



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 07:30 AM UTC

PDB ID : 9UOL / pdb_00009uol
EMDB ID : EMD-64381
Title : Cryo-EM structure of pyrene-modified TIP60 double mutant (G12C/S50C) with addition of Nile Red
Authors : Yamashita, M.; Kawakami, N.; Arai, R.; Ikeda, A.; Moriya, T.; Senda, T.; Miyamoto, K.
Deposited on : 2025-04-26
Resolution : 3.80 Å (reported)
Based on initial model : 7EQ9

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

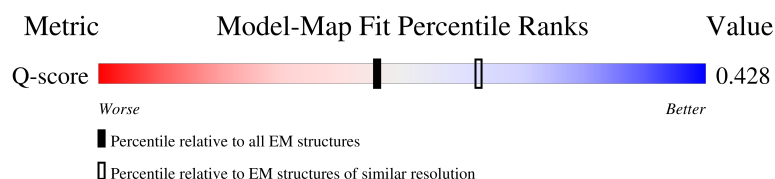
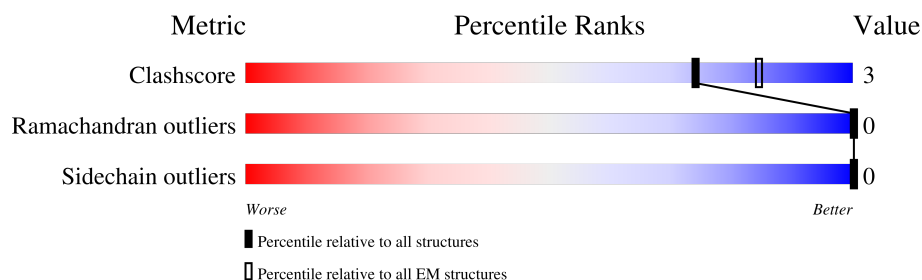
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



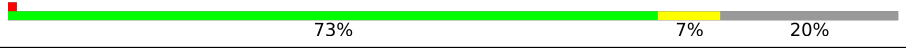
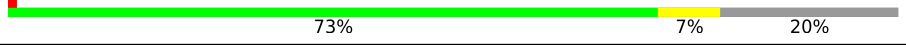
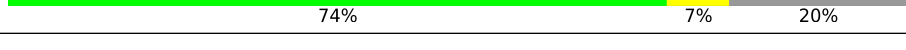
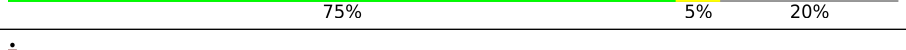
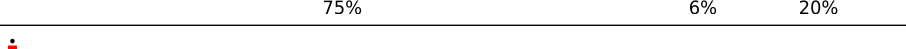
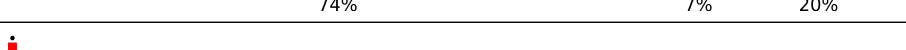
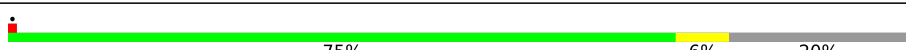
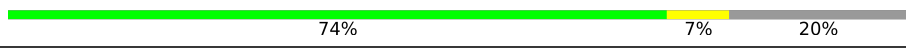
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	153	
1	AA	153	
1	AB	153	

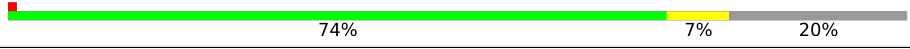
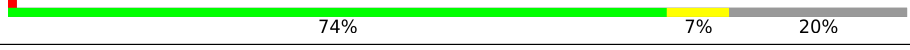
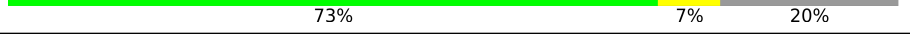
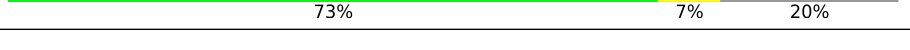
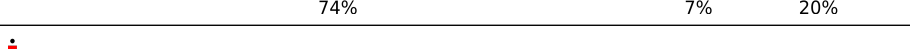
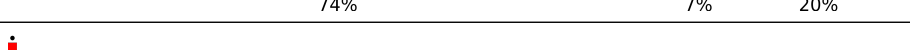
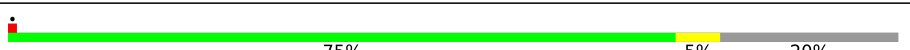
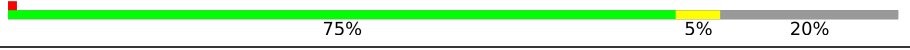
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	B	153	
1	BA	153	
1	BB	153	
1	C	153	
1	CA	153	
1	CB	153	
1	D	153	
1	DA	153	
1	DB	153	
1	E	153	
1	EA	153	
1	EB	153	
1	F	153	
1	FA	153	
1	FB	153	
1	G	153	
1	GA	153	
1	GB	153	
1	H	153	
1	HA	153	
1	HB	153	
1	I	153	
1	IA	153	
1	IB	153	
1	J	153	

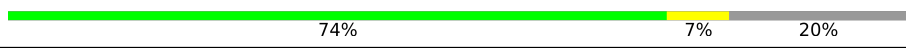
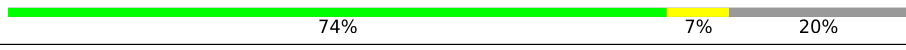
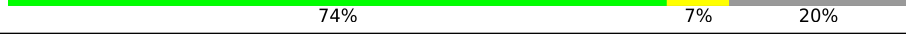
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	JA	153	
1	K	153	
1	KA	153	
1	L	153	
1	LA	153	
1	M	153	
1	MA	153	
1	N	153	
1	NA	153	
1	O	153	
1	OA	153	
1	P	153	
1	PA	153	
1	Q	153	
1	QA	153	
1	R	153	
1	RA	153	
1	S	153	
1	SA	153	
1	T	153	
1	TA	153	
1	UA	153	
1	V	153	
1	VA	153	
1	W	153	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	WA	153	 73%7%20%
1	X	153	 74%7%20%
1	XA	153	 74%7%20%
1	Y	153	 74%7%20%
1	YA	153	 73%7%20%
1	Z	153	 74%7%20%
1	ZA	153	 74%7%20%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 63180 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 TIP60 double mutant (G12C/S50C).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	B	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	C	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	D	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	E	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	F	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	G	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	H	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	I	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	J	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	K	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	L	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	M	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	N	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	O	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	P	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	Q	123	Total 1007	C 633	N 170	O 200	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	S	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	T	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	V	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	W	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	X	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	Y	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	Z	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	AA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	BA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	CA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	DA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	EA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	FA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	GA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	HA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	IA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	JA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	KA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	LA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	MA	123	Total 1007	C 633	N 170	O 200	S 4	0	0

Continued on next page...

Continued from previous page...

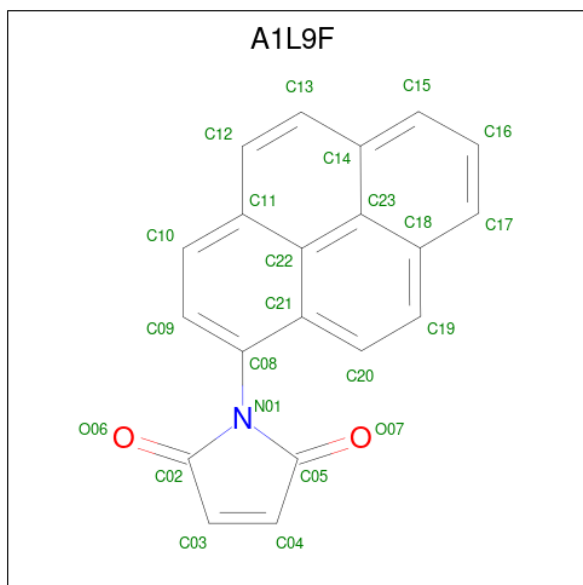
Mol	Chain	Residues	Atoms					AltConf	Trace
1	NA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	OA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	PA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	QA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	RA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	SA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	TA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	UA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	VA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	WA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	XA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	YA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	ZA	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	AB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	BB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	CB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	DB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	EB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	FB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	GB	123	Total 1007	C 633	N 170	O 200	S 4	0	0
1	HB	123	Total 1007	C 633	N 170	O 200	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	IB	123	Total	C	N	O	S	0	0
			1007	633	170	200	4		

- Molecule 2 is N-(1-pyrenyl)maleimide (CCD ID: A1L9F) (formula: C₂₀H₁₁NO₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			23	20	1	2	
2	A	1	Total	C	N	O	0
			23	20	1	2	
2	B	1	Total	C	N	O	0
			23	20	1	2	
2	B	1	Total	C	N	O	0
			23	20	1	2	
2	C	1	Total	C	N	O	0
			23	20	1	2	
2	C	1	Total	C	N	O	0
			23	20	1	2	
2	D	1	Total	C	N	O	0
			23	20	1	2	
2	D	1	Total	C	N	O	0
			23	20	1	2	
2	E	1	Total	C	N	O	0
			23	20	1	2	
2	E	1	Total	C	N	O	0
			23	20	1	2	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
2	F	1	Total 23	C 20	N 1	O 2	0
2	F	1	Total 23	C 20	N 1	O 2	0
2	G	1	Total 23	C 20	N 1	O 2	0
2	G	1	Total 23	C 20	N 1	O 2	0
2	H	1	Total 23	C 20	N 1	O 2	0
2	H	1	Total 23	C 20	N 1	O 2	0
2	I	1	Total 23	C 20	N 1	O 2	0
2	I	1	Total 23	C 20	N 1	O 2	0
2	J	1	Total 23	C 20	N 1	O 2	0
2	J	1	Total 23	C 20	N 1	O 2	0
2	K	1	Total 23	C 20	N 1	O 2	0
2	K	1	Total 23	C 20	N 1	O 2	0
2	L	1	Total 23	C 20	N 1	O 2	0
2	L	1	Total 23	C 20	N 1	O 2	0
2	M	1	Total 23	C 20	N 1	O 2	0
2	M	1	Total 23	C 20	N 1	O 2	0
2	N	1	Total 23	C 20	N 1	O 2	0
2	N	1	Total 23	C 20	N 1	O 2	0
2	O	1	Total 23	C 20	N 1	O 2	0
2	O	1	Total 23	C 20	N 1	O 2	0
2	P	1	Total 23	C 20	N 1	O 2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
2	P	1	Total 23	C 20	N 1	O 2	0
2	Q	1	Total 23	C 20	N 1	O 2	0
2	Q	1	Total 23	C 20	N 1	O 2	0
2	R	1	Total 23	C 20	N 1	O 2	0
2	R	1	Total 23	C 20	N 1	O 2	0
2	S	1	Total 23	C 20	N 1	O 2	0
2	S	1	Total 23	C 20	N 1	O 2	0
2	T	1	Total 23	C 20	N 1	O 2	0
2	T	1	Total 23	C 20	N 1	O 2	0
2	V	1	Total 23	C 20	N 1	O 2	0
2	V	1	Total 23	C 20	N 1	O 2	0
2	W	1	Total 23	C 20	N 1	O 2	0
2	W	1	Total 23	C 20	N 1	O 2	0
2	X	1	Total 23	C 20	N 1	O 2	0
2	X	1	Total 23	C 20	N 1	O 2	0
2	Y	1	Total 23	C 20	N 1	O 2	0
2	Y	1	Total 23	C 20	N 1	O 2	0
2	Z	1	Total 23	C 20	N 1	O 2	0
2	Z	1	Total 23	C 20	N 1	O 2	0
2	AA	1	Total 23	C 20	N 1	O 2	0
2	AA	1	Total 23	C 20	N 1	O 2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
2	BA	1	Total 23	C 20	N 1	O 2	0
2	BA	1	Total 23	C 20	N 1	O 2	0
2	CA	1	Total 23	C 20	N 1	O 2	0
2	CA	1	Total 23	C 20	N 1	O 2	0
2	DA	1	Total 23	C 20	N 1	O 2	0
2	DA	1	Total 23	C 20	N 1	O 2	0
2	EA	1	Total 23	C 20	N 1	O 2	0
2	EA	1	Total 23	C 20	N 1	O 2	0
2	FA	1	Total 23	C 20	N 1	O 2	0
2	FA	1	Total 23	C 20	N 1	O 2	0
2	GA	1	Total 23	C 20	N 1	O 2	0
2	GA	1	Total 23	C 20	N 1	O 2	0
2	HA	1	Total 23	C 20	N 1	O 2	0
2	HA	1	Total 23	C 20	N 1	O 2	0
2	IA	1	Total 23	C 20	N 1	O 2	0
2	IA	1	Total 23	C 20	N 1	O 2	0
2	JA	1	Total 23	C 20	N 1	O 2	0
2	JA	1	Total 23	C 20	N 1	O 2	0
2	KA	1	Total 23	C 20	N 1	O 2	0
2	KA	1	Total 23	C 20	N 1	O 2	0
2	LA	1	Total 23	C 20	N 1	O 2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
2	LA	1	Total 23	C 20	N 1	O 2	0
2	MA	1	Total 23	C 20	N 1	O 2	0
2	MA	1	Total 23	C 20	N 1	O 2	0
2	NA	1	Total 23	C 20	N 1	O 2	0
2	NA	1	Total 23	C 20	N 1	O 2	0
2	OA	1	Total 23	C 20	N 1	O 2	0
2	OA	1	Total 23	C 20	N 1	O 2	0
2	PA	1	Total 23	C 20	N 1	O 2	0
2	PA	1	Total 23	C 20	N 1	O 2	0
2	QA	1	Total 23	C 20	N 1	O 2	0
2	QA	1	Total 23	C 20	N 1	O 2	0
2	RA	1	Total 23	C 20	N 1	O 2	0
2	RA	1	Total 23	C 20	N 1	O 2	0
2	SA	1	Total 23	C 20	N 1	O 2	0
2	SA	1	Total 23	C 20	N 1	O 2	0
2	TA	1	Total 23	C 20	N 1	O 2	0
2	TA	1	Total 23	C 20	N 1	O 2	0
2	UA	1	Total 23	C 20	N 1	O 2	0
2	UA	1	Total 23	C 20	N 1	O 2	0
2	VA	1	Total 23	C 20	N 1	O 2	0
2	VA	1	Total 23	C 20	N 1	O 2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
2	WA	1	Total 23	C 20	N 1	O 2	0
2	WA	1	Total 23	C 20	N 1	O 2	0
2	XA	1	Total 23	C 20	N 1	O 2	0
2	XA	1	Total 23	C 20	N 1	O 2	0
2	YA	1	Total 23	C 20	N 1	O 2	0
2	YA	1	Total 23	C 20	N 1	O 2	0
2	ZA	1	Total 23	C 20	N 1	O 2	0
2	ZA	1	Total 23	C 20	N 1	O 2	0
2	AB	1	Total 23	C 20	N 1	O 2	0
2	AB	1	Total 23	C 20	N 1	O 2	0
2	BB	1	Total 23	C 20	N 1	O 2	0
2	BB	1	Total 23	C 20	N 1	O 2	0
2	CB	1	Total 23	C 20	N 1	O 2	0
2	CB	1	Total 23	C 20	N 1	O 2	0
2	DB	1	Total 23	C 20	N 1	O 2	0
2	DB	1	Total 23	C 20	N 1	O 2	0
2	EB	1	Total 23	C 20	N 1	O 2	0
2	EB	1	Total 23	C 20	N 1	O 2	0
2	FB	1	Total 23	C 20	N 1	O 2	0
2	FB	1	Total 23	C 20	N 1	O 2	0
2	GB	1	Total 23	C 20	N 1	O 2	0

Continued on next page...

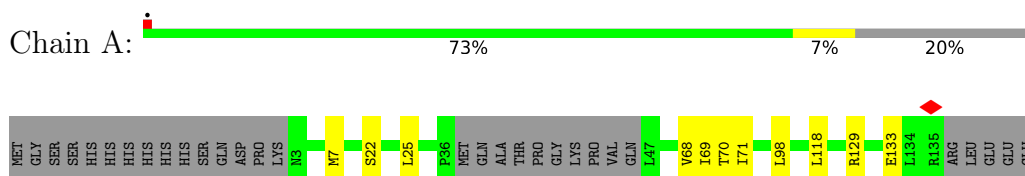
Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
2	GB	1	Total	C	N	O	0
			23	20	1	2	
2	HB	1	Total	C	N	O	0
			23	20	1	2	
2	HB	1	Total	C	N	O	0
			23	20	1	2	
2	IB	1	Total	C	N	O	0
			23	20	1	2	
2	IB	1	Total	C	N	O	0
			23	20	1	2	

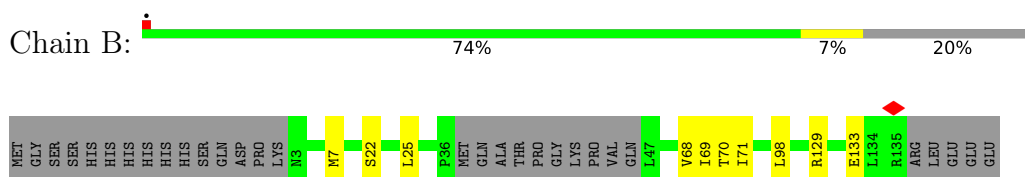
3 Residue-property plots [i](#)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

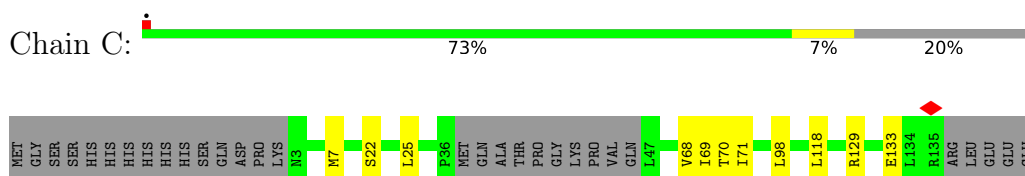
- Molecule 1: TIP60 double mutant (G12C/S50C)



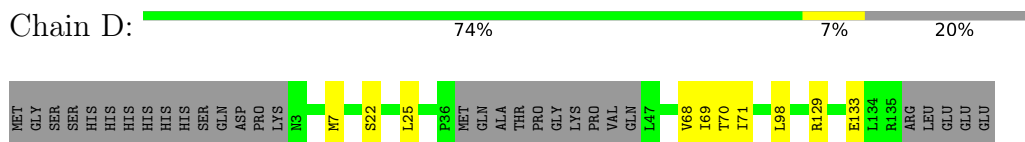
- Molecule 1: TIP60 double mutant (G12C/S50C)



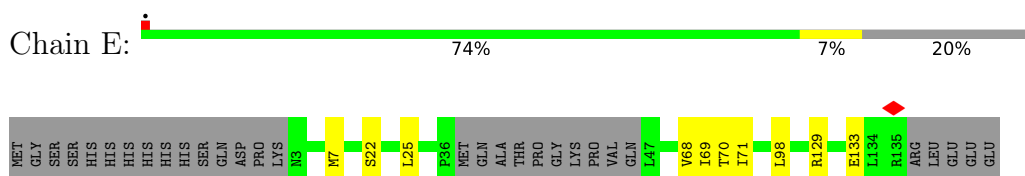
- Molecule 1: TIP60 double mutant (G12C/S50C)



- Molecule 1: TIP60 double mutant (G12C/S50C)

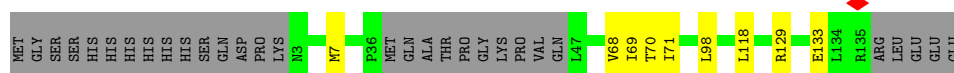


- Molecule 1: TIP60 double mutant (G12C/S50C)



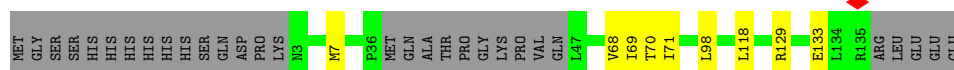
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain F:  75% 6% 20%



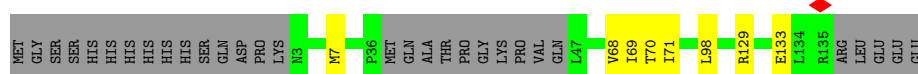
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain G:  75% 6% 20%



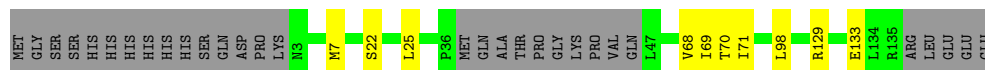
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain H:  75% 5% 20%



- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain I:  74% 7% 20%



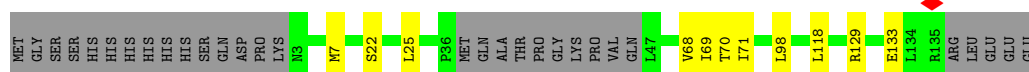
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain J:  74% 7% 20%



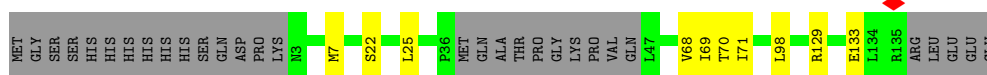
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain K:  73% 7% 20%

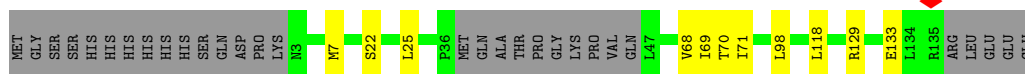


- Molecule 1: TIP60 double mutant (G12C/S50C)

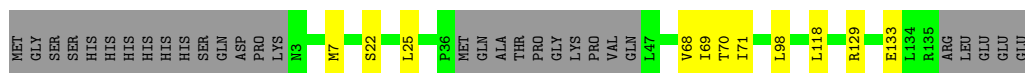
Chain L:  74% 7% 20%



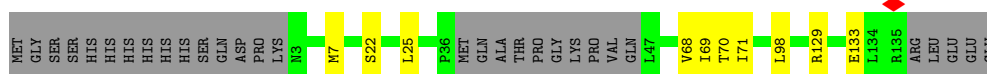
- Molecule 1: TIP60 double mutant (G12C/S50C)



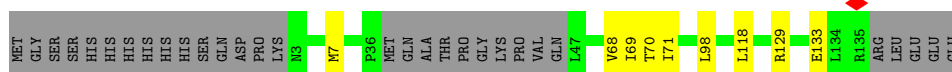
- Molecule 1: TIP60 double mutant (G12C/S50C)



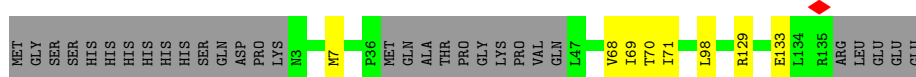
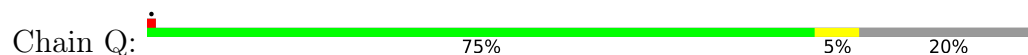
- Molecule 1: TIP60 double mutant (G12C/S50C)



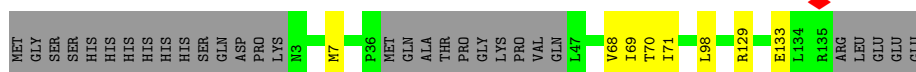
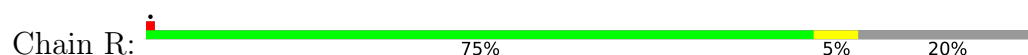
- Molecule 1: TIP60 double mutant (G12C/S50C)



- Molecule 1: TIP60 double mutant (G12C/S50C)

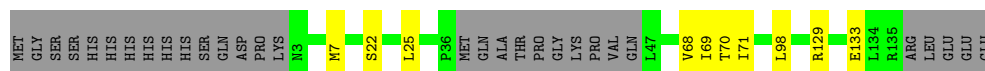


- Molecule 1: TIP60 double mutant (G12C/S50C)



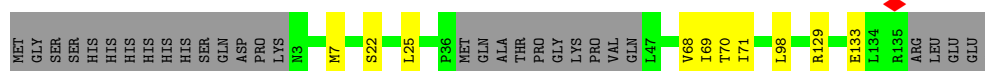
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain S:  74% 7% 20%



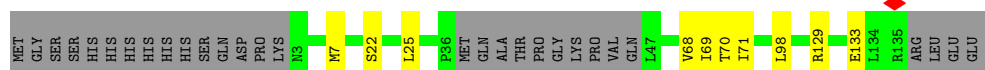
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain T:  74% 7% 20%



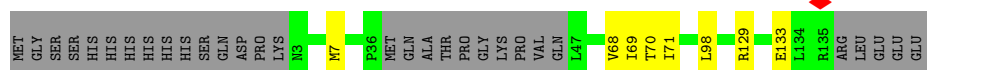
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain V:  74% 7% 20%



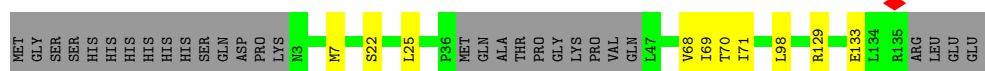
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain W:  75% 5% 20%



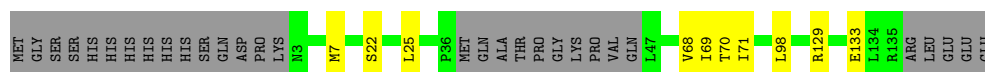
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain X:  74% 7% 20%



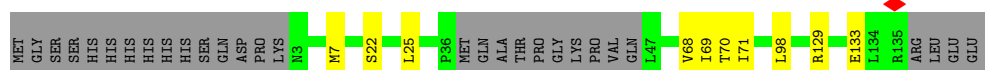
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain Y:  74% 7% 20%



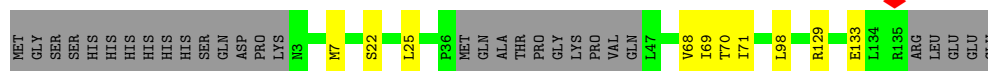
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain Z:  74% 7% 20%



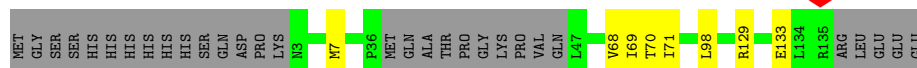
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain AA: 



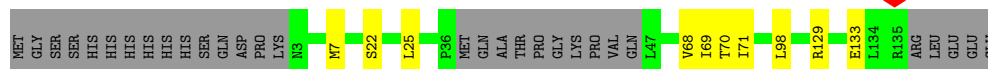
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain BA: 



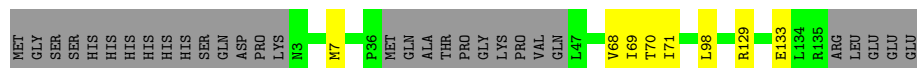
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain CA: 



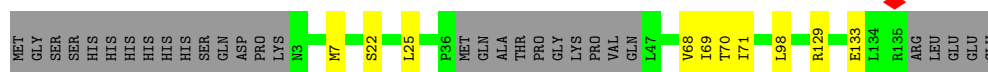
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain DA: 



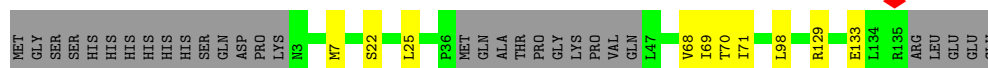
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain EA: 



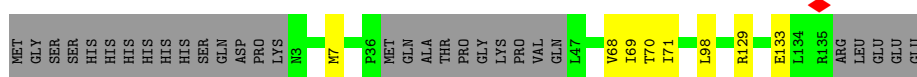
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain FA: 

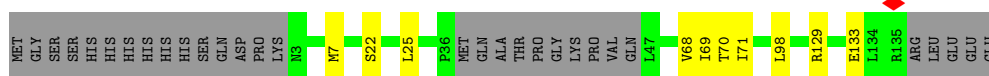
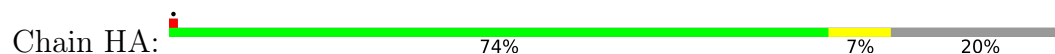


- Molecule 1: TIP60 double mutant (G12C/S50C)

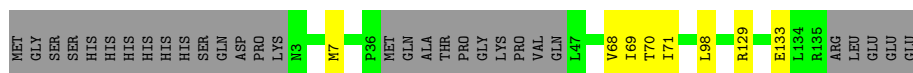
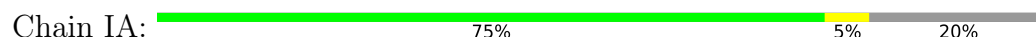
Chain GA: 



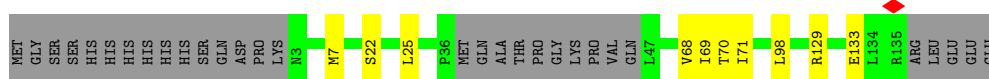
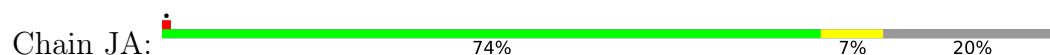
- Molecule 1: TIP60 double mutant (G12C/S50C)



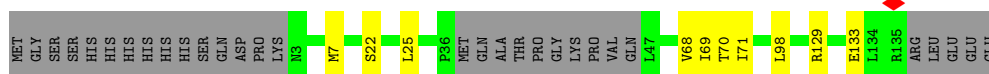
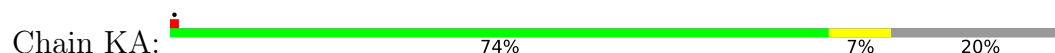
- Molecule 1: TIP60 double mutant (G12C/S50C)



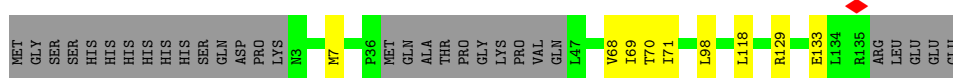
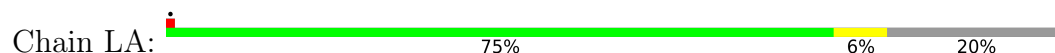
- Molecule 1: TIP60 double mutant (G12C/S50C)



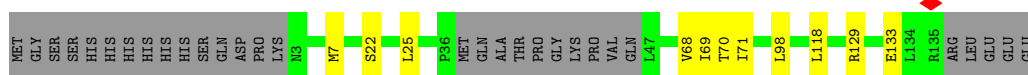
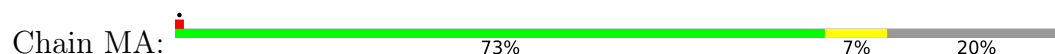
- Molecule 1: TIP60 double mutant (G12C/S50C)



- Molecule 1: TIP60 double mutant (G12C/S50C)

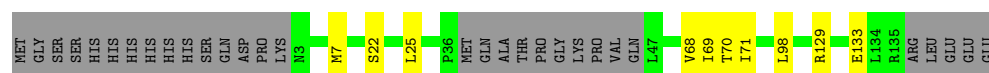


- Molecule 1: TIP60 double mutant (G12C/S50C)



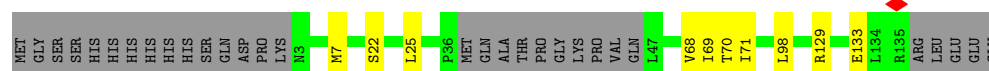
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain NA: 



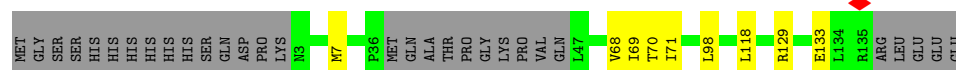
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain OA: 



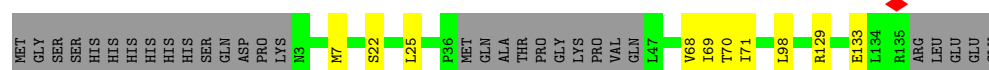
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain PA: 



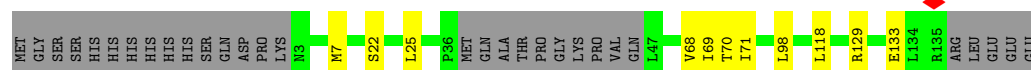
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain QA: 



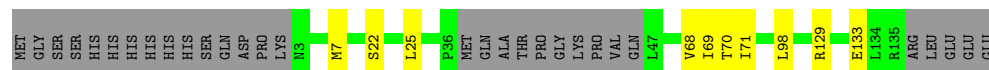
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain RA: 



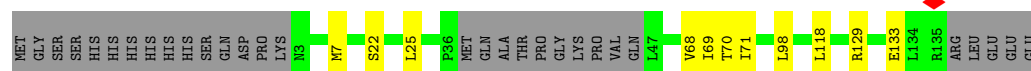
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain SA: 



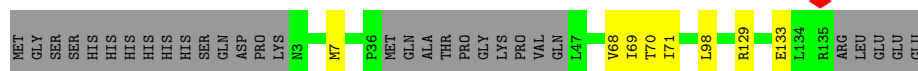
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain TA: 



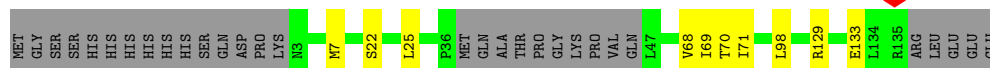
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain UA: 



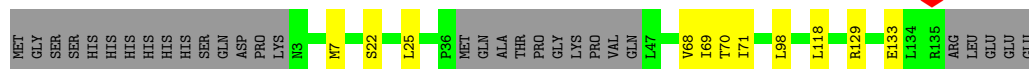
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain VA: 



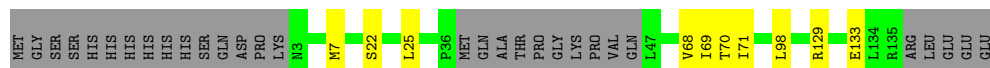
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain WA: 



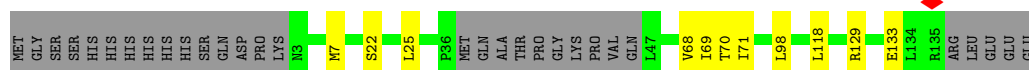
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain XA: 



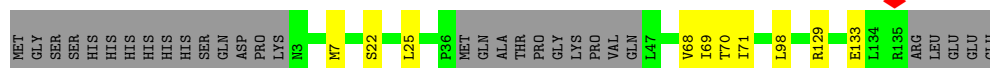
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain YA: 



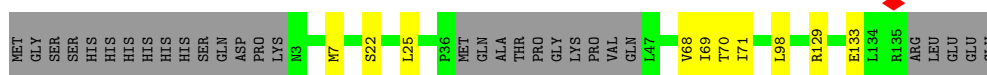
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain ZA: 

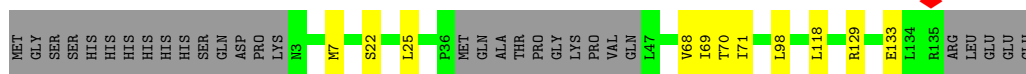
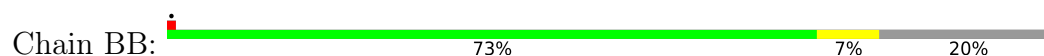


- Molecule 1: TIP60 double mutant (G12C/S50C)

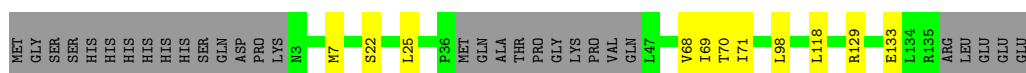
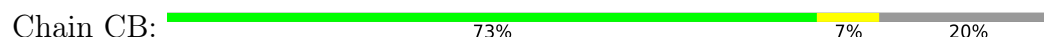
Chain AB: 



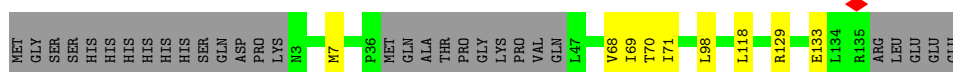
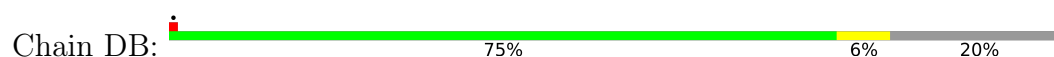
- Molecule 1: TIP60 double mutant (G12C/S50C)



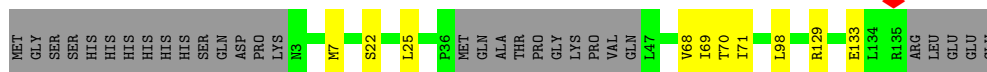
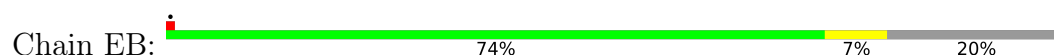
- Molecule 1: TIP60 double mutant (G12C/S50C)



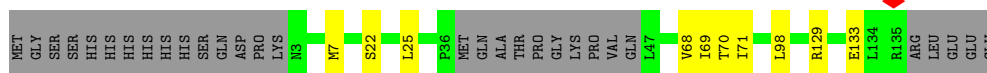
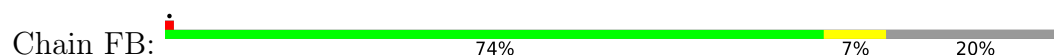
- Molecule 1: TIP60 double mutant (G12C/S50C)



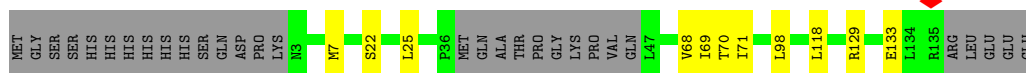
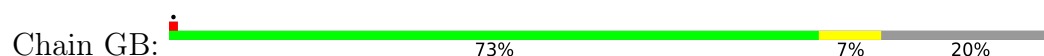
- Molecule 1: TIP60 double mutant (G12C/S50C)



- Molecule 1: TIP60 double mutant (G12C/S50C)



- Molecule 1: TIP60 double mutant (G12C/S50C)



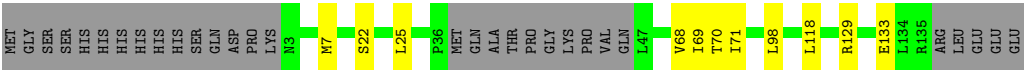
- Molecule 1: TIP60 double mutant (G12C/S50C)

Chain HB:

73%

7%

20%



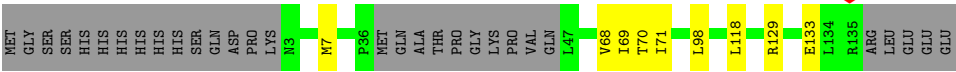
● Molecule 1: TIP60 double mutant (G12C/S50C)

Chain IB:

75%

6%

20%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	22050	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	92000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.015	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	425.088, 425.088, 425.088	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.107, 1.107, 1.107	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1L9F

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	0.11	0/1015	0.34	0/1365
1	AA	0.11	0/1015	0.34	0/1365
1	AB	0.11	0/1015	0.34	0/1365
1	B	0.11	0/1015	0.34	0/1365
1	BA	0.11	0/1015	0.34	0/1365
1	BB	0.11	0/1015	0.34	0/1365
1	C	0.11	0/1015	0.34	0/1365
1	CA	0.11	0/1015	0.34	0/1365
1	CB	0.11	0/1015	0.34	0/1365
1	D	0.11	0/1015	0.34	0/1365
1	DA	0.11	0/1015	0.34	0/1365
1	DB	0.11	0/1015	0.34	0/1365
1	E	0.11	0/1015	0.34	0/1365
1	EA	0.11	0/1015	0.34	0/1365
1	EB	0.11	0/1015	0.34	0/1365
1	F	0.11	0/1015	0.34	0/1365
1	FA	0.11	0/1015	0.34	0/1365
1	FB	0.11	0/1015	0.34	0/1365
1	G	0.11	0/1015	0.34	0/1365
1	GA	0.11	0/1015	0.34	0/1365
1	GB	0.11	0/1015	0.34	0/1365
1	H	0.11	0/1015	0.34	0/1365
1	HA	0.11	0/1015	0.34	0/1365
1	HB	0.11	0/1015	0.34	0/1365
1	I	0.11	0/1015	0.34	0/1365
1	IA	0.11	0/1015	0.34	0/1365
1	IB	0.11	0/1015	0.34	0/1365
1	J	0.11	0/1015	0.34	0/1365
1	JA	0.11	0/1015	0.34	0/1365
1	K	0.11	0/1015	0.34	0/1365
1	KA	0.11	0/1015	0.34	0/1365
1	L	0.11	0/1015	0.34	0/1365

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	LA	0.11	0/1015	0.34	0/1365
1	M	0.11	0/1015	0.34	0/1365
1	MA	0.11	0/1015	0.34	0/1365
1	N	0.11	0/1015	0.34	0/1365
1	NA	0.11	0/1015	0.34	0/1365
1	O	0.11	0/1015	0.34	0/1365
1	OA	0.11	0/1015	0.34	0/1365
1	P	0.11	0/1015	0.34	0/1365
1	PA	0.11	0/1015	0.34	0/1365
1	Q	0.11	0/1015	0.34	0/1365
1	QA	0.11	0/1015	0.34	0/1365
1	R	0.11	0/1015	0.34	0/1365
1	RA	0.11	0/1015	0.34	0/1365
1	S	0.11	0/1015	0.34	0/1365
1	SA	0.11	0/1015	0.34	0/1365
1	T	0.11	0/1015	0.34	0/1365
1	TA	0.11	0/1015	0.34	0/1365
1	UA	0.11	0/1015	0.34	0/1365
1	V	0.11	0/1015	0.34	0/1365
1	VA	0.11	0/1015	0.34	0/1365
1	W	0.11	0/1015	0.34	0/1365
1	WA	0.11	0/1015	0.34	0/1365
1	X	0.11	0/1015	0.34	0/1365
1	XA	0.11	0/1015	0.34	0/1365
1	Y	0.11	0/1015	0.34	0/1365
1	YA	0.11	0/1015	0.34	0/1365
1	Z	0.11	0/1015	0.34	0/1365
1	ZA	0.11	0/1015	0.34	0/1365
All	All	0.11	0/60900	0.34	0/81900

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1007	0	1044	9	0
1	AA	1007	0	1044	8	0
1	AB	1007	0	1044	8	0
1	B	1007	0	1044	8	0
1	BA	1007	0	1044	7	0
1	BB	1007	0	1044	8	0
1	C	1007	0	1044	9	0
1	CA	1007	0	1044	8	0
1	CB	1007	0	1044	9	0
1	D	1007	0	1044	7	0
1	DA	1007	0	1044	6	0
1	DB	1007	0	1044	8	0
1	E	1007	0	1044	7	0
1	EA	1007	0	1044	8	0
1	EB	1007	0	1044	7	0
1	F	1007	0	1044	7	0
1	FA	1007	0	1044	8	0
1	FB	1007	0	1044	8	0
1	G	1007	0	1044	7	0
1	GA	1007	0	1044	7	0
1	GB	1007	0	1044	8	0
1	H	1007	0	1044	7	0
1	HA	1007	0	1044	7	0
1	HB	1007	0	1044	9	0
1	I	1007	0	1044	8	0
1	IA	1007	0	1044	6	0
1	IB	1007	0	1044	8	0
1	J	1007	0	1044	8	0
1	JA	1007	0	1044	8	0
1	K	1007	0	1044	9	0
1	KA	1007	0	1044	7	0
1	L	1007	0	1044	8	0
1	LA	1007	0	1044	7	0
1	M	1007	0	1044	9	0
1	MA	1007	0	1044	9	0
1	N	1007	0	1044	8	0
1	NA	1007	0	1044	7	0
1	O	1007	0	1044	7	0
1	OA	1007	0	1044	8	0
1	P	1007	0	1044	7	0
1	PA	1007	0	1044	8	0
1	Q	1007	0	1044	6	0
1	QA	1007	0	1044	7	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	1007	0	1044	7	0
1	RA	1007	0	1044	8	0
1	S	1007	0	1044	8	0
1	SA	1007	0	1044	8	0
1	T	1007	0	1044	8	0
1	TA	1007	0	1044	9	0
1	UA	1007	0	1044	7	0
1	V	1007	0	1044	7	0
1	VA	1007	0	1044	7	0
1	W	1007	0	1044	6	0
1	WA	1007	0	1044	8	0
1	X	1007	0	1044	8	0
1	XA	1007	0	1044	8	0
1	Y	1007	0	1044	7	0
1	YA	1007	0	1044	9	0
1	Z	1007	0	1044	8	0
1	ZA	1007	0	1044	8	0
2	A	46	0	0	0	0
2	AA	46	0	0	0	0
2	AB	46	0	0	0	0
2	B	46	0	0	0	0
2	BA	46	0	0	0	0
2	BB	46	0	0	0	0
2	C	46	0	0	0	0
2	CA	46	0	0	0	0
2	CB	46	0	0	0	0
2	D	46	0	0	0	0
2	DA	46	0	0	0	0
2	DB	46	0	0	0	0
2	E	46	0	0	0	0
2	EA	46	0	0	0	0
2	EB	46	0	0	0	0
2	F	46	0	0	0	0
2	FA	46	0	0	0	0
2	FB	46	0	0	0	0
2	G	46	0	0	0	0
2	GA	46	0	0	0	0
2	GB	46	0	0	0	0
2	H	46	0	0	0	0
2	HA	46	0	0	0	0
2	HB	46	0	0	0	0
2	I	46	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	IA	46	0	0	0	0
2	IB	46	0	0	0	0
2	J	46	0	0	0	0
2	JA	46	0	0	0	0
2	K	46	0	0	0	0
2	KA	46	0	0	0	0
2	L	46	0	0	0	0
2	LA	46	0	0	0	0
2	M	46	0	0	0	0
2	MA	46	0	0	0	0
2	N	46	0	0	0	0
2	NA	46	0	0	0	0
2	O	46	0	0	0	0
2	OA	46	0	0	0	0
2	P	46	0	0	0	0
2	PA	46	0	0	0	0
2	Q	46	0	0	0	0
2	QA	46	0	0	0	0
2	R	46	0	0	0	0
2	RA	46	0	0	0	0
2	S	46	0	0	0	0
2	SA	46	0	0	0	0
2	T	46	0	0	0	0
2	TA	46	0	0	0	0
2	UA	46	0	0	0	0
2	V	46	0	0	0	0
2	VA	46	0	0	0	0
2	W	46	0	0	0	0
2	WA	46	0	0	0	0
2	X	46	0	0	0	0
2	XA	46	0	0	0	0
2	Y	46	0	0	0	0
2	YA	46	0	0	0	0
2	Z	46	0	0	0	0
2	ZA	46	0	0	0	0
All	All	63180	0	62640	401	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 401 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:DA:7:MET:HE1	1:DA:68:VAL:HG13	1.59	0.85
1:IA:7:MET:HE1	1:IA:68:VAL:HG13	1.59	0.85
1:GB:7:MET:HE1	1:GB:68:VAL:HG13	1.59	0.85
1:BB:7:MET:HE1	1:BB:68:VAL:HG13	1.59	0.85
1:AA:7:MET:HE1	1:AA:68:VAL:HG13	1.58	0.85

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	AA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	AB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	B	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	BA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	BB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	C	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	CA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	CB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	D	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	DA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	DB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	E	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	EA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	EB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	F	119/153 (78%)	116 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	FB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	G	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	GA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	GB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	H	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	HA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	HB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	I	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	IA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	IB	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	J	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	JA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	K	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	KA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	L	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	LA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	M	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	MA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	N	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	NA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	O	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	OA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	P	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	PA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	Q	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	QA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	R	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	RA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	S	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	SA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	TA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	UA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	V	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	VA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	W	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	WA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	X	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	XA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	Y	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	YA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	Z	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
1	ZA	119/153 (78%)	116 (98%)	3 (2%)	0	100	100
All	All	7140/9180 (78%)	6960 (98%)	180 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	119/146 (82%)	119 (100%)	0	100	100
1	AA	119/146 (82%)	119 (100%)	0	100	100
1	AB	119/146 (82%)	119 (100%)	0	100	100
1	B	119/146 (82%)	119 (100%)	0	100	100
1	BA	119/146 (82%)	119 (100%)	0	100	100
1	BB	119/146 (82%)	119 (100%)	0	100	100
1	C	119/146 (82%)	119 (100%)	0	100	100
1	CA	119/146 (82%)	119 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CB	119/146 (82%)	119 (100%)	0	100	100
1	D	119/146 (82%)	119 (100%)	0	100	100
1	DA	119/146 (82%)	119 (100%)	0	100	100
1	DB	119/146 (82%)	119 (100%)	0	100	100
1	E	119/146 (82%)	119 (100%)	0	100	100
1	EA	119/146 (82%)	119 (100%)	0	100	100
1	EB	119/146 (82%)	119 (100%)	0	100	100
1	F	119/146 (82%)	119 (100%)	0	100	100
1	FA	119/146 (82%)	119 (100%)	0	100	100
1	FB	119/146 (82%)	119 (100%)	0	100	100
1	G	119/146 (82%)	119 (100%)	0	100	100
1	GA	119/146 (82%)	119 (100%)	0	100	100
1	GB	119/146 (82%)	119 (100%)	0	100	100
1	H	119/146 (82%)	119 (100%)	0	100	100
1	HA	119/146 (82%)	119 (100%)	0	100	100
1	HB	119/146 (82%)	119 (100%)	0	100	100
1	I	119/146 (82%)	119 (100%)	0	100	100
1	IA	119/146 (82%)	119 (100%)	0	100	100
1	IB	119/146 (82%)	119 (100%)	0	100	100
1	J	119/146 (82%)	119 (100%)	0	100	100
1	JA	119/146 (82%)	119 (100%)	0	100	100
1	K	119/146 (82%)	119 (100%)	0	100	100
1	KA	119/146 (82%)	119 (100%)	0	100	100
1	L	119/146 (82%)	119 (100%)	0	100	100
1	LA	119/146 (82%)	119 (100%)	0	100	100
1	M	119/146 (82%)	119 (100%)	0	100	100
1	MA	119/146 (82%)	119 (100%)	0	100	100
1	N	119/146 (82%)	119 (100%)	0	100	100
1	NA	119/146 (82%)	119 (100%)	0	100	100
1	O	119/146 (82%)	119 (100%)	0	100	100
1	OA	119/146 (82%)	119 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	119/146 (82%)	119 (100%)	0	100	100
1	PA	119/146 (82%)	119 (100%)	0	100	100
1	Q	119/146 (82%)	119 (100%)	0	100	100
1	QA	119/146 (82%)	119 (100%)	0	100	100
1	R	119/146 (82%)	119 (100%)	0	100	100
1	RA	119/146 (82%)	119 (100%)	0	100	100
1	S	119/146 (82%)	119 (100%)	0	100	100
1	SA	119/146 (82%)	119 (100%)	0	100	100
1	T	119/146 (82%)	119 (100%)	0	100	100
1	TA	119/146 (82%)	119 (100%)	0	100	100
1	UA	119/146 (82%)	119 (100%)	0	100	100
1	V	119/146 (82%)	119 (100%)	0	100	100
1	VA	119/146 (82%)	119 (100%)	0	100	100
1	W	119/146 (82%)	119 (100%)	0	100	100
1	WA	119/146 (82%)	119 (100%)	0	100	100
1	X	119/146 (82%)	119 (100%)	0	100	100
1	XA	119/146 (82%)	119 (100%)	0	100	100
1	Y	119/146 (82%)	119 (100%)	0	100	100
1	YA	119/146 (82%)	119 (100%)	0	100	100
1	Z	119/146 (82%)	119 (100%)	0	100	100
1	ZA	119/146 (82%)	119 (100%)	0	100	100
All	All	7140/8760 (82%)	7140 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	85	HIS
1	CA	85	HIS
1	HB	85	HIS
1	ZA	85	HIS
1	CB	85	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

120 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	$\# Z > 2$
2	A1L9F	D	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	H	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	W	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	NA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	K	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	B	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	Z	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	L	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	KA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	XA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	EA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	HA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	FB	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	M	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1L9F	QA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	GA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	HB	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	N	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	X	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	CB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	BB	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	AB	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	OA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	R	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	TA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	AA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	SA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	Q	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	K	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	Y	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	EB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	G	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	XA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	T	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	HA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	IB	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	O	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	FA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	M	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	LA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	F	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	H	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	O	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	Z	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	GA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	CB	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	KA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	A	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	YA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1L9F	J	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	FA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	TA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	R	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	S	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	UA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	BA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	RA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	MA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	DB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	W	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	PA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	JA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	P	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	WA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	GB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	C	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	DA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	E	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	P	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	S	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	GB	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	D	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	V	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	DA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	B	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	IA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	J	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	L	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	MA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	V	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	IA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	JA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	Q	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	BA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1L9F	I	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	BB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	VA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	C	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	AB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	E	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	RA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	SA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	YA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	WA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	DB	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	IB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	QA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	T	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	Y	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	I	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	ZA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	UA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	CA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	OA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	PA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	EA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	LA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	AA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	VA	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	A	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	CA	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	EB	201	1	27,27,27	2.46	10 (37%)	41,41,41	0.87	0
2	A1L9F	X	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	FB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	N	201	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	HB	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	G	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	F	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0
2	A1L9F	NA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1L9F	ZA	202	1	27,27,27	2.45	10 (37%)	41,41,41	0.87	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
2	A1L9F	D	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	H	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	W	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	NA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	K	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	B	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	Z	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	L	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	KA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	XA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	EA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	HA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	FB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	M	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	QA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	GA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	HB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	N	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	X	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	CB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	BB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	AB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	OA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	R	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	TA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	AA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	SA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	Q	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	K	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	Y	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	EB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	G	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	XA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	T	201	1	-	0/4/17/17	0/5/5/5

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A1L9F	HA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	IB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	O	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	FA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	M	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	LA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	F	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	H	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	O	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	Z	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	GA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	CB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	KA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	A	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	YA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	J	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	FA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	TA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	R	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	S	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	UA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	BA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	RA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	MA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	DB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	W	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	PA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	JA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	P	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	WA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	GB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	C	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	DA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	E	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	P	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	S	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	GB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	D	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	V	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	DA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	B	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	IA	201	1	-	0/4/17/17	0/5/5/5

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A1L9F	J	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	L	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	MA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	V	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	IA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	JA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	Q	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	BA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	I	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	BB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	VA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	C	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	AB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	E	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	RA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	SA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	YA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	WA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	DB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	IB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	QA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	T	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	Y	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	I	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	ZA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	UA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	CA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	OA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	PA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	EA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	LA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	AA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	VA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	A	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	CA	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	EB	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	X	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	FB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	N	201	1	-	0/4/17/17	0/5/5/5
2	A1L9F	HB	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	G	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	F	202	1	-	0/4/17/17	0/5/5/5

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A1L9F	NA	202	1	-	0/4/17/17	0/5/5/5
2	A1L9F	ZA	202	1	-	0/4/17/17	0/5/5/5

The worst 5 of 1200 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	A1L9F	C04-C05	-5.44	1.38	1.48
2	F	201	A1L9F	C04-C05	-5.44	1.38	1.48
2	K	201	A1L9F	C04-C05	-5.44	1.38	1.48
2	P	201	A1L9F	C04-C05	-5.44	1.38	1.48
2	V	201	A1L9F	C04-C05	-5.44	1.38	1.48

There are no bond angle outliers.

There are no chirality outliers.

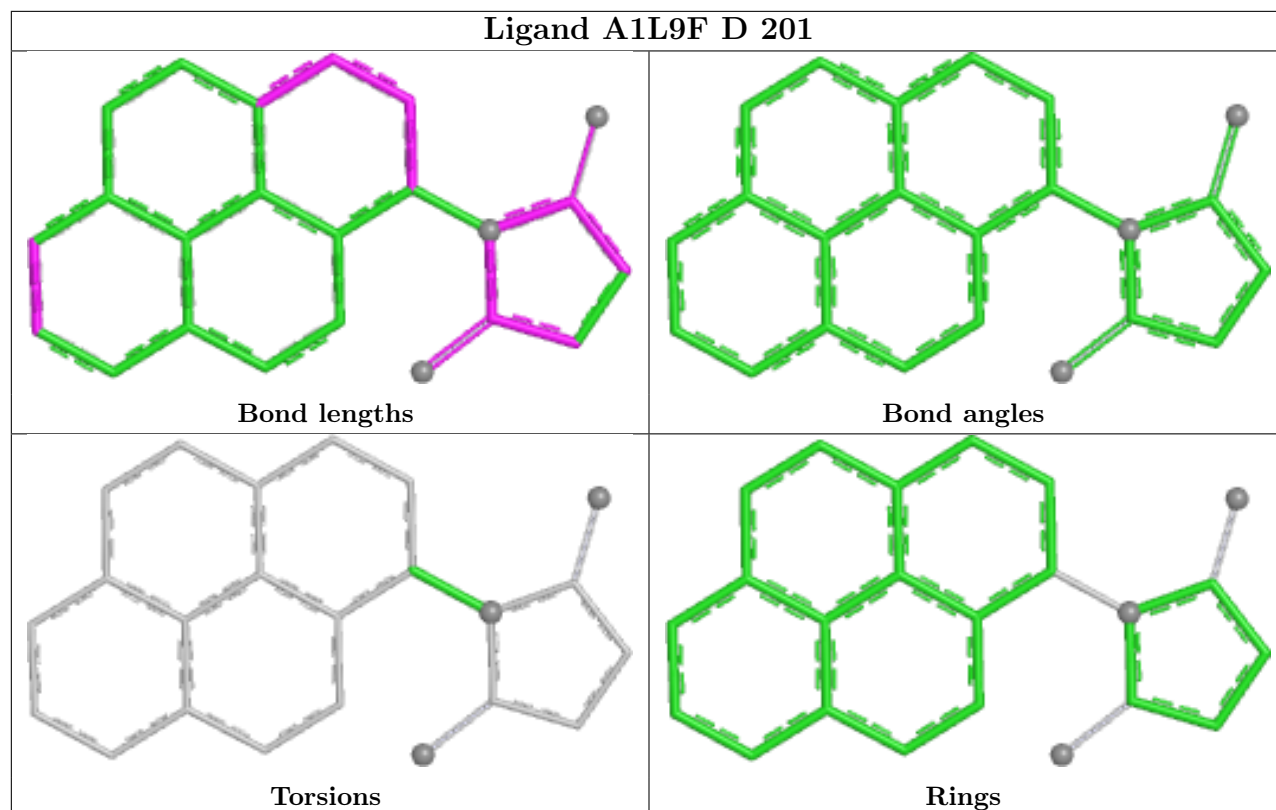
There are no torsion outliers.

There are no ring outliers.

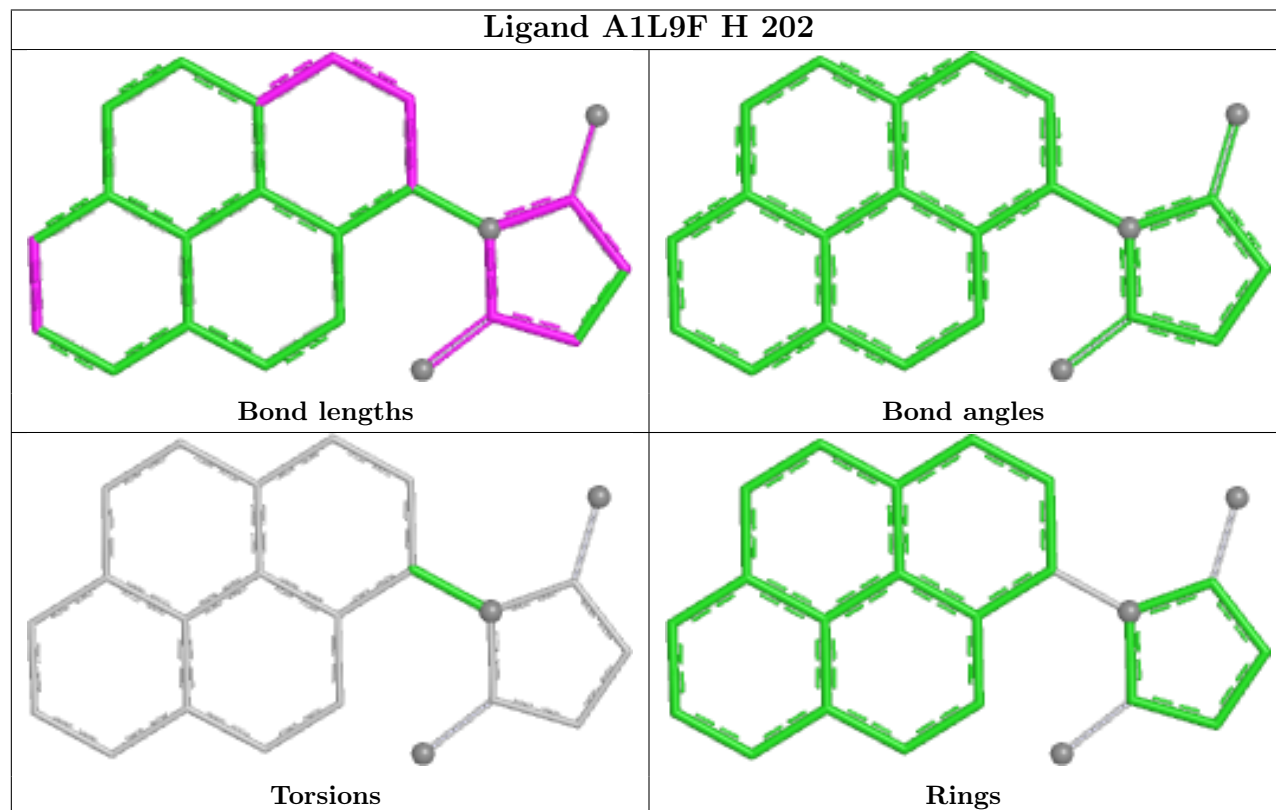
No monomer is involved in short contacts.

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

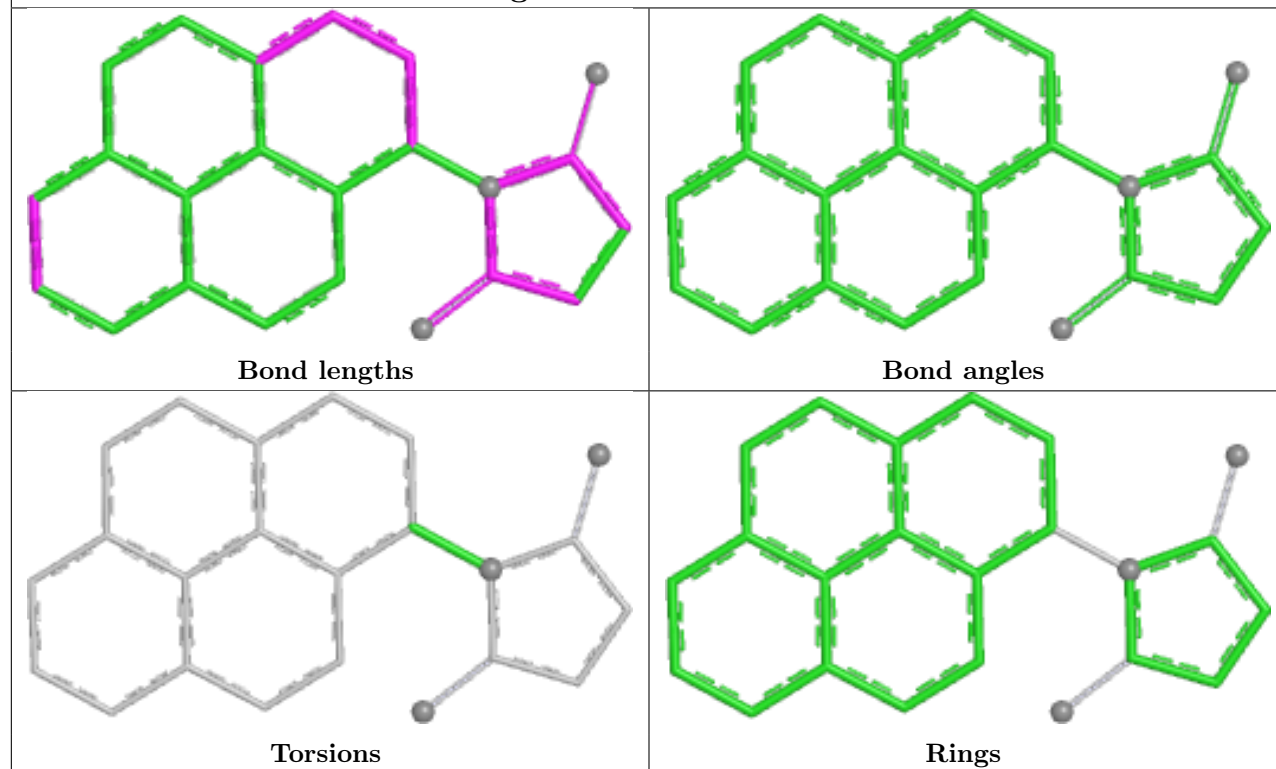
Ligand A1L9F D 201



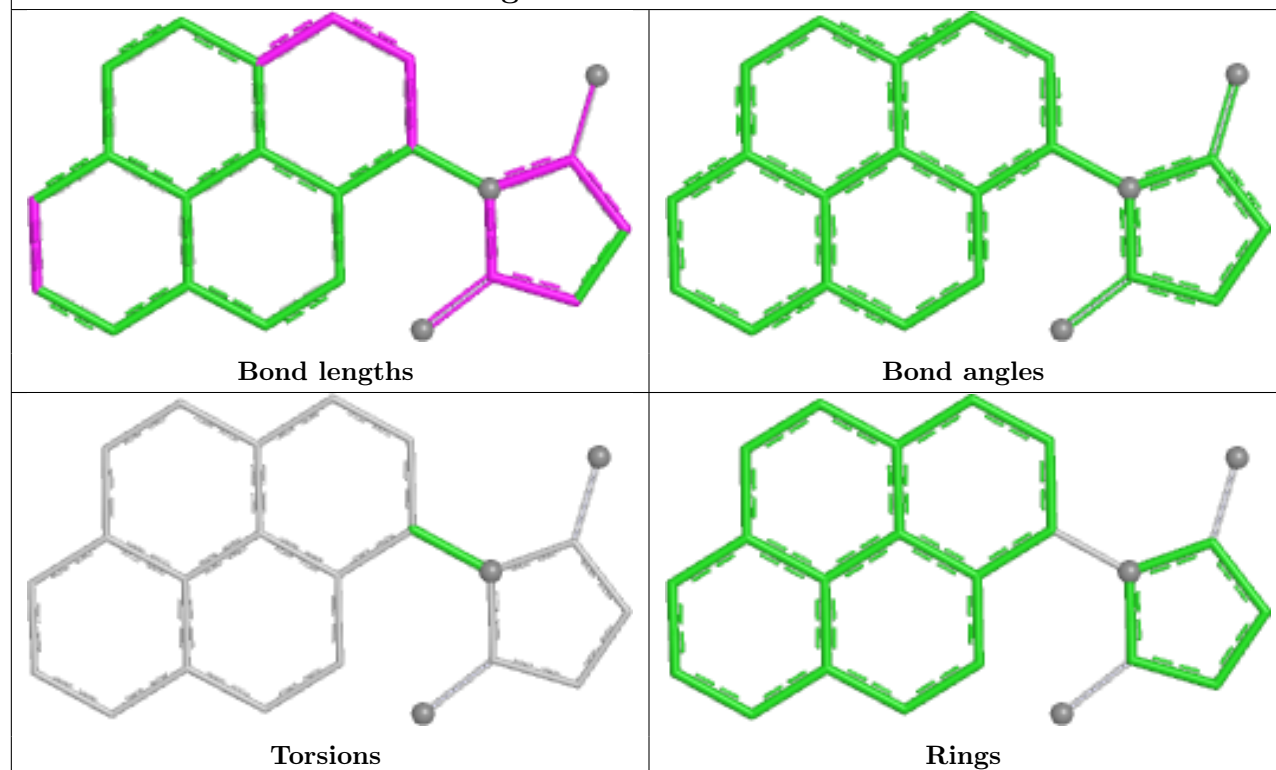
Ligand A1L9F H 202



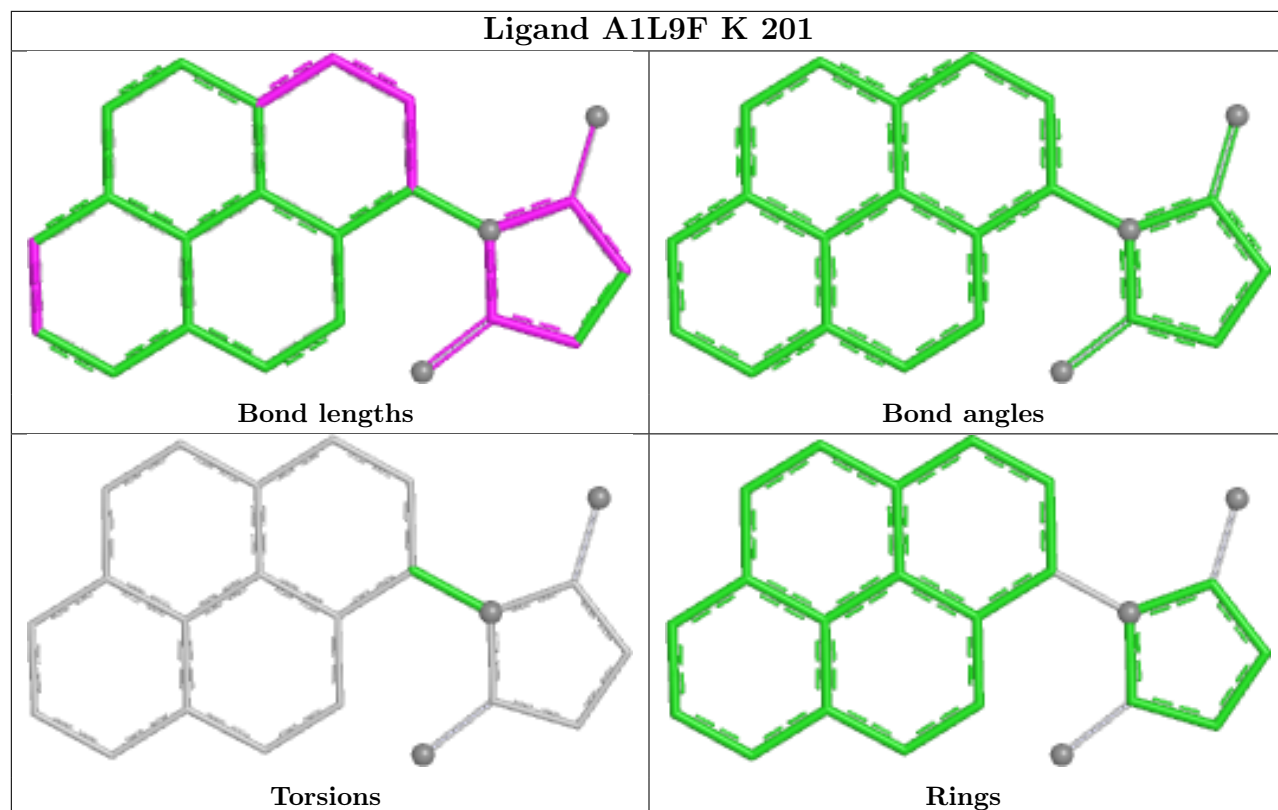
Ligand A1L9F W 202



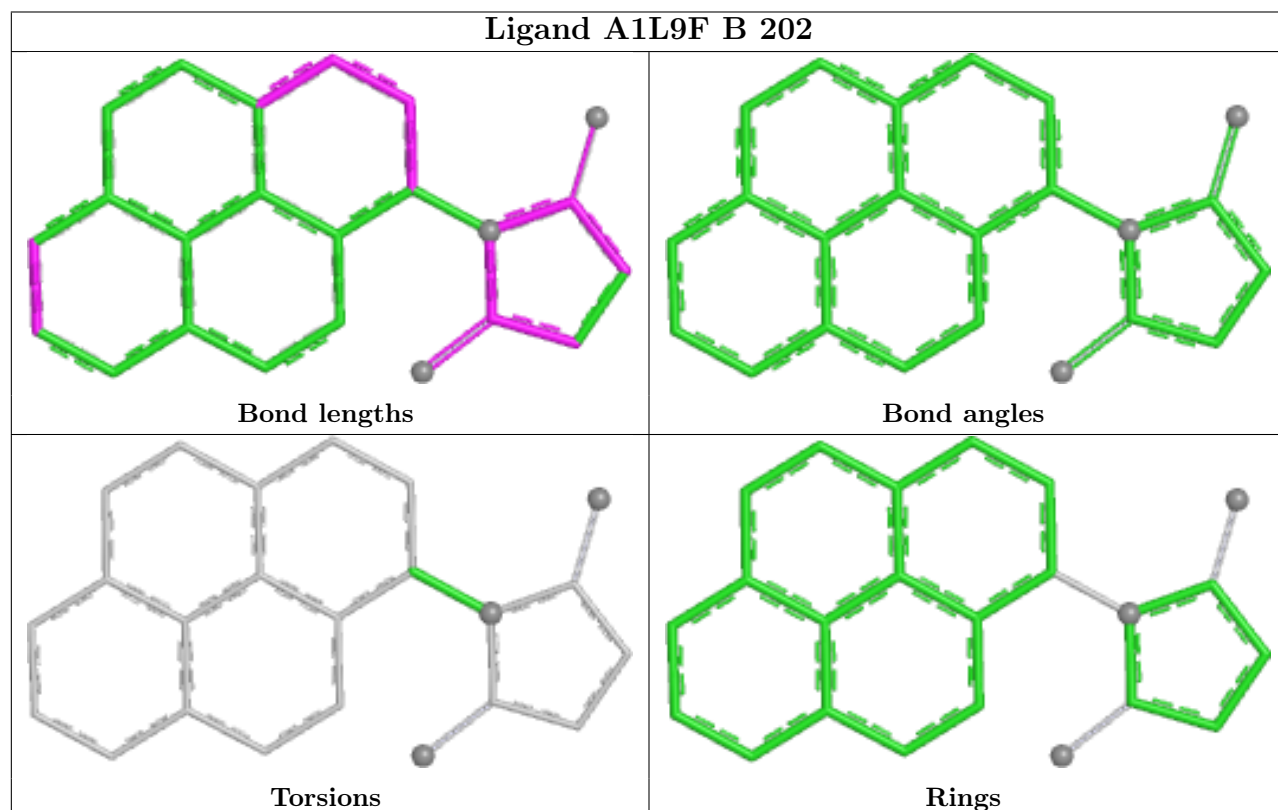
Ligand A1L9F NA 201



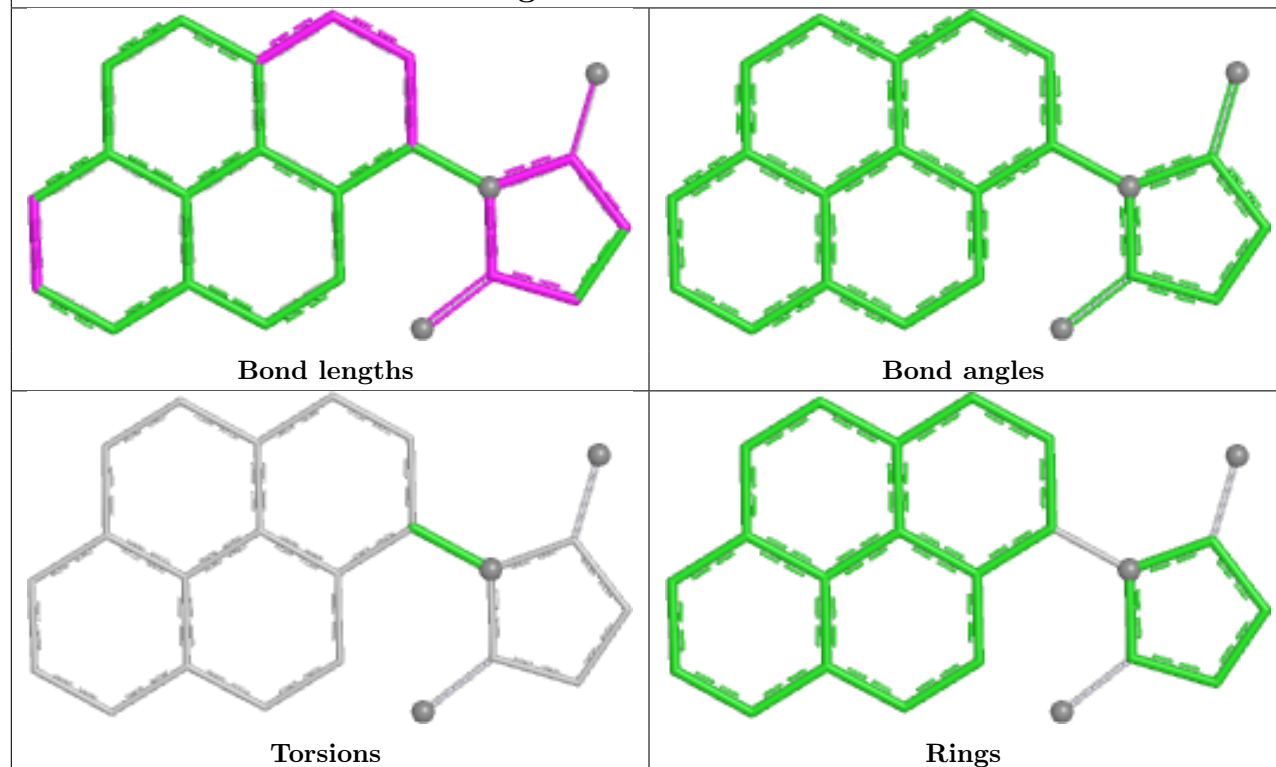
Ligand A1L9F K 201



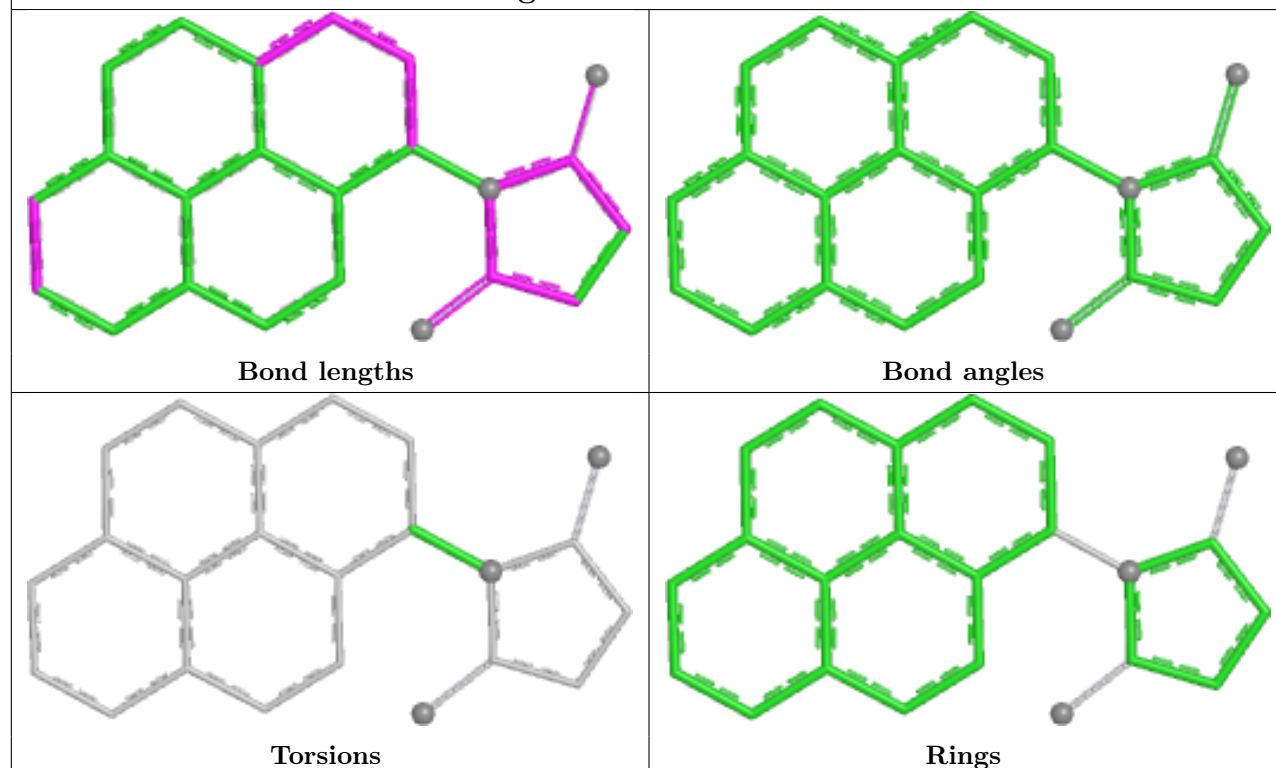
Ligand A1L9F B 202



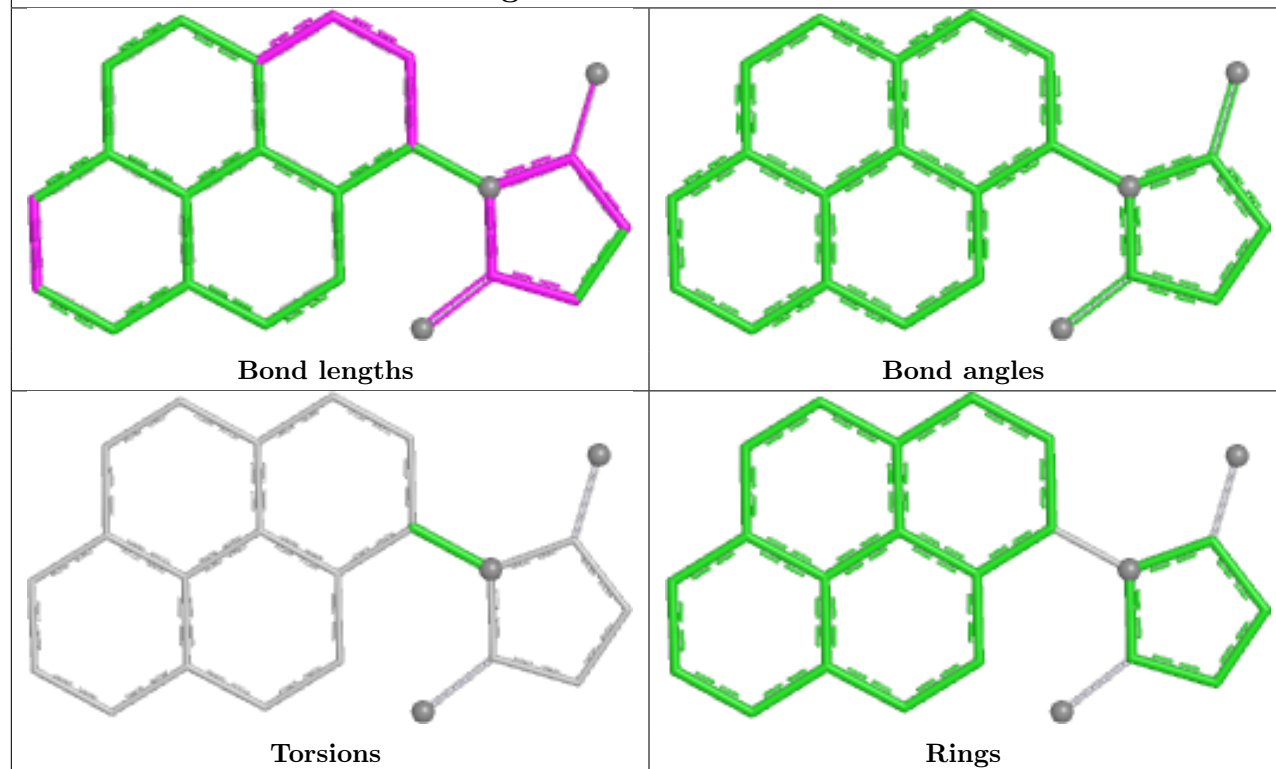
Ligand A1L9F Z 201



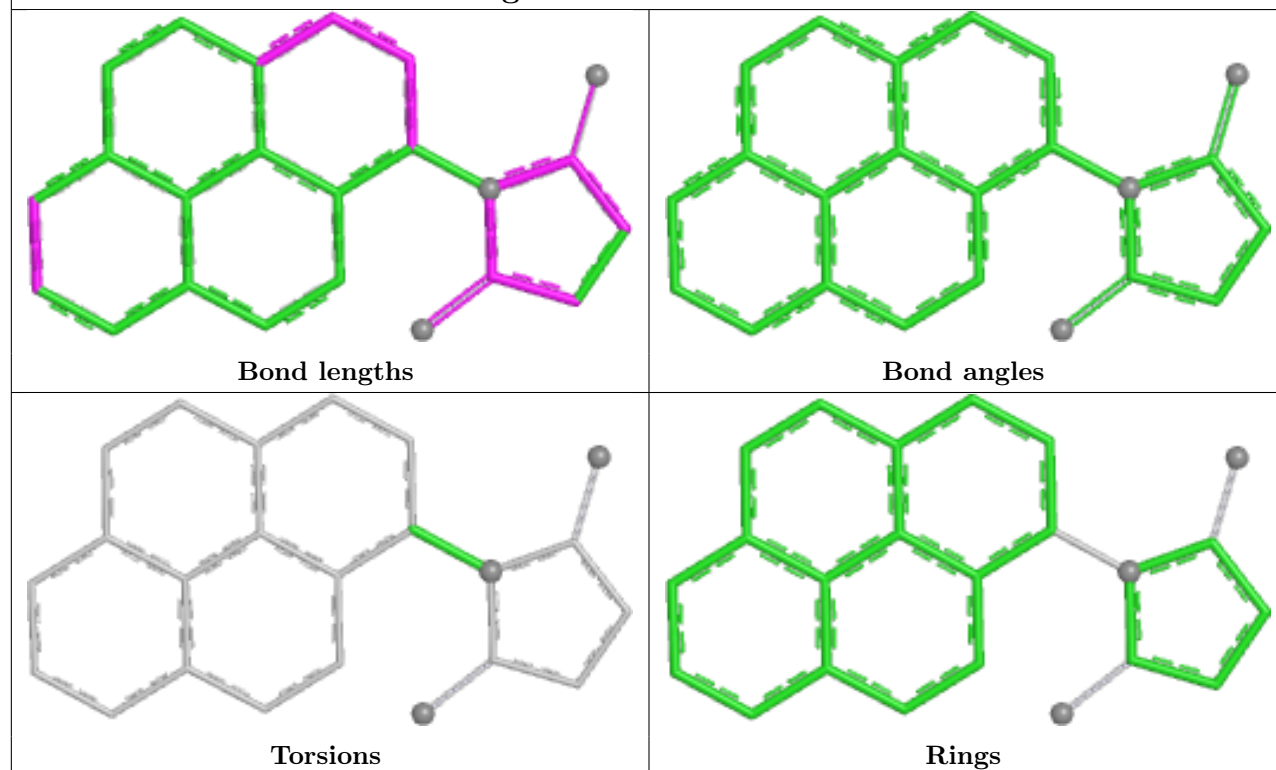
Ligand A1L9F L 202



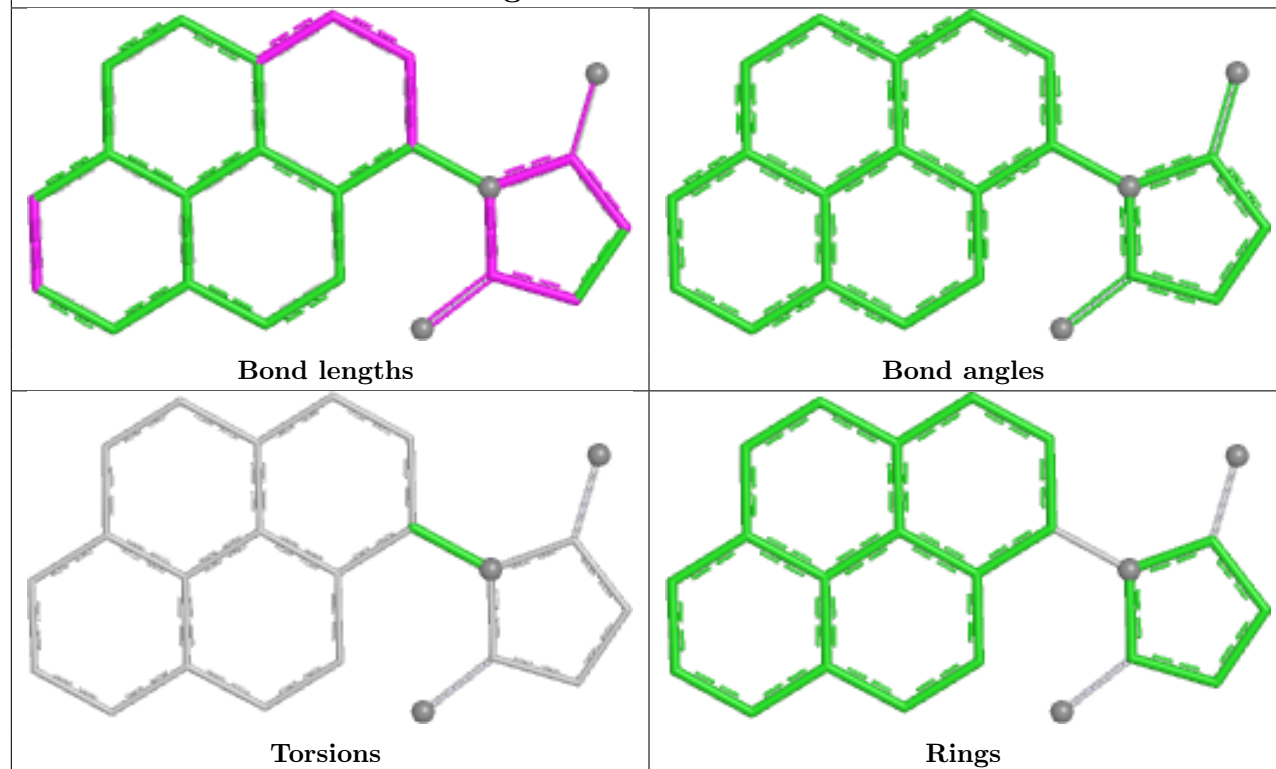
Ligand A1L9F KA 201



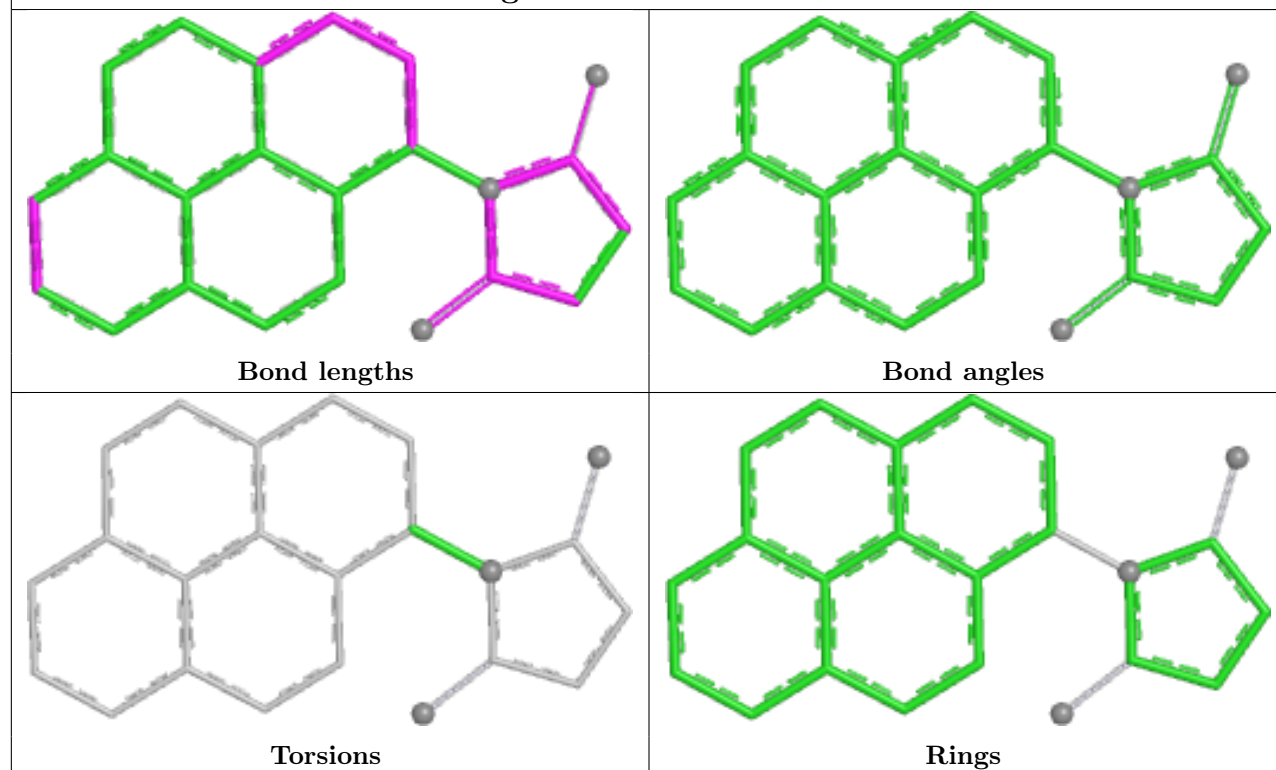
Ligand A1L9F XA 202



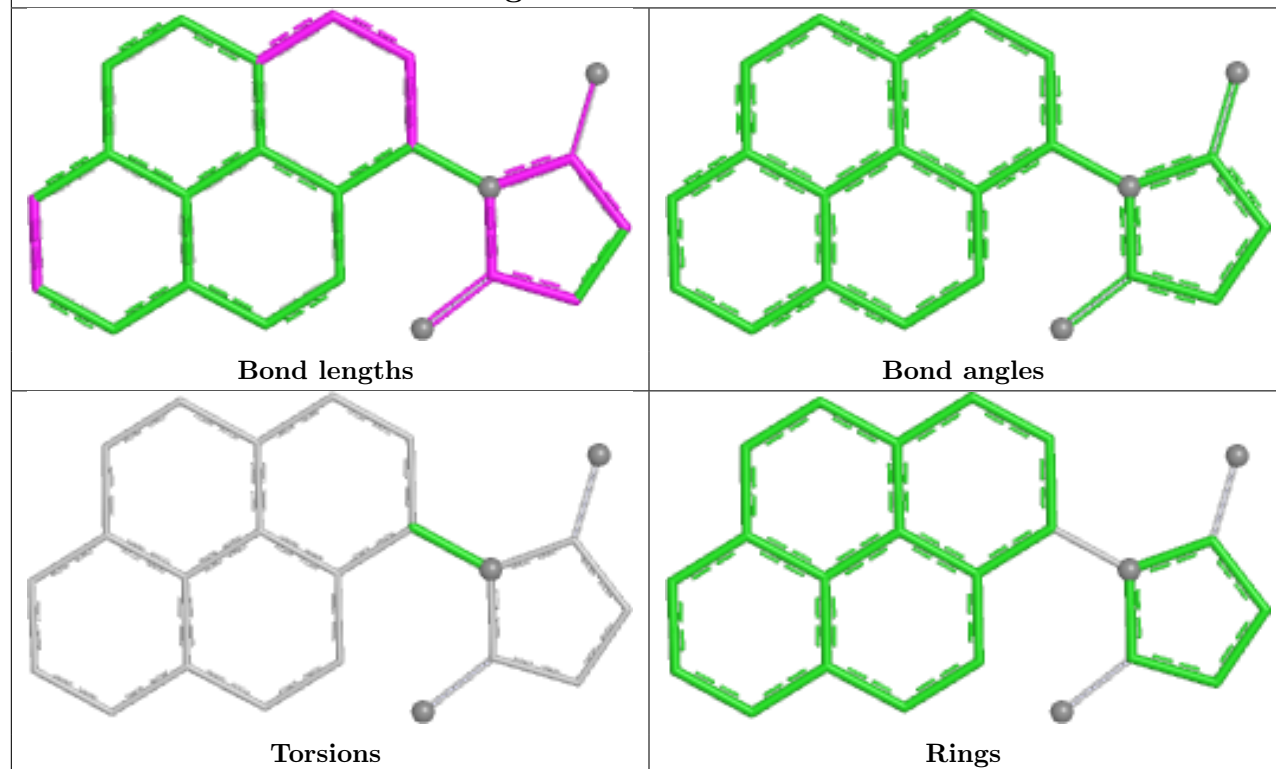
Ligand A1L9F EA 201



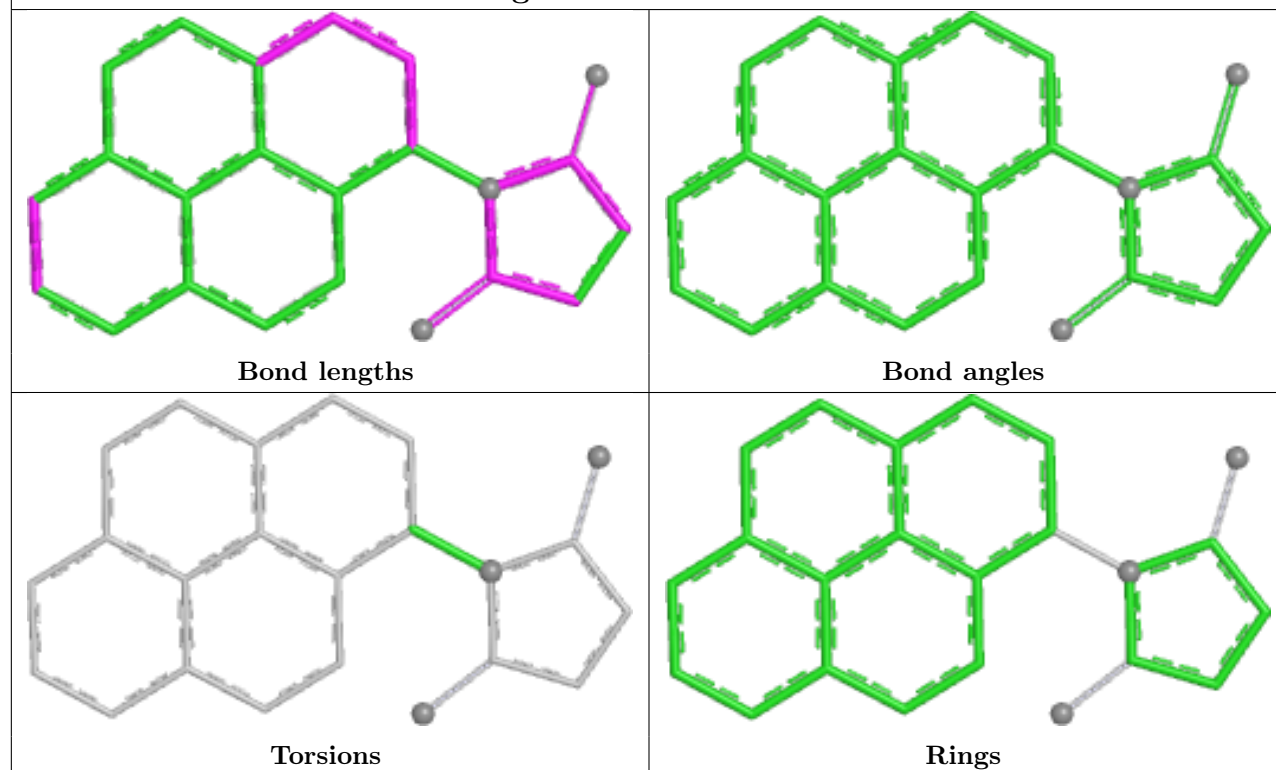
Ligand A1L9F HA 202



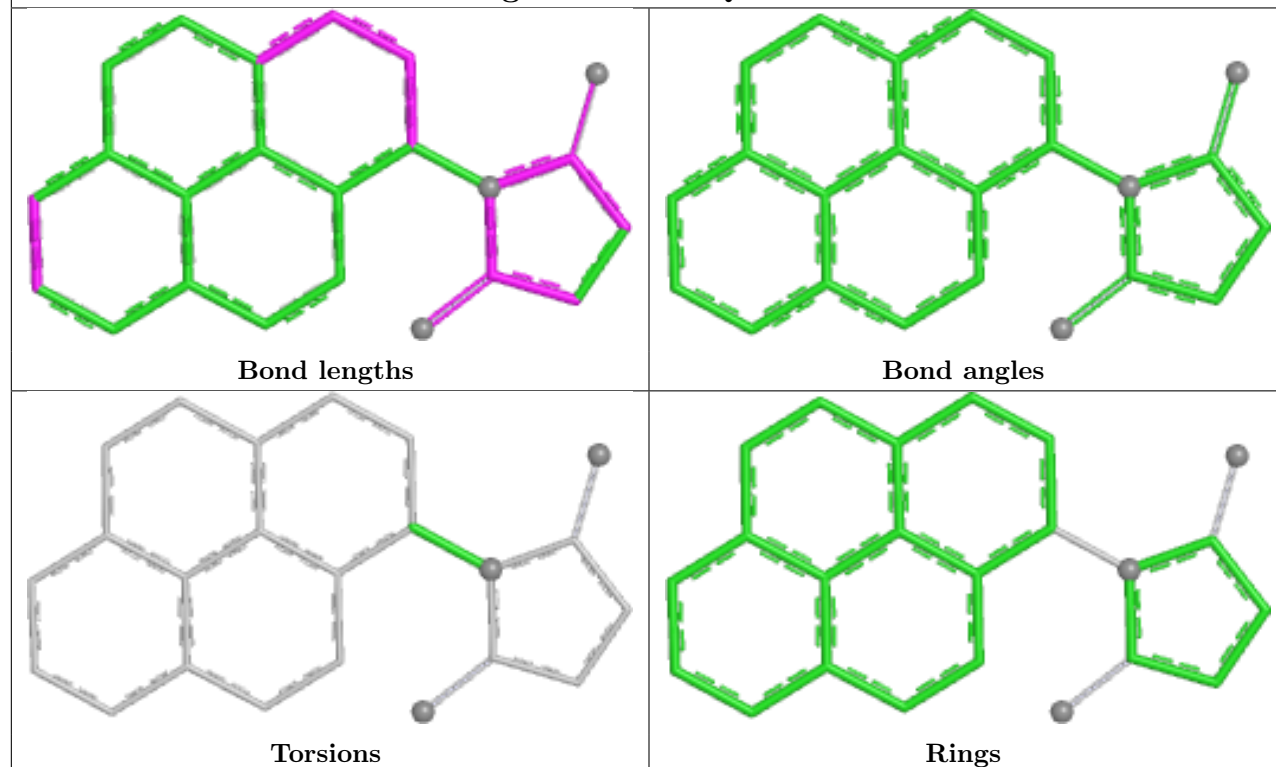
Ligand A1L9F FB 201



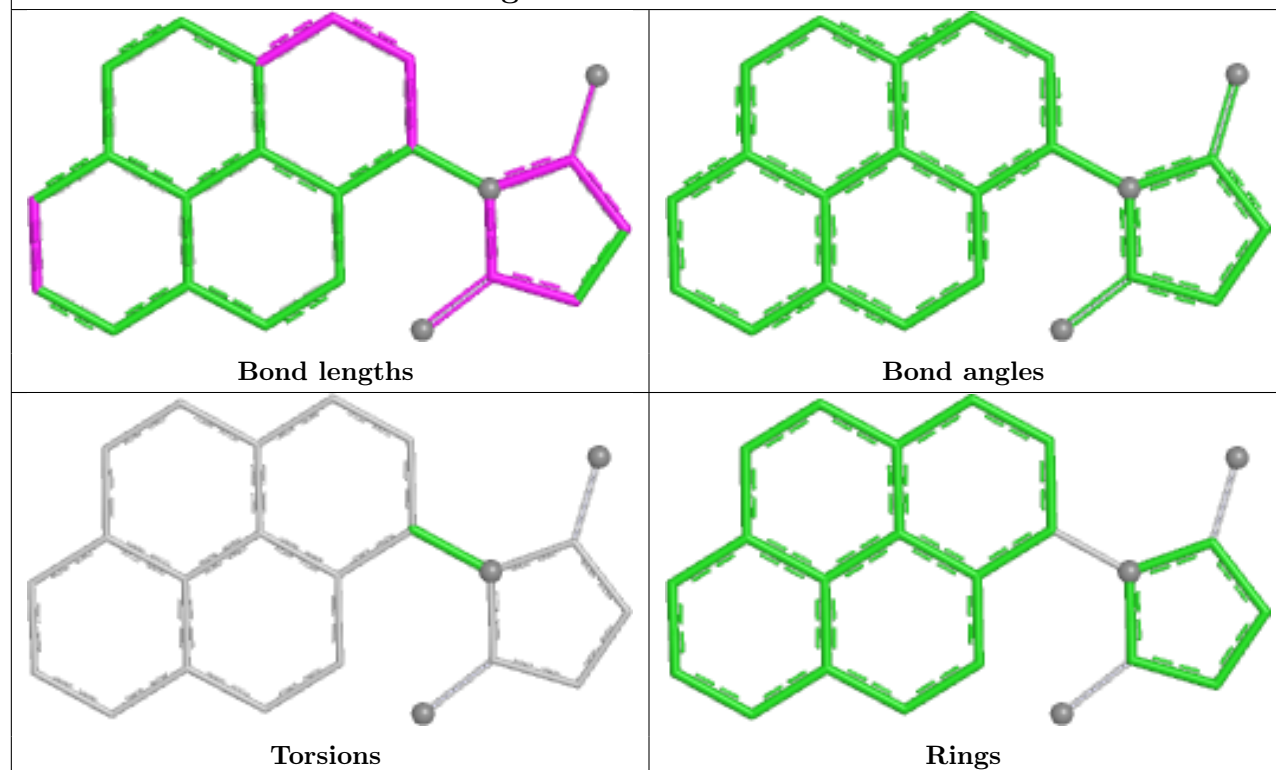
Ligand A1L9F M 201



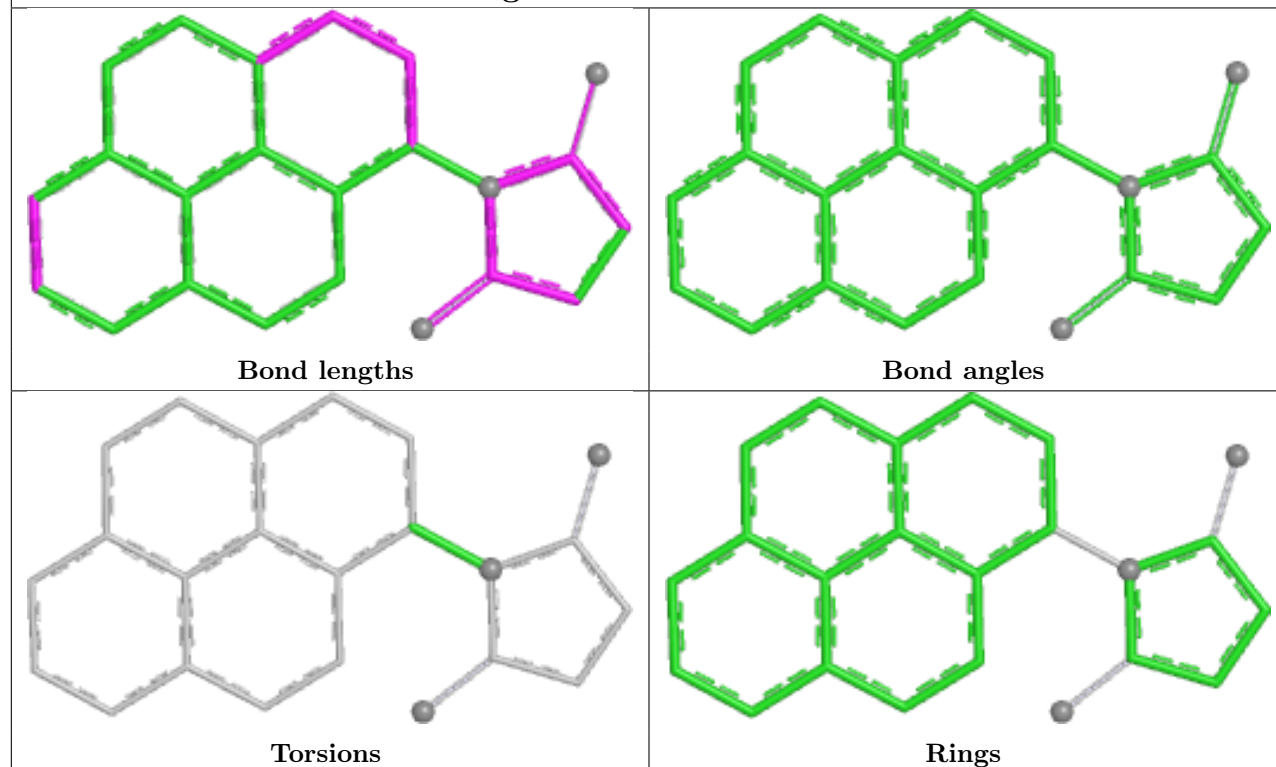
Ligand A1L9F QA 201



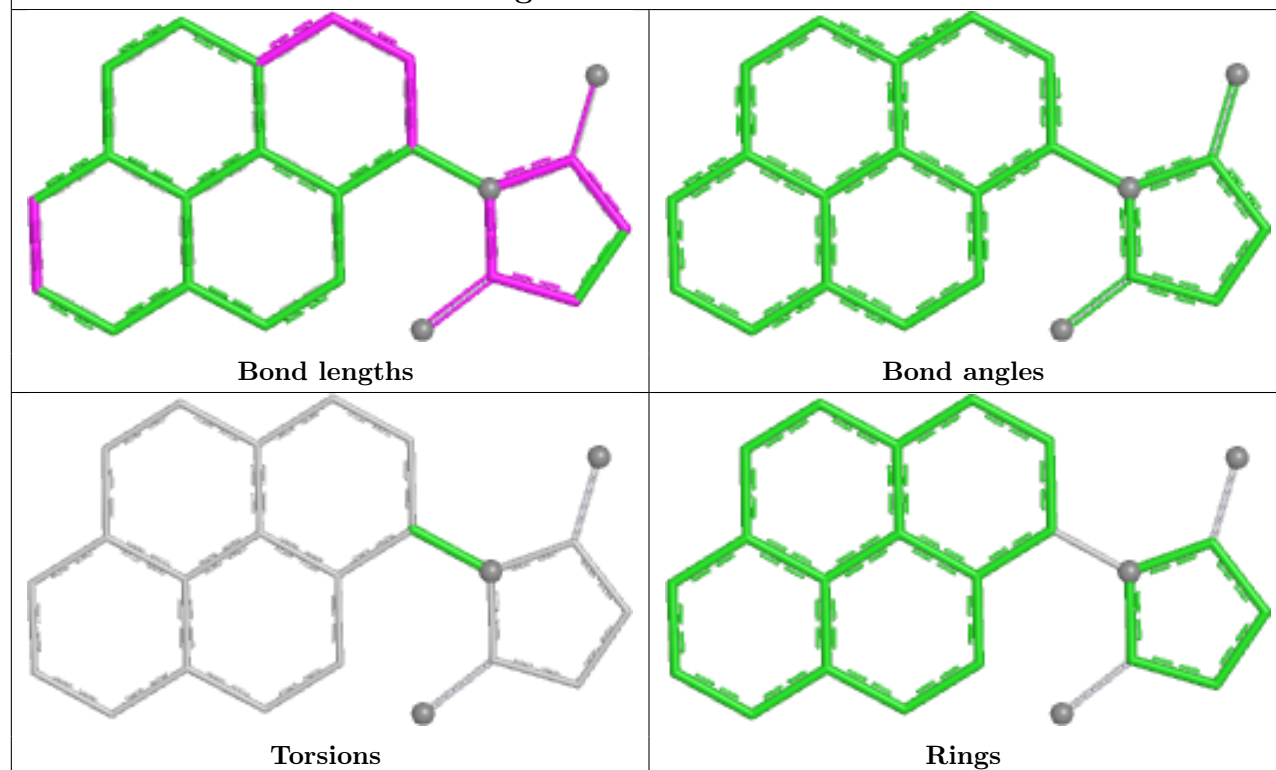
Ligand A1L9F GA 201



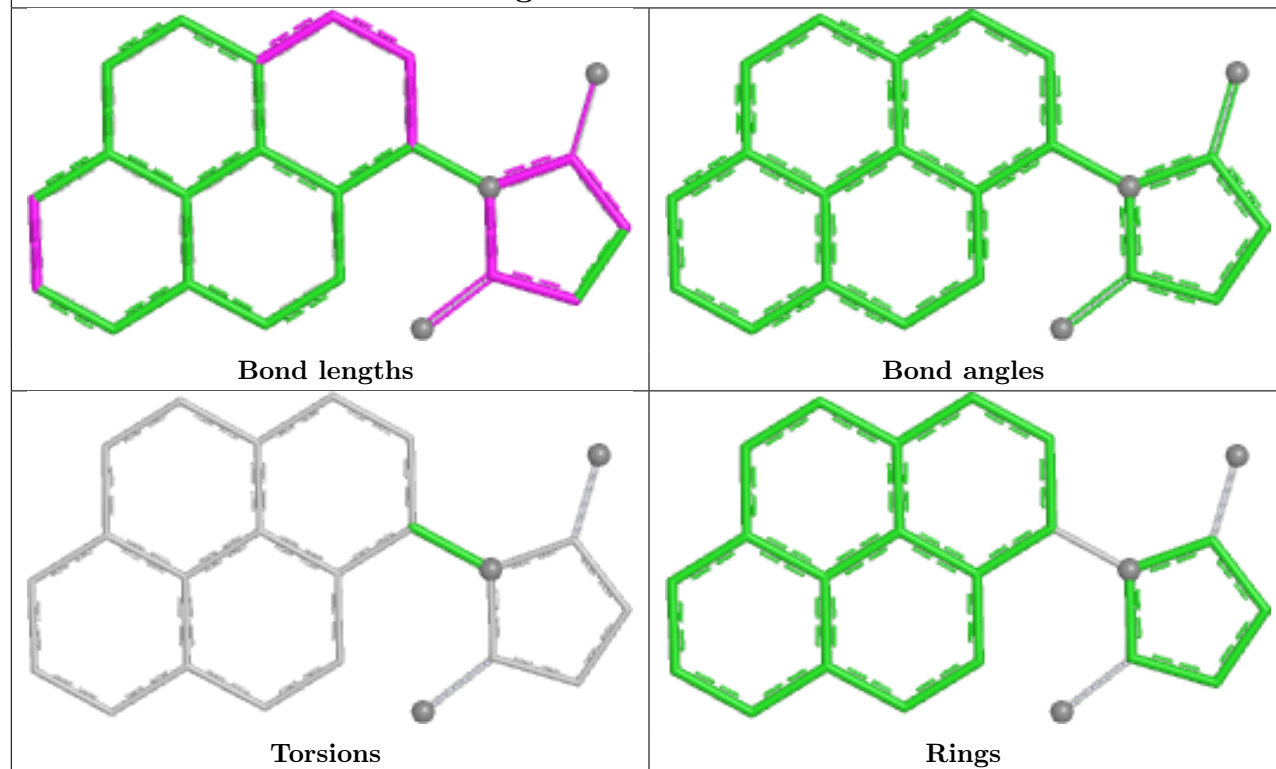
Ligand A1L9F HB 201



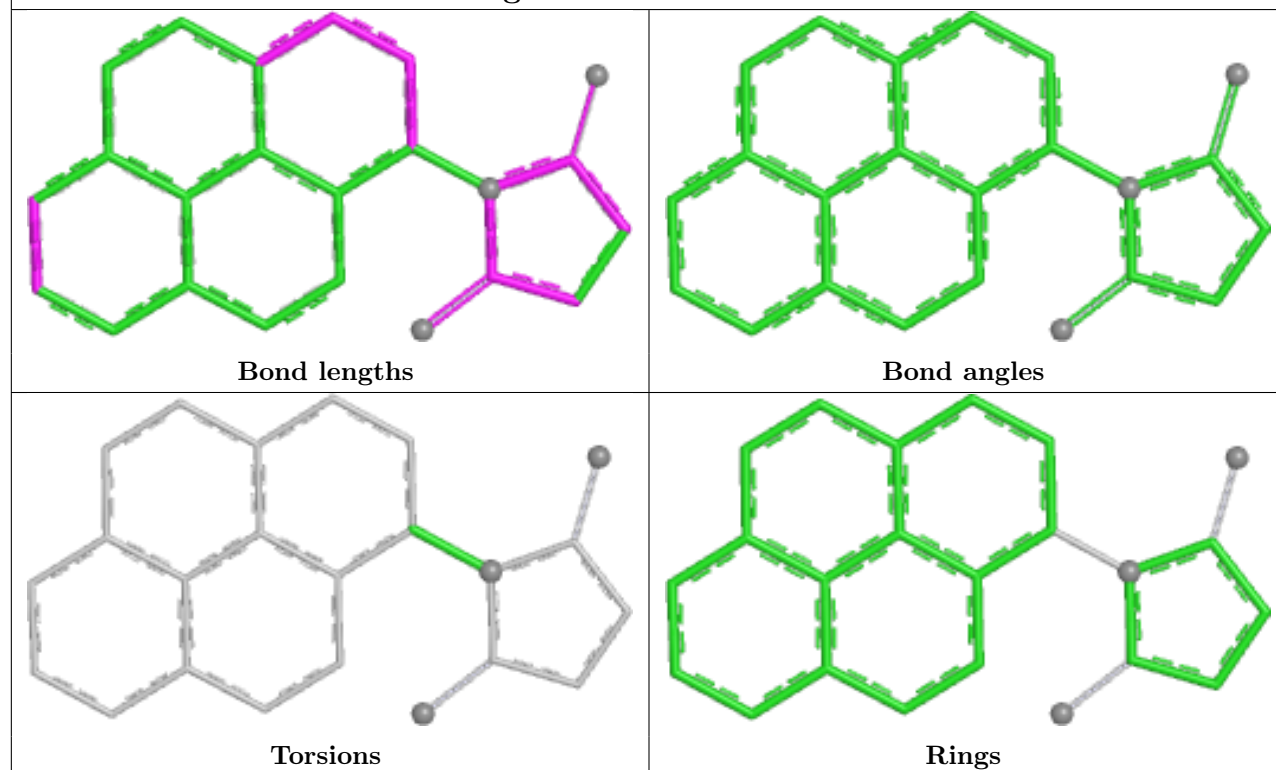
Ligand A1L9F N 202



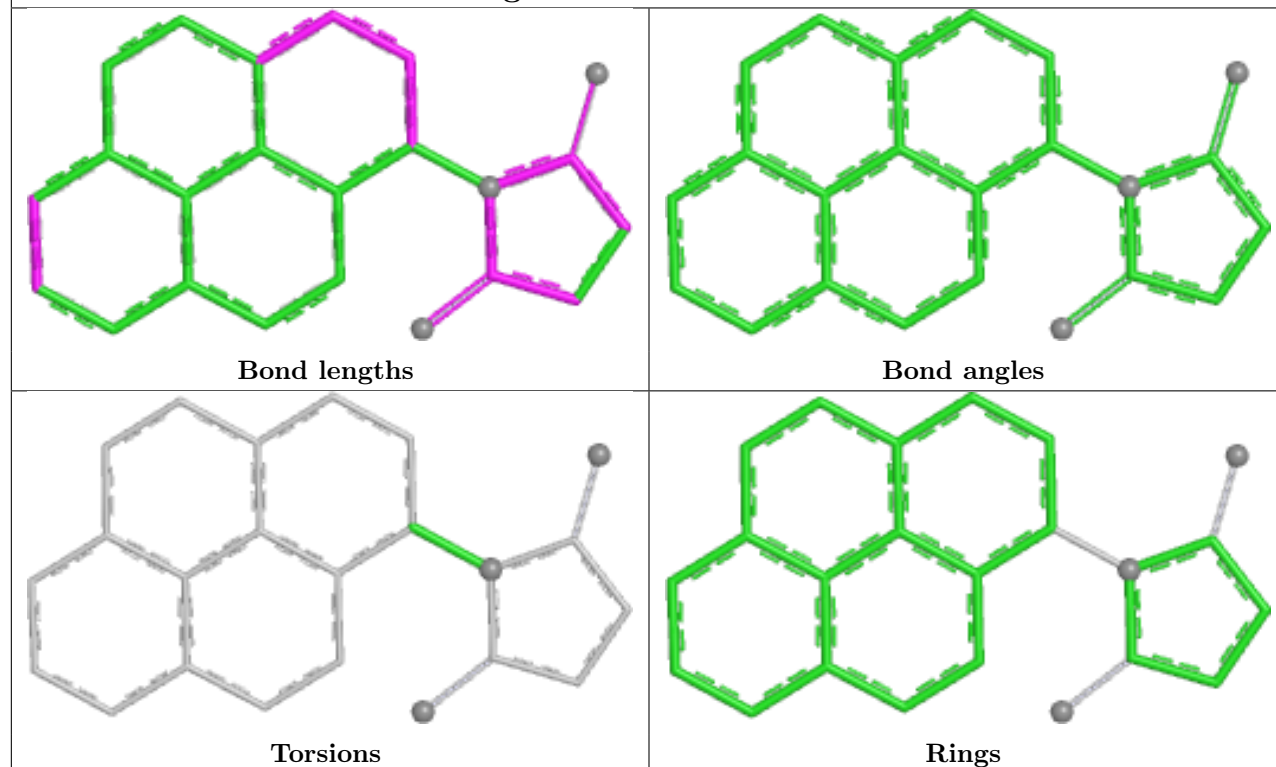
Ligand A1L9F X 201



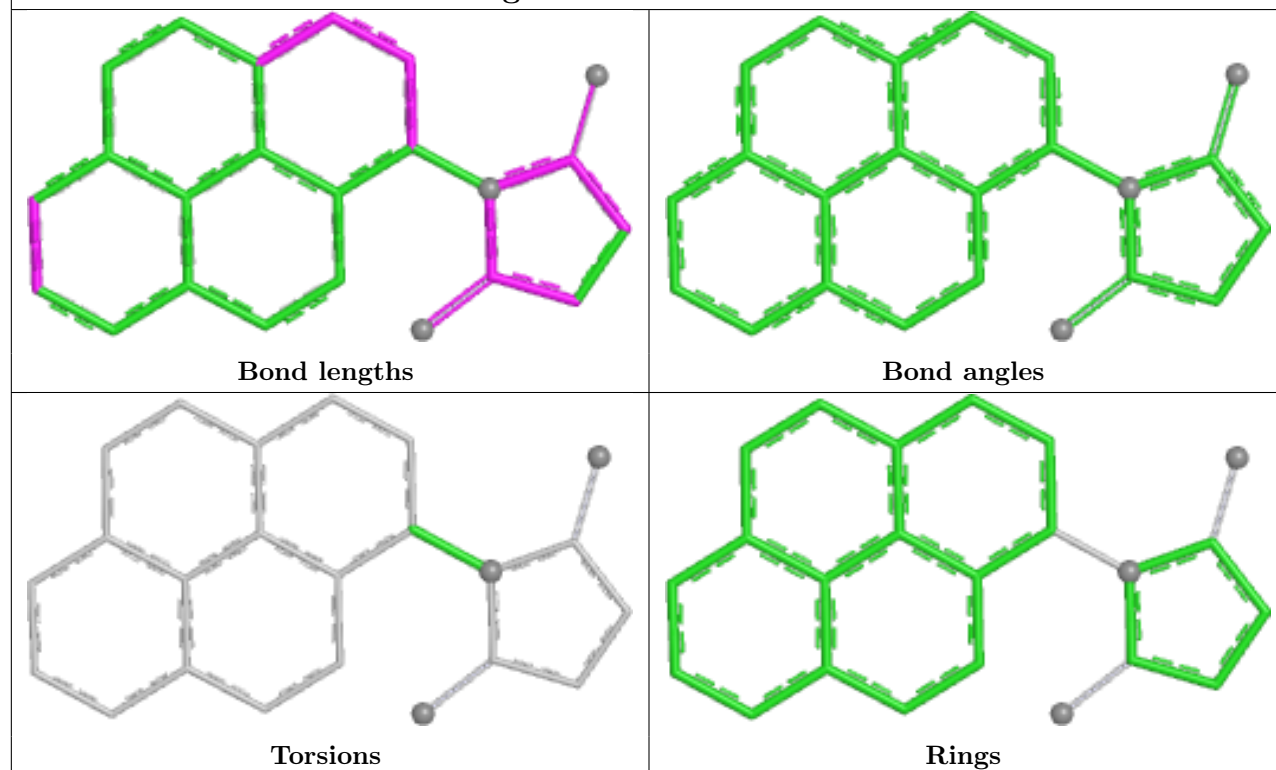
Ligand A1L9F CB 202



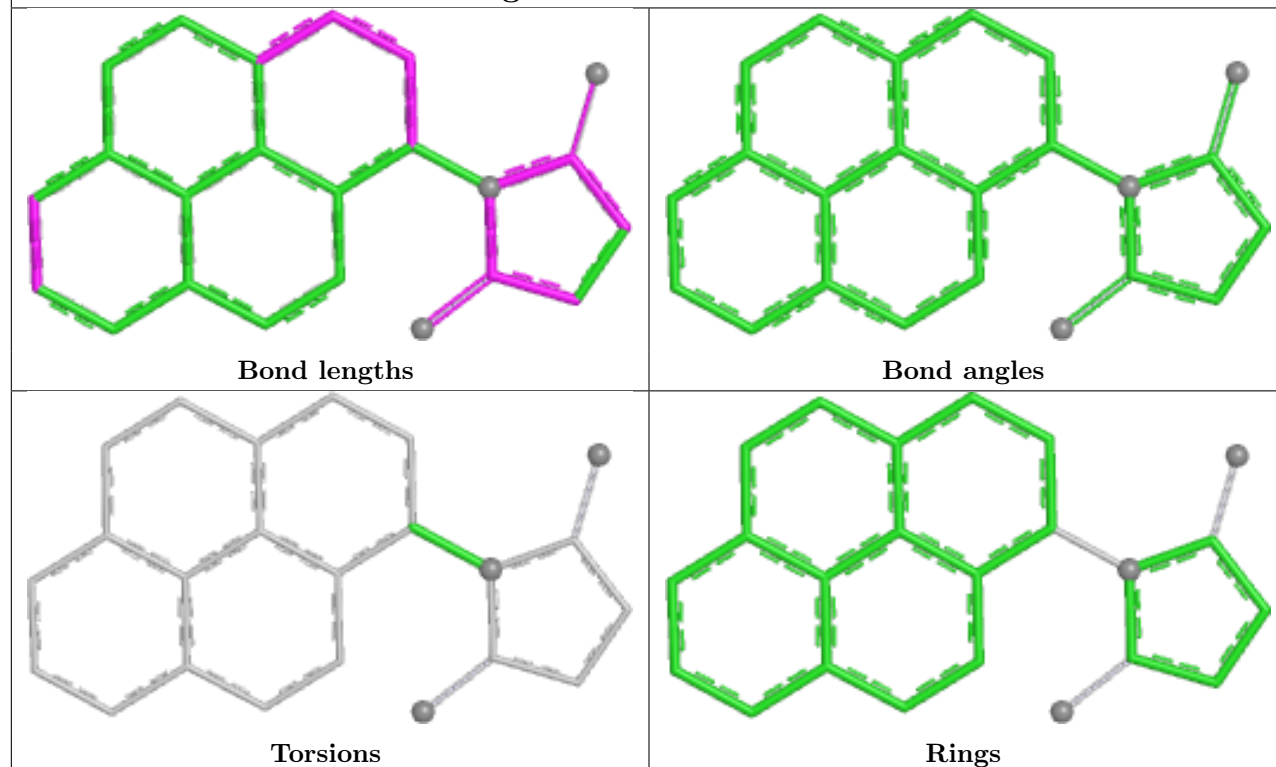
Ligand A1L9F BB 201



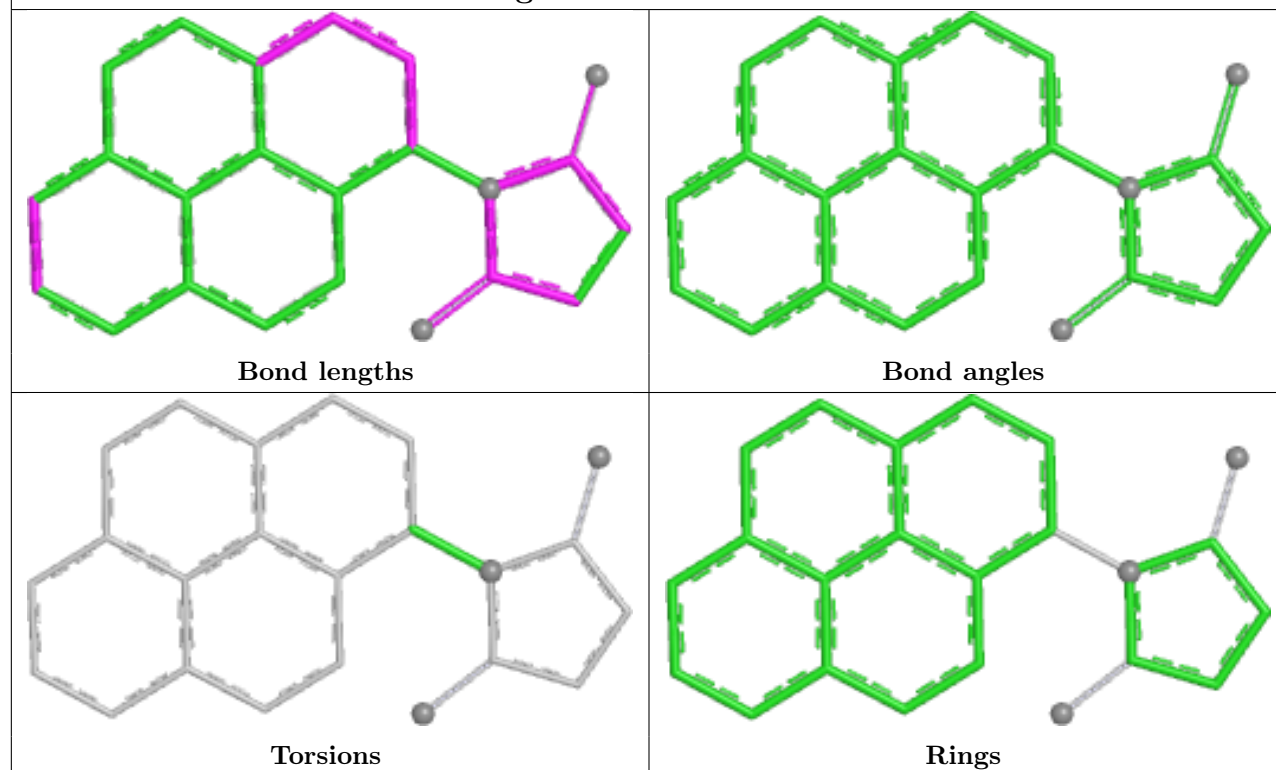
Ligand A1L9F AB 201



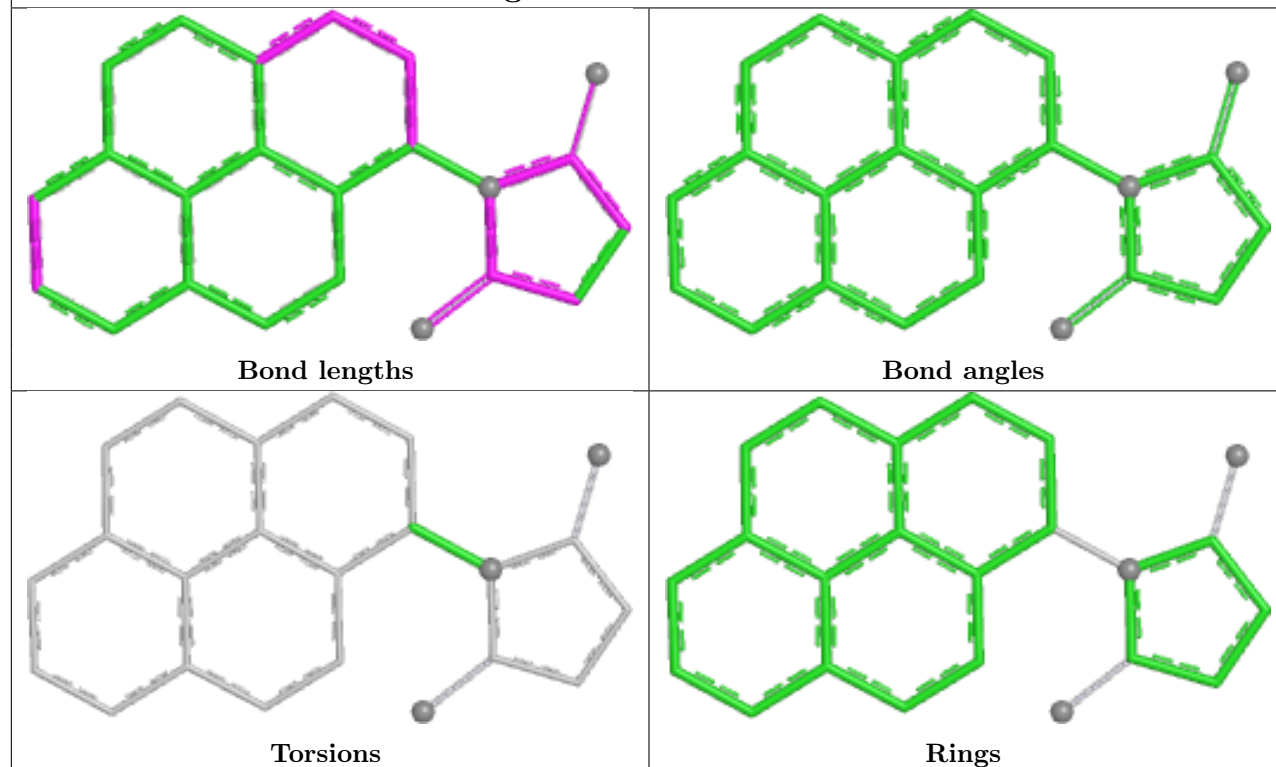
Ligand A1L9F OA 201



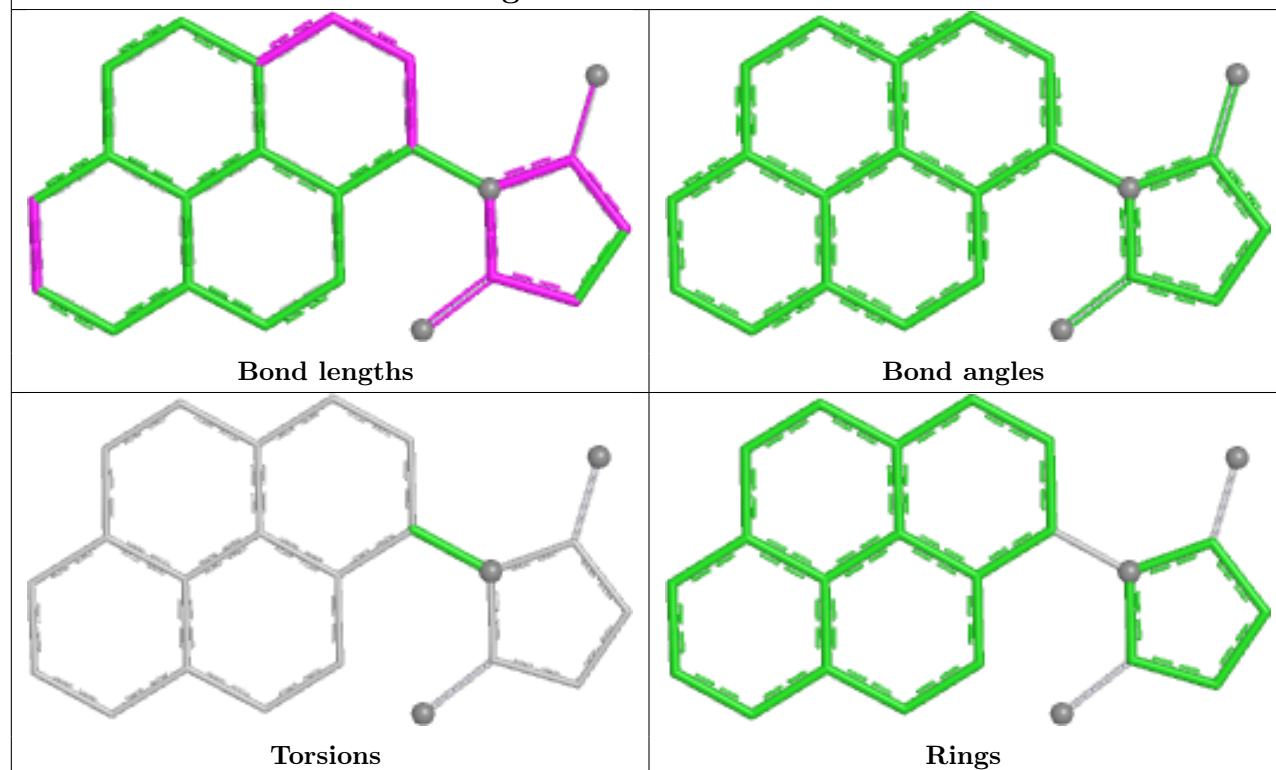
Ligand A1L9F R 201



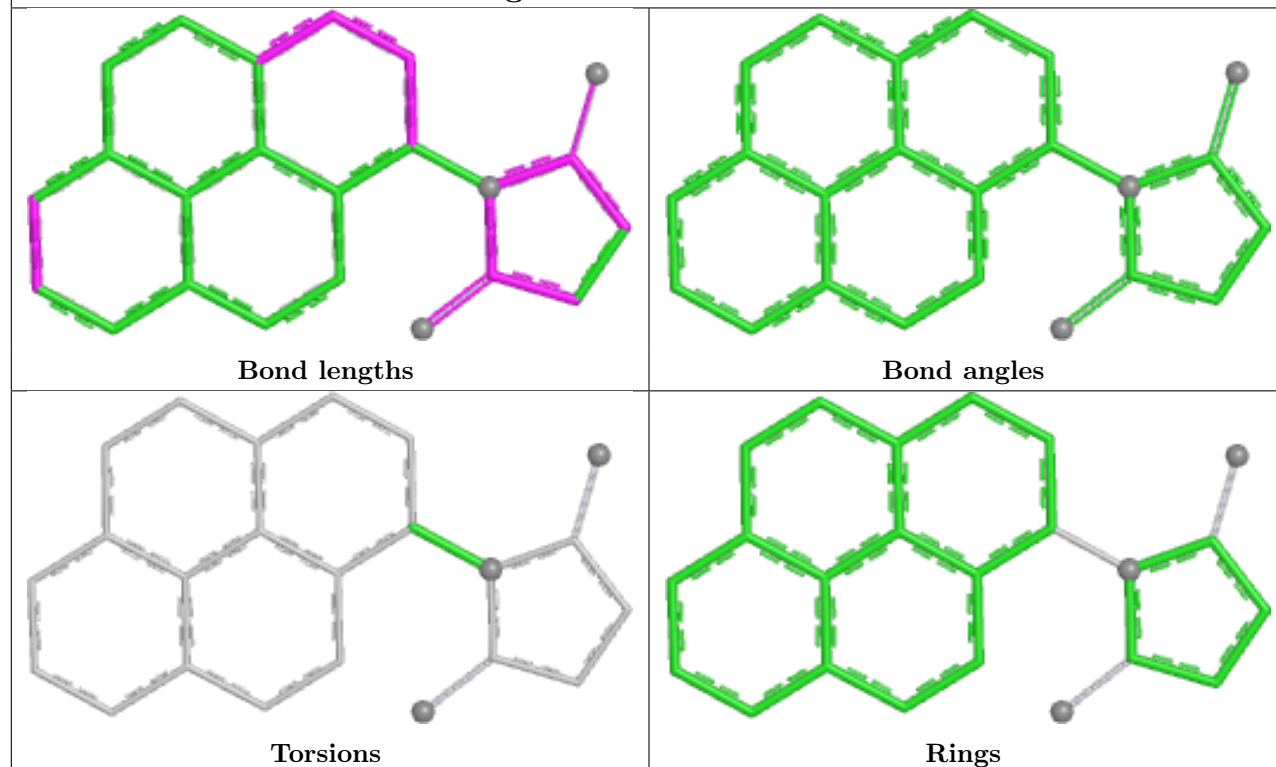
Ligand A1L9F TA 202



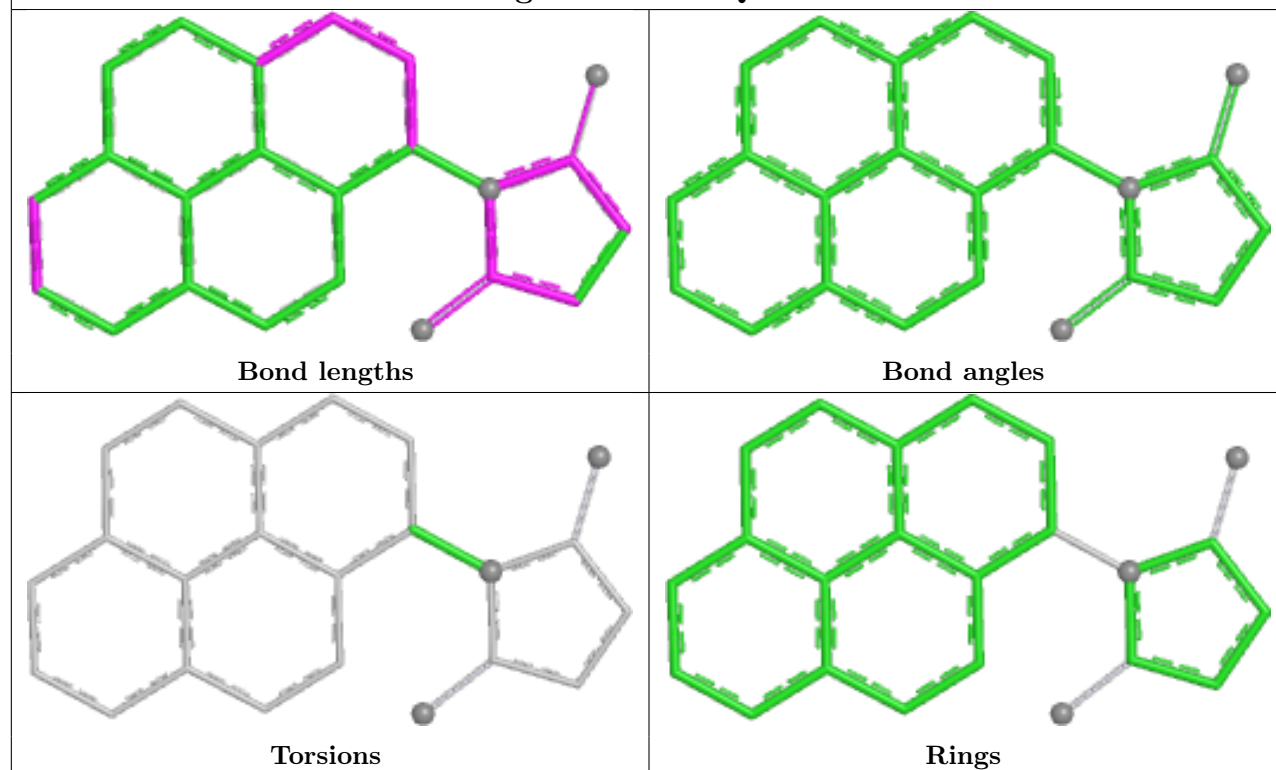
Ligand A1L9F AA 201



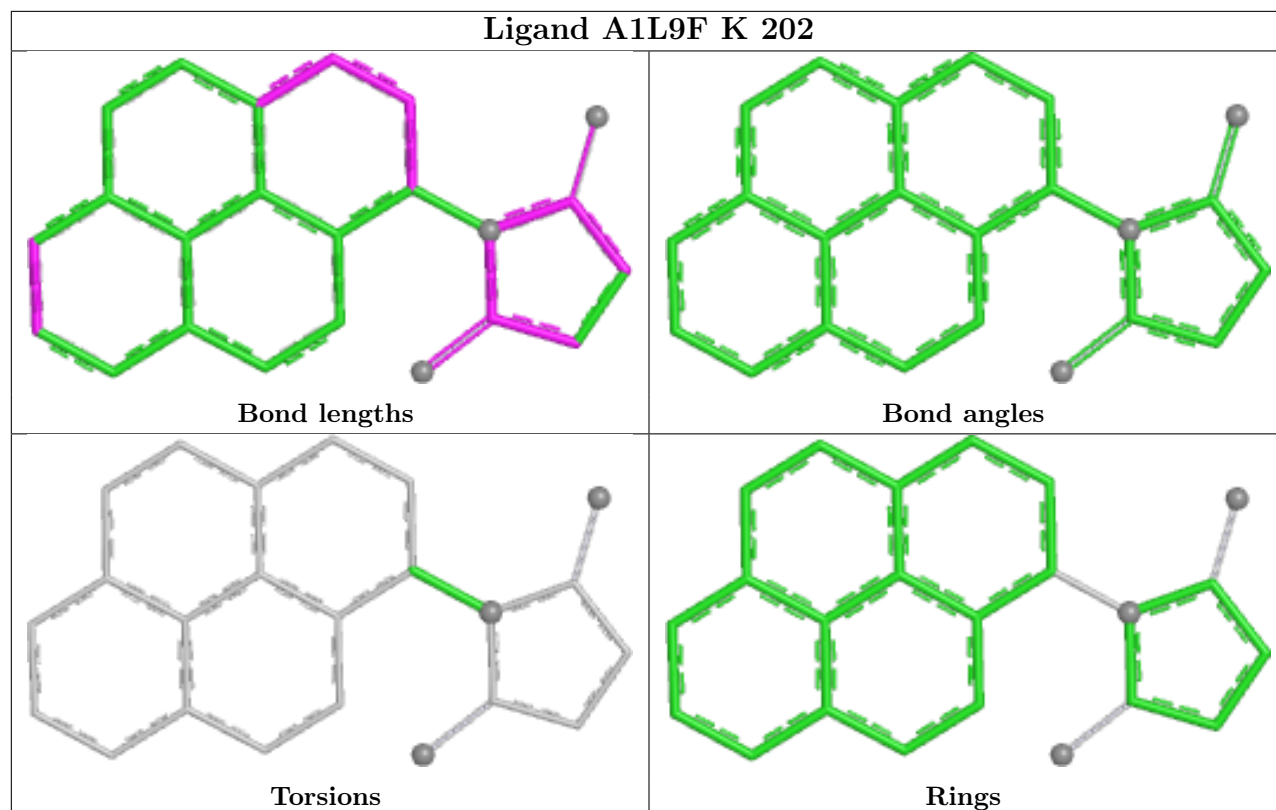
Ligand A1L9F SA 201



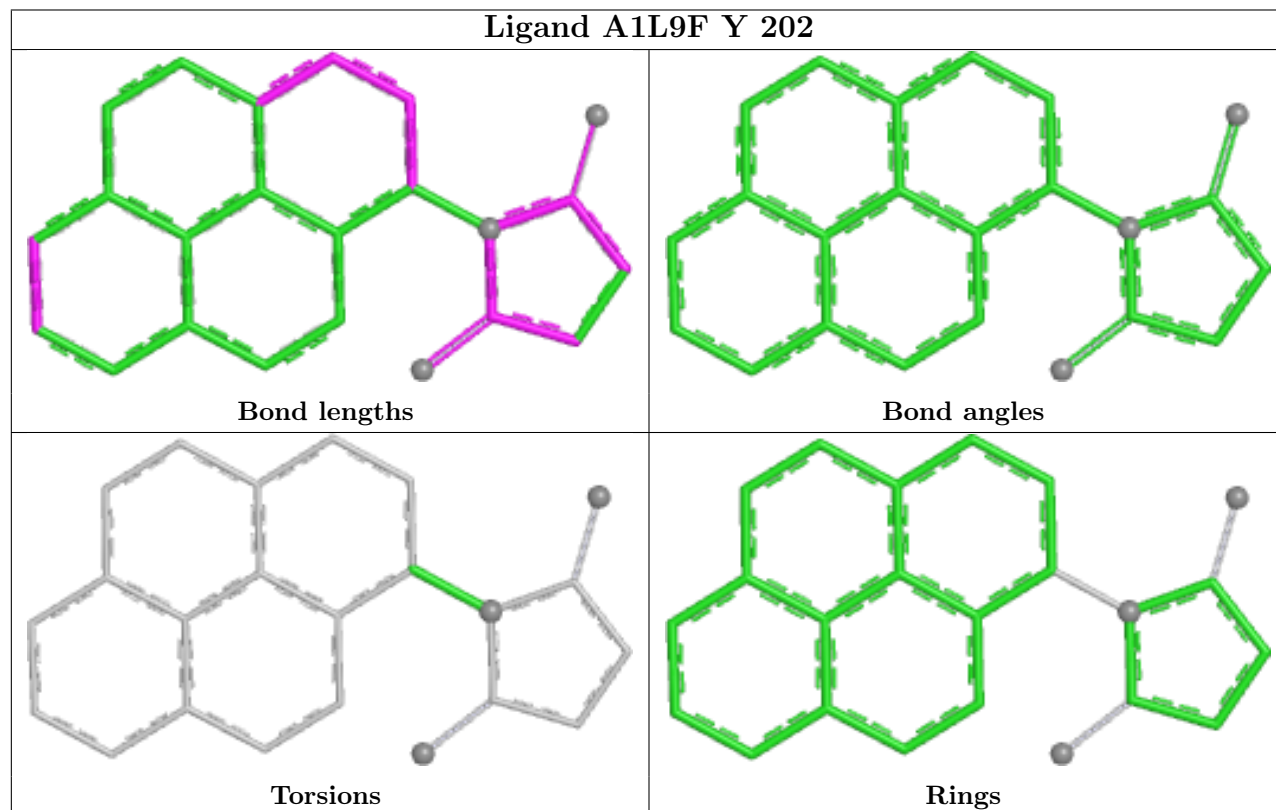
Ligand A1L9F Q 201



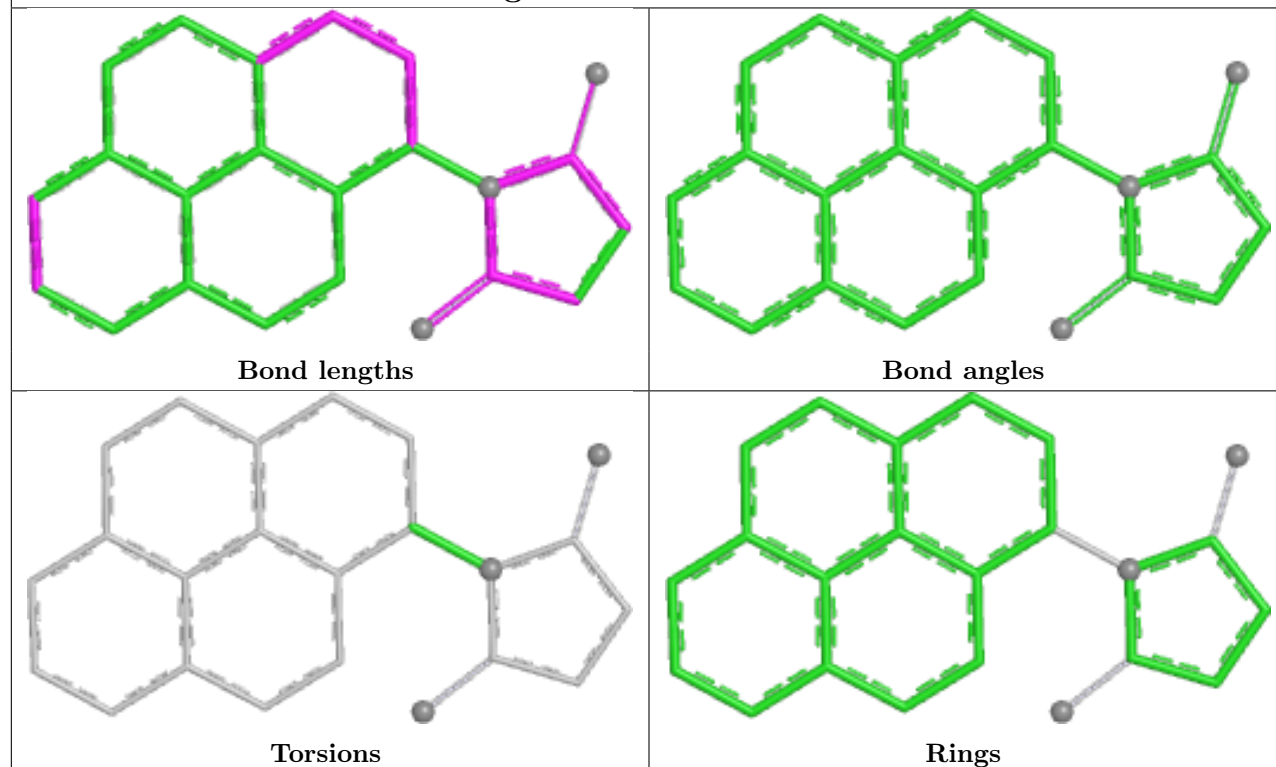
Ligand A1L9F K 202



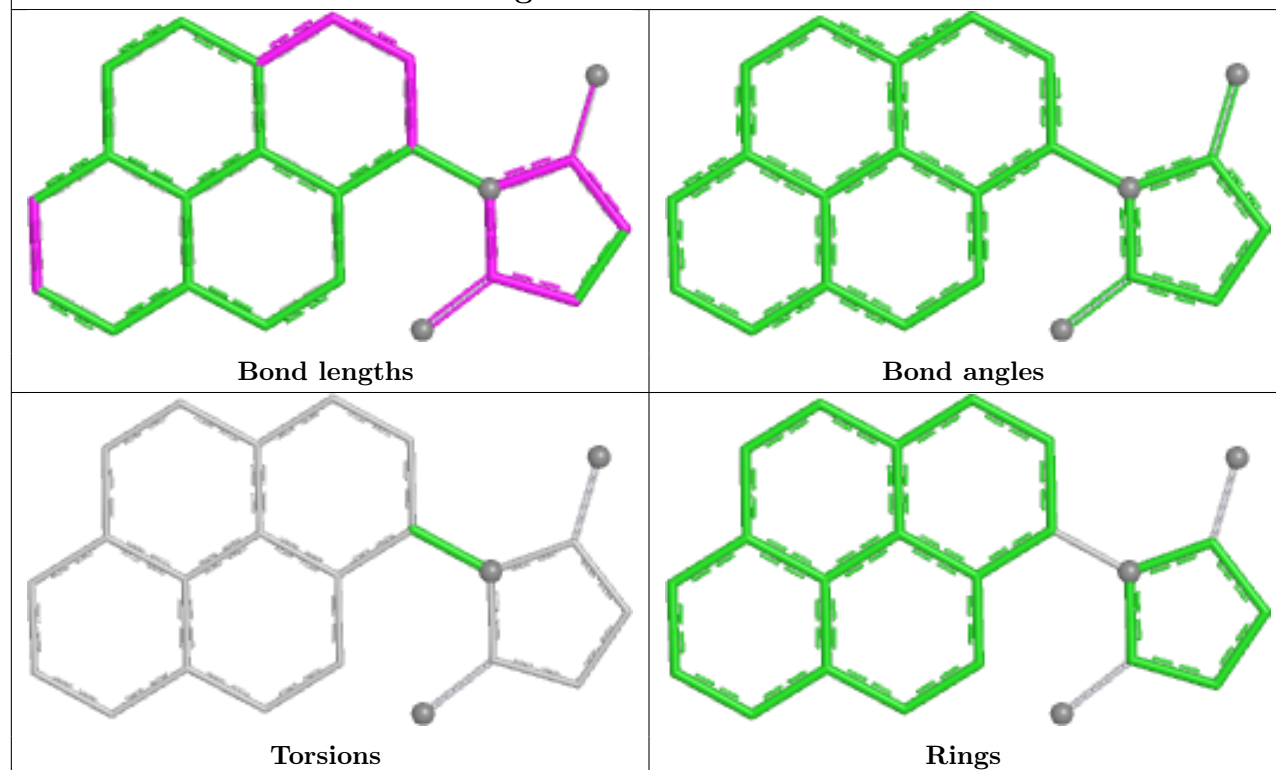
Ligand A1L9F Y 202



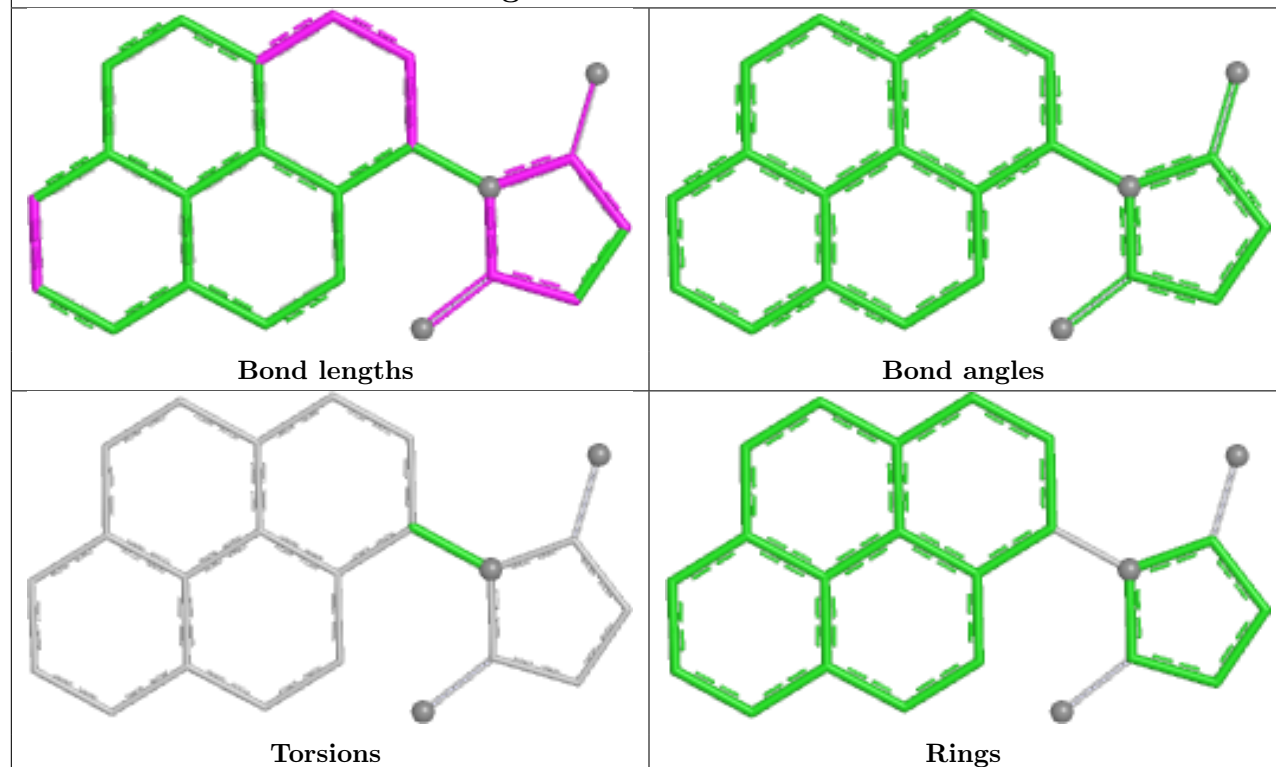
Ligand A1L9F EB 202



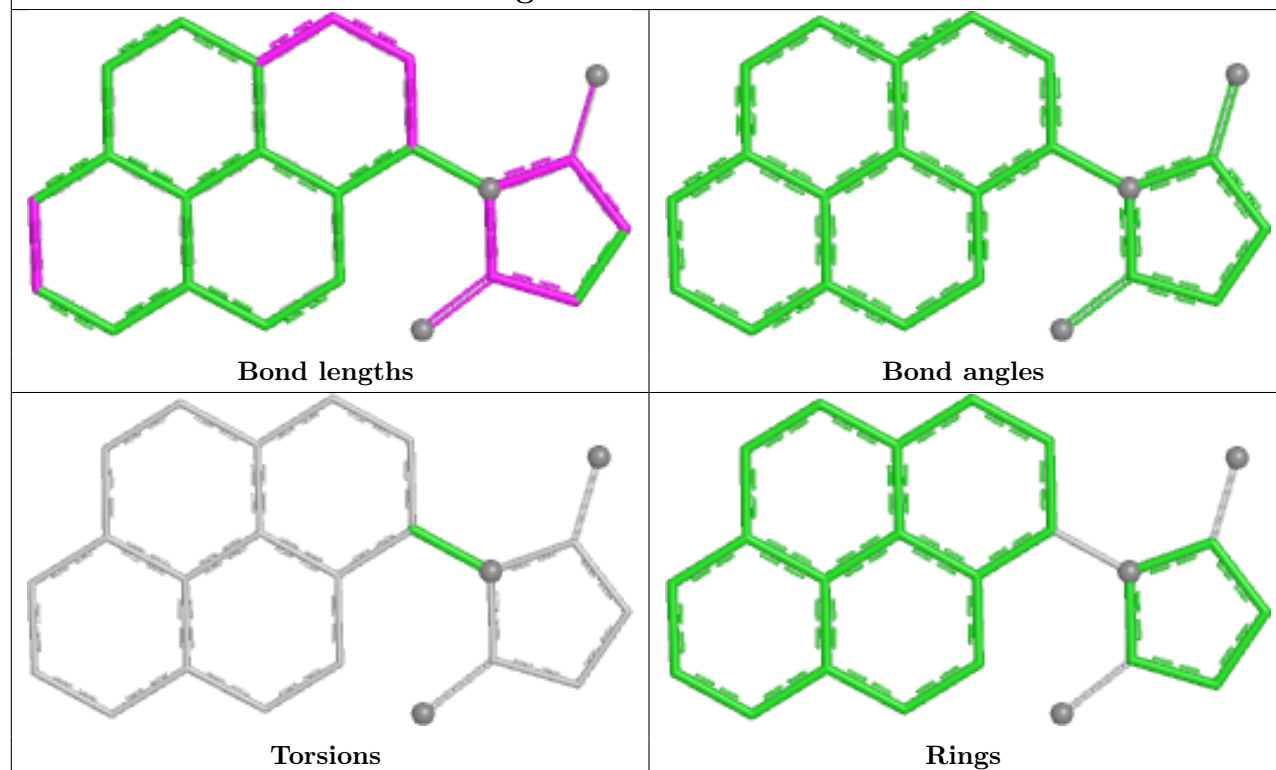
Ligand A1L9F G 201



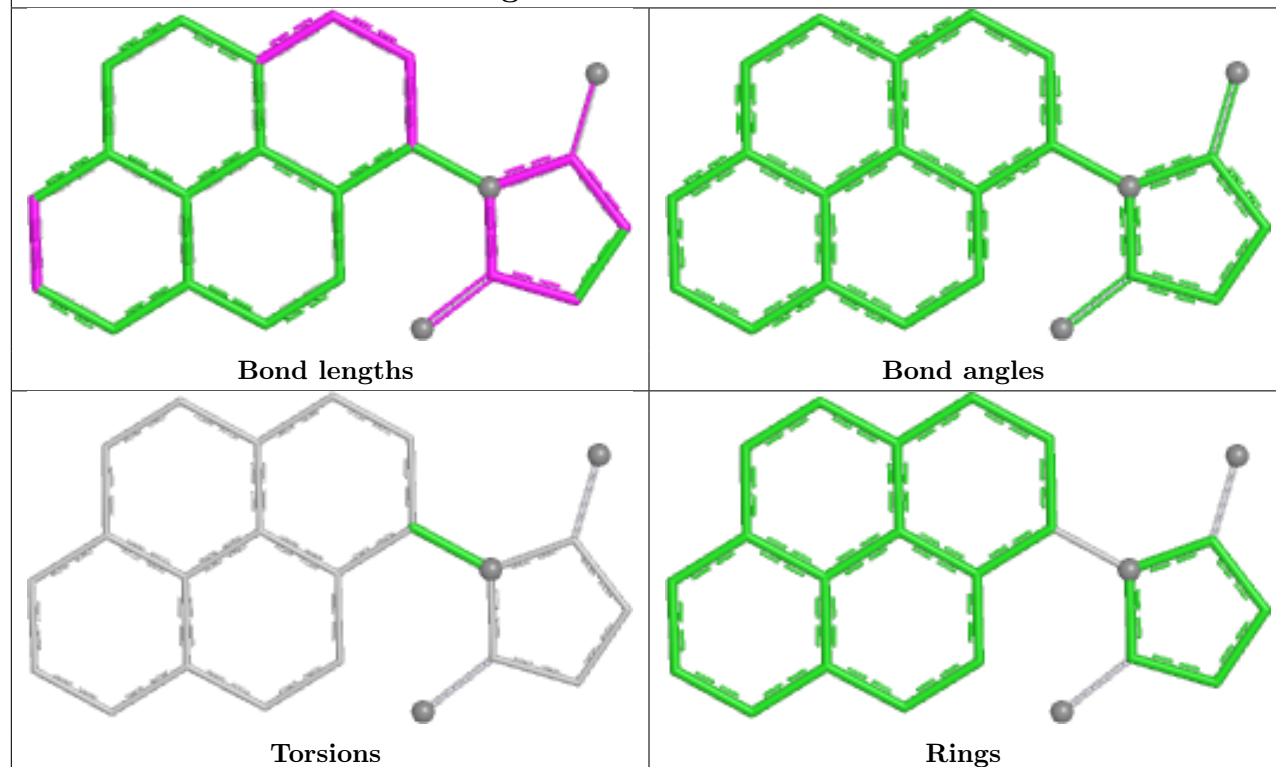
Ligand A1L9F XA 201



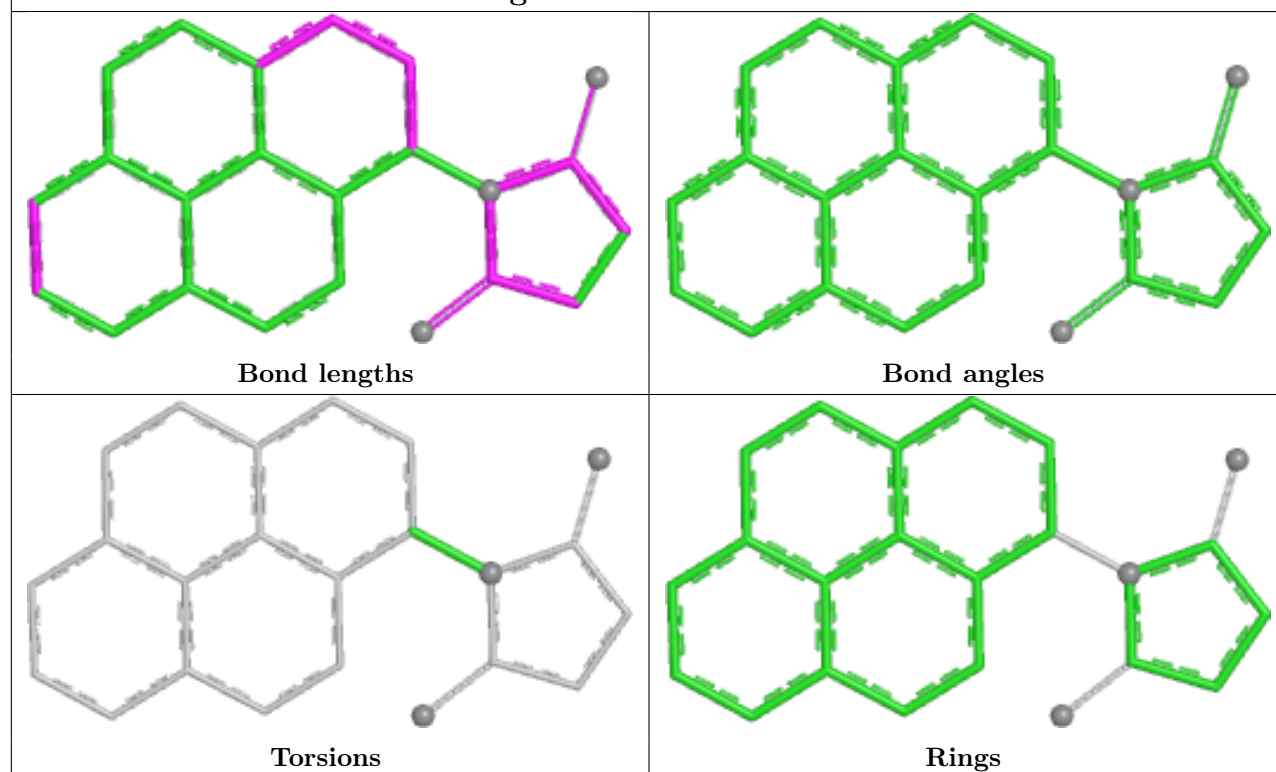
Ligand A1L9F T 201



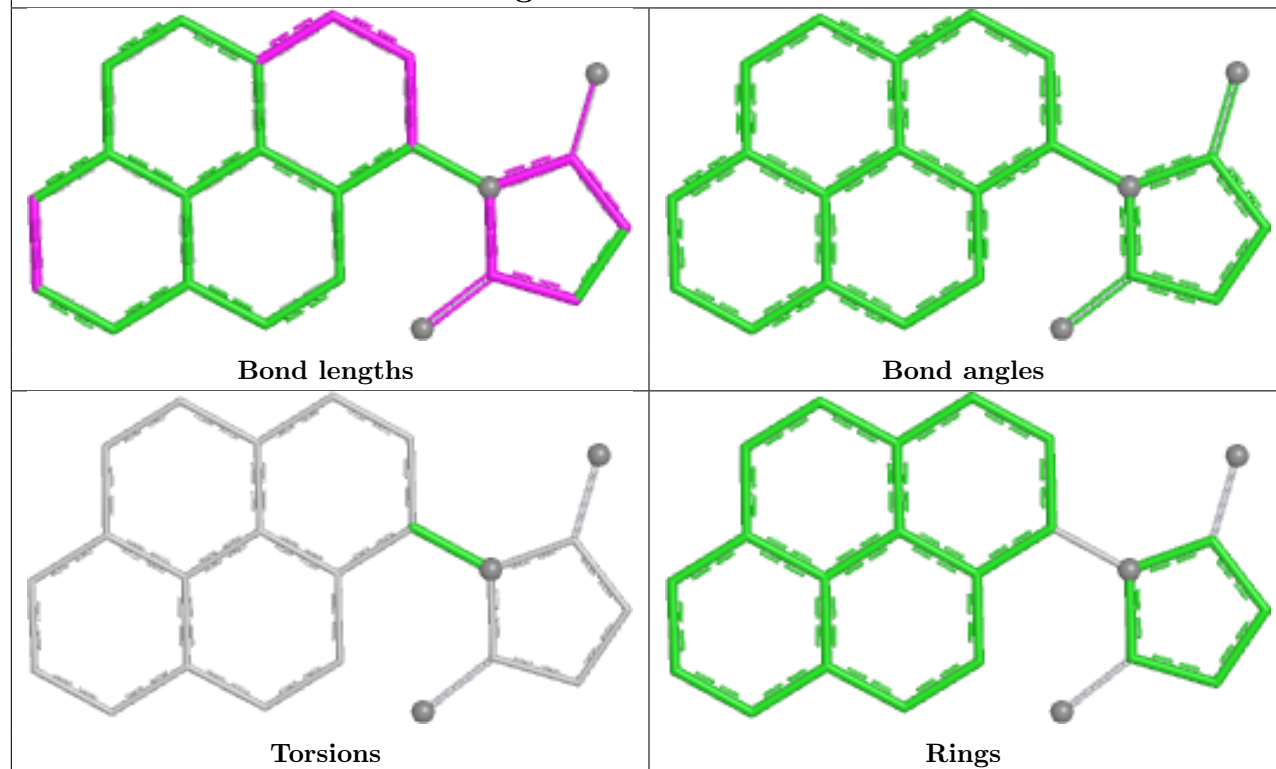
Ligand A1L9F HA 201



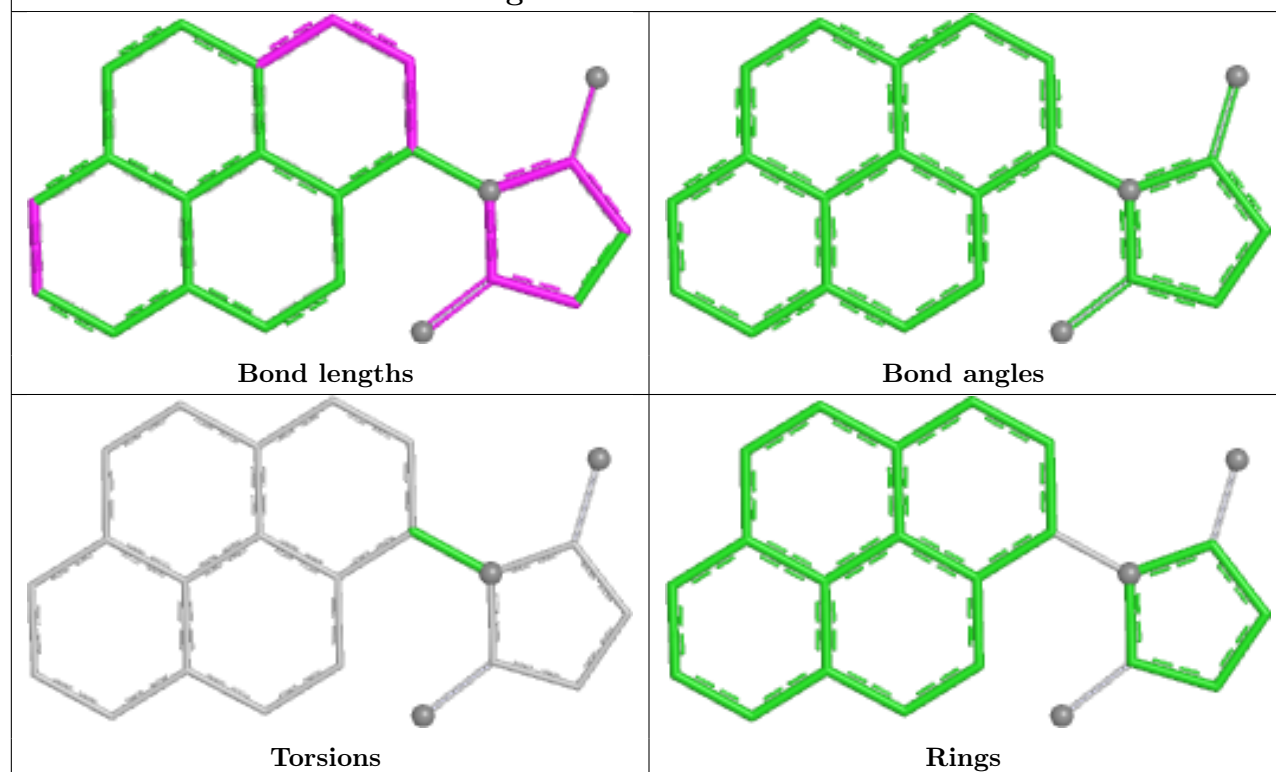
Ligand A1L9F IB 201



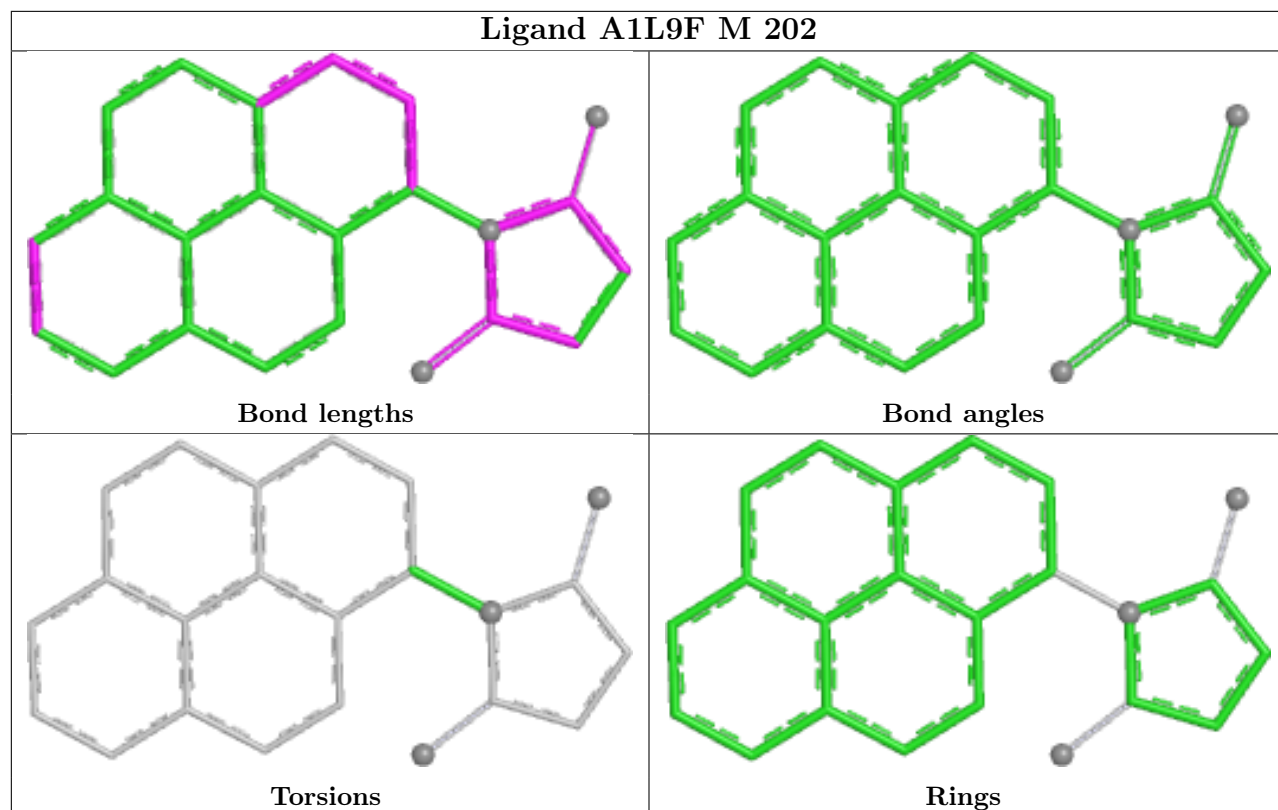
Ligand A1L9F O 202



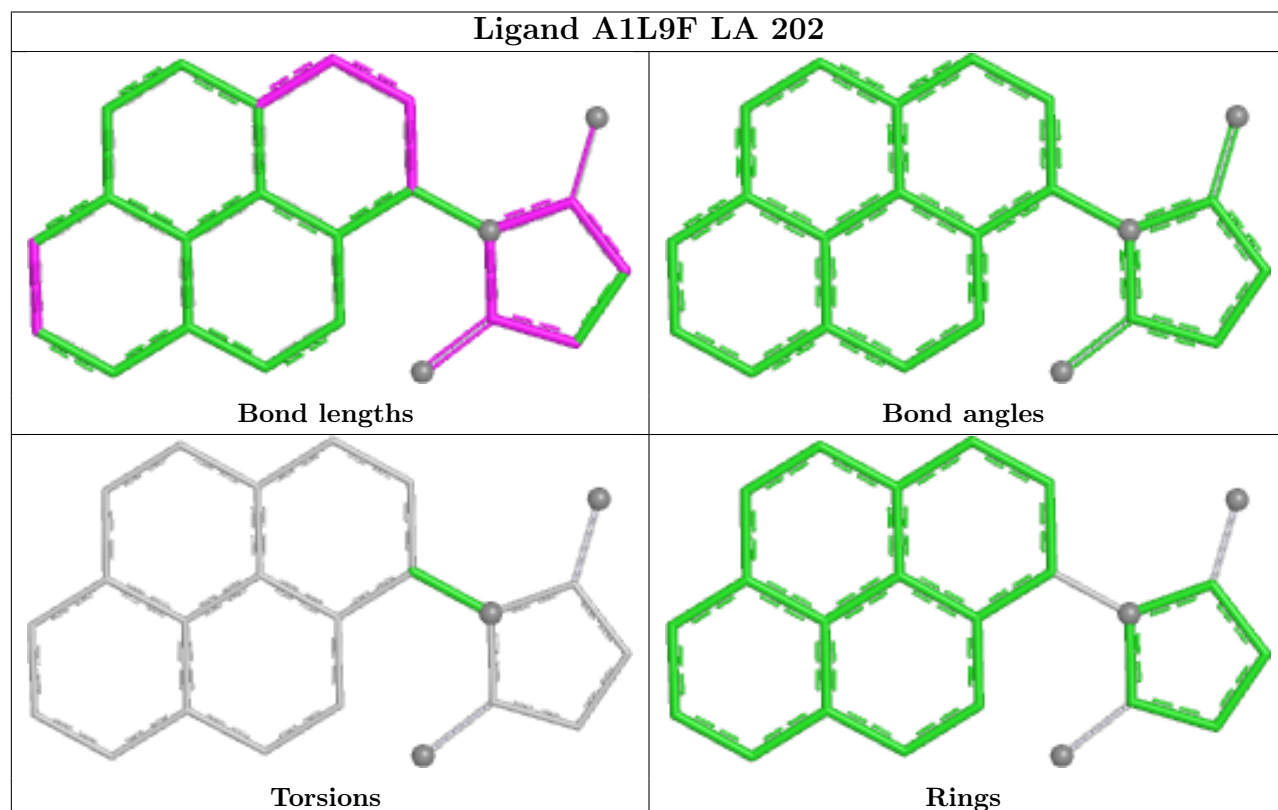
Ligand A1L9F FA 202



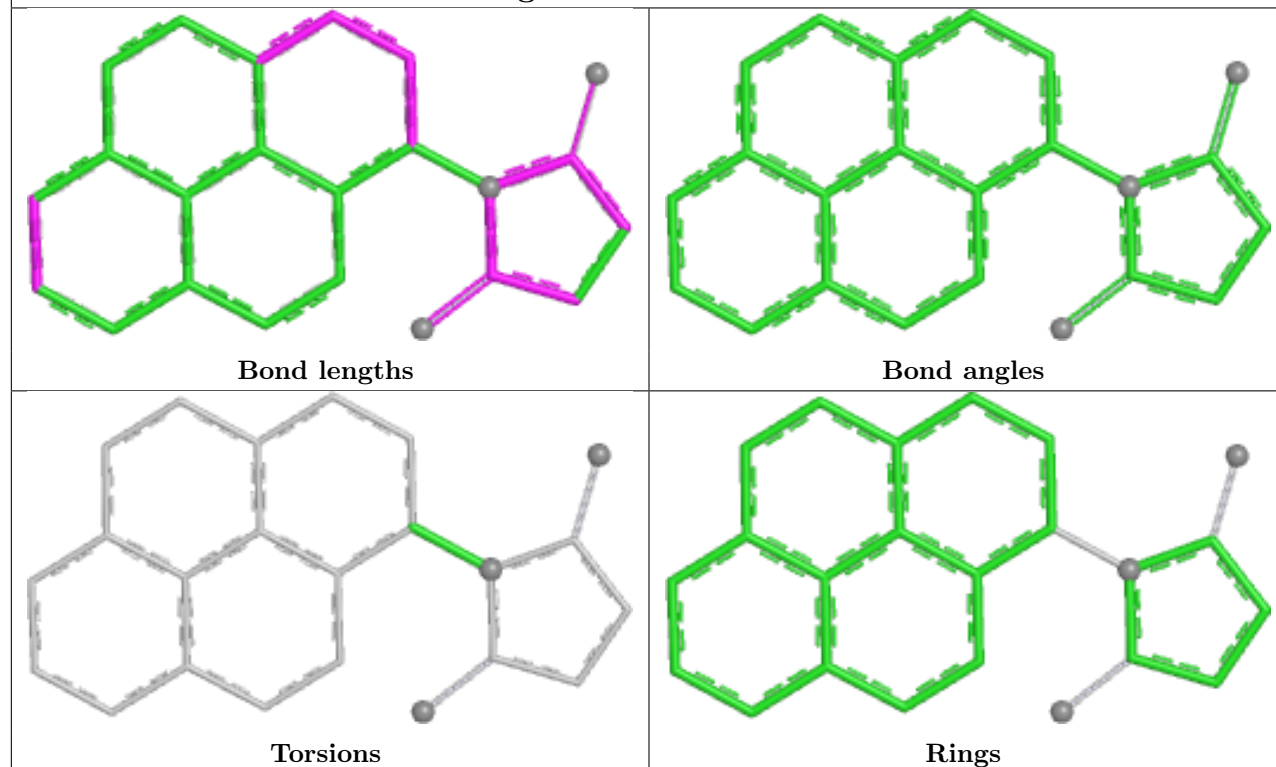
Ligand A1L9F M 202



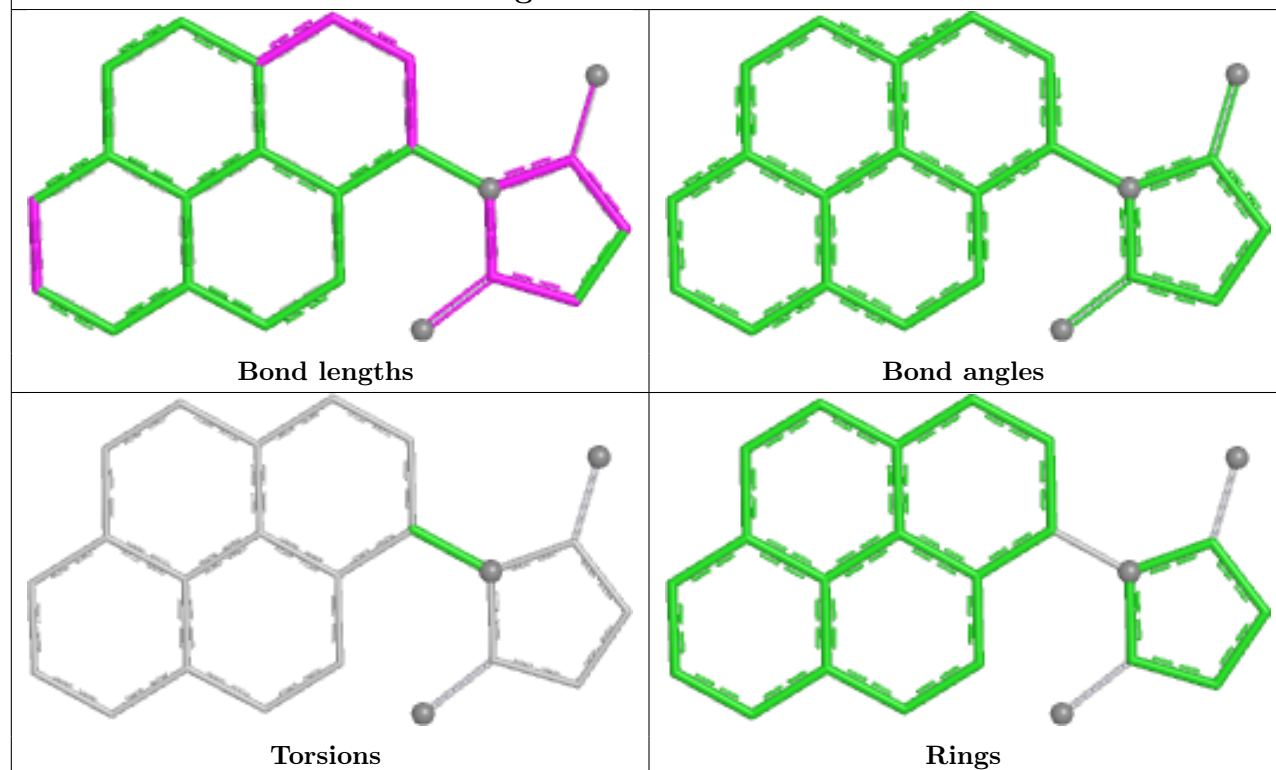
Ligand A1L9F LA 202



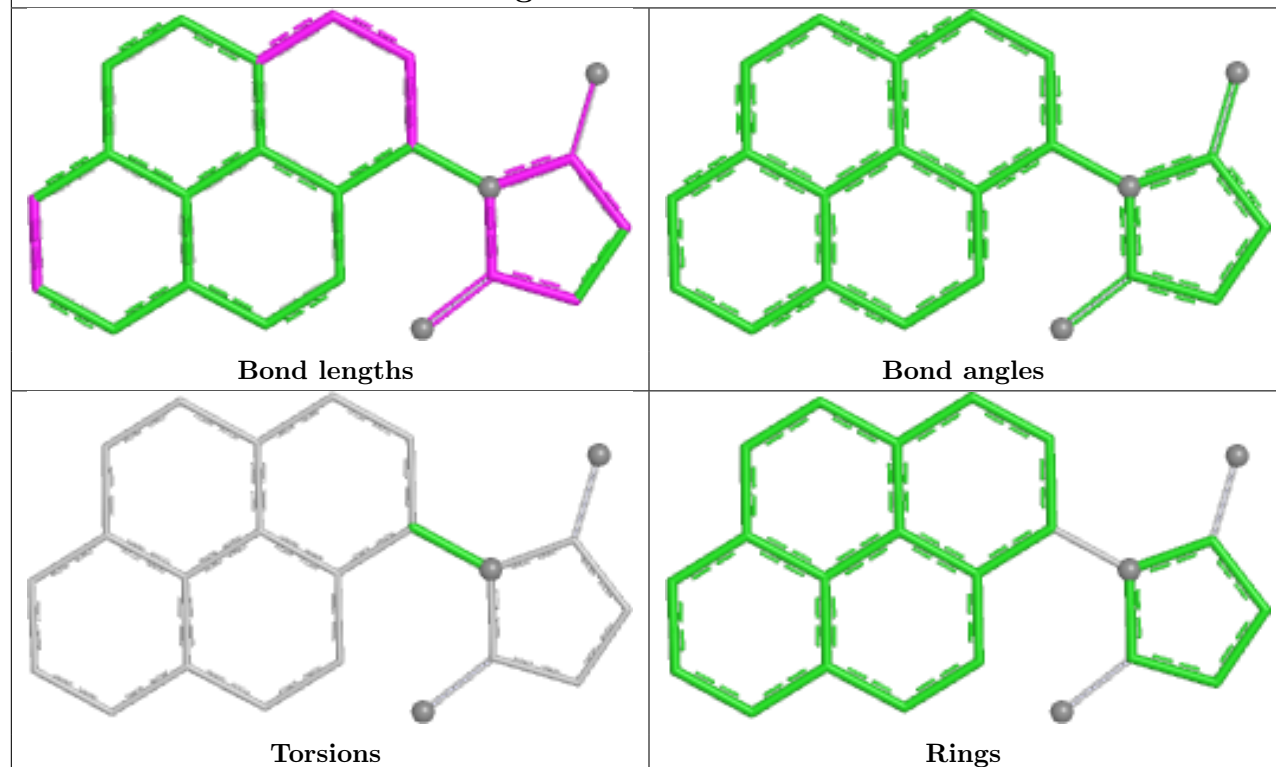
Ligand A1L9F F 201



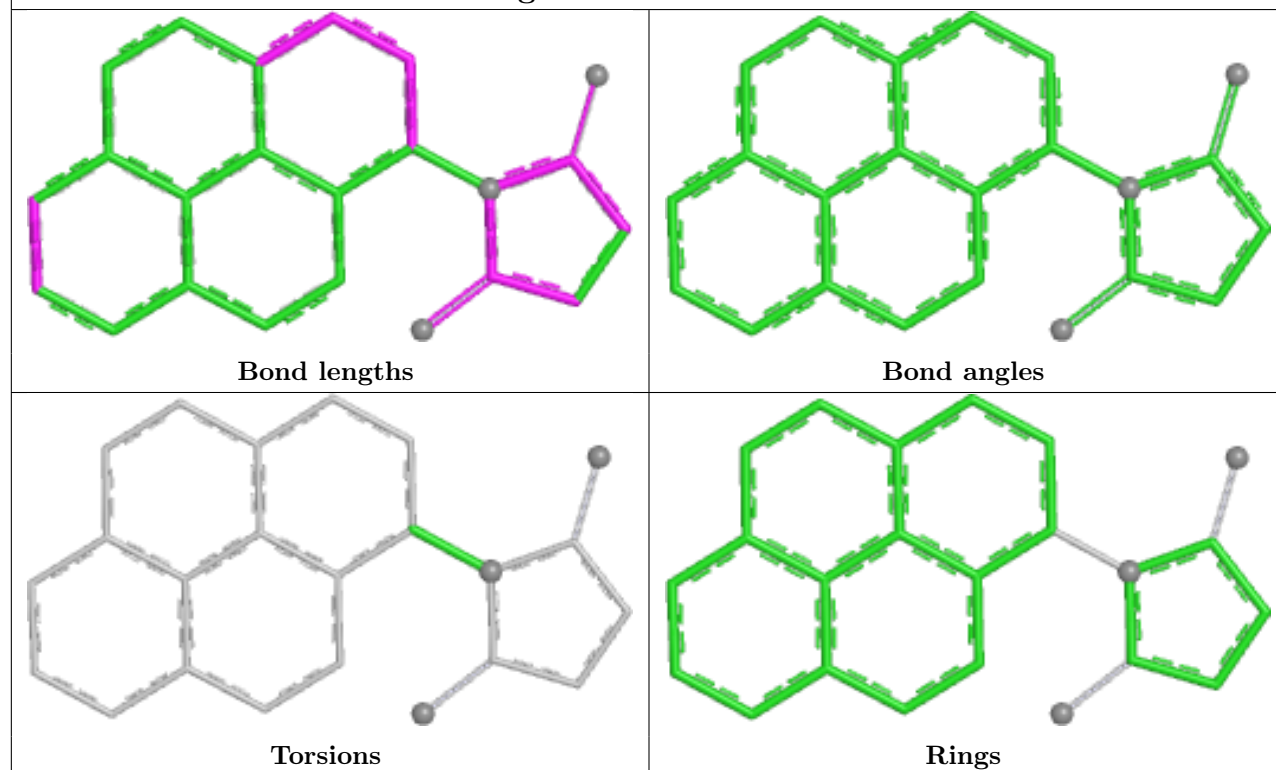
Ligand A1L9F H 201



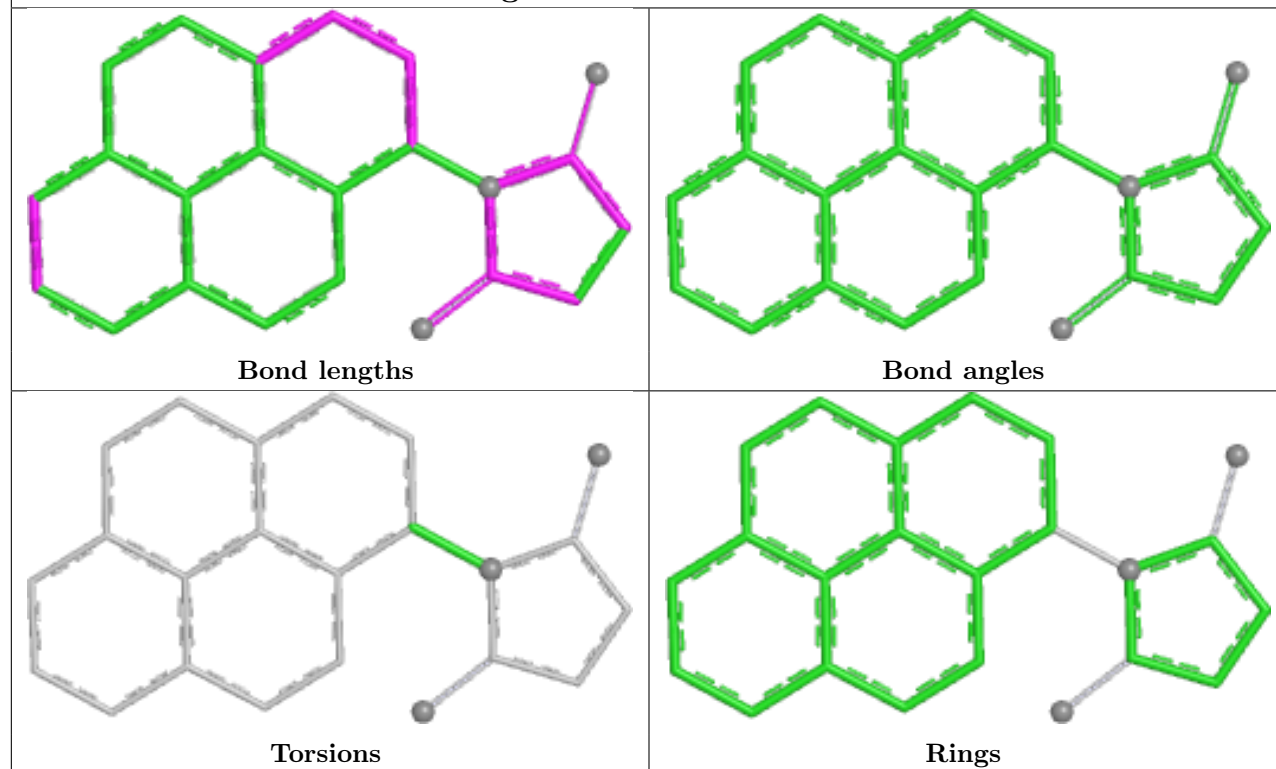
Ligand A1L9F O 201



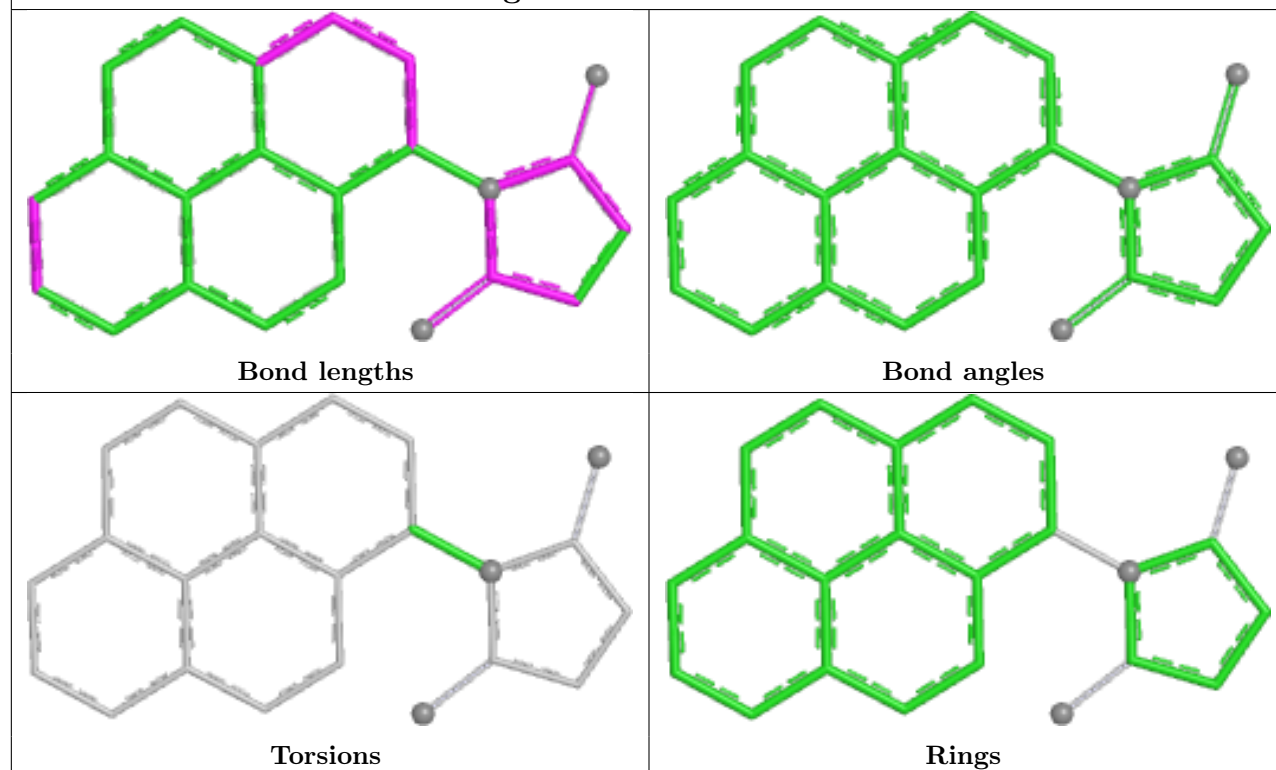
Ligand A1L9F Z 202



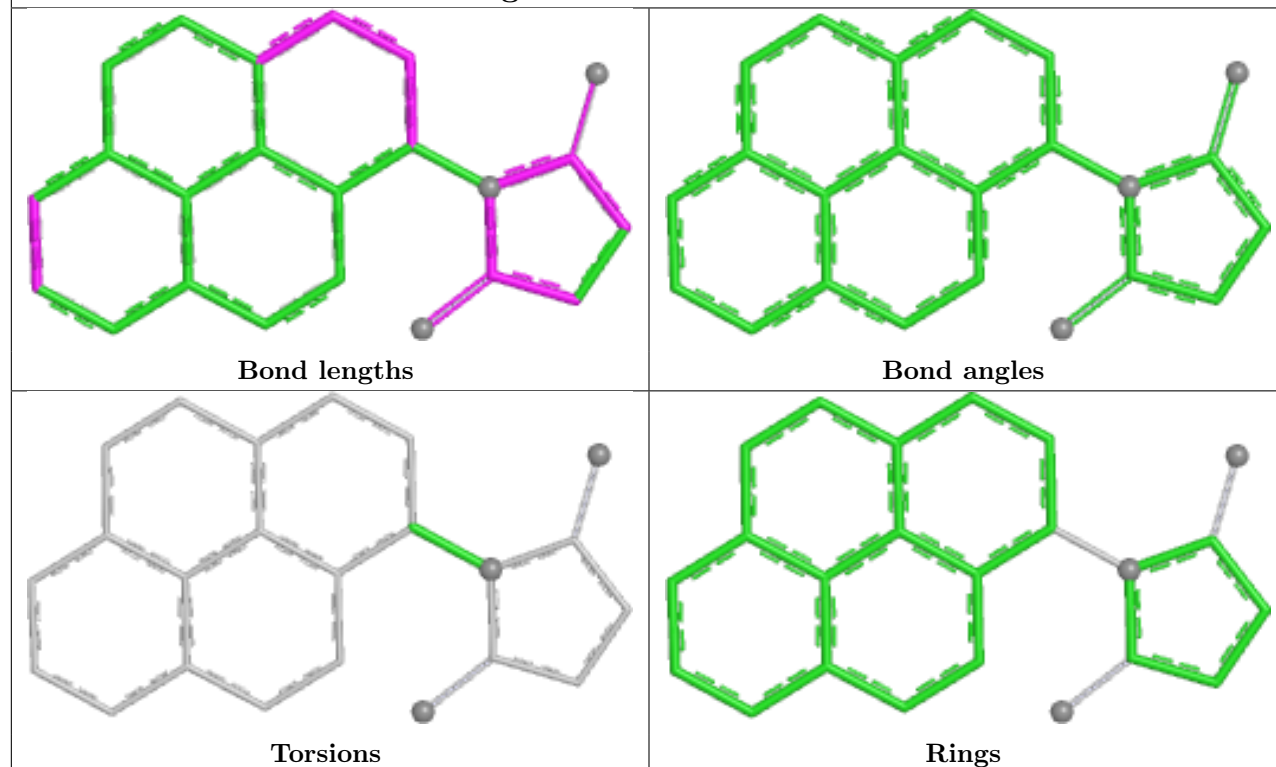
Ligand A1L9F GA 202



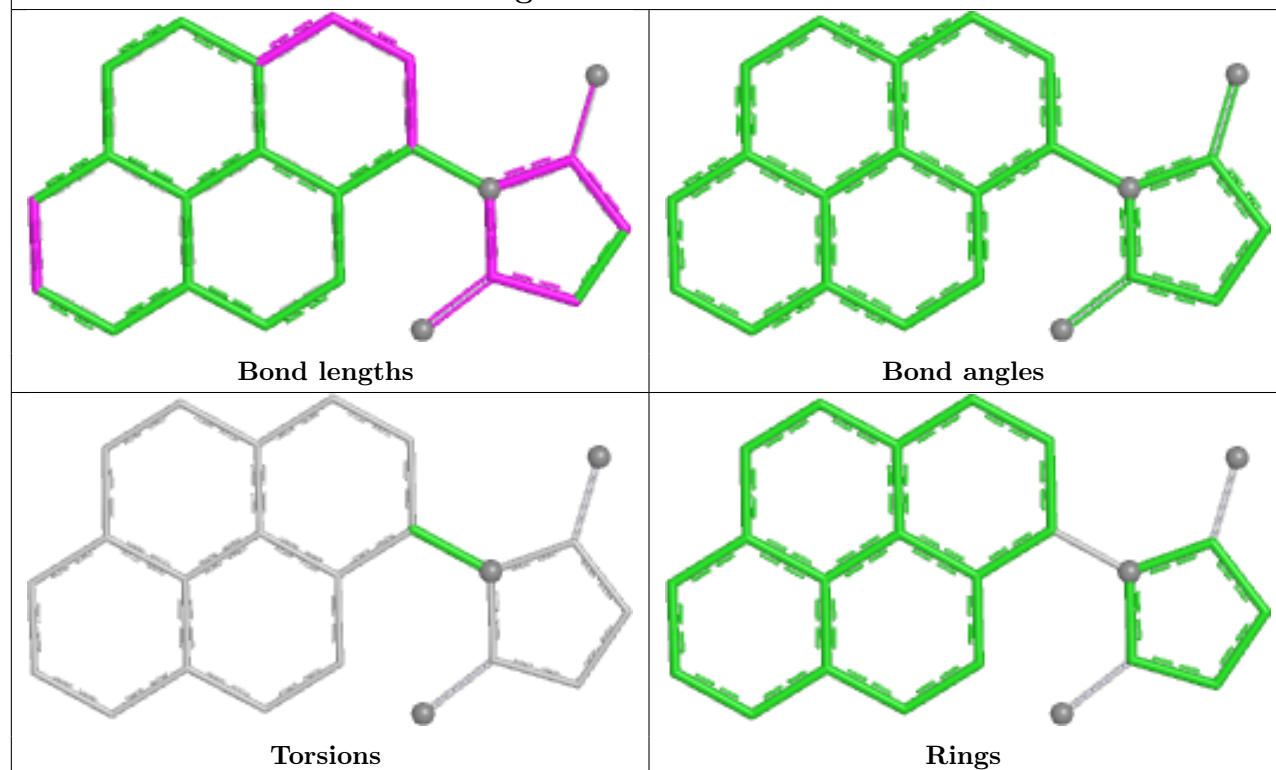
Ligand A1L9F CB 201



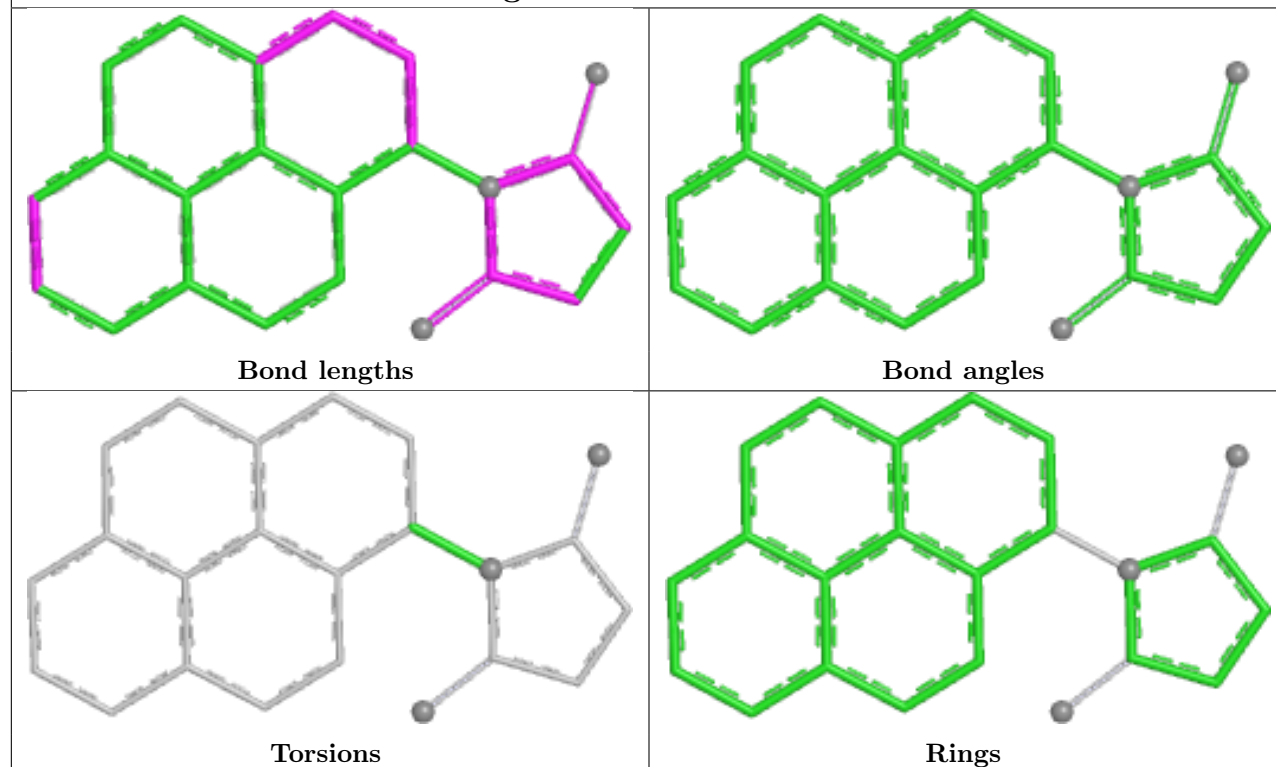
Ligand A1L9F KA 202



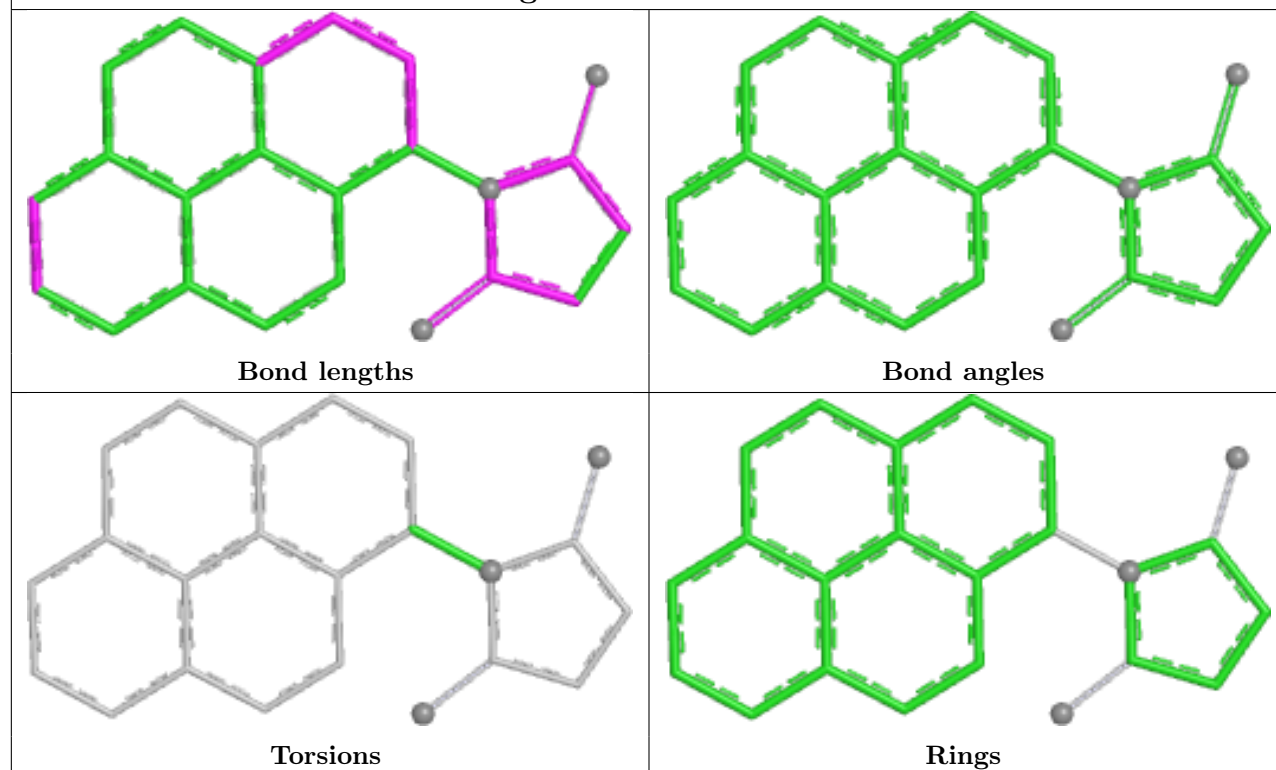
Ligand A1L9F A 201



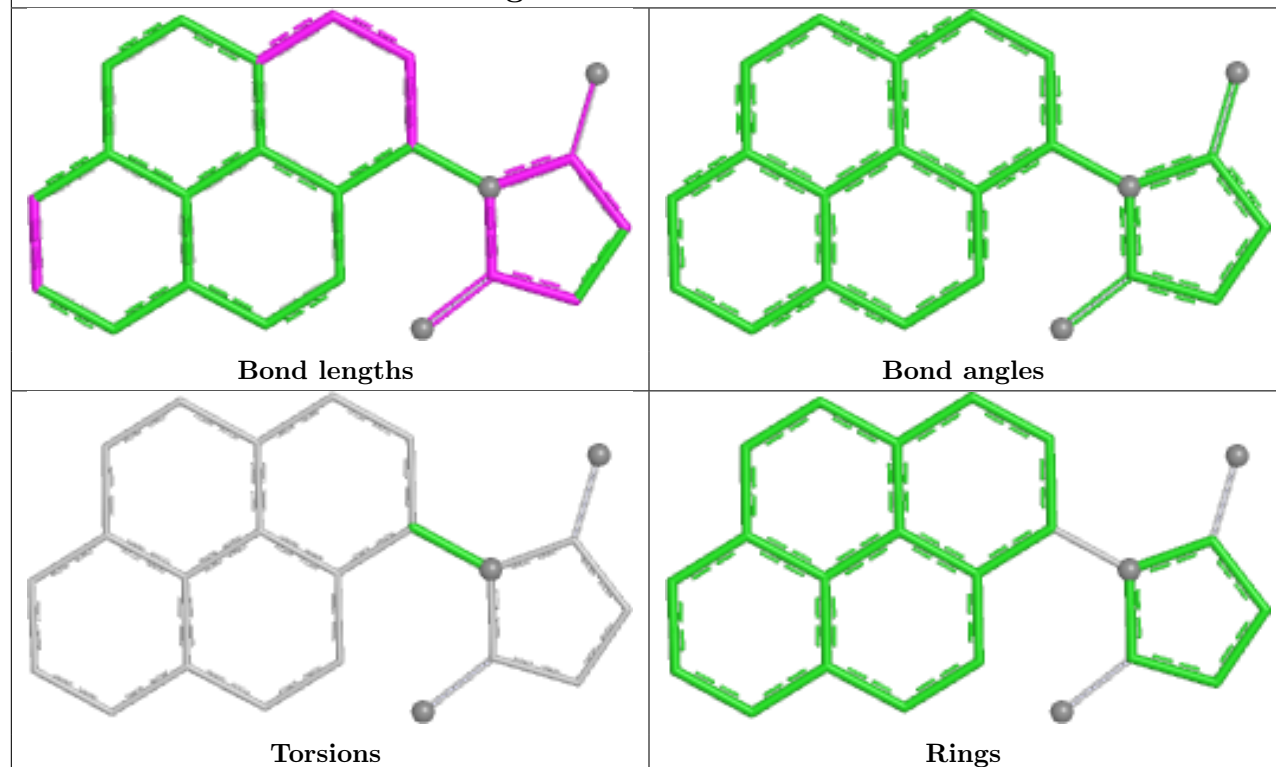
Ligand A1L9F YA 201



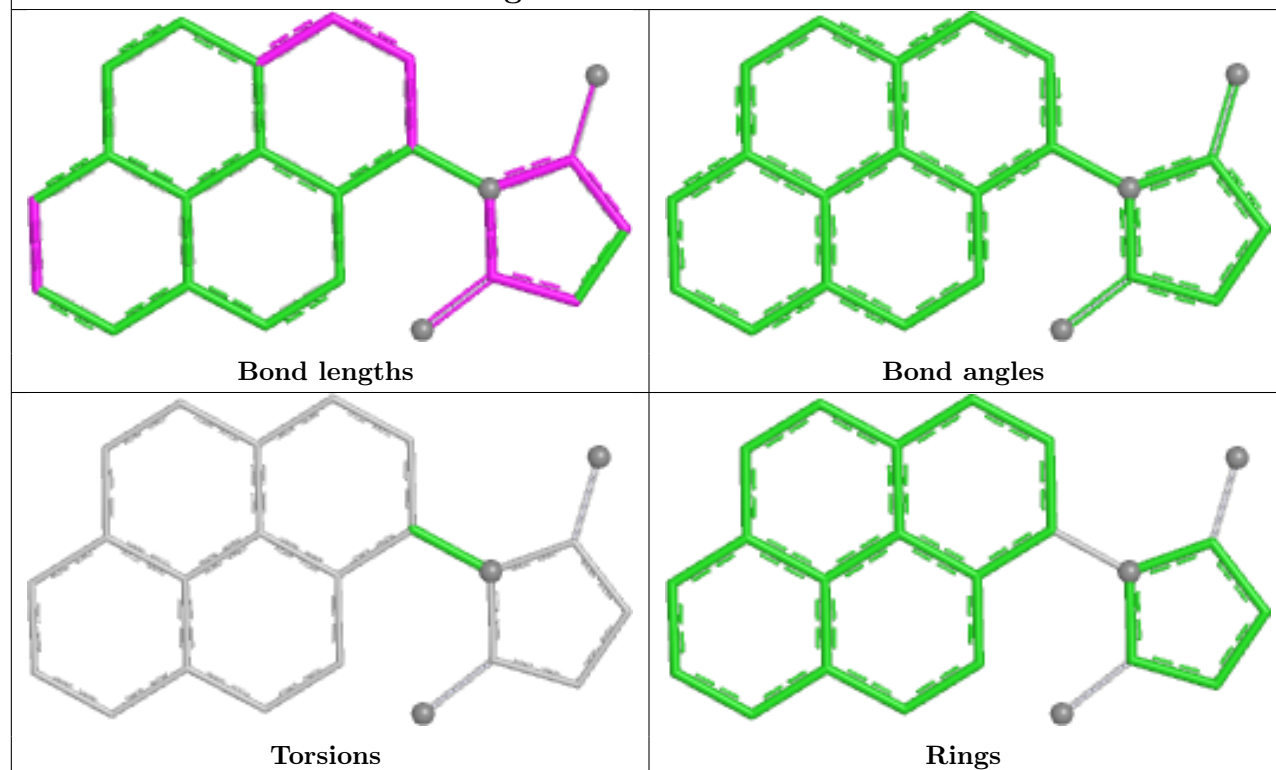
Ligand A1L9F J 202



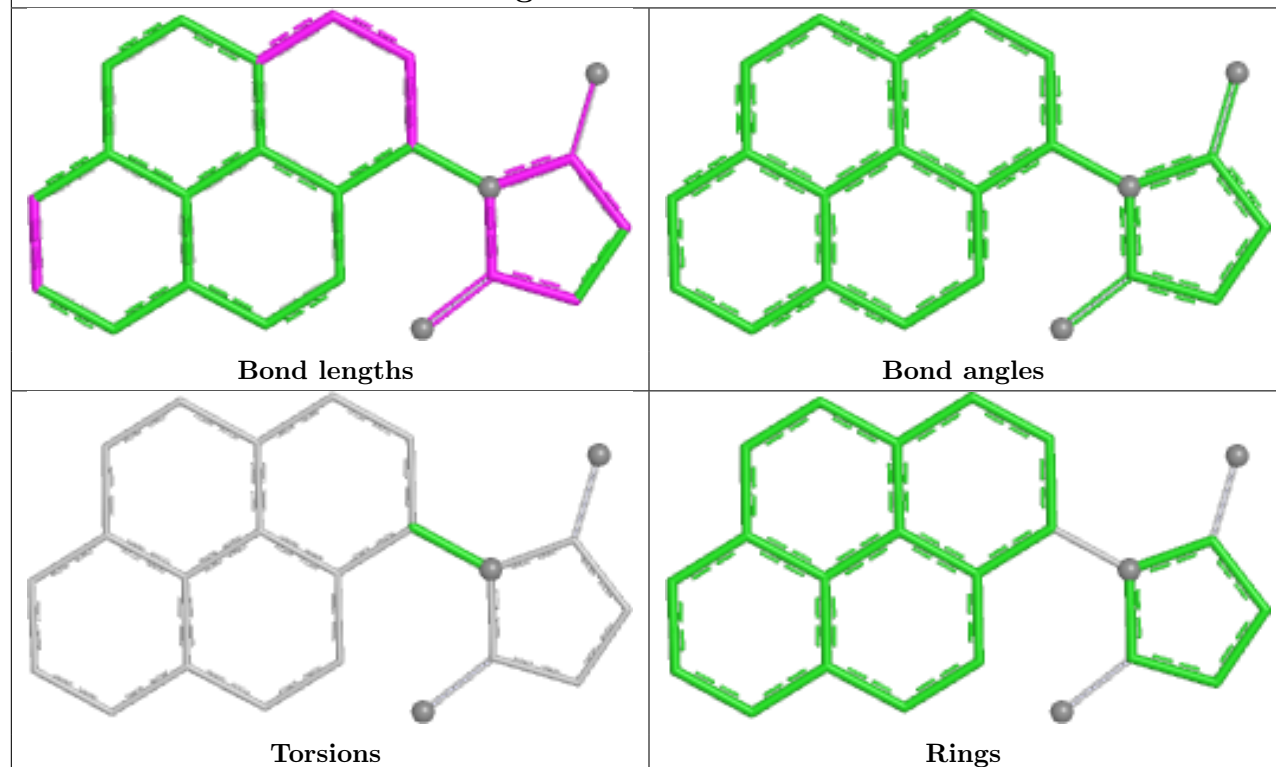
Ligand A1L9F FA 201



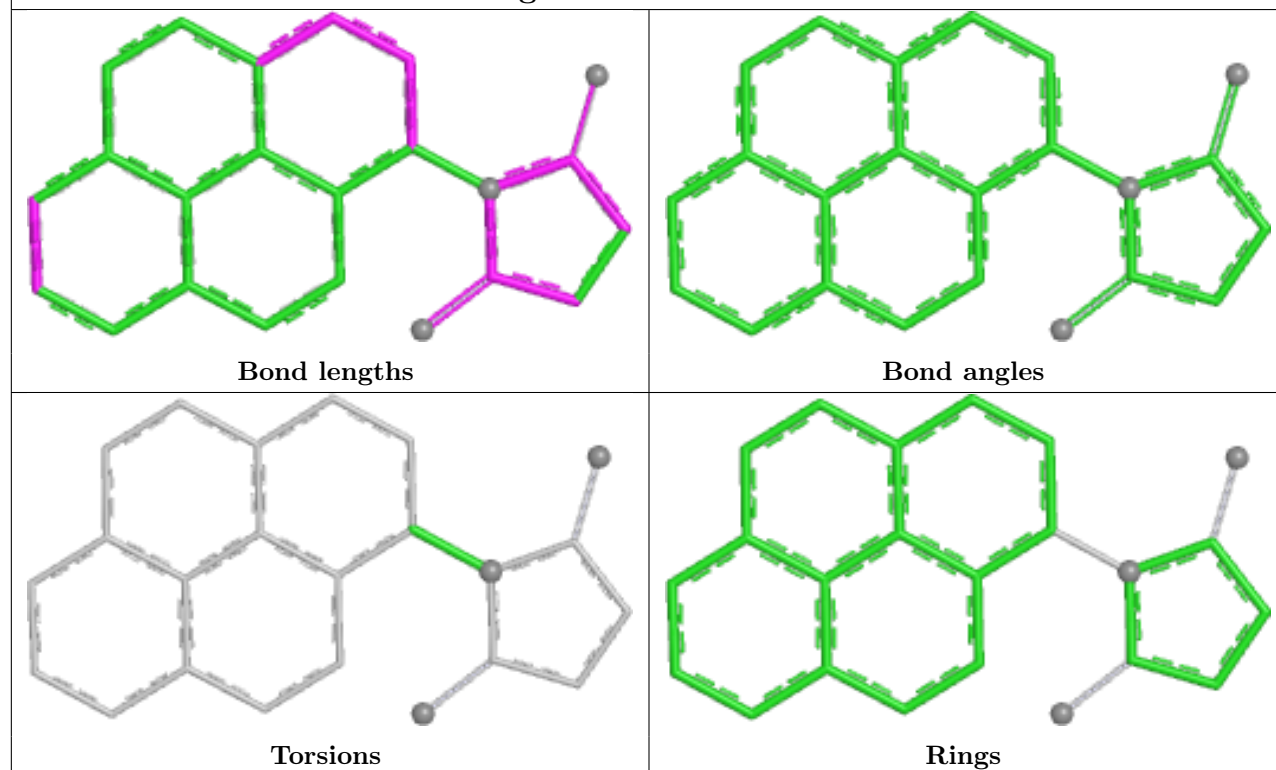
Ligand A1L9F TA 201



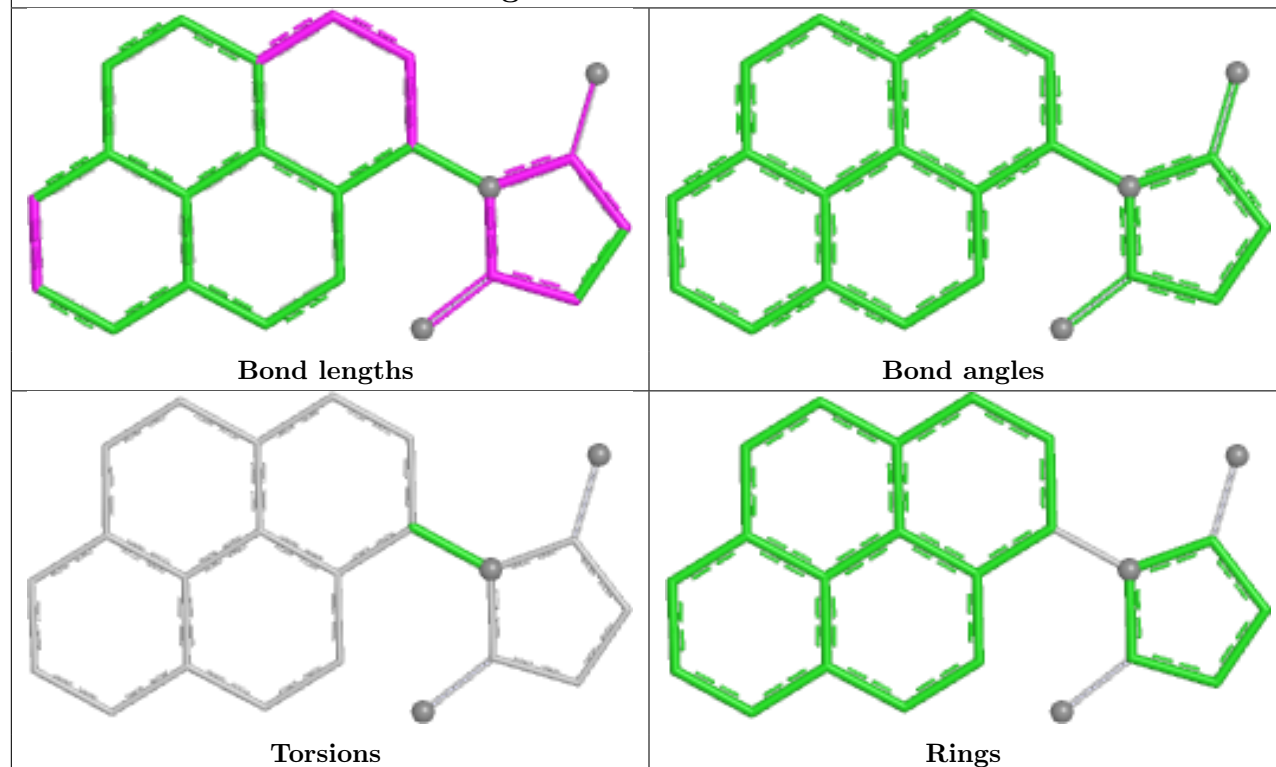
Ligand A1L9F R 202



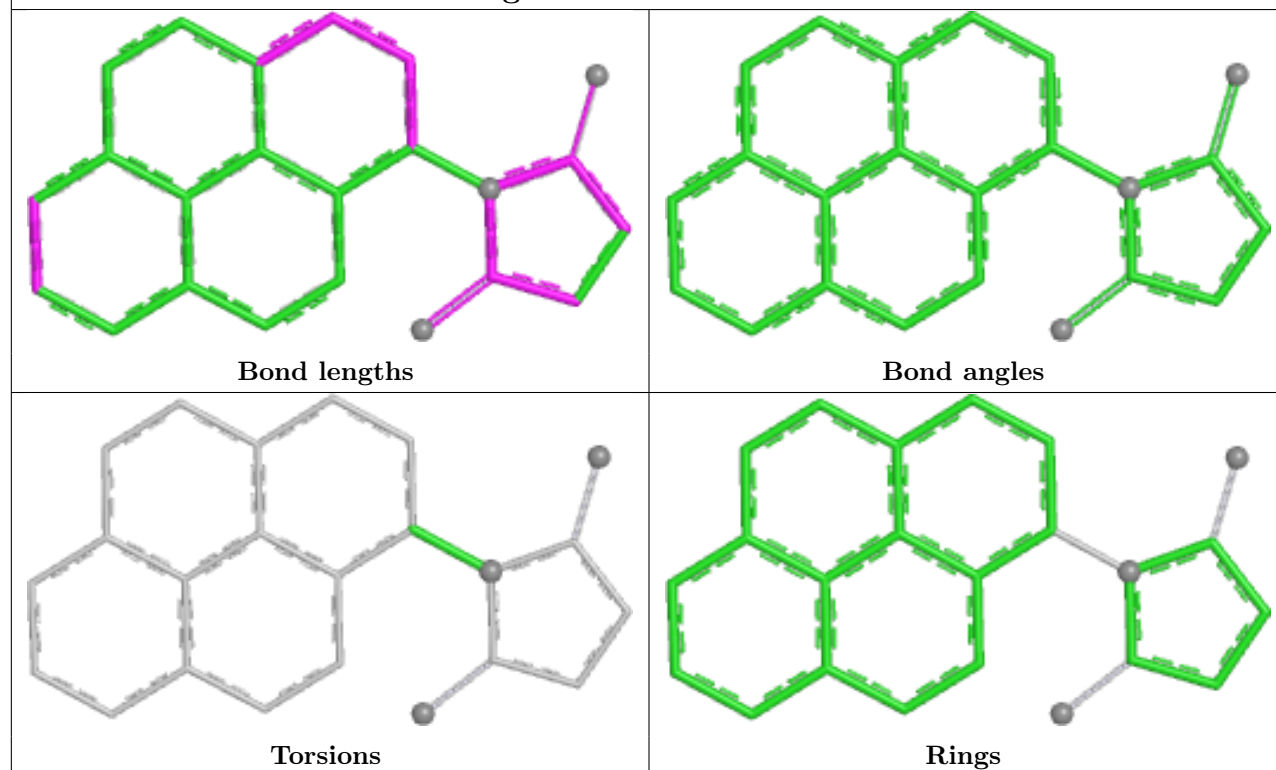
Ligand A1L9F S 201



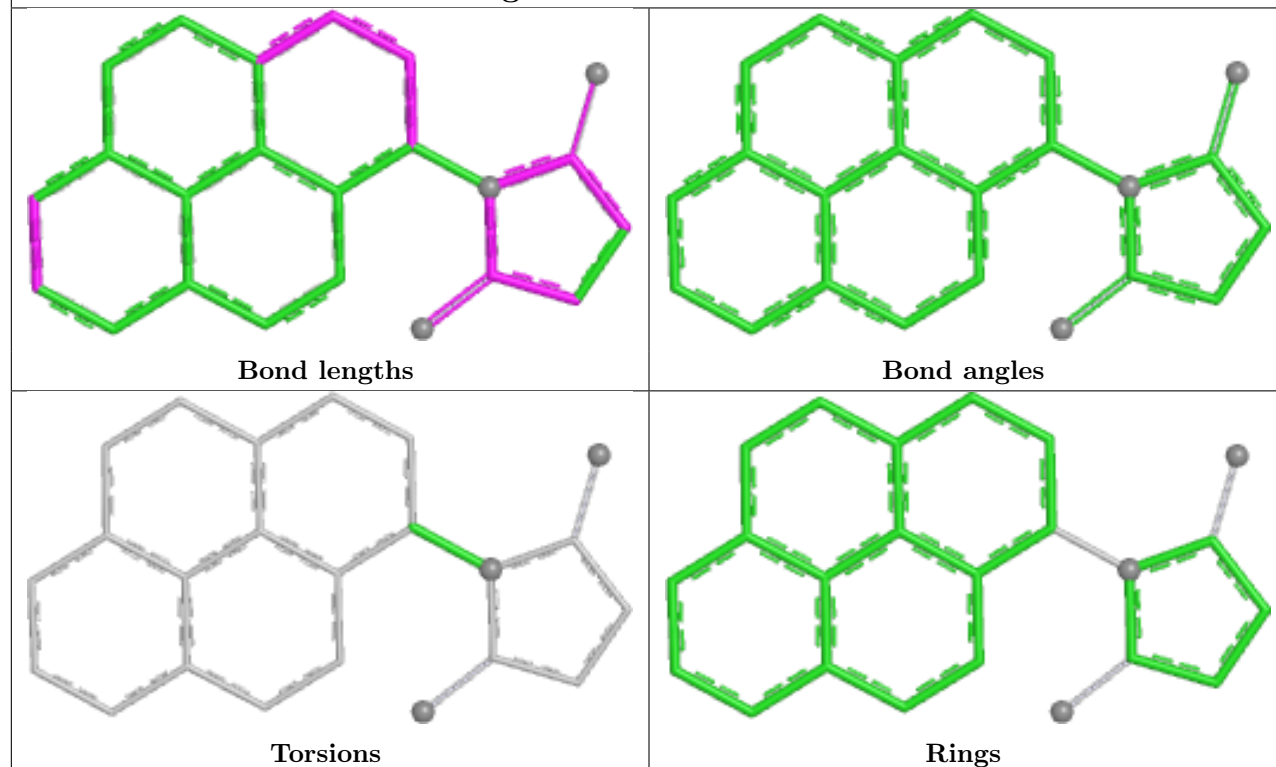
Ligand A1L9F UA 201



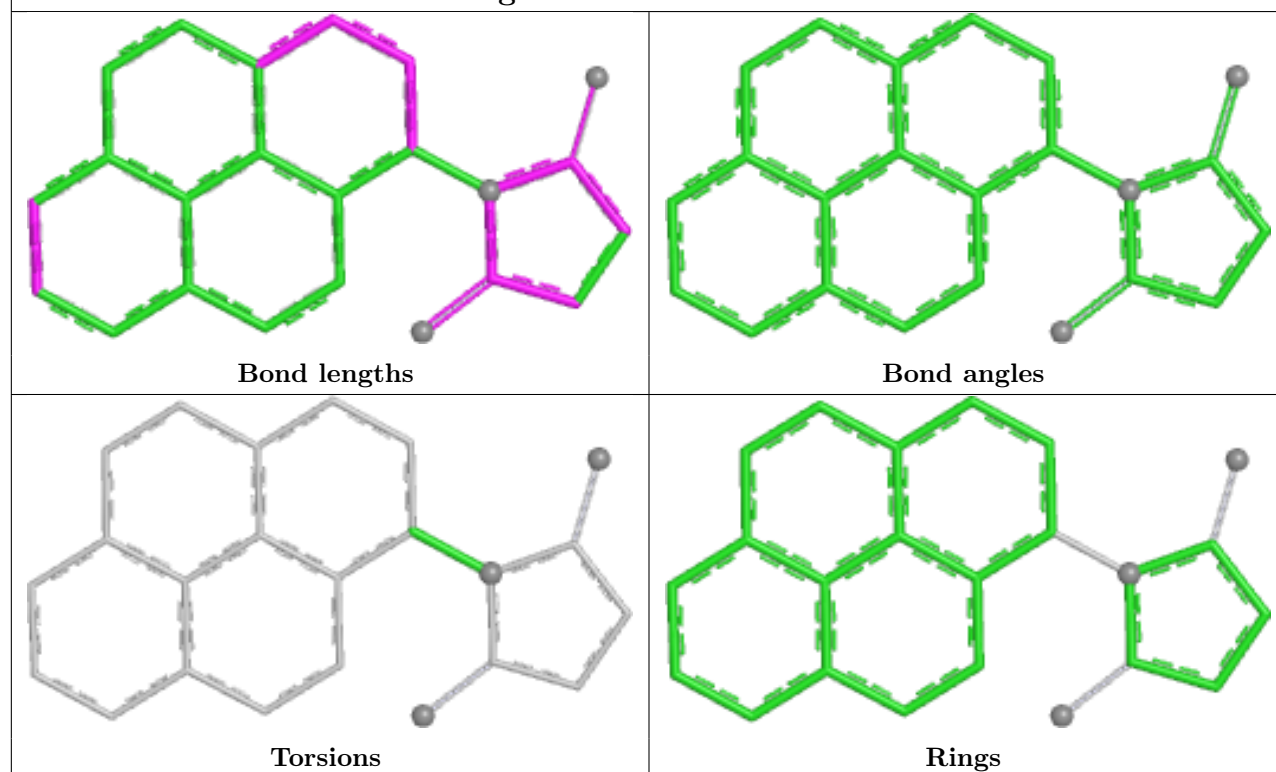
Ligand A1L9F BA 202



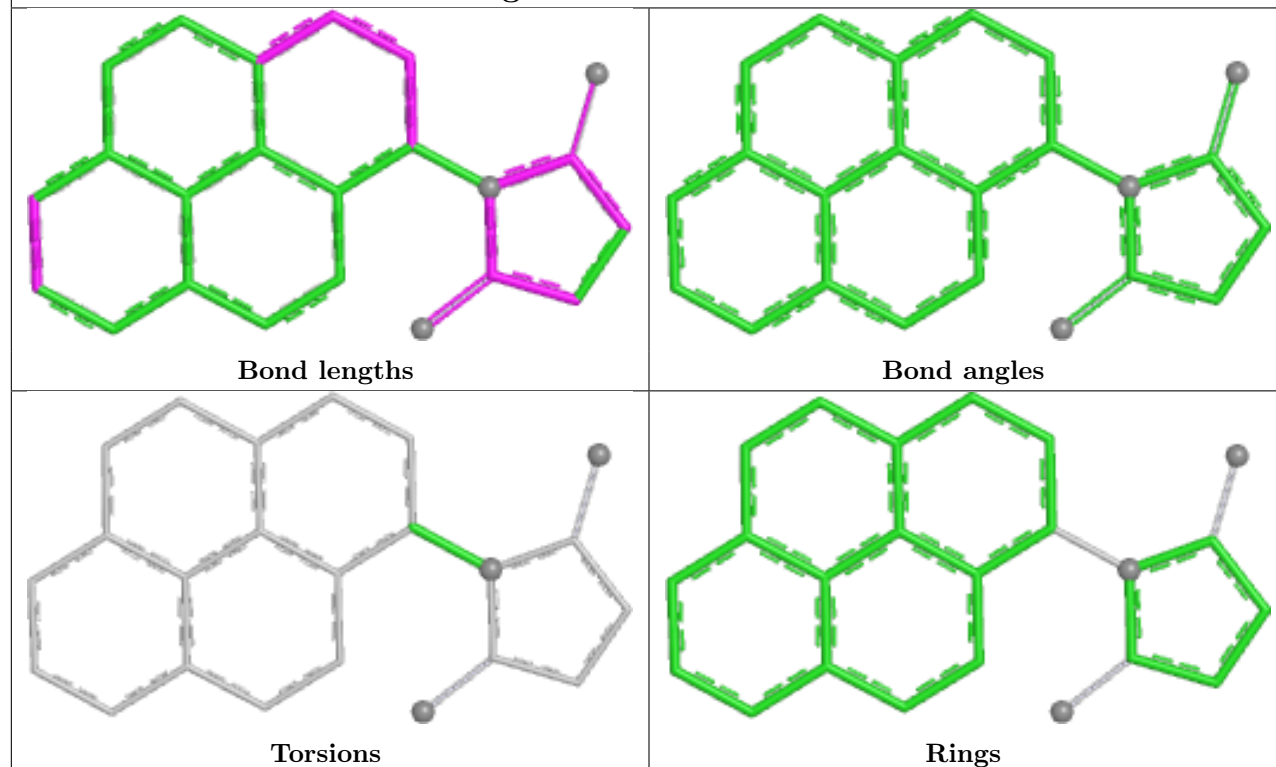
Ligand A1L9F RA 202



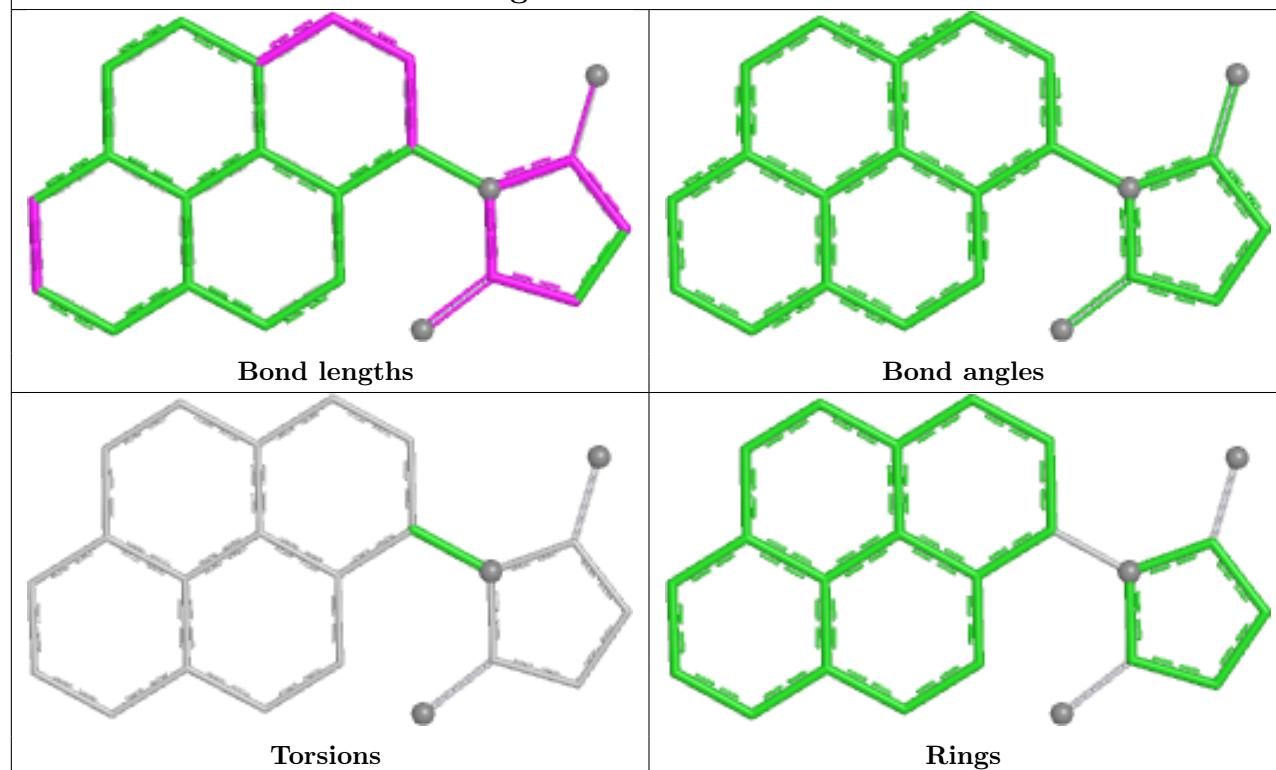
Ligand A1L9F MA 201



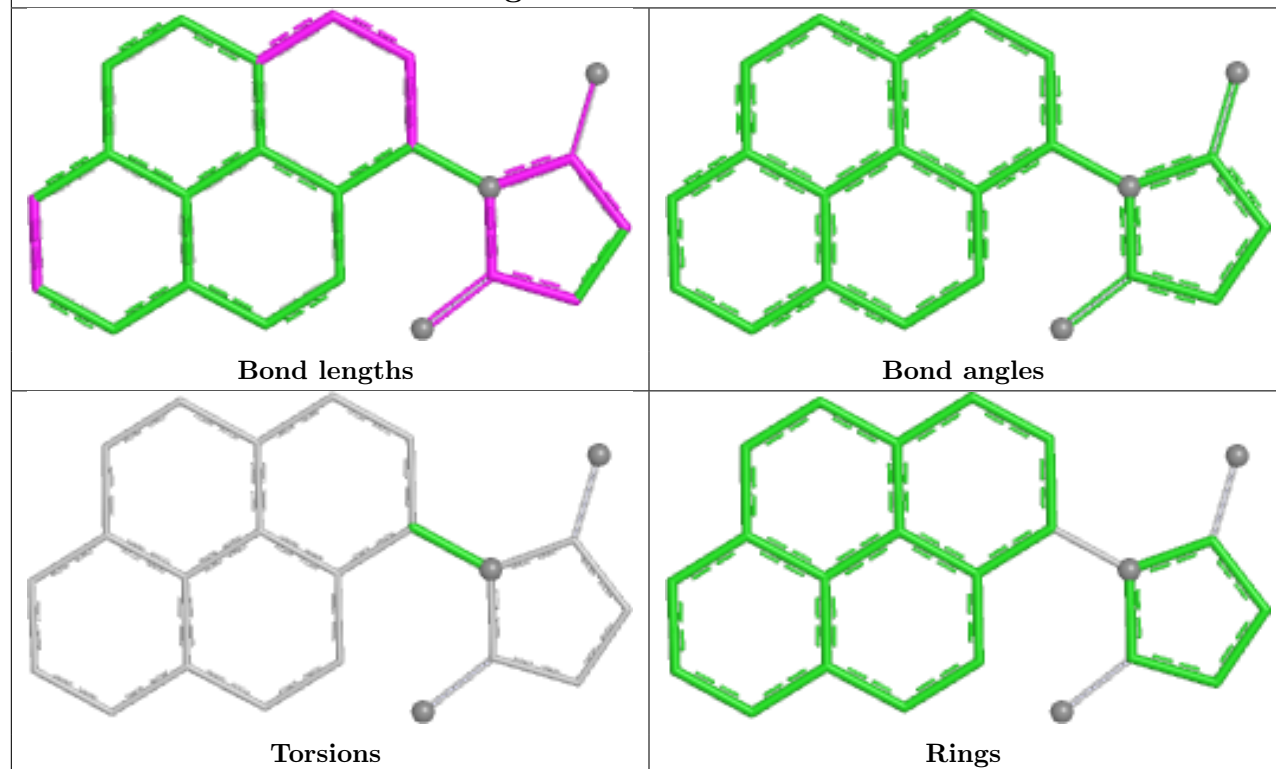
Ligand A1L9F DB 202



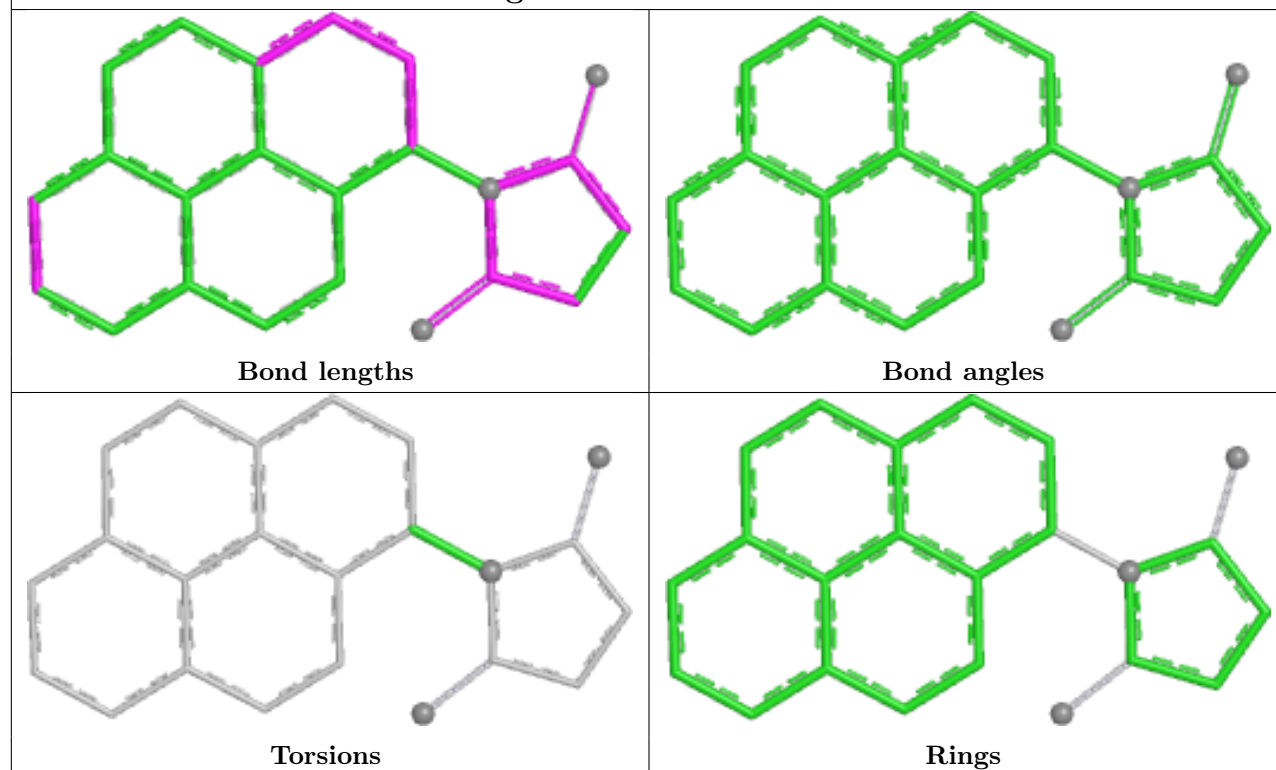
Ligand A1L9F W 201



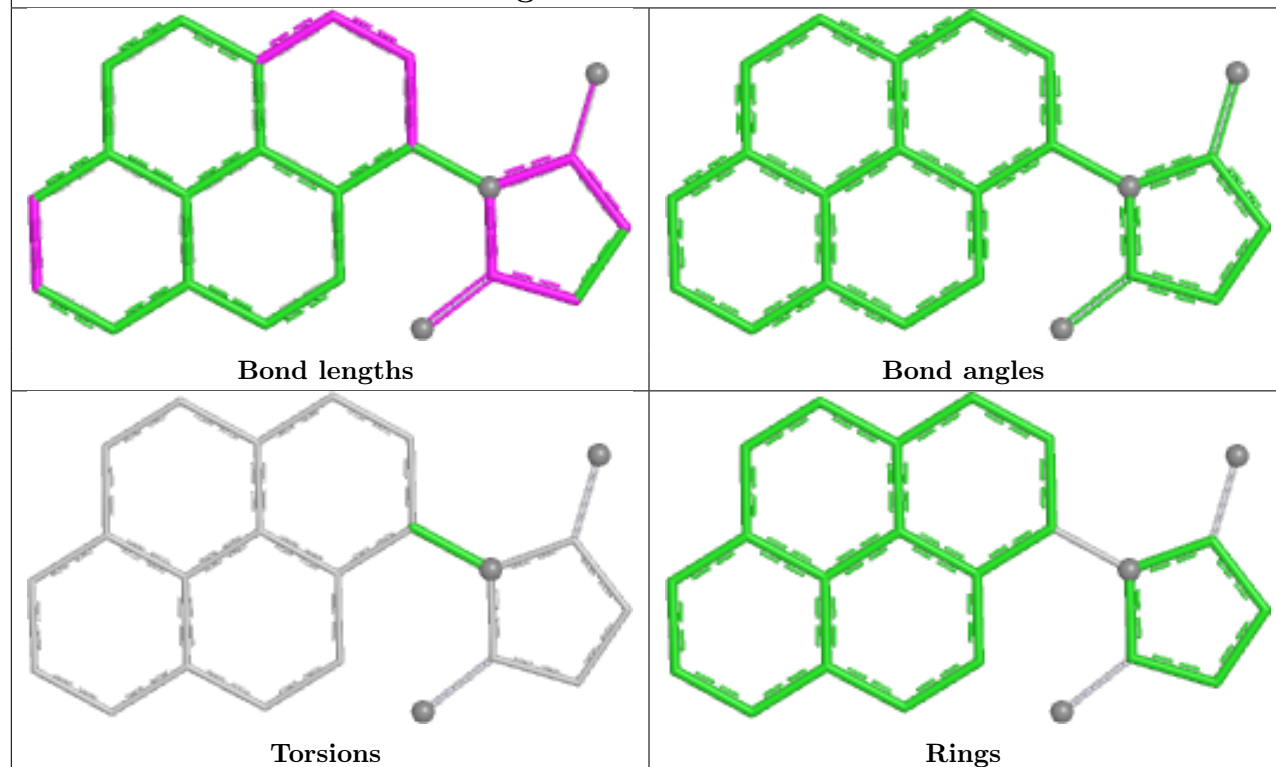
Ligand A1L9F PA 201



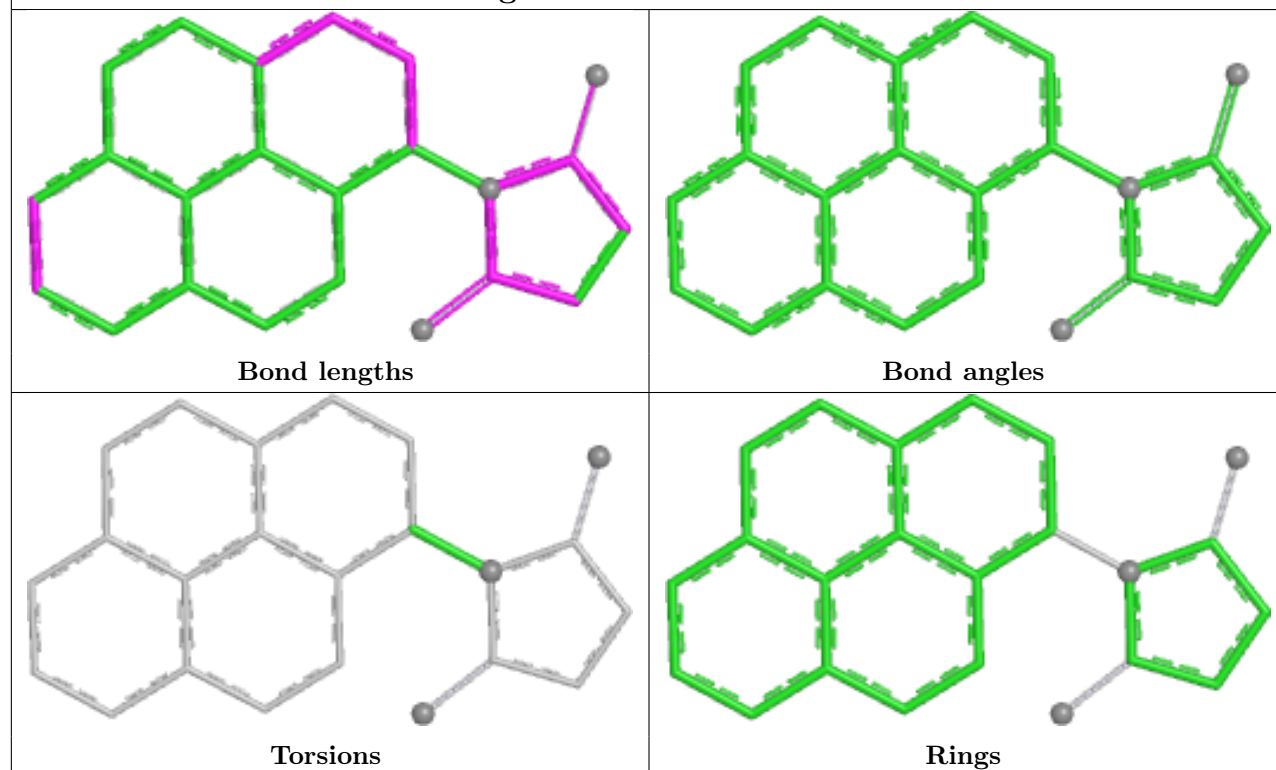
Ligand A1L9F JA 201



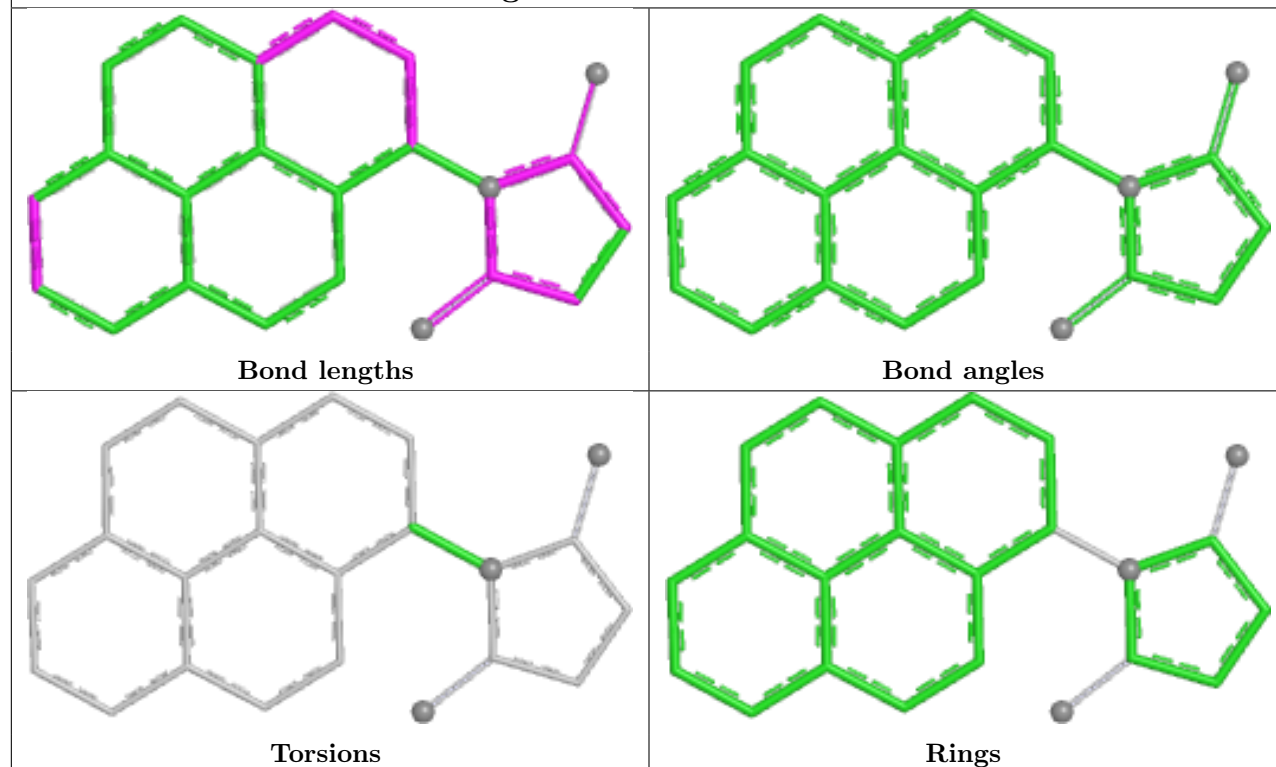
Ligand A1L9F P 202



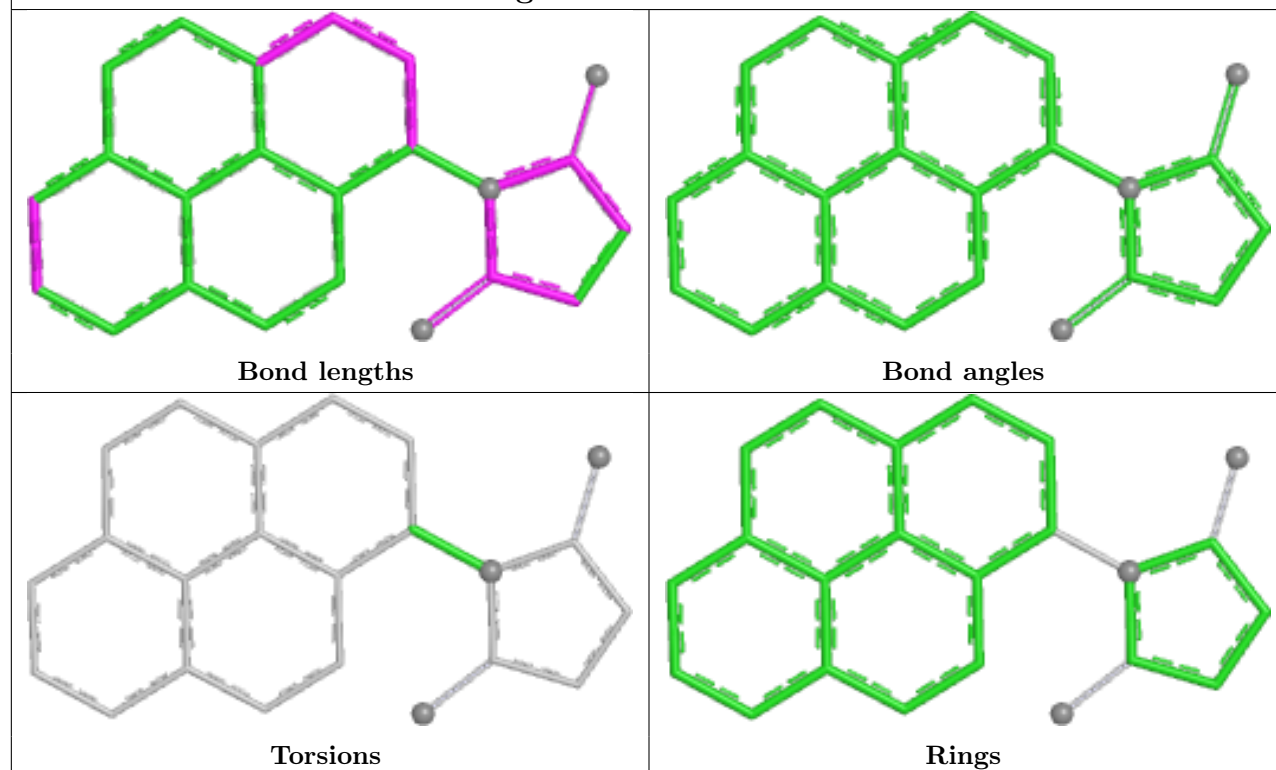
Ligand A1L9F WA 201



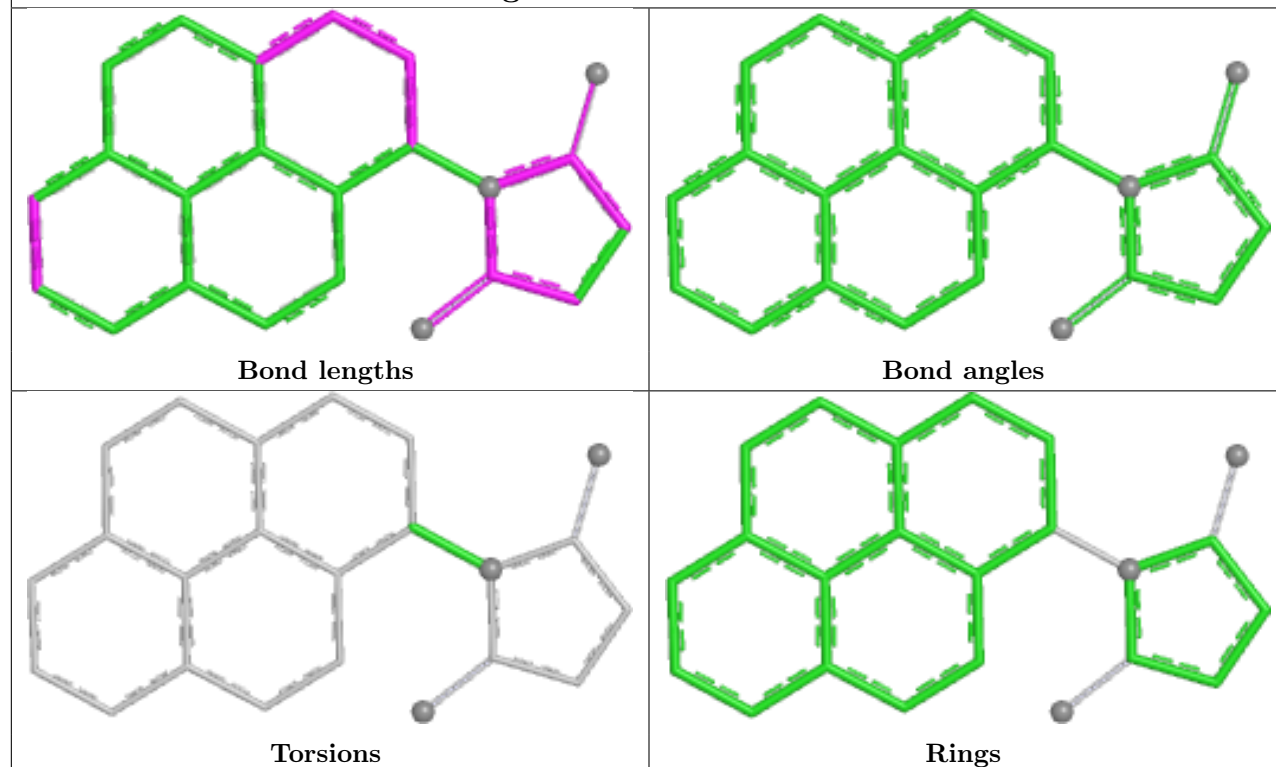
Ligand A1L9F GB 202



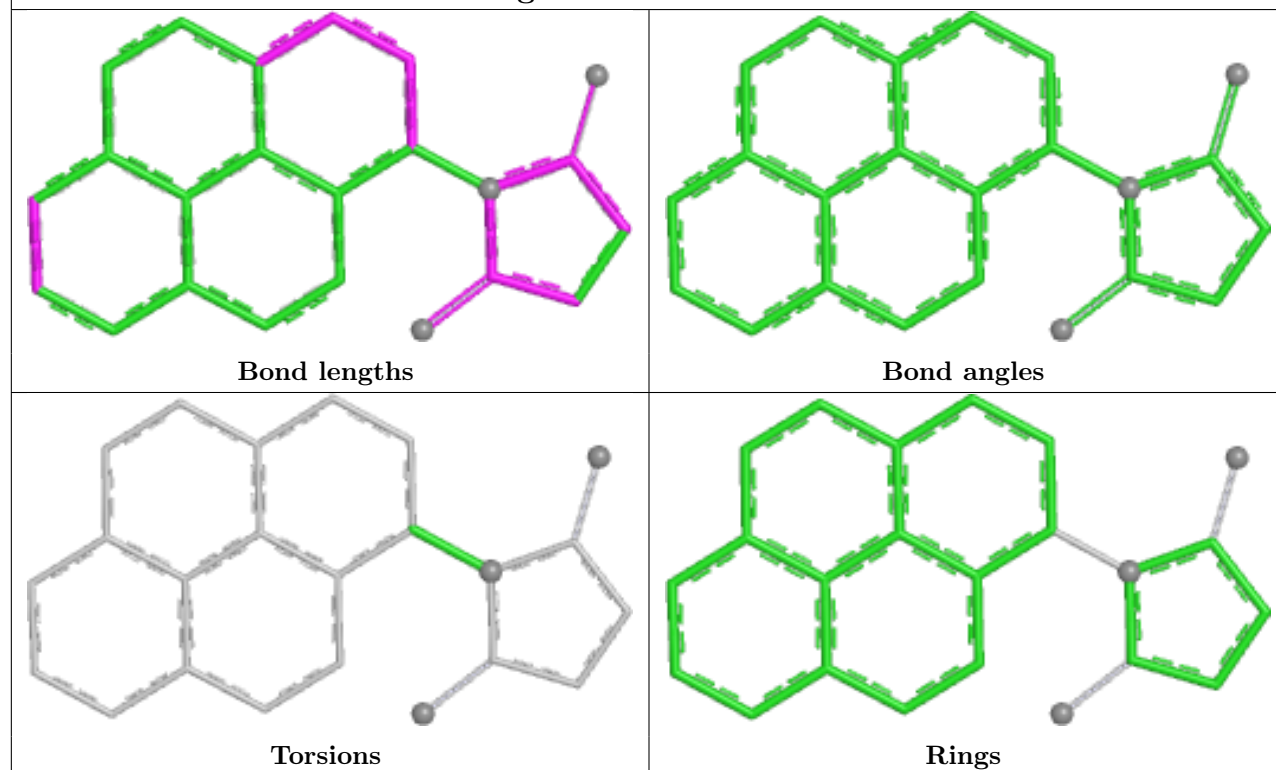
Ligand A1L9F C 201



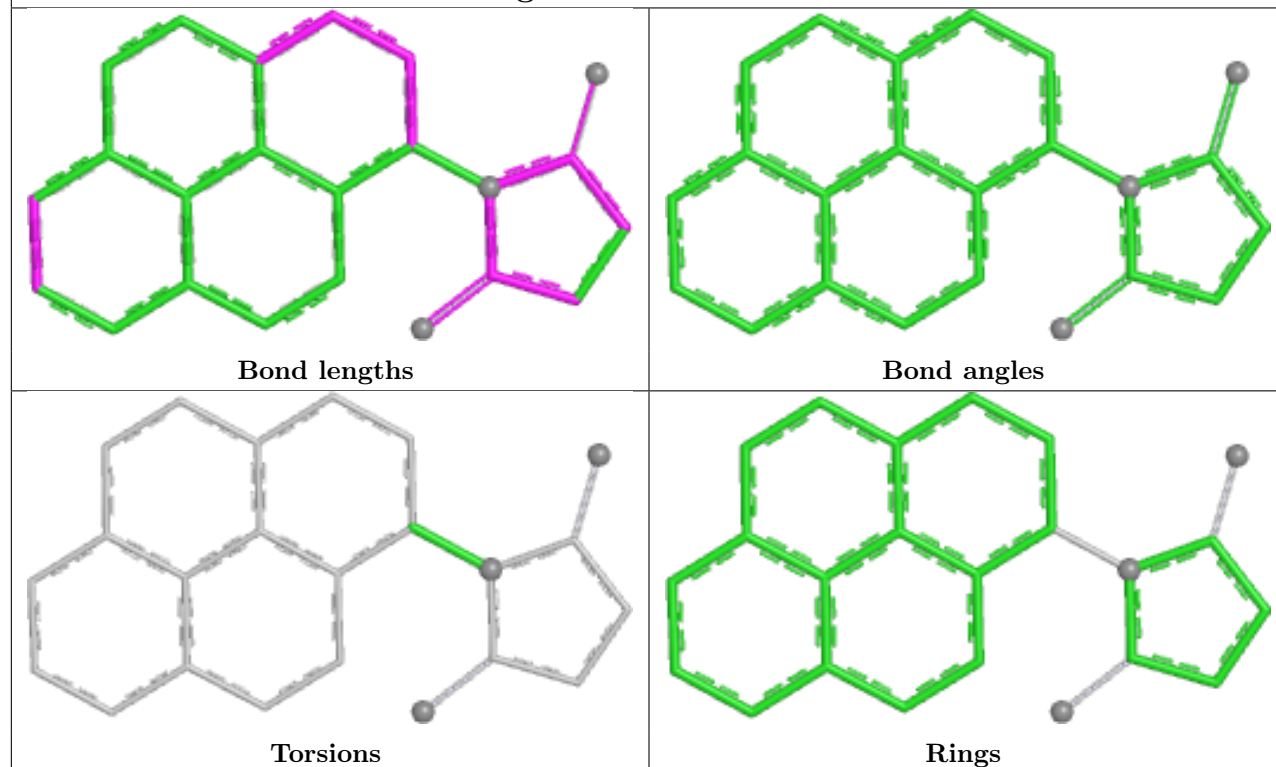
Ligand A1L9F DA 202



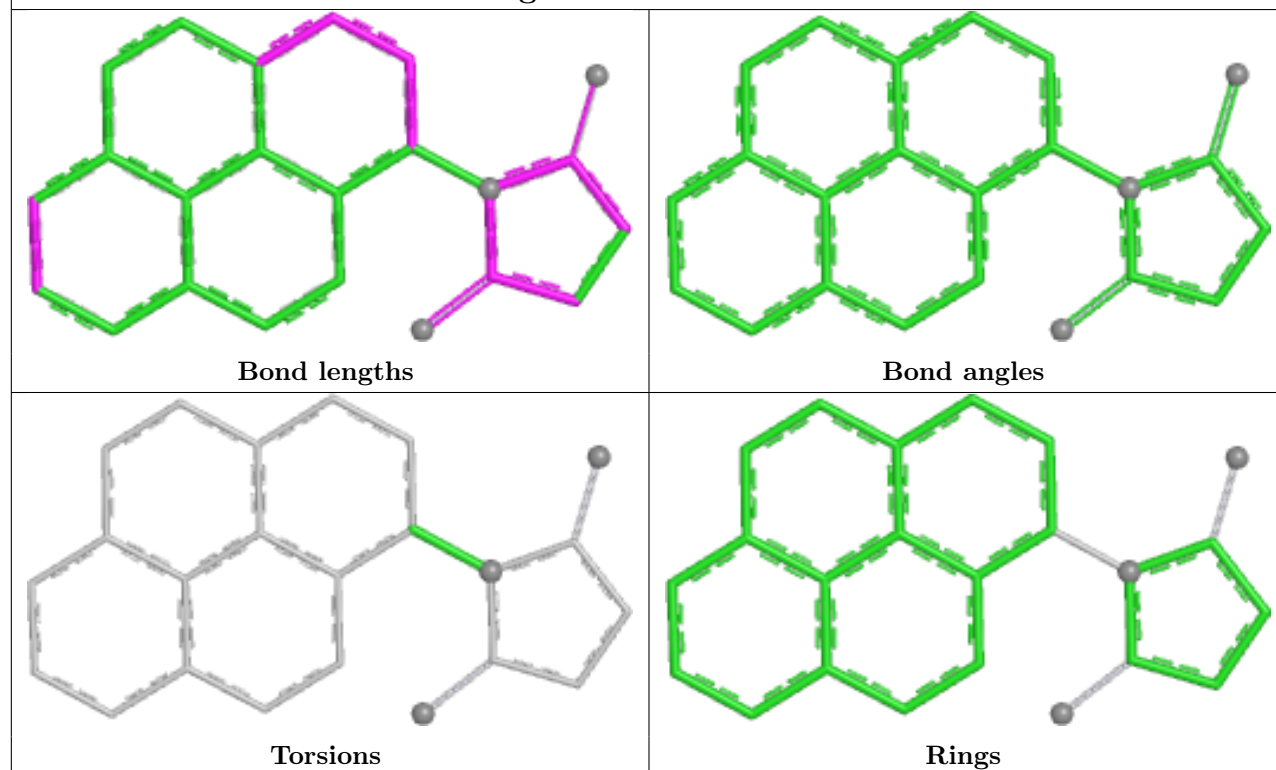
Ligand A1L9F E 201



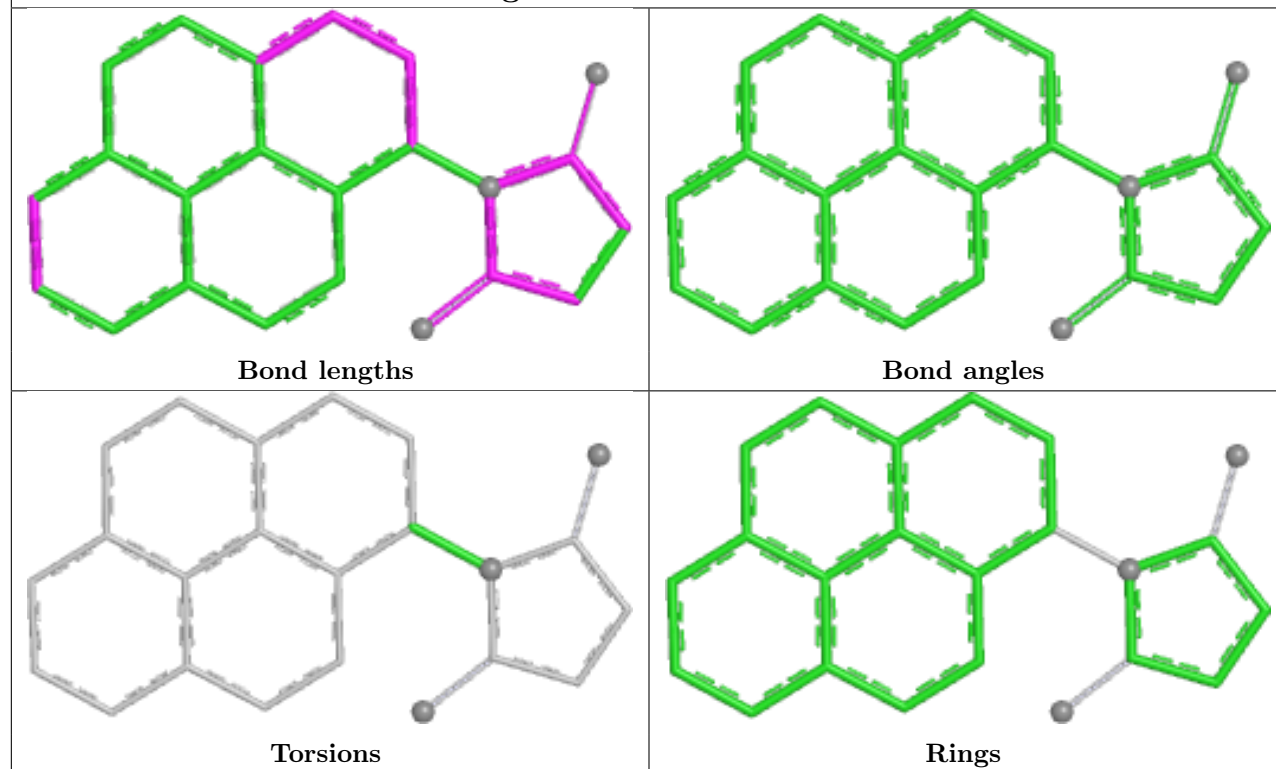
Ligand A1L9F P 201



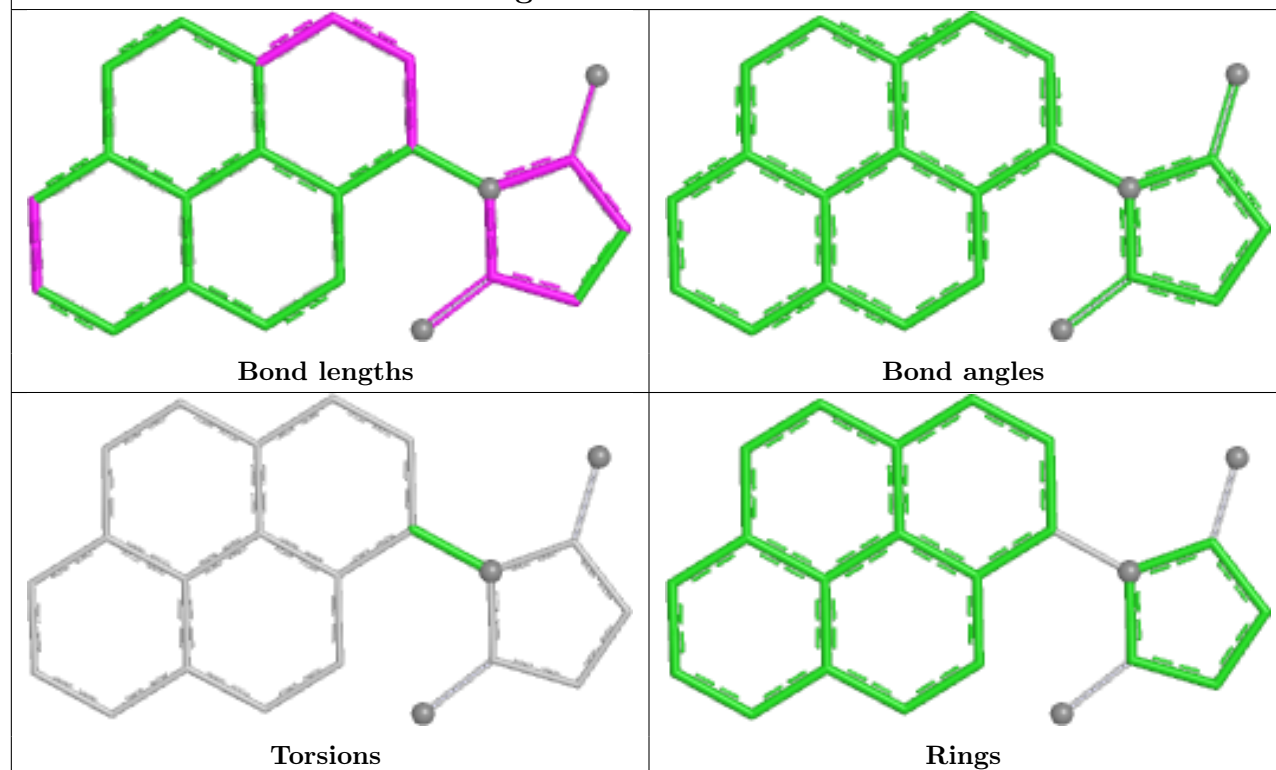
Ligand A1L9F S 202



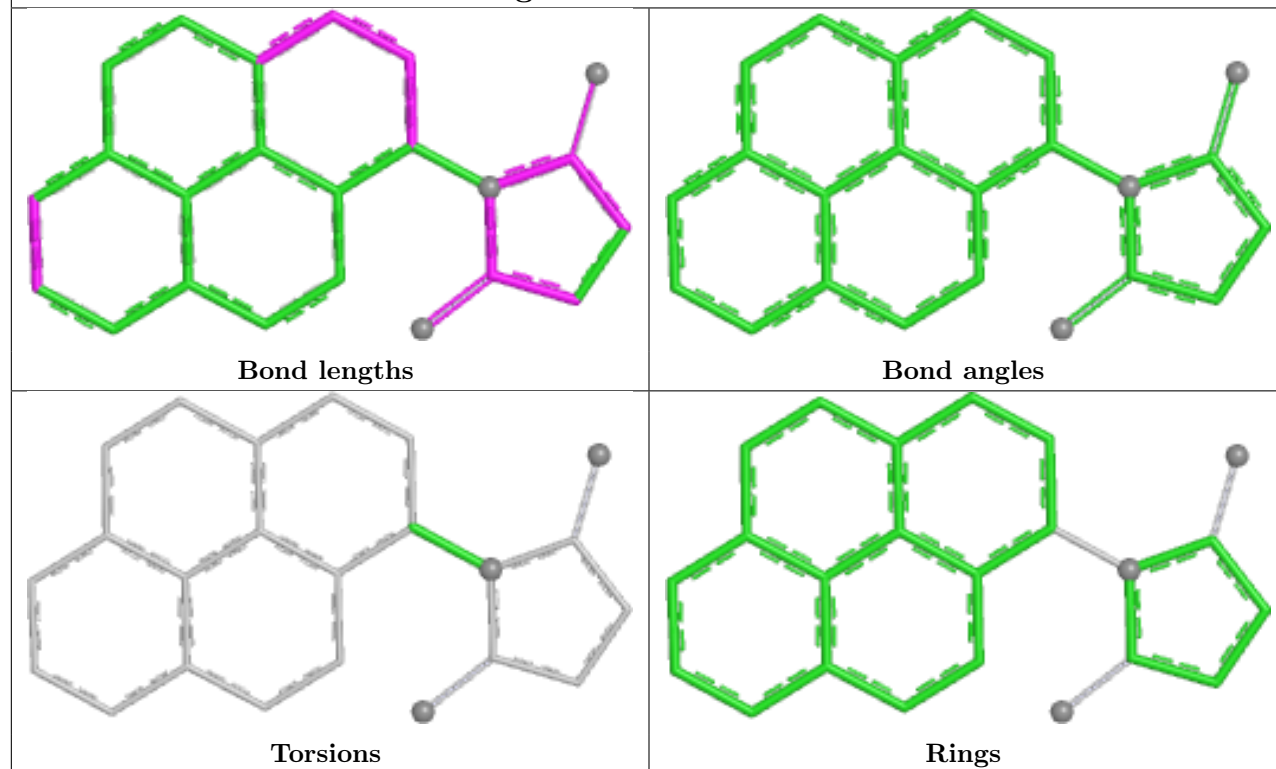
Ligand A1L9F GB 201



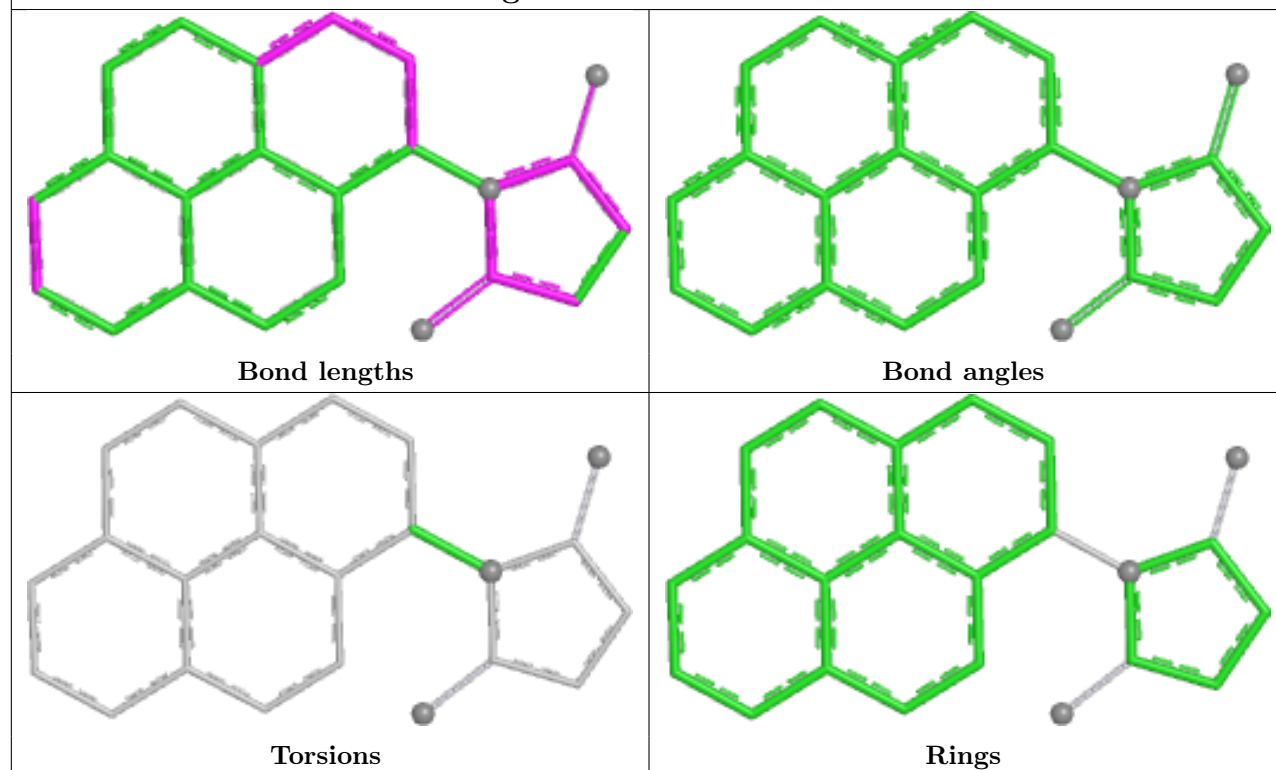
Ligand A1L9F D 202



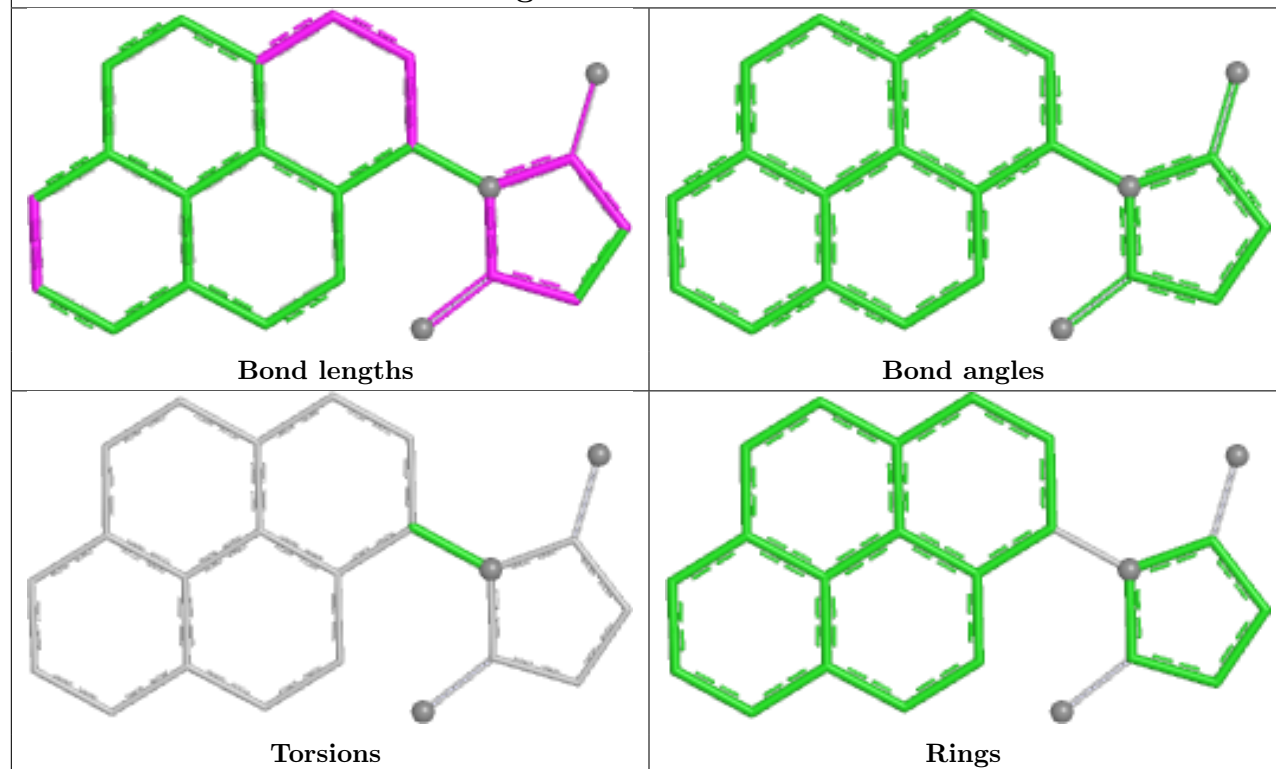
Ligand A1L9F V 202



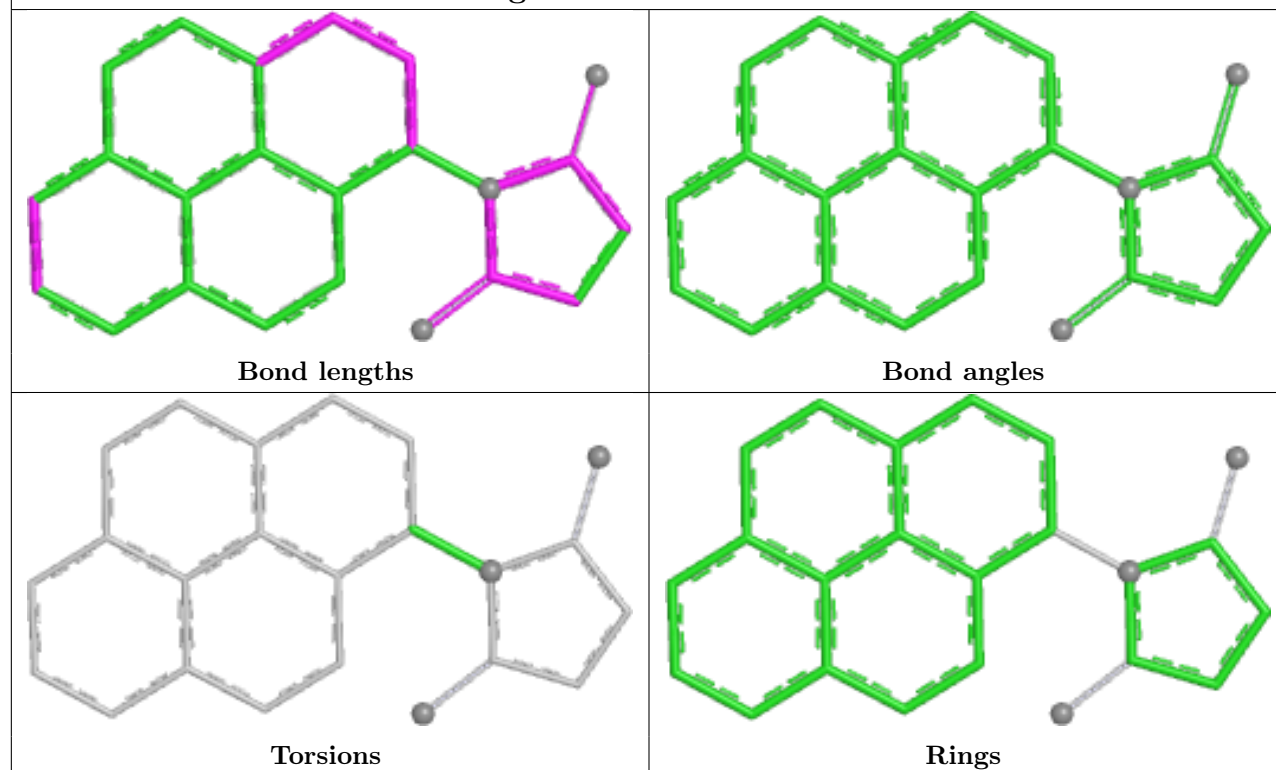
Ligand A1L9F DA 201



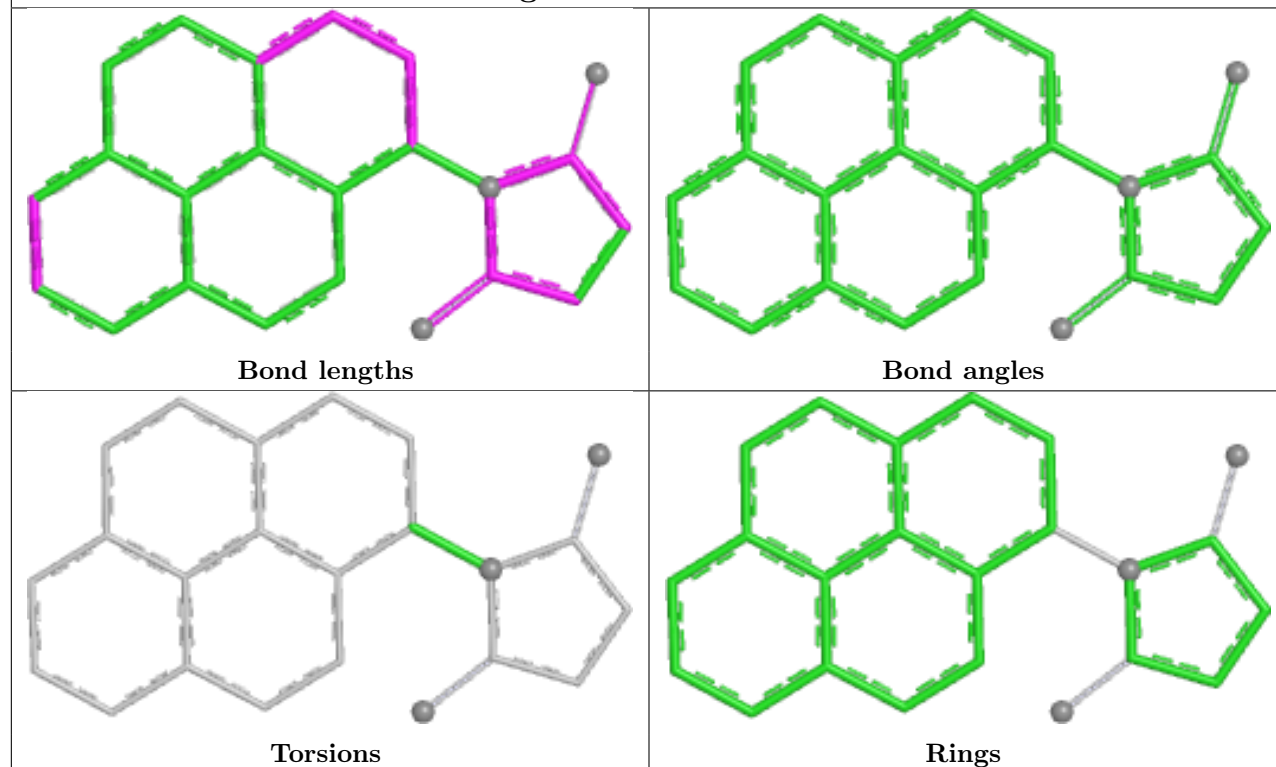
Ligand A1L9F B 201



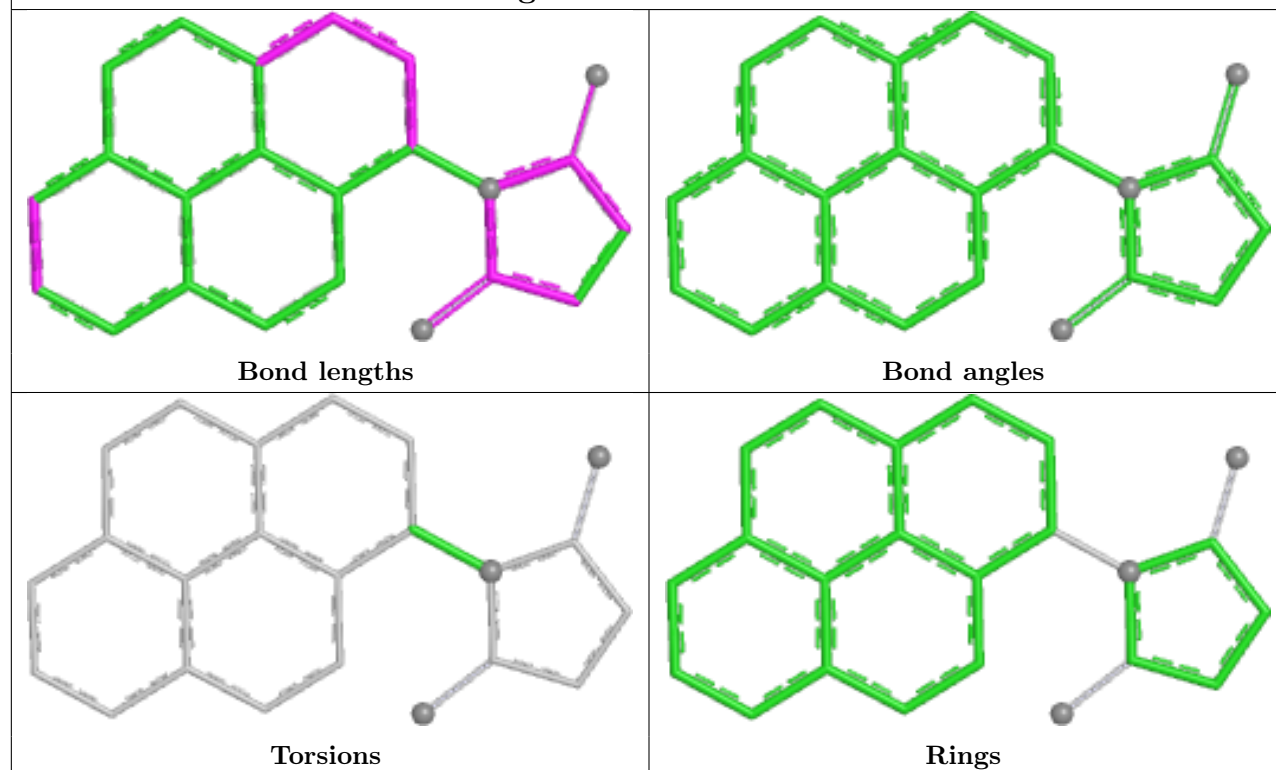
Ligand A1L9F IA 201



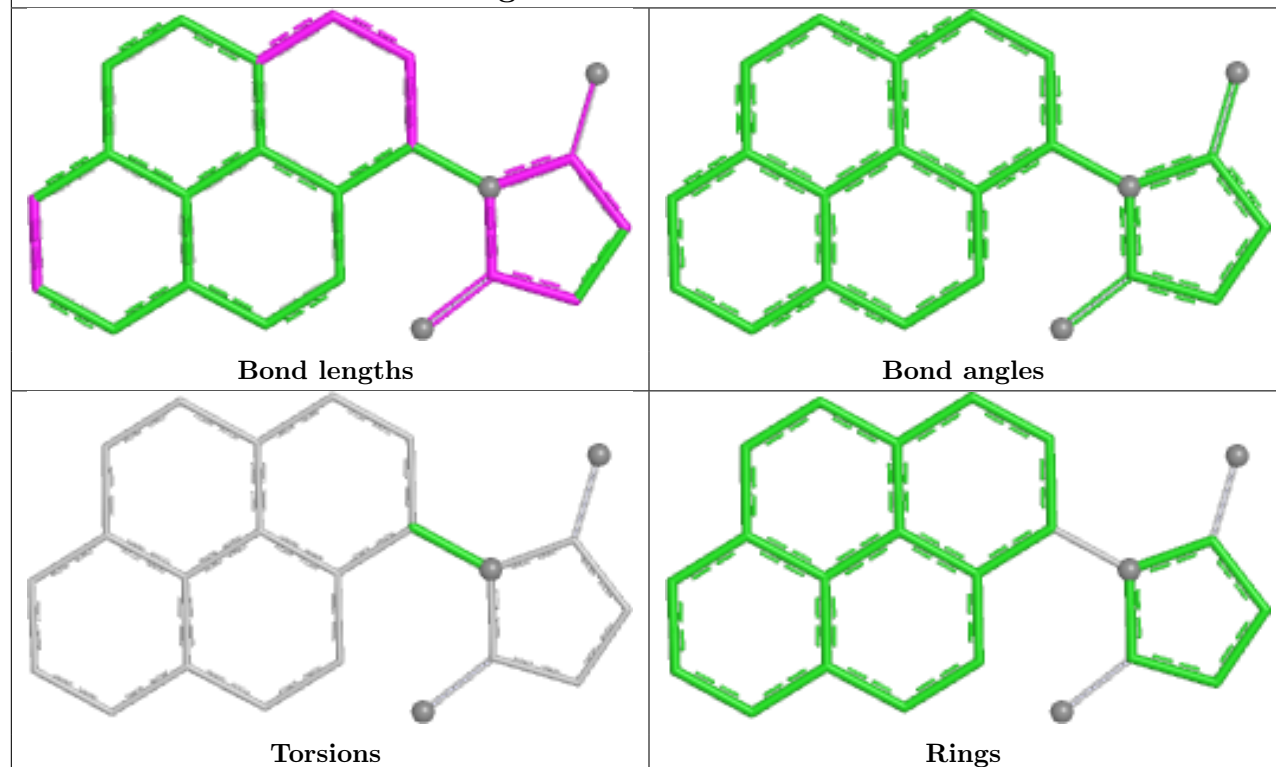
Ligand A1L9F J 201



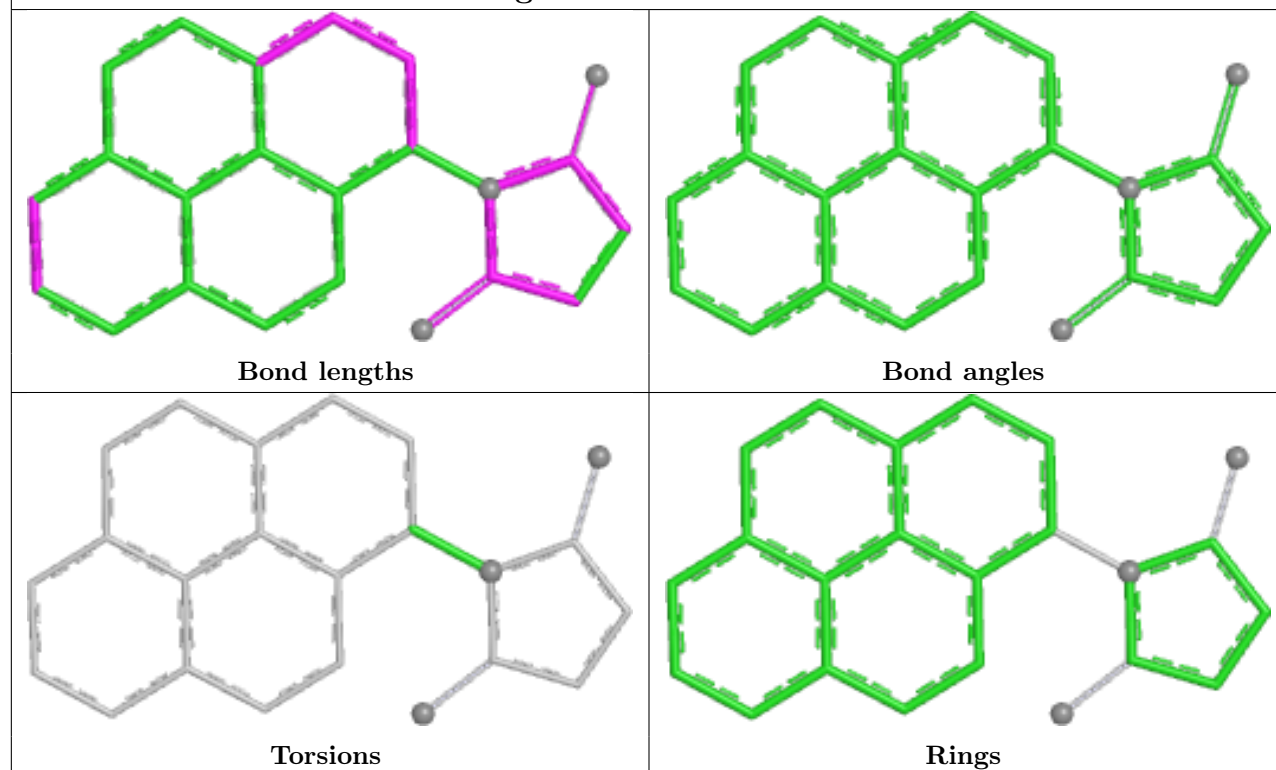
Ligand A1L9F L 201



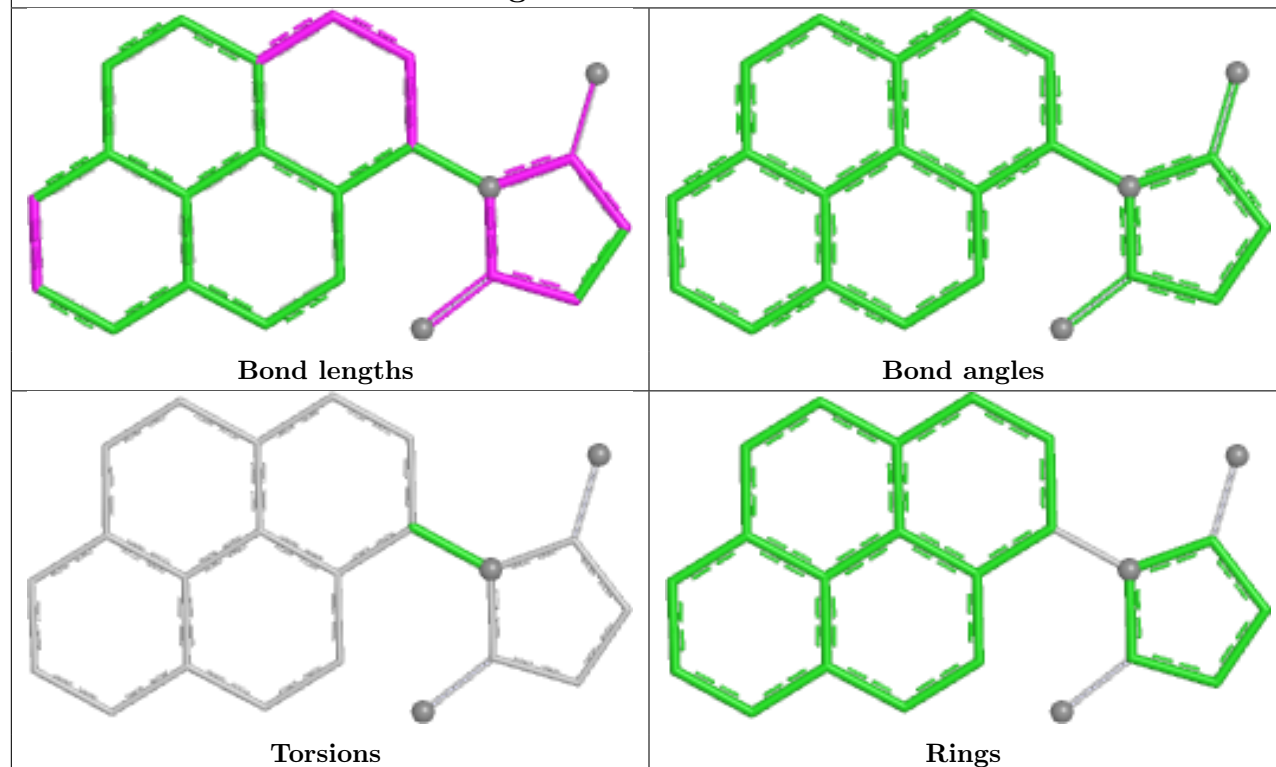
Ligand A1L9F MA 202



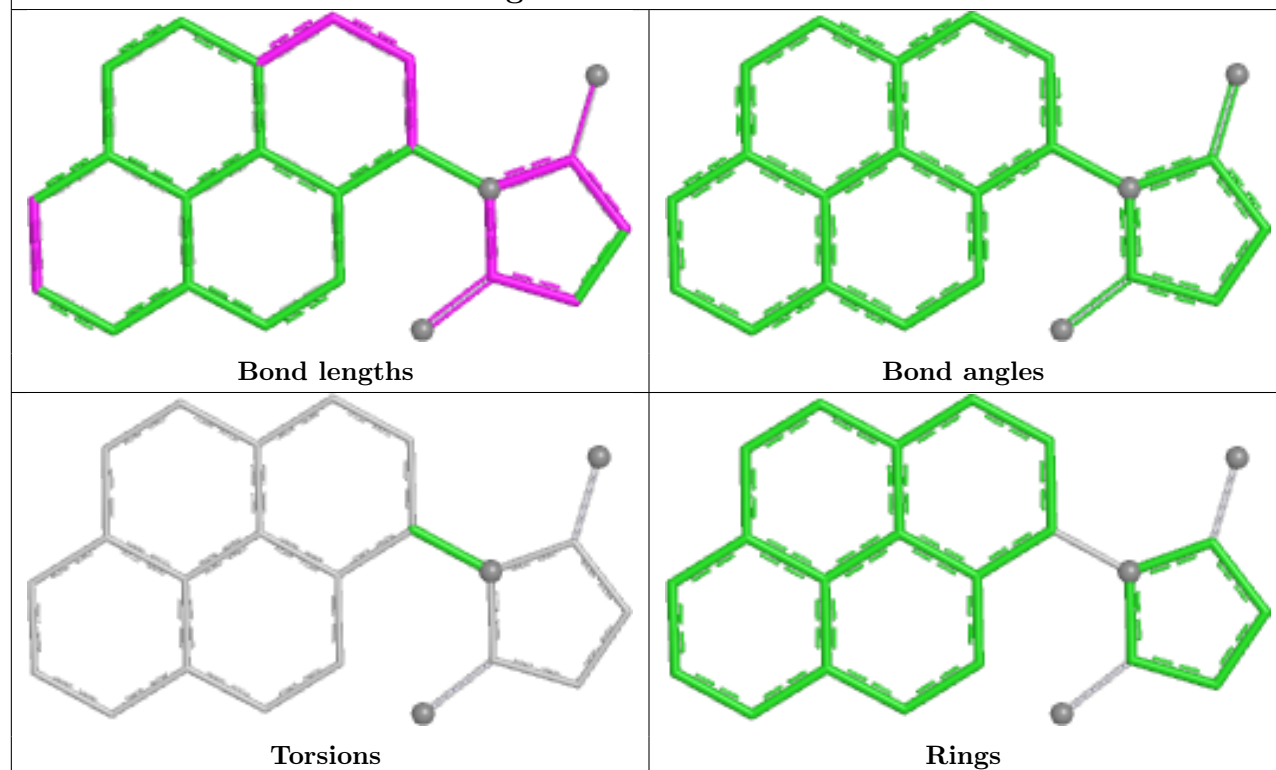
Ligand A1L9F V 201



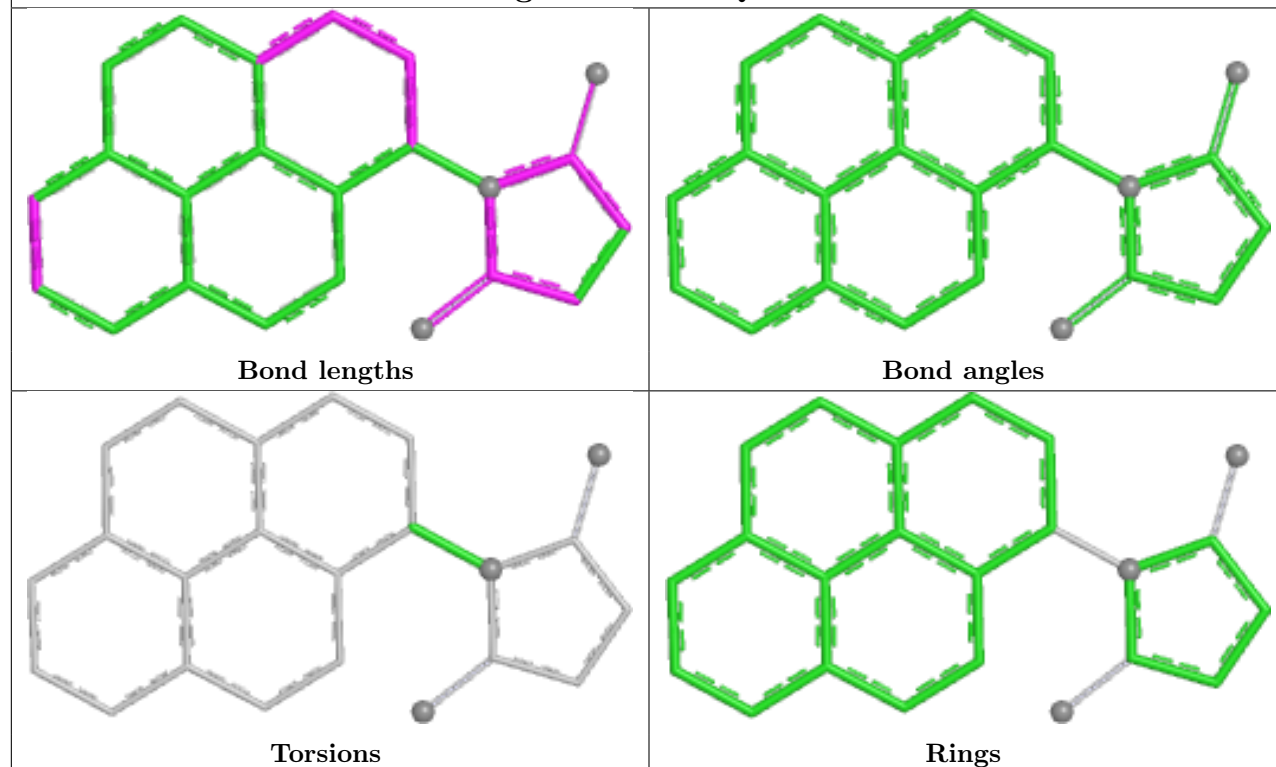
Ligand A1L9F IA 202



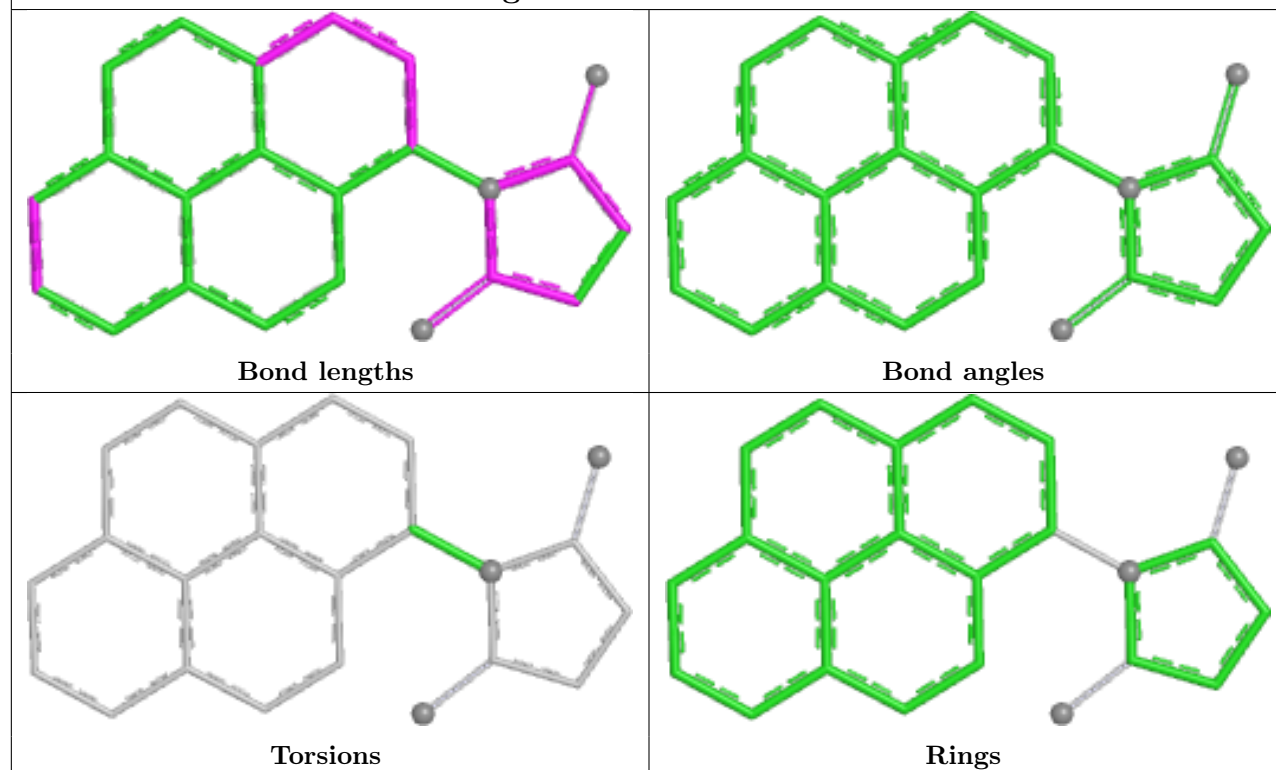
Ligand A1L9F JA 202



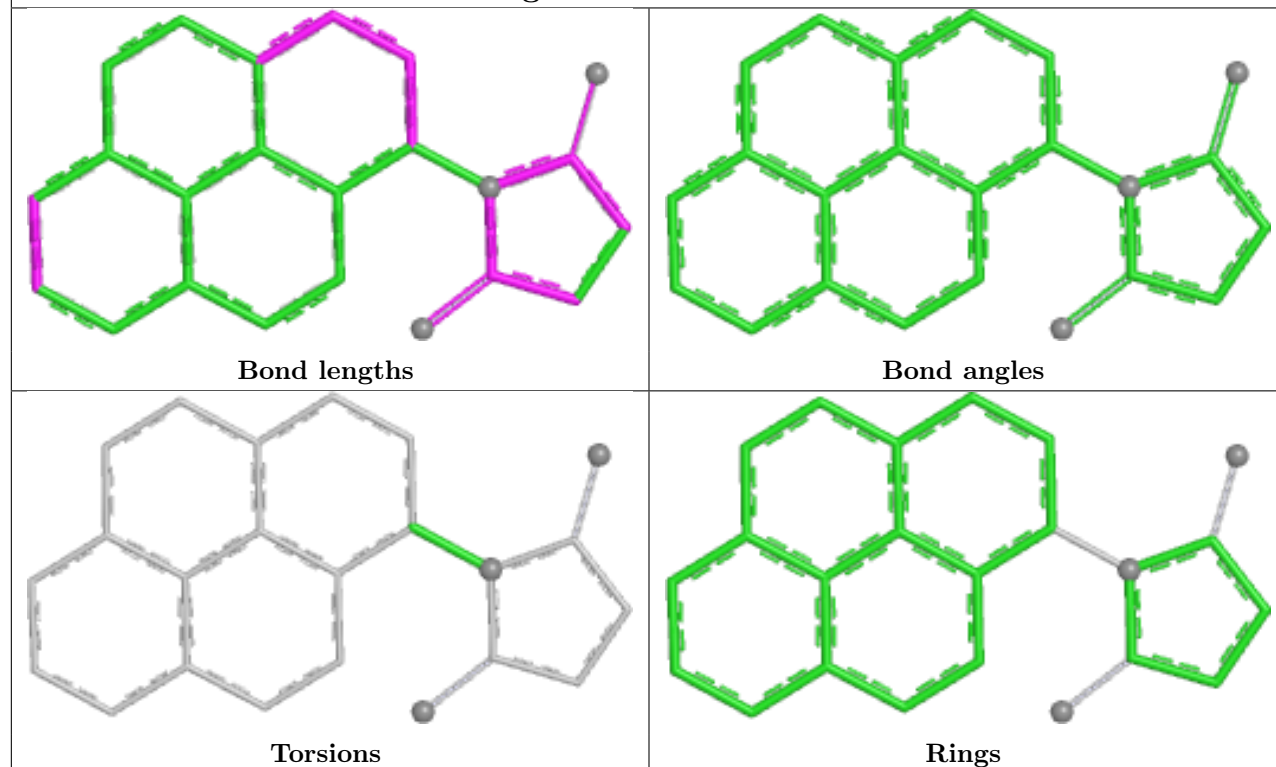
Ligand A1L9F Q 202



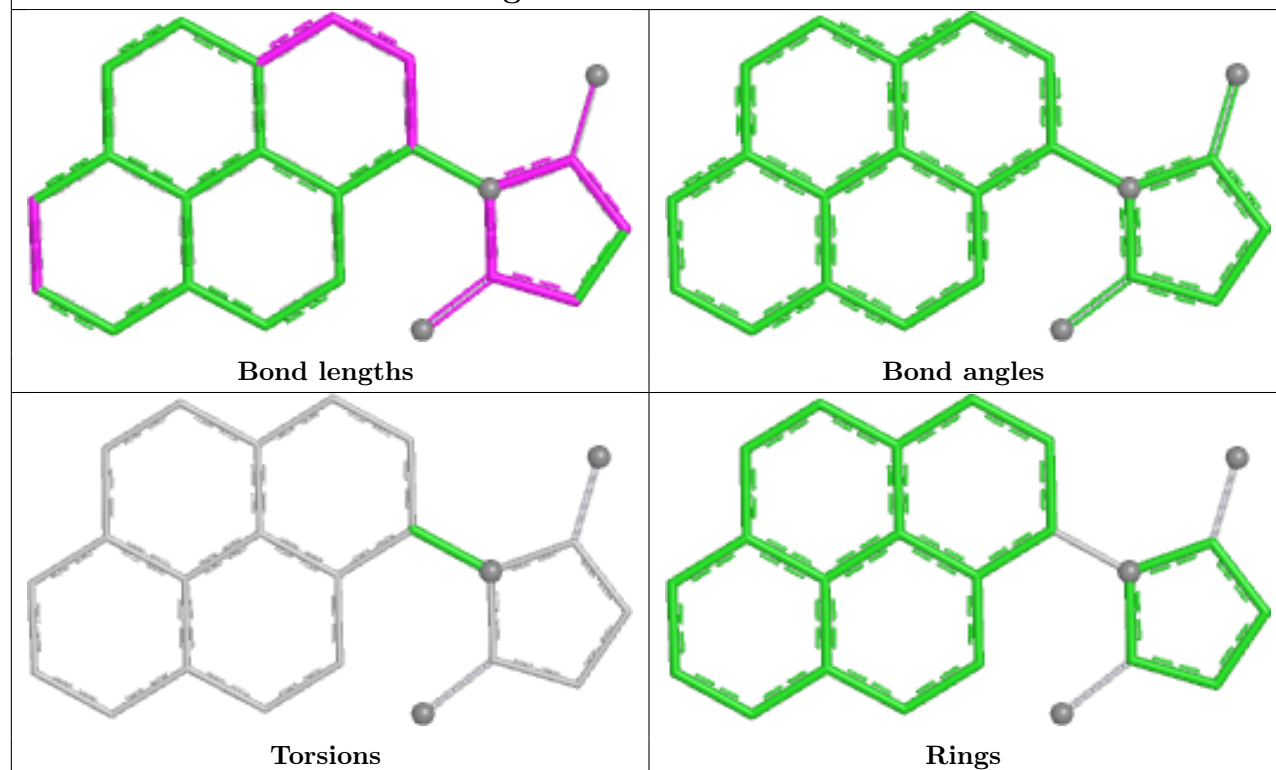
Ligand A1L9F BA 201



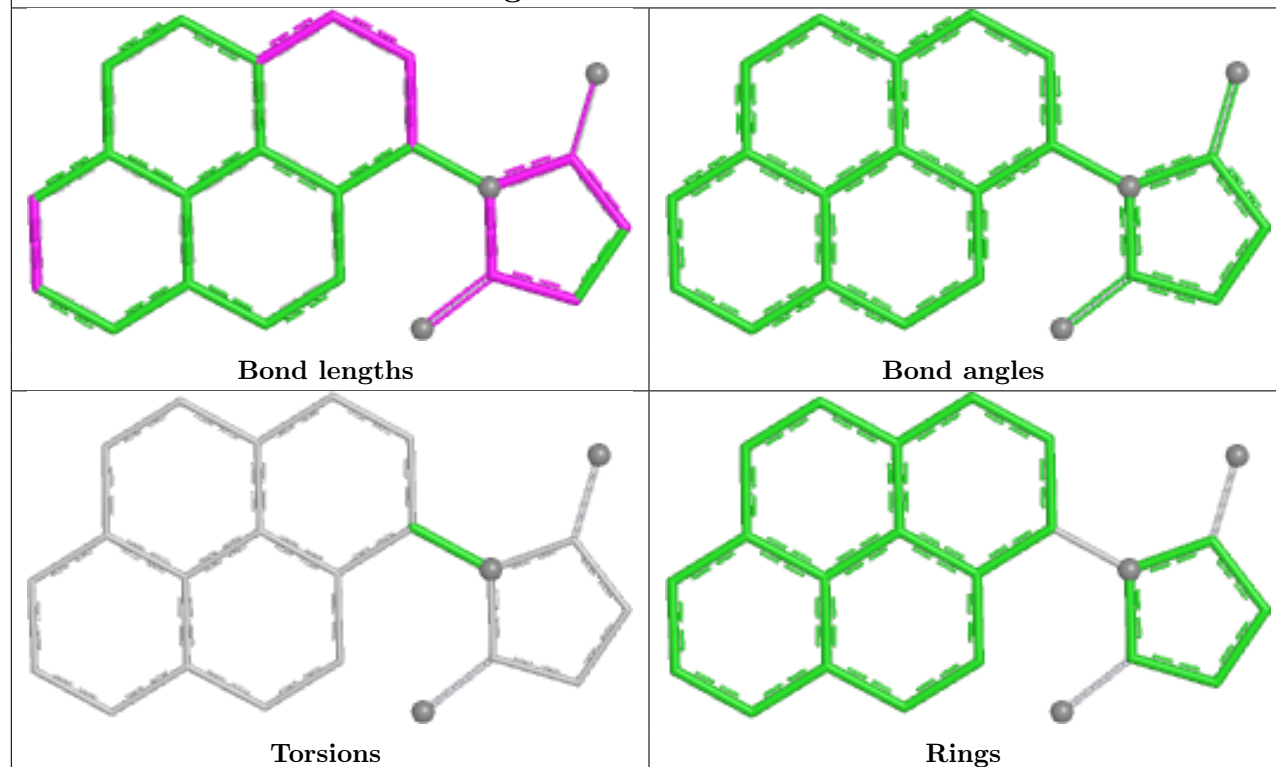
Ligand A1L9F I 201



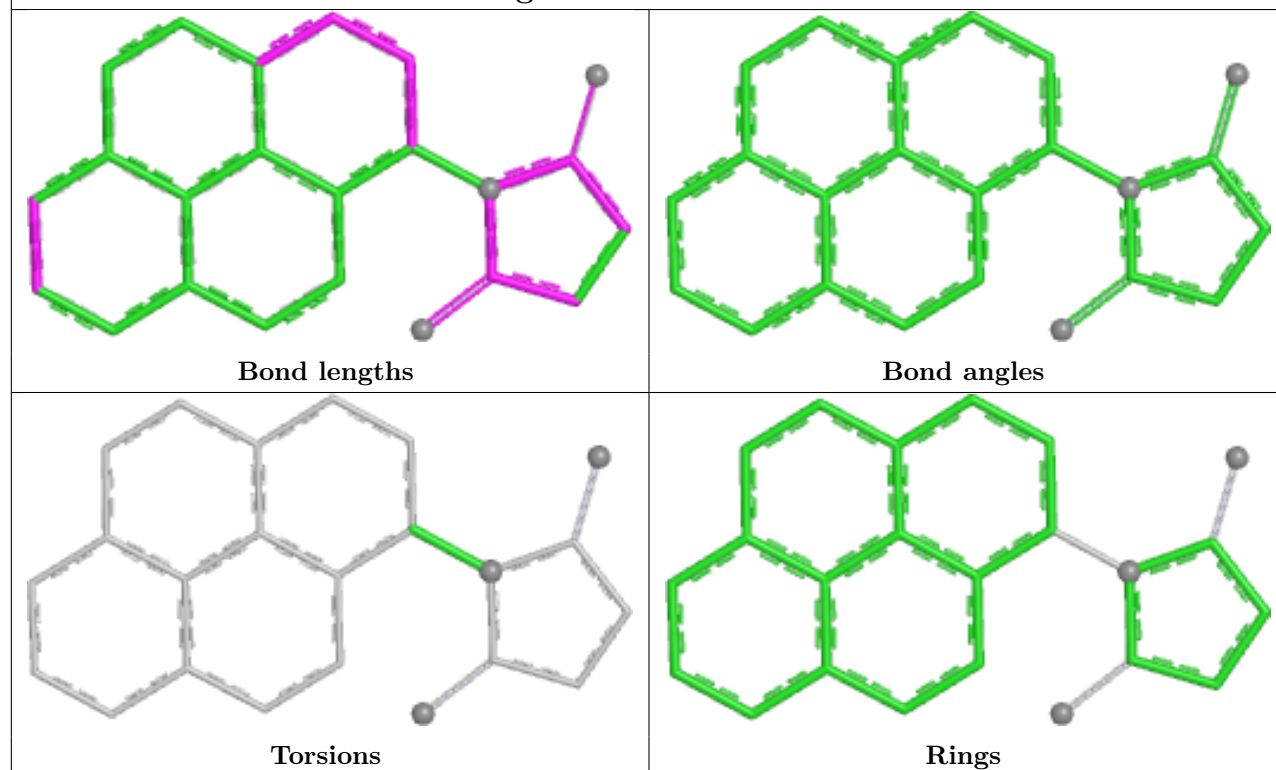
Ligand A1L9F BB 202



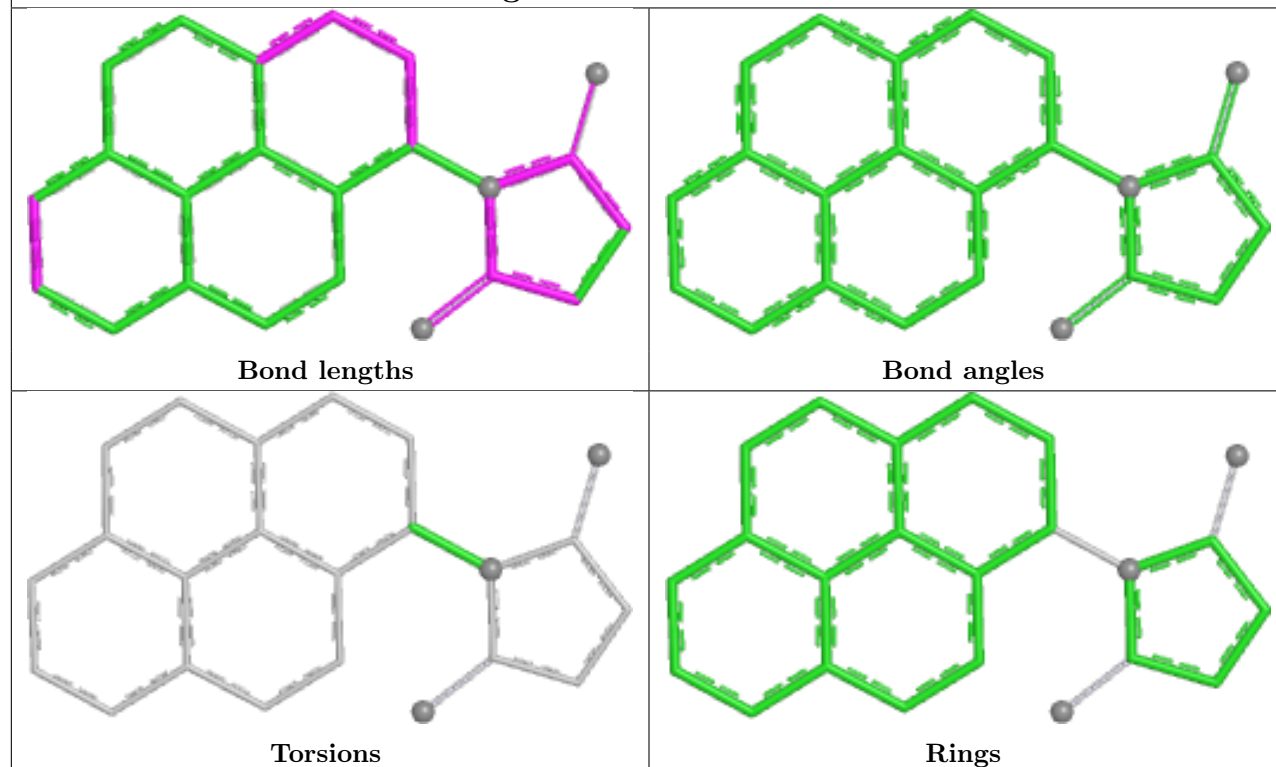
Ligand A1L9F VA 202



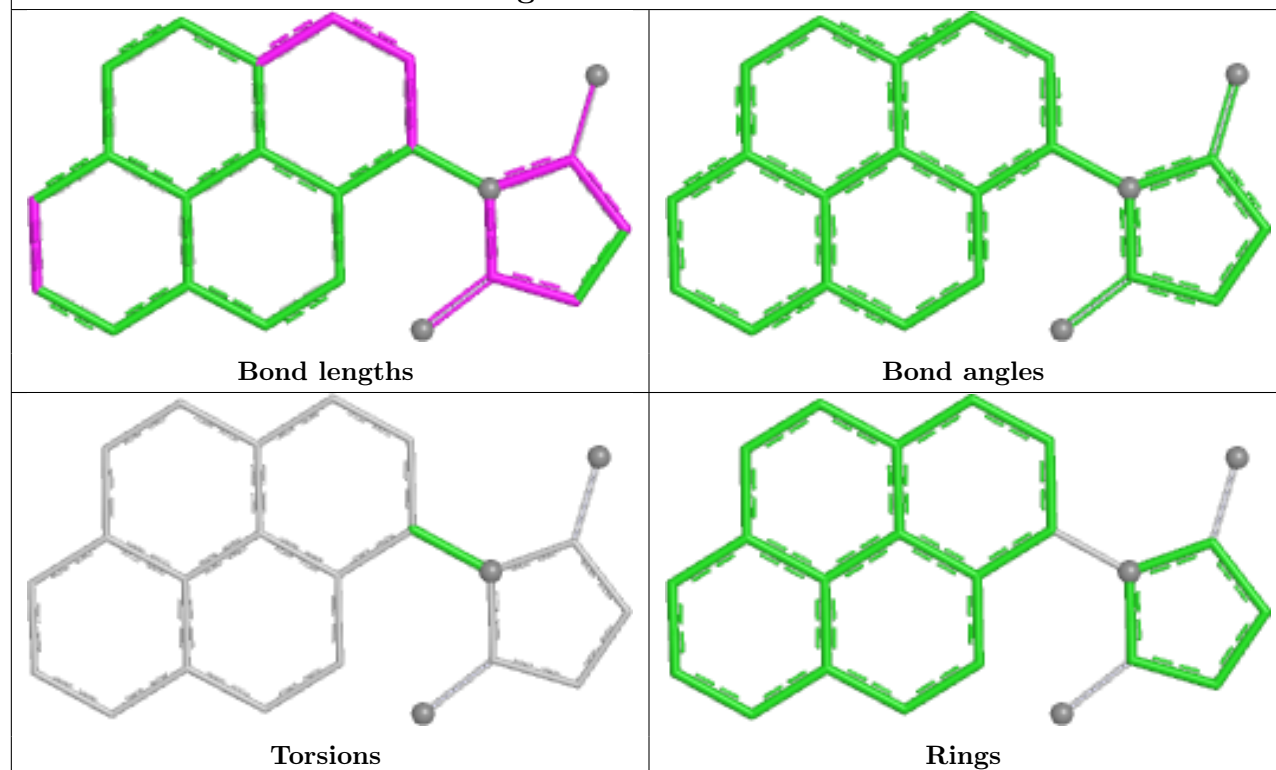
Ligand A1L9F C 202



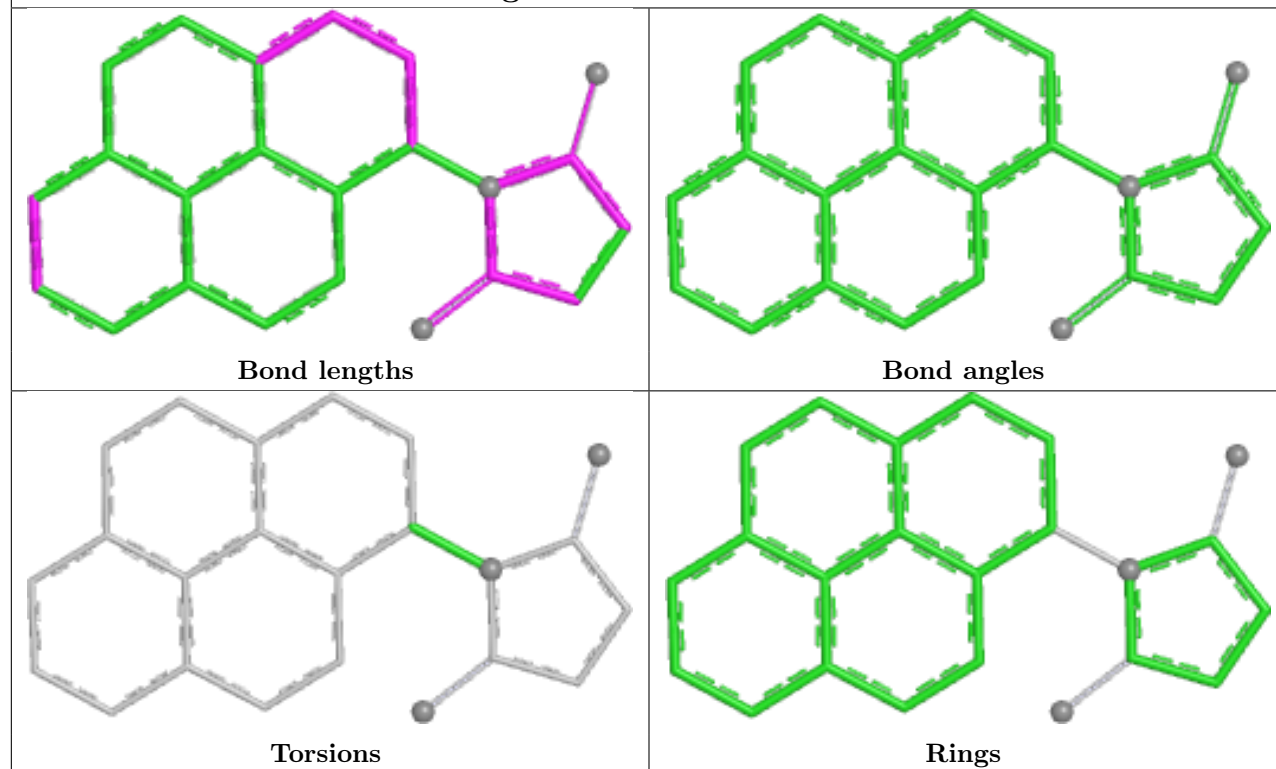
Ligand A1L9F AB 202



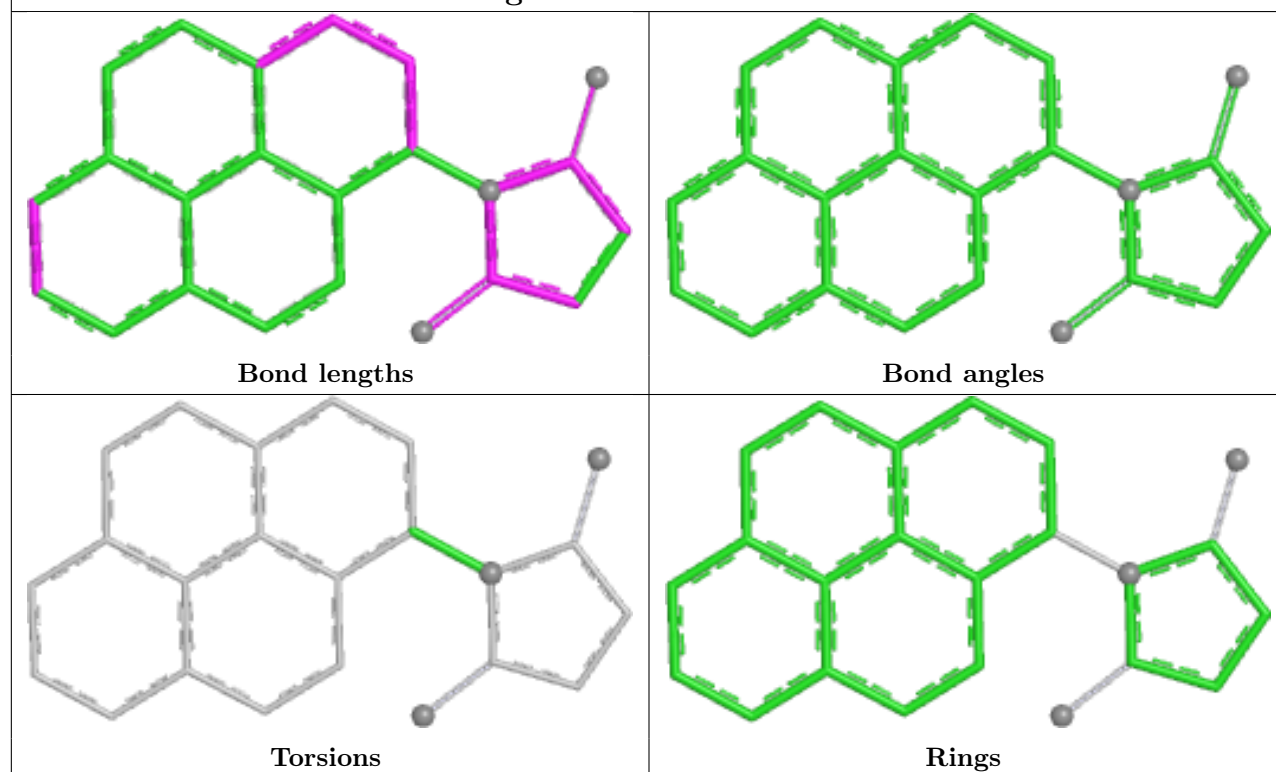
Ligand A1L9F E 202



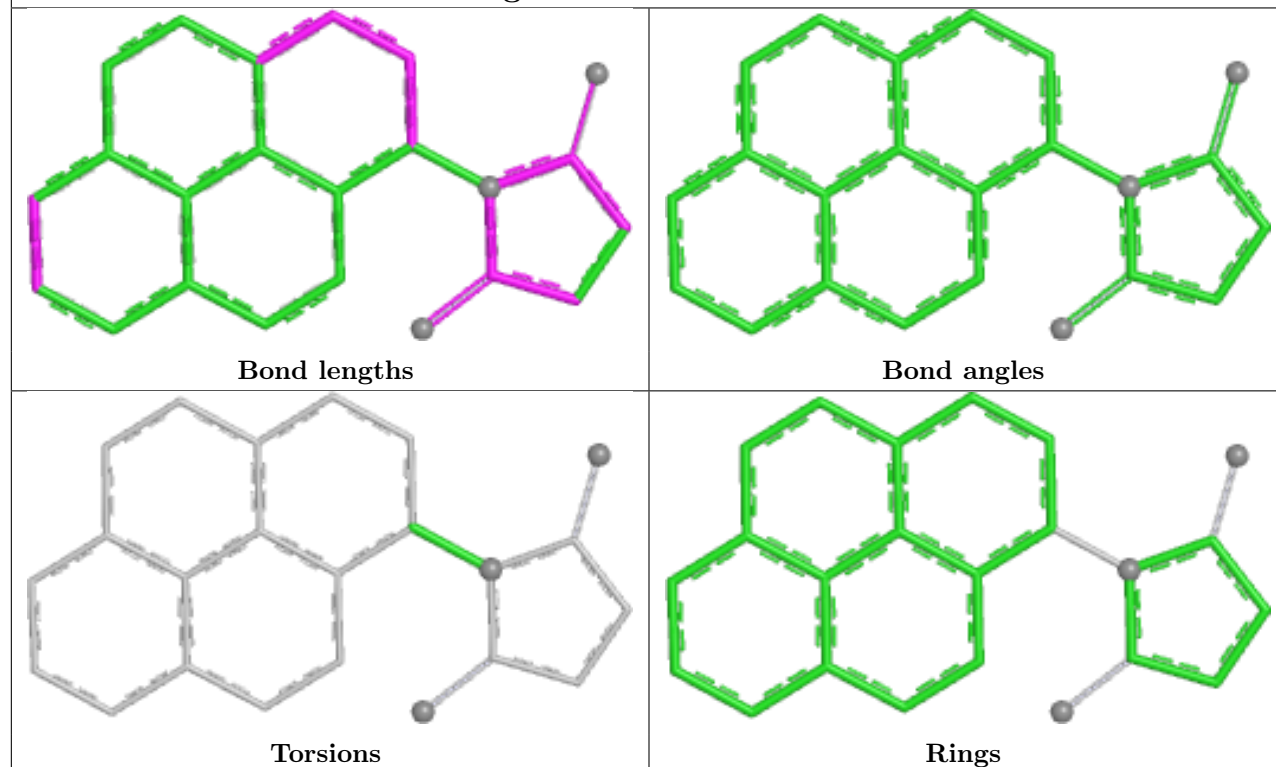
Ligand A1L9F RA 201



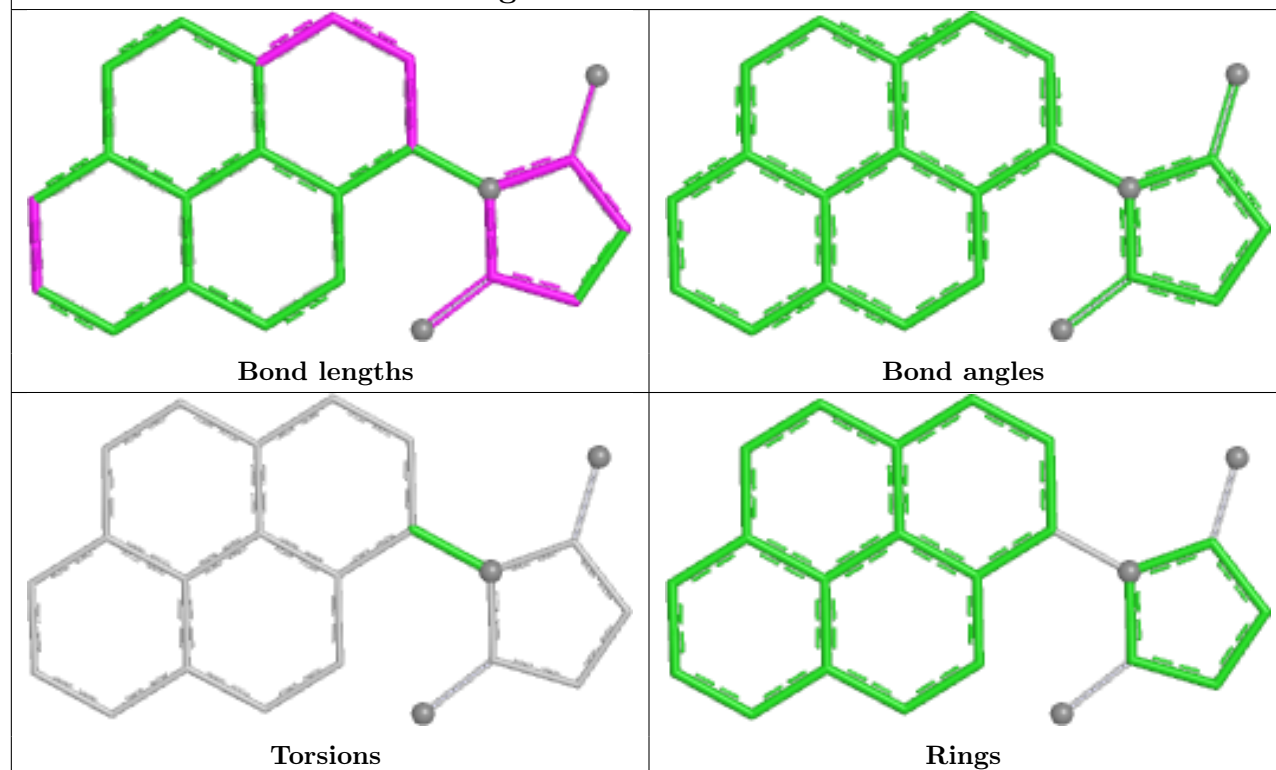
Ligand A1L9F SA 202



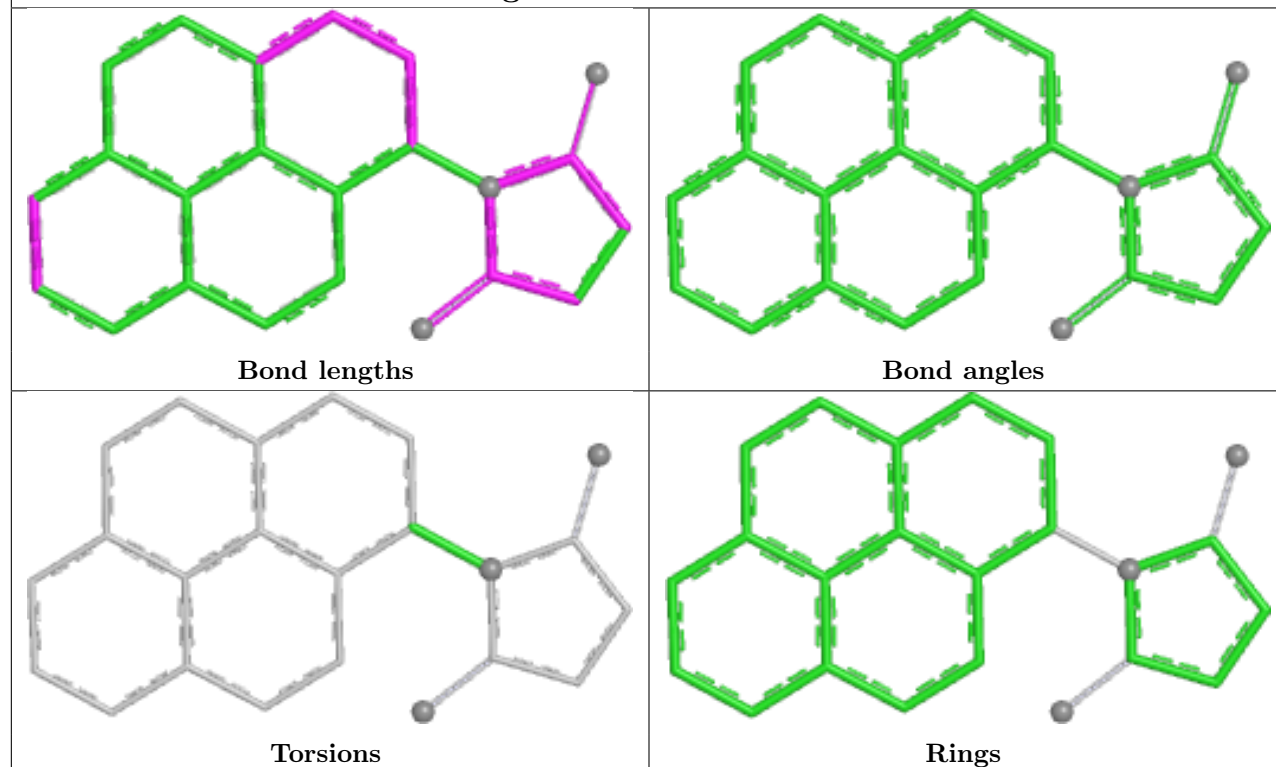
Ligand A1L9F YA 202



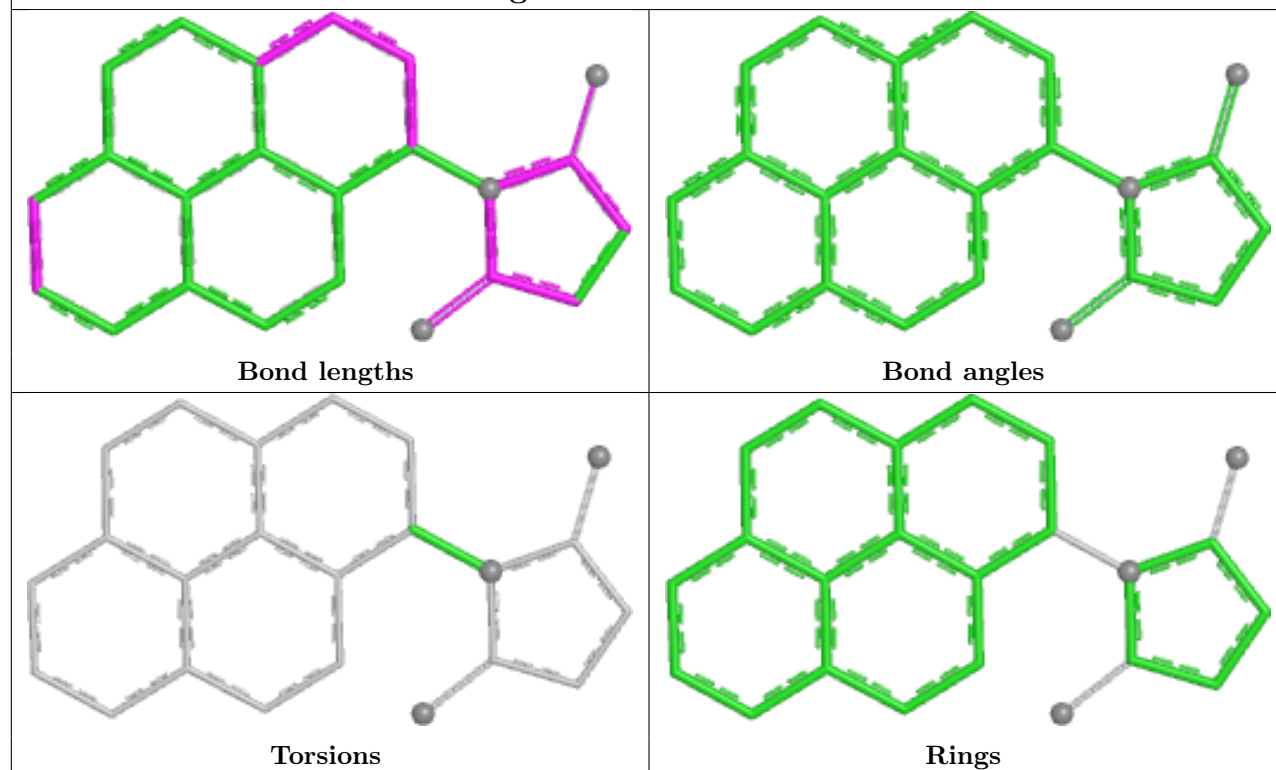
Ligand A1L9F WA 202



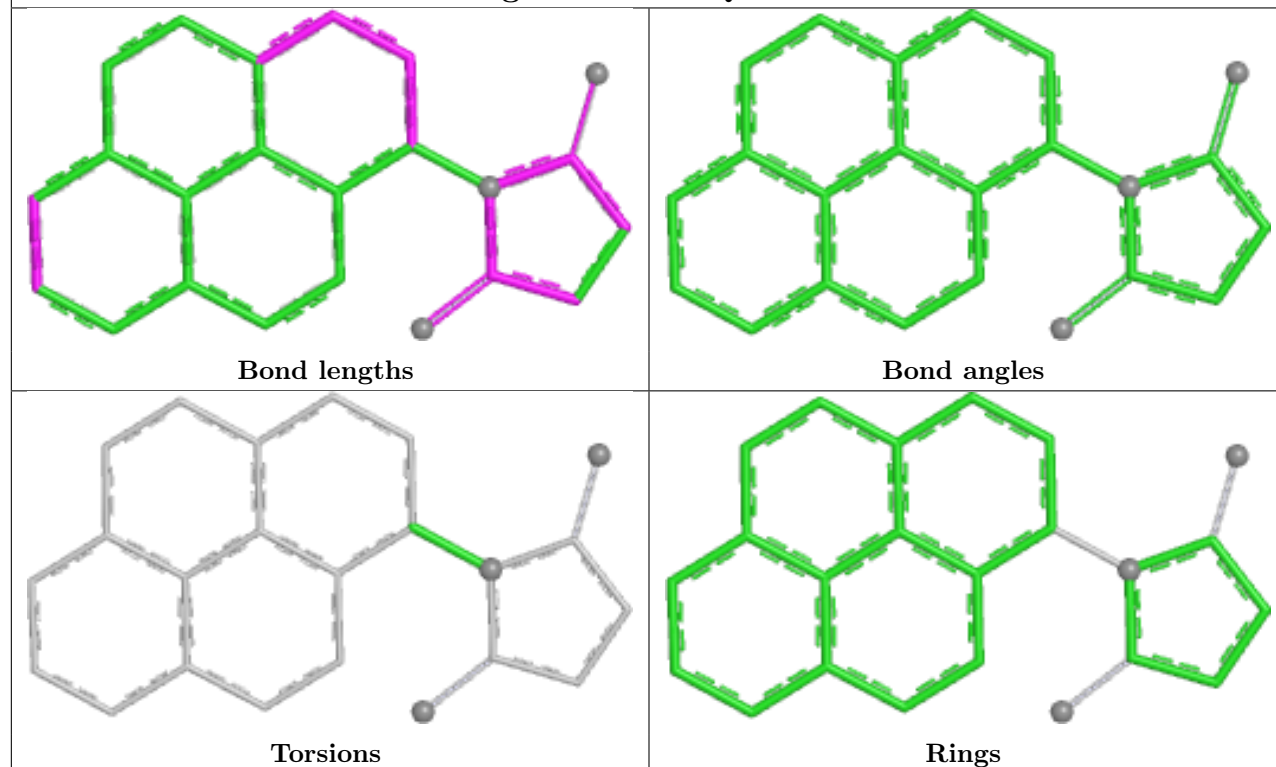
Ligand A1L9F DB 201



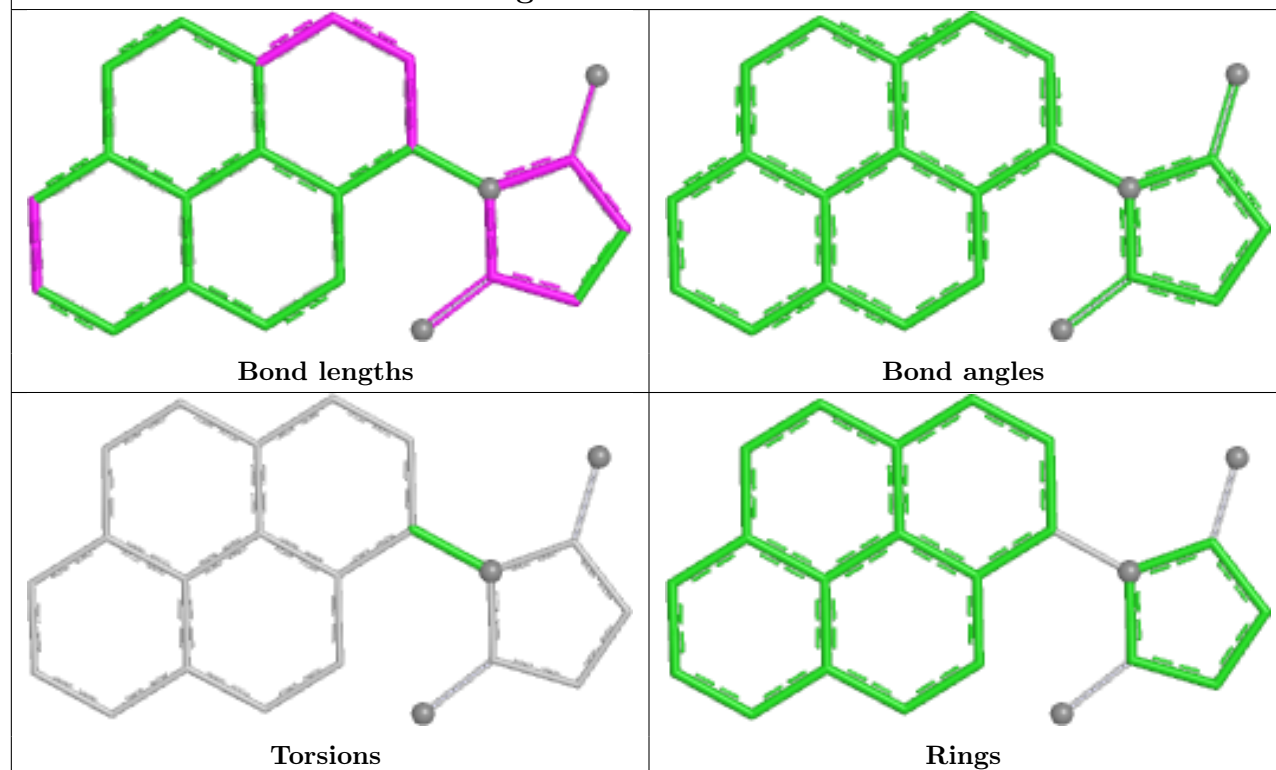
Ligand A1L9F IB 202



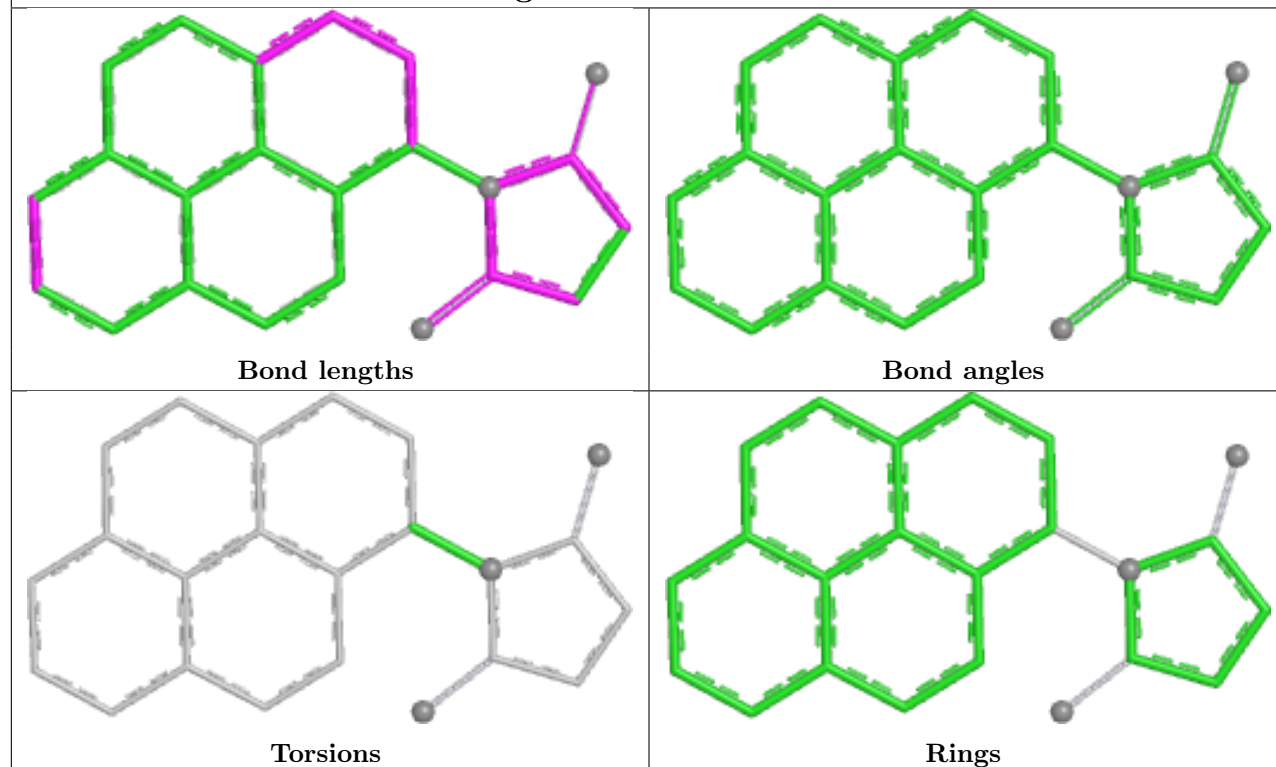
Ligand A1L9F QA 202



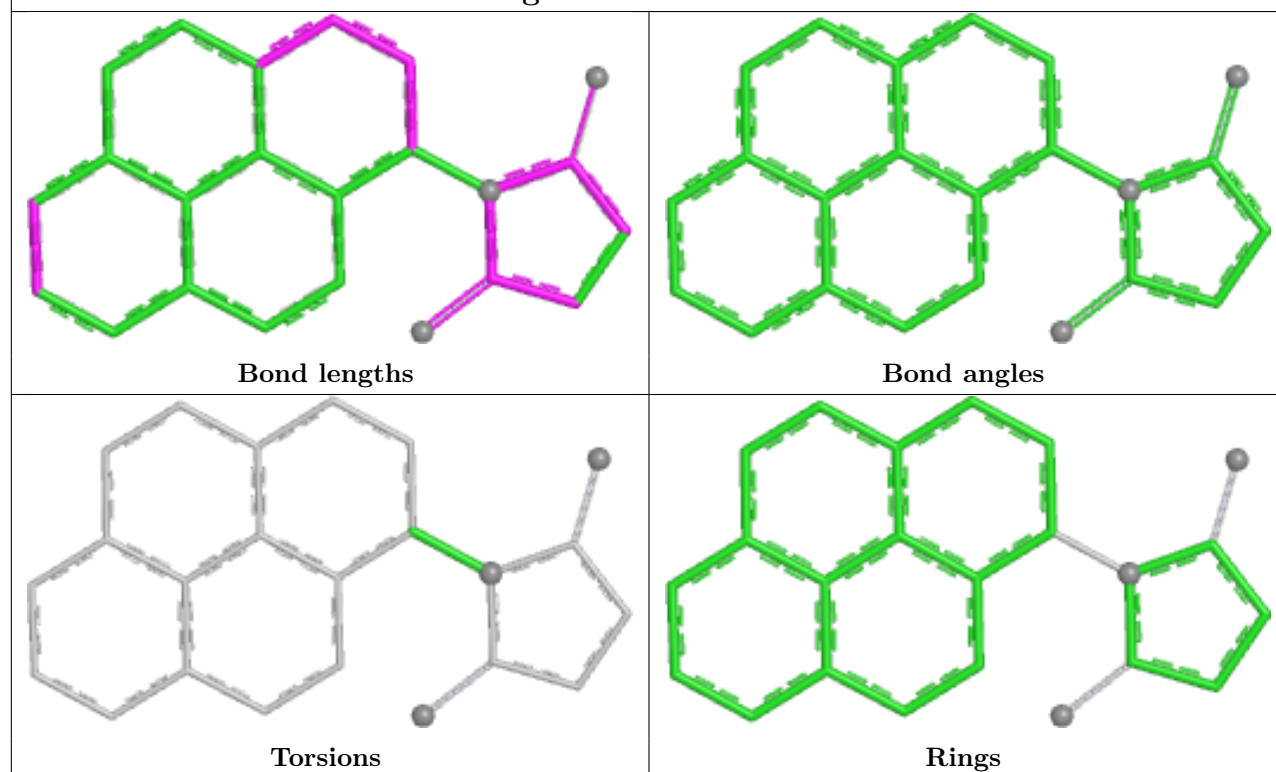
Ligand A1L9F T 202



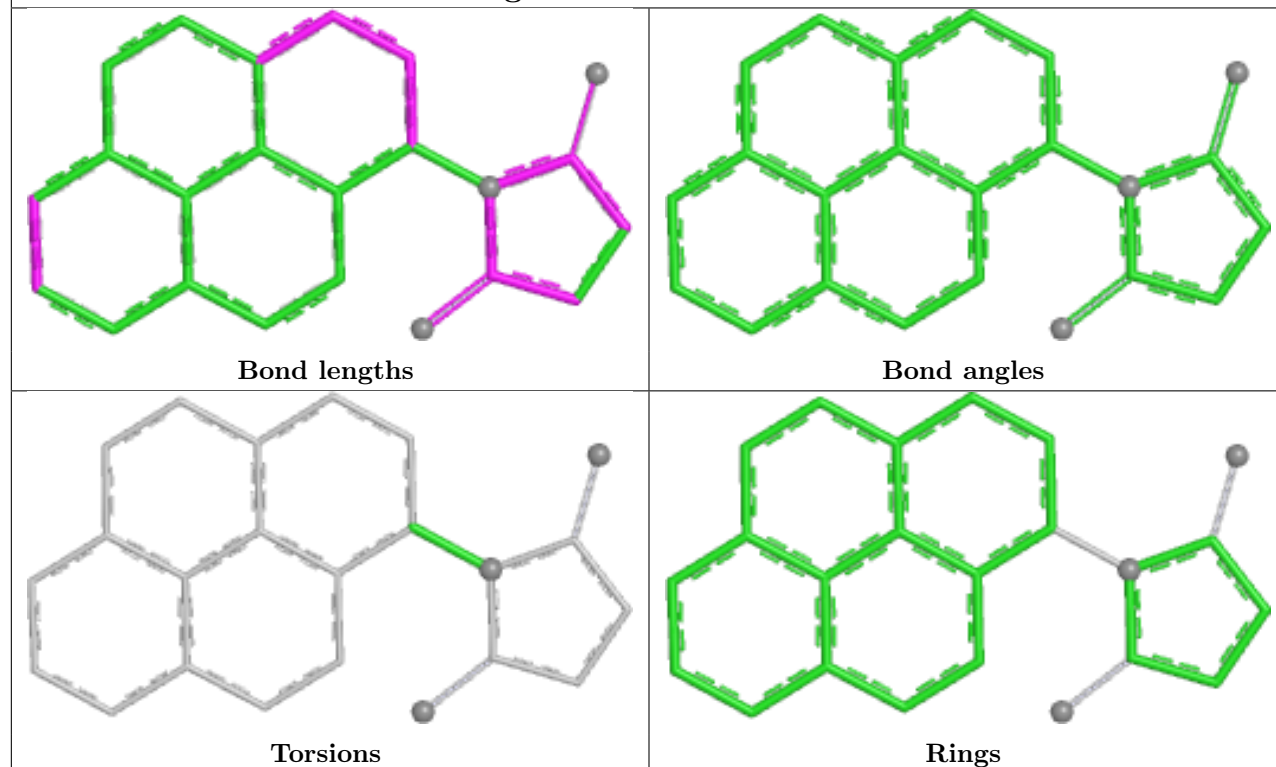
Ligand A1L9F Y 201



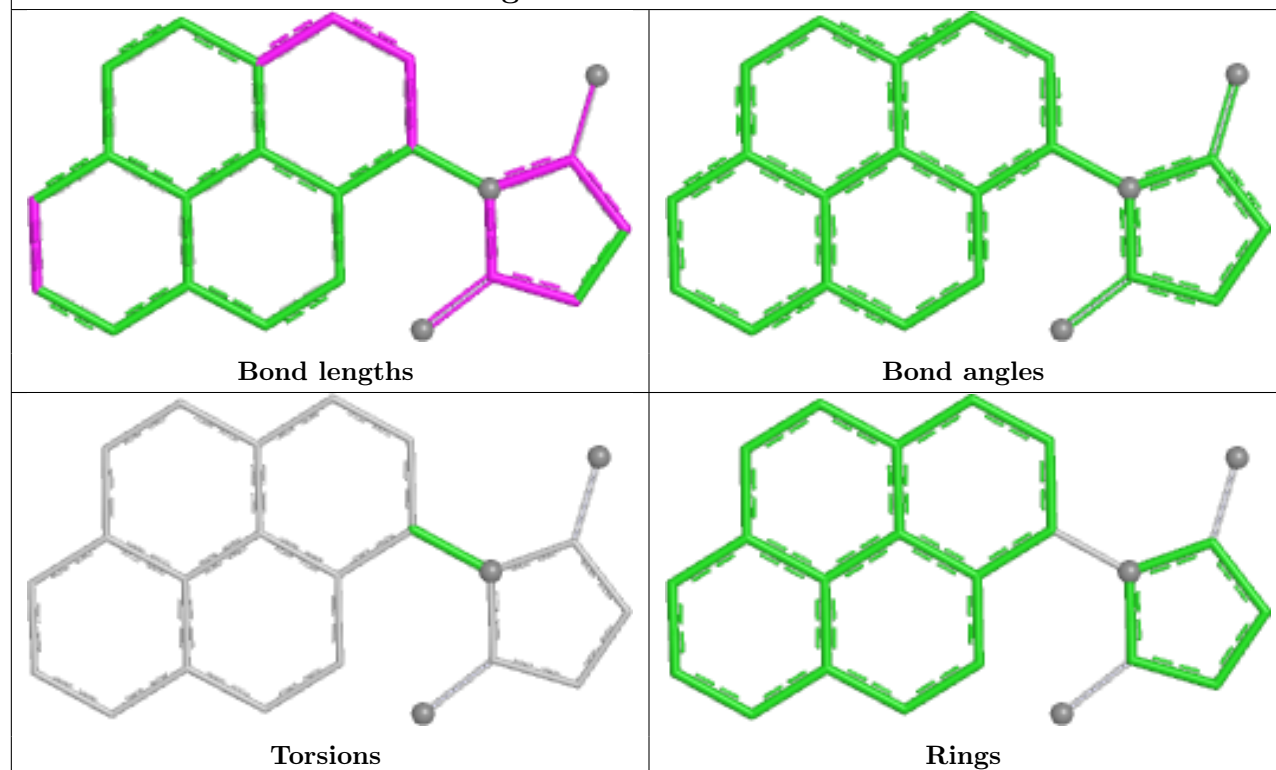
Ligand A1L9F I 202



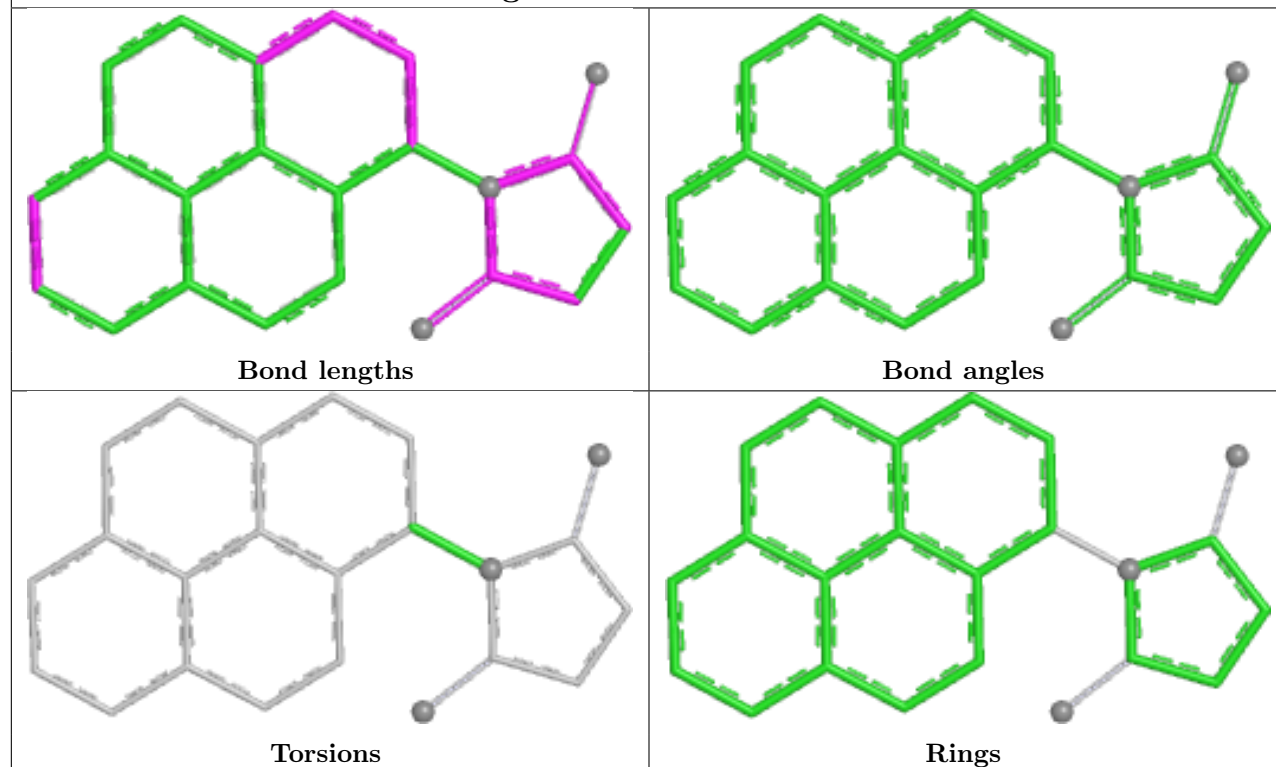
Ligand A1L9F ZA 201



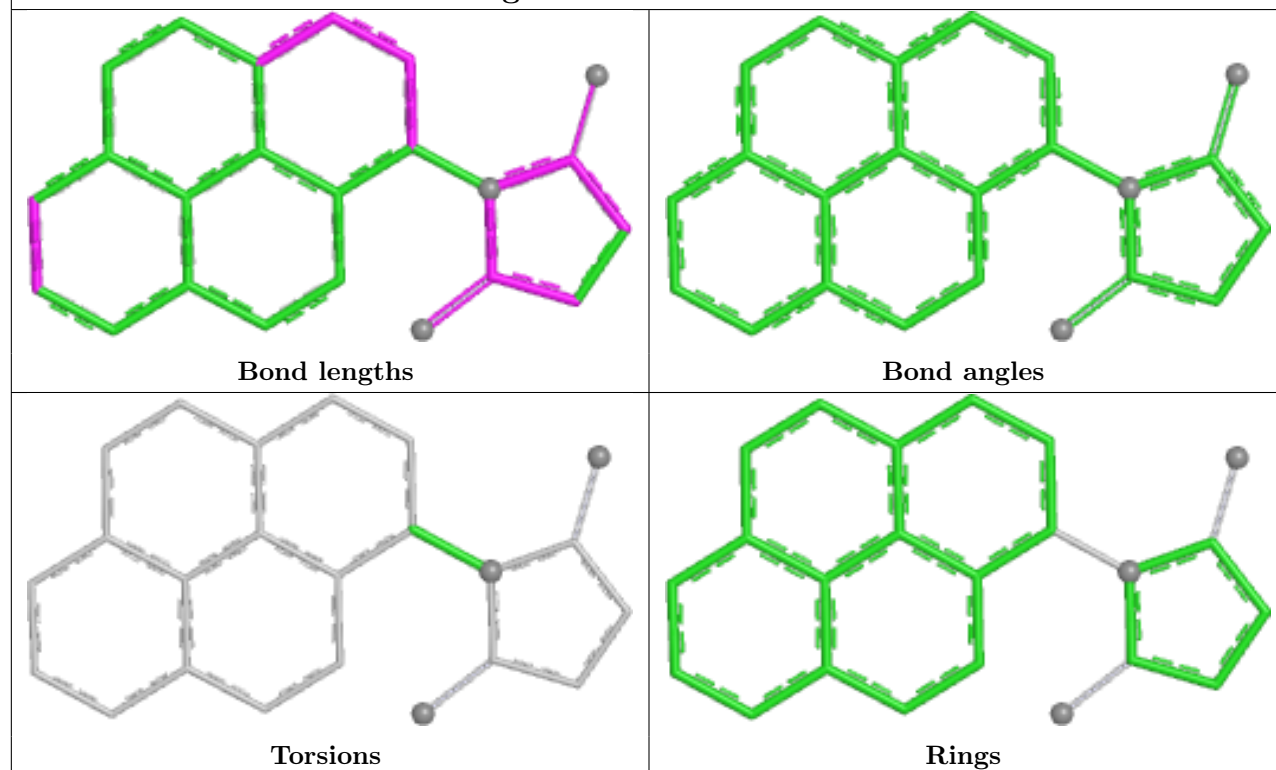
Ligand A1L9F UA 202



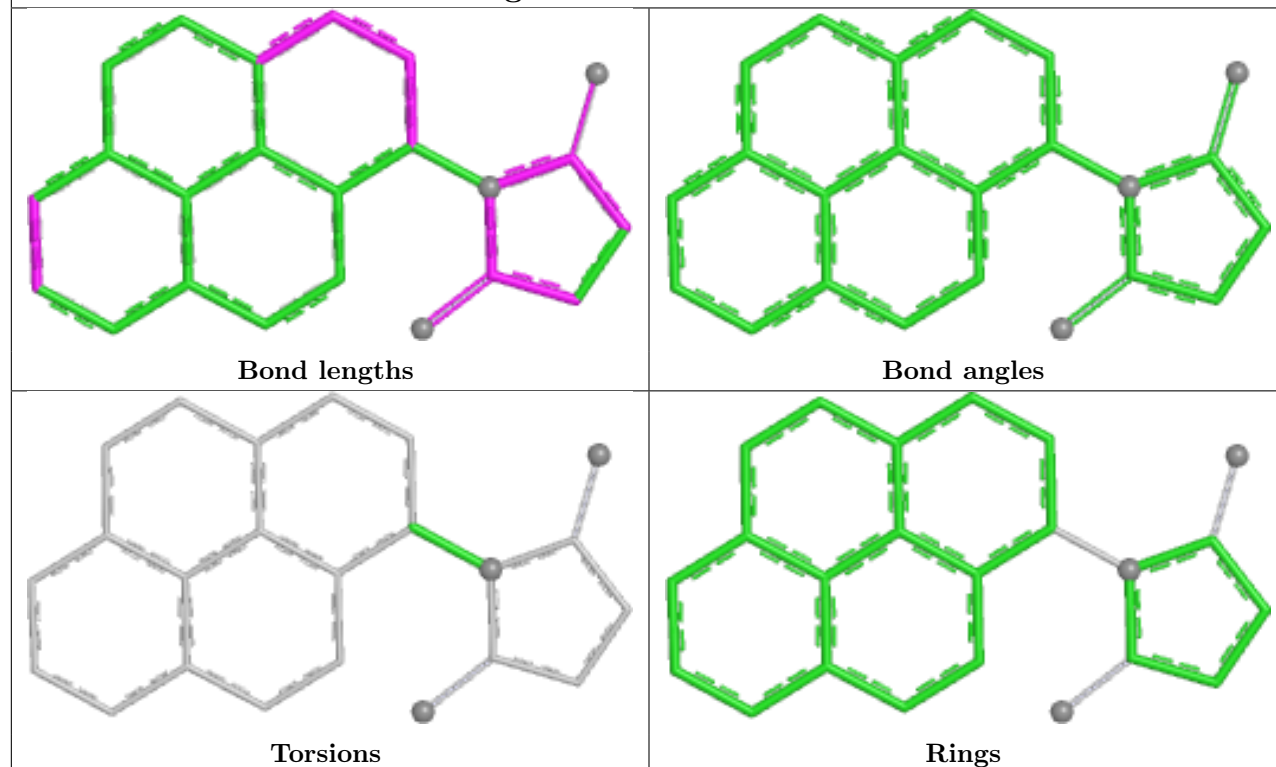
Ligand A1L9F CA 202



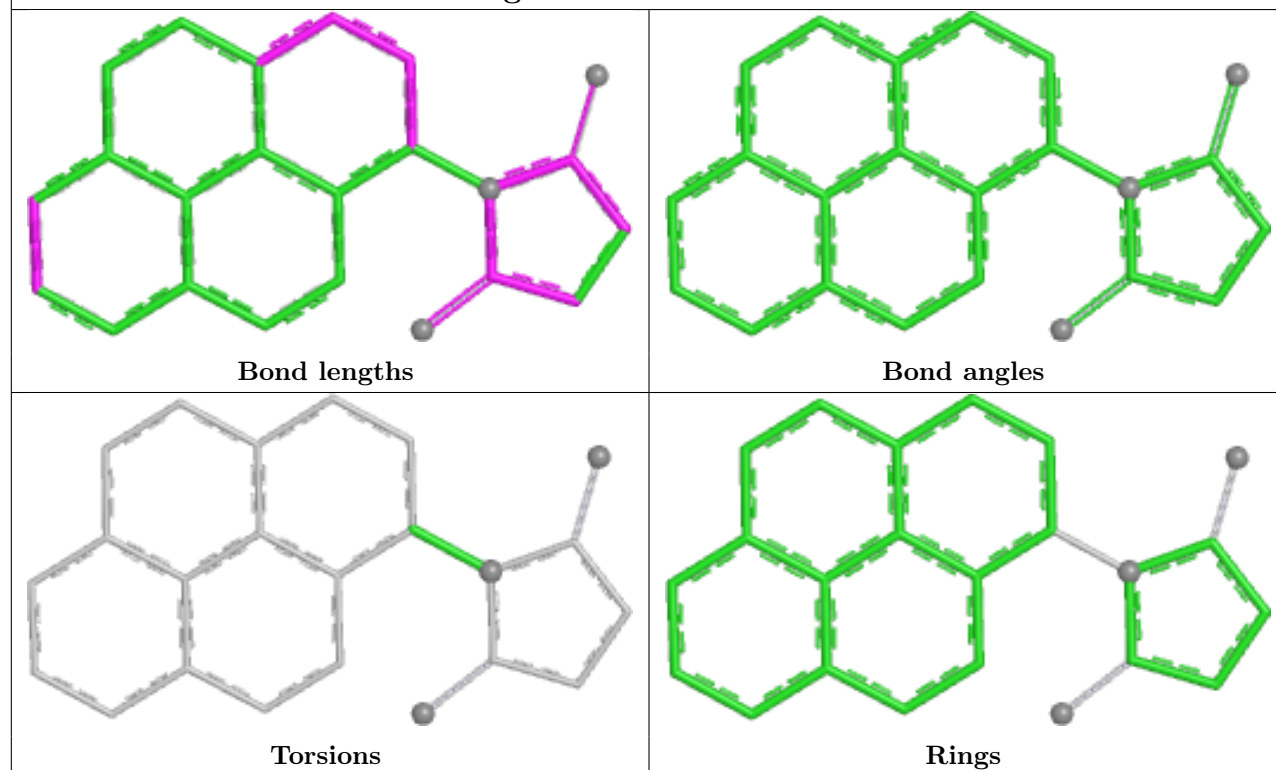
Ligand A1L9F OA 202



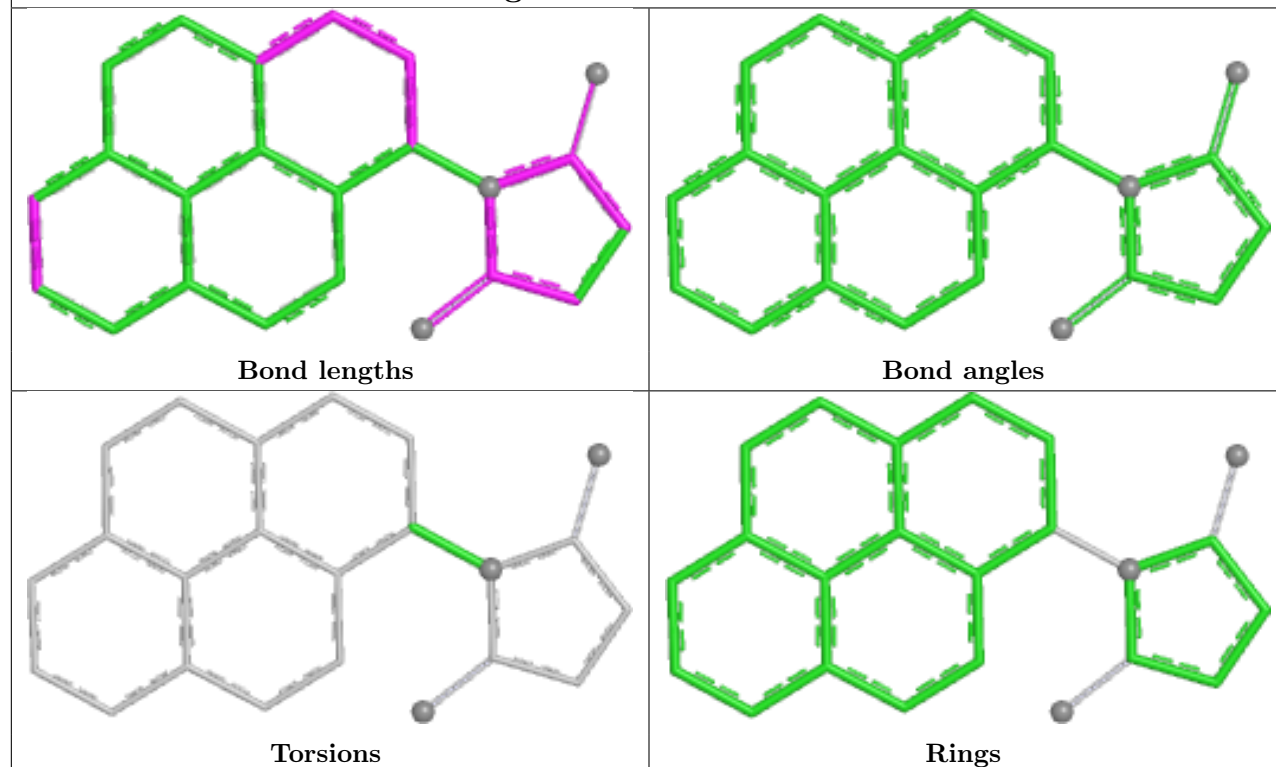
Ligand A1L9F PA 202



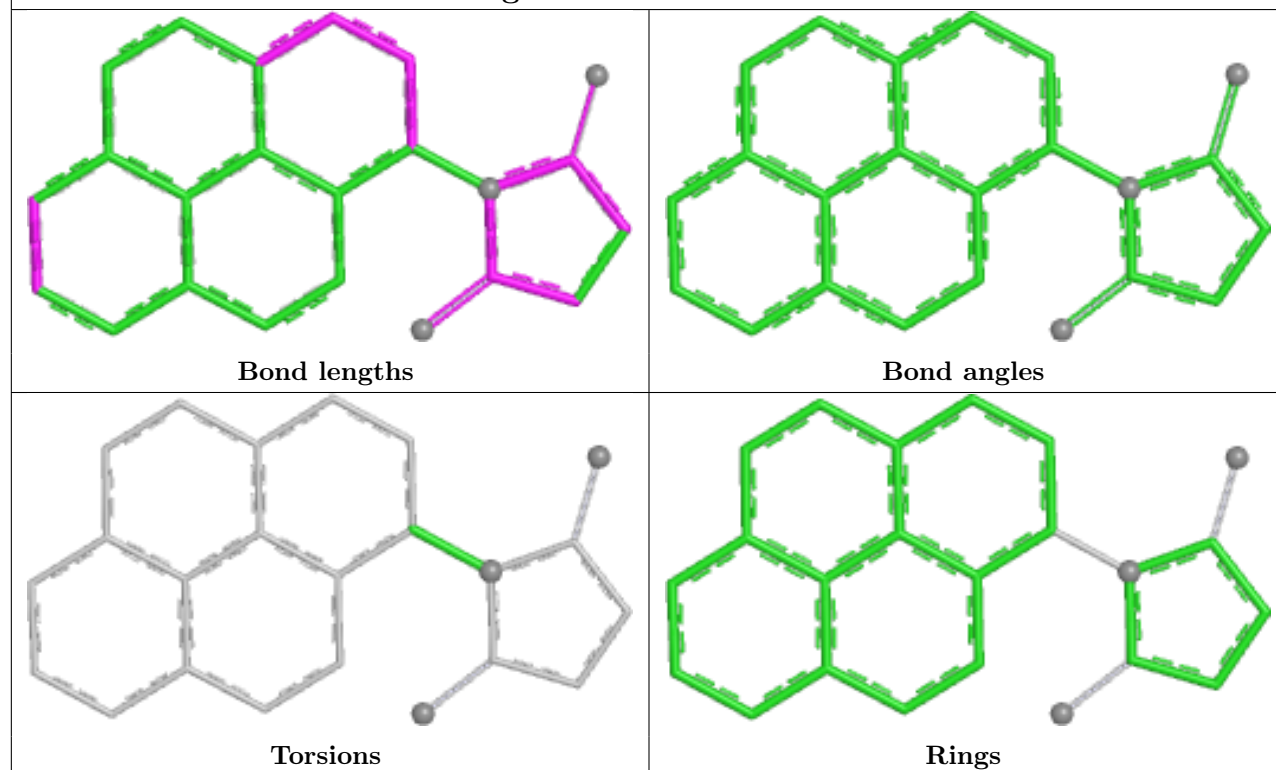
Ligand A1L9F EA 202



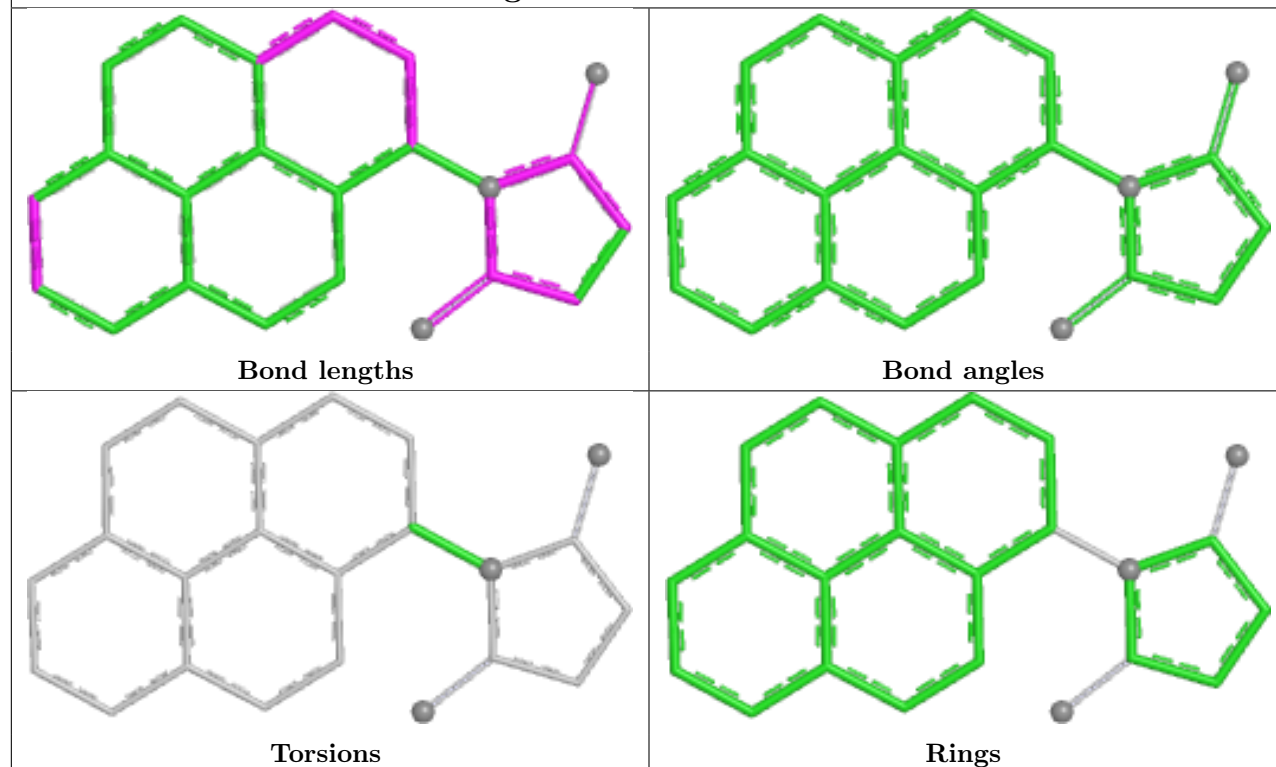
Ligand A1L9F LA 201



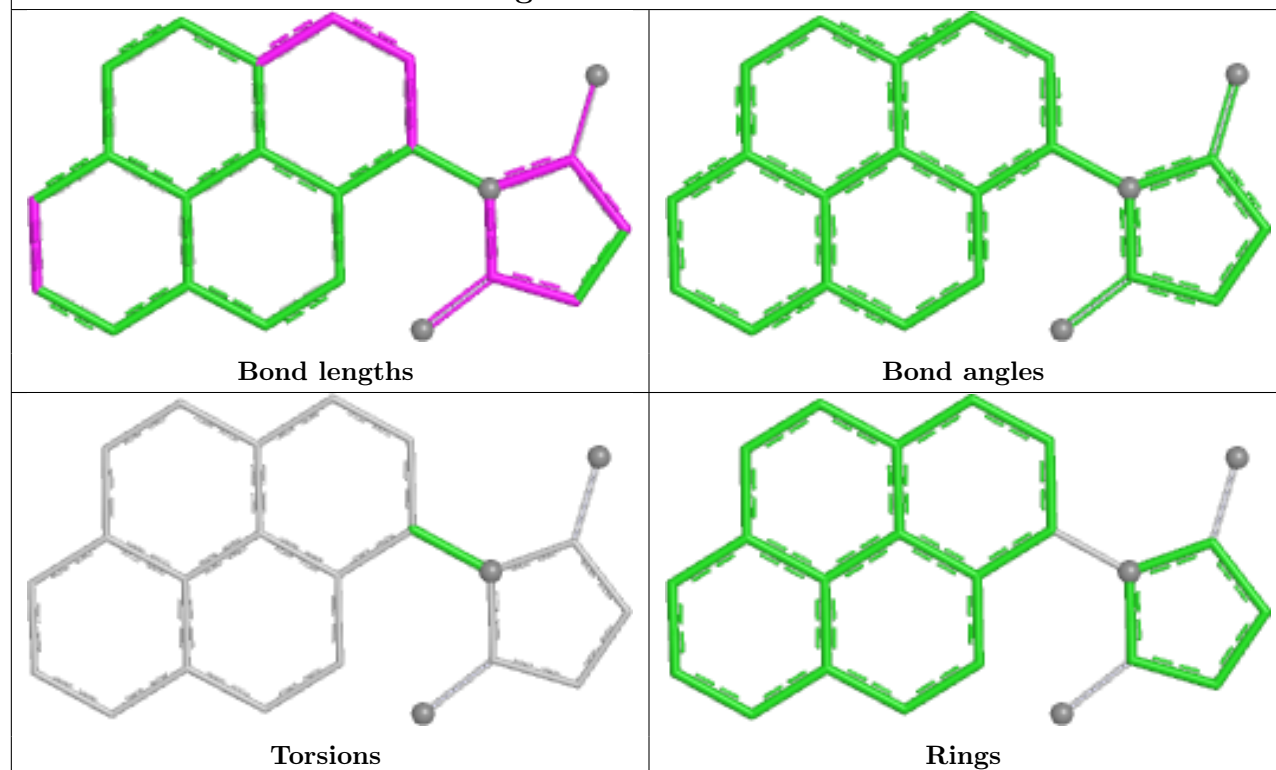
Ligand A1L9F AA 202



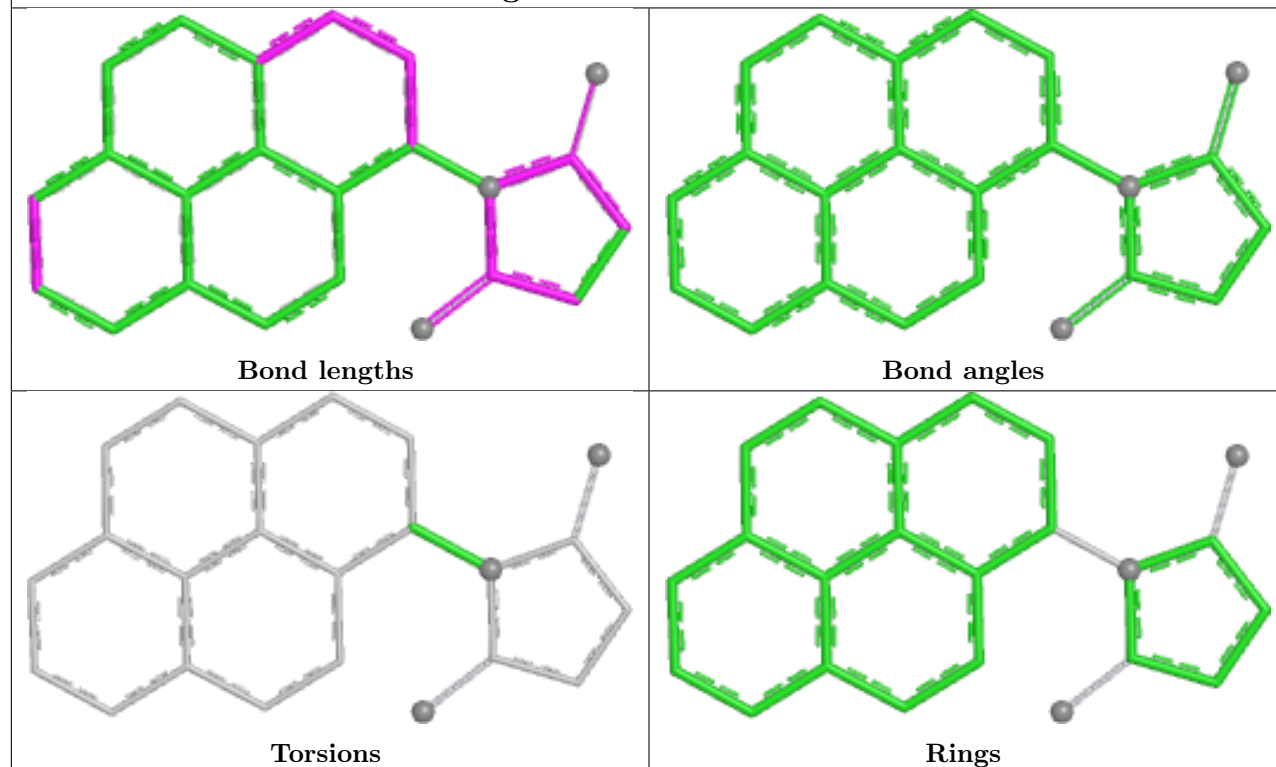
Ligand A1L9F VA 201



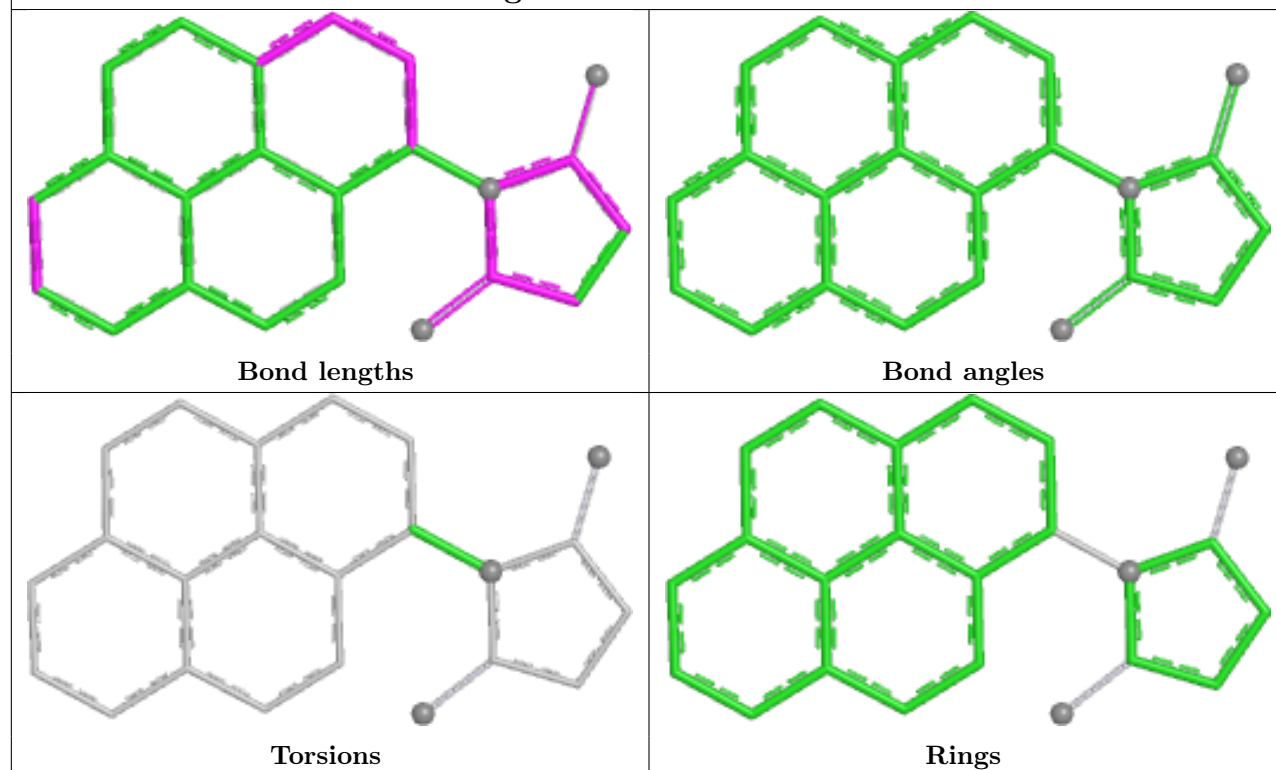
Ligand A1L9F A 202



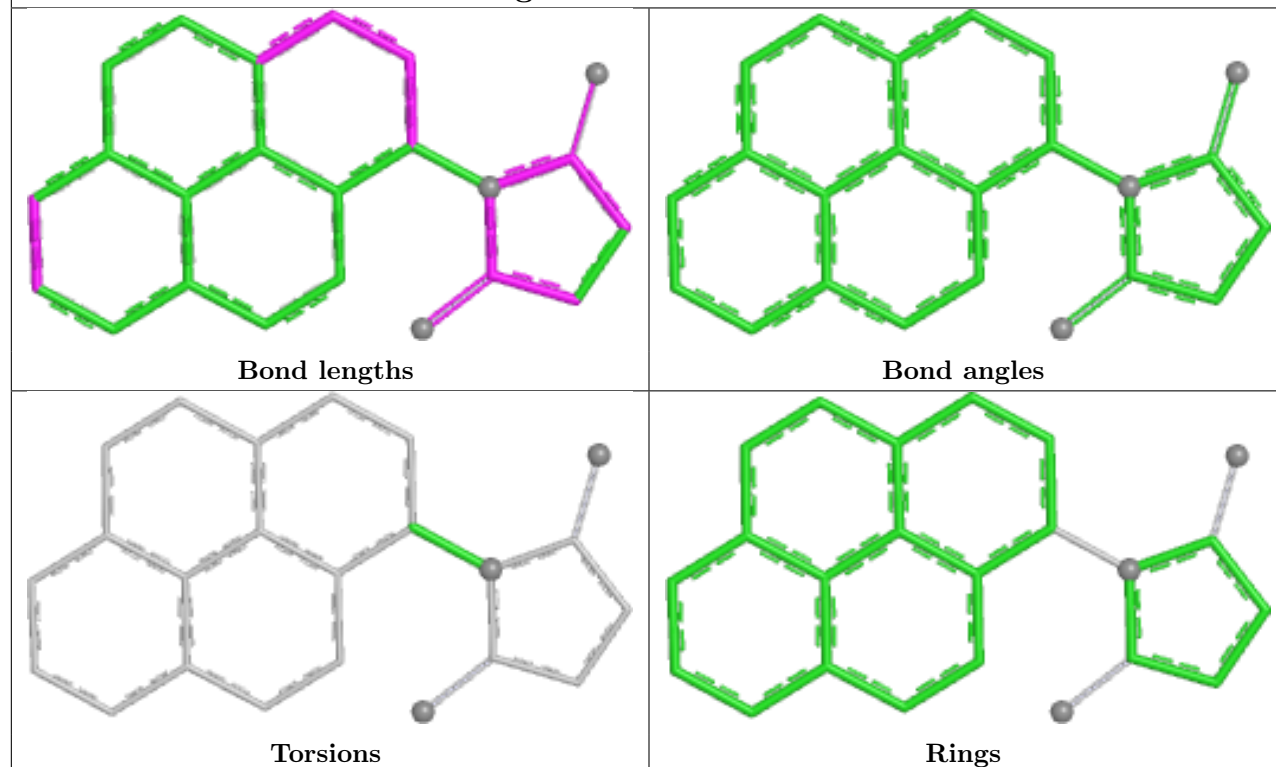
Ligand A1L9F CA 201



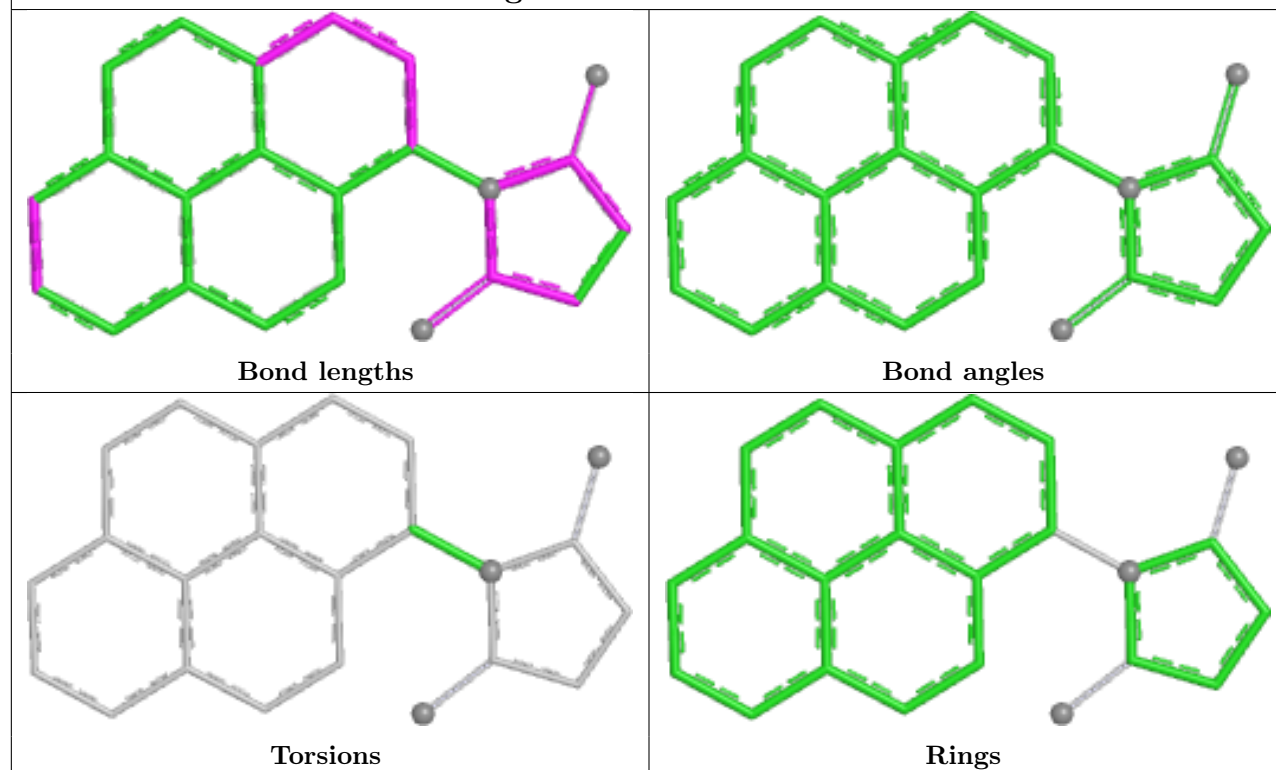
Ligand A1L9F EB 201



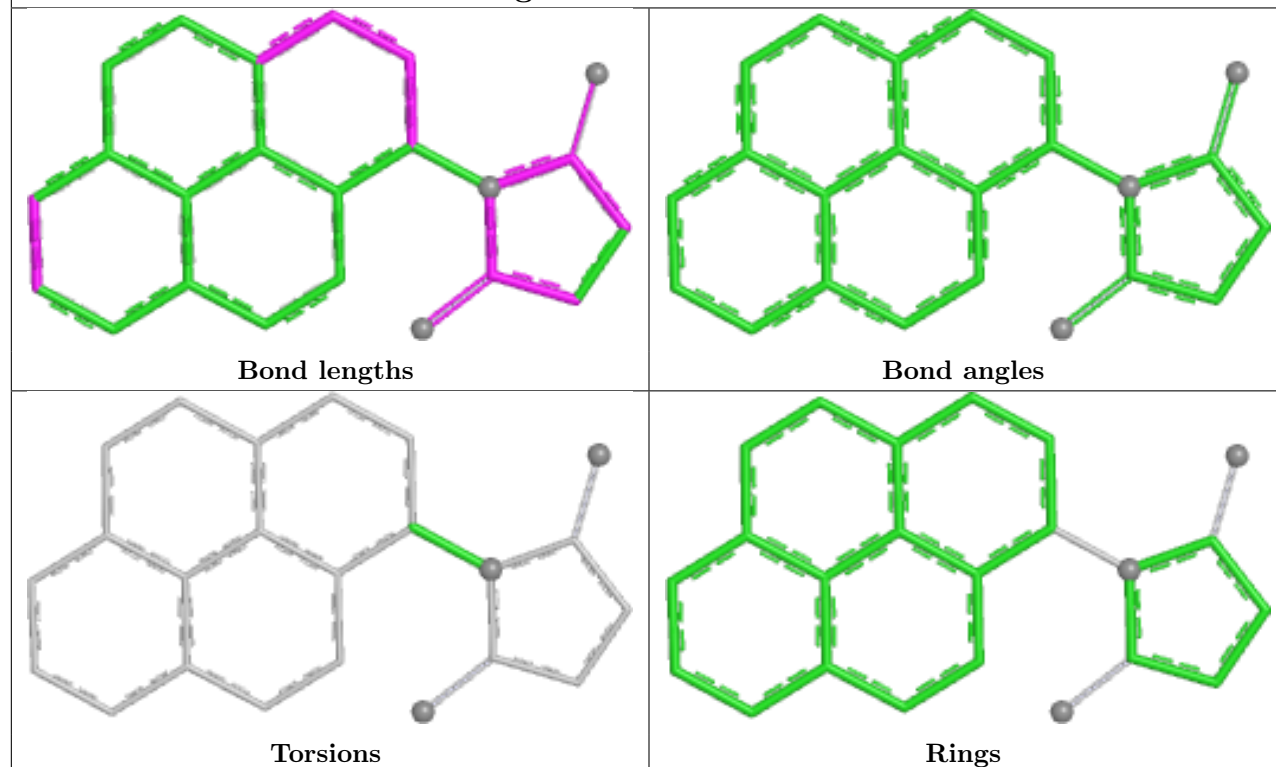
Ligand A1L9F X 202



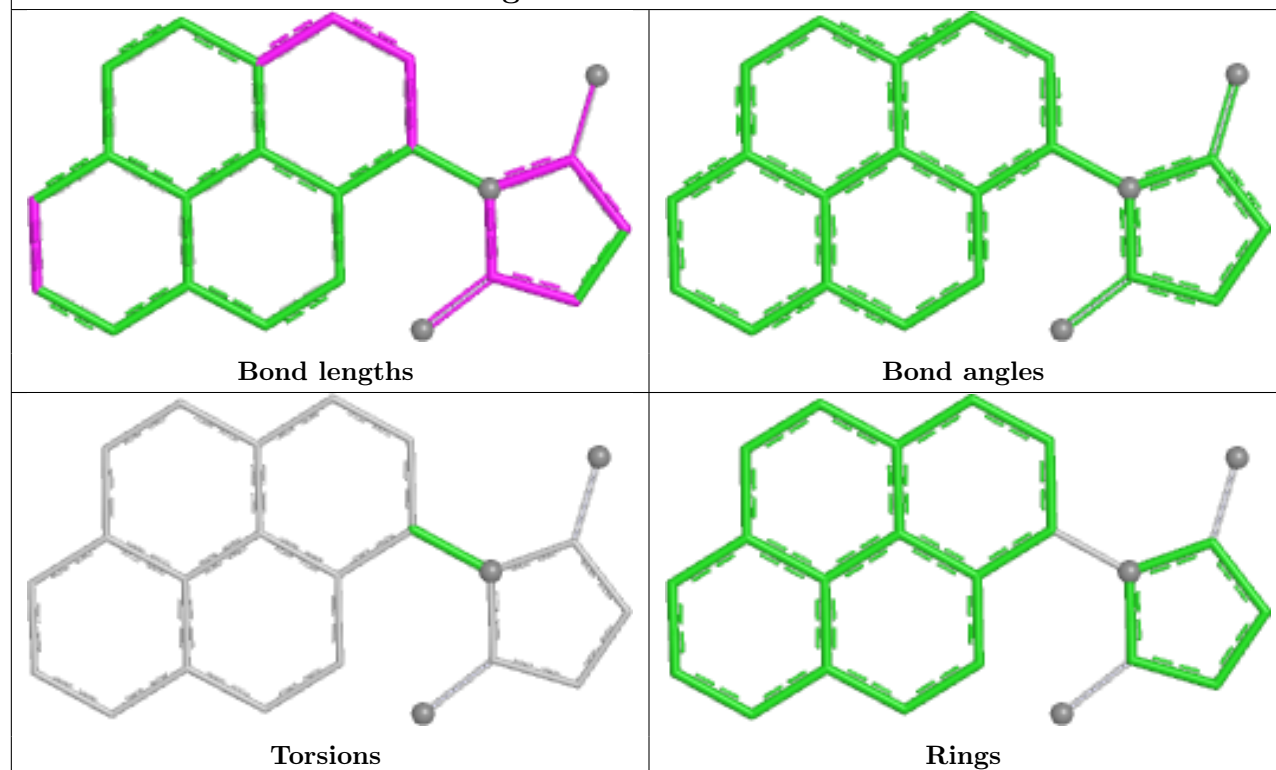
Ligand A1L9F FB 202



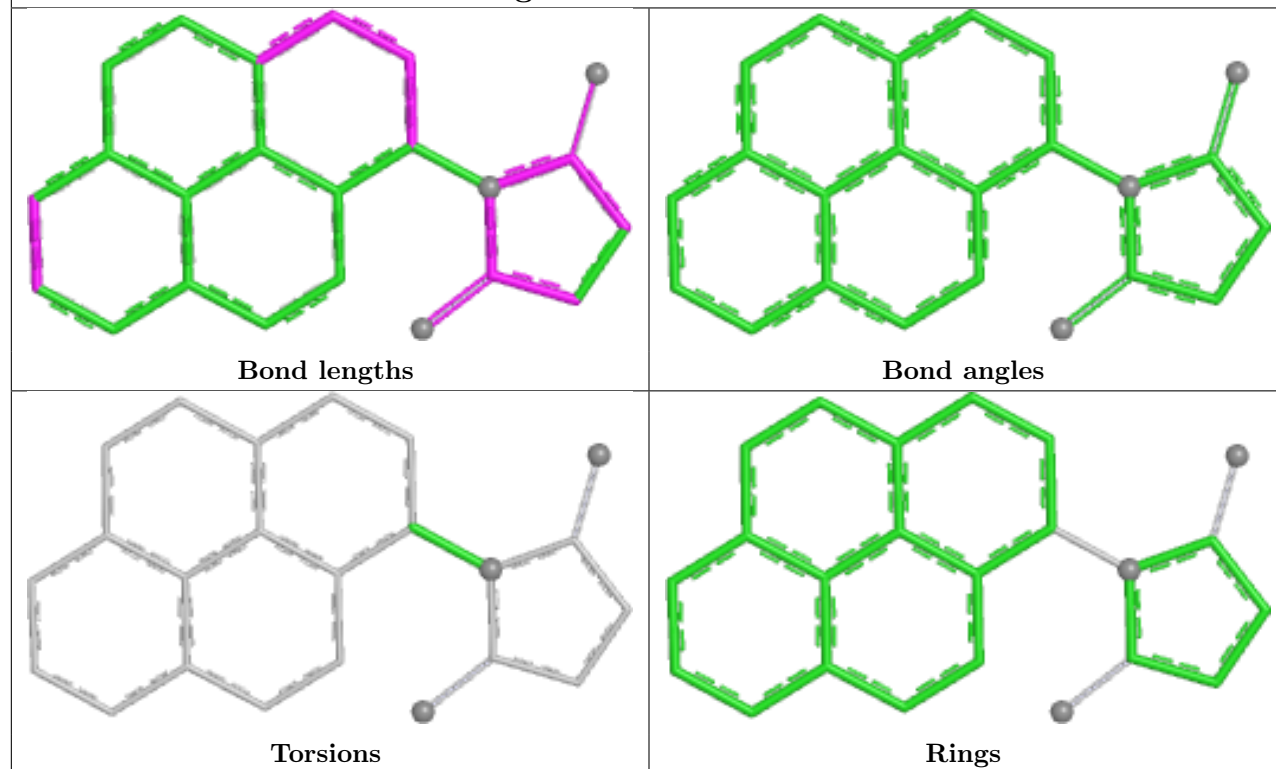
Ligand A1L9F N 201



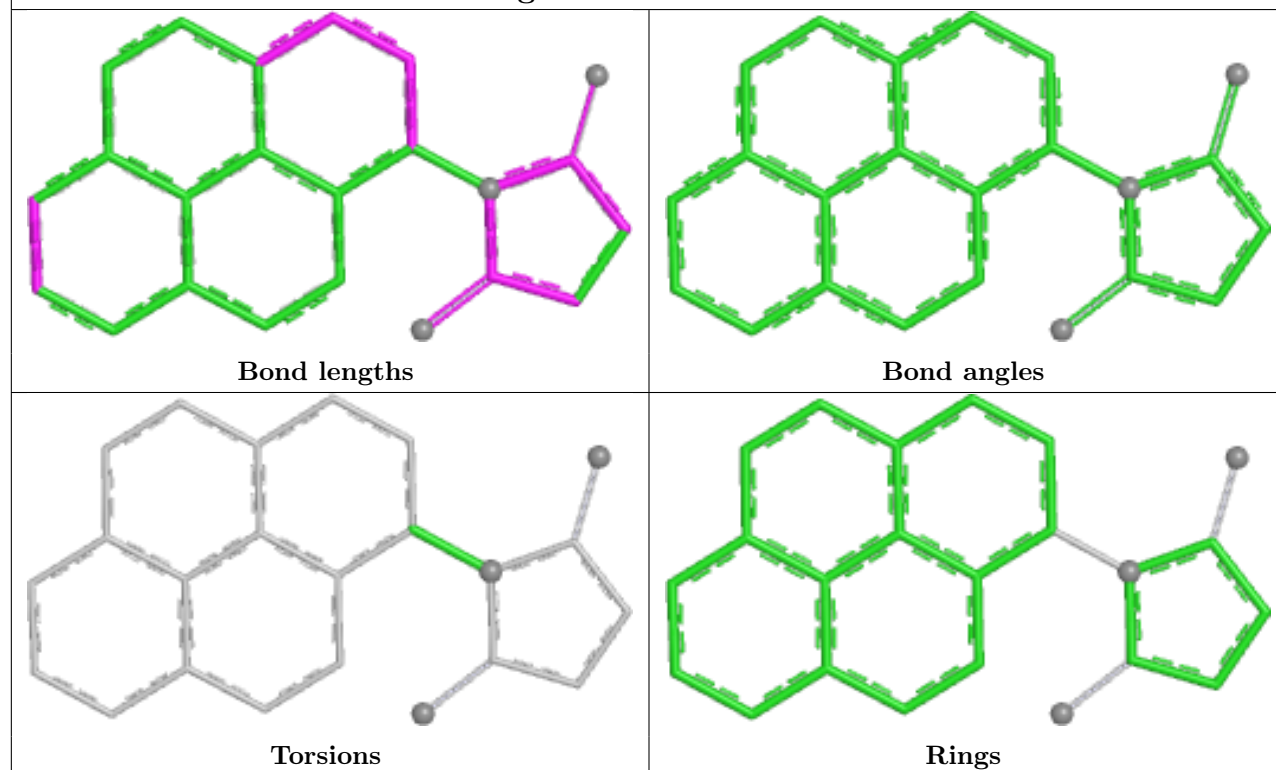
Ligand A1L9F HB 202



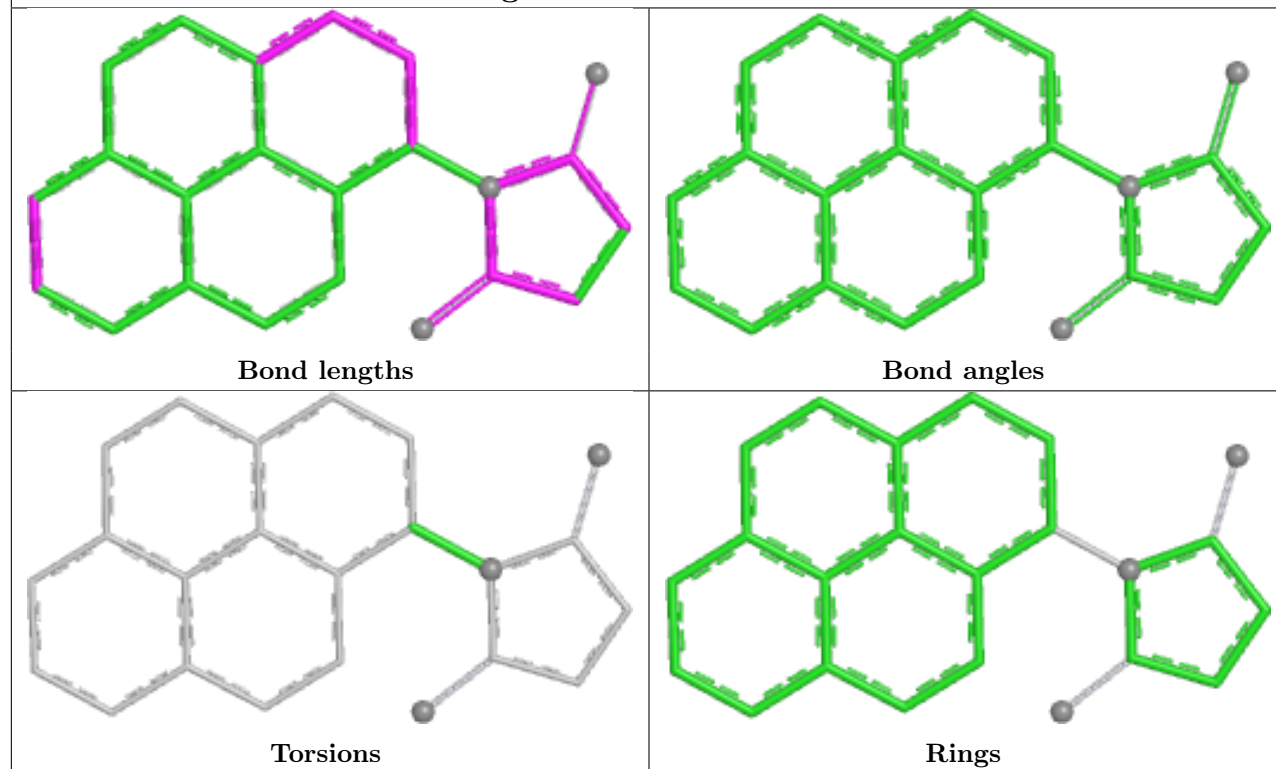
Ligand A1L9F G 202



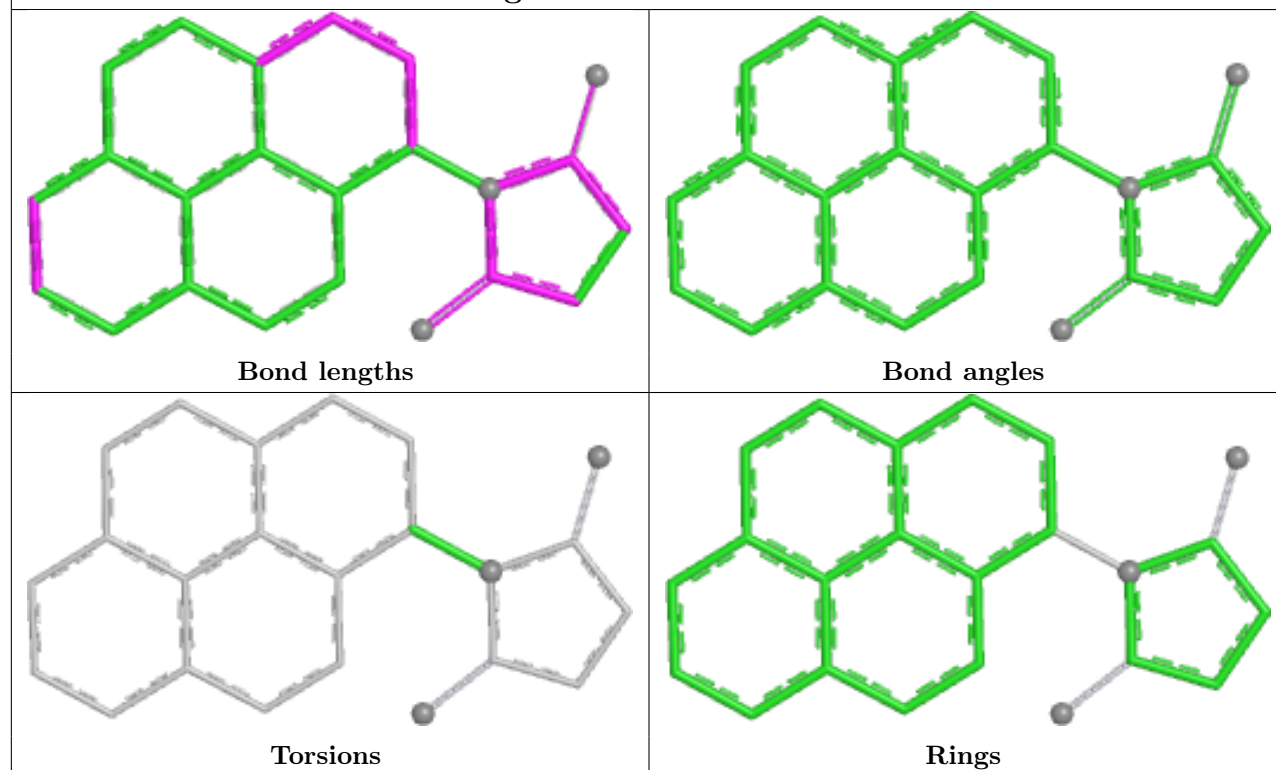
Ligand A1L9F F 202



Ligand A1L9F NA 202



Ligand A1L9F ZA 202



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.

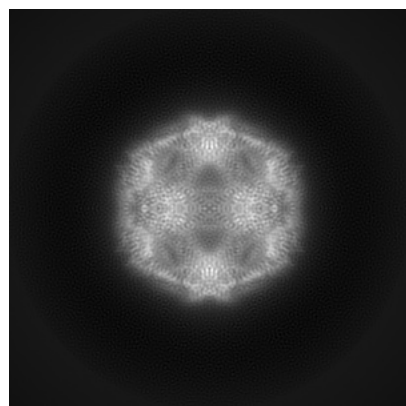
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64381. These allow visual inspection of the internal detail of the map and identification of artifacts.

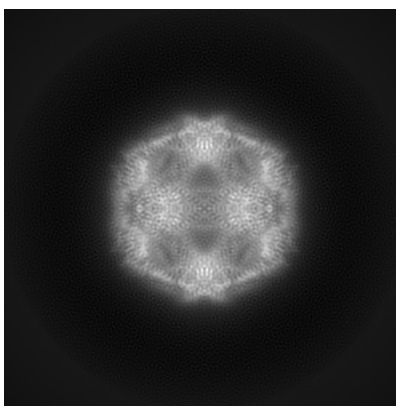
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

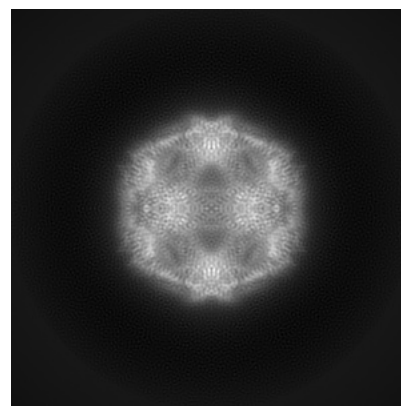
6.1.1 Primary map



X

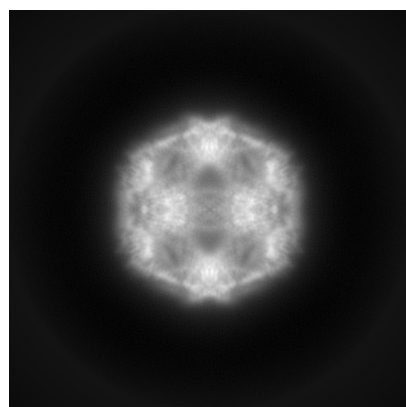


Y

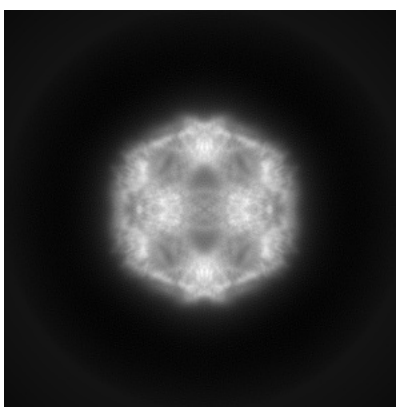


Z

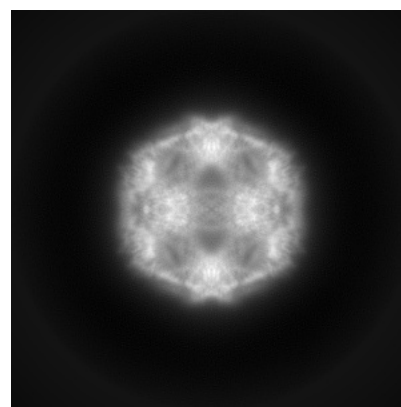
6.1.2 Raw map



X



Y

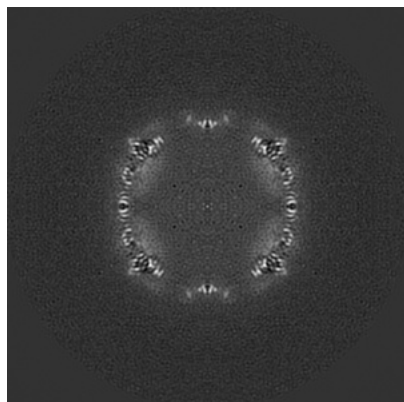


Z

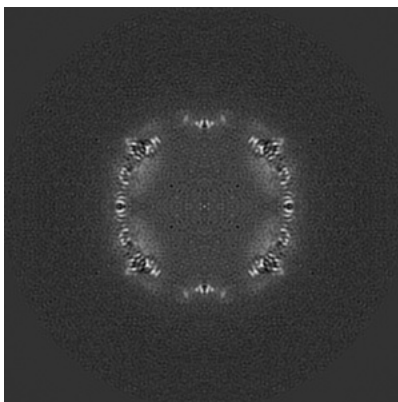
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

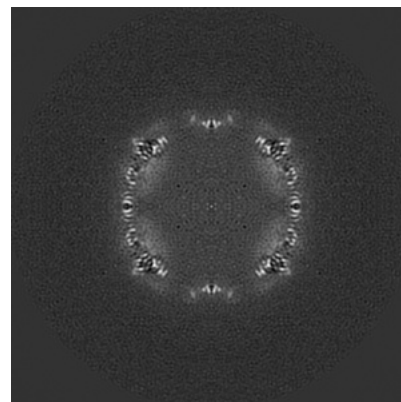
6.2.1 Primary map



X Index: 192

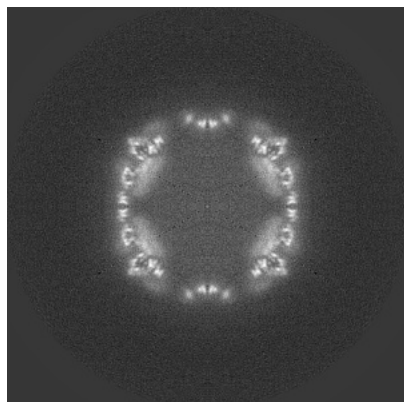


Y Index: 192

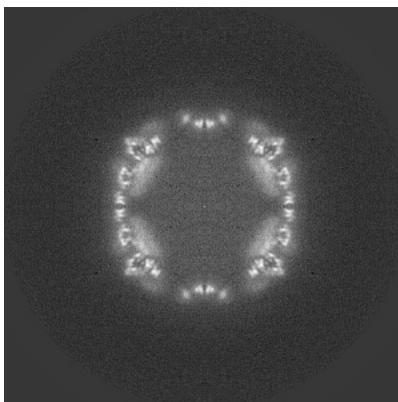


Z Index: 192

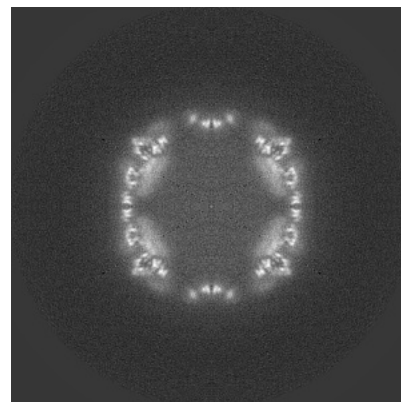
6.2.2 Raw map



X Index: 192



Y Index: 192

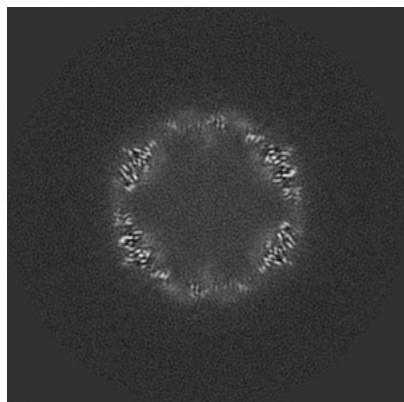


Z Index: 192

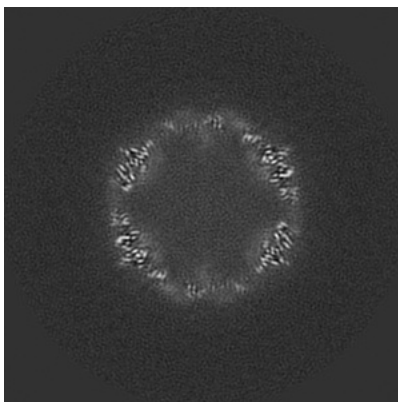
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

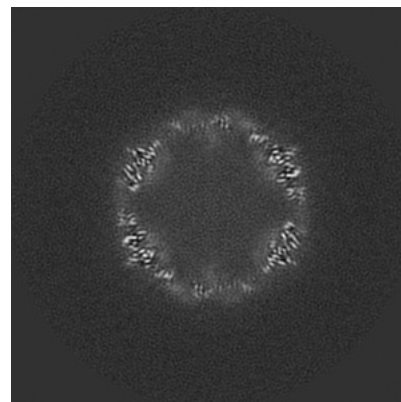
6.3.1 Primary map



X Index: 206

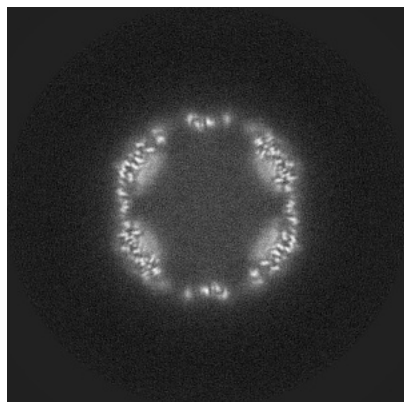


Y Index: 206

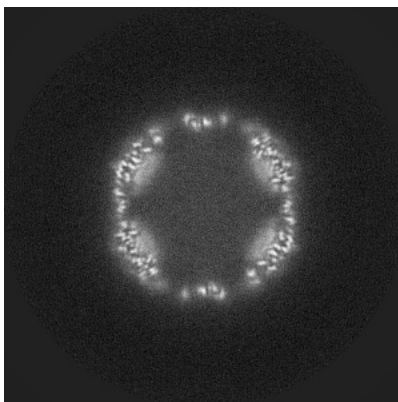


Z Index: 206

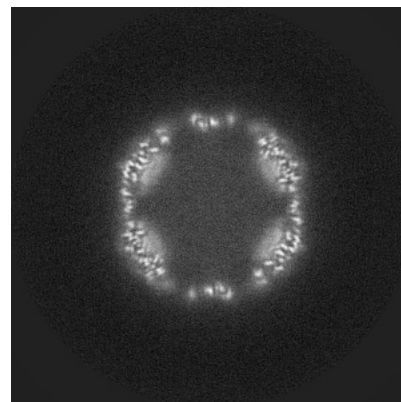
6.3.2 Raw map



X Index: 187



Y Index: 187

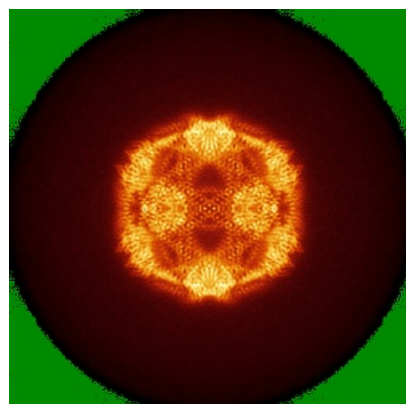


Z Index: 187

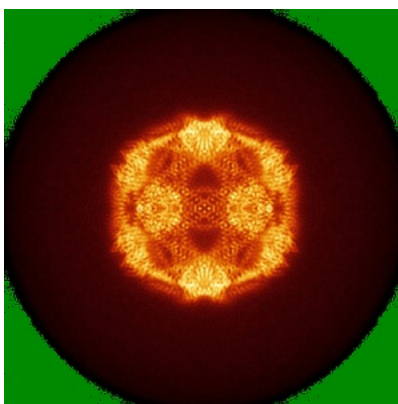
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

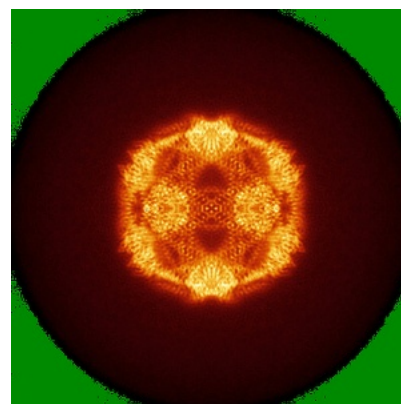
6.4.1 Primary map



X

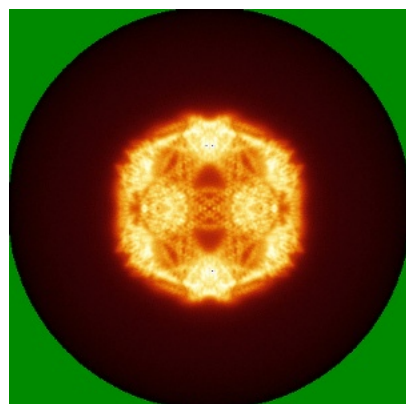


Y

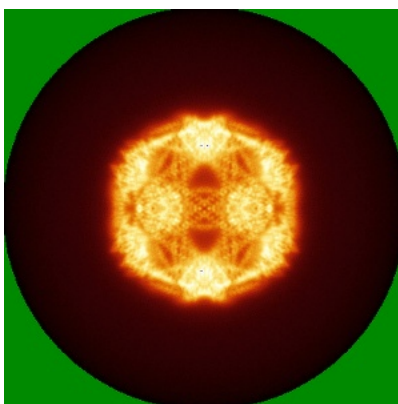


Z

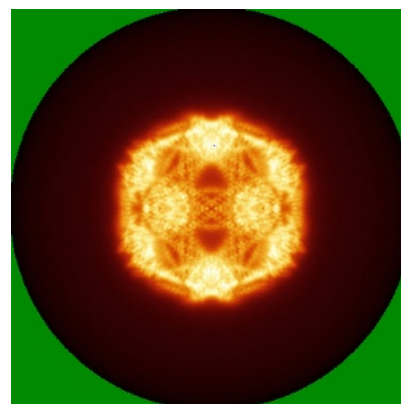
6.4.2 Raw map



X



Y

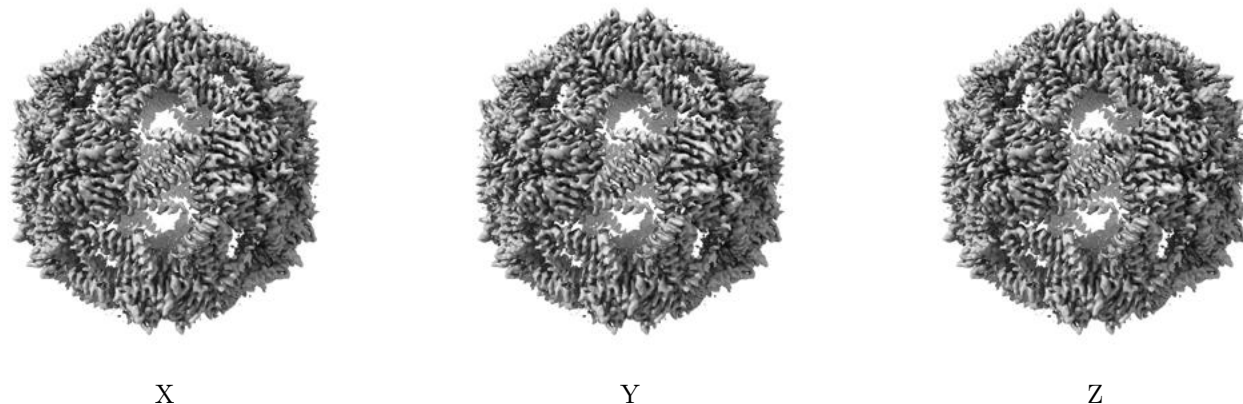


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

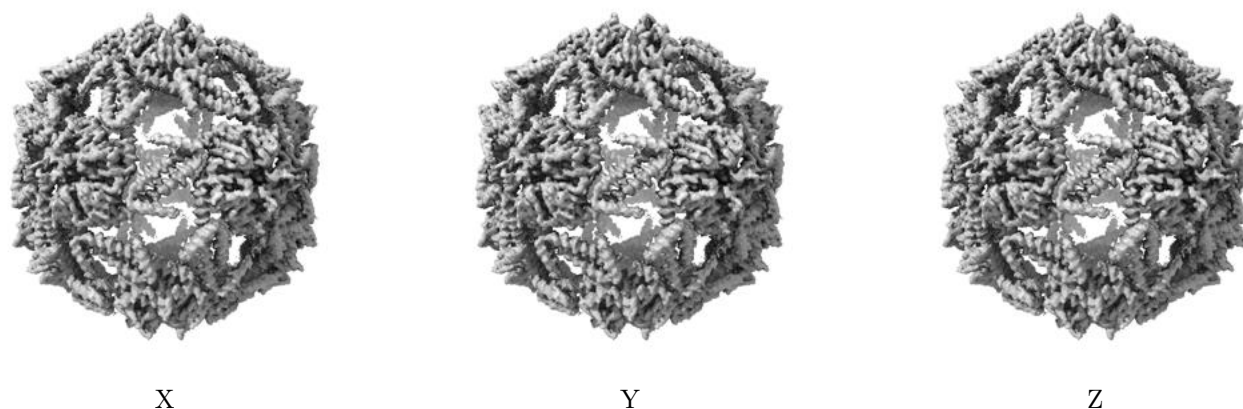
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

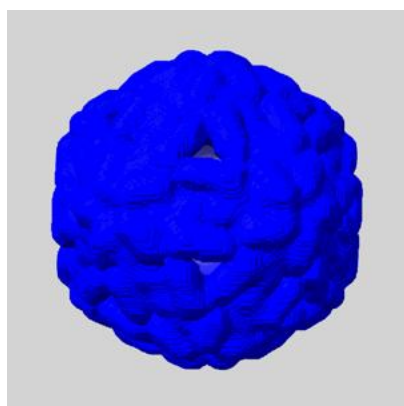
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

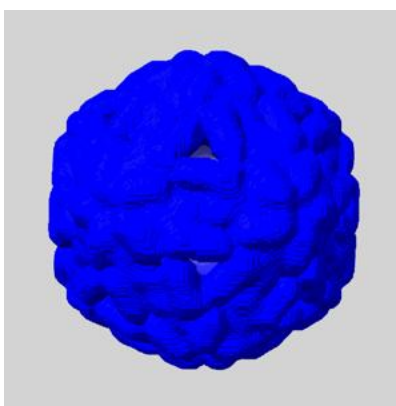
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

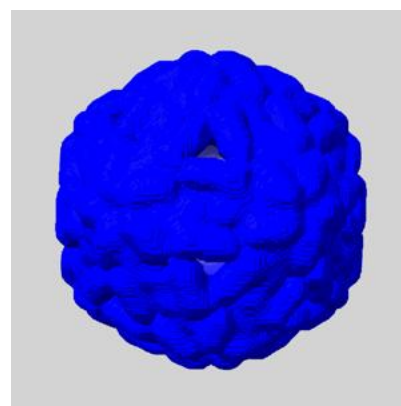
6.6.1 emd_64381_msk_1.map [i](#)



X



Y

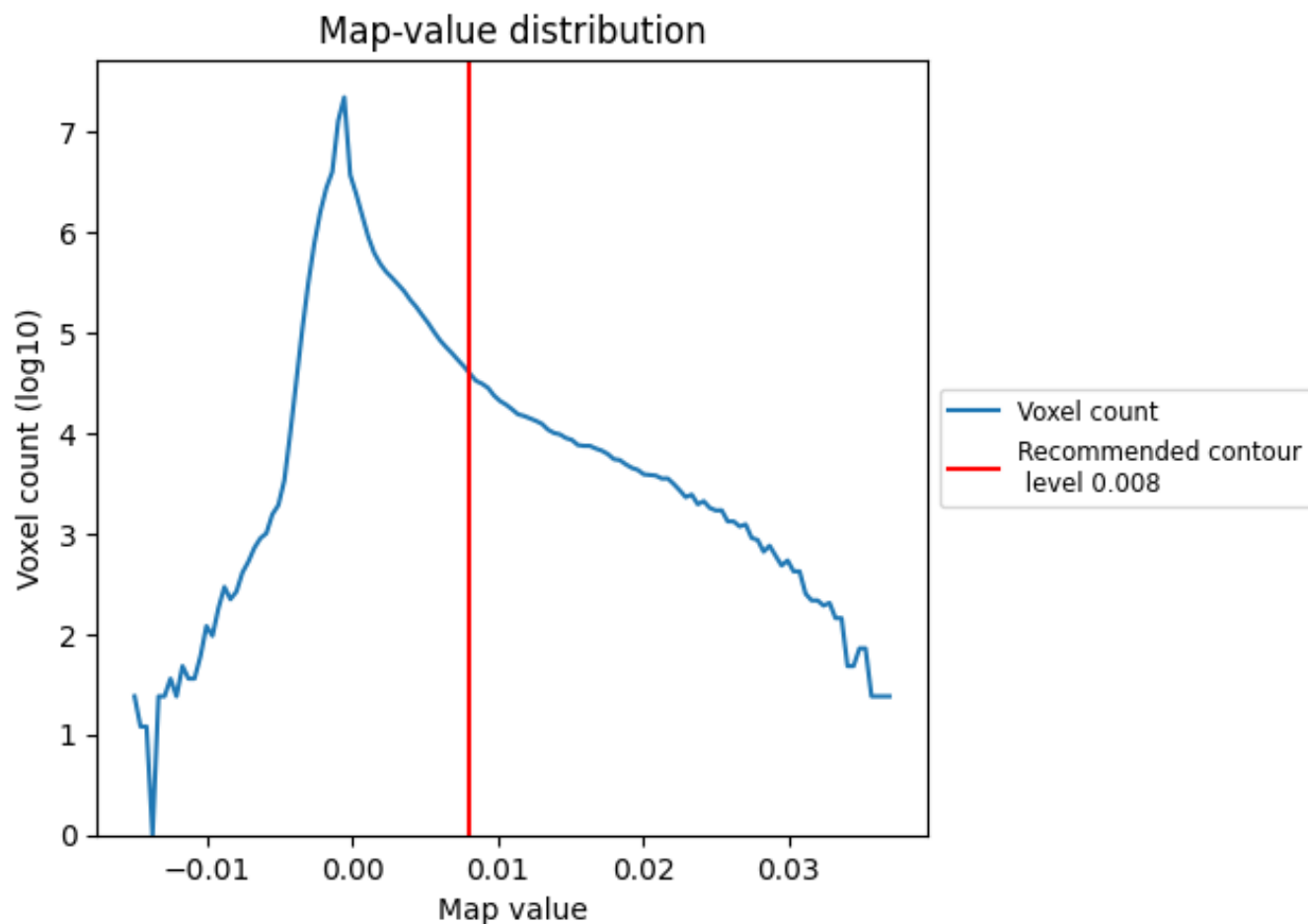


Z

7 Map analysis [i](#)

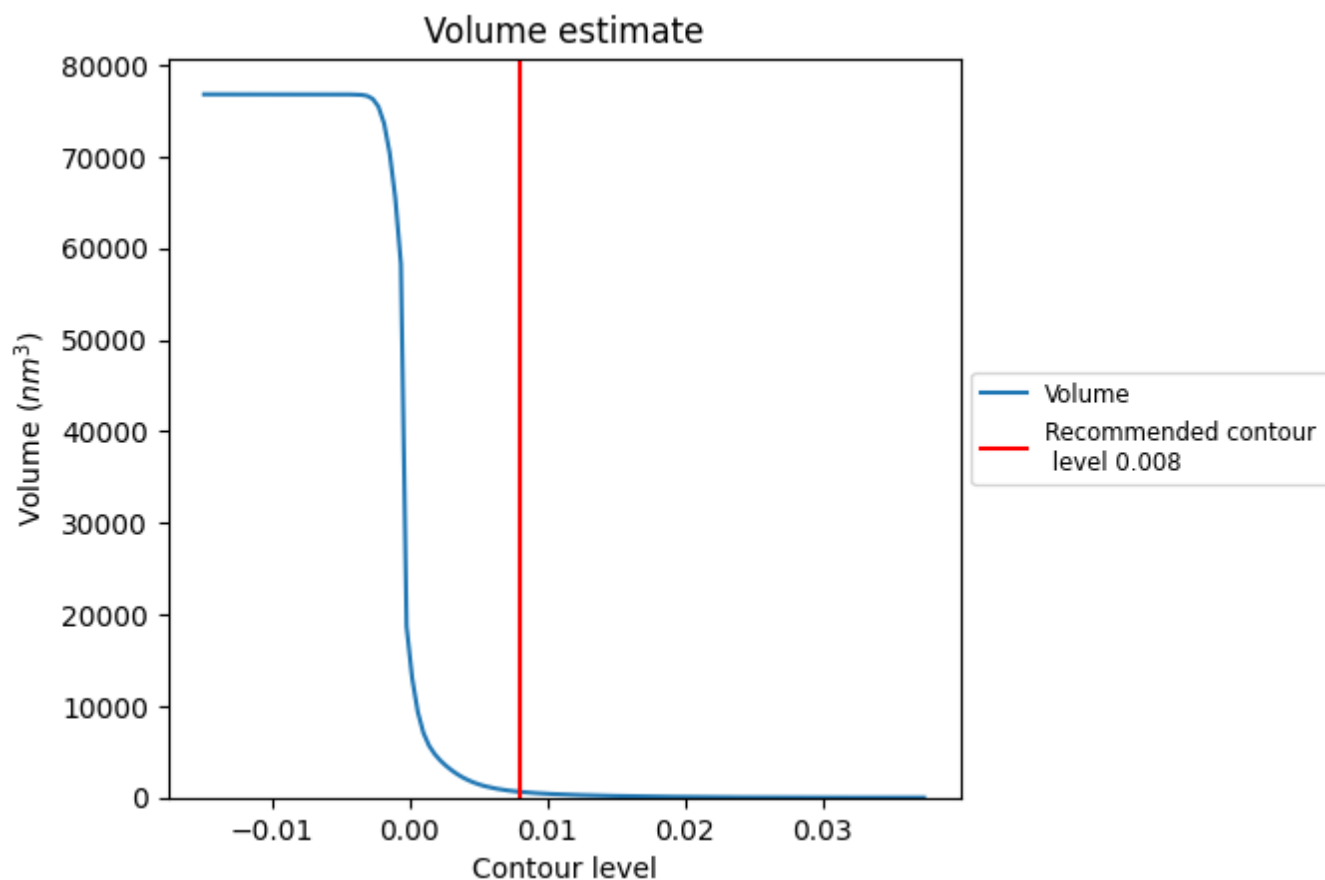
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

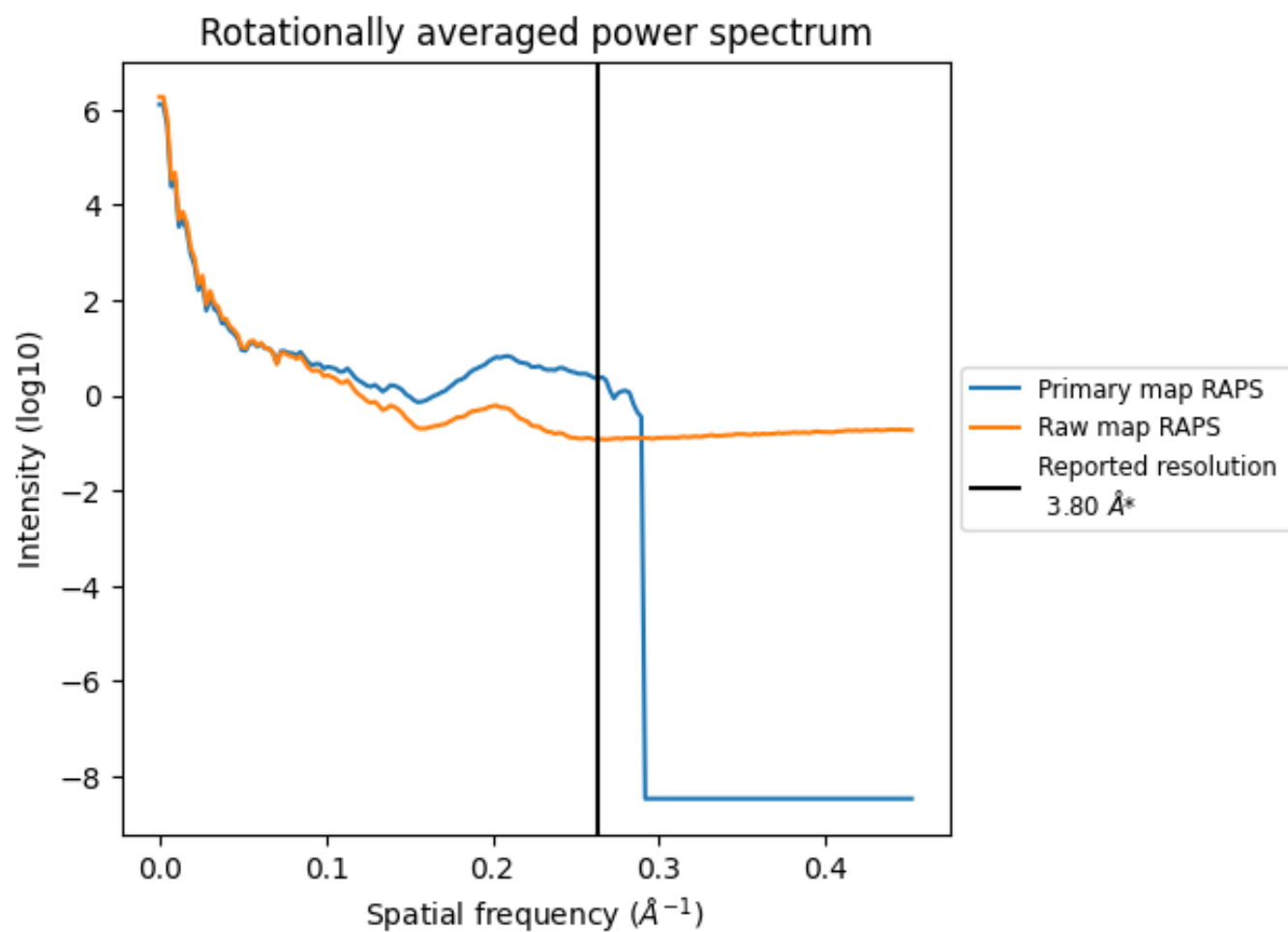
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 625 nm³; this corresponds to an approximate mass of 564 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

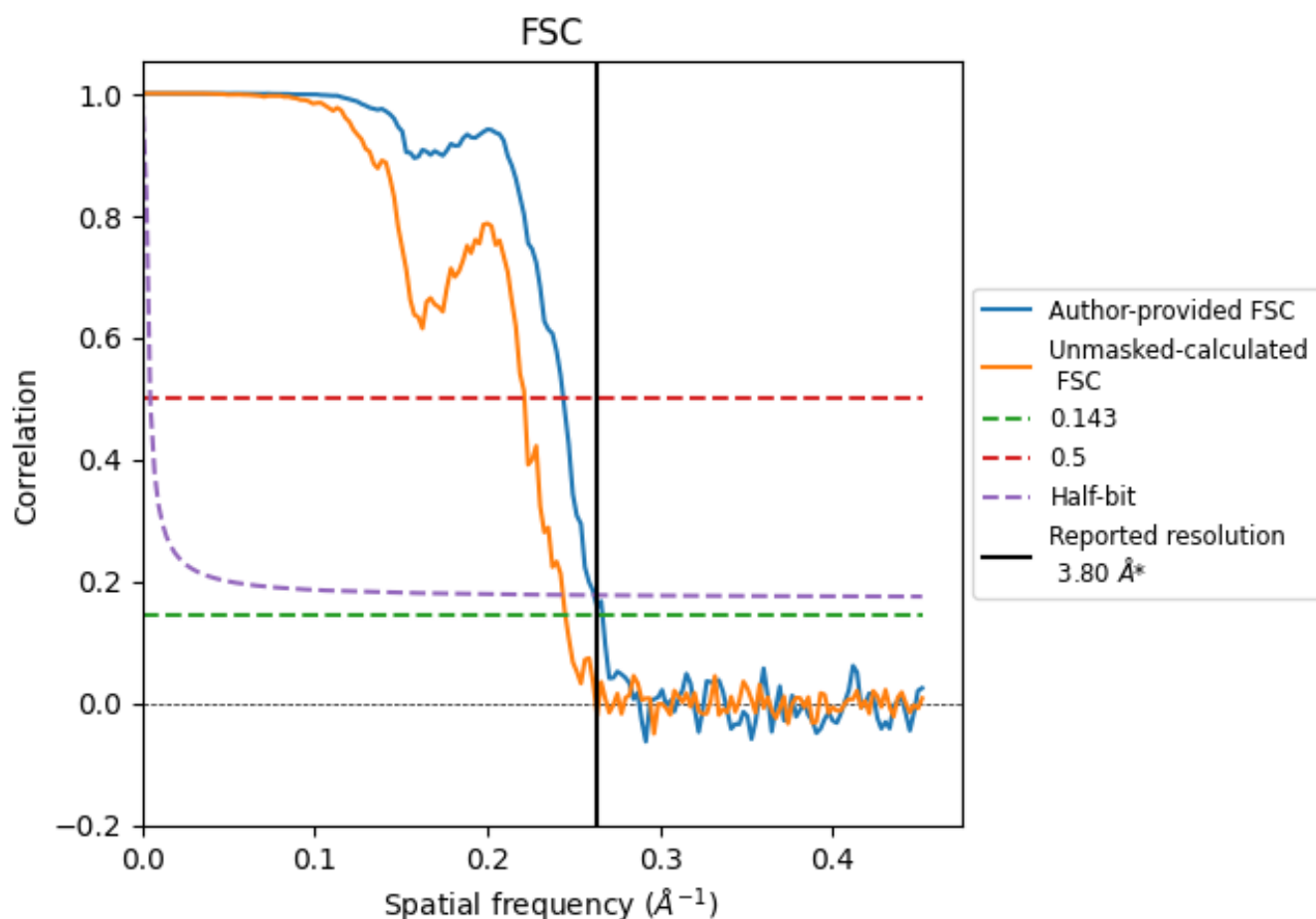


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

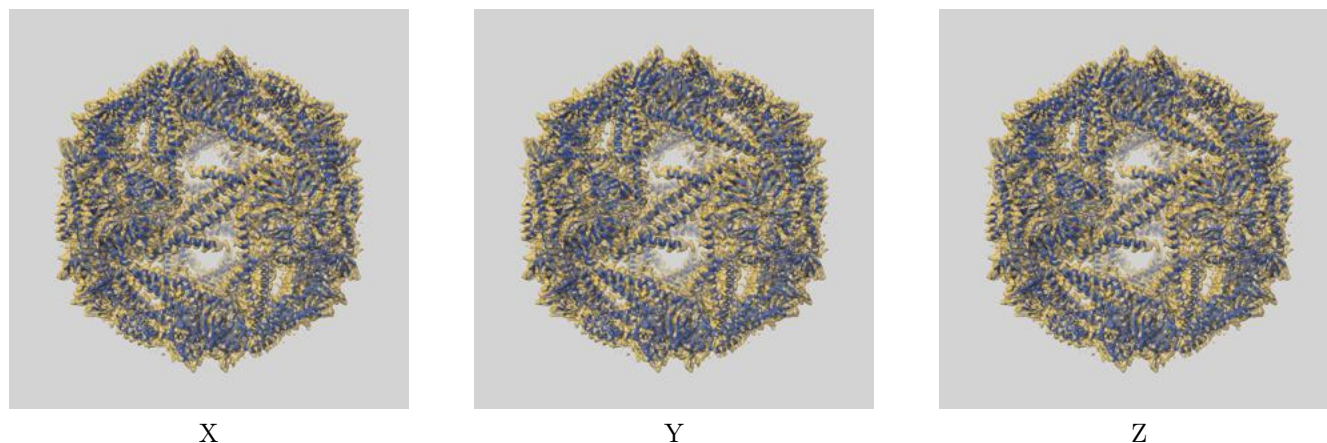
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.75	4.10	3.82
Unmasked-calculated*	4.08	4.52	4.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

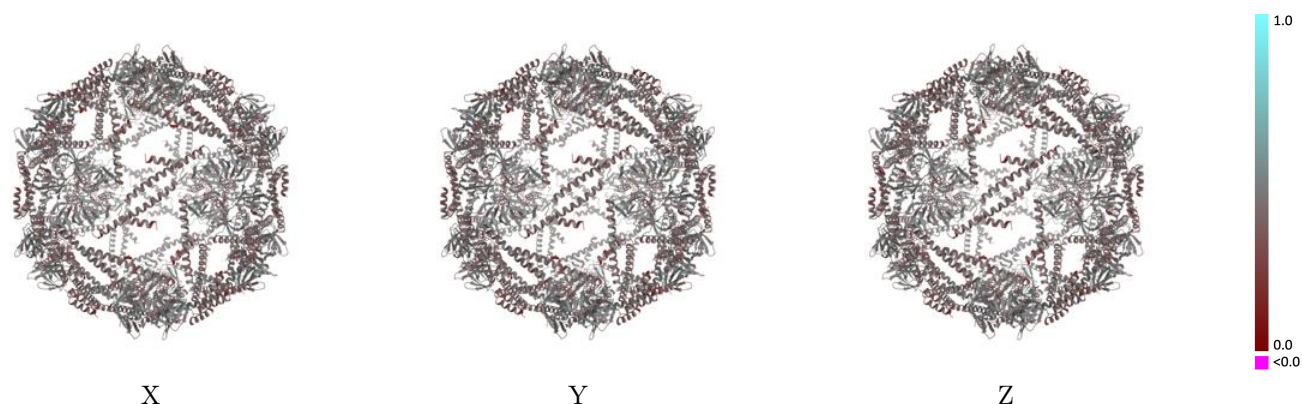
This section contains information regarding the fit between EMDB map EMD-64381 and PDB model 9UOL. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



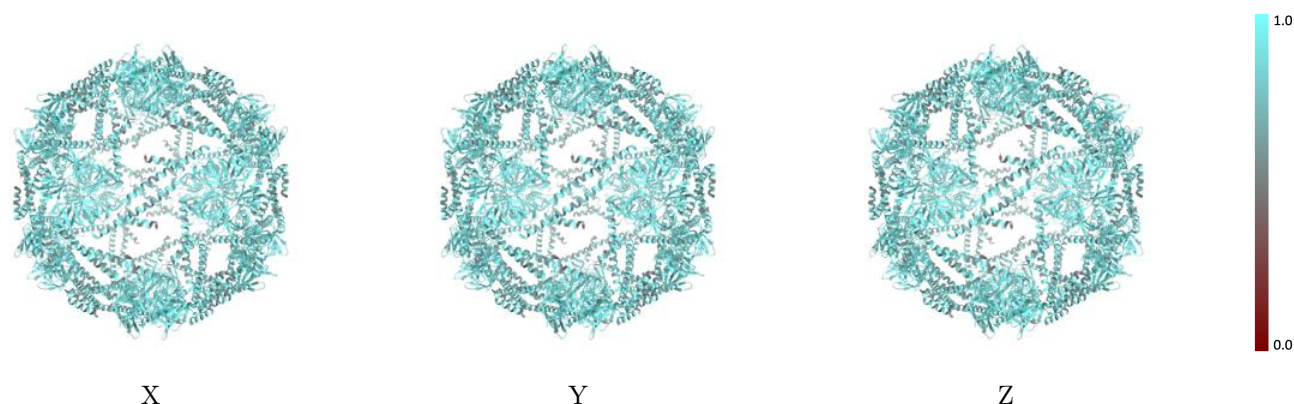
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



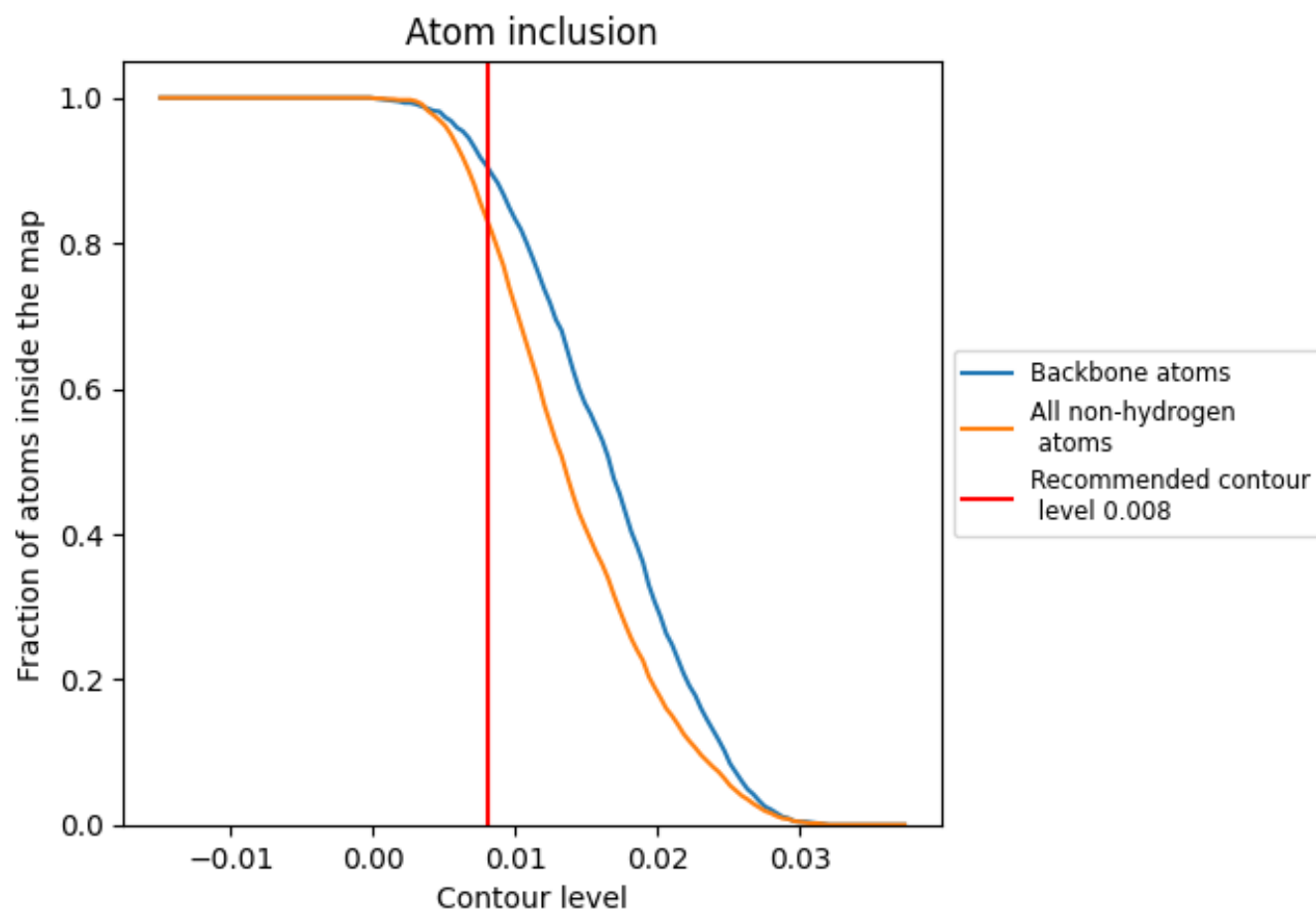
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8330	 0.4280
A	 0.8340	 0.4270
AA	 0.8340	 0.4300
AB	 0.8300	 0.4260
B	 0.8300	 0.4260
BA	 0.8300	 0.4270
BB	 0.8360	 0.4280
C	 0.8360	 0.4280
CA	 0.8360	 0.4290
CB	 0.8320	 0.4270
D	 0.8320	 0.4270
DA	 0.8320	 0.4240
DB	 0.8310	 0.4270
E	 0.8310	 0.4290
EA	 0.8310	 0.4290
EB	 0.8340	 0.4300
F	 0.8350	 0.4300
FA	 0.8340	 0.4310
FB	 0.8300	 0.4240
G	 0.8300	 0.4290
GA	 0.8300	 0.4260
GB	 0.8360	 0.4290
H	 0.8360	 0.4290
HA	 0.8360	 0.4250
HB	 0.8320	 0.4260
I	 0.8320	 0.4280
IA	 0.8320	 0.4270
IB	 0.8310	 0.4290
J	 0.8310	 0.4290
JA	 0.8310	 0.4280
K	 0.8350	 0.4280
KA	 0.8350	 0.4270
L	 0.8300	 0.4260
LA	 0.8300	 0.4260
M	 0.8360	 0.4300



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
MA	 0.8360	 0.4240
N	 0.8320	 0.4270
NA	 0.8320	 0.4310
O	 0.8310	 0.4270
OA	 0.8310	 0.4280
P	 0.8340	 0.4280
PA	 0.8340	 0.4310
Q	 0.8300	 0.4310
QA	 0.8300	 0.4260
R	 0.8360	 0.4290
RA	 0.8360	 0.4290
S	 0.8320	 0.4290
SA	 0.8320	 0.4260
T	 0.8310	 0.4300
TA	 0.8310	 0.4270
UA	 0.8350	 0.4300
V	 0.8350	 0.4260
VA	 0.8300	 0.4250
W	 0.8300	 0.4290
WA	 0.8360	 0.4310
X	 0.8360	 0.4290
XA	 0.8320	 0.4240
Y	 0.8320	 0.4280
YA	 0.8310	 0.4260
Z	 0.8310	 0.4310
ZA	 0.8350	 0.4280