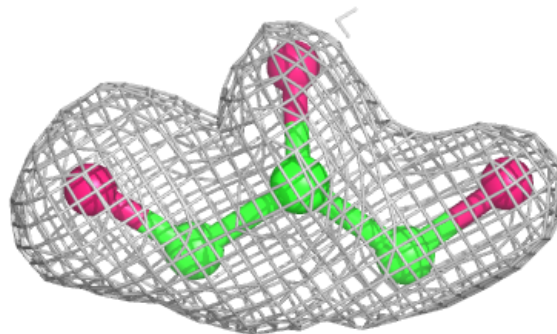
Electron density around IMD E 705:

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

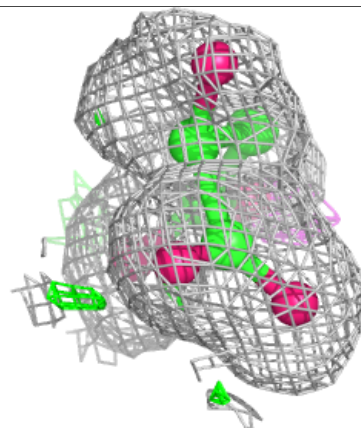
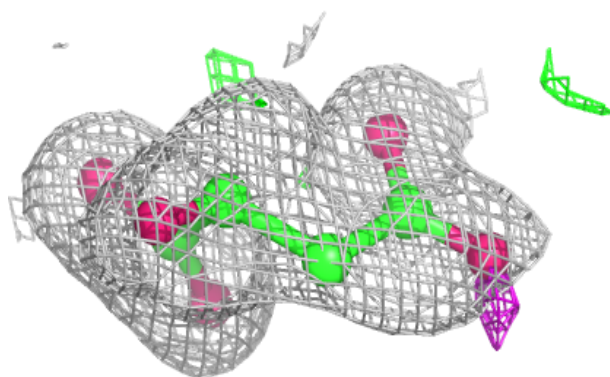
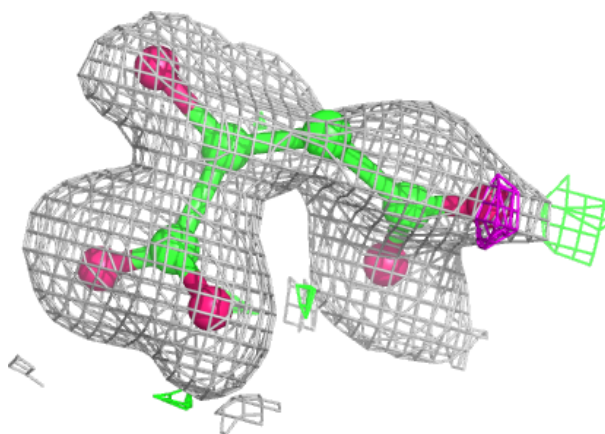


Electron density around GOL C 807:

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

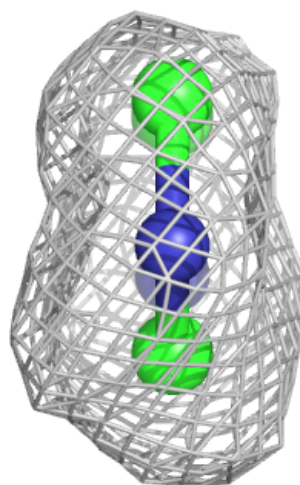
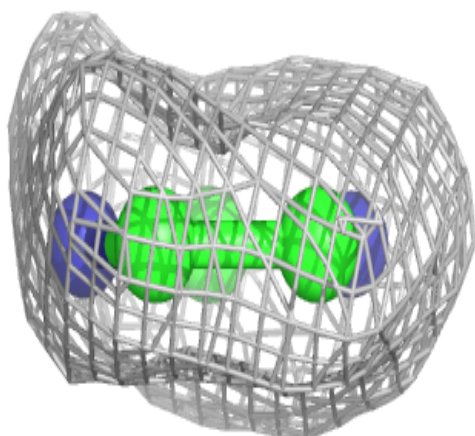
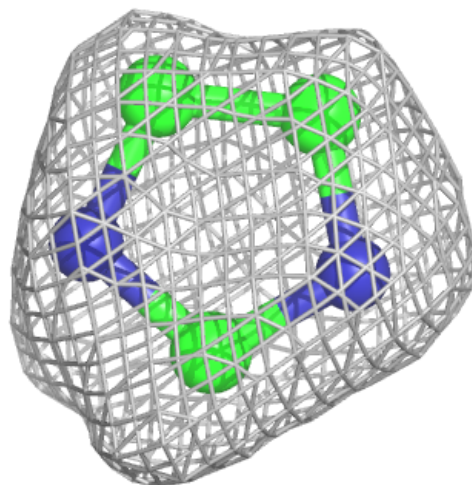
**Electron density around LMR D 702:**

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



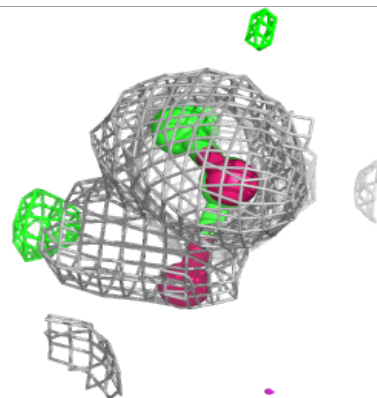
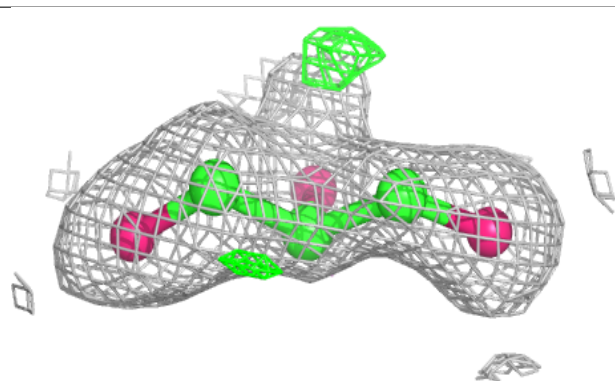
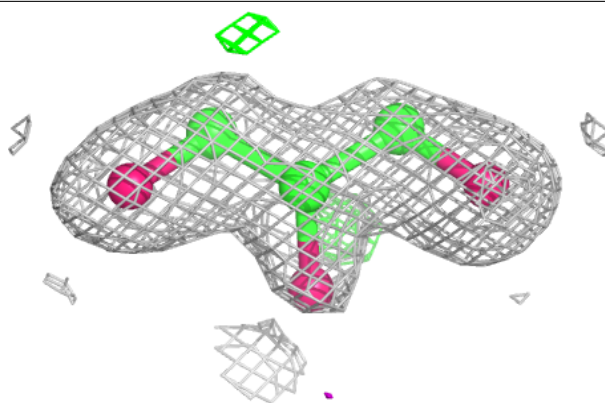
Electron density around IMD D 701:

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



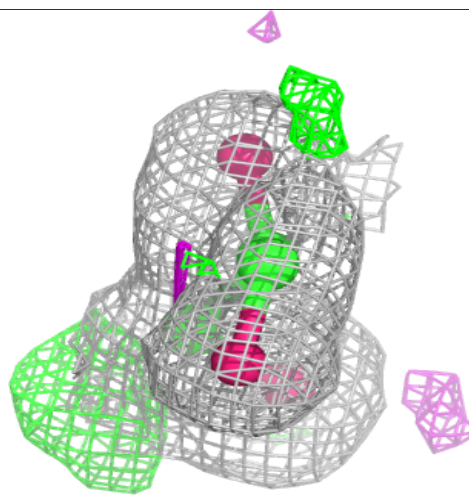
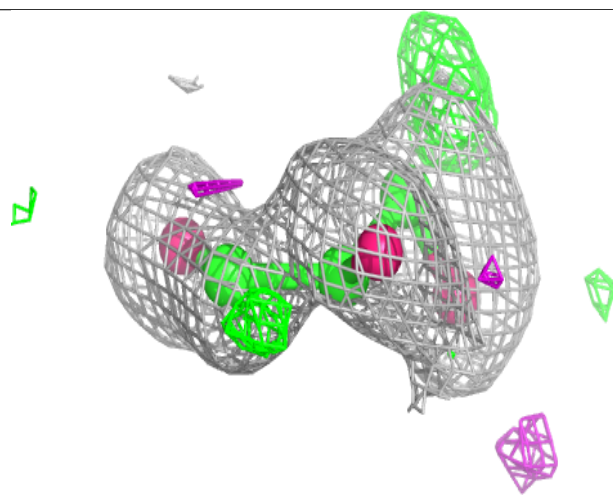
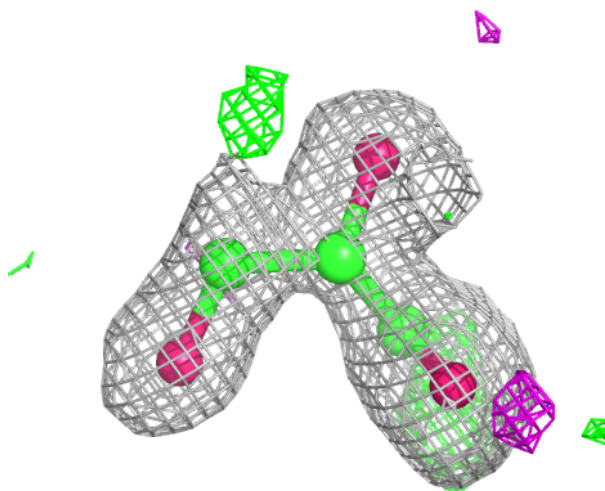
Electron density around GOL B 701:

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



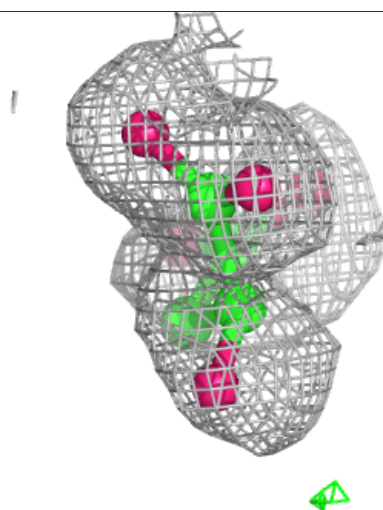
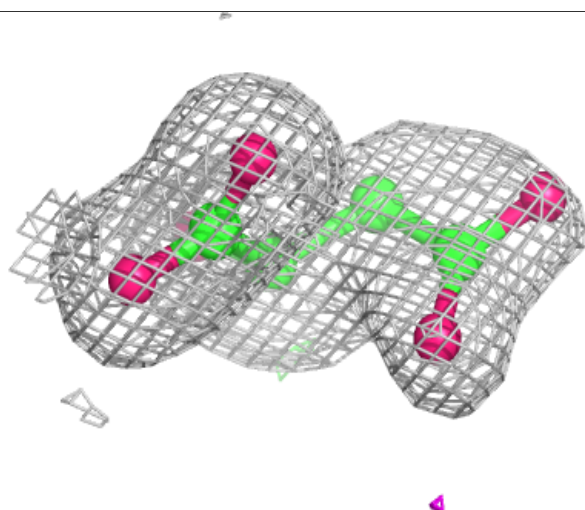
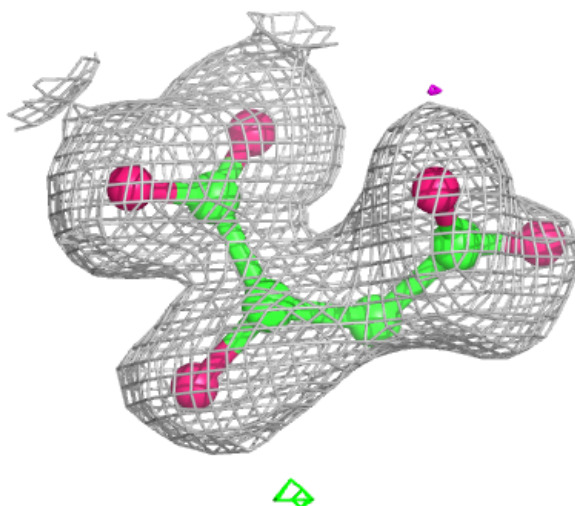
Electron density around GOL D 704:

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



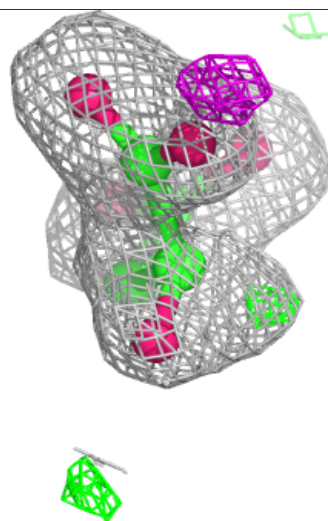
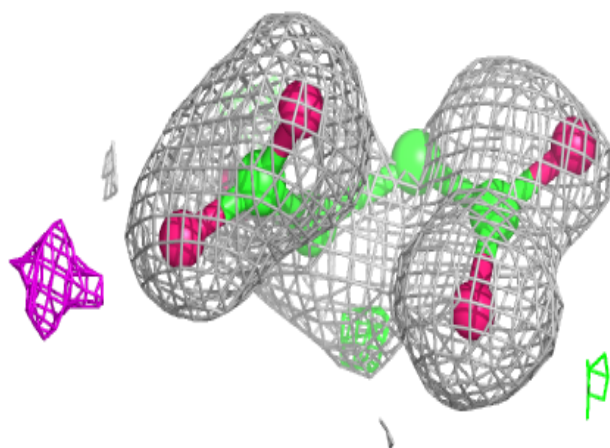
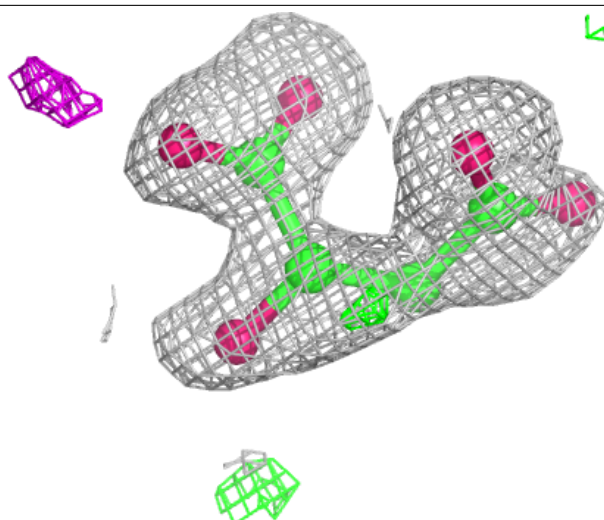
Electron density around LMR A 801:

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



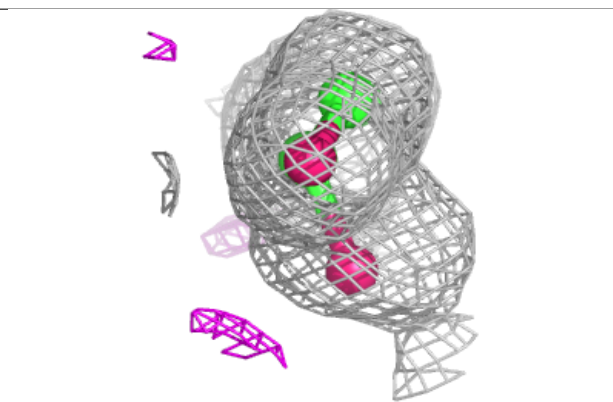
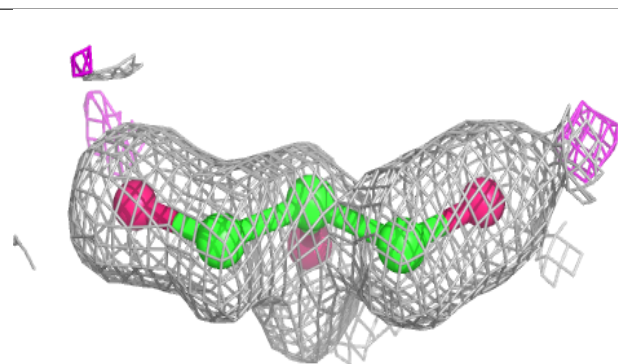
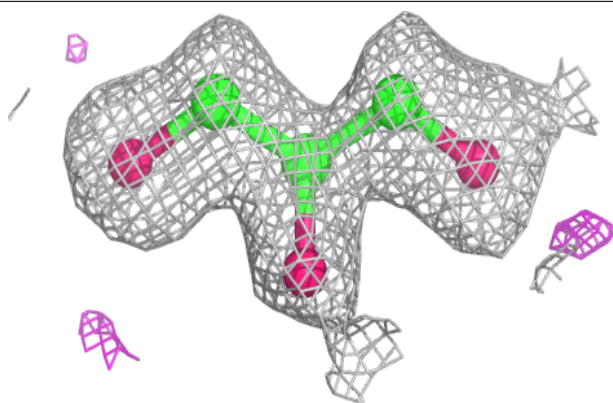
Electron density around LMR C 809:

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



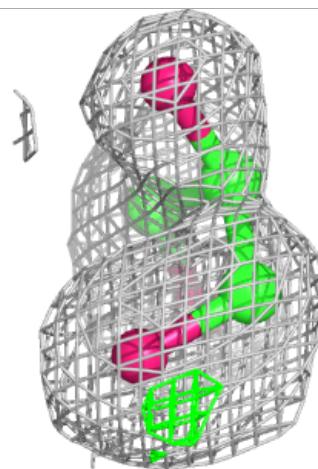
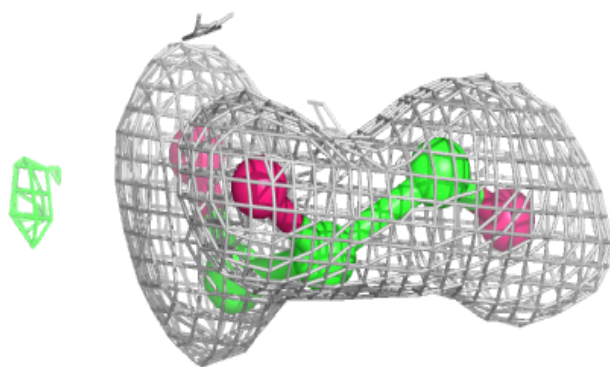
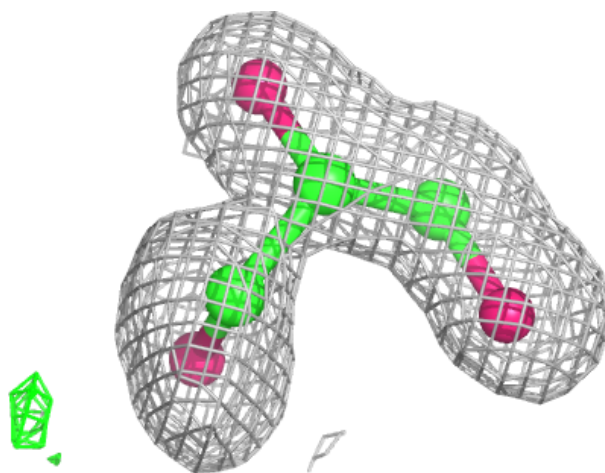
Electron density around GOL D 707:

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



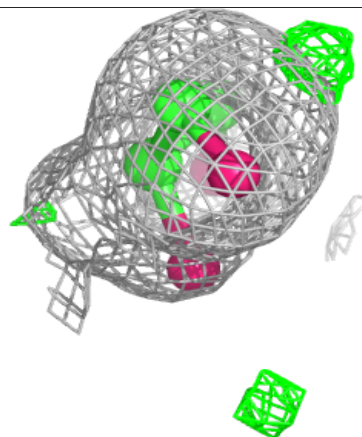
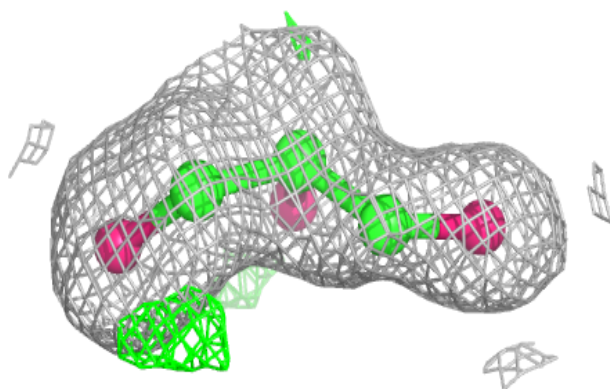
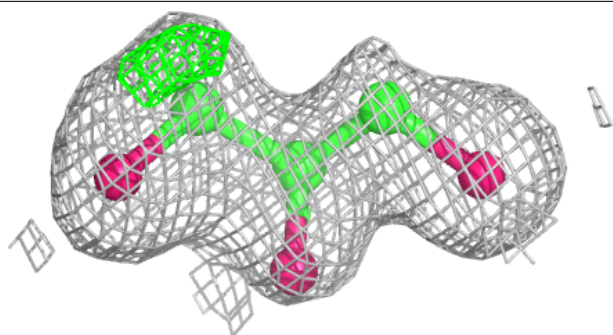
Electron density around GOL C 803:

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



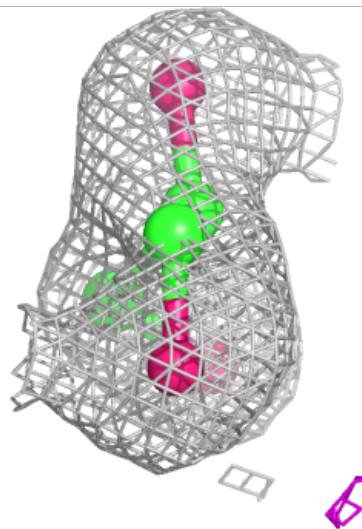
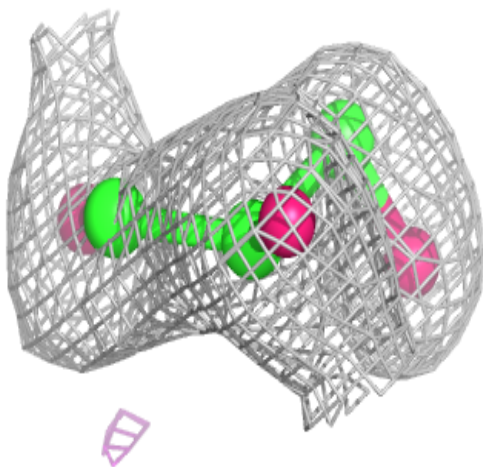
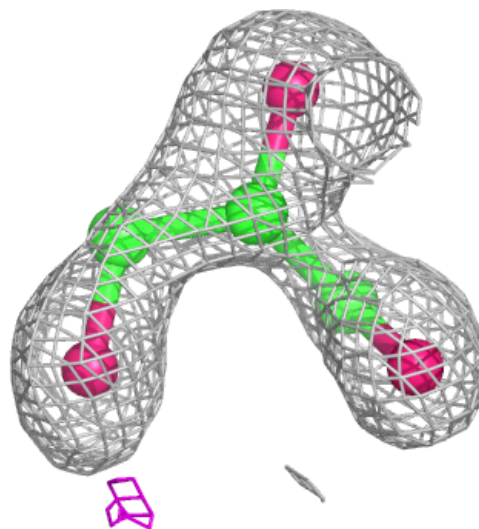
Electron density around GOL C 801:

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



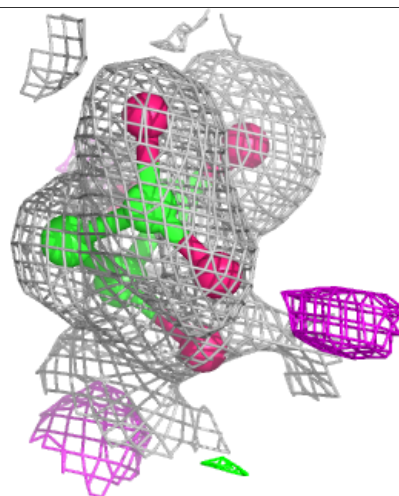
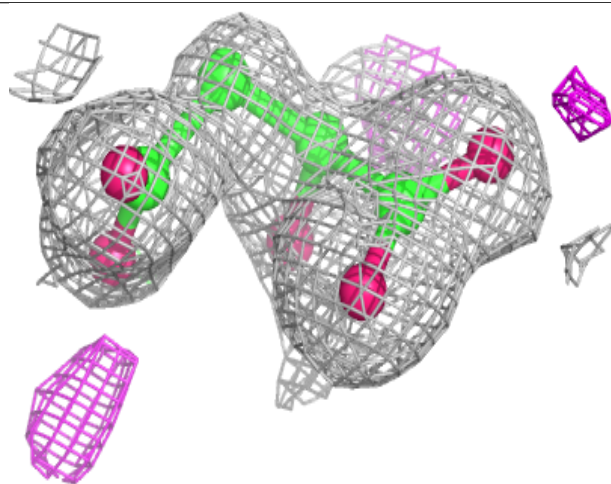
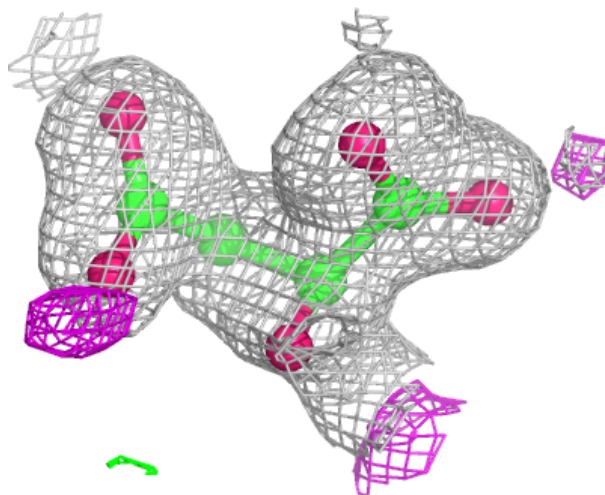
Electron density around GOL B 702:

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



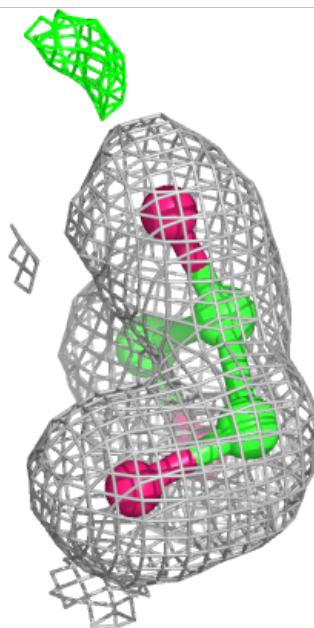
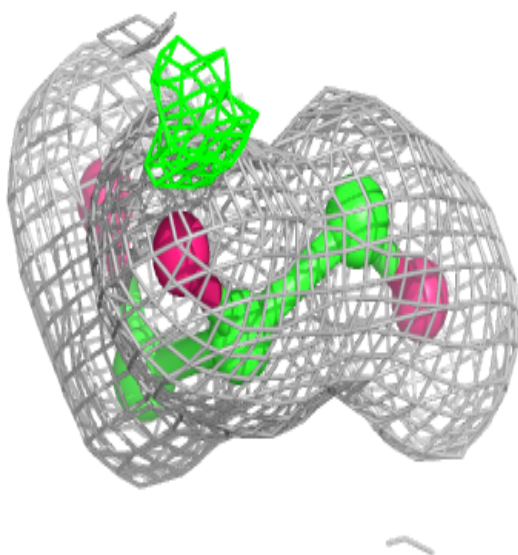
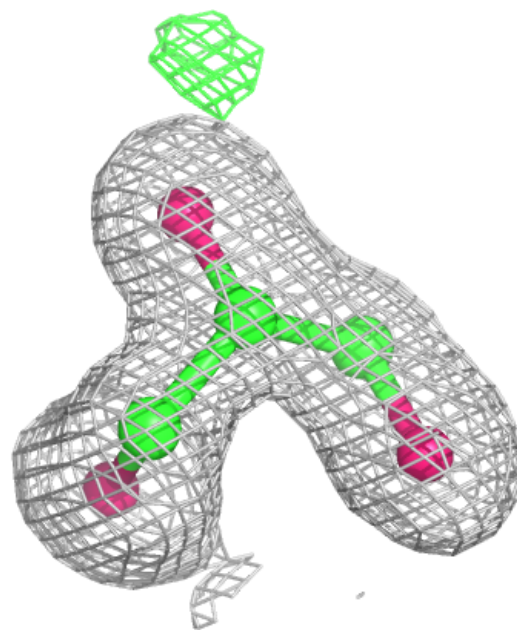
Electron density around LMR F 707:

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



Electron density around GOL E 706:

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.