



wwPDB EM Validation Summary Report ⓘ

Apr 8, 2024 – 11:35 AM EDT

PDB ID : 8TRO
EMDB ID : EMD-41585
Title : Rod from high-resolution phycobilisome quenched by OCP (local refinement)
Authors : Sauer, P.V.; Sutter, M.; Cupellini, L.
Deposited on : 2023-08-09
Resolution : 1.90 Å(reported)

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.dev92
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.1

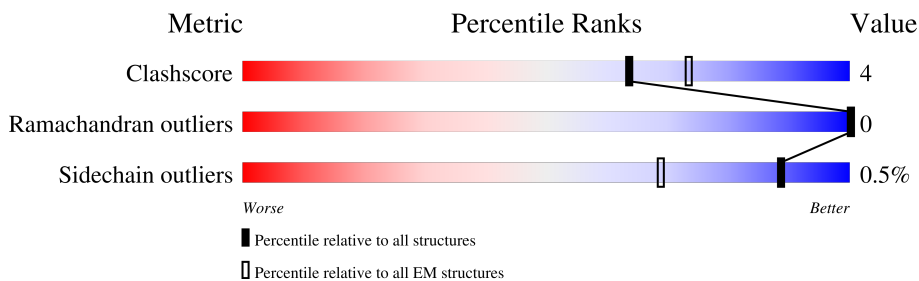
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 1.90 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.



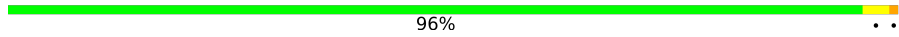

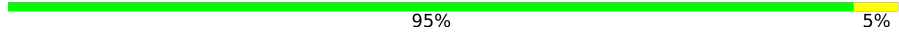
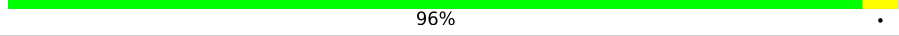
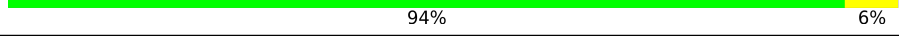
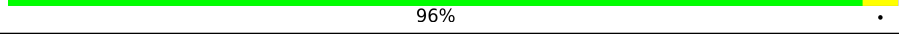
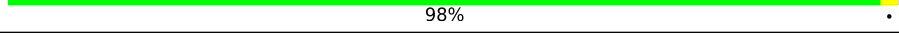
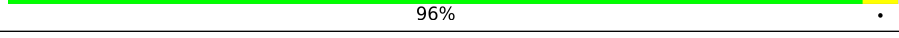
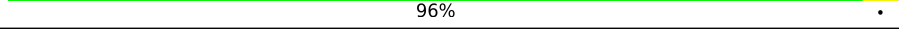
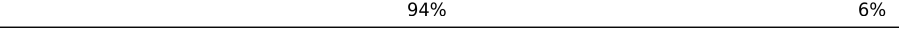
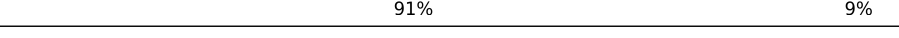
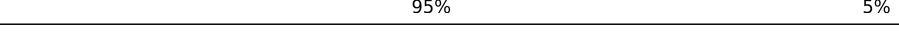
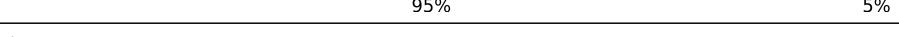
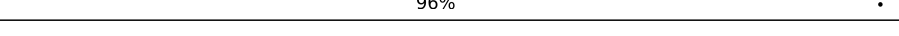
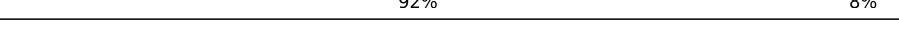
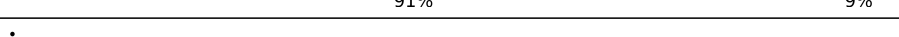
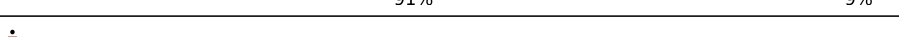
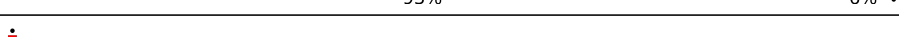
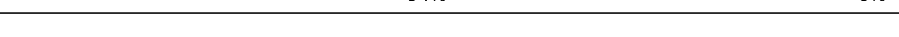






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	0	162	
1	2	162	
1	4	162	
1	6	162	
1	8	162	
1	A	162	
1	C	162	
1	E	162	

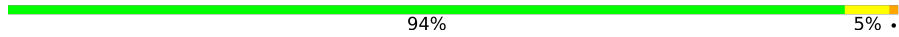
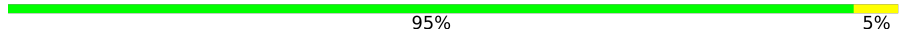

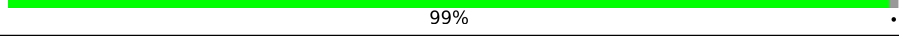
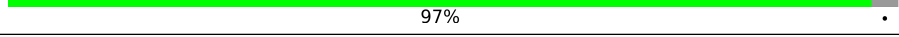

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Mol	Chain	Length	Quality of chain
1	G	162	 96% . .
1	I	162	 91% 9% .
1	K	162	 95% 5% .
1	M	162	 96% .
1	O	162	 94% 6% .
1	Q	162	 96% .
1	S	162	 98% .
1	U	162	 96% .
1	W	162	 96% .
1	Y	162	 94% 6% .
2	1	172	 91% 9% .
2	3	172	 95% 5% .
2	5	172	 95% 5% .
2	7	172	 96% .
2	9	172	 92% 8% .
2	B	172	 91% 9% .
2	D	172	 91% 9% .
2	F	172	 93% 6% .
2	H	172	 94% 6% .
2	J	172	 94% 6% .
2	L	172	 99% .
2	N	172	 93% 7% .
2	P	172	 94% 6% .
2	R	172	 90% 10% .
2	T	172	 95% 5% .

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Mol	Chain	Length	Quality of chain
2	V	172	 94% 5%
2	X	172	 95% 5%
2	Z	172	 93% 6%
3	a	249	 78% 22%
4	b	291	 99%
5	c	273	 97%
6	d	83	 89% 11%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 110442 atoms, of which 52922 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 C-phycoyanin alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	0	162	2446	775	1206	215	247	3	0	0
1	2	162	2446	775	1206	215	247	3	0	0
1	4	162	2446	775	1206	215	247	3	0	0
1	6	162	2446	775	1206	215	247	3	0	0
1	8	162	2446	775	1206	215	247	3	0	0
1	A	162	2446	775	1206	215	247	3	0	0
1	C	162	2446	775	1206	215	247	3	0	0
1	E	162	2446	775	1206	215	247	3	0	0
1	G	162	2446	775	1206	215	247	3	0	0
1	I	162	2446	775	1206	215	247	3	0	0
1	K	162	2446	775	1206	215	247	3	0	0
1	M	162	2446	775	1206	215	247	3	0	0
1	O	162	2446	775	1206	215	247	3	0	0
1	Q	162	2446	775	1206	215	247	3	0	0
1	S	162	2446	775	1206	215	247	3	0	0
1	U	162	2446	775	1206	215	247	3	0	0
1	W	162	2446	775	1206	215	247	3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace	
1	Y	162	Total	C	H	N	O	S	0	0
			2446	775	1206	215	247	3		

- Molecule 2 is a protein called C-phycoyanin beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	1	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	3	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	5	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	7	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	9	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	B	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	D	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	F	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	H	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	J	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	L	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	N	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	P	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	R	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	T	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	V	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	X	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		
2	Z	172	Total	C	H	N	O	S	0	0
			2534	785	1263	228	251	7		

- Molecule 3 is a protein called Phycobilisome rod-core linker polypeptide CpcG.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	a	194	3194	1031	1577	286	298	2	0	0

- Molecule 4 is a protein called Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated, rod 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	b	289	4545	1438	2263	408	433	3	0	0

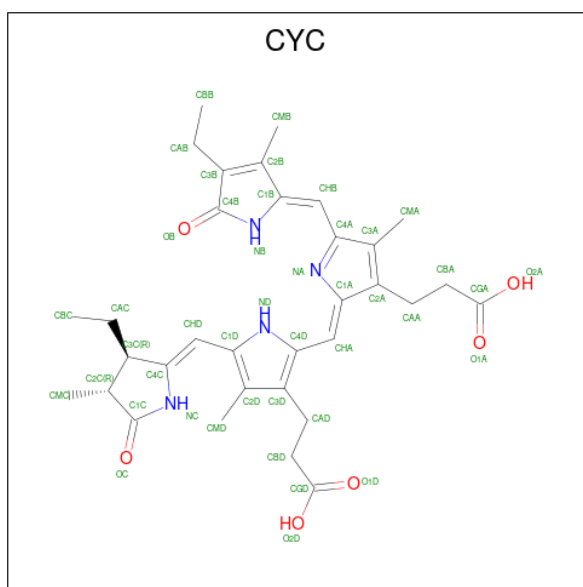
- Molecule 5 is a protein called Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated, rod 2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	c	266	4202	1317	2080	393	409	3	0	0

- Molecule 6 is a protein called Phycobilisome 8.9 kDa linker polypeptide, phycocyanin-associated, rod.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	d	74	1162	358	579	113	110	2	0	0

- Molecule 7 is PHYCOCYANOBILIN (three-letter code: CYC) (formula: $C_{33}H_{40}N_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf		
			Total	C	H	N		O	
7	0	1	Total	80	33	37	4	6	0
7	1	1	Total	80	33	37	4	6	0
7	1	1	Total	79	33	36	4	6	0
7	2	1	Total	80	33	37	4	6	0
7	3	1	Total	79	33	36	4	6	0
7	3	1	Total	80	33	37	4	6	0
7	4	1	Total	80	33	37	4	6	0
7	5	1	Total	80	33	37	4	6	0
7	5	1	Total	80	33	37	4	6	0
7	6	1	Total	80	33	37	4	6	0
7	7	1	Total	80	33	37	4	6	0
7	7	1	Total	79	33	36	4	6	0
7	8	1	Total	80	33	37	4	6	0
7	9	1	Total	79	33	36	4	6	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
7	9	1	Total 80	C 33	H 37	N 4	O 6	0
7	A	1	Total 80	C 33	H 37	N 4	O 6	0
7	B	1	Total 80	C 33	H 37	N 4	O 6	0
7	B	1	Total 80	C 33	H 37	N 4	O 6	0
7	C	1	Total 80	C 33	H 37	N 4	O 6	0
7	D	1	Total 79	C 33	H 36	N 4	O 6	0
7	D	1	Total 80	C 33	H 37	N 4	O 6	0
7	E	1	Total 80	C 33	H 37	N 4	O 6	0
7	F	1	Total 79	C 33	H 36	N 4	O 6	0
7	F	1	Total 80	C 33	H 37	N 4	O 6	0
7	G	1	Total 80	C 33	H 37	N 4	O 6	0
7	H	1	Total 80	C 33	H 37	N 4	O 6	0
7	H	1	Total 79	C 33	H 36	N 4	O 6	0
7	I	1	Total 79	C 33	H 36	N 4	O 6	0
7	J	1	Total 79	C 33	H 36	N 4	O 6	0
7	J	1	Total 80	C 33	H 37	N 4	O 6	0
7	K	1	Total 80	C 33	H 37	N 4	O 6	0
7	L	1	Total 79	C 33	H 36	N 4	O 6	0
7	L	1	Total 80	C 33	H 37	N 4	O 6	0
7	M	1	Total 80	C 33	H 37	N 4	O 6	0
7	N	1	Total 80	C 33	H 37	N 4	O 6	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
7	N	1	Total 79	C 33	H 36	N 4	O 6	0
7	O	1	Total 80	C 33	H 37	N 4	O 6	0
7	P	1	Total 80	C 33	H 37	N 4	O 6	0
7	P	1	Total 80	C 33	H 37	N 4	O 6	0
7	Q	1	Total 80	C 33	H 37	N 4	O 6	0
7	R	1	Total 79	C 33	H 36	N 4	O 6	0
7	R	1	Total 80	C 33	H 37	N 4	O 6	0
7	S	1	Total 80	C 33	H 37	N 4	O 6	0
7	T	1	Total 79	C 33	H 36	N 4	O 6	0
7	T	1	Total 80	C 33	H 37	N 4	O 6	0
7	U	1	Total 80	C 33	H 37	N 4	O 6	0
7	V	1	Total 79	C 33	H 36	N 4	O 6	0
7	V	1	Total 80	C 33	H 37	N 4	O 6	0
7	W	1	Total 80	C 33	H 37	N 4	O 6	0
7	X	1	Total 79	C 33	H 36	N 4	O 6	0
7	X	1	Total 80	C 33	H 37	N 4	O 6	0
7	Y	1	Total 80	C 33	H 37	N 4	O 6	0
7	Z	1	Total 79	C 33	H 36	N 4	O 6	0
7	Z	1	Total 79	C 33	H 36	N 4	O 6	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		AltConf
8	0	74	Total 74	O 74	0
8	1	90	Total 90	O 90	0
8	2	85	Total 85	O 85	0
8	3	66	Total 66	O 66	0
8	4	78	Total 78	O 78	0
8	5	83	Total 83	O 83	0
8	6	89	Total 89	O 89	0
8	7	83	Total 83	O 83	0
8	8	60	Total 60	O 60	0
8	9	92	Total 92	O 92	0
8	A	57	Total 57	O 57	0
8	B	91	Total 91	O 91	0
8	C	52	Total 52	O 52	0
8	D	96	Total 96	O 96	0
8	E	70	Total 70	O 70	0
8	F	92	Total 92	O 92	0
8	G	75	Total 75	O 75	0
8	H	67	Total 67	O 67	0
8	I	61	Total 61	O 61	0
8	J	75	Total 75	O 75	0
8	K	72	Total 72	O 72	0
8	L	90	Total 90	O 90	0

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Mol	Chain	Residues	Atoms		AltConf
8	M	95	Total 95	O 95	0
8	N	119	Total 119	O 119	0
8	O	86	Total 86	O 86	0
8	P	91	Total 91	O 91	0
8	Q	76	Total 76	O 76	0
8	R	85	Total 85	O 85	0
8	S	90	Total 90	O 90	0
8	T	123	Total 123	O 123	0
8	U	87	Total 87	O 87	0
8	V	84	Total 84	O 84	0
8	W	87	Total 87	O 87	0
8	X	96	Total 96	O 96	0
8	Y	69	Total 69	O 69	0
8	Z	82	Total 82	O 82	0
8	a	130	Total 130	O 130	0
8	b	143	Total 143	O 143	0
8	c	115	Total 115	O 115	0
8	d	40	Total 40	O 40	0

3 Residue-property plots

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: C-phycoerythrin alpha subunit

Chain 0:  95% 5%



- Molecule 1: C-phycoerythrin alpha subunit

Chain 2:  93% 7%



- Molecule 1: C-phycoerythrin alpha subunit

Chain 4:  93% 7%



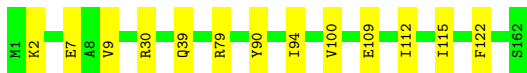
- Molecule 1: C-phycoerythrin alpha subunit

Chain 6:  95% 5%



- Molecule 1: C-phycoerythrin alpha subunit

Chain 8:  92% 8%



- Molecule 1: C-phycoerythrin alpha subunit

Chain A:  96%



• Molecule 1: C-phycoerythrin alpha subunit

Chain C:  94% 6%



• Molecule 1: C-phycoerythrin alpha subunit

Chain E:  96%




• Molecule 1: C-phycoerythrin alpha subunit

Chain G:  96%



• Molecule 1: C-phycoerythrin alpha subunit

Chain I:  91% 9%



• Molecule 1: C-phycoerythrin alpha subunit

Chain K:  95% 5%



• Molecule 1: C-phycoerythrin alpha subunit

Chain M:  96%



• Molecule 1: C-phycoerythrin alpha subunit

Chain O:  94% 6%



• Molecule 1: C-phycoerythrin alpha subunit

Chain Q:  96% .



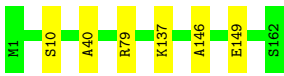
• Molecule 1: C-phycoerythrin alpha subunit

Chain S:  98% .



• Molecule 1: C-phycoerythrin alpha subunit

Chain U:  96% .



• Molecule 1: C-phycoerythrin alpha subunit

Chain W:  96% .




• Molecule 1: C-phycoerythrin alpha subunit

Chain Y:  94% 6%



• Molecule 2: C-phycoerythrin beta subunit

Chain 1:  91% 9%



• Molecule 2: C-phycoerythrin beta subunit

Chain 3:  95% 5%



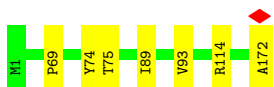
• Molecule 2: C-phyco cyanin beta subunit

Chain 5:  95% 5%



• Molecule 2: C-phyco cyanin beta subunit

Chain 7:  96% .

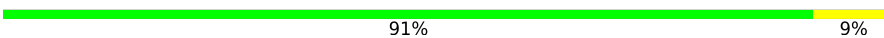


• Molecule 2: C-phyco cyanin beta subunit

Chain 9:  92% 8%



• Molecule 2: C-phyco cyanin beta subunit

Chain B:  91% 9%



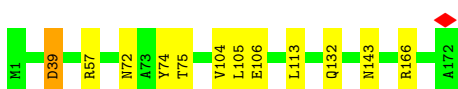
• Molecule 2: C-phyco cyanin beta subunit

Chain D:  91% 9%



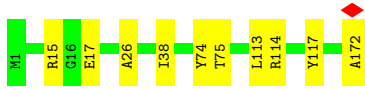
• Molecule 2: C-phyco cyanin beta subunit

Chain F:  93% 6% .



• Molecule 2: C-phyco cyanin beta subunit

Chain H:  94% 6%



- Molecule 2: C-phycoyanin beta subunit

Chain J:  94% 6%



- Molecule 2: C-phycoyanin beta subunit

Chain L:  99% .



- Molecule 2: C-phycoyanin beta subunit

Chain N:  93% 7%

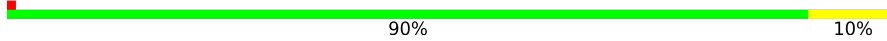


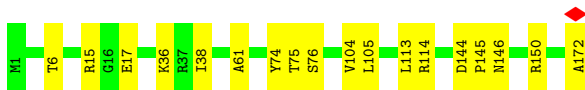
- Molecule 2: C-phycoyanin beta subunit

Chain P:  94% 6%



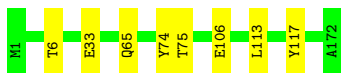
- Molecule 2: C-phycoyanin beta subunit

Chain R:  90% 10%



- Molecule 2: C-phycoyanin beta subunit

Chain T:  95% 5%



- Molecule 2: C-phycoyanin beta subunit

Chain V:  94% 5%



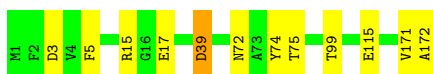
- Molecule 2: C-phyco cyanin beta subunit

Chain X:  95% 5%




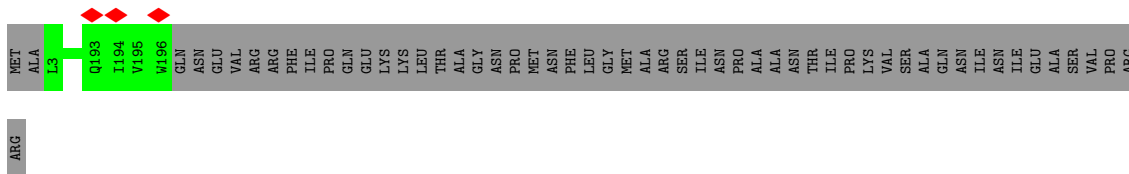
- Molecule 2: C-phyco cyanin beta subunit

Chain Z:  93% 6%



- Molecule 3: Phycobilisome rod-core linker polypeptide CpcG

Chain a:  78% 22%



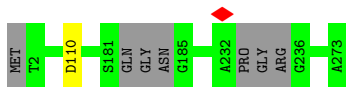
- Molecule 4: Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated, rod 1

Chain b:  99%




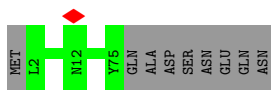
- Molecule 5: Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated, rod 2

Chain c:  97%



- Molecule 6: Phycobilisome 8.9 kDa linker polypeptide, phycocyanin-associated, rod

Chain d:  89% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	435854	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.688	Depositor
Minimum map value	-1.543	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	372.224, 372.224, 372.224	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0	0.32	0/1261	0.49	0/1709
1	2	0.33	0/1261	0.49	0/1709
1	4	0.33	0/1261	0.49	0/1709
1	6	0.32	0/1261	0.49	0/1709
1	8	0.33	0/1261	0.48	0/1709
1	A	0.32	0/1261	0.48	0/1709
1	C	0.32	0/1261	0.50	0/1709
1	E	0.32	0/1261	0.49	0/1709
1	G	0.34	0/1261	0.49	0/1709
1	I	0.32	0/1261	0.49	0/1709
1	K	0.34	0/1261	0.50	0/1709
1	M	0.32	0/1261	0.50	0/1709
1	O	0.34	0/1261	0.49	0/1709
1	Q	0.34	0/1261	0.50	0/1709
1	S	0.34	0/1261	0.51	0/1709
1	U	0.34	0/1261	0.49	0/1709
1	W	0.33	0/1261	0.49	0/1709
1	Y	0.32	0/1261	0.49	0/1709
2	1	0.32	0/1275	0.53	0/1725
2	3	0.31	0/1275	0.53	0/1725
2	5	0.31	0/1275	0.54	0/1725
2	7	0.31	0/1275	0.52	0/1725
2	9	0.31	0/1275	0.53	0/1725
2	B	0.31	0/1275	0.52	0/1725
2	D	0.29	0/1275	0.51	0/1725
2	F	0.32	0/1275	0.52	0/1725
2	H	0.32	0/1275	0.53	0/1725
2	J	0.32	0/1275	0.53	0/1725
2	L	0.30	0/1275	0.52	0/1725
2	N	0.33	0/1275	0.54	0/1725
2	P	0.31	0/1275	0.52	0/1725
2	R	0.32	0/1275	0.53	0/1725

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	T	0.33	0/1275	0.55	0/1725
2	V	0.33	0/1275	0.53	0/1725
2	X	0.32	0/1275	0.53	0/1725
2	Z	0.31	0/1275	0.53	0/1725
3	a	0.34	0/1656	0.56	0/2240
4	b	0.33	0/2327	0.57	0/3149
5	c	0.32	0/2156	0.58	0/2907
6	d	0.34	0/591	0.59	0/796
All	All	0.32	0/52378	0.52	0/70904

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1240	1206	1206	5	0
1	2	1240	1206	1206	7	0
1	4	1240	1206	1206	6	0
1	6	1240	1206	1206	4	0
1	8	1240	1206	1206	7	0
1	A	1240	1206	1206	4	0
1	C	1240	1206	1206	6	0
1	E	1240	1206	1206	3	0
1	G	1240	1206	1206	4	0
1	I	1240	1206	1206	7	0
1	K	1240	1206	1206	7	0
1	M	1240	1206	1206	4	0
1	O	1240	1206	1206	5	0
1	Q	1240	1206	1206	2	0
1	S	1240	1206	1206	3	0
1	U	1240	1206	1206	4	0
1	W	1240	1206	1206	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Y	1240	1206	1206	6	0
2	1	1271	1263	1262	13	0
2	3	1271	1263	1262	8	0
2	5	1271	1263	1262	6	0
2	7	1271	1263	1262	5	0
2	9	1271	1263	1262	10	0
2	B	1271	1263	1262	11	0
2	D	1271	1263	1262	12	0
2	F	1271	1263	1262	11	0
2	H	1271	1263	1262	7	0
2	J	1271	1263	1262	7	0
2	L	1271	1263	1262	2	0
2	N	1271	1263	1262	10	0
2	P	1271	1263	1262	7	0
2	R	1271	1263	1262	12	0
2	T	1271	1263	1262	5	0
2	V	1271	1263	1262	10	0
2	X	1271	1263	1262	6	0
2	Z	1271	1263	1262	8	0
3	a	1617	1577	1576	0	0
4	b	2282	2263	2261	0	0
5	c	2122	2080	2076	0	0
6	d	583	579	578	0	0
7	0	43	37	37	3	0
7	1	86	73	74	11	0
7	2	43	37	37	5	0
7	3	86	73	74	9	0
7	4	43	37	37	2	0
7	5	86	74	74	9	0
7	6	43	37	37	3	0
7	7	86	73	74	8	0
7	8	43	37	37	3	0
7	9	86	73	74	9	0
7	A	43	37	37	2	0
7	B	86	74	74	9	0
7	C	43	37	37	3	0
7	D	86	73	74	10	0
7	E	43	37	37	3	0
7	F	86	73	74	10	0
7	G	43	37	37	3	0
7	H	86	73	74	7	0
7	I	43	36	37	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	J	86	73	74	8	0
7	K	43	37	37	3	0
7	L	86	73	74	6	0
7	M	43	37	37	2	0
7	N	86	73	74	11	0
7	O	43	37	37	4	0
7	P	86	74	74	9	0
7	Q	43	37	37	4	0
7	R	86	73	74	10	0
7	S	43	37	37	4	0
7	T	86	73	74	10	0
7	U	43	37	37	4	0
7	V	86	73	74	10	0
7	W	43	37	37	3	0
7	X	86	73	74	11	0
7	Y	43	37	37	4	0
7	Z	86	72	74	8	0
8	0	74	0	0	0	0
8	1	90	0	0	4	0
8	2	85	0	0	2	0
8	3	66	0	0	2	0
8	4	78	0	0	0	0
8	5	83	0	0	2	0
8	6	89	0	0	0	0
8	7	83	0	0	2	0
8	8	60	0	0	1	0
8	9	92	0	0	4	0
8	A	57	0	0	1	0
8	B	91	0	0	1	0
8	C	52	0	0	1	0
8	D	96	0	0	1	0
8	E	70	0	0	1	0
8	F	92	0	0	4	0
8	G	75	0	0	1	0
8	H	67	0	0	2	0
8	I	61	0	0	2	0
8	J	75	0	0	2	0
8	K	72	0	0	3	0
8	L	90	0	0	0	0
8	M	95	0	0	1	0
8	N	119	0	0	4	0
8	O	86	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	P	91	0	0	1	0
8	Q	76	0	0	1	0
8	R	85	0	0	1	0
8	S	90	0	0	0	0
8	T	123	0	0	2	0
8	U	87	0	0	2	0
8	V	84	0	0	3	0
8	W	87	0	0	0	0
8	X	96	0	0	0	0
8	Y	69	0	0	1	0
8	Z	82	0	0	1	0
8	a	130	0	0	0	0
8	b	143	0	0	0	0
8	c	115	0	0	0	0
8	d	40	0	0	0	0
All	All	57520	52922	52913	407	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 4.

The worst 5 of 407 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)
7:9:202:CYC:HMA1	7:9:202:CYC:HB	1.32	0.94
7:7:201:CYC:HMA1	7:7:201:CYC:HB	1.35	0.92
7:1:201:CYC:HB	7:1:201:CYC:HMA1	1.32	0.91
7:5:202:CYC:HMA1	7:5:202:CYC:HB	1.35	0.90
2:B:77:ARG:NH2	1:C:109:GLU:OE2	2.08	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	0	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
1	2	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
1	4	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
1	6	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
1	8	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
1	A	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
1	C	160/162 (99%)	155 (97%)	5 (3%)	0	100	100
1	E	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
1	G	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
1	I	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
1	K	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
1	M	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
1	O	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
1	Q	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
1	S	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
1	U	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
1	W	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
1	Y	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
2	1	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	3	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	5	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	7	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	9	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	B	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	D	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	F	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	H	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	J	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	L	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	N	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	P	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	R	169/172 (98%)	166 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	T	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	V	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	X	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	Z	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
3	a	192/249 (77%)	186 (97%)	6 (3%)	0	100	100
4	b	287/291 (99%)	282 (98%)	5 (2%)	0	100	100
5	c	260/273 (95%)	259 (100%)	1 (0%)	0	100	100
6	d	72/83 (87%)	71 (99%)	1 (1%)	0	100	100
All	All	6733/6908 (98%)	6628 (98%)	105 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	0	126/126 (100%)	126 (100%)	0	100	100
1	2	126/126 (100%)	125 (99%)	1 (1%)	81	82
1	4	126/126 (100%)	126 (100%)	0	100	100
1	6	126/126 (100%)	124 (98%)	2 (2%)	62	60
1	8	126/126 (100%)	124 (98%)	2 (2%)	62	60
1	A	126/126 (100%)	126 (100%)	0	100	100
1	C	126/126 (100%)	126 (100%)	0	100	100
1	E	126/126 (100%)	124 (98%)	2 (2%)	62	60
1	G	126/126 (100%)	125 (99%)	1 (1%)	81	82
1	I	126/126 (100%)	125 (99%)	1 (1%)	81	82
1	K	126/126 (100%)	126 (100%)	0	100	100
1	M	126/126 (100%)	125 (99%)	1 (1%)	81	82
1	O	126/126 (100%)	125 (99%)	1 (1%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	126/126 (100%)	123 (98%)	3 (2%)	49	43
1	S	126/126 (100%)	126 (100%)	0	100	100
1	U	126/126 (100%)	125 (99%)	1 (1%)	81	82
1	W	126/126 (100%)	126 (100%)	0	100	100
1	Y	126/126 (100%)	125 (99%)	1 (1%)	81	82
2	1	127/127 (100%)	127 (100%)	0	100	100
2	3	127/127 (100%)	127 (100%)	0	100	100
2	5	127/127 (100%)	127 (100%)	0	100	100
2	7	127/127 (100%)	127 (100%)	0	100	100
2	9	127/127 (100%)	127 (100%)	0	100	100
2	B	127/127 (100%)	127 (100%)	0	100	100
2	D	127/127 (100%)	127 (100%)	0	100	100
2	F	127/127 (100%)	126 (99%)	1 (1%)	81	82
2	H	127/127 (100%)	127 (100%)	0	100	100
2	J	127/127 (100%)	127 (100%)	0	100	100
2	L	127/127 (100%)	126 (99%)	1 (1%)	81	82
2	N	127/127 (100%)	127 (100%)	0	100	100
2	P	127/127 (100%)	127 (100%)	0	100	100
2	R	127/127 (100%)	127 (100%)	0	100	100
2	T	127/127 (100%)	126 (99%)	1 (1%)	81	82
2	V	127/127 (100%)	125 (98%)	2 (2%)	62	60
2	X	127/127 (100%)	126 (99%)	1 (1%)	81	82
2	Z	127/127 (100%)	126 (99%)	1 (1%)	81	82
3	a	175/221 (79%)	175 (100%)	0	100	100
4	b	244/246 (99%)	243 (100%)	1 (0%)	91	91
5	c	225/230 (98%)	224 (100%)	1 (0%)	91	91
6	d	63/71 (89%)	63 (100%)	0	100	100
All	All	5261/5322 (99%)	5236 (100%)	25 (0%)	89	89

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	70	GLN

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Mol	Chain	Res	Type
1	U	10	SER
5	c	110	ASP
2	T	65	GLN
2	V	106	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
2	V	132	GLN
5	c	131	ASN
1	W	57	GLN
1	Y	139	ASN
6	d	4	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

18 non-standard protein/DNA/RNA residues 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	MEN	T	72	2	7,8,9	0.18	0	6,9,11	0.55	0
2	MEN	3	72	2	7,8,9	0.18	0	6,9,11	0.44	0
2	MEN	B	72	2	7,8,9	0.18	0	6,9,11	0.62	0
2	MEN	H	72	2	7,8,9	0.21	0	6,9,11	0.77	0
2	MEN	V	72	2	7,8,9	0.19	0	6,9,11	0.76	0
2	MEN	Z	72	2	7,8,9	0.23	0	6,9,11	0.44	0
2	MEN	D	72	2	7,8,9	0.16	0	6,9,11	0.60	0
2	MEN	X	72	2	7,8,9	0.18	0	6,9,11	0.81	0
2	MEN	R	72	2	7,8,9	0.16	0	6,9,11	0.91	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MEN	N	72	2	7,8,9	0.25	0	6,9,11	0.74	0
2	MEN	P	72	2	7,8,9	0.17	0	6,9,11	0.52	0
2	MEN	L	72	2	7,8,9	0.20	0	6,9,11	0.76	0
2	MEN	J	72	2	7,8,9	0.18	0	6,9,11	0.85	0
2	MEN	1	72	2	7,8,9	0.18	0	6,9,11	0.65	0
2	MEN	9	72	2	7,8,9	0.20	0	6,9,11	0.72	0
2	MEN	7	72	2	7,8,9	0.19	0	6,9,11	0.70	0
2	MEN	5	72	2	7,8,9	0.20	0	6,9,11	0.75	0
2	MEN	F	72	2	7,8,9	0.18	0	6,9,11	0.68	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	T	72	2	-	2/7/8/10	-
2	MEN	3	72	2	-	2/7/8/10	-
2	MEN	B	72	2	-	3/7/8/10	-
2	MEN	H	72	2	-	2/7/8/10	-
2	MEN	V	72	2	-	2/7/8/10	-
2	MEN	Z	72	2	-	3/7/8/10	-
2	MEN	D	72	2	-	2/7/8/10	-
2	MEN	X	72	2	-	3/7/8/10	-
2	MEN	R	72	2	-	2/7/8/10	-
2	MEN	N	72	2	-	2/7/8/10	-
2	MEN	P	72	2	-	2/7/8/10	-
2	MEN	L	72	2	-	2/7/8/10	-
2	MEN	J	72	2	-	2/7/8/10	-
2	MEN	1	72	2	-	2/7/8/10	-
2	MEN	9	72	2	-	2/7/8/10	-
2	MEN	7	72	2	-	2/7/8/10	-
2	MEN	5	72	2	-	2/7/8/10	-
2	MEN	F	72	2	-	2/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	72	MEN	O-C-CA-CB
2	X	72	MEN	O-C-CA-CB
2	Z	72	MEN	O-C-CA-CB
2	3	72	MEN	CA-CB-CG-OD1
2	7	72	MEN	CA-CB-CG-OD1

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Z	72	MEN	1	0
2	D	72	MEN	1	0
2	X	72	MEN	1	0
2	F	72	MEN	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

54 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	$\# Z > 2$
7	CYC	F	202	2	42,46,46	0.49	1 (2%)	50,67,67	0.61	1 (2%)
7	CYC	5	202	2	42,46,46	0.51	1 (2%)	50,67,67	1.06	3 (6%)
7	CYC	V	201	2	42,46,46	0.67	1 (2%)	50,67,67	0.72	2 (4%)
7	CYC	H	202	2	42,46,46	0.55	1 (2%)	50,67,67	0.75	2 (4%)
7	CYC	5	201	2	42,46,46	0.61	1 (2%)	50,67,67	0.70	2 (4%)
7	CYC	D	202	2	42,46,46	0.68	1 (2%)	50,67,67	0.67	3 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	CYC	H	201	2	42,46,46	0.47	1 (2%)	50,67,67	0.64	2 (4%)
7	CYC	C	201	1	42,46,46	0.57	1 (2%)	50,67,67	0.66	2 (4%)
7	CYC	R	202	2	42,46,46	0.54	1 (2%)	50,67,67	0.64	2 (4%)
7	CYC	M	201	1	42,46,46	0.60	1 (2%)	50,67,67	0.72	2 (4%)
7	CYC	1	201	2	42,46,46	0.52	1 (2%)	50,67,67	0.97	2 (4%)
7	CYC	9	202	2	42,46,46	0.45	0	50,67,67	0.98	3 (6%)
7	CYC	D	201	2	42,46,46	0.54	1 (2%)	50,67,67	0.73	3 (6%)
7	CYC	I	201	1	42,46,46	0.52	1 (2%)	50,67,67	0.64	2 (4%)
7	CYC	8	201	1	42,46,46	0.53	1 (2%)	50,67,67	0.73	2 (4%)
7	CYC	Z	202	2	42,46,46	0.37	0	50,67,67	0.68	2 (4%)
7	CYC	Q	201	1	42,46,46	0.51	1 (2%)	50,67,67	0.72	2 (4%)
7	CYC	L	202	2	42,46,46	0.49	1 (2%)	50,67,67	0.58	2 (4%)
7	CYC	9	201	2	42,46,46	0.69	1 (2%)	50,67,67	0.74	2 (4%)
7	CYC	F	201	2	42,46,46	0.60	1 (2%)	50,67,67	0.75	3 (6%)
7	CYC	A	201	1	42,46,46	0.71	1 (2%)	50,67,67	0.66	2 (4%)
7	CYC	3	201	2	42,46,46	0.71	1 (2%)	50,67,67	0.71	3 (6%)
7	CYC	L	201	2	42,46,46	0.74	1 (2%)	50,67,67	0.78	3 (6%)
7	CYC	S	201	1	42,46,46	0.51	0	50,67,67	0.68	2 (4%)
7	CYC	0	201	1	42,46,46	0.48	0	50,67,67	0.71	2 (4%)
7	CYC	Z	201	2	42,46,46	0.59	1 (2%)	50,67,67	0.74	2 (4%)
7	CYC	T	202	2	42,46,46	0.41	0	50,67,67	0.74	3 (6%)
7	CYC	K	201	1	42,46,46	0.56	1 (2%)	50,67,67	0.65	2 (4%)
7	CYC	U	201	1	42,46,46	0.45	0	50,67,67	0.66	2 (4%)
7	CYC	V	202	2	42,46,46	0.55	1 (2%)	50,67,67	0.64	1 (2%)
7	CYC	W	201	1	42,46,46	0.54	1 (2%)	50,67,67	0.66	2 (4%)
7	CYC	J	201	2	42,46,46	0.61	1 (2%)	50,67,67	0.74	3 (6%)
7	CYC	J	202	2	42,46,46	0.53	1 (2%)	50,67,67	0.64	2 (4%)
7	CYC	P	202	2	42,46,46	0.51	1 (2%)	50,67,67	0.69	2 (4%)
7	CYC	P	201	2	42,46,46	0.68	1 (2%)	50,67,67	0.67	2 (4%)
7	CYC	2	201	1	42,46,46	0.50	1 (2%)	50,67,67	0.64	2 (4%)
7	CYC	T	201	2	42,46,46	0.62	1 (2%)	50,67,67	0.75	2 (4%)
7	CYC	N	201	2	42,46,46	0.51	1 (2%)	50,67,67	0.63	2 (4%)
7	CYC	B	202	2	42,46,46	0.73	1 (2%)	50,67,67	0.75	4 (8%)
7	CYC	7	202	2	42,46,46	0.58	1 (2%)	50,67,67	0.74	3 (6%)
7	CYC	X	201	2	42,46,46	0.69	1 (2%)	50,67,67	0.79	3 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	CYC	6	201	1	42,46,46	0.65	1 (2%)	50,67,67	0.64	2 (4%)
7	CYC	7	201	2	42,46,46	0.59	1 (2%)	50,67,67	0.93	3 (6%)
7	CYC	N	202	2	42,46,46	0.46	0	50,67,67	0.72	2 (4%)
7	CYC	Y	201	1	42,46,46	0.69	1 (2%)	50,67,67	0.65	2 (4%)
7	CYC	B	201	2	42,46,46	0.55	1 (2%)	50,67,67	0.60	1 (2%)
7	CYC	3	202	2	42,46,46	0.51	1 (2%)	50,67,67	0.60	2 (4%)
7	CYC	R	201	2	42,46,46	0.73	1 (2%)	50,67,67	0.79	3 (6%)
7	CYC	X	202	2	42,46,46	0.42	0	50,67,67	0.90	3 (6%)
7	CYC	E	201	1	42,46,46	0.59	1 (2%)	50,67,67	0.62	2 (4%)
7	CYC	4	201	1	42,46,46	0.65	1 (2%)	50,67,67	0.70	2 (4%)
7	CYC	G	201	1	42,46,46	0.61	1 (2%)	50,67,67	0.68	2 (4%)
7	CYC	1	202	2	42,46,46	0.57	1 (2%)	50,67,67	0.78	3 (6%)
7	CYC	O	201	1	42,46,46	0.52	1 (2%)	50,67,67	0.68	2 (4%)

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
7	CYC	F	202	2	-	7/25/74/74	0/4/4/4
7	CYC	5	202	2	-	7/25/74/74	0/4/4/4
7	CYC	V	201	2	-	8/25/74/74	0/4/4/4
7	CYC	H	202	2	-	4/25/74/74	0/4/4/4
7	CYC	5	201	2	-	4/25/74/74	0/4/4/4
7	CYC	D	202	2	-	6/25/74/74	0/4/4/4
7	CYC	H	201	2	-	8/25/74/74	0/4/4/4
7	CYC	C	201	1	-	11/25/74/74	0/4/4/4
7	CYC	R	202	2	-	7/25/74/74	0/4/4/4
7	CYC	M	201	1	-	11/25/74/74	0/4/4/4
7	CYC	1	201	2	-	6/25/74/74	0/4/4/4
7	CYC	9	202	2	-	3/25/74/74	0/4/4/4
7	CYC	D	201	2	-	8/25/74/74	0/4/4/4
7	CYC	I	201	1	-	11/25/74/74	0/4/4/4
7	CYC	8	201	1	-	10/25/74/74	0/4/4/4
7	CYC	Z	202	2	-	8/25/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	CYC	Q	201	1	-	9/25/74/74	0/4/4/4
7	CYC	L	202	2	-	7/25/74/74	0/4/4/4
7	CYC	9	201	2	-	6/25/74/74	0/4/4/4
7	CYC	F	201	2	-	5/25/74/74	0/4/4/4
7	CYC	A	201	1	-	11/25/74/74	0/4/4/4
7	CYC	3	201	2	-	7/25/74/74	0/4/4/4
7	CYC	L	201	2	-	7/25/74/74	0/4/4/4
7	CYC	S	201	1	-	11/25/74/74	0/4/4/4
7	CYC	0	201	1	-	11/25/74/74	0/4/4/4
7	CYC	Z	201	2	-	6/25/74/74	0/4/4/4
7	CYC	T	202	2	-	11/25/74/74	0/4/4/4
7	CYC	K	201	1	-	11/25/74/74	0/4/4/4
7	CYC	U	201	1	-	9/25/74/74	0/4/4/4
7	CYC	V	202	2	-	10/25/74/74	0/4/4/4
7	CYC	W	201	1	-	11/25/74/74	0/4/4/4
7	CYC	J	201	2	-	6/25/74/74	0/4/4/4
7	CYC	J	202	2	-	7/25/74/74	0/4/4/4
7	CYC	P	202	2	-	4/25/74/74	0/4/4/4
7	CYC	P	201	2	-	8/25/74/74	0/4/4/4
7	CYC	2	201	1	-	9/25/74/74	0/4/4/4
7	CYC	T	201	2	-	6/25/74/74	0/4/4/4
7	CYC	N	201	2	-	8/25/74/74	0/4/4/4
7	CYC	B	202	2	-	6/25/74/74	0/4/4/4
7	CYC	7	202	2	-	8/25/74/74	0/4/4/4
7	CYC	X	201	2	-	8/25/74/74	0/4/4/4
7	CYC	6	201	1	-	11/25/74/74	0/4/4/4
7	CYC	7	201	2	-	5/25/74/74	0/4/4/4
7	CYC	N	202	2	-	4/25/74/74	0/4/4/4
7	CYC	Y	201	1	-	8/25/74/74	0/4/4/4
7	CYC	B	201	2	-	8/25/74/74	0/4/4/4
7	CYC	3	202	2	-	4/25/74/74	0/4/4/4
7	CYC	R	201	2	-	6/25/74/74	0/4/4/4
7	CYC	X	202	2	-	8/25/74/74	0/4/4/4
7	CYC	E	201	1	-	11/25/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	CYC	4	201	1	-	9/25/74/74	0/4/4/4
7	CYC	G	201	1	-	10/25/74/74	0/4/4/4
7	CYC	1	202	2	-	6/25/74/74	0/4/4/4
7	CYC	O	201	1	-	11/25/74/74	0/4/4/4

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	L	201	CYC	CHA-C1A	4.18	1.38	1.35
7	B	202	CYC	CHA-C1A	4.16	1.38	1.35
7	3	201	CYC	CHA-C1A	4.14	1.38	1.35
7	R	201	CYC	CHA-C1A	4.07	1.38	1.35
7	A	201	CYC	CHA-C1A	3.81	1.38	1.35

The worst 5 of 122 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	1	201	CYC	C1B-CHB-C4A	4.76	139.72	128.08
7	5	202	CYC	C1B-CHB-C4A	4.60	139.32	128.08
7	9	202	CYC	C1B-CHB-C4A	4.34	138.69	128.08
7	7	201	CYC	C1B-CHB-C4A	4.32	138.65	128.08
7	X	202	CYC	C1B-CHB-C4A	3.98	137.80	128.08

There are no chirality outliers.

5 of 422 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	0	201	CYC	NA-C4A-CHB-C1B
7	0	201	CYC	C3A-C4A-CHB-C1B
7	0	201	CYC	C4C-C3C-CAC-CBC
7	0	201	CYC	ND-C1D-CHD-C4C
7	0	201	CYC	C2D-C1D-CHD-C4C

There are no ring outliers.

54 monomers are involved in 224 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	F	202	CYC	4	0
7	5	202	CYC	4	0
7	V	201	CYC	6	0

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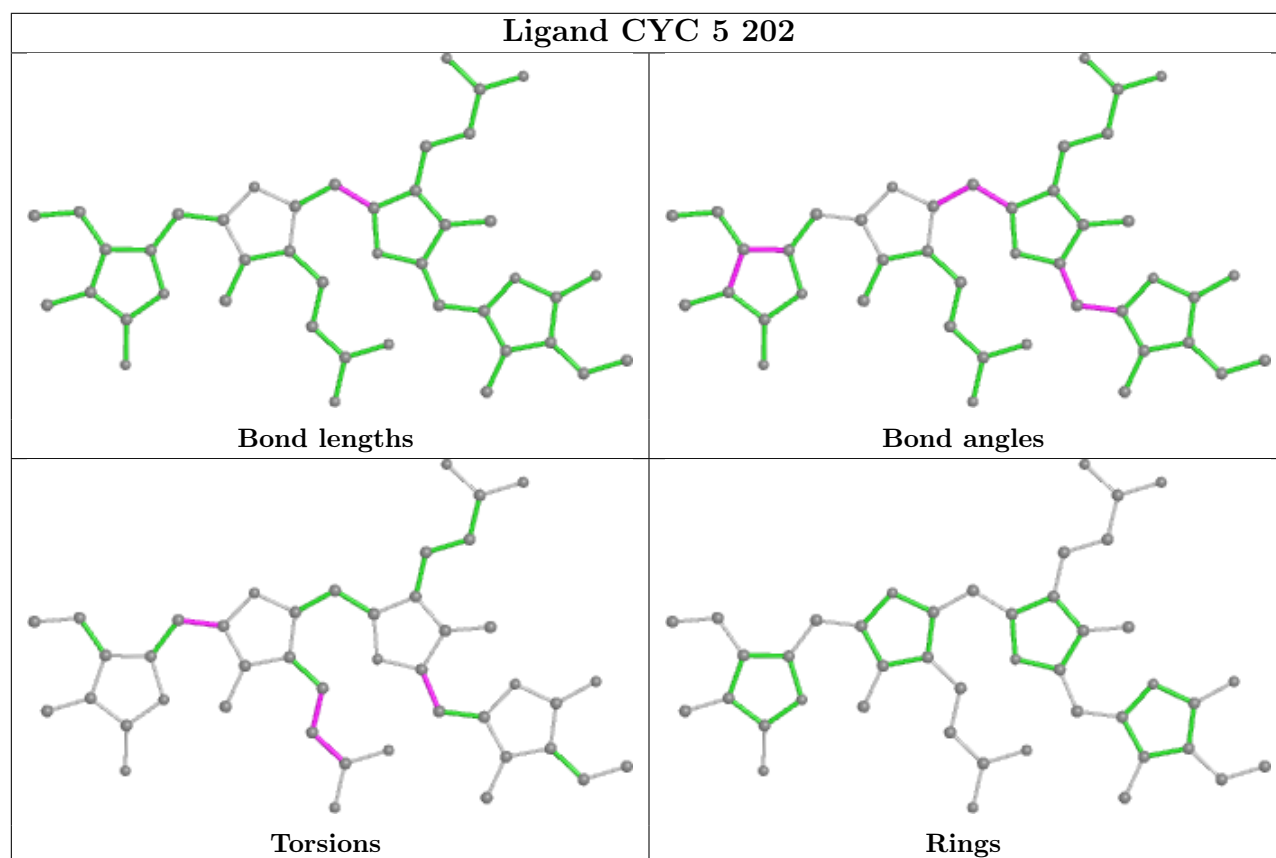
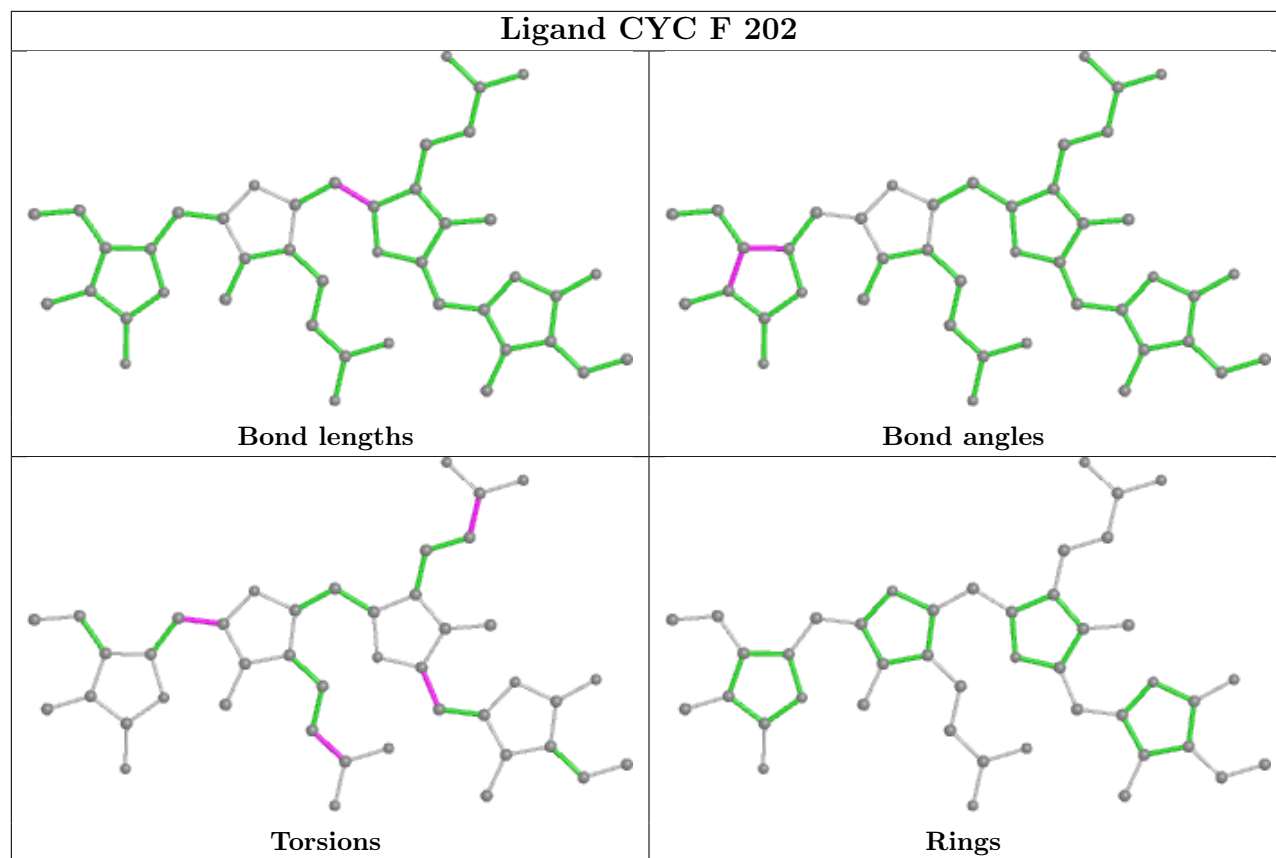
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	202	CYC	5	0
7	5	201	CYC	5	0
7	D	202	CYC	3	0
7	H	201	CYC	2	0
7	C	201	CYC	3	0
7	R	202	CYC	4	0
7	M	201	CYC	2	0
7	1	201	CYC	5	0
7	9	202	CYC	3	0
7	D	201	CYC	7	0
7	I	201	CYC	4	0
7	8	201	CYC	3	0
7	Z	202	CYC	3	0
7	Q	201	CYC	4	0
7	L	202	CYC	2	0
7	9	201	CYC	6	0
7	F	201	CYC	6	0
7	A	201	CYC	2	0
7	3	201	CYC	7	0
7	L	201	CYC	4	0
7	S	201	CYC	4	0
7	0	201	CYC	3	0
7	Z	201	CYC	5	0
7	T	202	CYC	5	0
7	K	201	CYC	3	0
7	U	201	CYC	4	0
7	V	202	CYC	4	0
7	W	201	CYC	3	0
7	J	201	CYC	4	0
7	J	202	CYC	4	0
7	P	202	CYC	5	0
7	P	201	CYC	4	0
7	2	201	CYC	5	0
7	T	201	CYC	5	0
7	N	201	CYC	3	0
7	B	202	CYC	6	0
7	7	202	CYC	5	0
7	X	201	CYC	5	0
7	6	201	CYC	3	0
7	7	201	CYC	3	0
7	N	202	CYC	8	0
7	Y	201	CYC	4	0

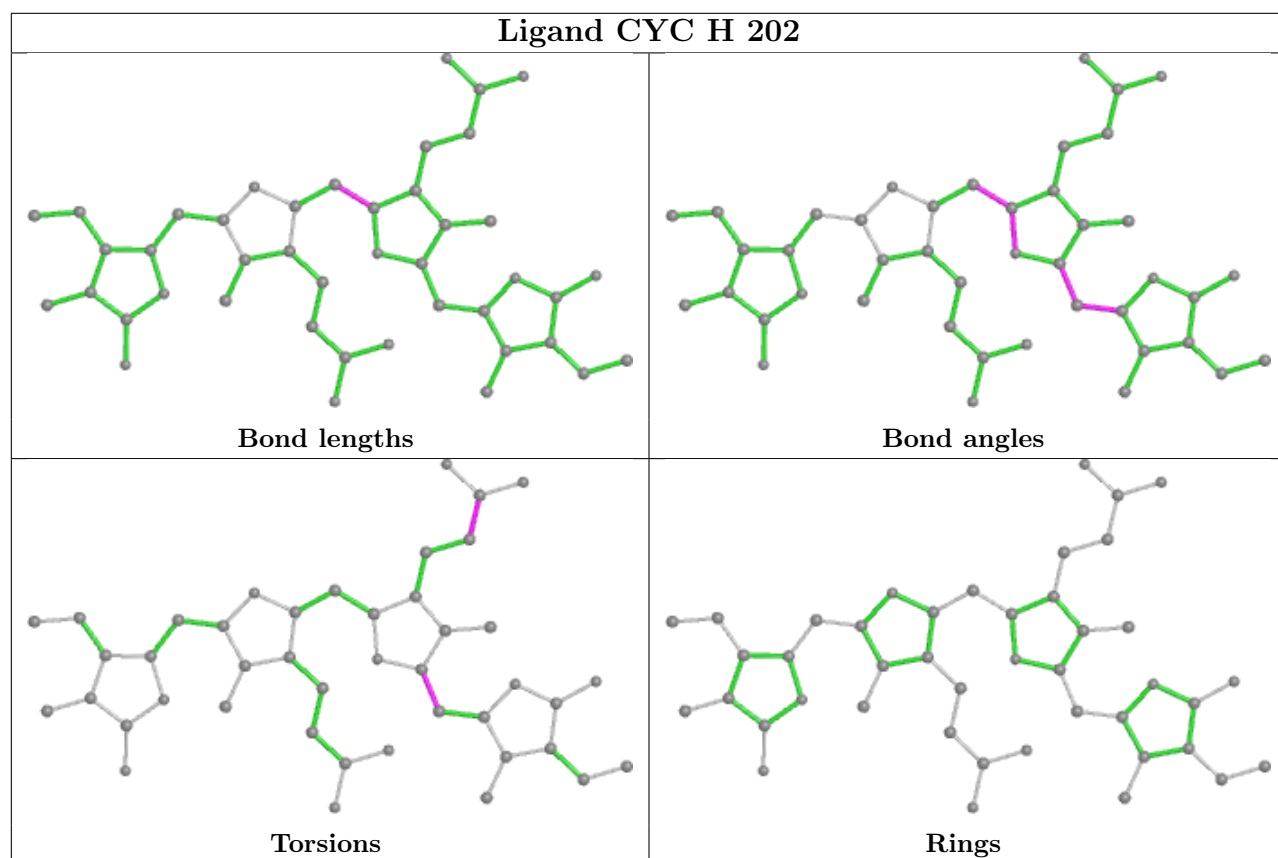
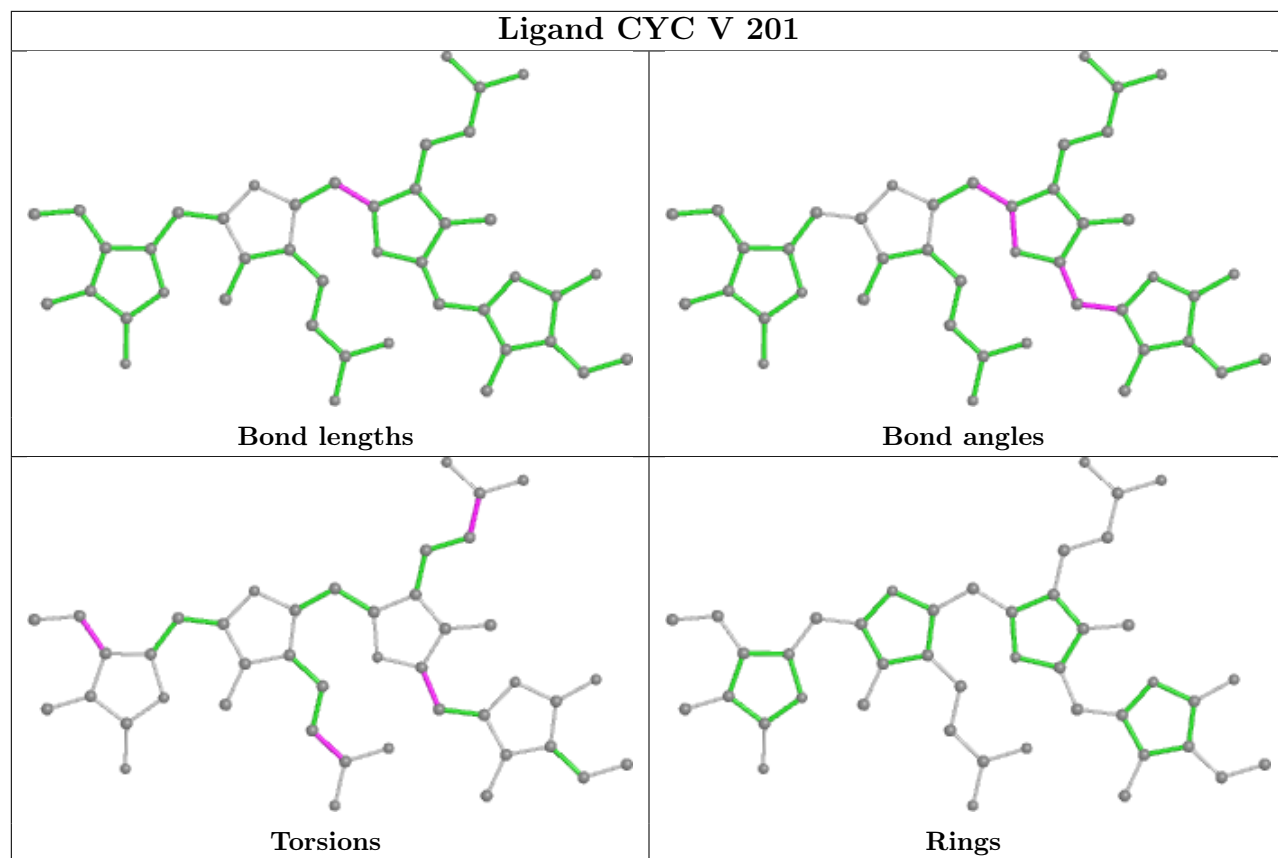
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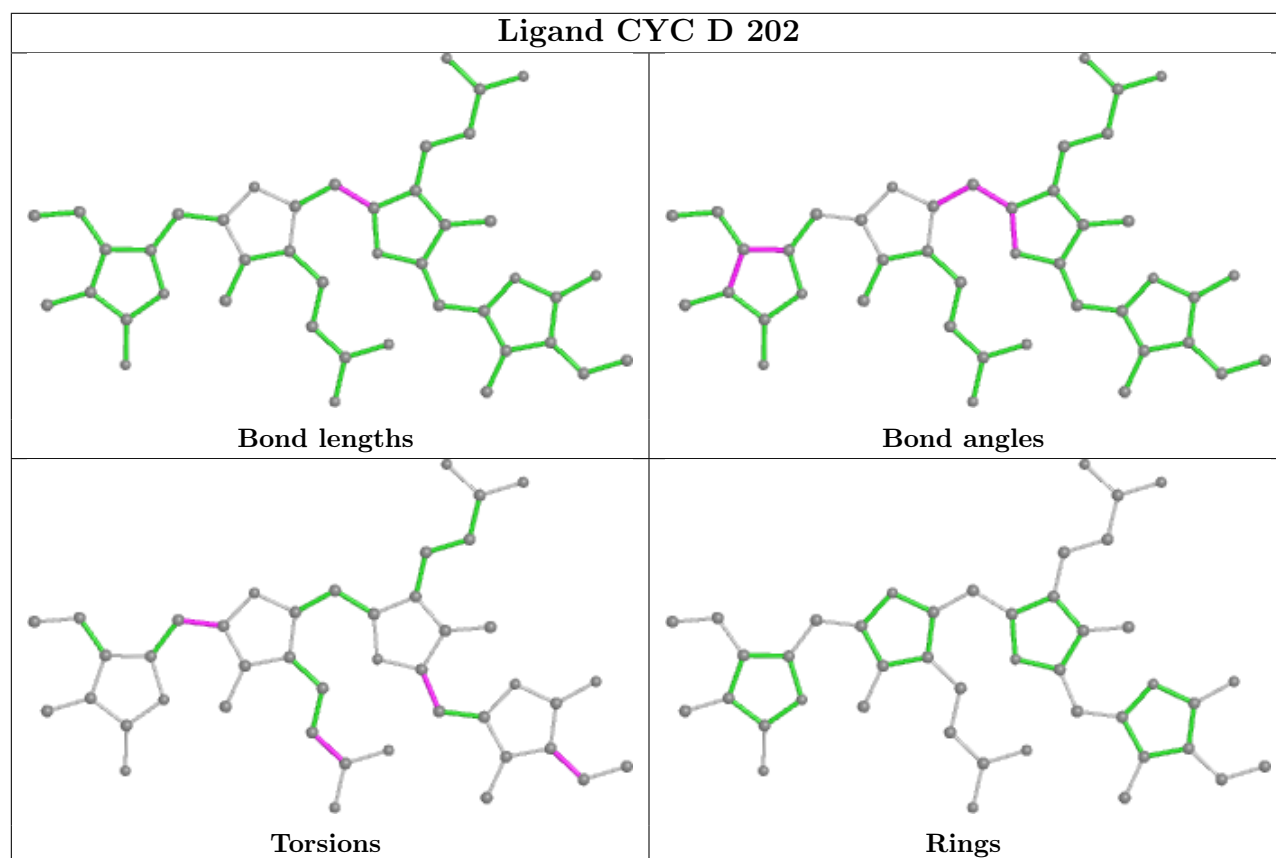
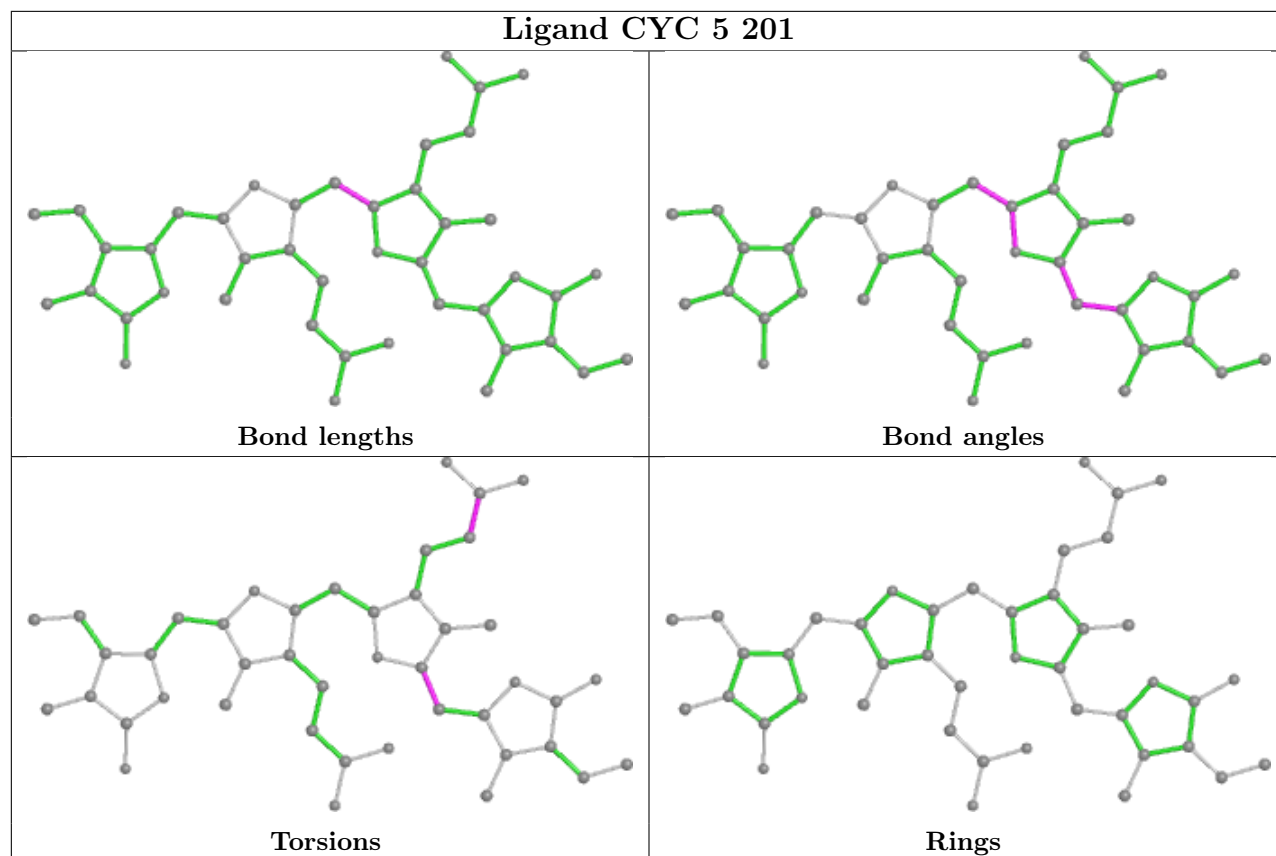
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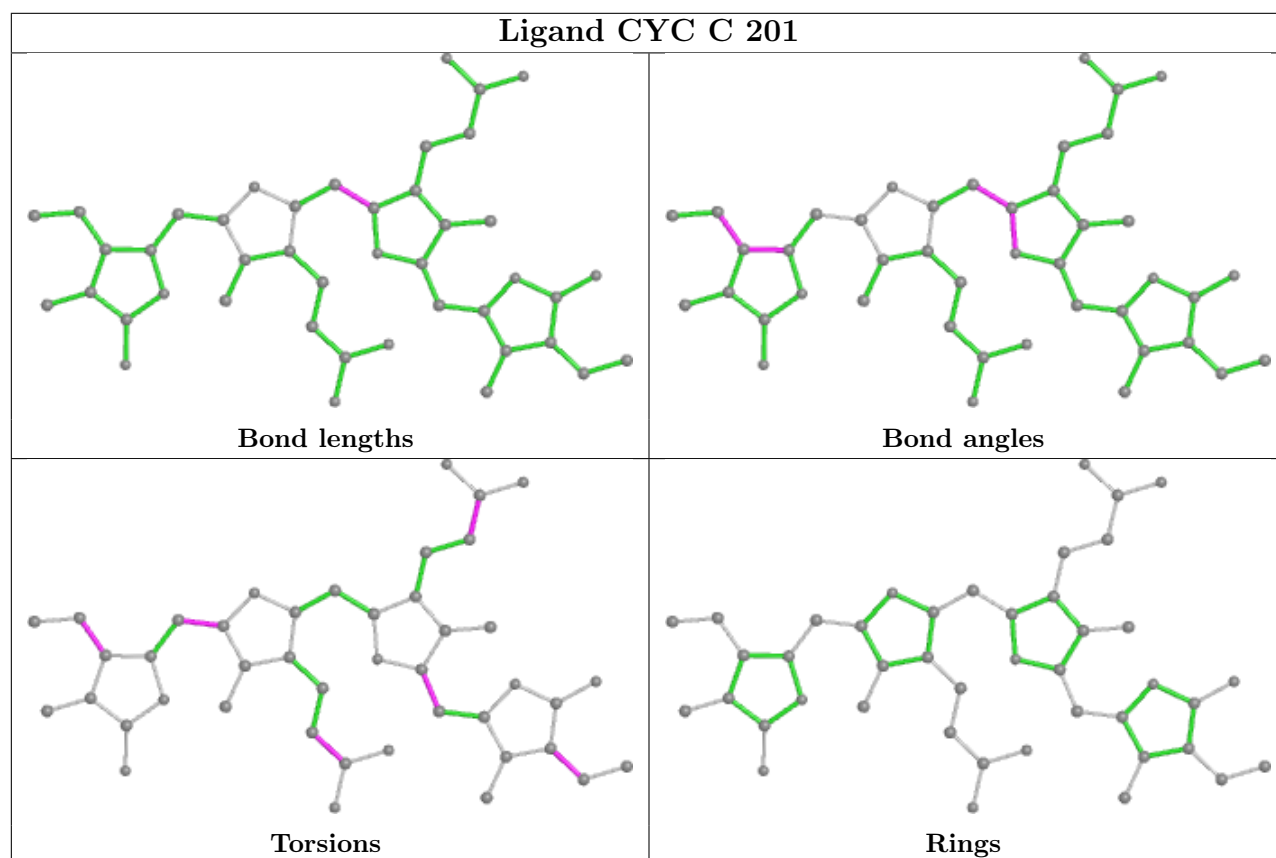
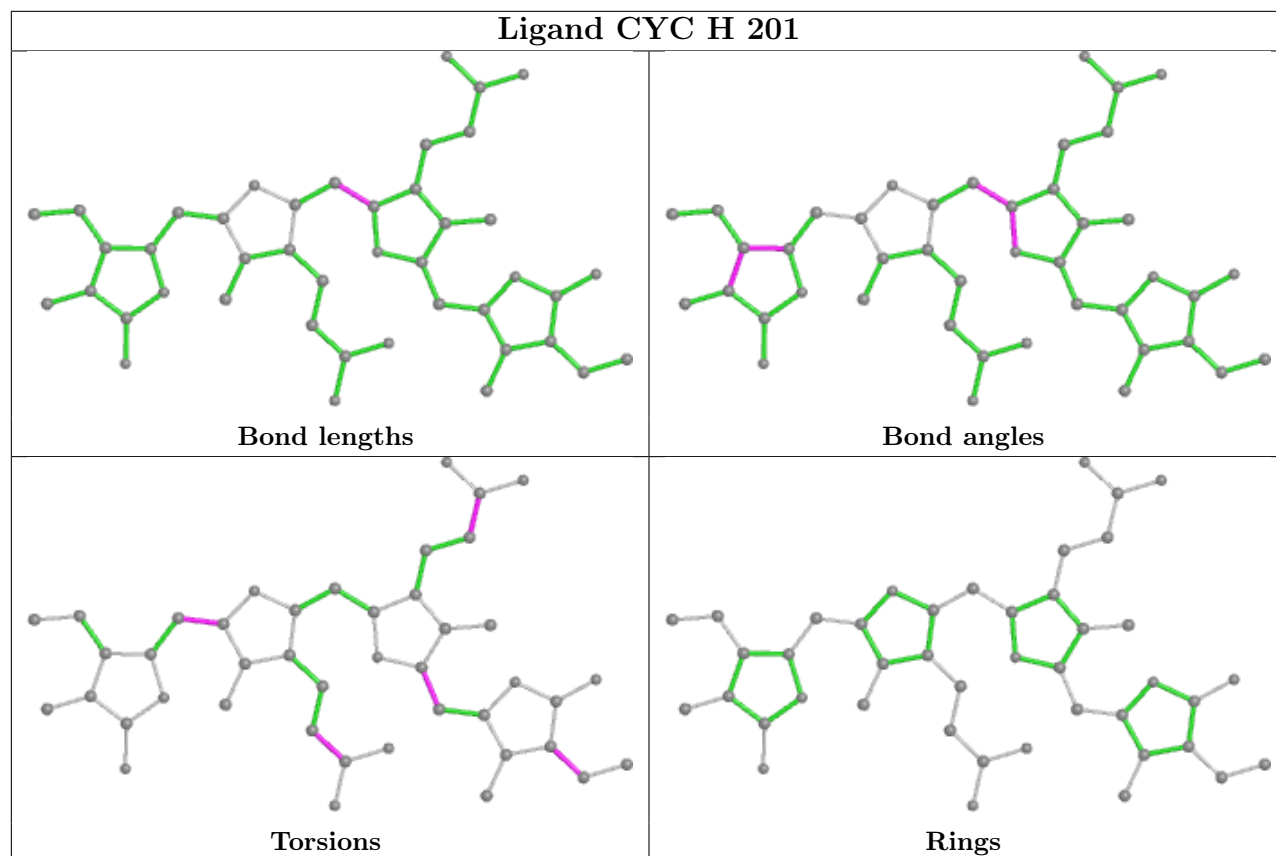
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	201	CYC	3	0
7	3	202	CYC	2	0
7	R	201	CYC	6	0
7	X	202	CYC	6	0
7	E	201	CYC	3	0
7	4	201	CYC	2	0
7	G	201	CYC	3	0
7	1	202	CYC	6	0
7	O	201	CYC	4	0

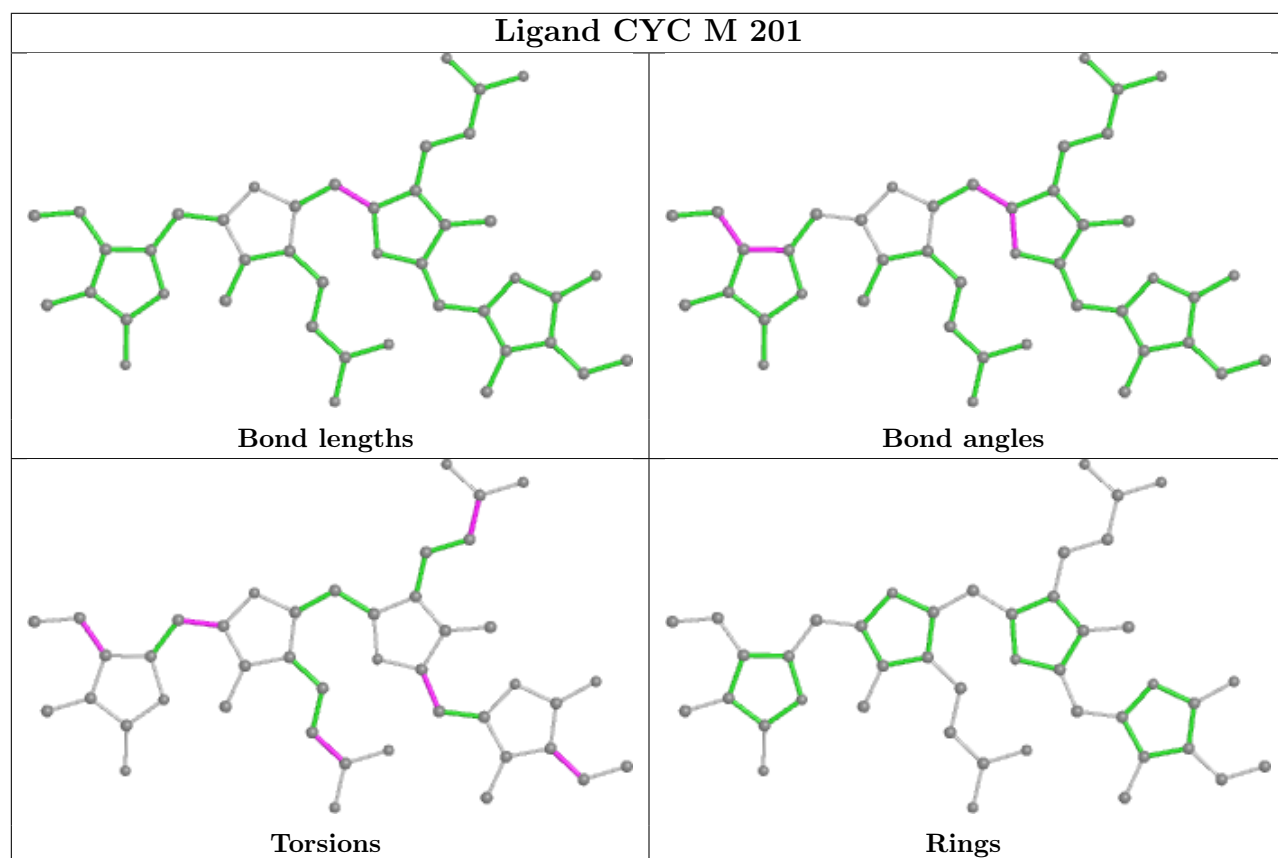
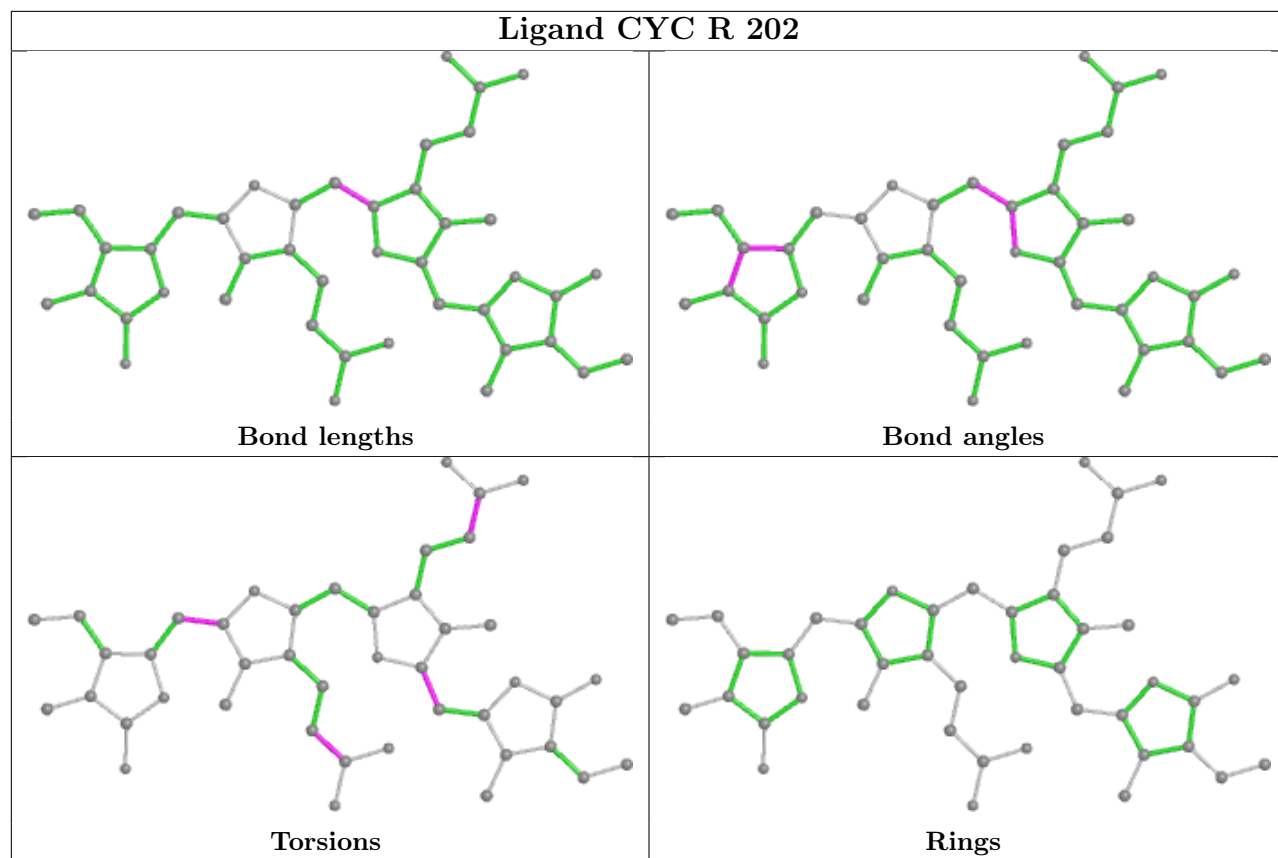
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

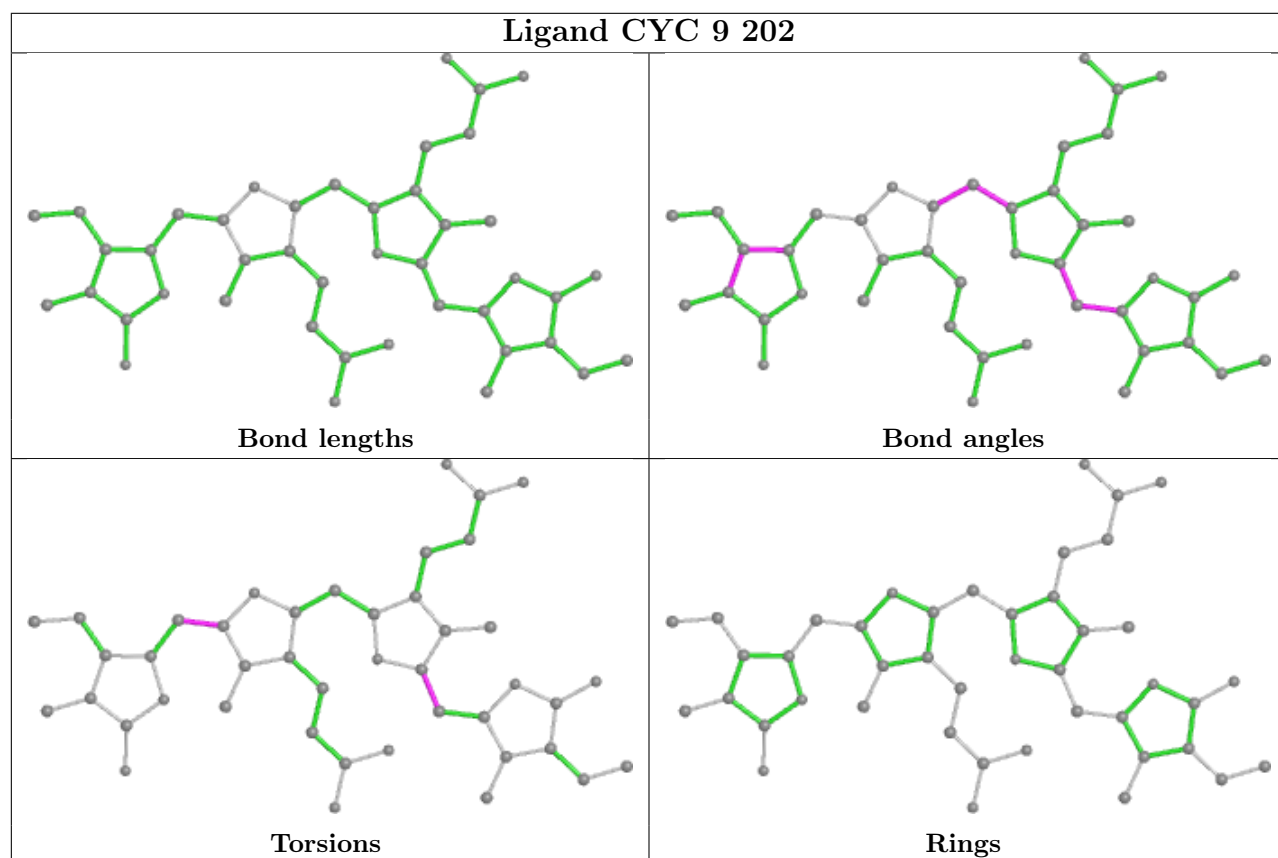
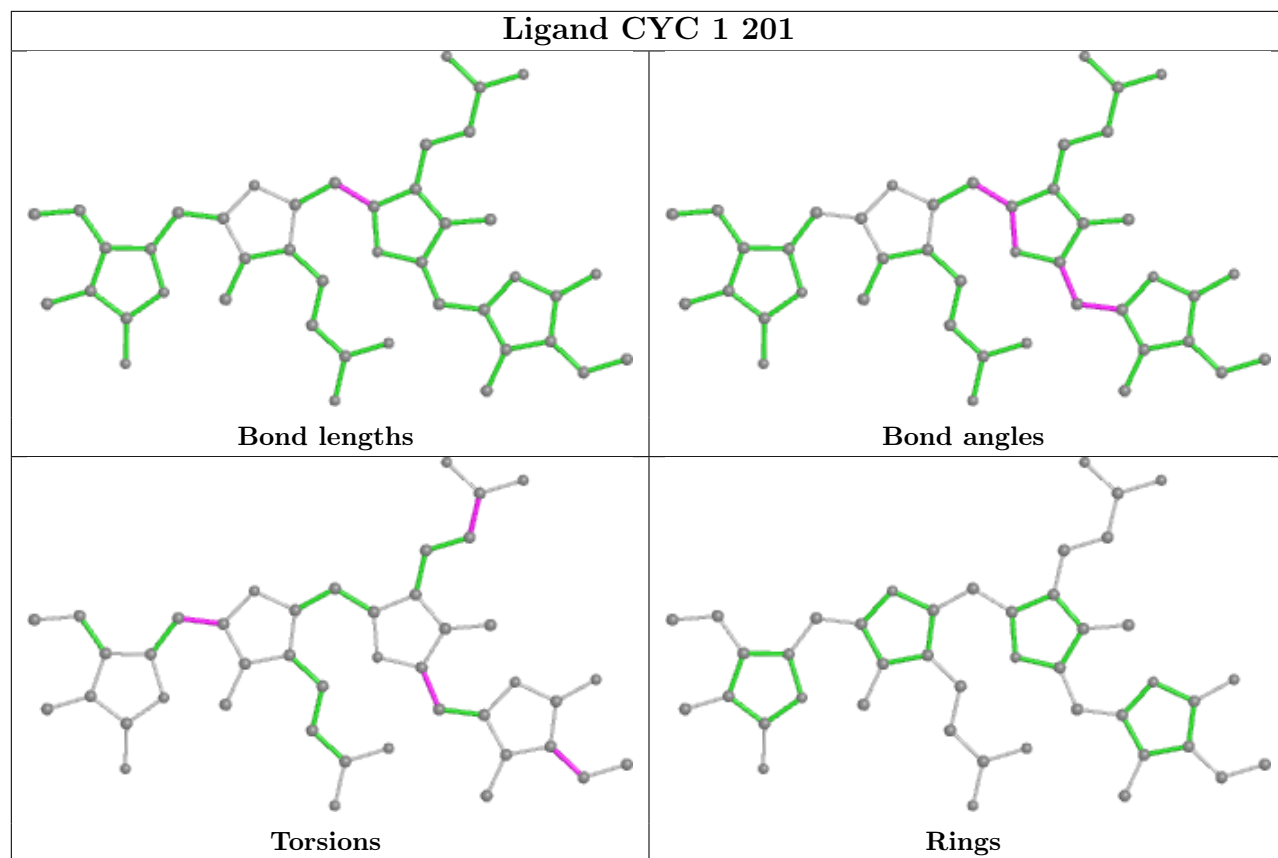


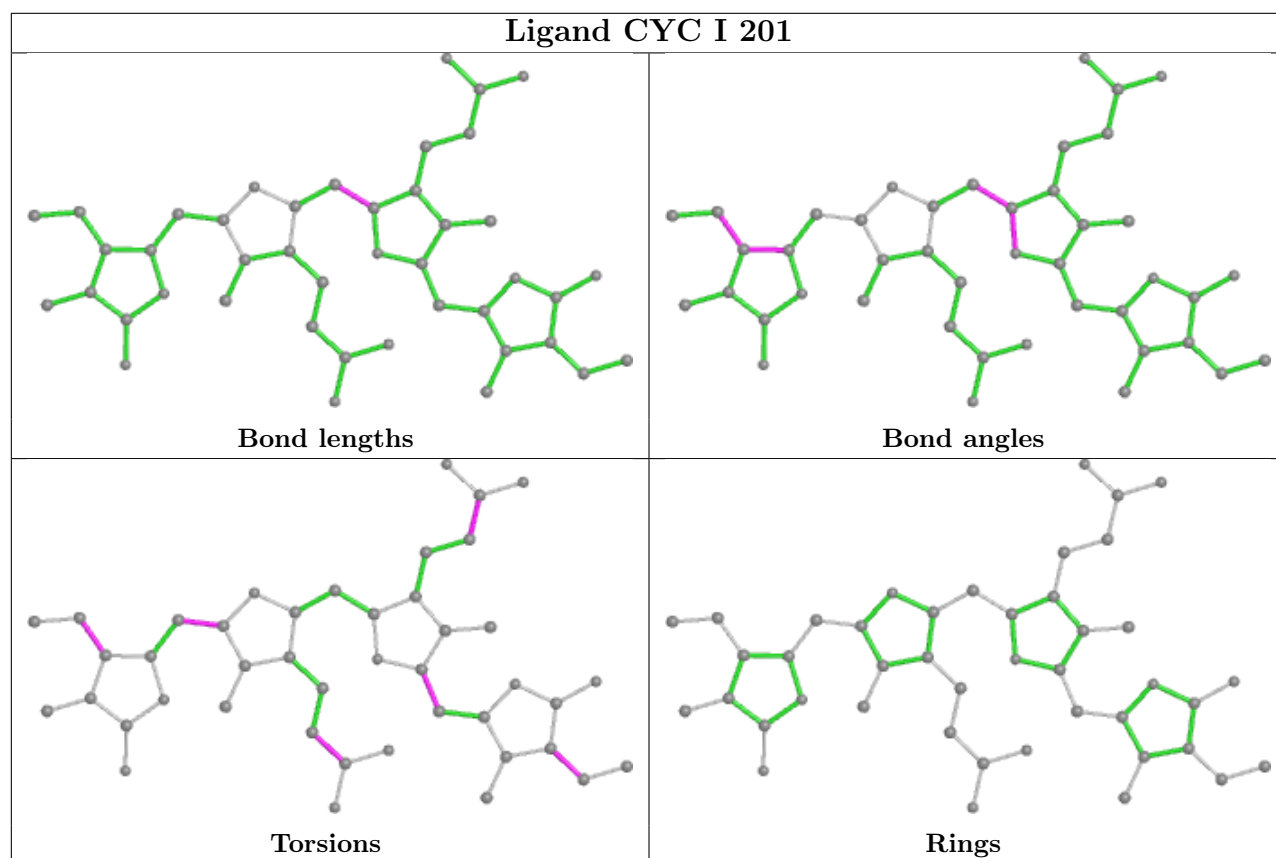
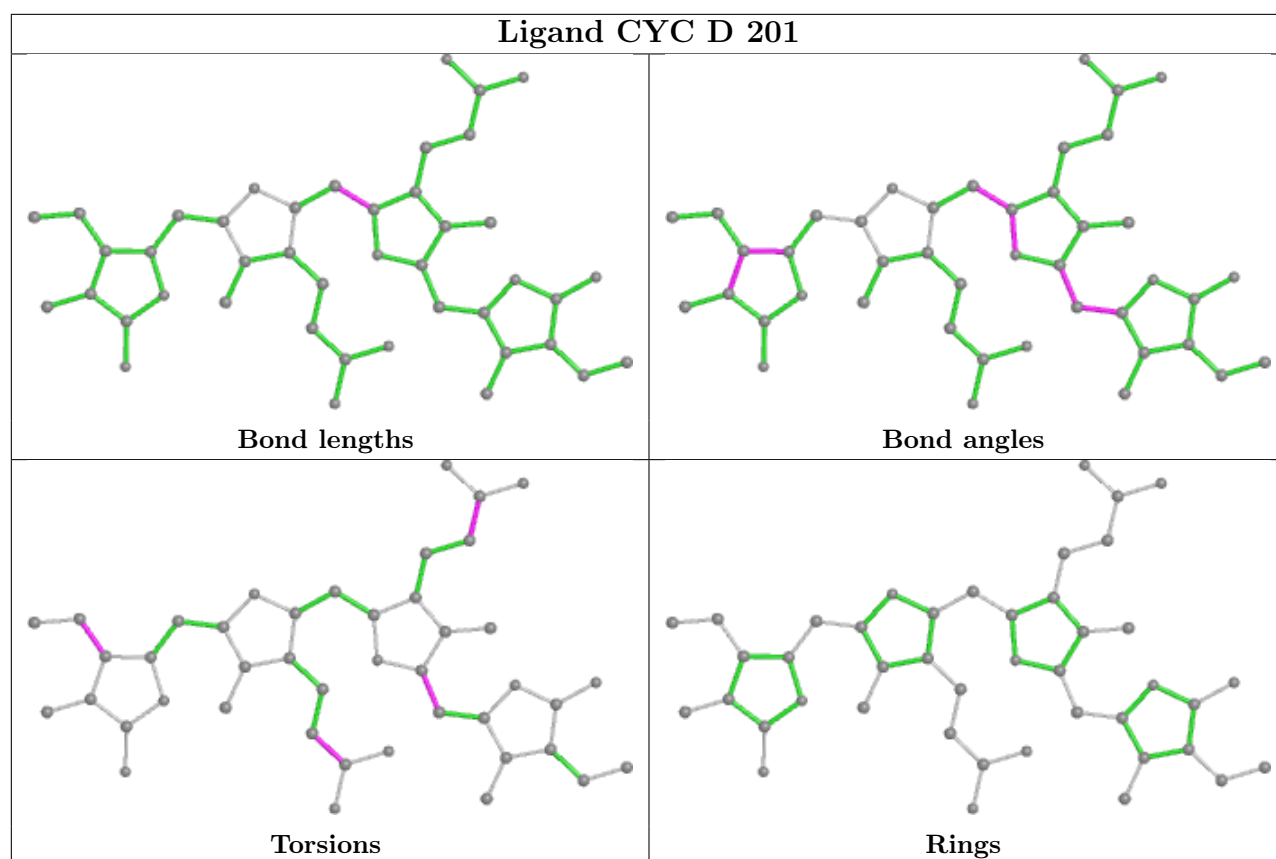


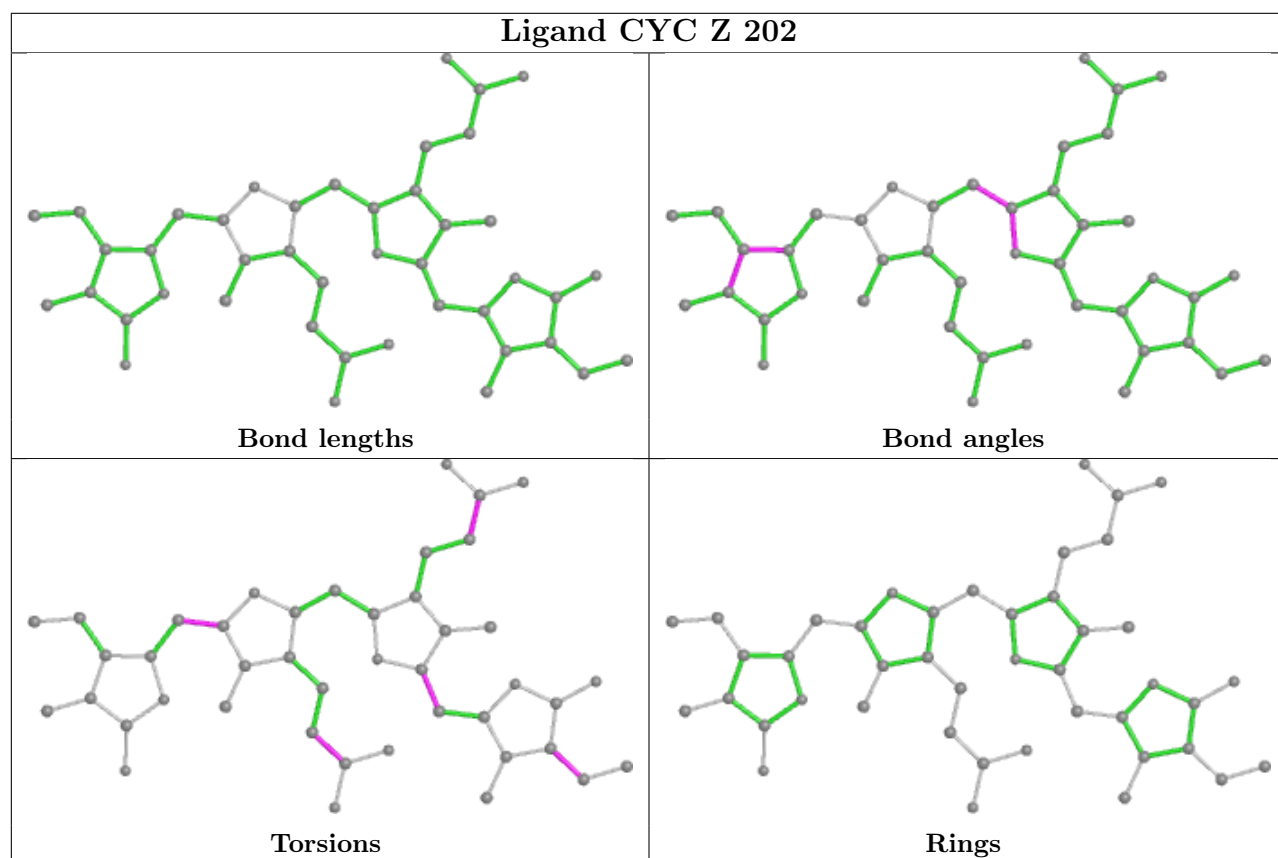
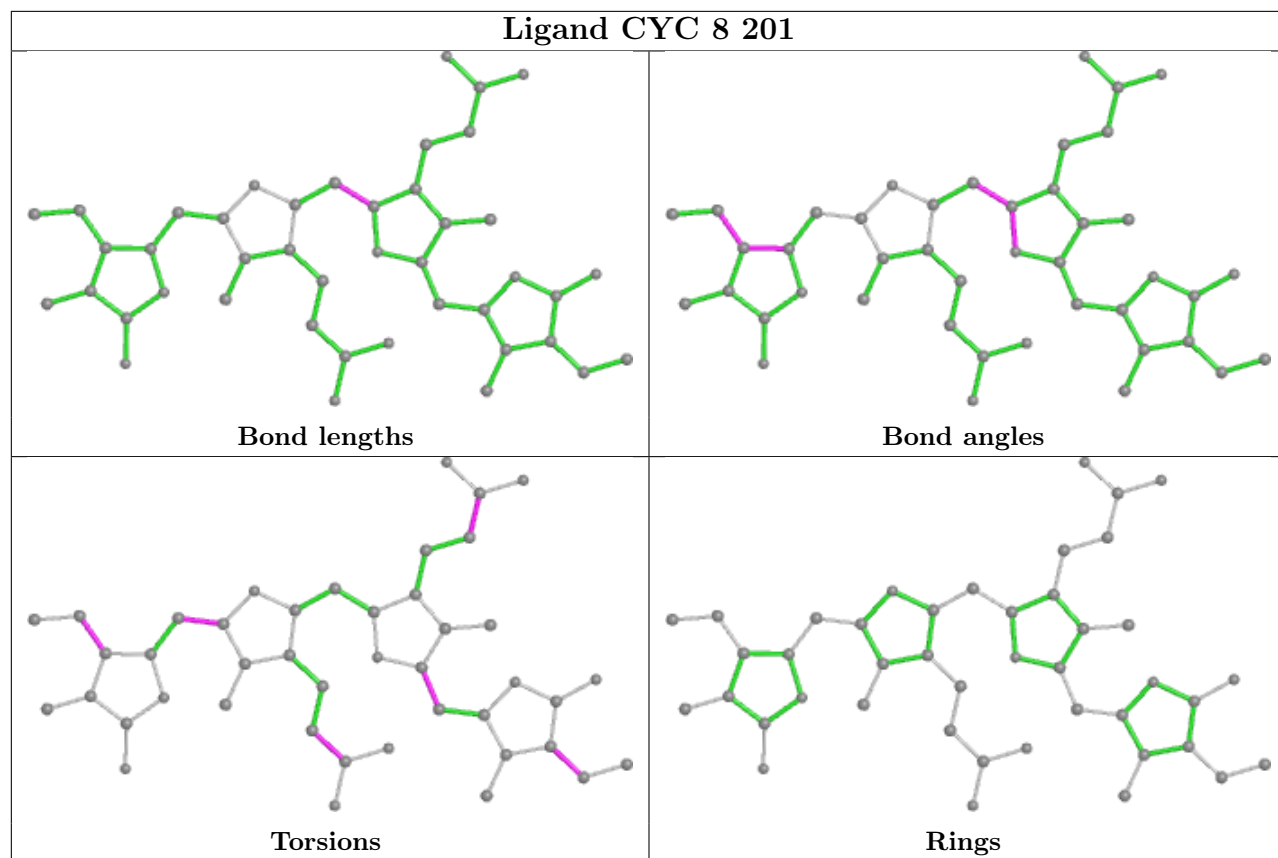


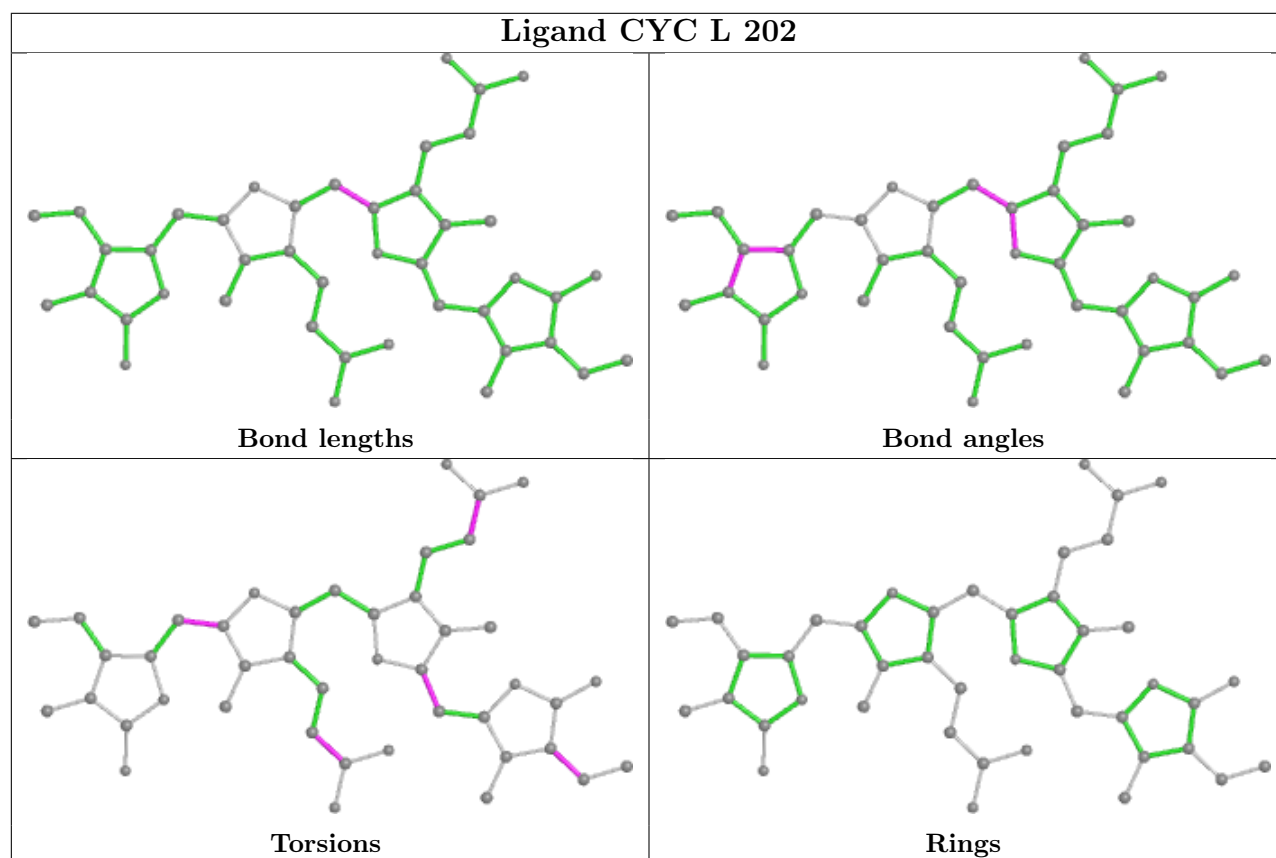
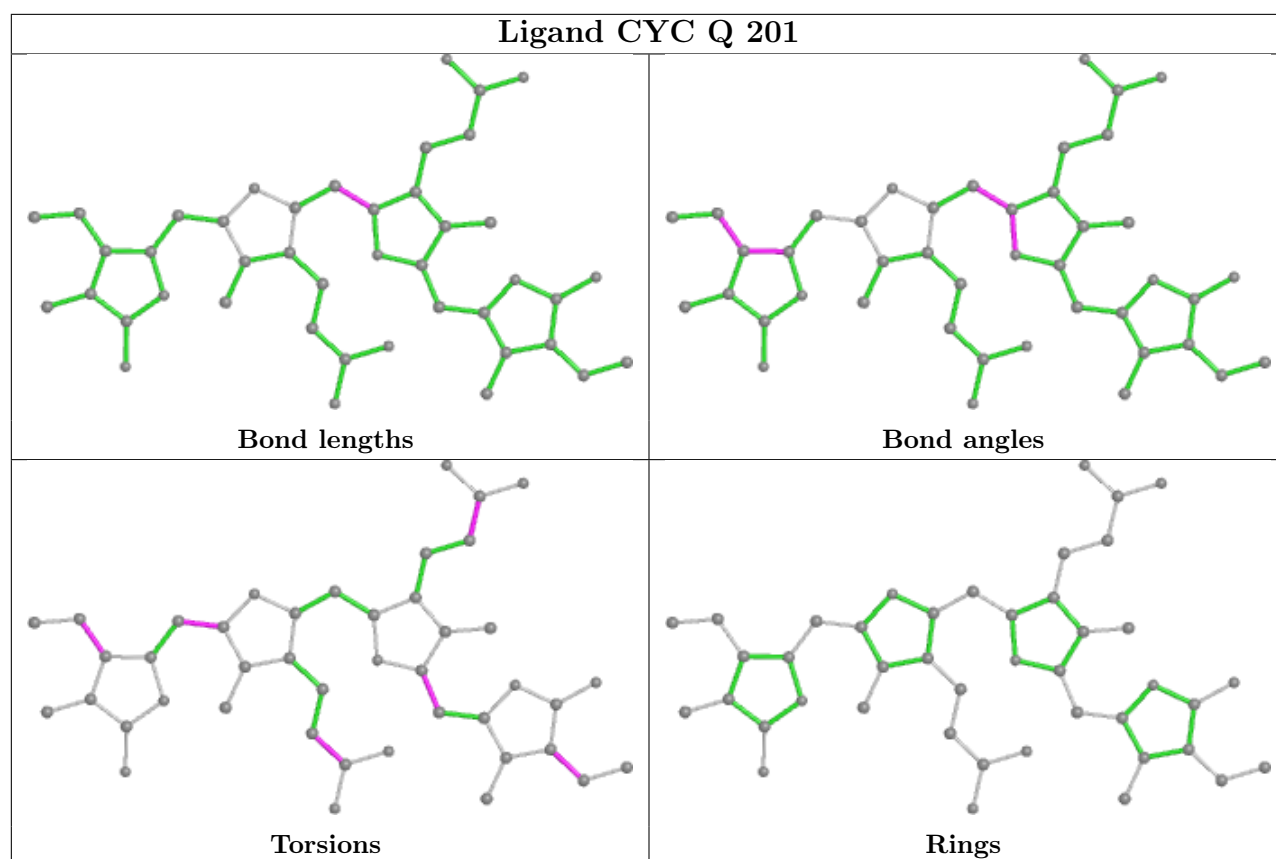


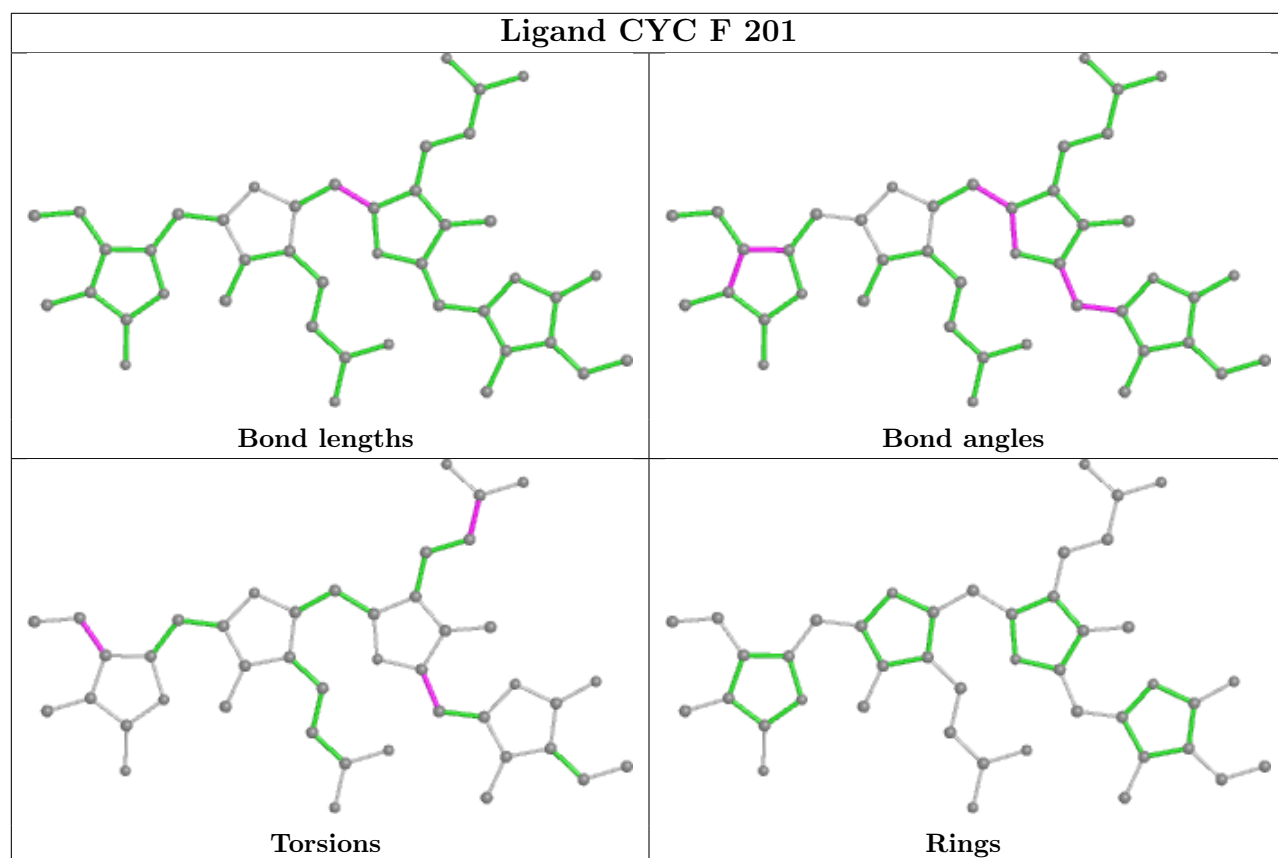
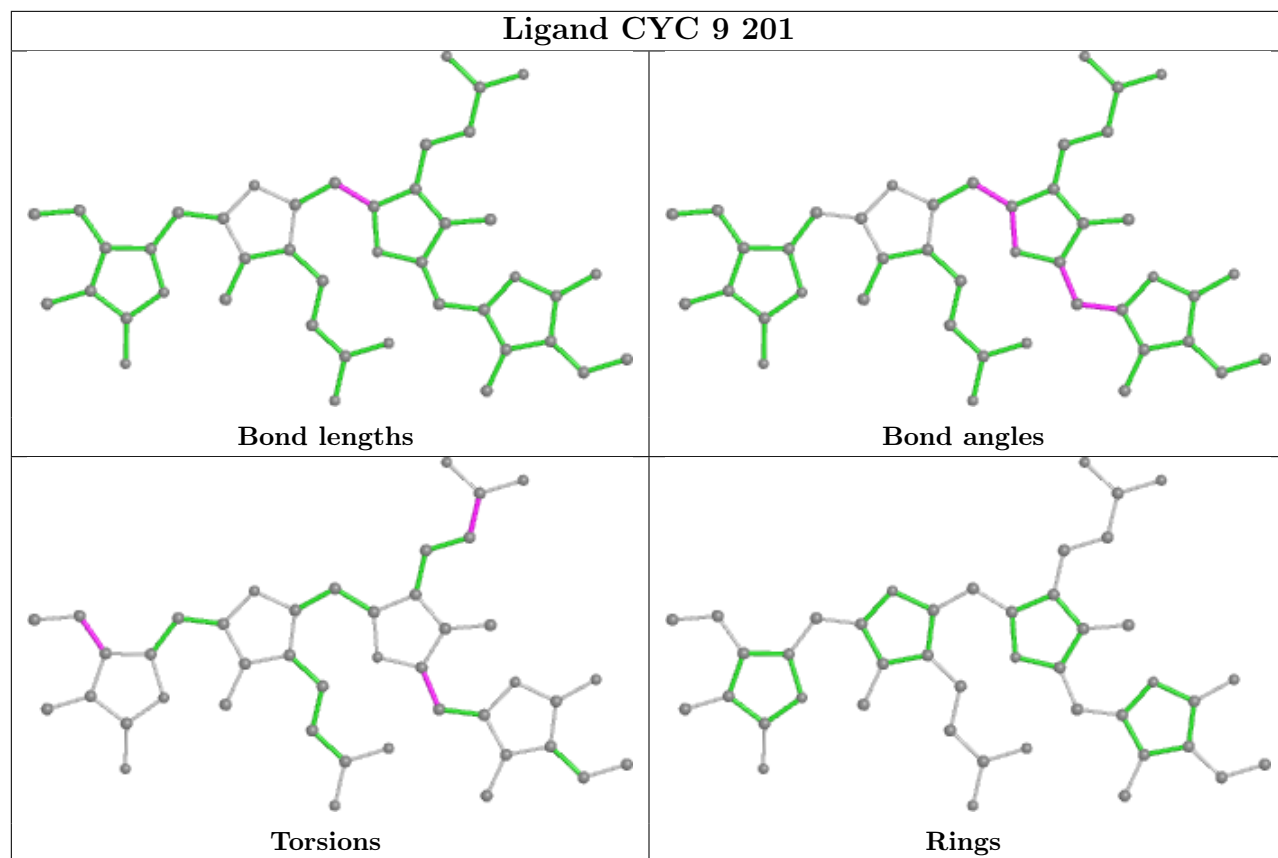


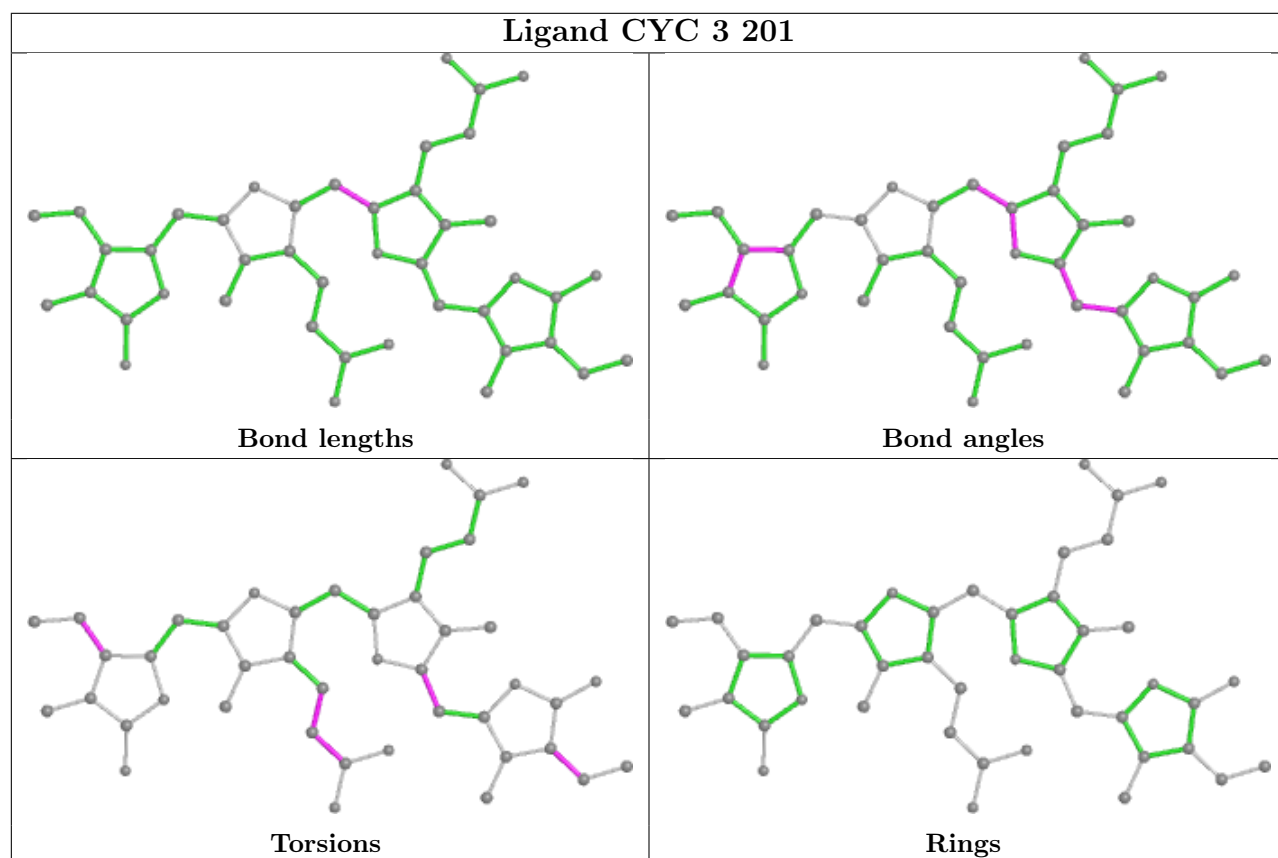
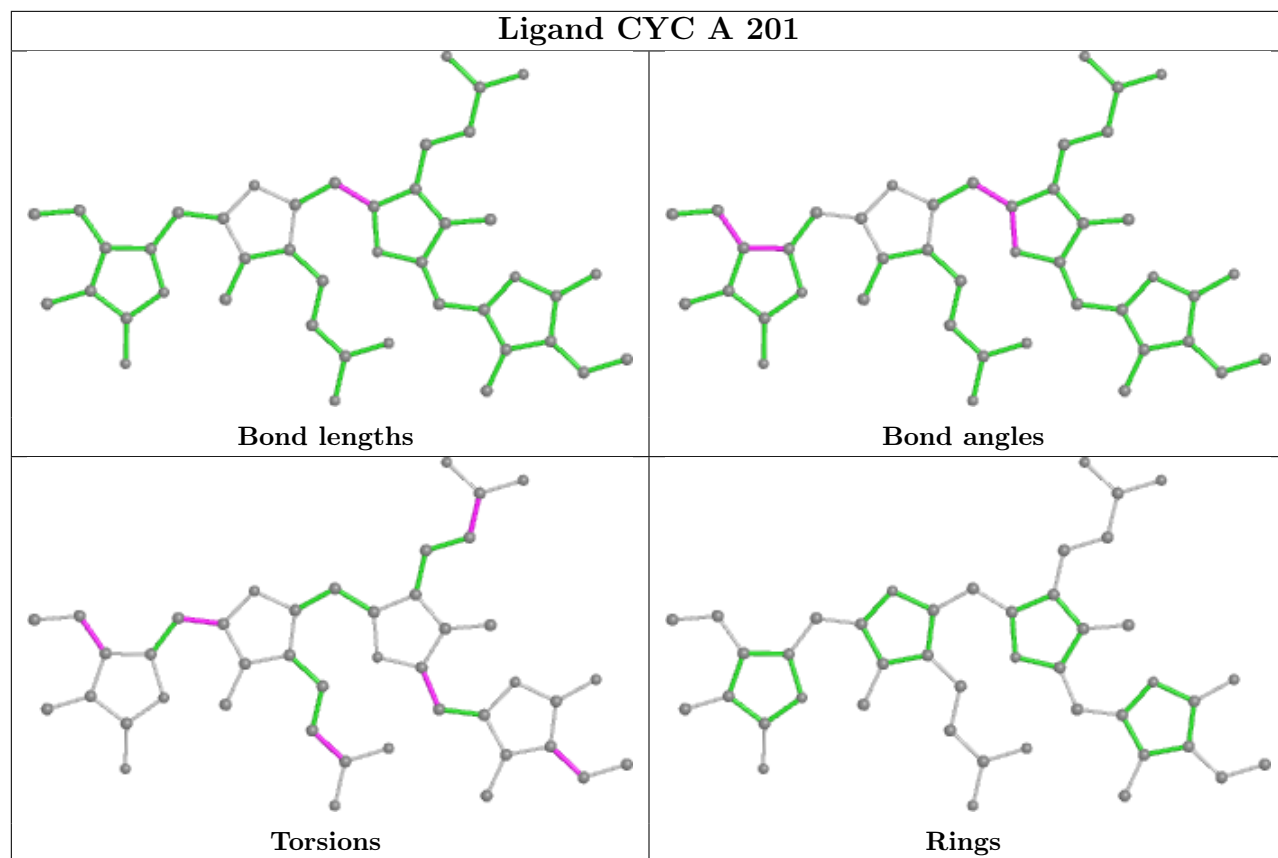


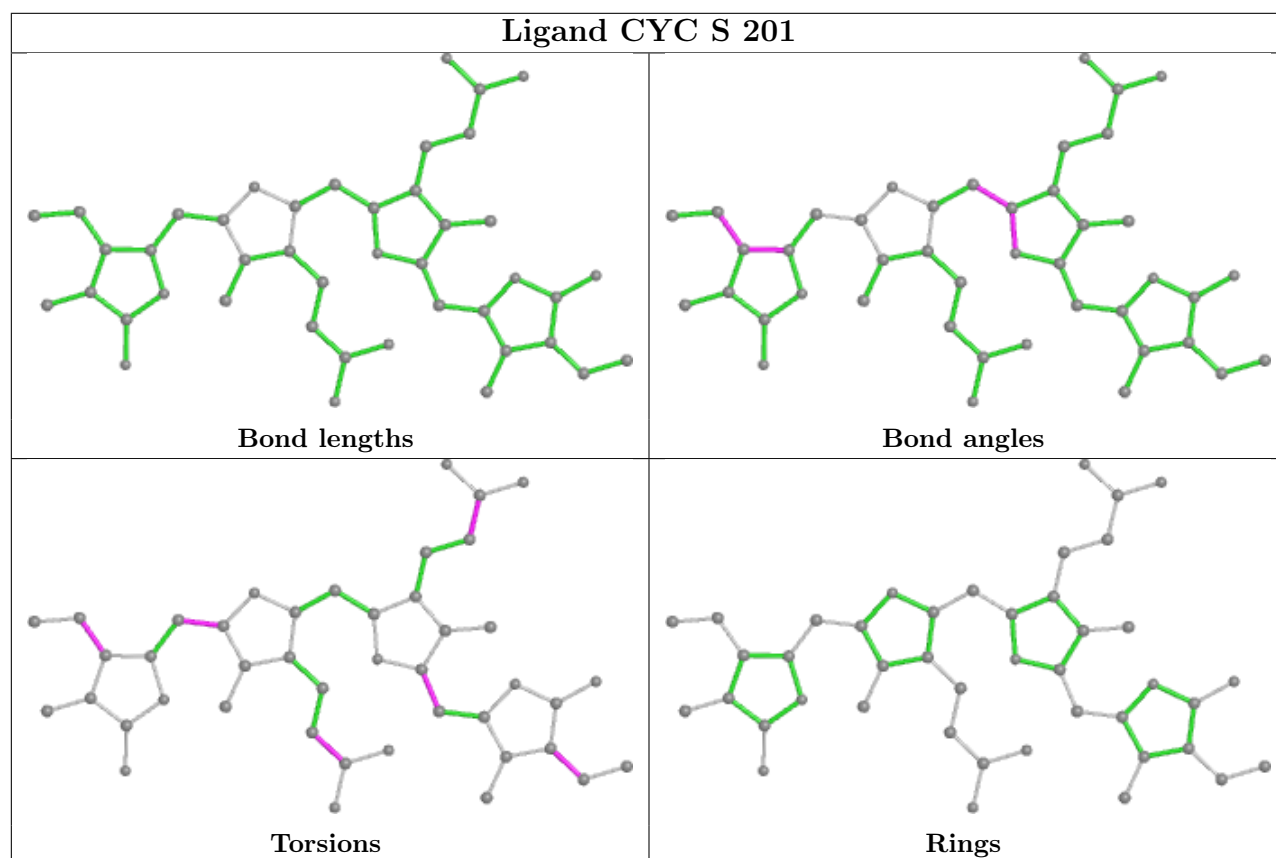
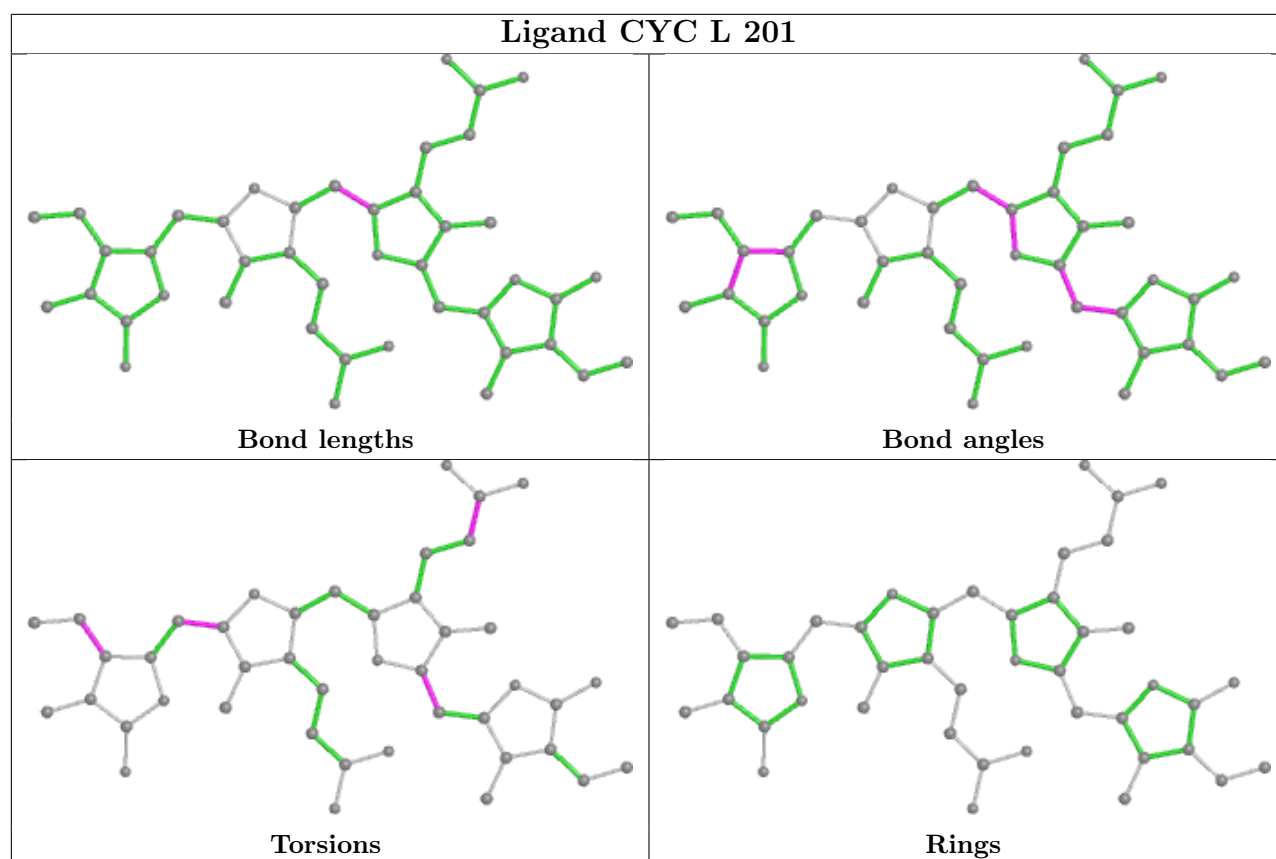


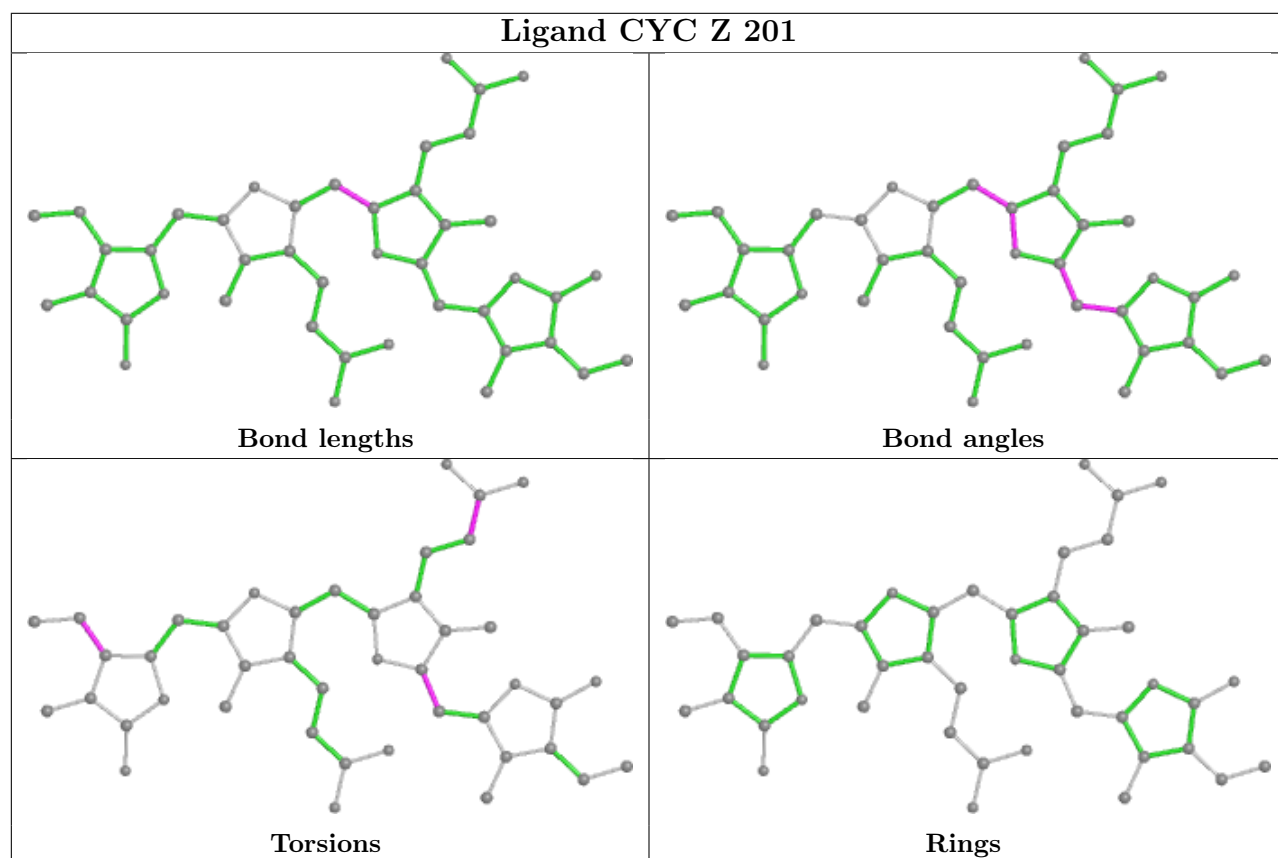
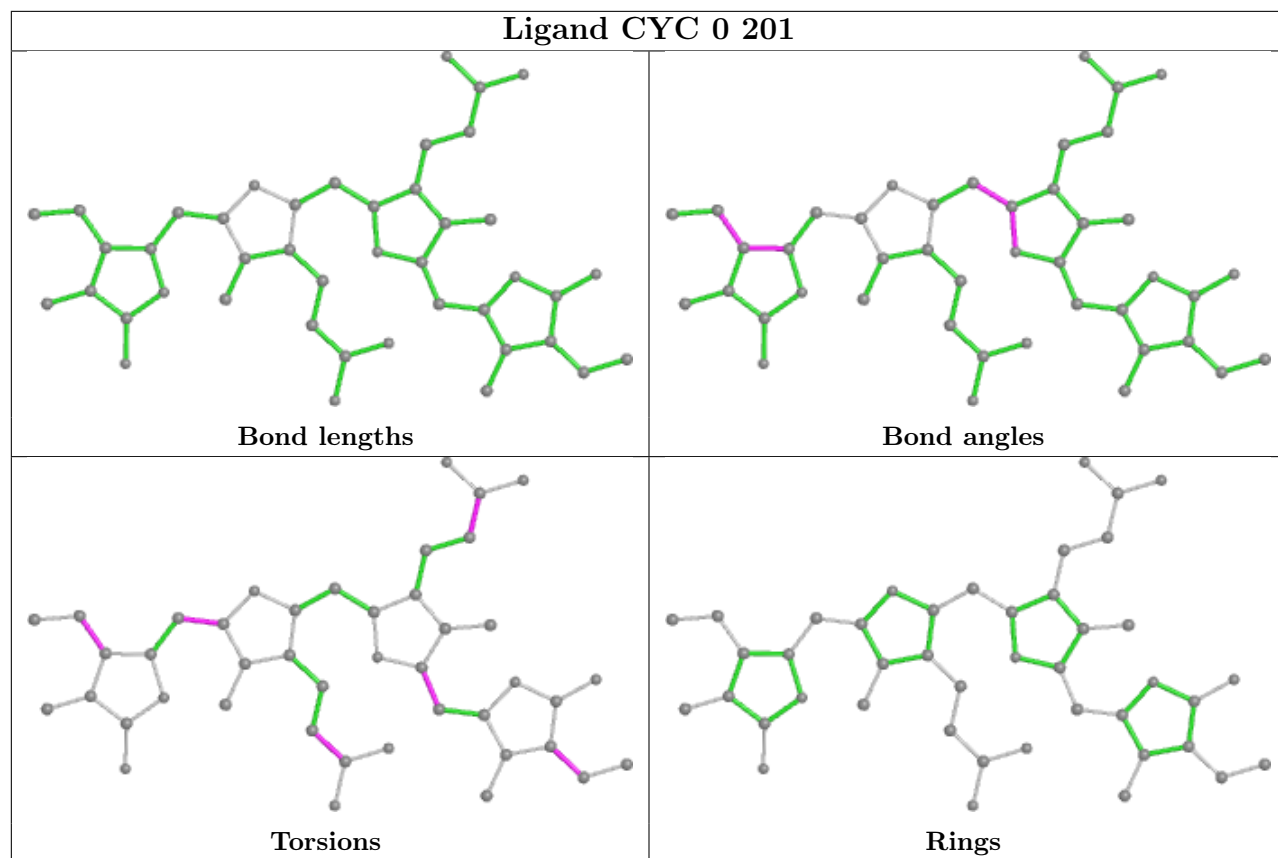


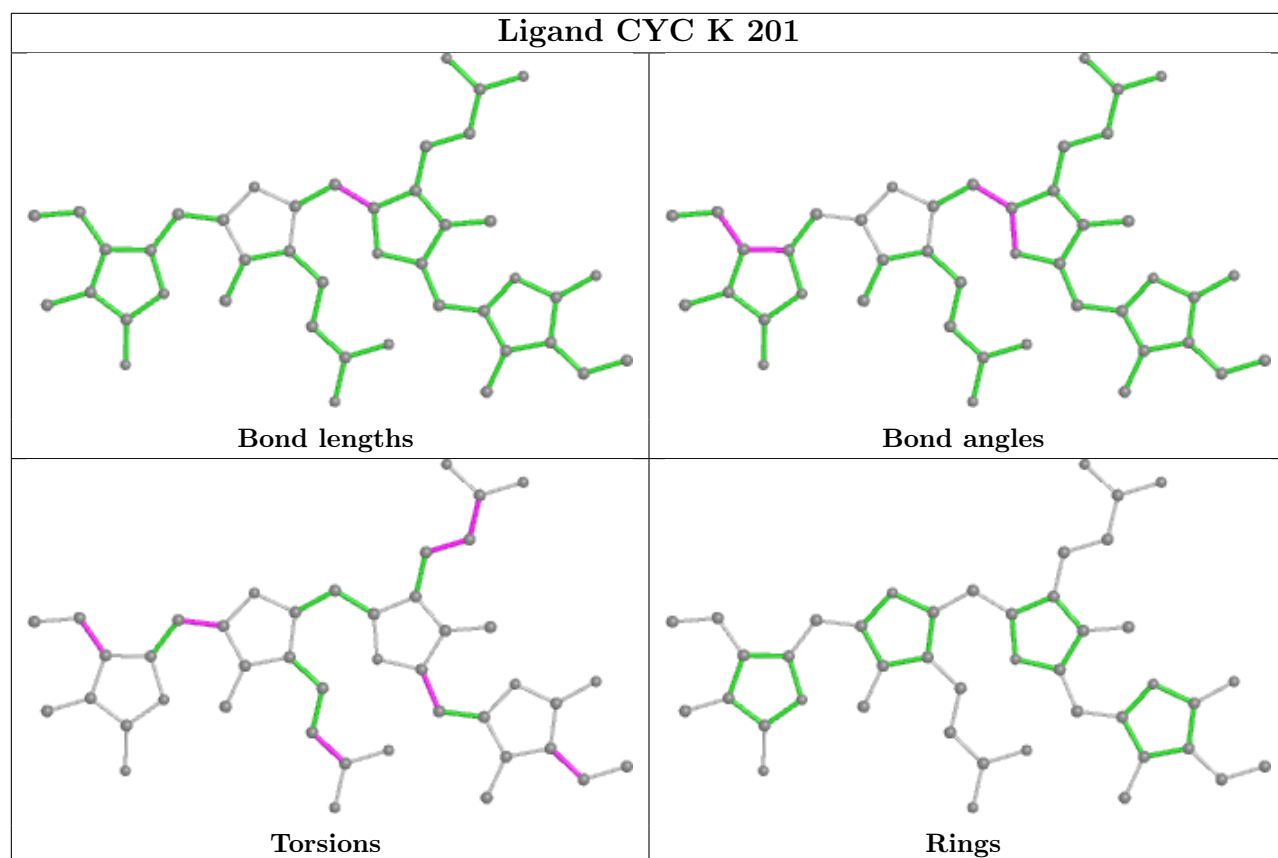
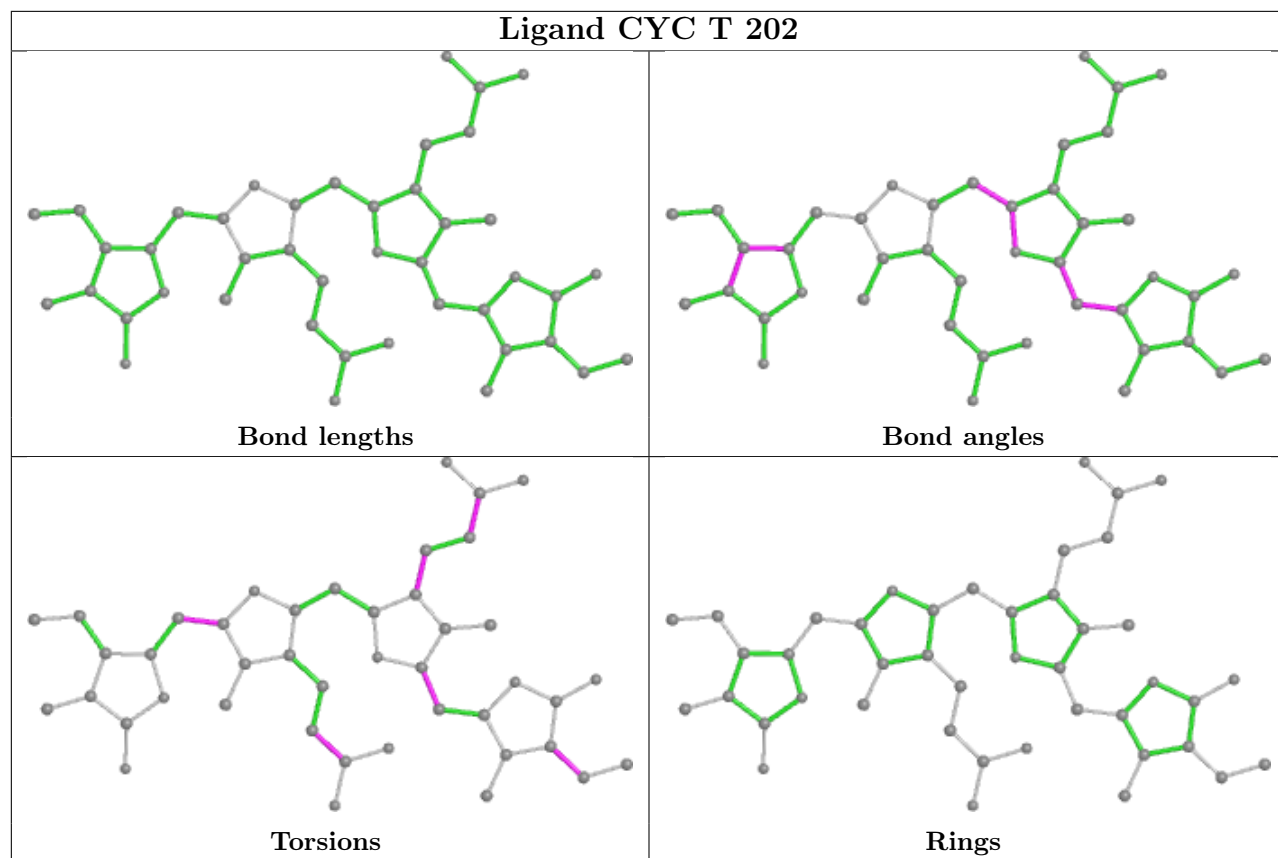


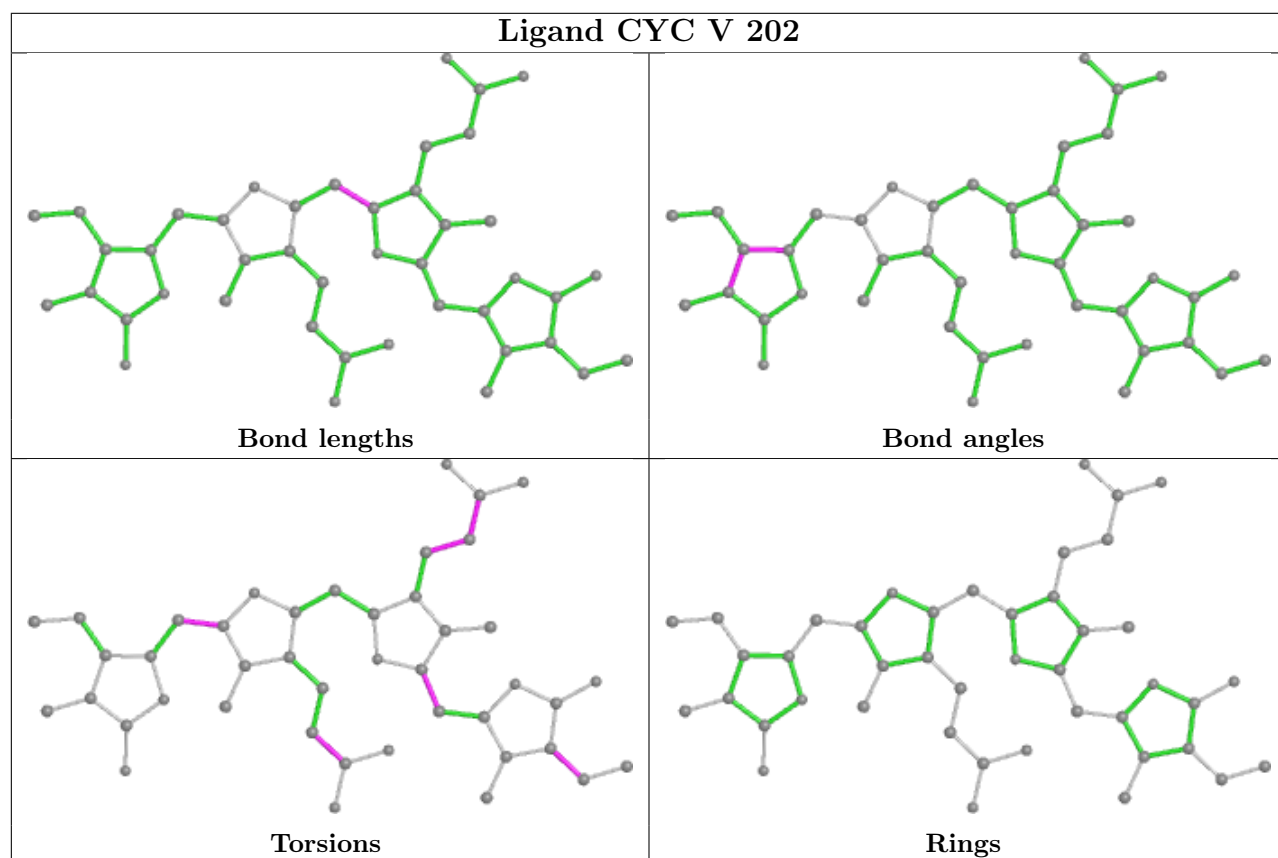
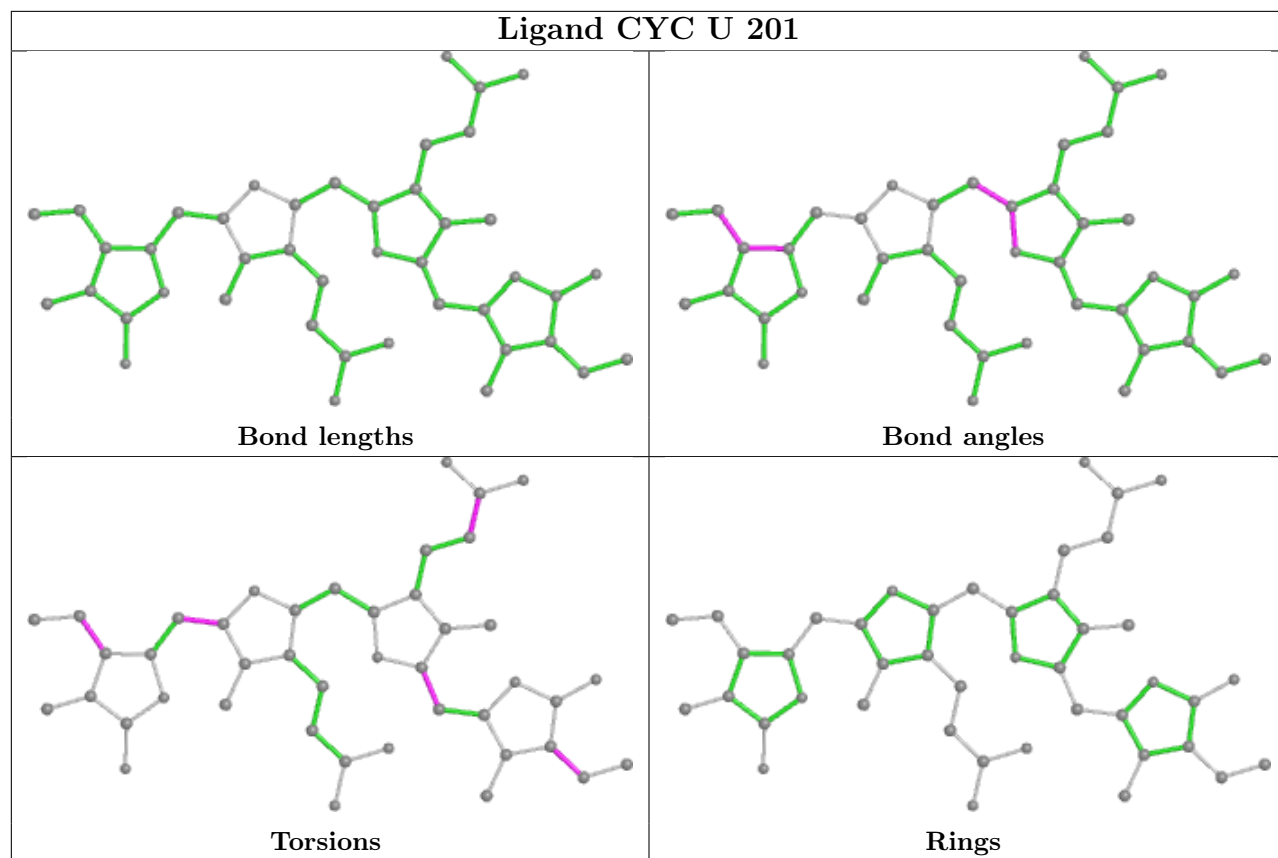


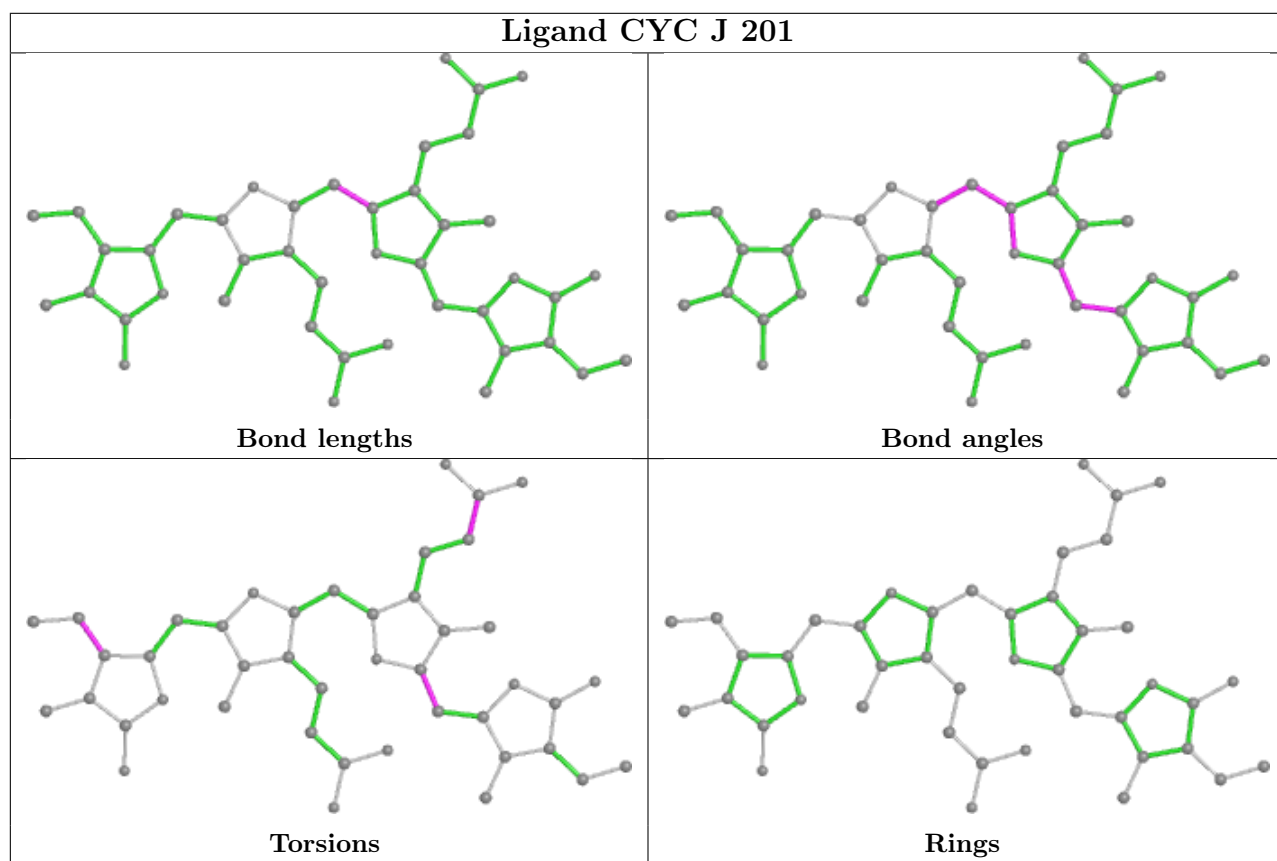
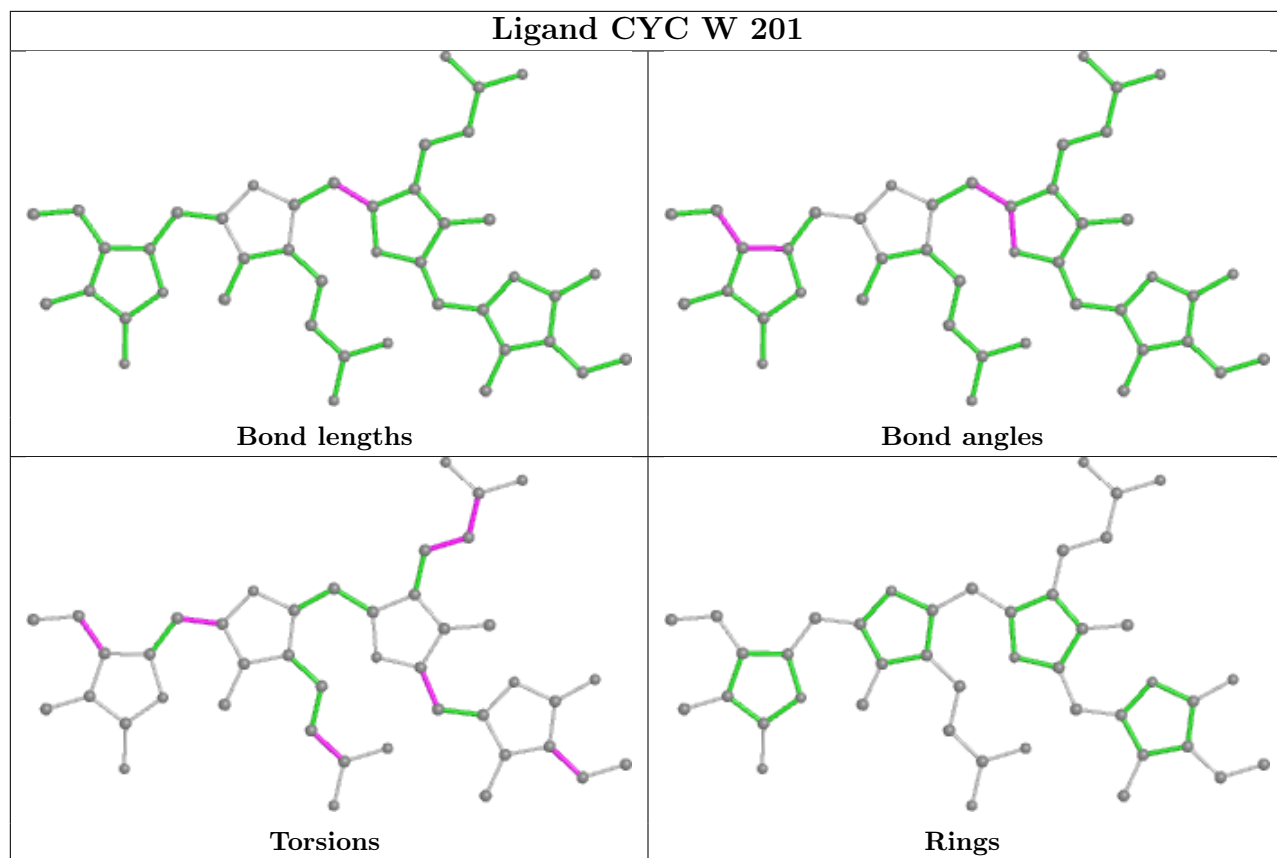


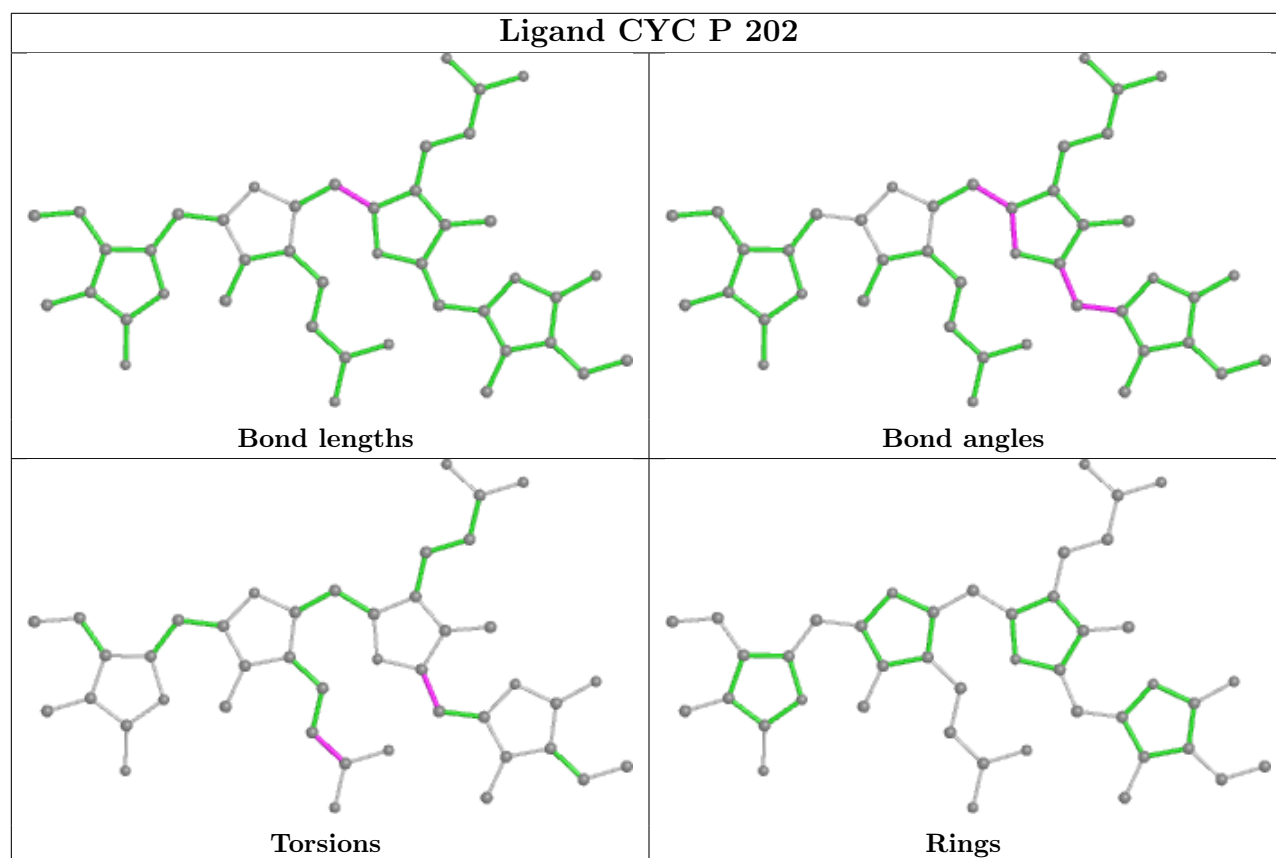
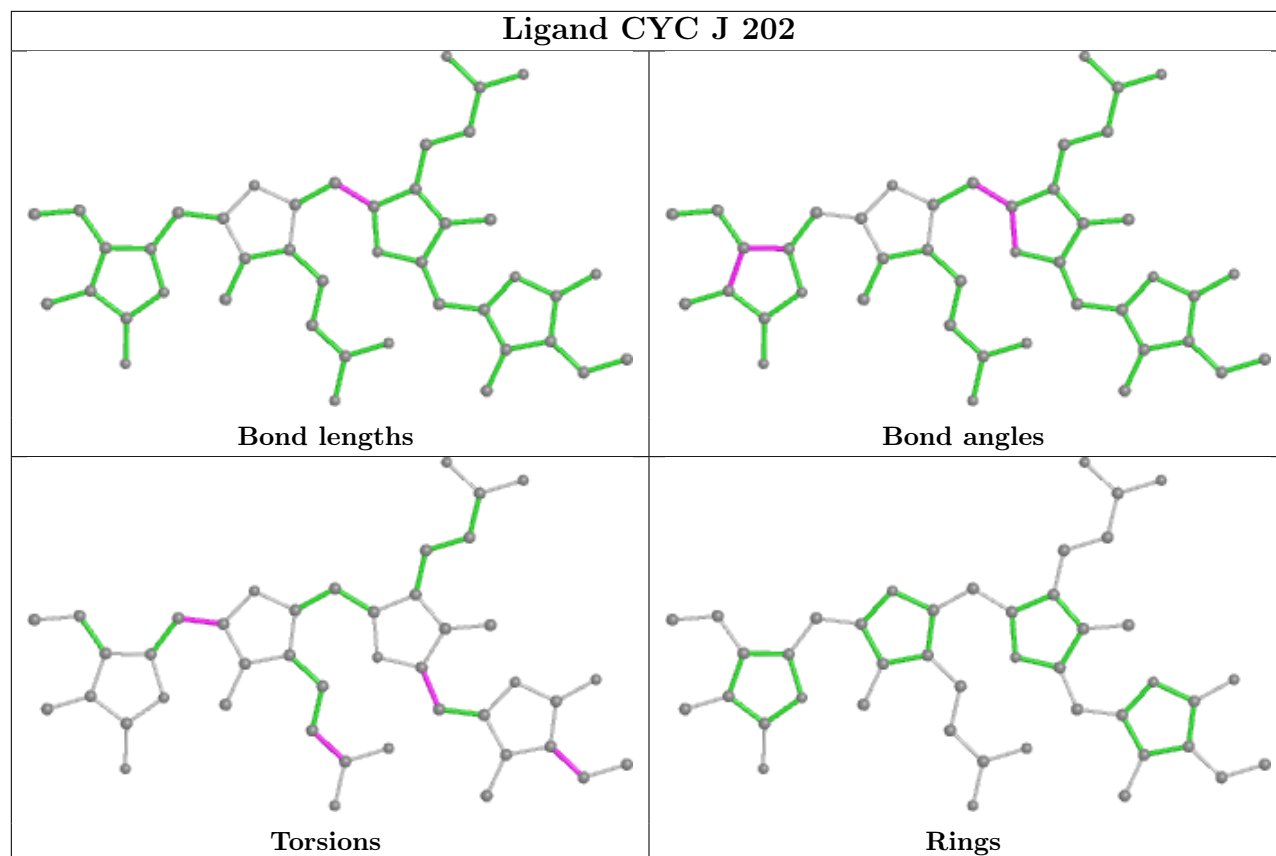


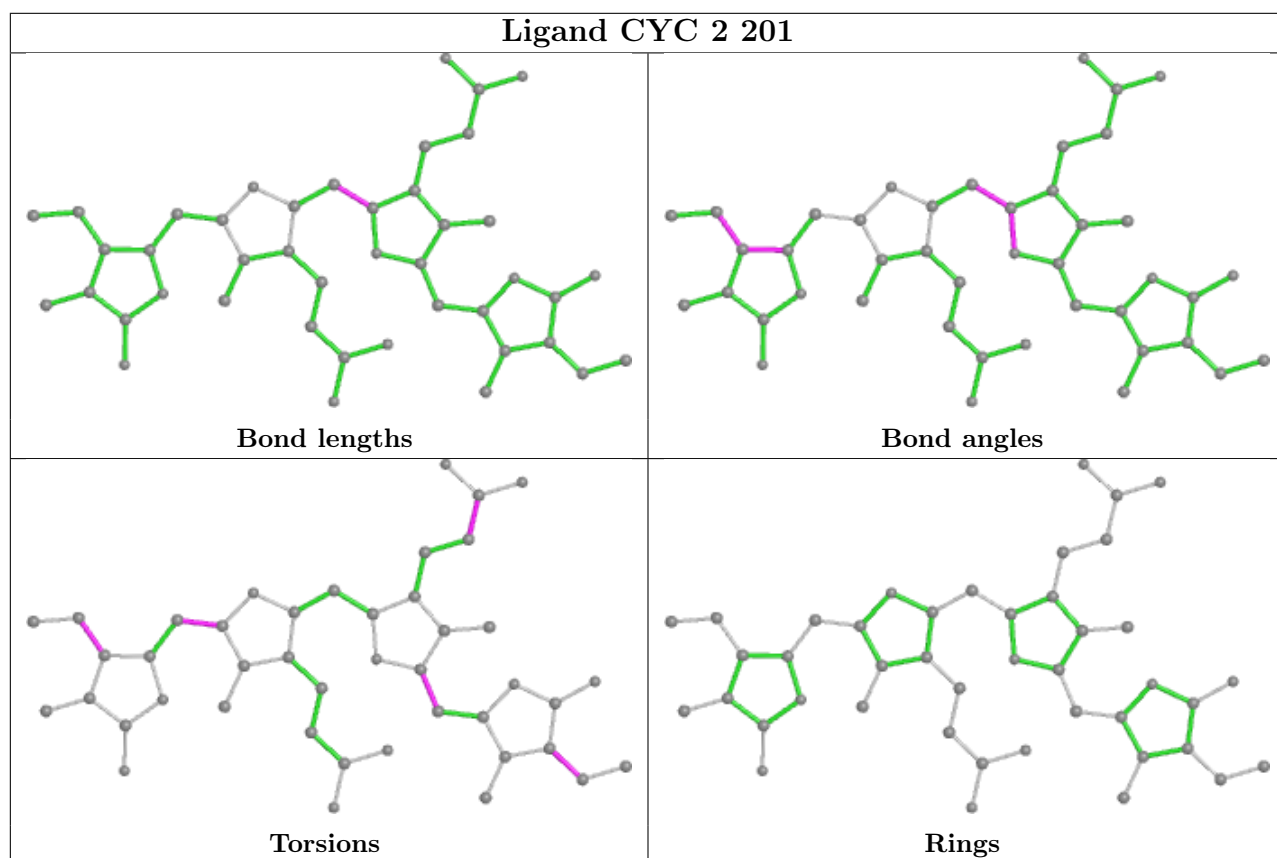
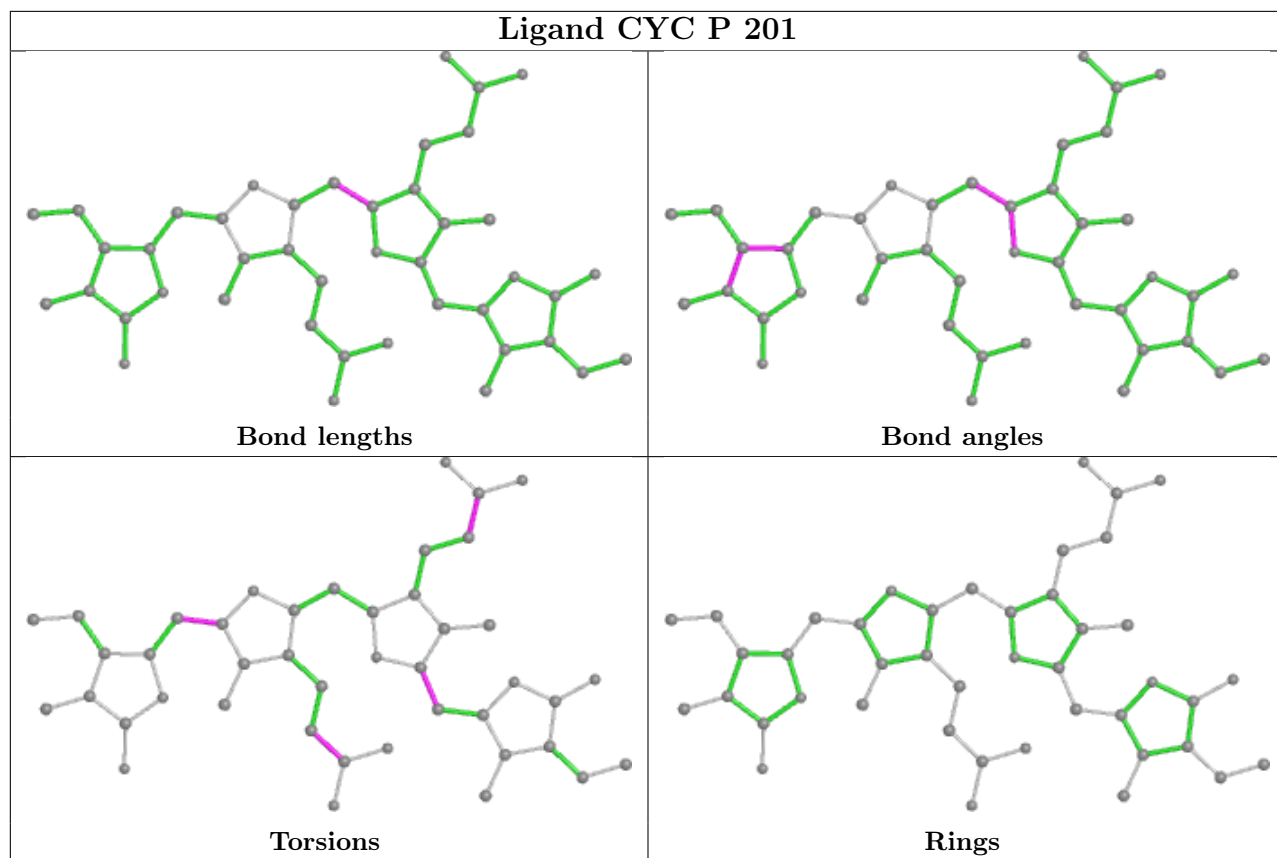


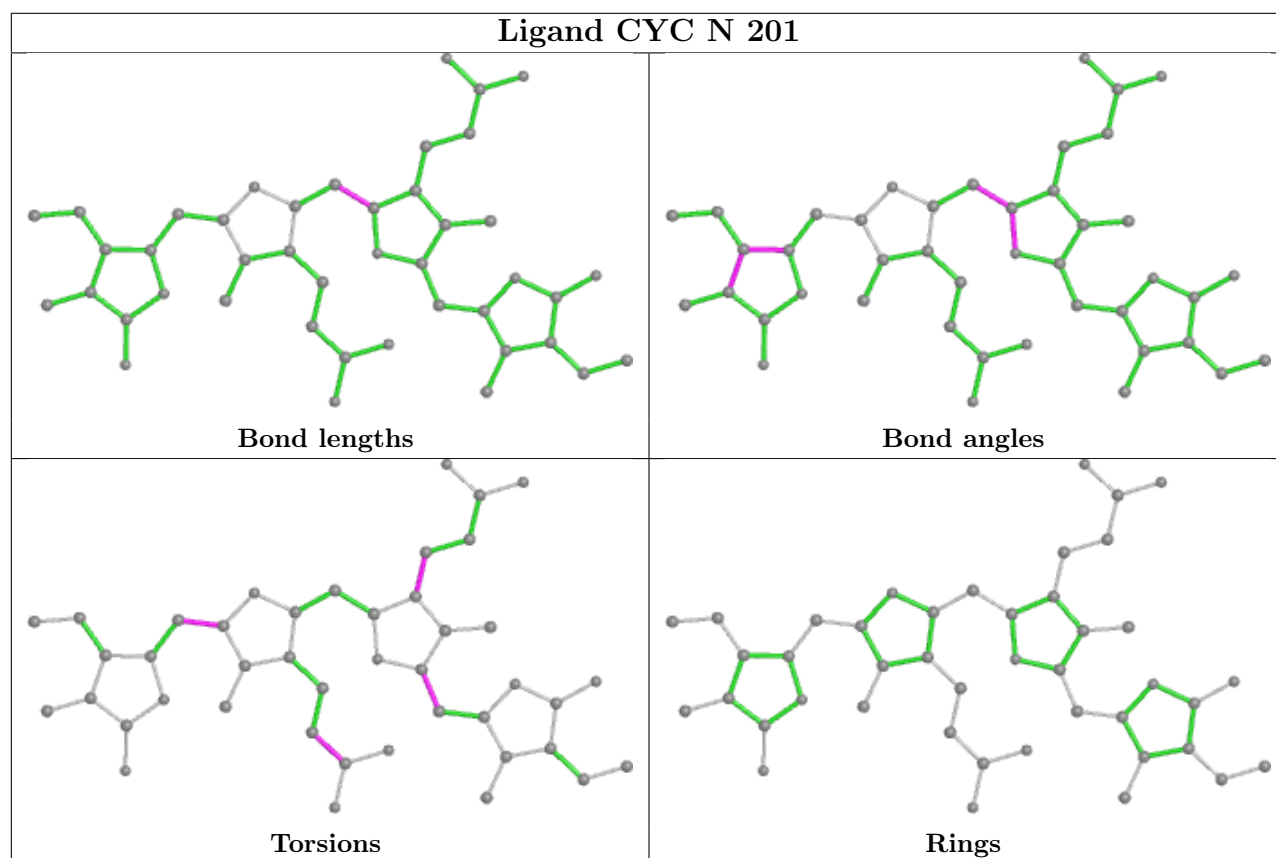
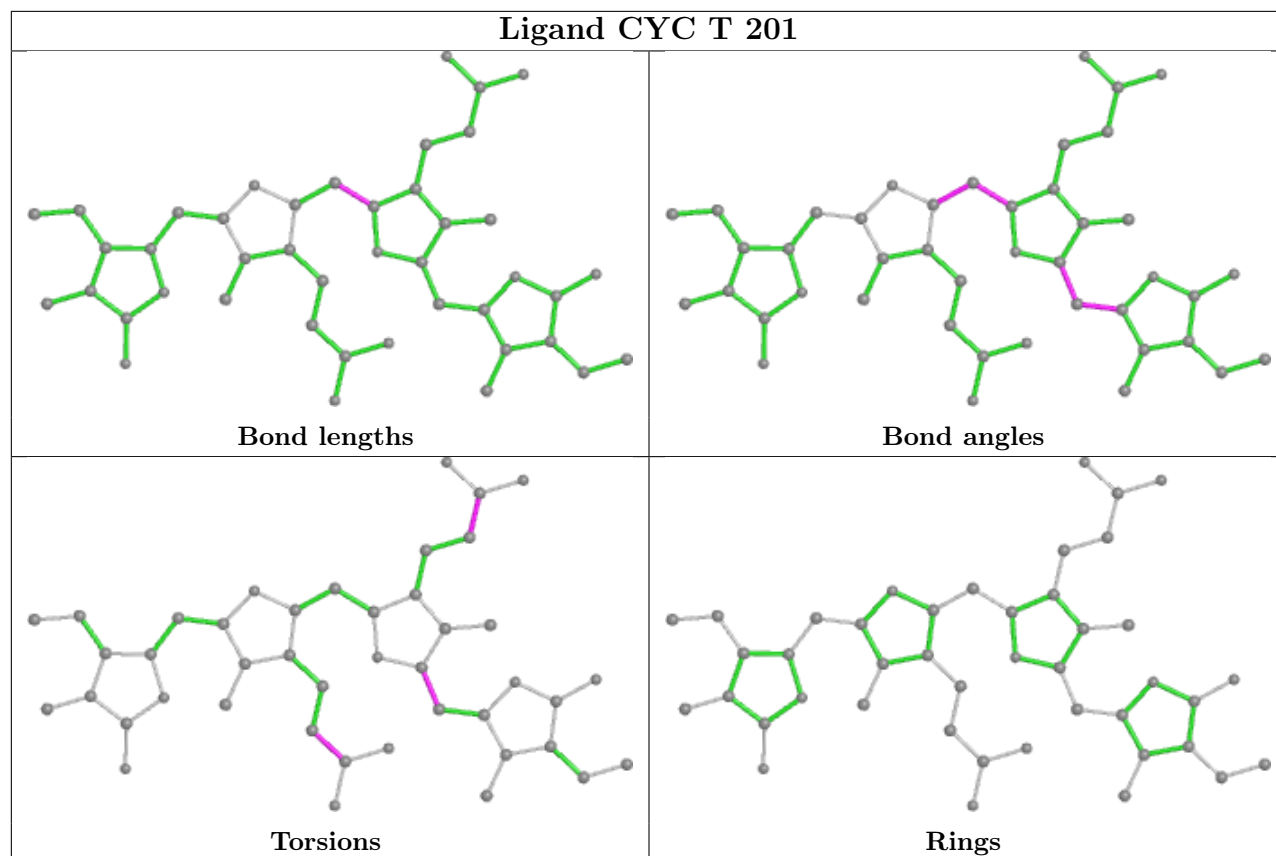


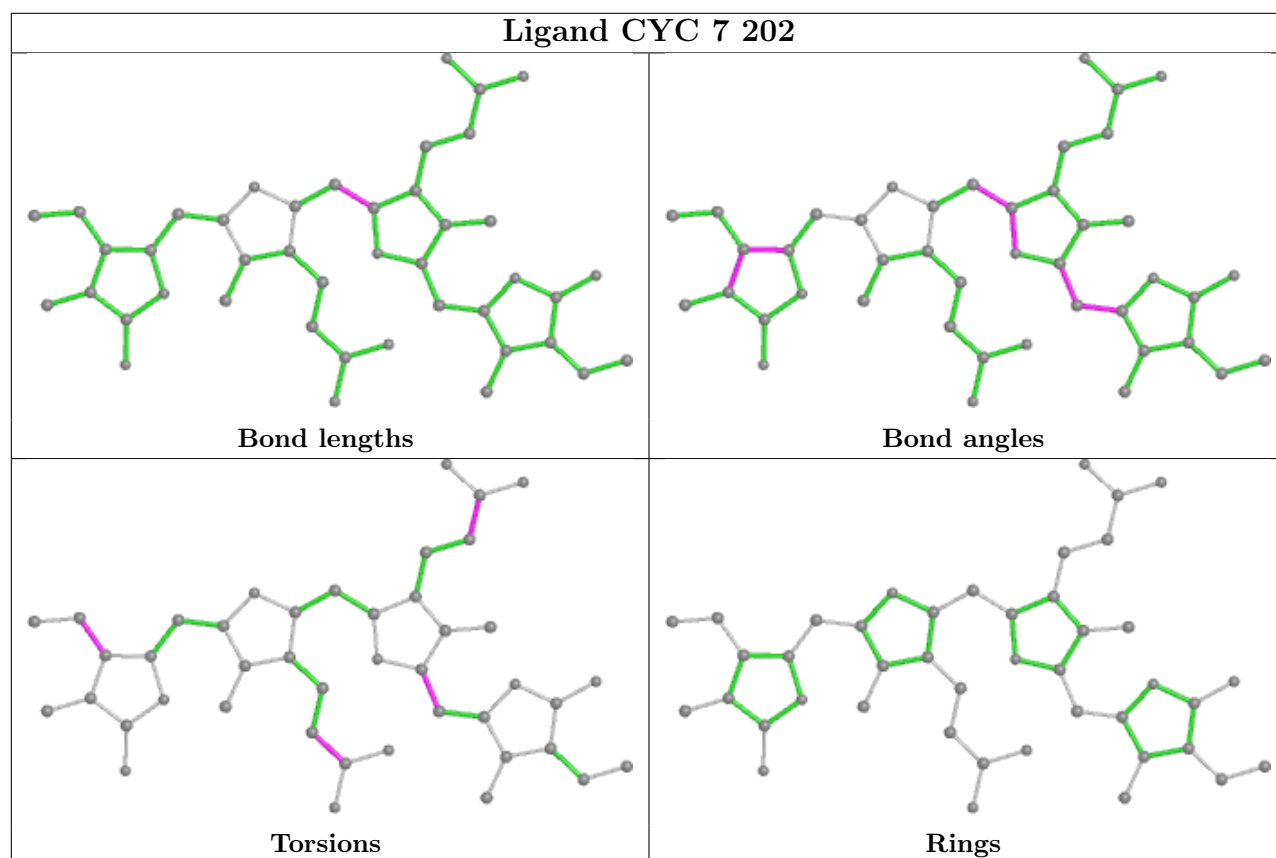
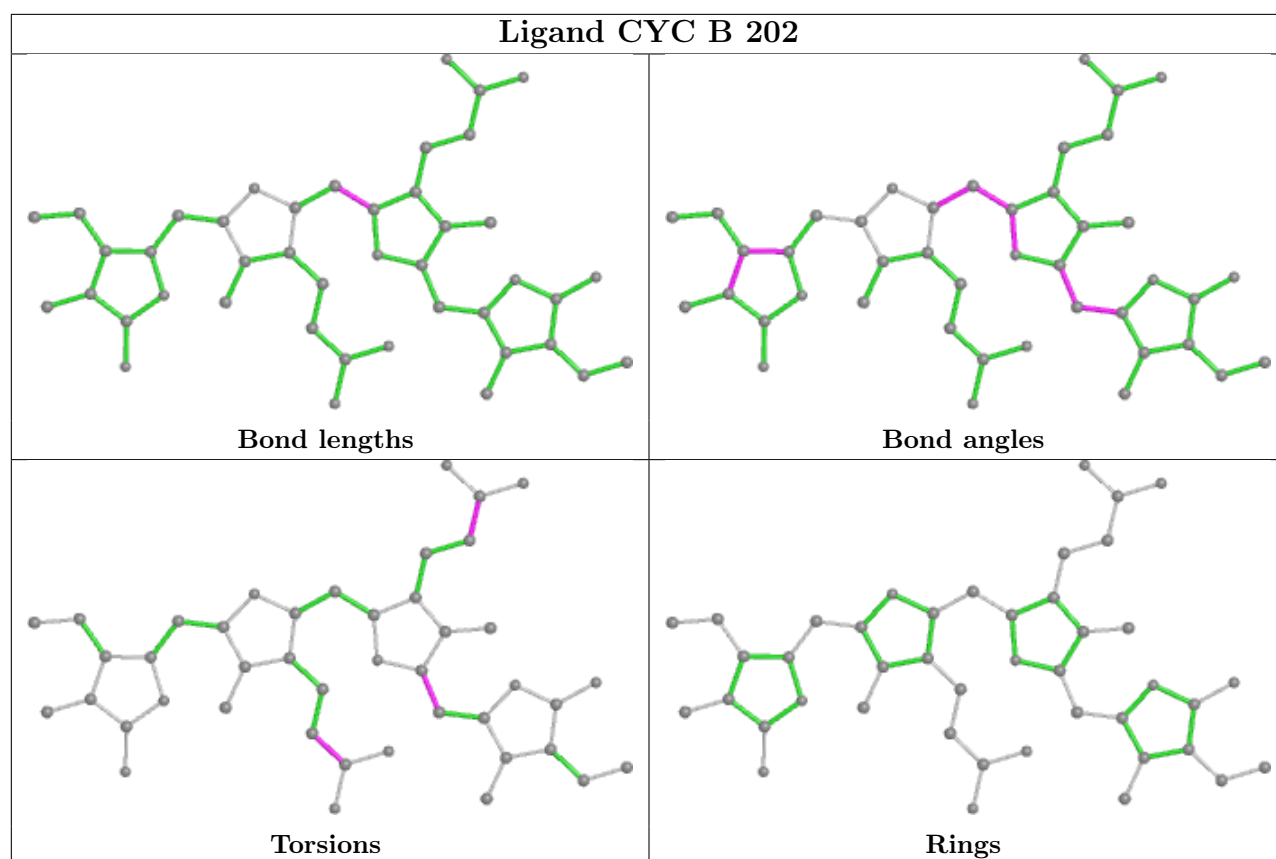


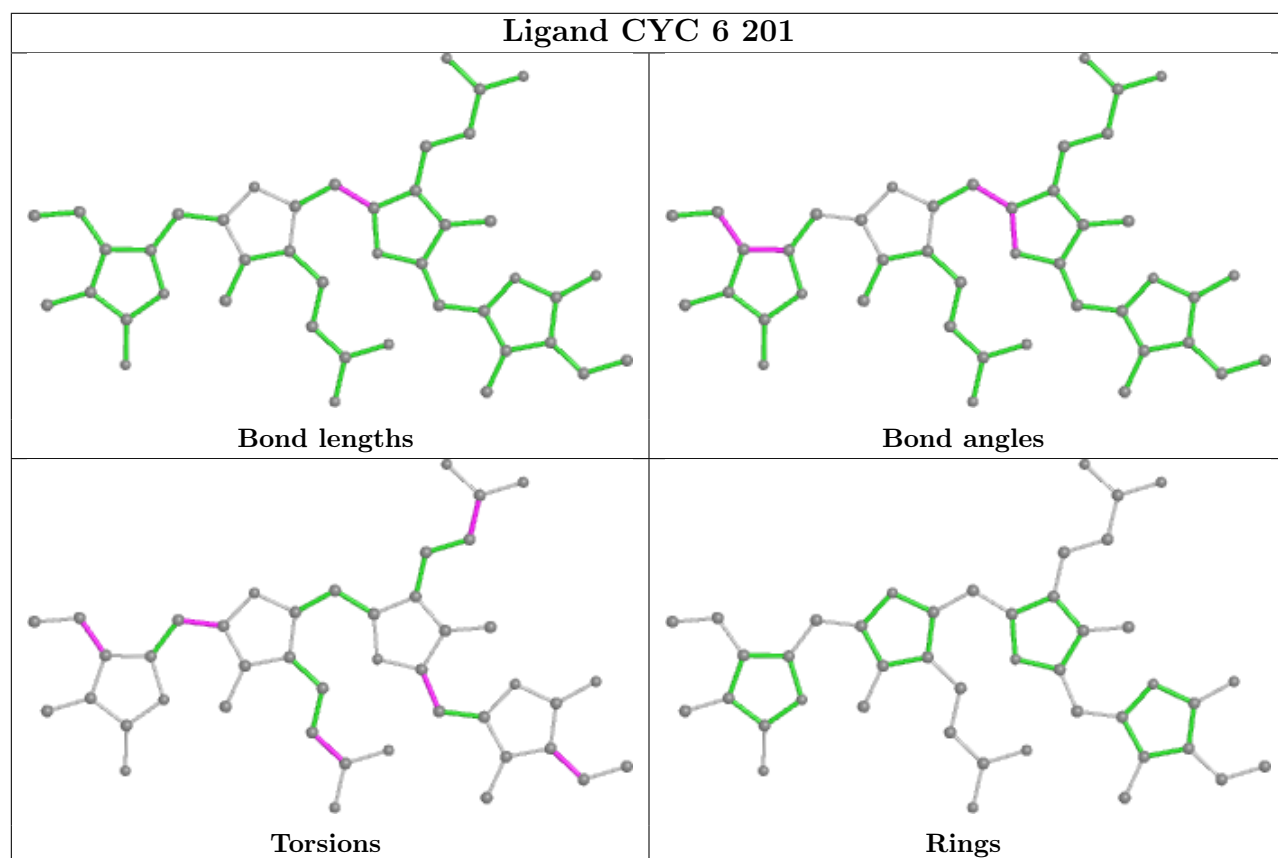
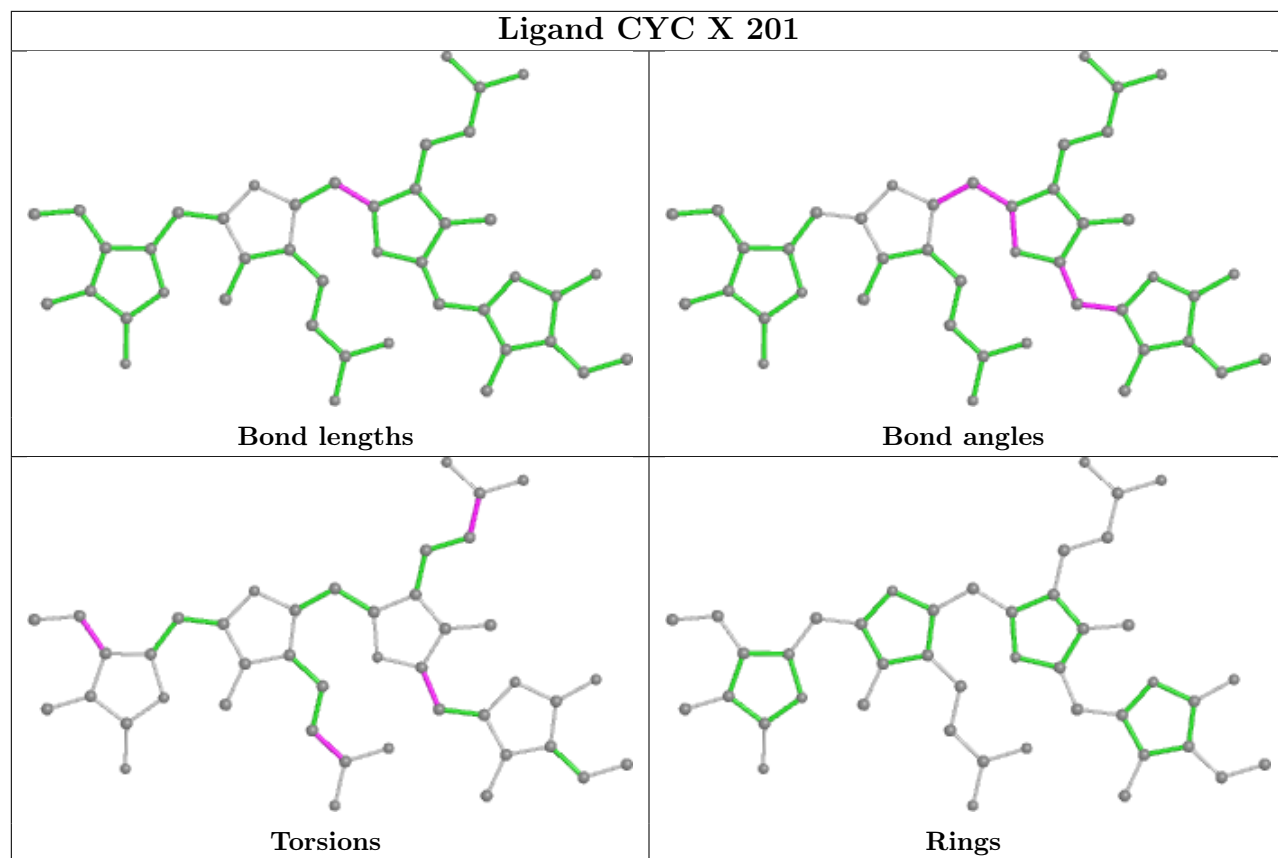


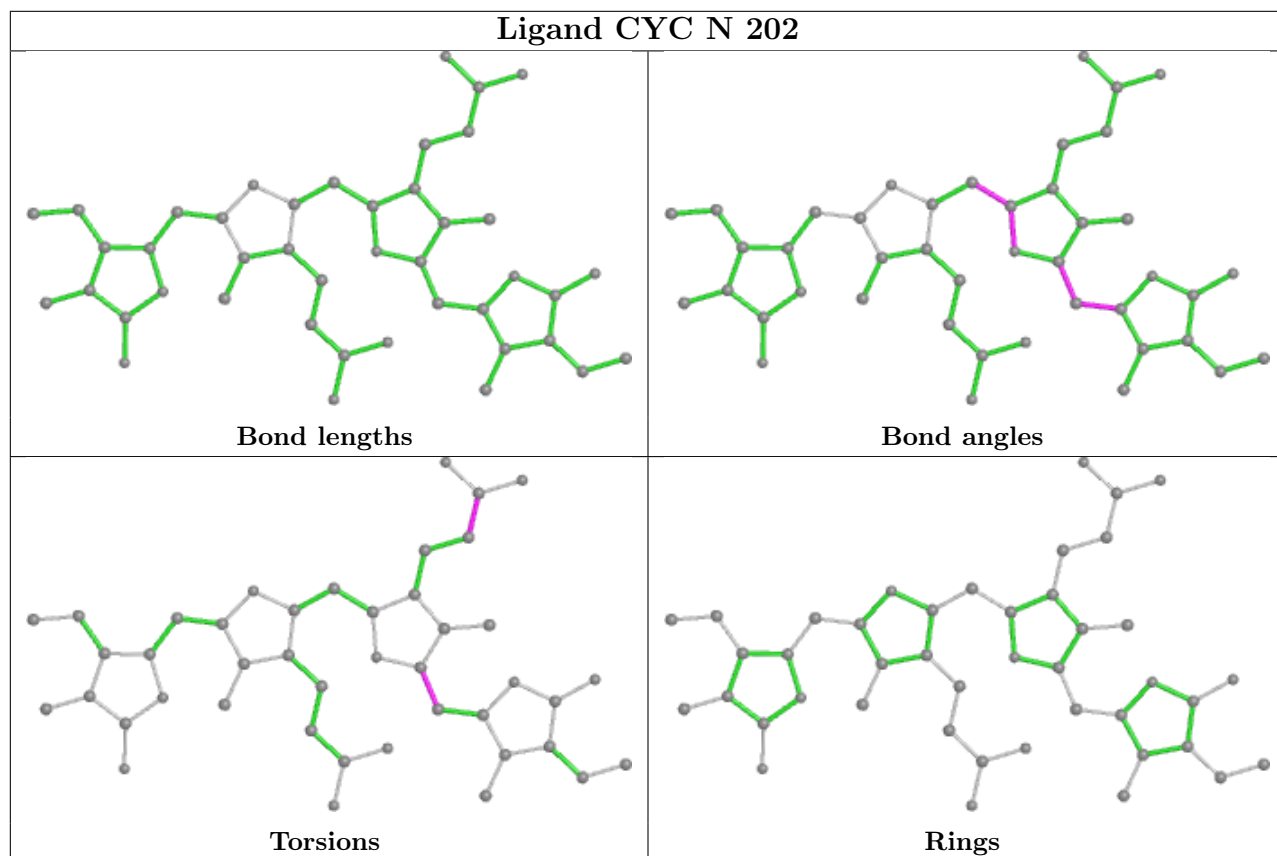
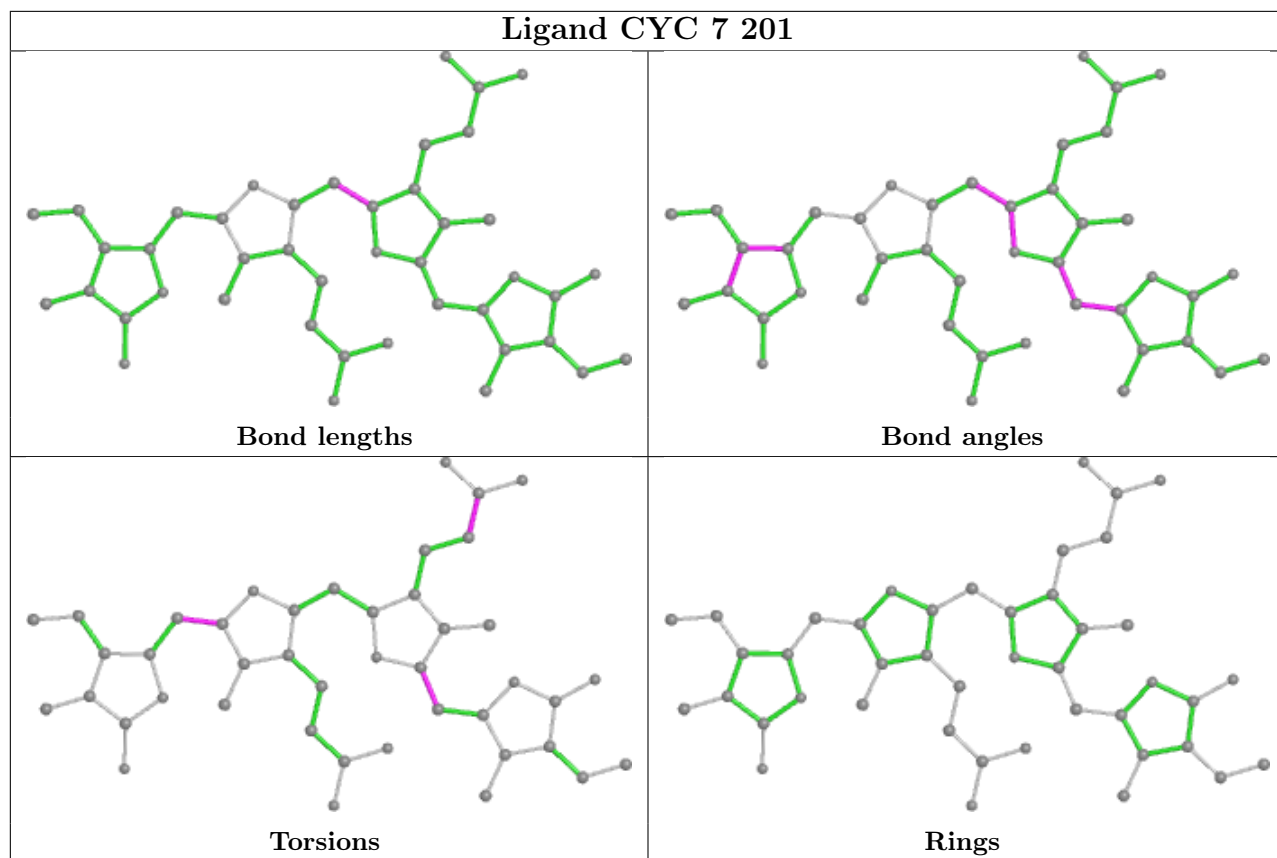


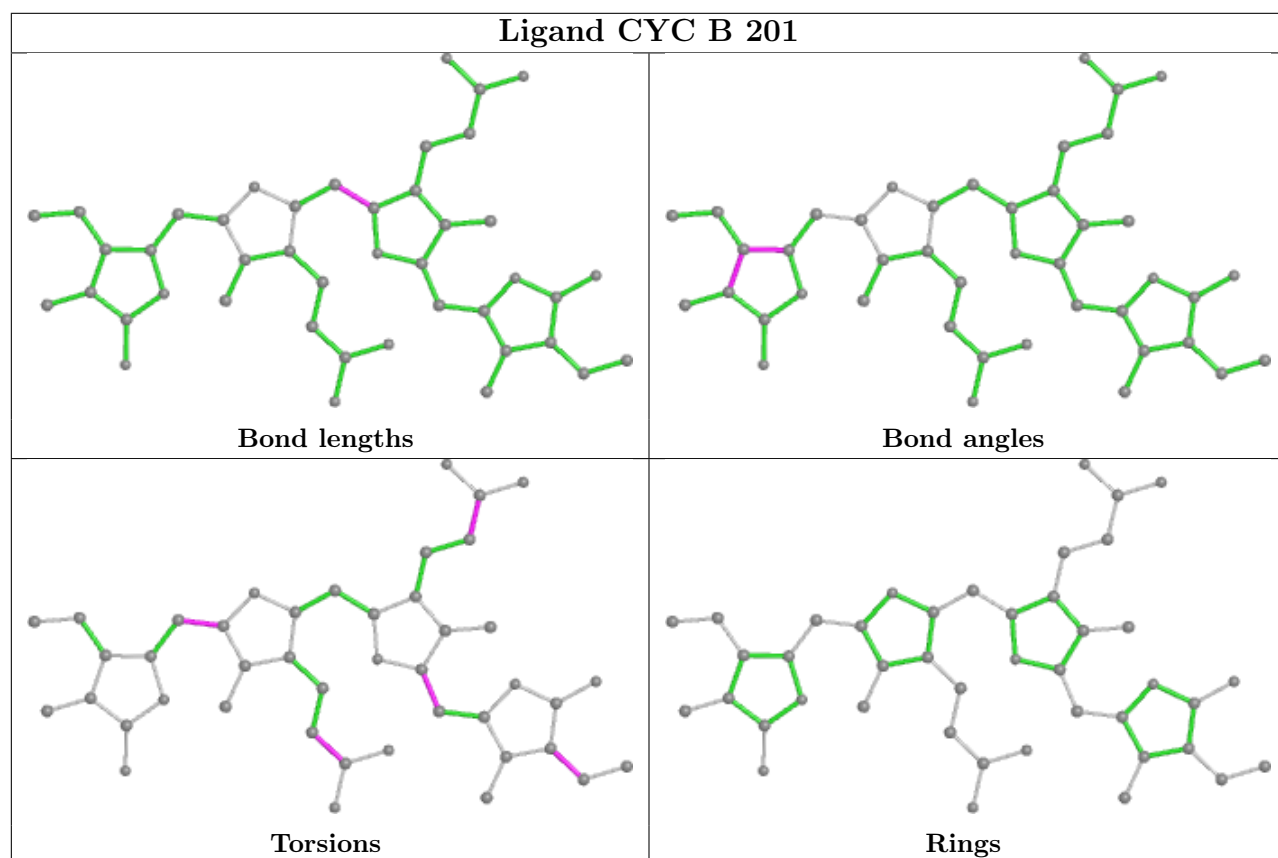
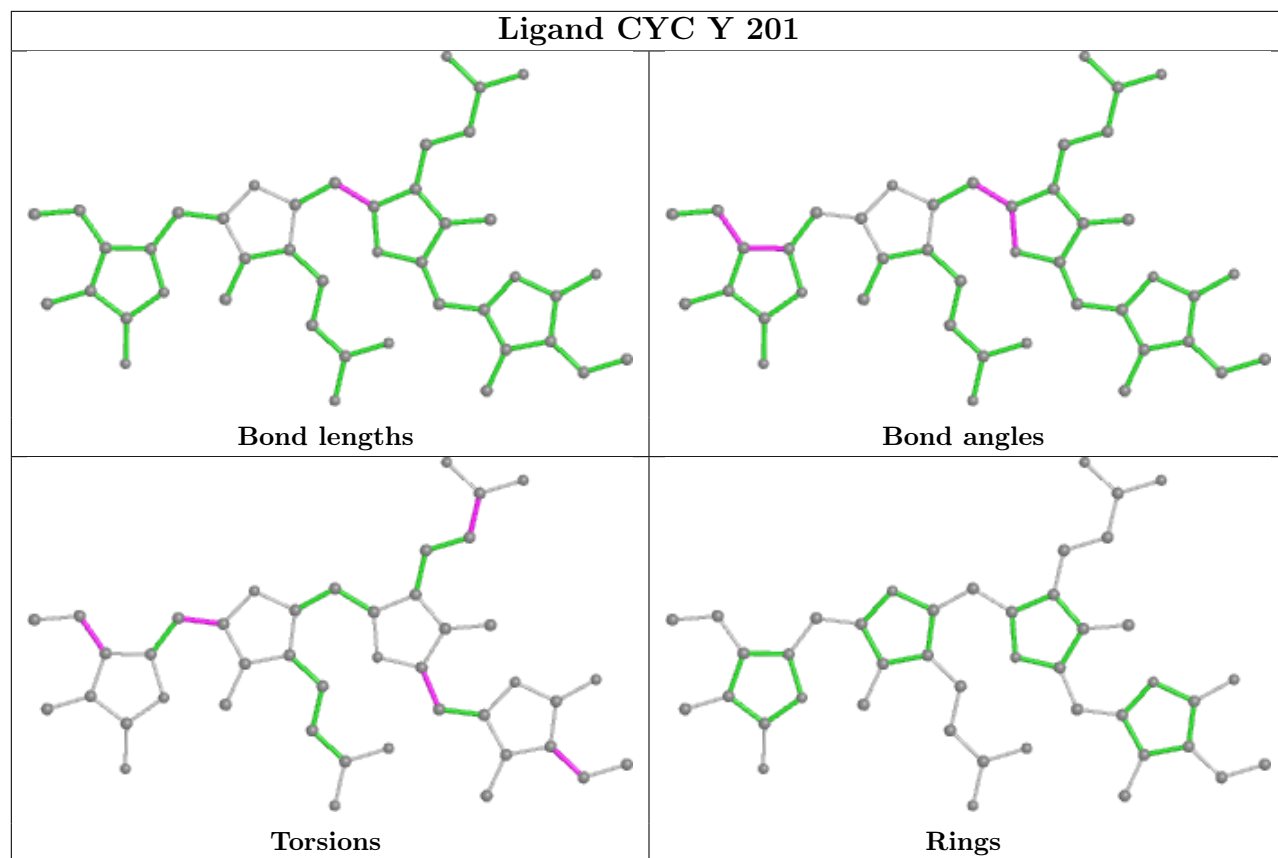


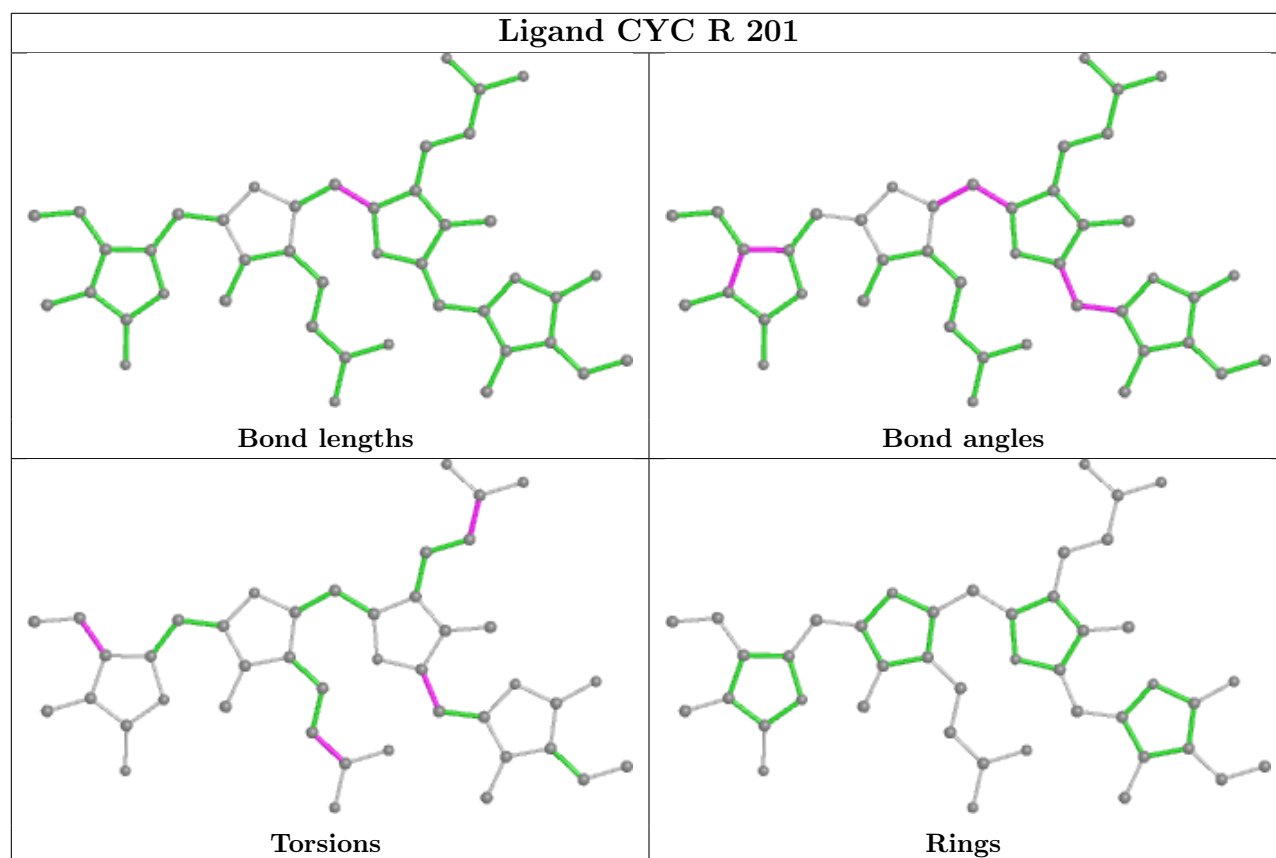
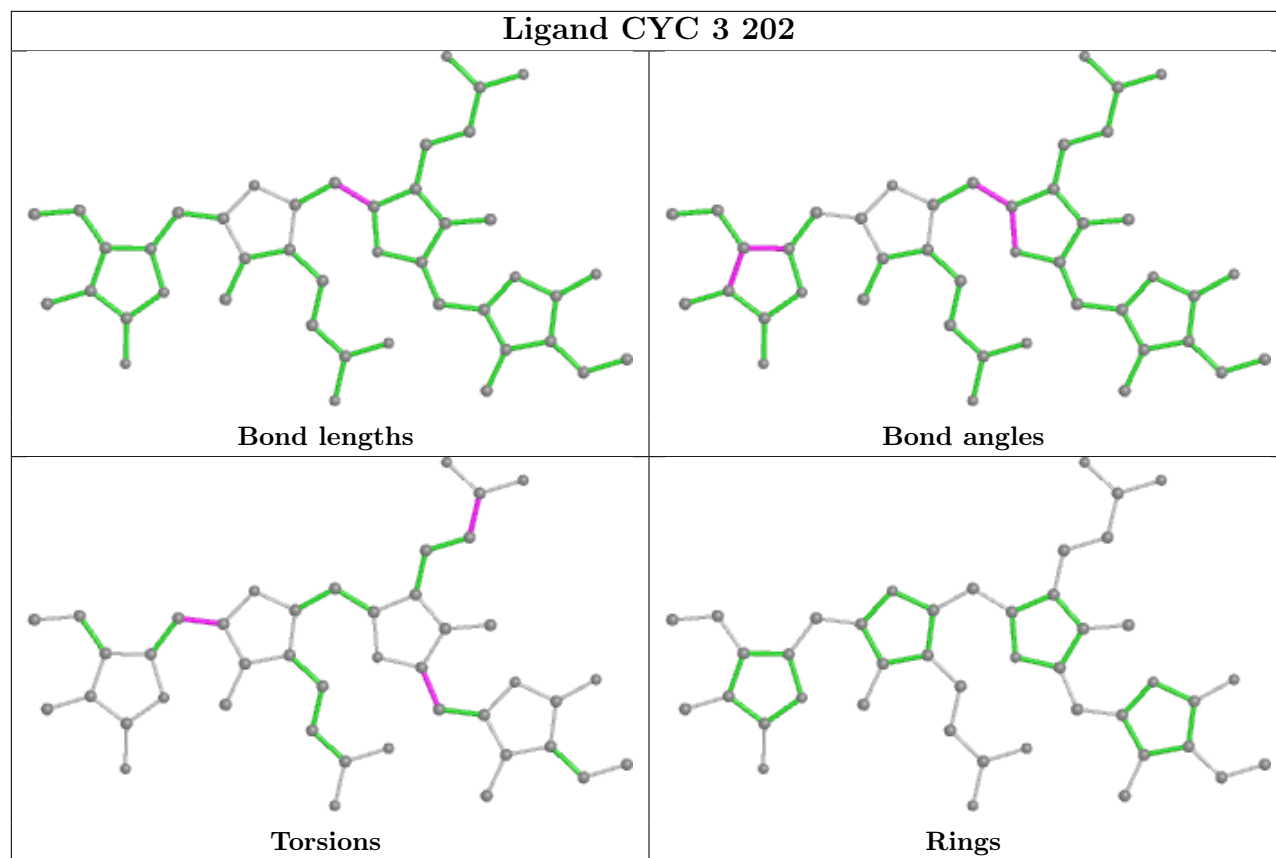


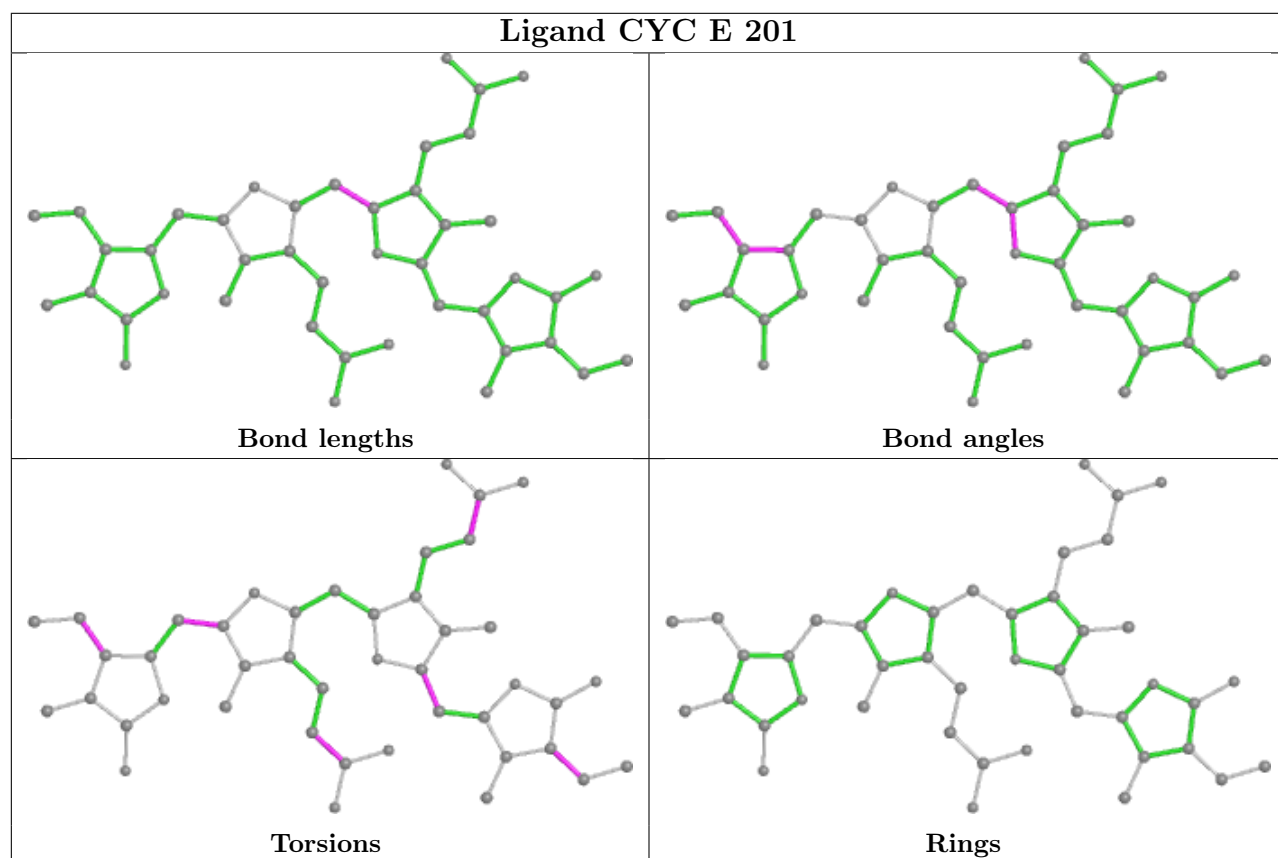
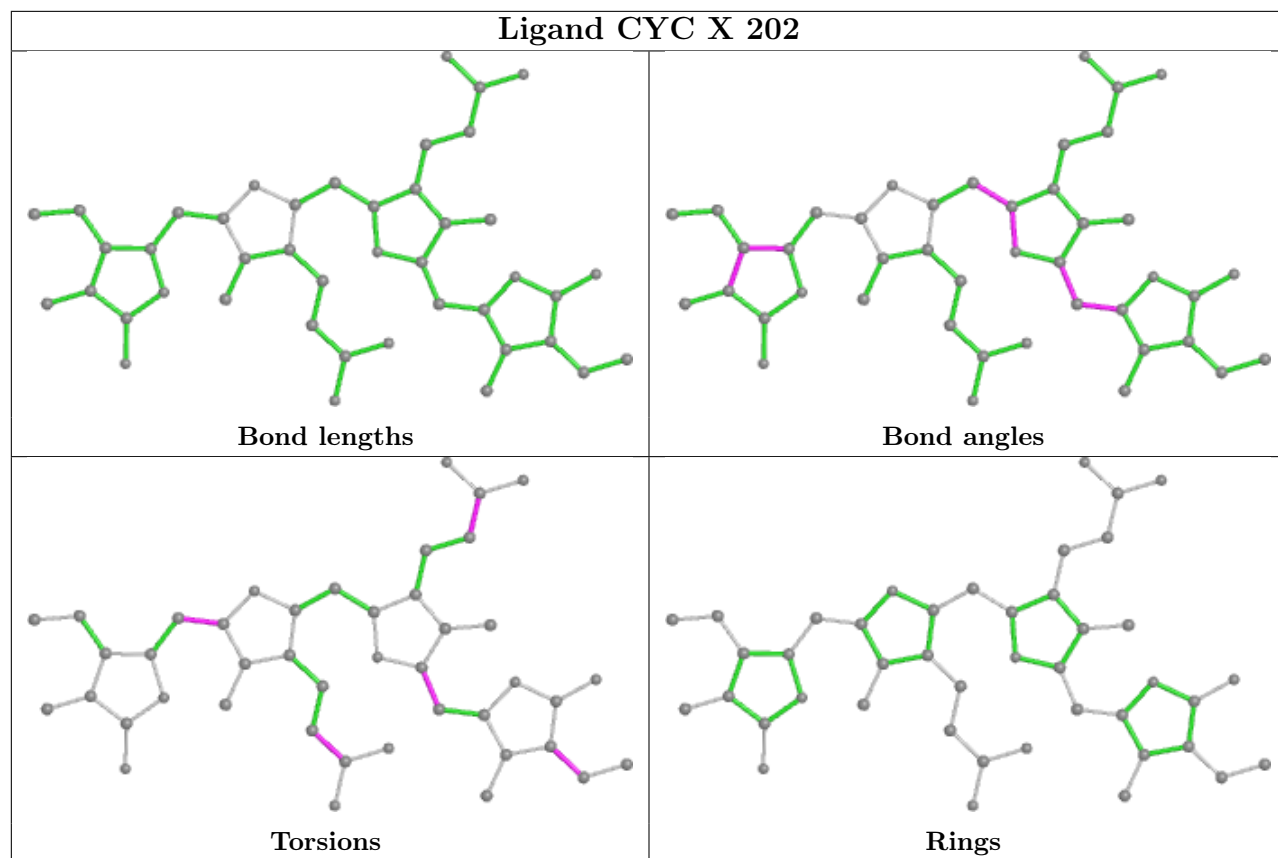


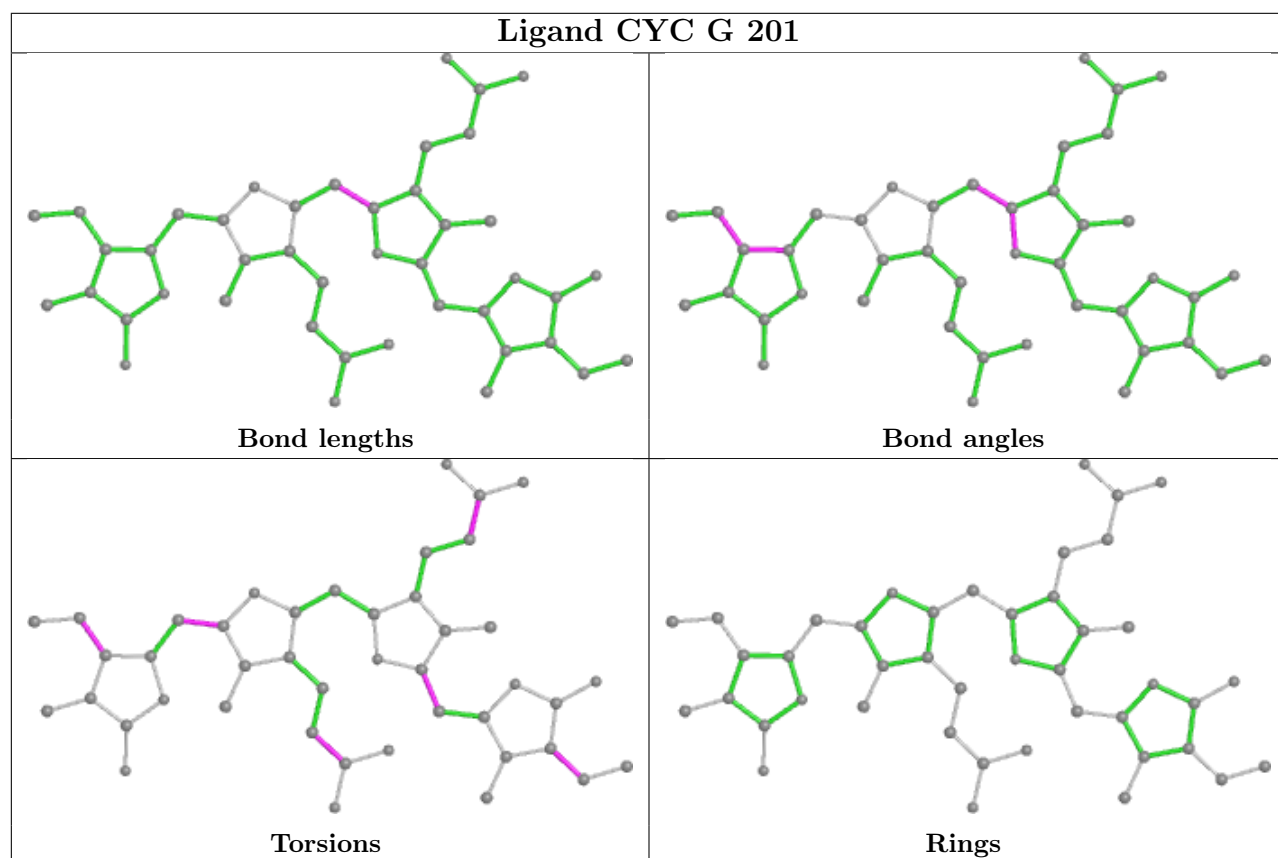
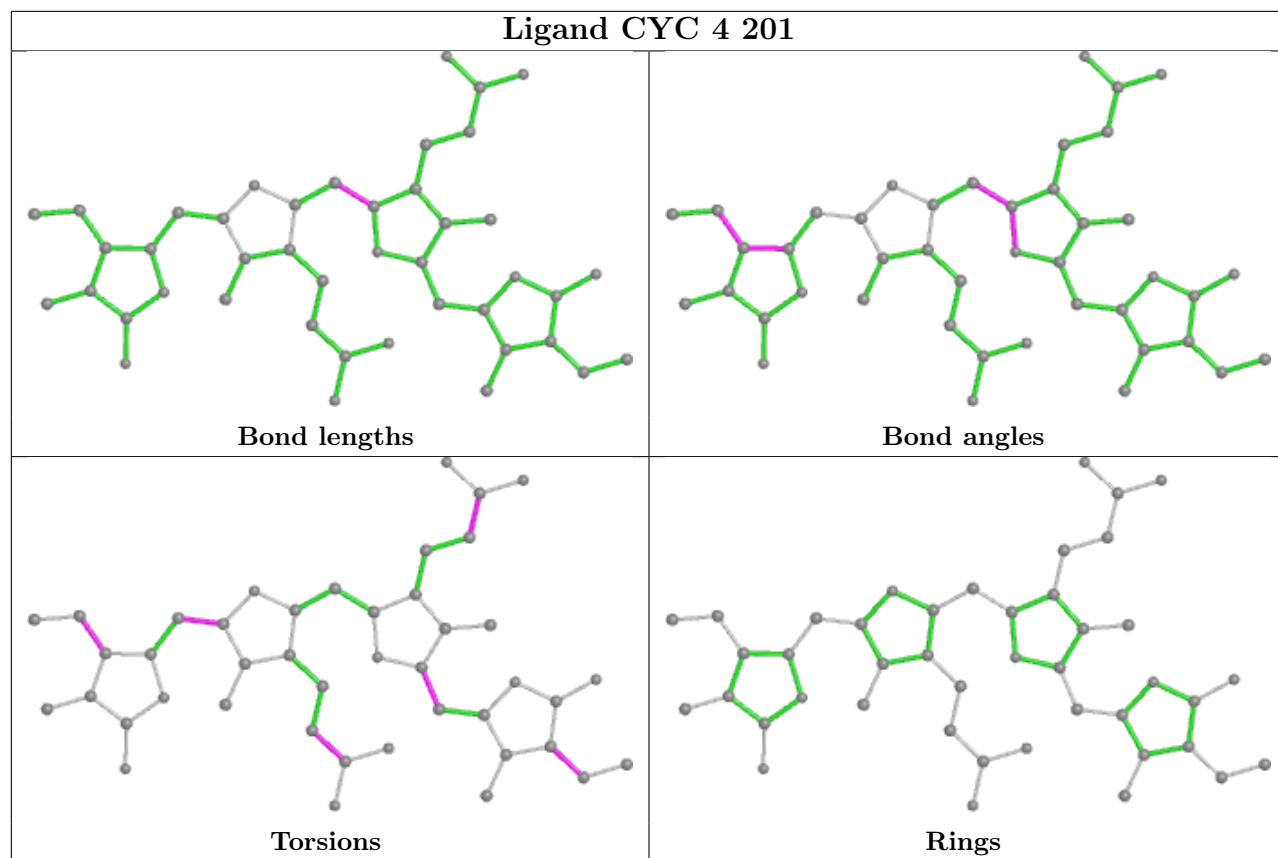


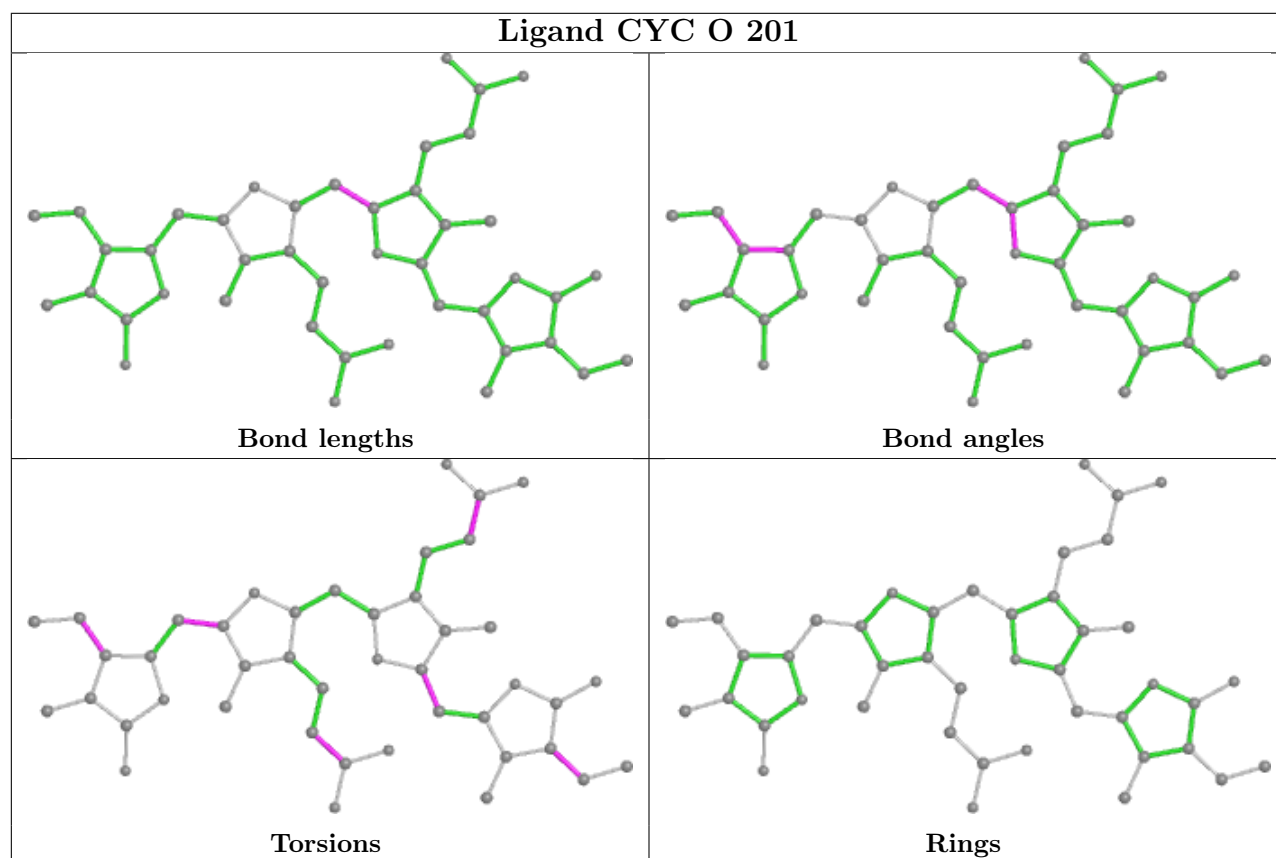
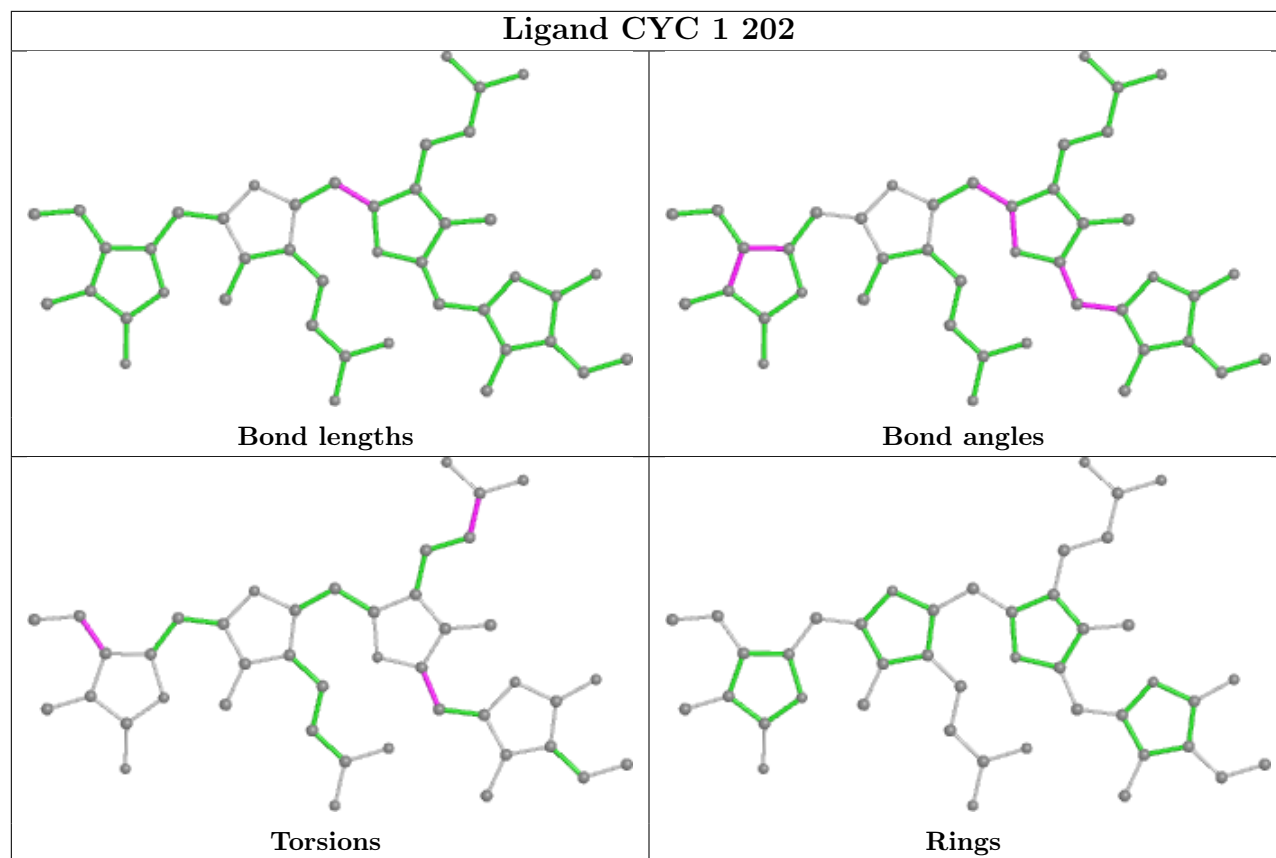












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

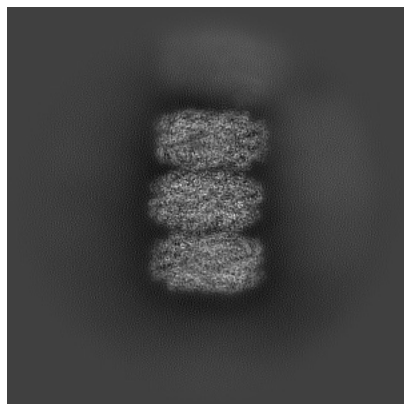
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41585. These allow visual inspection of the internal detail of the map and identification of artifacts.

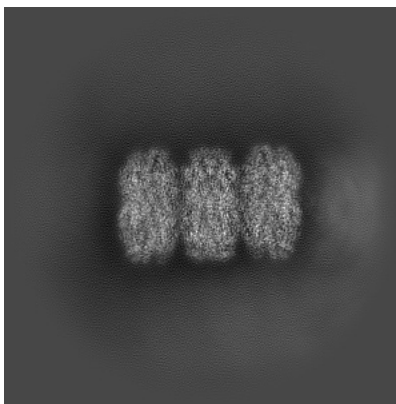
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

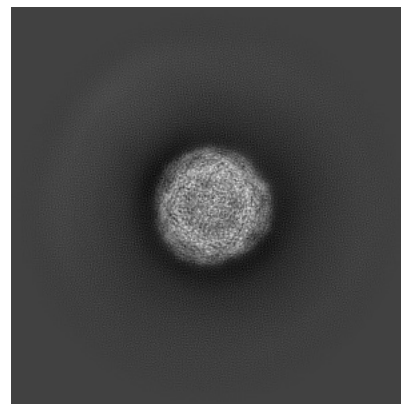
6.1.1 Primary map



X

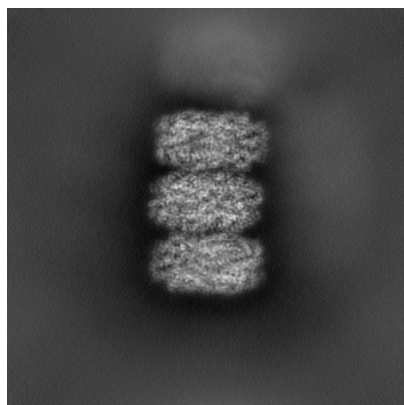


Y

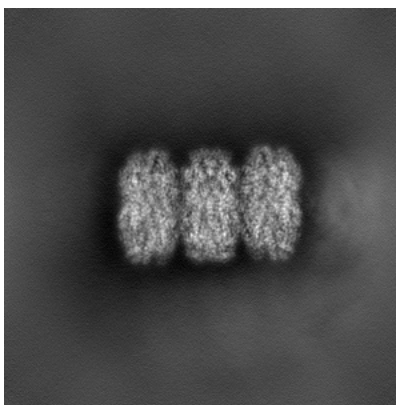


Z

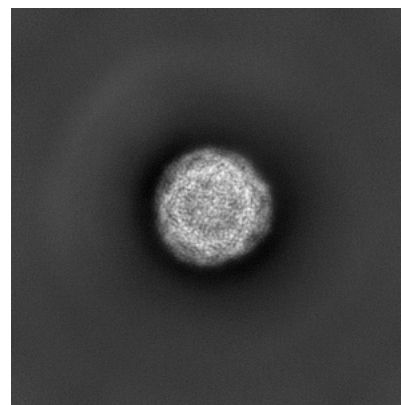
6.1.2 Raw map



X



Y

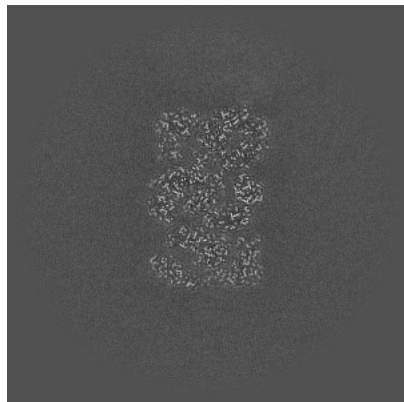


Z

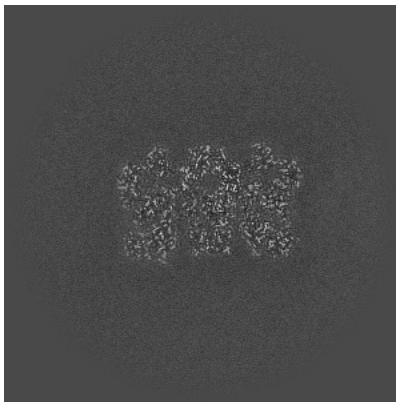
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

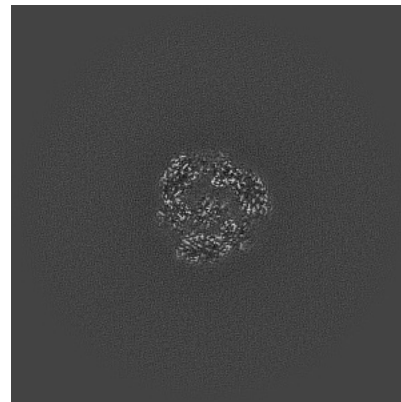
6.2.1 Primary map



X Index: 256

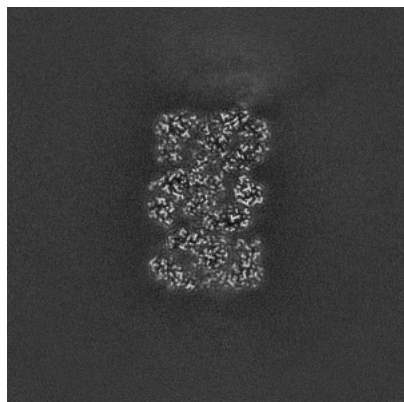


Y Index: 256

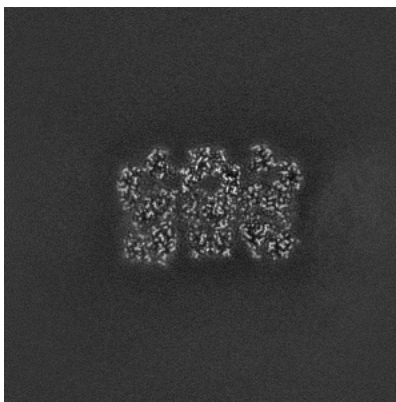


Z Index: 256

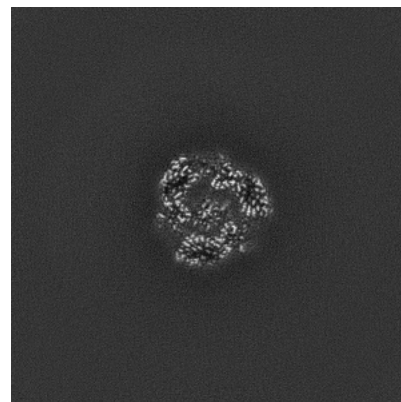
6.2.2 Raw map



X Index: 256



Y Index: 256

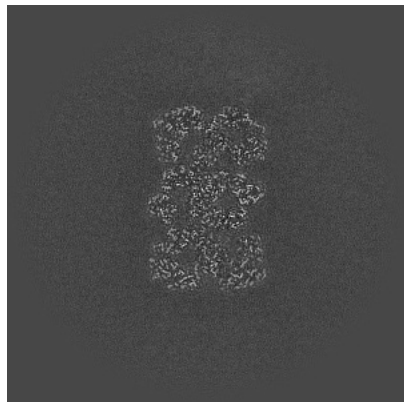


Z Index: 256

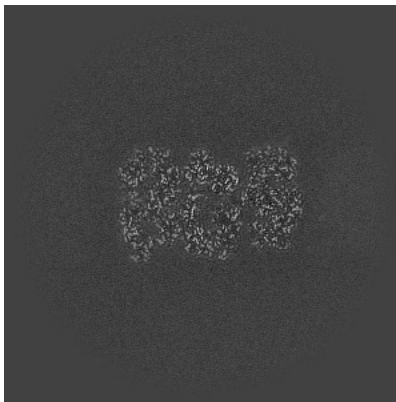
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

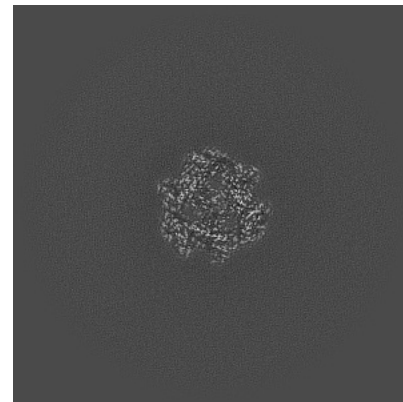
6.3.1 Primary map



X Index: 249

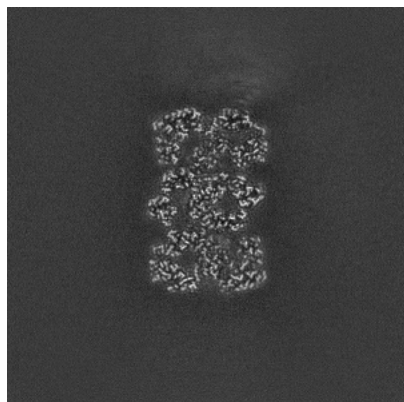


Y Index: 277

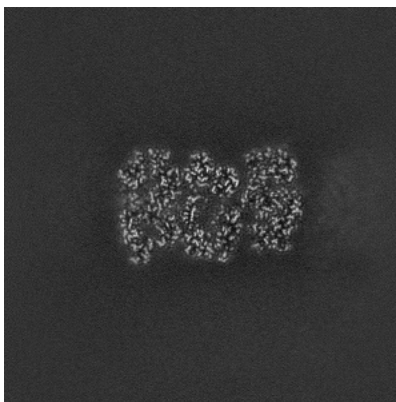


Z Index: 281

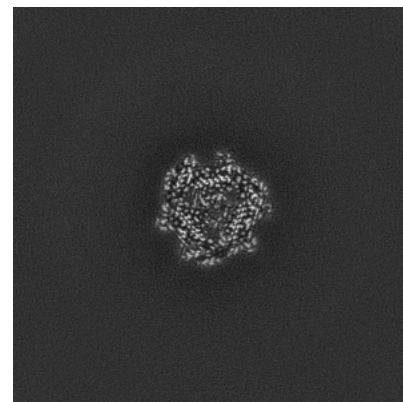
6.3.2 Raw map



X Index: 249



Y Index: 277

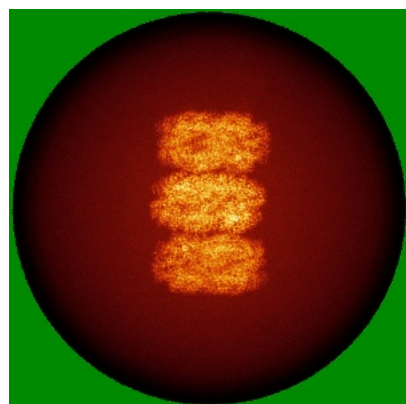


Z Index: 245

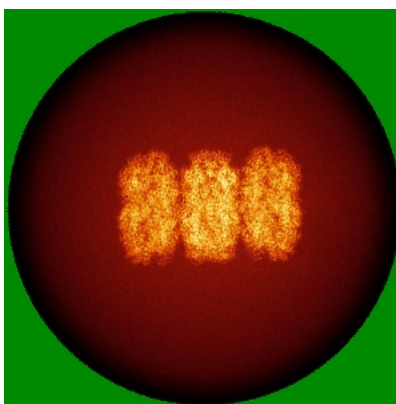
The images above show the largest variance slices of the map in three orthogonal directions.

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

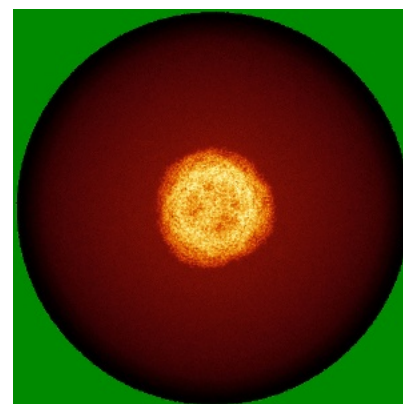
6.4.1 Primary map



X

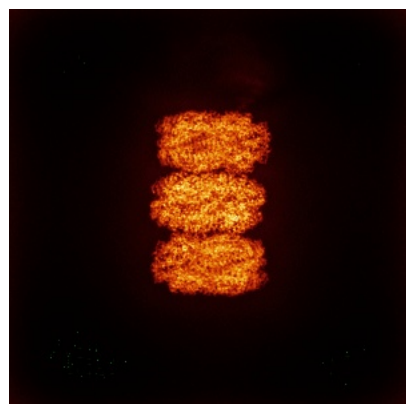


Y

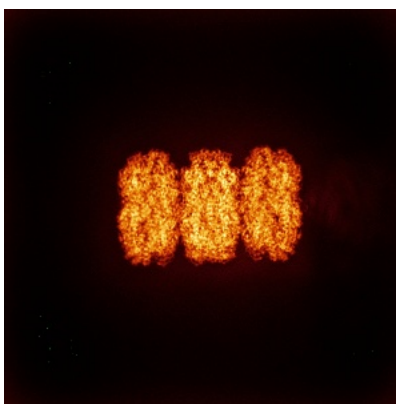


Z

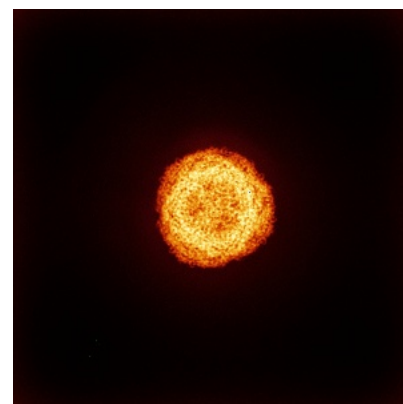
6.4.2 Raw map



X



Y



Z

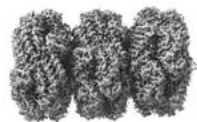
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



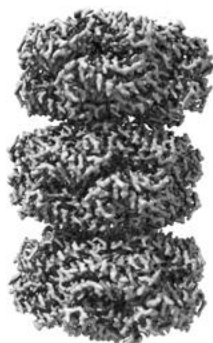
Y



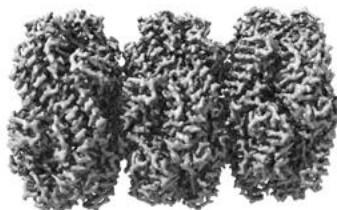
Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. 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



X



Y



Z

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.

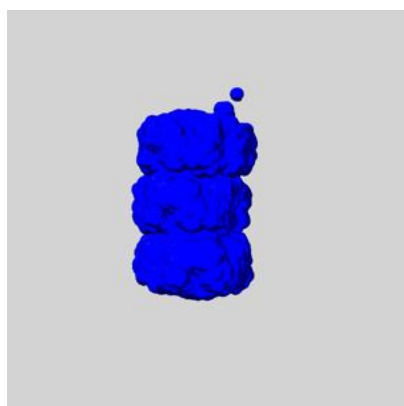
6.6 Mask visualisation [i](#)

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

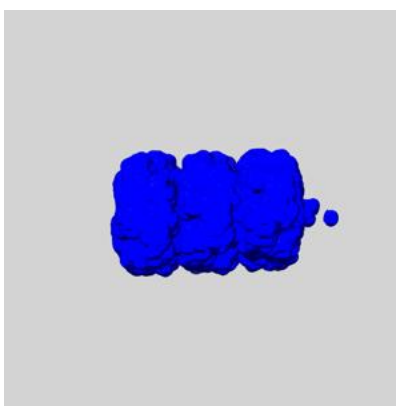
A mask typically either:

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

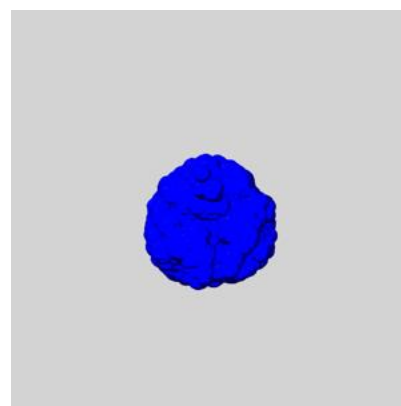
6.6.1 emd_41585_msk_1.map [i](#)



X



Y

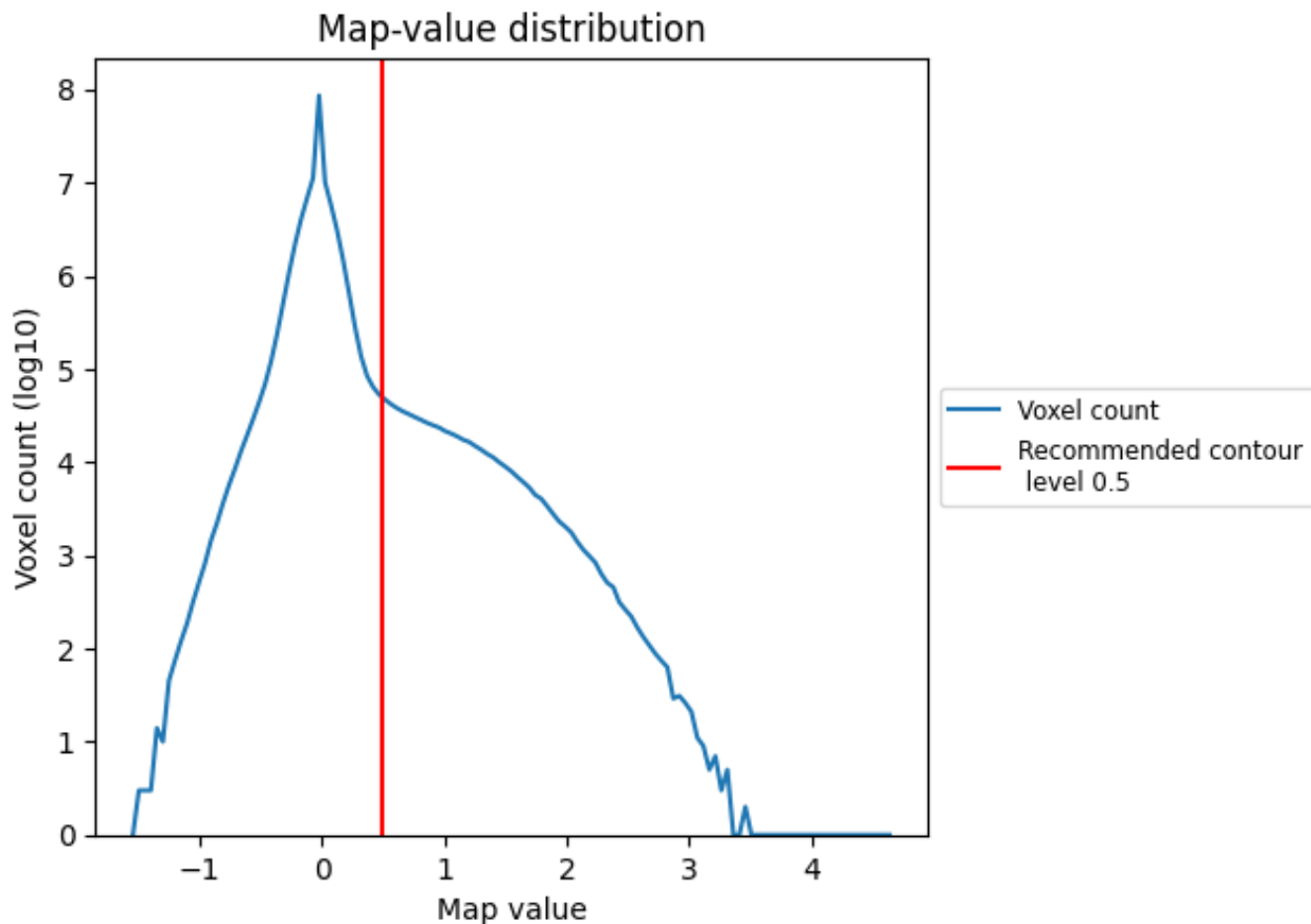


Z

7 Map analysis [i](#)

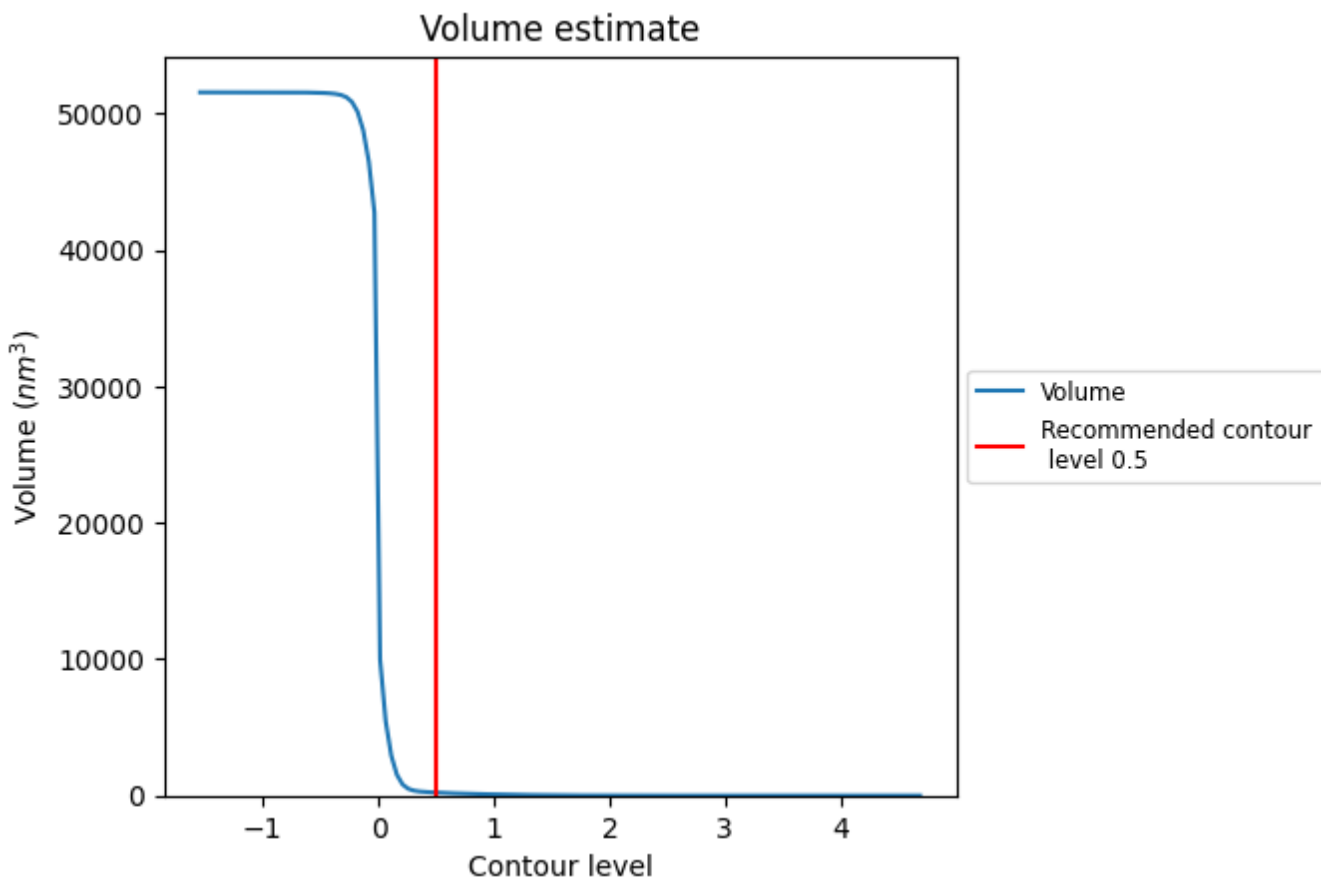
This section contains the results of statistical analysis of the map.

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.

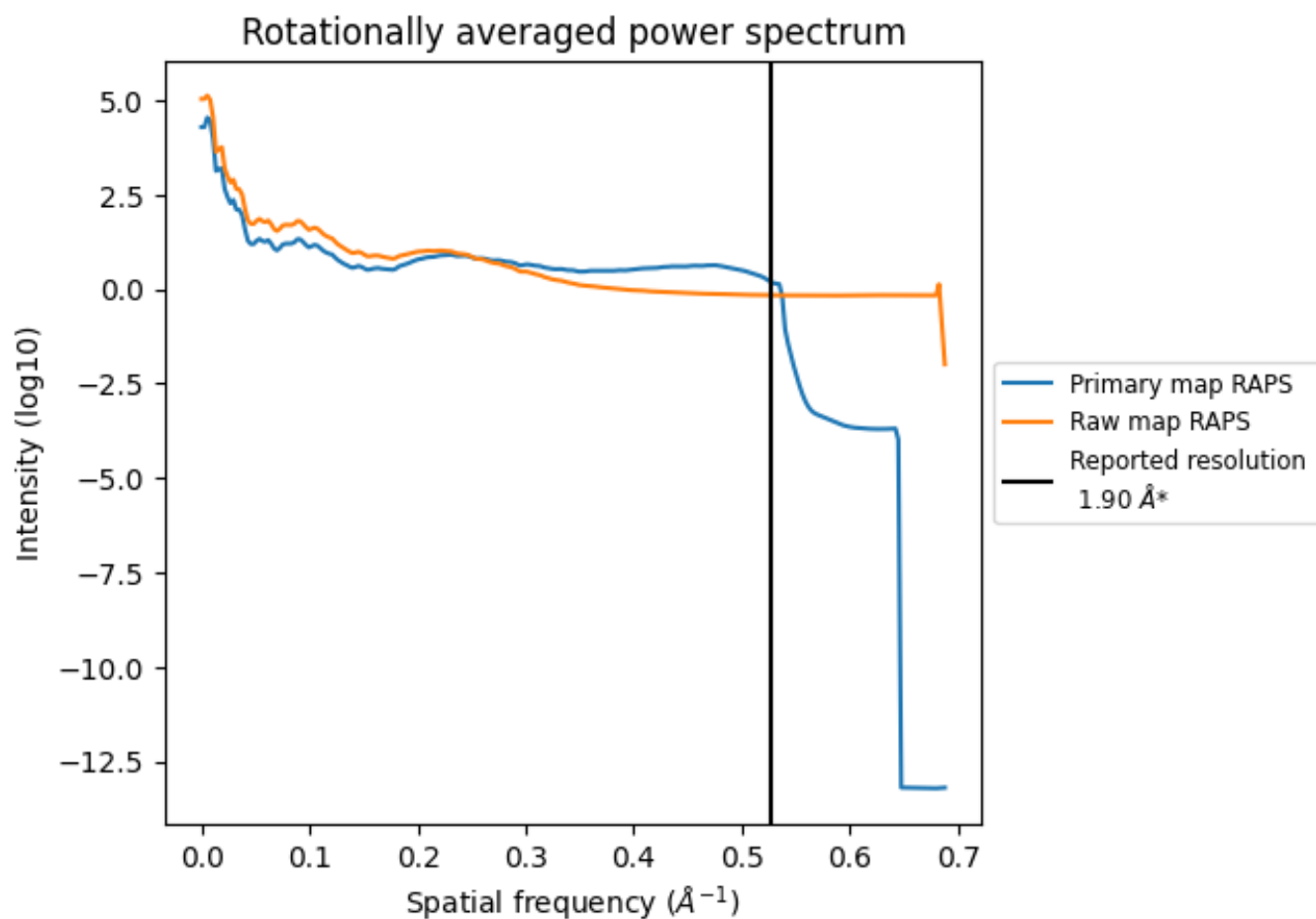
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 217 nm³; this corresponds to an approximate mass of 196 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 [i](#)

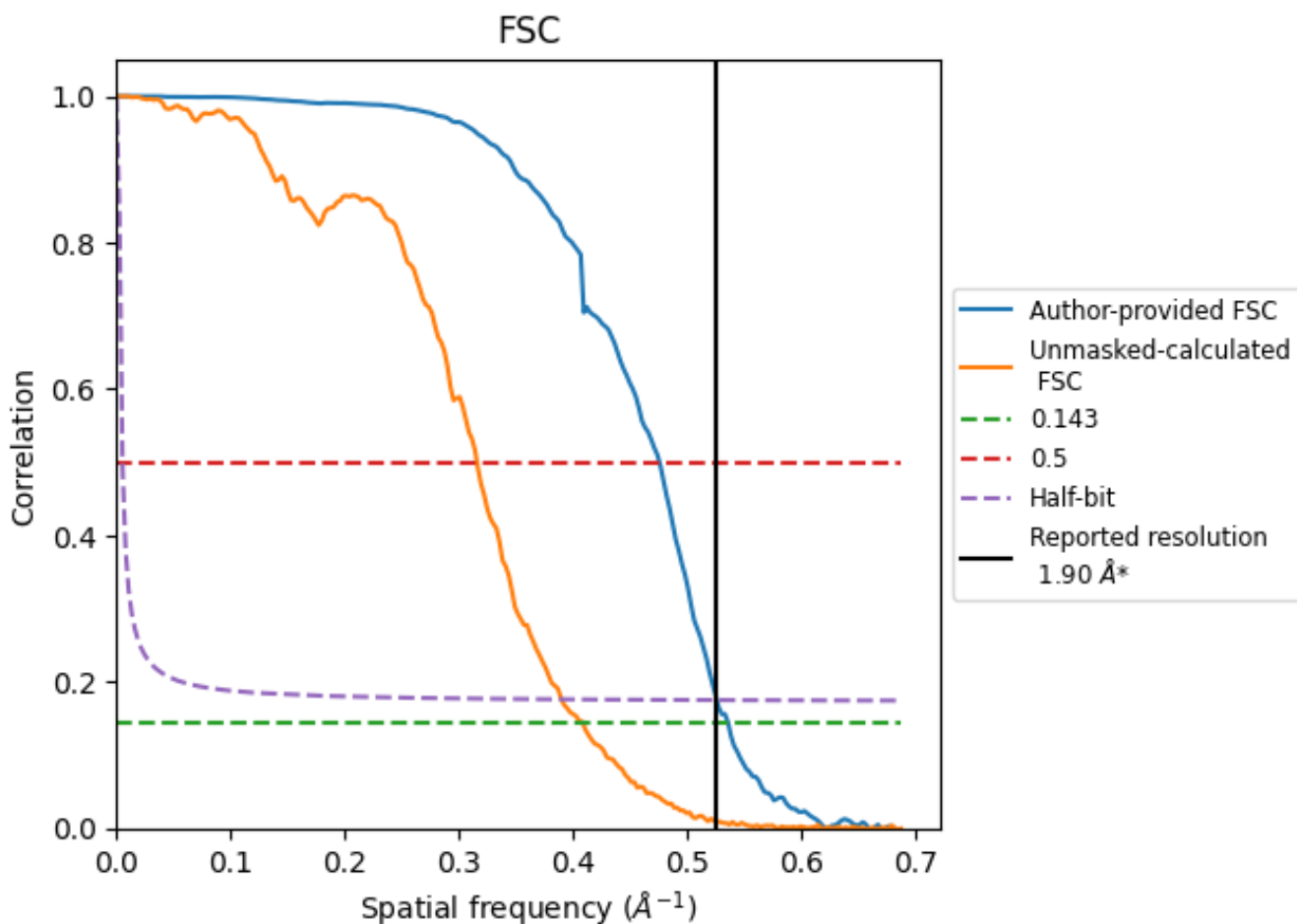


*Reported resolution corresponds to spatial frequency of 0.526 \AA^{-1}

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 0.526 \AA^{-1}

8.2 Resolution estimates [i](#)

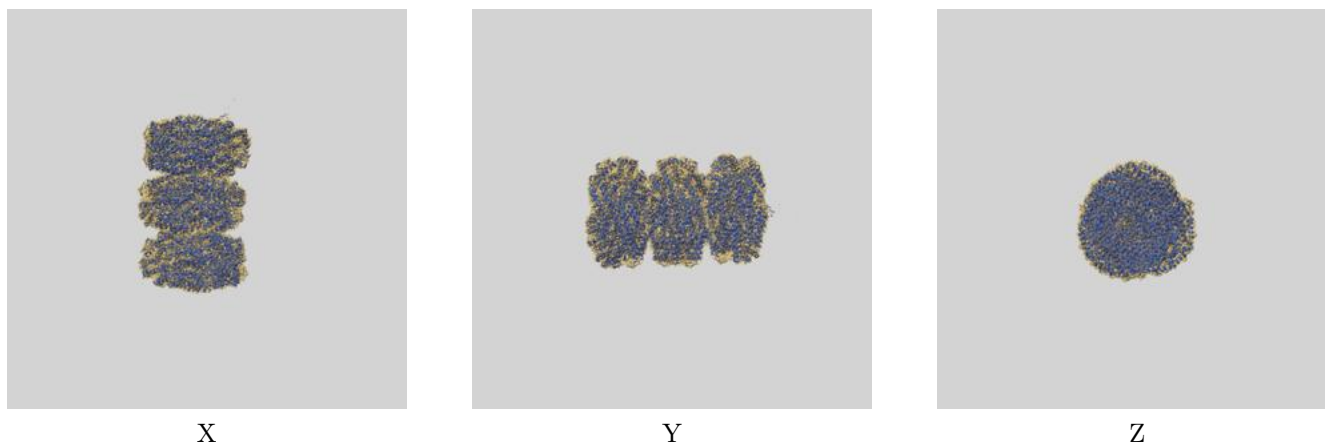
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.90	-	-
Author-provided FSC curve	1.86	2.10	1.90
Unmasked-calculated*	2.45	3.16	2.56

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.45 differs from the reported value 1.9 by more than 10 %

9 Map-model fit [i](#)

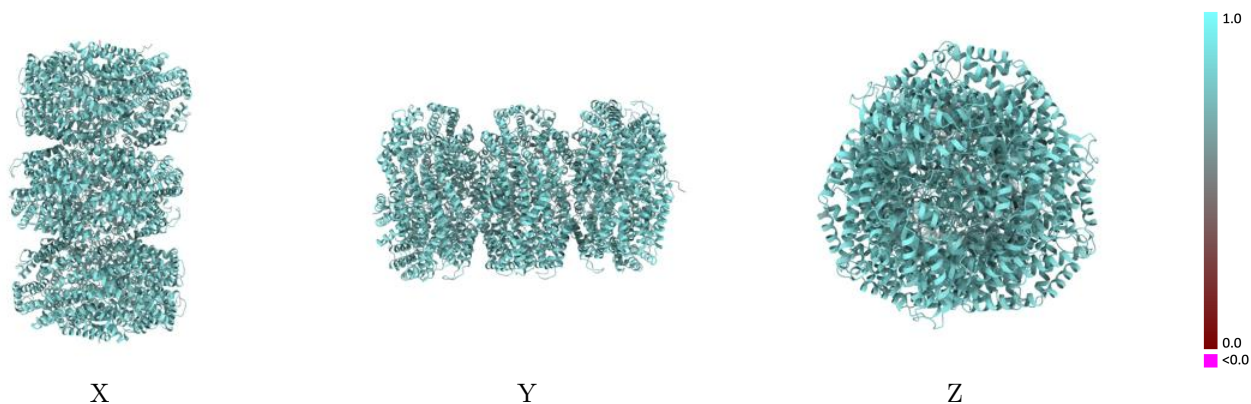
This section contains information regarding the fit between EMDB map EMD-41585 and PDB model 8TRO. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



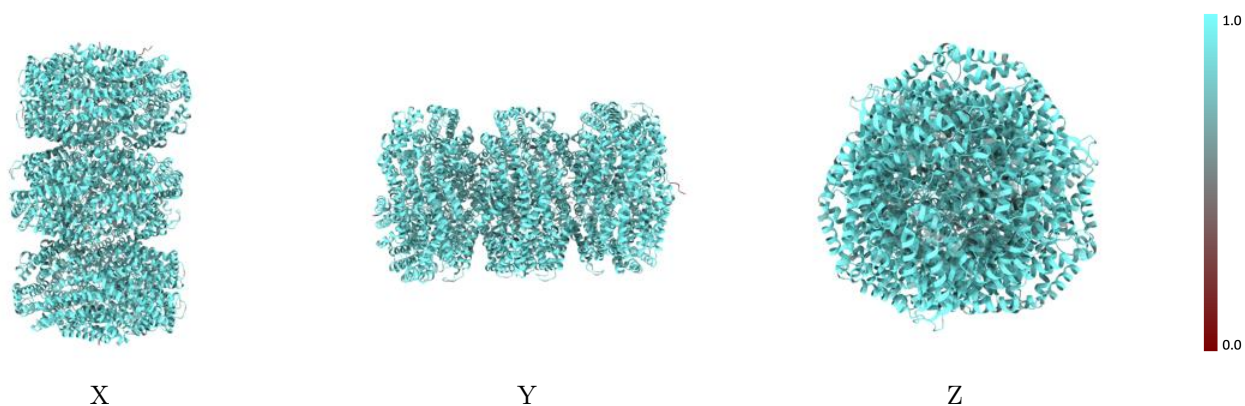
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



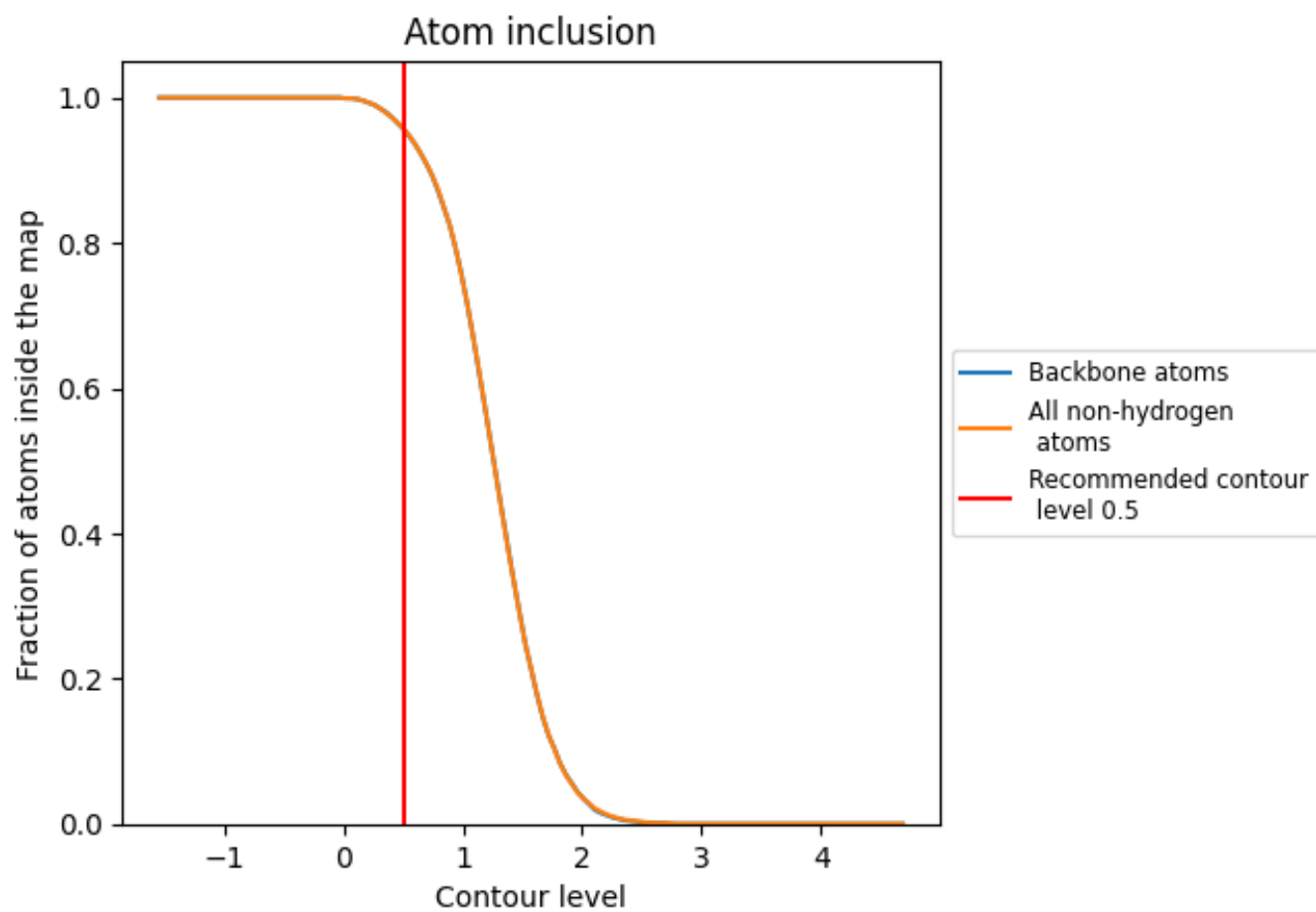
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.7910
0	 0.9630	 0.7950
1	 0.9570	 0.7980
2	 0.9470	 0.7810
3	 0.9480	 0.7790
4	 0.9600	 0.7920
5	 0.9520	 0.7970
6	 0.9670	 0.7970
7	 0.9440	 0.7830
8	 0.9500	 0.7710
9	 0.9560	 0.7880
A	 0.9470	 0.7680
B	 0.9520	 0.7790
C	 0.9470	 0.7760
D	 0.9550	 0.7790
E	 0.9450	 0.7790
F	 0.9530	 0.7790
G	 0.9570	 0.7850
H	 0.9580	 0.7890
I	 0.9520	 0.7720
J	 0.9550	 0.7840
K	 0.9530	 0.7800
L	 0.9580	 0.7960
M	 0.9680	 0.8020
N	 0.9750	 0.8120
O	 0.9680	 0.8010
P	 0.9670	 0.7960
Q	 0.9640	 0.7940
R	 0.9570	 0.7910
S	 0.9710	 0.8060
T	 0.9800	 0.8180
U	 0.9770	 0.8030
V	 0.9660	 0.8030
W	 0.9680	 0.8000
X	 0.9620	 0.7990



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Chain	Atom inclusion	Q-score
Y	 0.9540	 0.7790
Z	 0.9650	 0.8040
a	 0.9410	 0.7960
b	 0.9680	 0.8090
c	 0.9500	 0.7910
d	 0.8820	 0.7550