



# wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:25 PM UTC

PDB ID : 9I1R / pdb\_00009i1r  
EMDB ID : EMD-52573  
Title : Structure of the bicylindrical allophycocyanin core expressed during far-red light photoacclimation (FaRLiP)  
Authors : Consoli, G.; Leong, H.F.; Davis, G.A.; Richardson, T.; McInnes, A.; Murray, J.W.; Fantuzzi, A.; Rutherford, A.W.  
Deposited on : 2025-01-16  
Resolution : 2.51 Å (reported)  
Based on initial model : 8UHE

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

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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

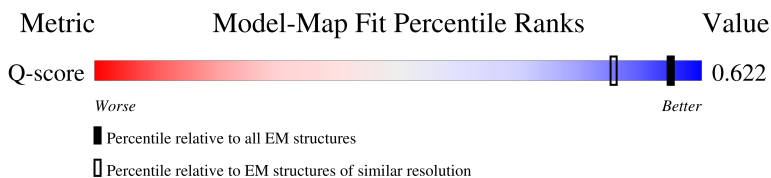
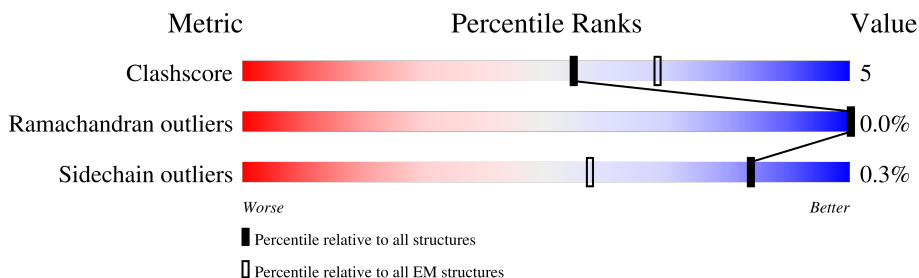
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*




The reported resolution of this entry is 2.51 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.













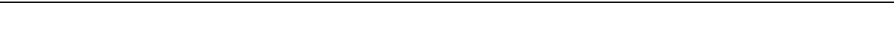

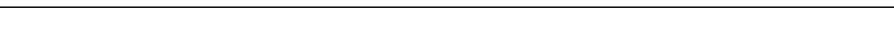
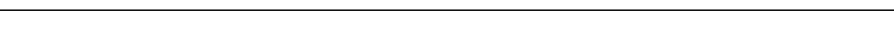




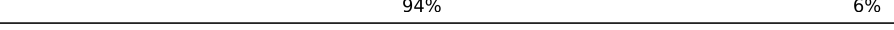



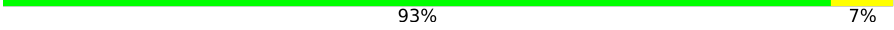


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7159 ( 2.01 - 3.01 )

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	158	
1	E	158	
1	G	158	












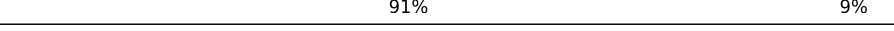







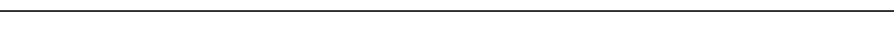

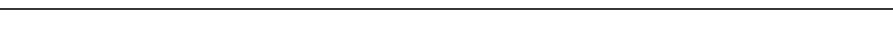
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Mol	Chain	Length	Quality of chain
1	M	158	 89% 10% .
1	O	158	 91% 8% .
1	Q	158	 89% 9% ..
1	T	158	 84% 15% ..
1	V	158	 84% 15% ..
1	X	158	 83% 16% ..
1	a	158	 87% 12% .
1	e	158	 85% 14% ..
1	g	158	 85% 14% .
1	m	158	 90% 9% .
1	o	158	 88% 11% ..
1	q	158	 87% 11% ..
1	t	158	 85% 13% ..
1	v	158	 86% 13% .
1	x	158	 81% 18% ..
2	B	161	 83% 17% .
2	D	161	 91% 9%
2	F	161	 94% 6%
2	H	161	 91% 9%
2	L	161	 83% 17% .
2	N	161	 88% 12%
2	P	161	 93% 7%
2	R	161	 89% 11%
2	U	161	 89% 11%
2	W	161	 90% 10%

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Mol	Chain	Length	Quality of chain
2	Y	161	 89% 11%
2	b	161	 83% 16% .
2	d	161	 90% 10%
2	f	161	 88% 12%
2	h	161	 91% 9%
2	l	161	 82% 17% .
2	n	161	 90% 10%
2	p	161	 92% 8%
2	r	161	 88% 12%
2	u	161	 89% 11%
2	w	161	 91% 9%
2	y	161	 91% 9%
3	C	175	 85% 14% .
3	c	175	 83% 16% .
4	I	159	 88% 11% .
4	i	159	 89% 10% .
5	J	169	 88% 12%
5	j	169	 91% 9%
6	K	780	 77% 9% 14%
6	k	780	 78% 8% 14%
7	S	67	 88% 12%
7	s	67	 91% 9%

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 71362 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 Phycocyanin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	E	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	G	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	M	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	O	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	Q	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	T	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	V	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	X	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	a	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	e	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	g	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	m	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	o	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	q	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	t	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		
1	v	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	x	157	Total	C	N	O	S	0	0
			1260	787	219	247	7		

- Molecule 2 is a protein called Allophycocyanin beta subunit apoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	D	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	F	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	H	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	L	160	Total	C	N	O	S	0	0
			1217	762	210	237	8		
2	N	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	P	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	R	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	U	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	W	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	Y	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	b	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	d	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	f	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	h	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	l	160	Total	C	N	O	S	0	0
			1217	762	210	237	8		
2	n	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	p	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	r	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	u	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	w	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		
2	y	161	Total	C	N	O	S	0	0
			1224	765	211	240	8		

- Molecule 3 is a protein called Phycocyanin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	174	Total	C	N	O	S	0	0
			1392	885	243	256	8		
3	c	174	Total	C	N	O	S	0	0
			1392	885	243	256	8		

- Molecule 4 is a protein called Phycocyanin.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	158	Total	C	N	O	S	0	0
			1270	800	220	242	8		
4	i	158	Total	C	N	O	S	0	0
			1270	800	220	242	8		

- Molecule 5 is a protein called Allophycocyanin beta-18 subunit apoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	169	Total	C	N	O	S	0	0
			1316	831	220	258	7		
5	j	169	Total	C	N	O	S	0	0
			1316	831	220	258	7		

- Molecule 6 is a protein called Phycobiliprotein ApcE.

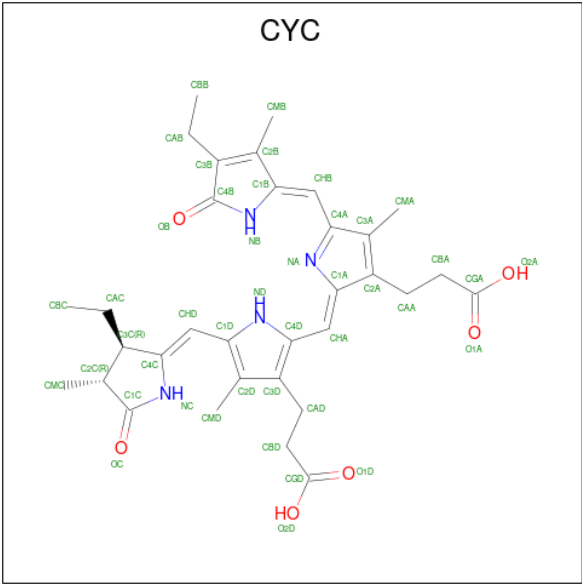
Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	669	Total	C	N	O	S	0	0
			5318	3387	939	978	14		
6	k	669	Total	C	N	O	S	0	0
			5318	3387	939	978	14		

- Molecule 7 is a protein called Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-as

sociated, core.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	S	67	Total 546	347	101	92	6	0	0
7	s	67	Total 546	347	101	92	6	0	0

- Molecule 8 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: C<sub>33</sub>H<sub>40</sub>N<sub>4</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
8	A	1	Total 43	33	4	6	0
8	B	1	Total 43	33	4	6	0
8	C	1	Total 43	33	4	6	0
8	D	1	Total 43	33	4	6	0
8	E	1	Total 43	33	4	6	0
8	F	1	Total 43	33	4	6	0
8	G	1	Total 43	33	4	6	0
8	H	1	Total 43	33	4	6	0

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Mol	Chain	Residues	Atoms				AltConf
8	I	1	Total 43	C 33	N 4	O 6	0
8	J	1	Total 43	C 33	N 4	O 6	0
8	K	1	Total 43	C 33	N 4	O 6	0
8	L	1	Total 43	C 33	N 4	O 6	0
8	M	1	Total 43	C 33	N 4	O 6	0
8	N	1	Total 43	C 33	N 4	O 6	0
8	O	1	Total 43	C 33	N 4	O 6	0
8	P	1	Total 43	C 33	N 4	O 6	0
8	Q	1	Total 43	C 33	N 4	O 6	0
8	R	1	Total 43	C 33	N 4	O 6	0
8	T	1	Total 43	C 33	N 4	O 6	0
8	U	1	Total 43	C 33	N 4	O 6	0
8	V	1	Total 43	C 33	N 4	O 6	0
8	W	1	Total 43	C 33	N 4	O 6	0
8	X	1	Total 43	C 33	N 4	O 6	0
8	Y	1	Total 43	C 33	N 4	O 6	0
8	a	1	Total 43	C 33	N 4	O 6	0
8	b	1	Total 43	C 33	N 4	O 6	0
8	c	1	Total 43	C 33	N 4	O 6	0
8	d	1	Total 43	C 33	N 4	O 6	0
8	e	1	Total 43	C 33	N 4	O 6	0

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Mol	Chain	Residues	Atoms				AltConf
8	f	1	Total 43	C 33	N 4	O 6	0
8	g	1	Total 43	C 33	N 4	O 6	0
8	h	1	Total 43	C 33	N 4	O 6	0
8	i	1	Total 43	C 33	N 4	O 6	0
8	j	1	Total 43	C 33	N 4	O 6	0
8	k	1	Total 43	C 33	N 4	O 6	0
8	l	1	Total 43	C 33	N 4	O 6	0
8	m	1	Total 43	C 33	N 4	O 6	0
8	n	1	Total 43	C 33	N 4	O 6	0
8	o	1	Total 43	C 33	N 4	O 6	0
8	p	1	Total 43	C 33	N 4	O 6	0
8	q	1	Total 43	C 33	N 4	O 6	0
8	r	1	Total 43	C 33	N 4	O 6	0
8	t	1	Total 43	C 33	N 4	O 6	0
8	u	1	Total 43	C 33	N 4	O 6	0
8	v	1	Total 43	C 33	N 4	O 6	0
8	w	1	Total 43	C 33	N 4	O 6	0
8	x	1	Total 43	C 33	N 4	O 6	0
8	y	1	Total 43	C 33	N 4	O 6	0


- Molecule 9 is water.

Mol	Chain	Residues	Atoms		AltConf
9	G	1	Total 1	O 1	0
9	I	1	Total 1	O 1	0
9	J	1	Total 1	O 1	0
9	K	1	Total 1	O 1	0
9	R	2	Total 2	O 2	0
9	T	3	Total 3	O 3	0
9	U	1	Total 1	O 1	0
9	g	1	Total 1	O 1	0
9	i	1	Total 1	O 1	0
9	j	1	Total 1	O 1	0
9	k	1	Total 1	O 1	0
9	r	2	Total 2	O 2	0
9	t	3	Total 3	O 3	0
9	u	1	Total 1	O 1	0

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


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

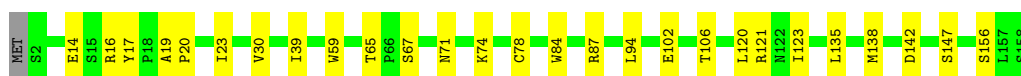
- Molecule 1: Phycocyanin

Chain A:  85% 14% ..




- Molecule 1: Phycocyanin

Chain E:  82% 17% .



- Molecule 1: Phycocyanin

Chain G:  84% 15% .



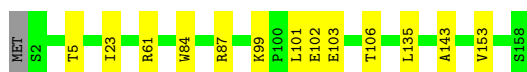
- Molecule 1: Phycocyanin

Chain M:  89% 10% .




- Molecule 1: Phycocyanin

Chain O:  91% 8% .




- Molecule 1: Phycocyanin

Chain Q:  89% 9% ..




- Molecule 1: Phycocyanin

Chain T:  84% 15% ..




- Molecule 1: Phycocyanin

Chain V:  84% 15% ..




- Molecule 1: Phycocyanin

Chain X:  83% 16% ..




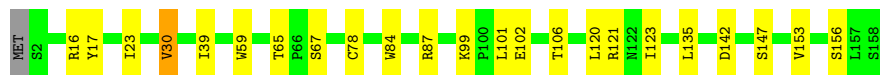
- Molecule 1: Phycocyanin

Chain a:  87% 12% .




- Molecule 1: Phycocyanin

Chain e:  85% 14% ..




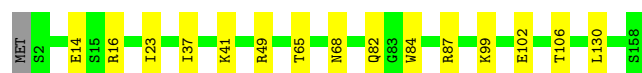
- Molecule 1: Phycocyanin

Chain g:  85% 14% .




- Molecule 1: Phycocyanin

Chain m:  90% 9%




• Molecule 1: Phycocyanin

Chain o:  88% 11%




• Molecule 1: Phycocyanin

Chain q:  87% 11%




• Molecule 1: Phycocyanin

Chain t:  85% 13%




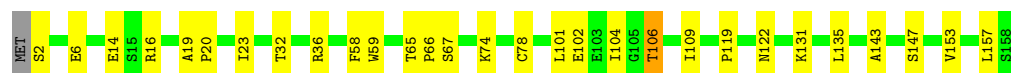
• Molecule 1: Phycocyanin

Chain v:  86% 13%




• Molecule 1: Phycocyanin

Chain x:  81% 18%



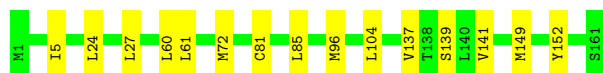
• Molecule 2: Allophycocyanin beta subunit apoprotein

Chain B:  83% 17%



• Molecule 2: Allophycocyanin beta subunit apoprotein

Chain D:  91% 9%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain F:  94% 6%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain H:  91% 9%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain L:  83% 17%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain N:  88% 12%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain P:  93% 7%




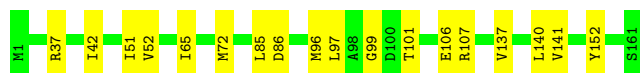
- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain R:  89% 11%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain U:  89% 11%




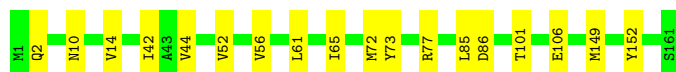
- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain W:  90% 10%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain Y:  89% 11%



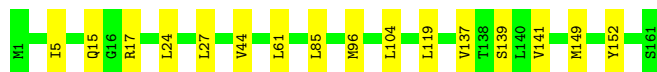
- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain b:  83% 16%




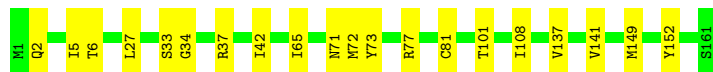
- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain d:  90% 10%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain f:  88% 12%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain h:  91% 9%




- Molecule 2: Allophycocyanin beta subunit apoprotein



Chain l:  82% 17%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain n:  90% 10%




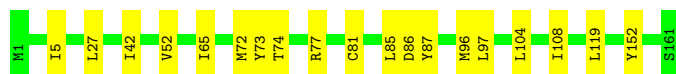
- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain p:  92% 8%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain r:  88% 12%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain u:  89% 11%



- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain w:  91% 9%




- Molecule 2: Allophycocyanin beta subunit apoprotein

Chain y:  91% 9%




- Molecule 3: Phycocyanin

Chain C:  85% 14%




- Molecule 3: Phycocyanin

Chain c:  83% 16%




- Molecule 4: Phycocyanin

Chain I:  88% 11%




- Molecule 4: Phycocyanin

Chain i:  89% 10%




- Molecule 5: Allophycocyanin beta-18 subunit apoprotein

Chain J:  88% 12%




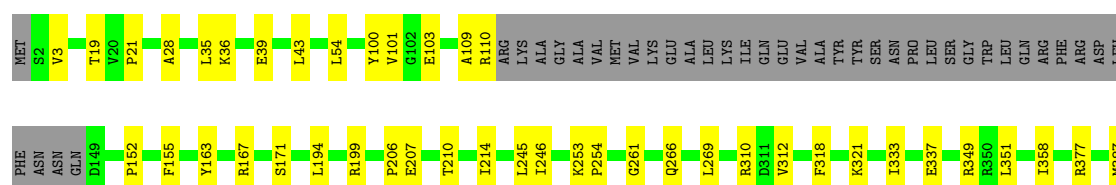
- Molecule 5: Allophycocyanin beta-18 subunit apoprotein

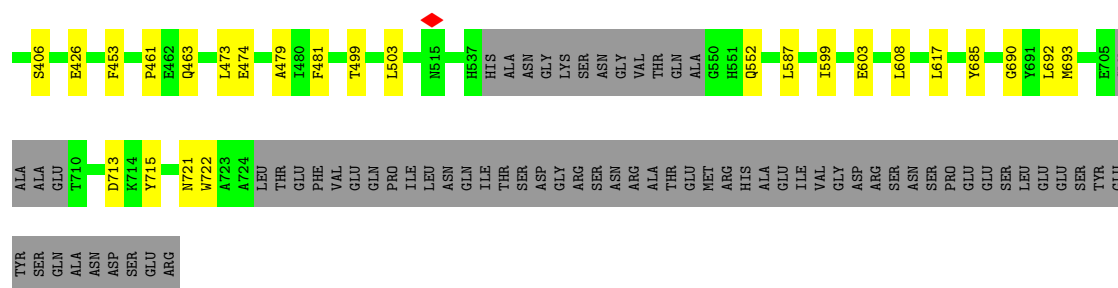
Chain j:  91% 9%



- Molecule 6: Phycobiliprotein ApcE

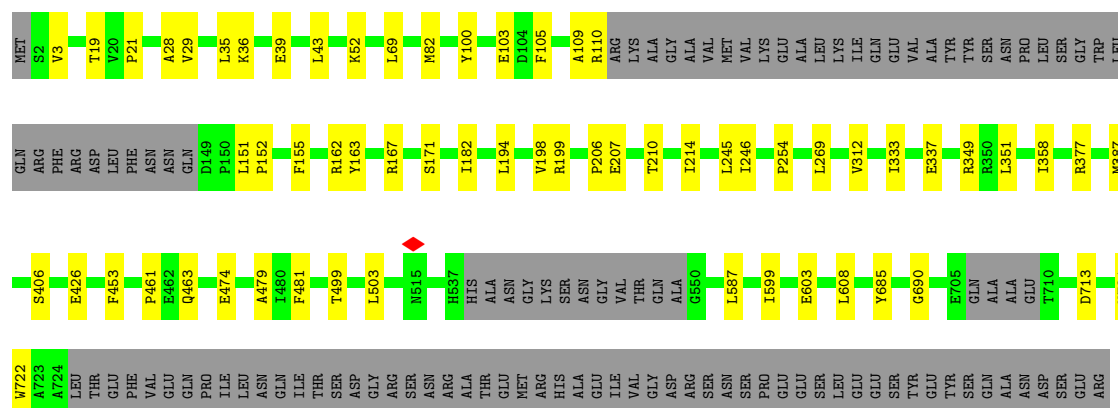
Chain K:  77% 9% 14%





• Molecule 6: Phycobiliprotein ApcE

Chain k: 78% 8% 14%



• Molecule 7: Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-associated, core

Chain S: 88% 12%



• Molecule 7: Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-associated, core

Chain s: 91% 9%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	36300	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)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.487	Depositor
Minimum map value	-0.637	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	506.1, 506.1, 506.1	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.723, 0.723, 0.723	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	A	0.17	0/1279	0.30	0/1725
1	E	0.20	0/1279	0.27	0/1725
1	G	0.20	0/1279	0.28	0/1725
1	M	0.21	0/1279	0.27	0/1725
1	O	0.18	0/1279	0.28	0/1725
1	Q	0.18	0/1279	0.26	0/1725
1	T	0.22	0/1279	0.29	0/1725
1	V	0.19	0/1279	0.28	0/1725
1	X	0.20	0/1279	0.28	0/1725
1	a	0.18	0/1279	0.34	0/1725
1	e	0.20	0/1279	0.26	0/1725
1	g	0.20	0/1279	0.28	0/1725
1	m	0.21	0/1279	0.27	0/1725
1	o	0.19	0/1279	0.28	0/1725
1	q	0.18	0/1279	0.29	0/1725
1	t	0.22	0/1279	0.30	0/1725
1	v	0.20	0/1279	0.27	0/1725
1	x	0.20	0/1279	0.29	0/1725
2	B	0.19	0/1230	0.29	0/1662
2	D	0.21	0/1230	0.27	0/1662
2	F	0.18	0/1230	0.29	0/1662
2	H	0.22	0/1230	0.31	0/1662
2	L	0.21	0/1223	0.30	0/1654
2	N	0.18	0/1230	0.28	0/1662
2	P	0.19	0/1230	0.28	0/1662
2	R	0.19	0/1230	0.29	0/1662
2	U	0.20	0/1230	0.30	0/1662
2	W	0.20	0/1230	0.28	0/1662
2	Y	0.22	0/1230	0.31	0/1662
2	b	0.19	0/1230	0.29	0/1662
2	d	0.20	0/1230	0.27	0/1662
2	f	0.18	0/1230	0.30	0/1662

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	h	0.21	0/1230	0.30	0/1662
2	l	0.20	0/1223	0.29	0/1654
2	n	0.18	0/1230	0.27	0/1662
2	p	0.19	0/1230	0.28	0/1662
2	r	0.19	0/1230	0.28	0/1662
2	u	0.20	0/1230	0.31	0/1662
2	w	0.21	0/1230	0.30	0/1662
2	y	0.22	0/1230	0.31	0/1662
3	C	0.19	0/1419	0.28	0/1920
3	c	0.20	0/1419	0.28	0/1920
4	I	0.22	0/1292	0.29	0/1749
4	i	0.22	0/1292	0.30	0/1749
5	J	0.22	0/1324	0.30	0/1789
5	j	0.23	0/1324	0.31	0/1789
6	K	0.22	0/5443	0.29	0/7364
6	k	0.22	0/5443	0.29	0/7364
7	S	0.21	0/555	0.32	0/743
7	s	0.20	0/555	0.32	0/743
All	All	0.20	0/70134	0.29	0/94728

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	A	1260	0	1253	13	0
1	E	1260	0	1253	17	0
1	G	1260	0	1253	15	0
1	M	1260	0	1253	10	0
1	O	1260	0	1253	8	0
1	Q	1260	0	1253	10	0
1	T	1260	0	1253	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V	1260	0	1253	13	0
1	X	1260	0	1253	16	0
1	a	1260	0	1253	10	0
1	e	1260	0	1253	15	0
1	g	1260	0	1253	14	0
1	m	1260	0	1253	10	0
1	o	1260	0	1253	10	0
1	q	1260	0	1253	11	0
1	t	1260	0	1253	14	0
1	v	1260	0	1253	16	0
1	x	1260	0	1253	18	0
2	B	1224	0	1227	19	0
2	D	1224	0	1227	12	0
2	F	1224	0	1227	7	0
2	H	1224	0	1227	9	0
2	L	1217	0	1222	17	0
2	N	1224	0	1227	15	0
2	P	1224	0	1227	8	0
2	R	1224	0	1227	13	0
2	U	1224	0	1227	11	0
2	W	1224	0	1227	11	0
2	Y	1224	0	1227	11	0
2	b	1224	0	1227	19	0
2	d	1224	0	1227	11	0
2	f	1224	0	1227	15	0
2	h	1224	0	1227	10	0
2	l	1217	0	1222	21	0
2	n	1224	0	1227	13	0
2	p	1224	0	1227	8	0
2	r	1224	0	1227	15	0
2	u	1224	0	1227	12	0
2	w	1224	0	1227	10	0
2	y	1224	0	1227	10	0
3	C	1392	0	1410	17	0
3	c	1392	0	1410	20	0
4	I	1270	0	1272	13	0
4	i	1270	0	1272	11	0
5	J	1316	0	1329	14	0
5	j	1316	0	1329	12	0
6	K	5318	0	5254	46	0
6	k	5318	0	5254	45	0
7	S	546	0	578	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	s	546	0	578	5	0
8	A	43	0	37	5	0
8	B	43	0	37	3	0
8	C	43	0	38	4	0
8	D	43	0	37	4	0
8	E	43	0	37	4	0
8	F	43	0	37	2	0
8	G	43	0	37	5	0
8	H	43	0	37	6	0
8	I	43	0	37	5	0
8	J	43	0	38	3	0
8	K	43	0	38	3	0
8	L	43	0	37	2	0
8	M	43	0	37	4	0
8	N	43	0	37	2	0
8	O	43	0	37	5	0
8	P	43	0	37	1	0
8	Q	43	0	37	4	0
8	R	43	0	37	5	0
8	T	43	0	37	3	0
8	U	43	0	37	4	0
8	V	43	0	37	4	0
8	W	43	0	37	3	0
8	X	43	0	37	5	0
8	Y	43	0	37	1	0
8	a	43	0	37	3	0
8	b	43	0	37	5	0
8	c	43	0	38	4	0
8	d	43	0	37	4	0
8	e	43	0	37	4	0
8	f	43	0	37	3	0
8	g	43	0	37	5	0
8	h	43	0	37	5	0
8	i	43	0	37	5	0
8	j	43	0	38	2	0
8	k	43	0	38	3	0
8	l	43	0	37	2	0
8	m	43	0	37	4	0
8	n	43	0	37	2	0
8	o	43	0	37	6	0
8	p	43	0	37	1	0
8	q	43	0	37	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	r	43	0	37	5	0
8	t	43	0	37	3	0
8	u	43	0	37	4	0
8	v	43	0	37	6	0
8	w	43	0	37	3	0
8	x	43	0	37	5	0
8	y	43	0	37	1	0
9	G	1	0	0	0	0
9	I	1	0	0	0	0
9	J	1	0	0	0	0
9	K	1	0	0	0	0
9	R	2	0	0	0	0
9	T	3	0	0	0	0
9	U	1	0	0	0	0
9	g	1	0	0	0	0
9	i	1	0	0	0	0
9	j	1	0	0	0	0
9	k	1	0	0	0	0
9	r	2	0	0	0	0
9	t	3	0	0	0	0
9	u	1	0	0	0	0
All	All	71362	0	71006	726	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 5.

The worst 5 of 726 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)
8:C:201:CYC:HMD1	8:C:201:CYC:HC	1.39	0.86
1:v:102:GLU:HA	1:v:106:THR:HB	1.57	0.86
1:V:102:GLU:HA	1:V:106:THR:HB	1.56	0.85
8:c:201:CYC:HMD1	8:c:201:CYC:HC	1.39	0.84
8:e:201:CYC:HB	8:e:201:CYC:HMA1	1.44	0.83

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	155/158 (98%)	155 (100%)	0	0	100	100
1	E	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	G	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	M	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	O	155/158 (98%)	155 (100%)	0	0	100	100
1	Q	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	T	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	V	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	X	155/158 (98%)	155 (100%)	0	0	100	100
1	a	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	e	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	g	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	m	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	o	155/158 (98%)	155 (100%)	0	0	100	100
1	q	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	t	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	v	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	x	155/158 (98%)	155 (100%)	0	0	100	100
2	B	158/161 (98%)	157 (99%)	0	1 (1%)	21	38
2	D	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	F	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	H	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	L	157/161 (98%)	155 (99%)	1 (1%)	1 (1%)	21	38
2	N	158/161 (98%)	156 (99%)	1 (1%)	1 (1%)	21	38
2	P	158/161 (98%)	157 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	R	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	U	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	W	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	Y	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	b	158/161 (98%)	157 (99%)	0	1 (1%)	21	38
2	d	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	f	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	h	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	l	157/161 (98%)	155 (99%)	2 (1%)	0	100	100
2	n	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	p	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	r	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	u	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	w	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	y	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
3	C	172/175 (98%)	168 (98%)	4 (2%)	0	100	100
3	c	172/175 (98%)	168 (98%)	4 (2%)	0	100	100
4	I	156/159 (98%)	154 (99%)	2 (1%)	0	100	100
4	i	156/159 (98%)	154 (99%)	2 (1%)	0	100	100
5	J	166/169 (98%)	162 (98%)	4 (2%)	0	100	100
5	j	166/169 (98%)	162 (98%)	4 (2%)	0	100	100
6	K	661/780 (85%)	641 (97%)	20 (3%)	0	100	100
6	k	661/780 (85%)	643 (97%)	18 (3%)	0	100	100
7	S	65/67 (97%)	65 (100%)	0	0	100	100
7	s	65/67 (97%)	65 (100%)	0	0	100	100
All	All	8704/9086 (96%)	8589 (99%)	111 (1%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	74	THR
2	L	74	THR
2	N	74	THR

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Mol	Chain	Res	Type
2	b	74	THR

### 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	139/140 (99%)	137 (99%)	2 (1%)	59	81
1	E	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	G	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	M	139/140 (99%)	139 (100%)	0	100	100
1	O	139/140 (99%)	139 (100%)	0	100	100
1	Q	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	T	139/140 (99%)	137 (99%)	2 (1%)	59	81
1	V	139/140 (99%)	137 (99%)	2 (1%)	59	81
1	X	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	a	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	e	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	g	139/140 (99%)	139 (100%)	0	100	100
1	m	139/140 (99%)	139 (100%)	0	100	100
1	o	139/140 (99%)	137 (99%)	2 (1%)	59	81
1	q	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	t	139/140 (99%)	138 (99%)	1 (1%)	76	89
1	v	139/140 (99%)	139 (100%)	0	100	100
1	x	139/140 (99%)	138 (99%)	1 (1%)	76	89
2	B	128/128 (100%)	128 (100%)	0	100	100
2	D	128/128 (100%)	128 (100%)	0	100	100
2	F	128/128 (100%)	128 (100%)	0	100	100
2	H	128/128 (100%)	128 (100%)	0	100	100
2	L	127/128 (99%)	127 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	N	128/128 (100%)	128 (100%)	0	100	100
2	P	128/128 (100%)	128 (100%)	0	100	100
2	R	128/128 (100%)	128 (100%)	0	100	100
2	U	128/128 (100%)	128 (100%)	0	100	100
2	W	128/128 (100%)	128 (100%)	0	100	100
2	Y	128/128 (100%)	128 (100%)	0	100	100
2	b	128/128 (100%)	128 (100%)	0	100	100
2	d	128/128 (100%)	128 (100%)	0	100	100
2	f	128/128 (100%)	128 (100%)	0	100	100
2	h	128/128 (100%)	128 (100%)	0	100	100
2	l	127/128 (99%)	127 (100%)	0	100	100
2	n	128/128 (100%)	128 (100%)	0	100	100
2	p	128/128 (100%)	127 (99%)	1 (1%)	73	88
2	r	128/128 (100%)	128 (100%)	0	100	100
2	u	128/128 (100%)	128 (100%)	0	100	100
2	w	128/128 (100%)	128 (100%)	0	100	100
2	y	128/128 (100%)	128 (100%)	0	100	100
3	C	150/151 (99%)	150 (100%)	0	100	100
3	c	150/151 (99%)	150 (100%)	0	100	100
4	I	140/141 (99%)	140 (100%)	0	100	100
4	i	140/141 (99%)	140 (100%)	0	100	100
5	J	144/144 (100%)	144 (100%)	0	100	100
5	j	144/144 (100%)	144 (100%)	0	100	100
6	K	560/657 (85%)	559 (100%)	1 (0%)	87	95
6	k	560/657 (85%)	560 (100%)	0	100	100
7	S	60/60 (100%)	60 (100%)	0	100	100
7	s	60/60 (100%)	60 (100%)	0	100	100
All	All	7424/7642 (97%)	7405 (100%)	19 (0%)	84	94

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	o	118	ILE

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Mol	Chain	Res	Type
1	t	106	THR
1	x	106	THR
1	q	106	THR
1	V	106	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
2	r	110	ASN
2	u	47	ASN
2	y	28	GLN
1	Q	28	ASN
2	P	28	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

24 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	B	71	2	7,8,9	0.56	0	4,9,11	0.51	0
2	MEN	w	71	2	7,8,9	0.55	0	4,9,11	0.55	0
2	MEN	r	71	2	7,8,9	0.55	0	4,9,11	0.57	0
2	MEN	H	71	2	7,8,9	0.54	0	4,9,11	0.55	0
5	MEN	J	72	5	7,8,9	0.54	0	4,9,11	0.48	0
2	MEN	P	71	2	7,8,9	0.53	0	4,9,11	0.56	0
2	MEN	R	71	2	7,8,9	0.53	0	4,9,11	0.57	0
2	MEN	W	71	2	7,8,9	0.54	0	4,9,11	0.52	0
2	MEN	y	71	2	7,8,9	0.57	0	4,9,11	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	MEN	j	72	5	7,8,9	0.54	0	4,9,11	0.50	0
2	MEN	l	71	2	7,8,9	0.54	0	4,9,11	0.50	0
2	MEN	h	71	2	7,8,9	0.55	0	4,9,11	0.51	0
2	MEN	D	71	2	7,8,9	0.57	0	4,9,11	0.53	0
2	MEN	U	71	2	7,8,9	0.54	0	4,9,11	0.45	0
2	MEN	Y	71	2	7,8,9	0.56	0	4,9,11	0.52	0
2	MEN	p	71	2	7,8,9	0.54	0	4,9,11	0.57	0
2	MEN	N	71	2	7,8,9	0.54	0	4,9,11	0.54	0
2	MEN	d	71	2	7,8,9	0.56	0	4,9,11	0.53	0
2	MEN	u	71	2	7,8,9	0.54	0	4,9,11	0.47	0
2	MEN	F	71	2	7,8,9	0.55	0	4,9,11	0.60	0
2	MEN	n	71	2	7,8,9	0.53	0	4,9,11	0.54	0
2	MEN	L	71	2	7,8,9	0.54	0	4,9,11	0.50	0
2	MEN	f	71	2	7,8,9	0.55	0	4,9,11	0.59	0
2	MEN	b	71	2	7,8,9	0.57	0	4,9,11	0.51	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	B	71	2	-	2/7/8/10	-
2	MEN	w	71	2	-	2/7/8/10	-
2	MEN	r	71	2	-	2/7/8/10	-
2	MEN	H	71	2	-	2/7/8/10	-
5	MEN	J	72	5	-	2/7/8/10	-
2	MEN	P	71	2	-	2/7/8/10	-
2	MEN	R	71	2	-	2/7/8/10	-
2	MEN	W	71	2	-	2/7/8/10	-
2	MEN	y	71	2	-	2/7/8/10	-
5	MEN	j	72	5	-	2/7/8/10	-
2	MEN	l	71	2	-	2/7/8/10	-
2	MEN	h	71	2	-	2/7/8/10	-
2	MEN	D	71	2	-	2/7/8/10	-
2	MEN	U	71	2	-	2/7/8/10	-
2	MEN	Y	71	2	-	2/7/8/10	-
2	MEN	p	71	2	-	2/7/8/10	-
2	MEN	N	71	2	-	2/7/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	d	71	2	-	2/7/8/10	-
2	MEN	u	71	2	-	2/7/8/10	-
2	MEN	F	71	2	-	2/7/8/10	-
2	MEN	n	71	2	-	2/7/8/10	-
2	MEN	L	71	2	-	2/7/8/10	-
2	MEN	f	71	2	-	2/7/8/10	-
2	MEN	b	71	2	-	2/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	J	72	MEN	C-CA-CB-CG
5	j	72	MEN	C-CA-CB-CG
5	J	72	MEN	N-CA-CB-CG
5	j	72	MEN	N-CA-CB-CG
2	B	71	MEN	CA-CB-CG-OD1

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	71	MEN	1	0
5	j	72	MEN	1	0
2	h	71	MEN	1	0
2	F	71	MEN	1	0
2	f	71	MEN	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

48 ligands are modelled in this entry.



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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
8	CYC	K	801	-	46,46,46	0.92	0	63,67,67	1.11	5 (7%)
8	CYC	q	201	1	46,46,46	0.96	0	63,67,67	1.24	7 (11%)
8	CYC	X	201	1	46,46,46	0.96	0	63,67,67	1.26	6 (9%)
8	CYC	c	201	-	46,46,46	0.93	0	63,67,67	1.14	5 (7%)
8	CYC	u	201	2	46,46,46	0.92	0	63,67,67	1.06	4 (6%)
8	CYC	y	201	2	46,46,46	0.93	0	63,67,67	1.02	3 (4%)
8	CYC	F	201	2	46,46,46	0.92	0	63,67,67	0.91	2 (3%)
8	CYC	i	201	4	46,46,46	0.98	0	63,67,67	1.30	8 (12%)
8	CYC	J	201	-	46,46,46	0.93	0	63,67,67	1.04	4 (6%)
8	CYC	A	201	1	46,46,46	0.94	0	63,67,67	1.29	7 (11%)
8	CYC	W	201	2	46,46,46	0.96	0	63,67,67	1.11	7 (11%)
8	CYC	N	201	2	46,46,46	0.91	0	63,67,67	0.85	3 (4%)
8	CYC	D	201	2	46,46,46	0.95	0	63,67,67	1.13	5 (7%)
8	CYC	m	201	1	46,46,46	0.96	0	63,67,67	1.31	8 (12%)
8	CYC	o	201	1	46,46,46	0.94	0	63,67,67	1.31	7 (11%)
8	CYC	h	201	2	46,46,46	0.95	0	63,67,67	1.09	6 (9%)
8	CYC	Y	201	2	46,46,46	0.93	0	63,67,67	1.02	3 (4%)
8	CYC	p	201	2	46,46,46	0.91	0	63,67,67	0.94	3 (4%)
8	CYC	E	201	1	46,46,46	0.97	0	63,67,67	1.26	7 (11%)
8	CYC	U	201	2	46,46,46	0.92	0	63,67,67	1.07	4 (6%)
8	CYC	V	201	1	46,46,46	0.95	0	63,67,67	1.26	7 (11%)
8	CYC	M	201	1	46,46,46	0.97	0	63,67,67	1.31	8 (12%)
8	CYC	d	201	2	46,46,46	0.95	0	63,67,67	1.14	5 (7%)
8	CYC	H	201	2	46,46,46	0.95	0	63,67,67	1.09	6 (9%)
8	CYC	w	201	2	46,46,46	0.95	0	63,67,67	1.11	7 (11%)
8	CYC	e	201	1	46,46,46	0.97	0	63,67,67	1.27	7 (11%)
8	CYC	L	201	2	46,46,46	0.93	0	63,67,67	0.99	2 (3%)
8	CYC	f	201	2	46,46,46	0.91	0	63,67,67	0.91	2 (3%)
8	CYC	t	201	1	46,46,46	0.99	0	63,67,67	1.28	9 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	CYC	P	201	2	46,46,46	0.92	0	63,67,67	0.93	2 (3%)
8	CYC	O	201	1	46,46,46	0.95	0	63,67,67	1.31	7 (11%)
8	CYC	n	201	2	46,46,46	0.91	0	63,67,67	0.86	2 (3%)
8	CYC	a	201	1	46,46,46	0.94	0	63,67,67	1.30	7 (11%)
8	CYC	I	201	4	46,46,46	0.98	0	63,67,67	1.30	9 (14%)
8	CYC	l	201	2	46,46,46	0.92	0	63,67,67	0.99	2 (3%)
8	CYC	G	201	1	46,46,46	0.96	0	63,67,67	1.21	5 (7%)
8	CYC	x	201	1	46,46,46	0.96	0	63,67,67	1.23	6 (9%)
8	CYC	Q	201	1	46,46,46	0.95	0	63,67,67	1.24	6 (9%)
8	CYC	C	201	-	46,46,46	0.94	0	63,67,67	1.13	4 (6%)
8	CYC	B	201	2	46,46,46	0.92	0	63,67,67	1.01	4 (6%)
8	CYC	j	201	-	46,46,46	0.92	0	63,67,67	1.04	4 (6%)
8	CYC	T	201	1	46,46,46	0.99	0	63,67,67	1.28	9 (14%)
8	CYC	k	801	-	46,46,46	0.92	0	63,67,67	1.11	5 (7%)
8	CYC	r	201	2	46,46,46	0.91	0	63,67,67	0.97	3 (4%)
8	CYC	b	201	2	46,46,46	0.91	0	63,67,67	1.06	5 (7%)
8	CYC	v	201	1	46,46,46	0.94	0	63,67,67	1.20	5 (7%)
8	CYC	R	201	2	46,46,46	0.92	0	63,67,67	0.96	3 (4%)
8	CYC	g	201	1	46,46,46	0.96	0	63,67,67	1.22	6 (9%)

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
8	CYC	K	801	-	-	8/26/74/74	0/4/4/4
8	CYC	q	201	1	-	9/26/74/74	0/4/4/4
8	CYC	X	201	1	-	9/26/74/74	0/4/4/4
8	CYC	c	201	-	-	12/26/74/74	0/4/4/4
8	CYC	u	201	2	-	12/26/74/74	0/4/4/4
8	CYC	y	201	2	-	8/26/74/74	0/4/4/4
8	CYC	F	201	2	-	10/26/74/74	0/4/4/4
8	CYC	i	201	4	-	8/26/74/74	0/4/4/4
8	CYC	J	201	-	-	7/26/74/74	0/4/4/4
8	CYC	A	201	1	-	8/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	CYC	W	201	2	-	10/26/74/74	0/4/4/4
8	CYC	N	201	2	-	8/26/74/74	0/4/4/4
8	CYC	D	201	2	-	5/26/74/74	0/4/4/4
8	CYC	m	201	1	-	8/26/74/74	0/4/4/4
8	CYC	o	201	1	-	8/26/74/74	0/4/4/4
8	CYC	h	201	2	-	7/26/74/74	0/4/4/4
8	CYC	Y	201	2	-	8/26/74/74	0/4/4/4
8	CYC	p	201	2	-	7/26/74/74	0/4/4/4
8	CYC	E	201	1	-	6/26/74/74	0/4/4/4
8	CYC	U	201	2	-	12/26/74/74	0/4/4/4
8	CYC	V	201	1	-	4/26/74/74	0/4/4/4
8	CYC	M	201	1	-	8/26/74/74	0/4/4/4
8	CYC	d	201	2	-	4/26/74/74	0/4/4/4
8	CYC	H	201	2	-	7/26/74/74	0/4/4/4
8	CYC	w	201	2	-	10/26/74/74	0/4/4/4
8	CYC	e	201	1	-	7/26/74/74	0/4/4/4
8	CYC	L	201	2	-	10/26/74/74	0/4/4/4
8	CYC	f	201	2	-	10/26/74/74	0/4/4/4
8	CYC	t	201	1	-	6/26/74/74	0/4/4/4
8	CYC	P	201	2	-	7/26/74/74	0/4/4/4
8	CYC	O	201	1	-	8/26/74/74	0/4/4/4
8	CYC	n	201	2	-	8/26/74/74	0/4/4/4
8	CYC	a	201	1	-	8/26/74/74	0/4/4/4
8	CYC	I	201	4	-	8/26/74/74	0/4/4/4
8	CYC	l	201	2	-	9/26/74/74	0/4/4/4
8	CYC	G	201	1	-	11/26/74/74	0/4/4/4
8	CYC	x	201	1	-	12/26/74/74	0/4/4/4
8	CYC	Q	201	1	-	9/26/74/74	0/4/4/4
8	CYC	C	201	-	-	12/26/74/74	0/4/4/4
8	CYC	B	201	2	-	7/26/74/74	0/4/4/4
8	CYC	j	201	-	-	7/26/74/74	0/4/4/4
8	CYC	T	201	1	-	6/26/74/74	0/4/4/4
8	CYC	k	801	-	-	7/26/74/74	0/4/4/4
8	CYC	r	201	2	-	9/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	CYC	b	201	2	-	11/26/74/74	0/4/4/4
8	CYC	v	201	1	-	8/26/74/74	0/4/4/4
8	CYC	R	201	2	-	9/26/74/74	0/4/4/4
8	CYC	g	201	1	-	10/26/74/74	0/4/4/4

There are no bond length outliers.

The worst 5 of 251 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	o	201	CYC	C1D-CHD-C4C	4.35	135.19	127.76
8	O	201	CYC	C1D-CHD-C4C	4.23	134.98	127.76
8	M	201	CYC	C1D-CHD-C4C	4.15	134.85	127.76
8	m	201	CYC	C1D-CHD-C4C	4.13	134.81	127.76
8	a	201	CYC	C1D-CHD-C4C	4.01	134.62	127.76

There are no chirality outliers.

5 of 402 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	201	CYC	NA-C4A-CHB-C1B
8	A	201	CYC	C3A-C4A-CHB-C1B
8	C	201	CYC	NA-C4A-CHB-C1B
8	C	201	CYC	C3A-C4A-CHB-C1B
8	C	201	CYC	C2C-C3C-CAC-CBC

There are no ring outliers.

48 monomers are involved in 176 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	K	801	CYC	3	0
8	q	201	CYC	4	0
8	X	201	CYC	5	0
8	c	201	CYC	4	0
8	u	201	CYC	4	0
8	y	201	CYC	1	0
8	F	201	CYC	2	0
8	i	201	CYC	5	0
8	J	201	CYC	3	0
8	A	201	CYC	5	0
8	W	201	CYC	3	0

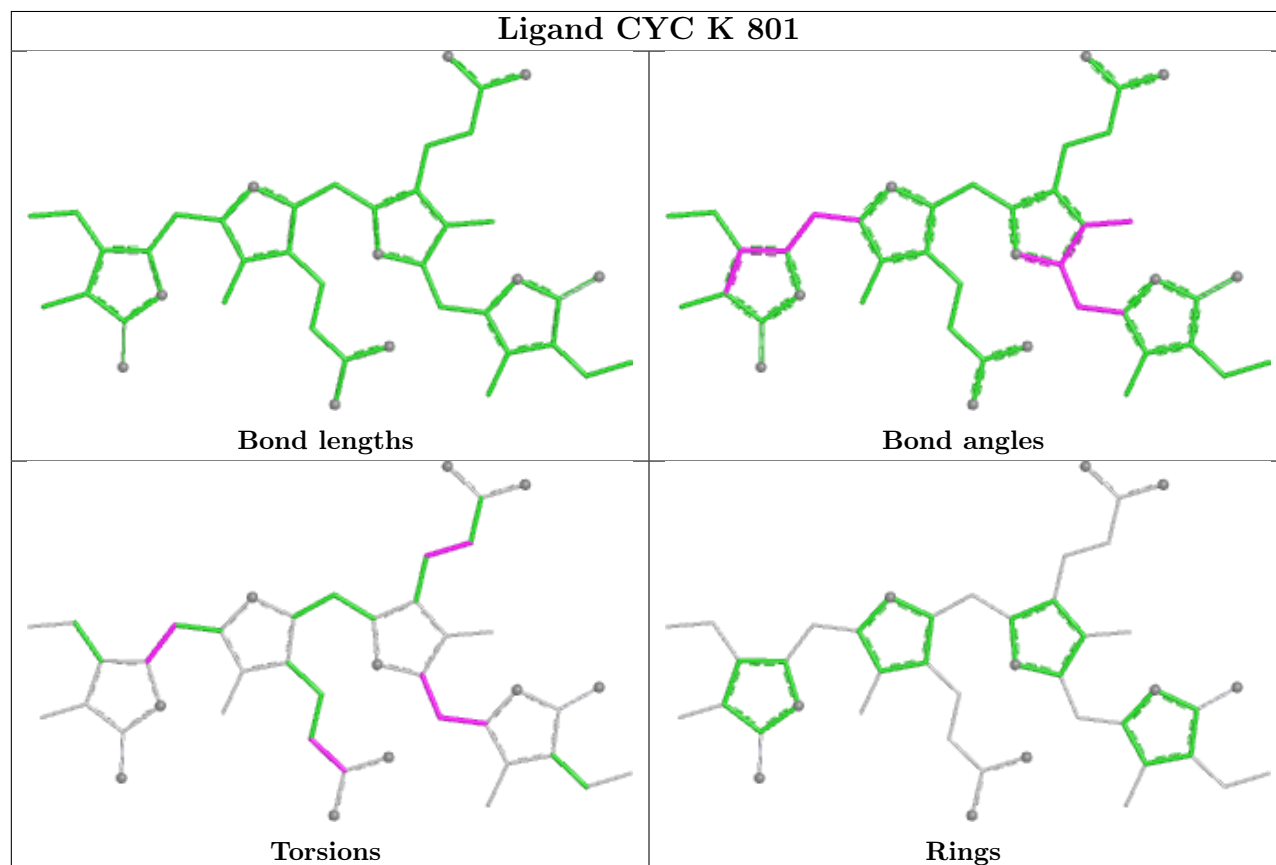
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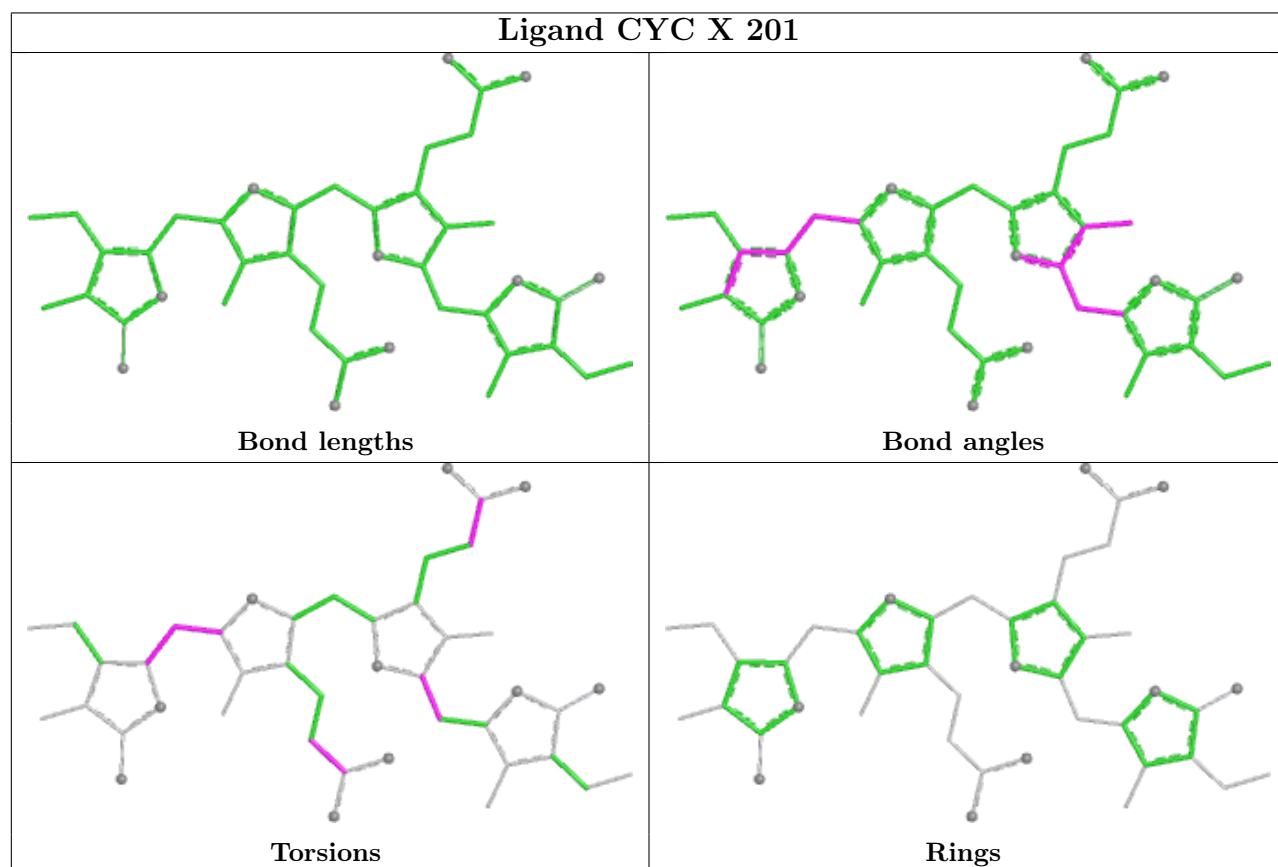
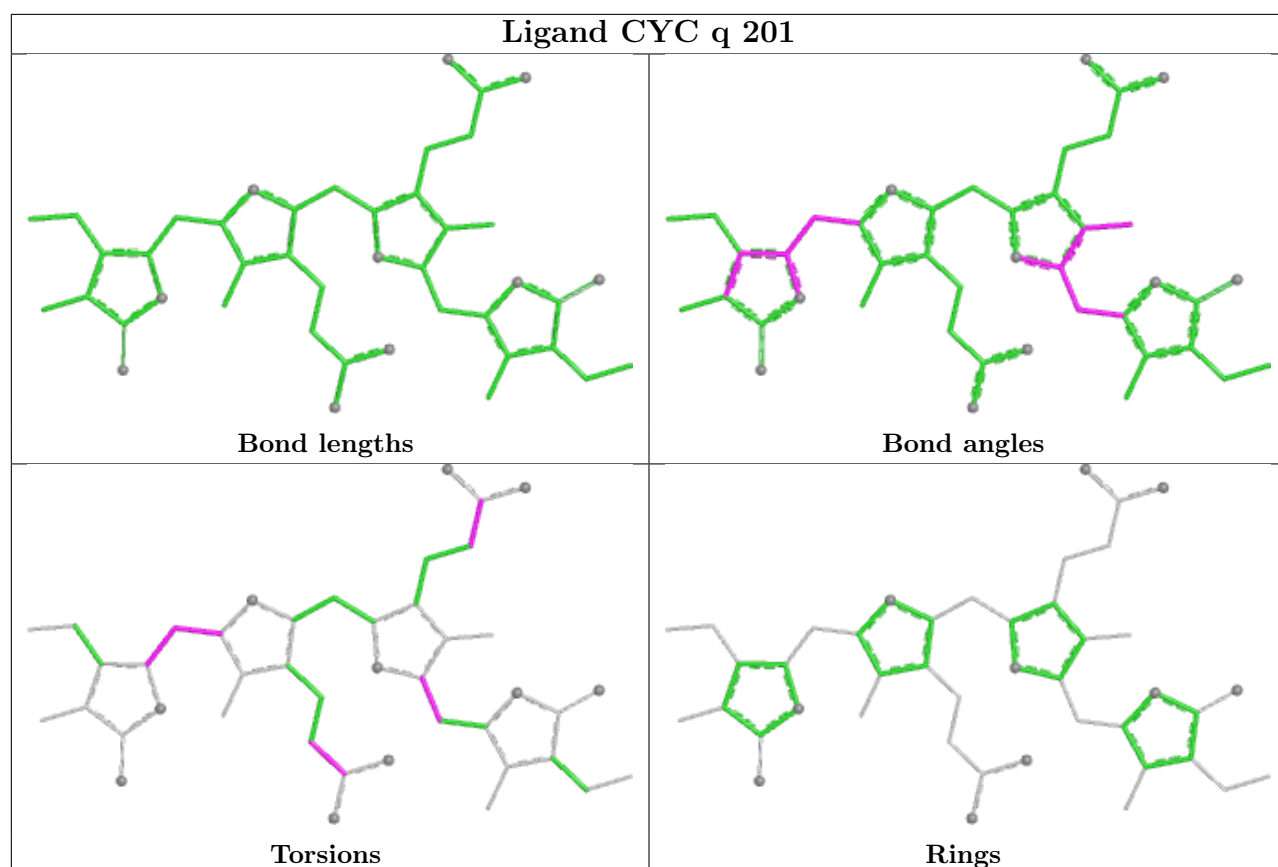
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	N	201	CYC	2	0
8	D	201	CYC	4	0
8	m	201	CYC	4	0
8	o	201	CYC	6	0
8	h	201	CYC	5	0
8	Y	201	CYC	1	0
8	p	201	CYC	1	0
8	E	201	CYC	4	0
8	U	201	CYC	4	0
8	V	201	CYC	4	0
8	M	201	CYC	4	0
8	d	201	CYC	4	0
8	H	201	CYC	6	0
8	w	201	CYC	3	0
8	e	201	CYC	4	0
8	L	201	CYC	2	0
8	f	201	CYC	3	0
8	t	201	CYC	3	0
8	P	201	CYC	1	0
8	O	201	CYC	5	0
8	n	201	CYC	2	0
8	a	201	CYC	3	0
8	I	201	CYC	5	0
8	l	201	CYC	2	0
8	G	201	CYC	5	0
8	x	201	CYC	5	0
8	Q	201	CYC	4	0
8	C	201	CYC	4	0
8	B	201	CYC	3	0
8	j	201	CYC	2	0
8	T	201	CYC	3	0
8	k	801	CYC	3	0
8	r	201	CYC	5	0
8	b	201	CYC	5	0
8	v	201	CYC	6	0
8	R	201	CYC	5	0
8	g	201	CYC	5	0

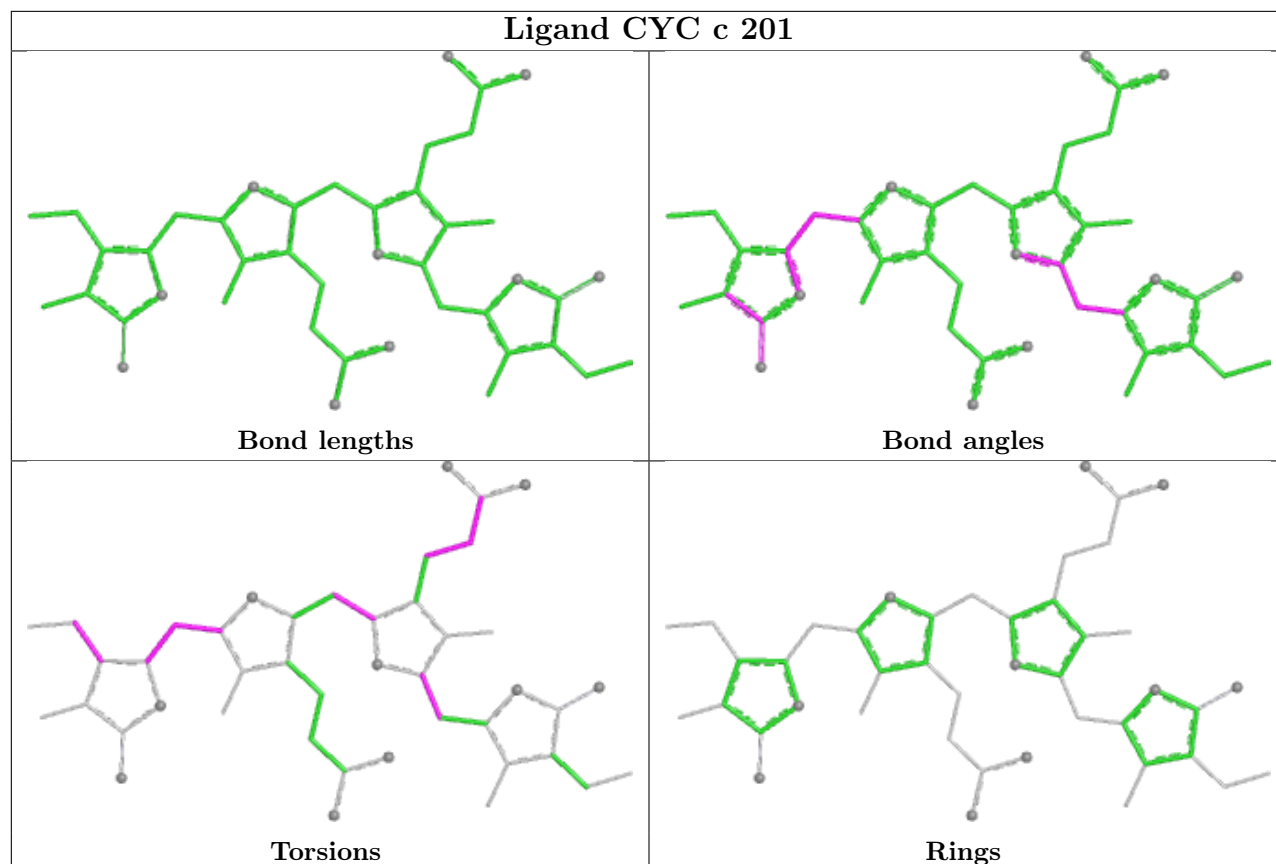
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

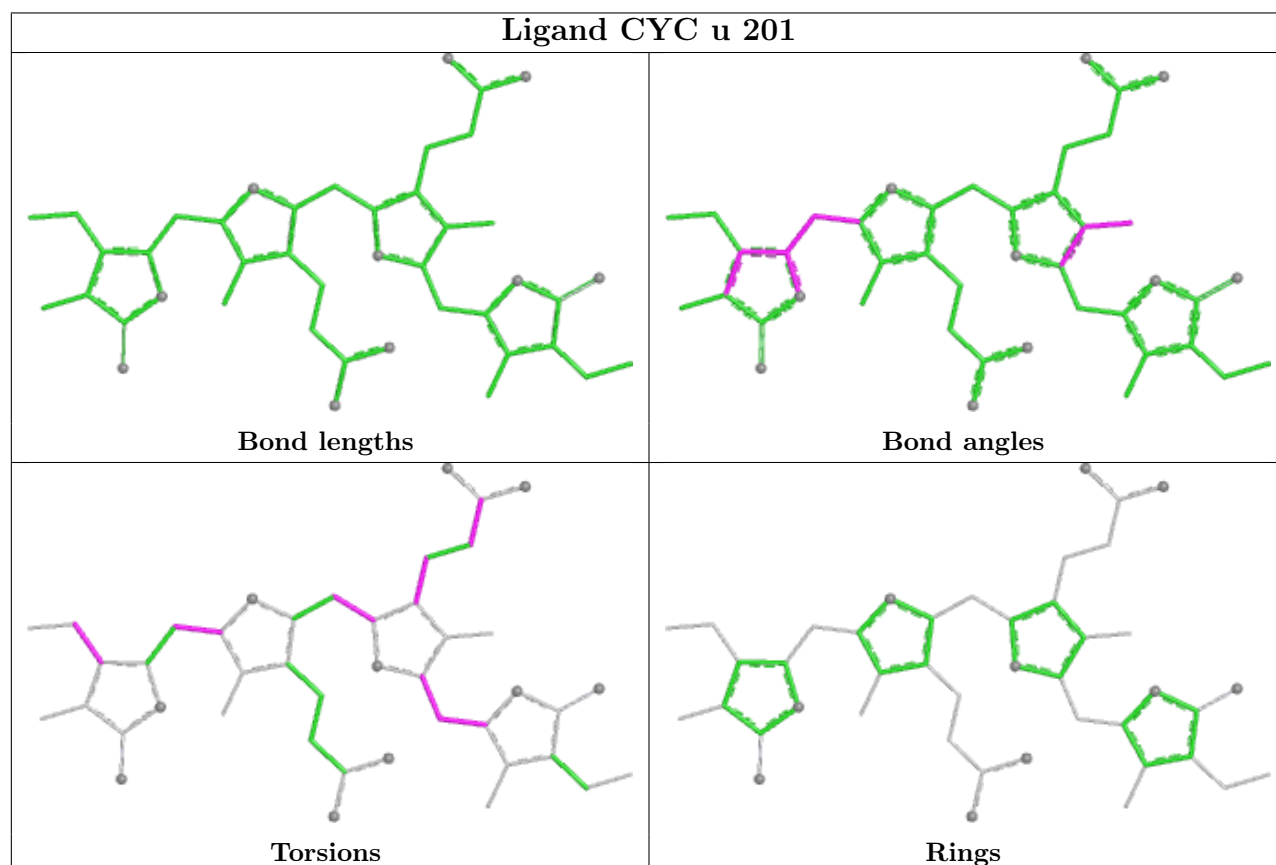




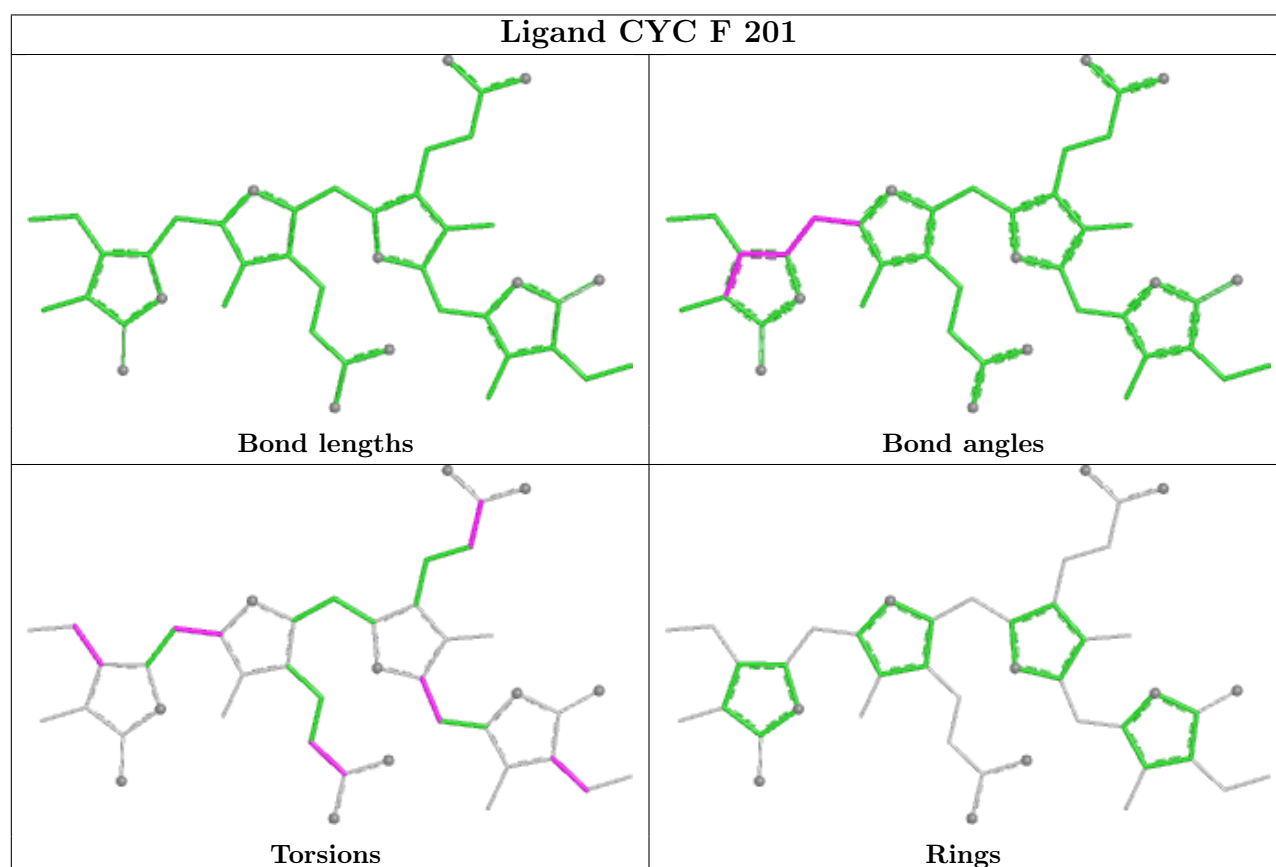
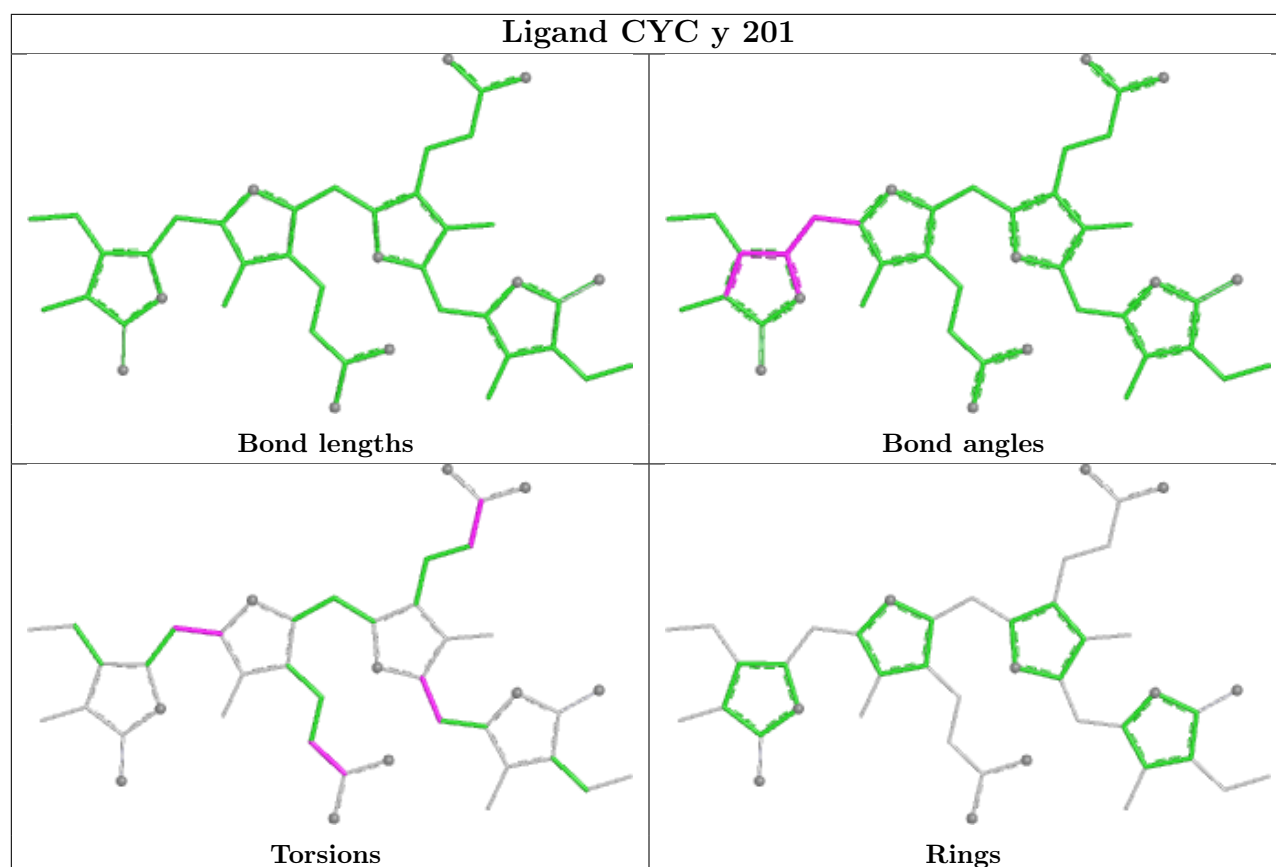
## Ligand CYC c 201



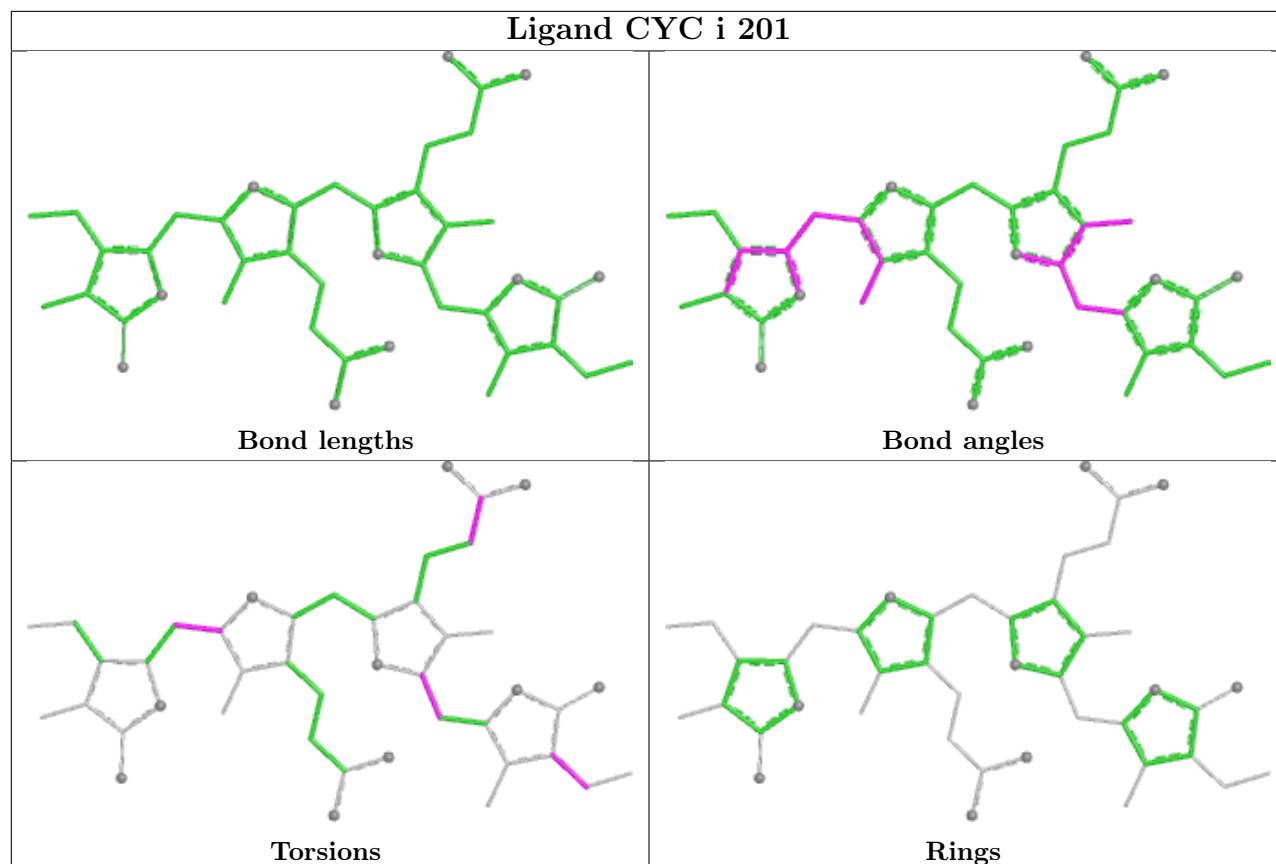
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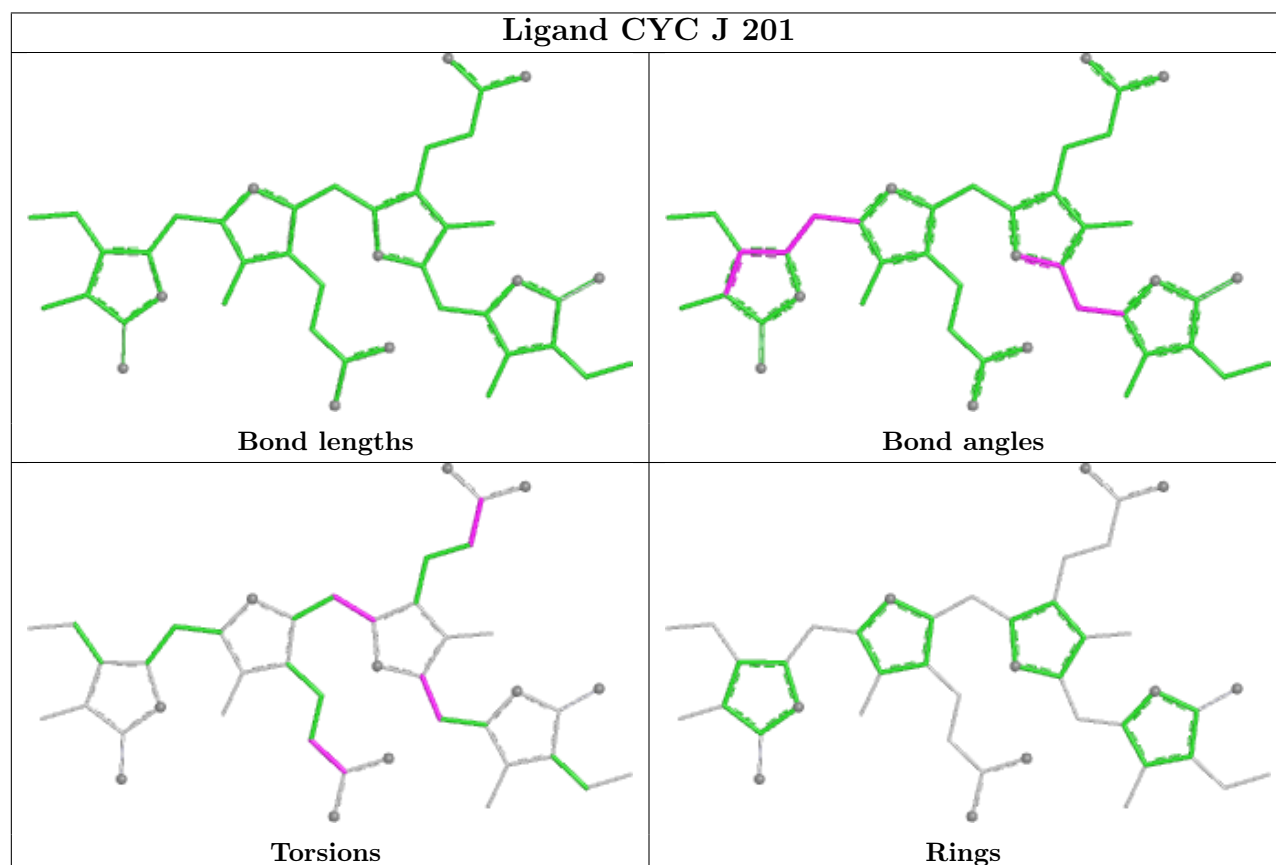


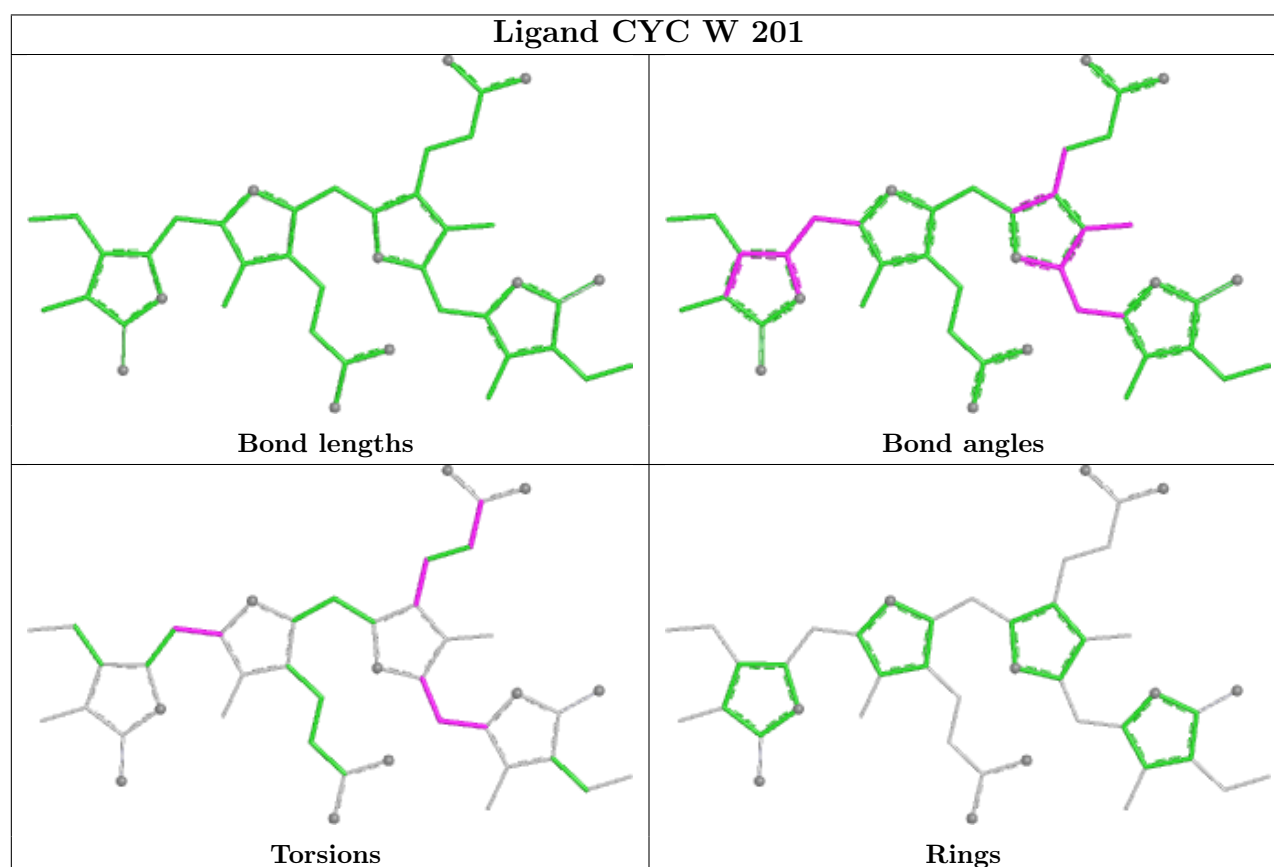
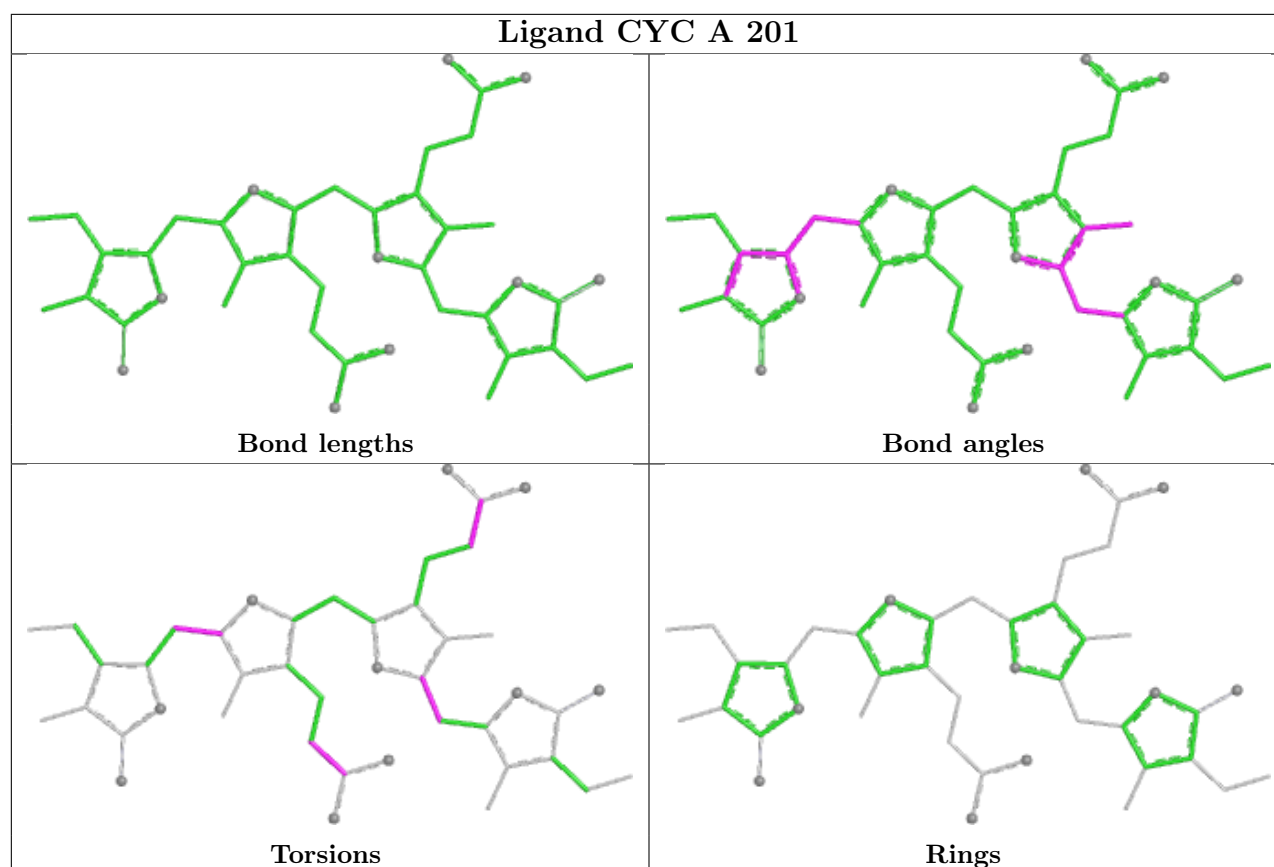


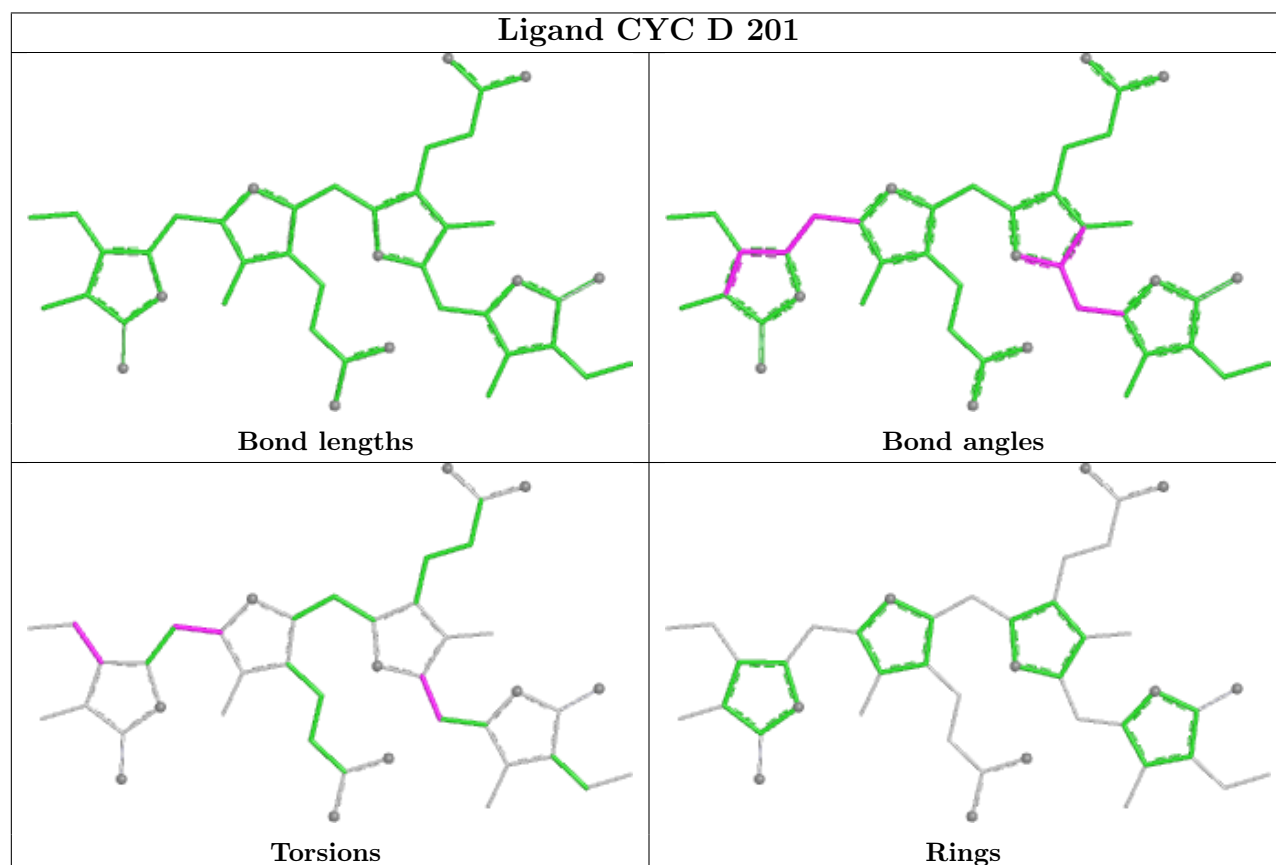
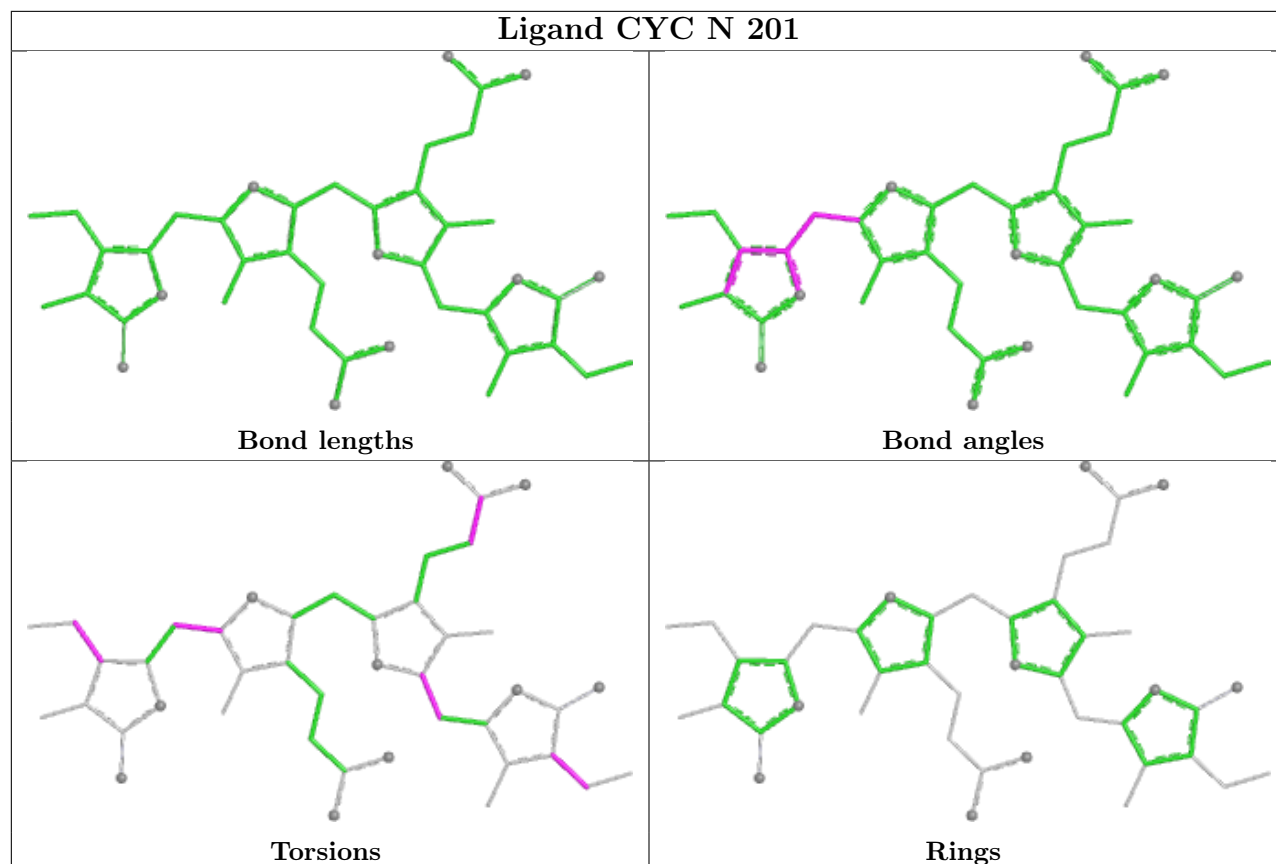
## Ligand CYC i 201

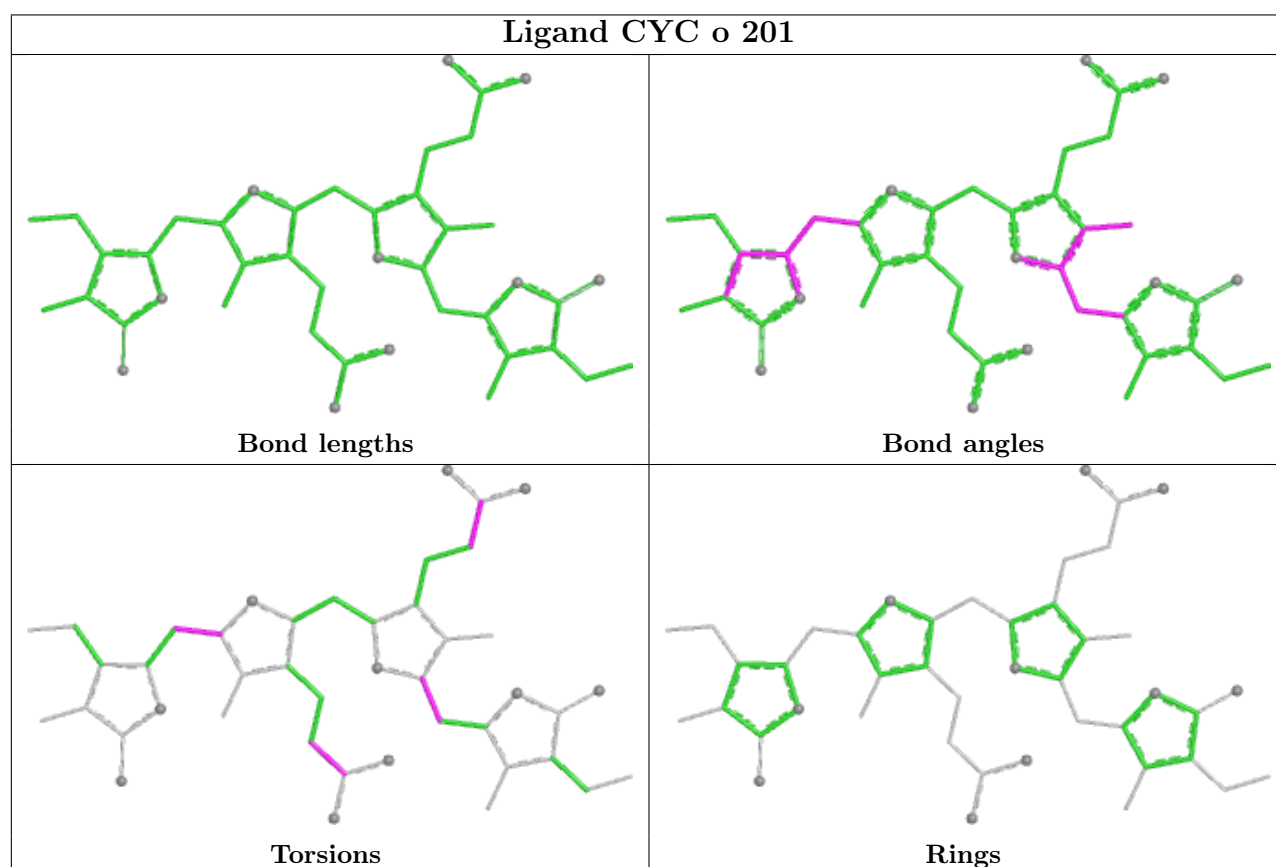
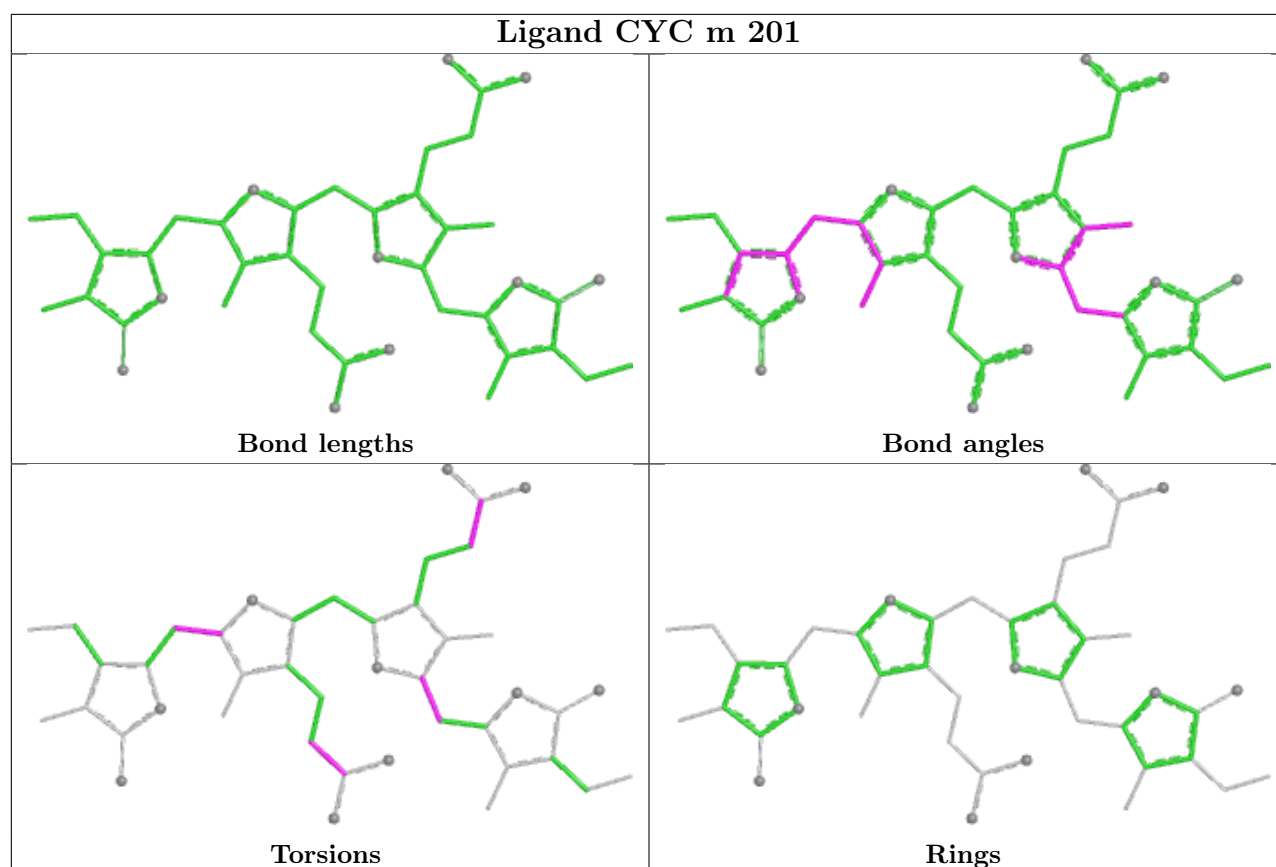


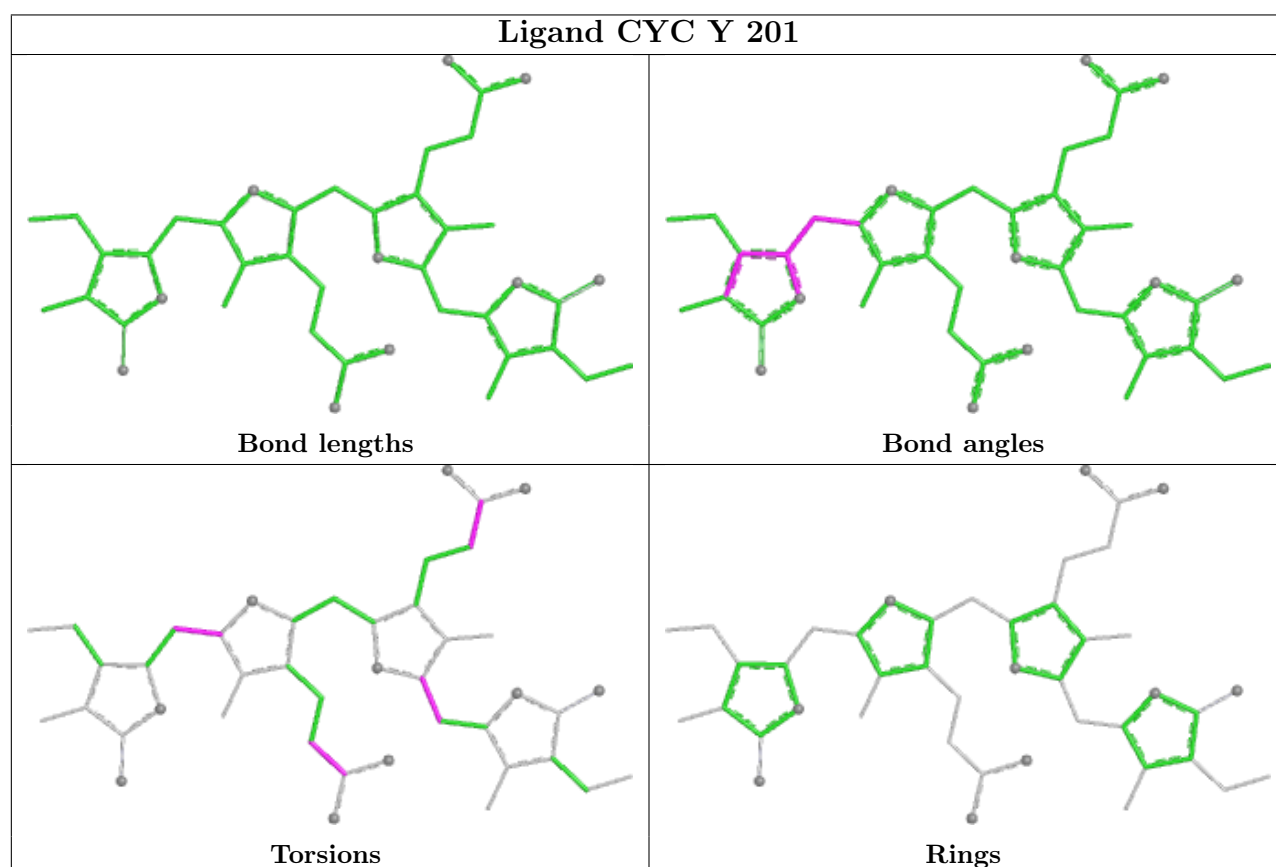
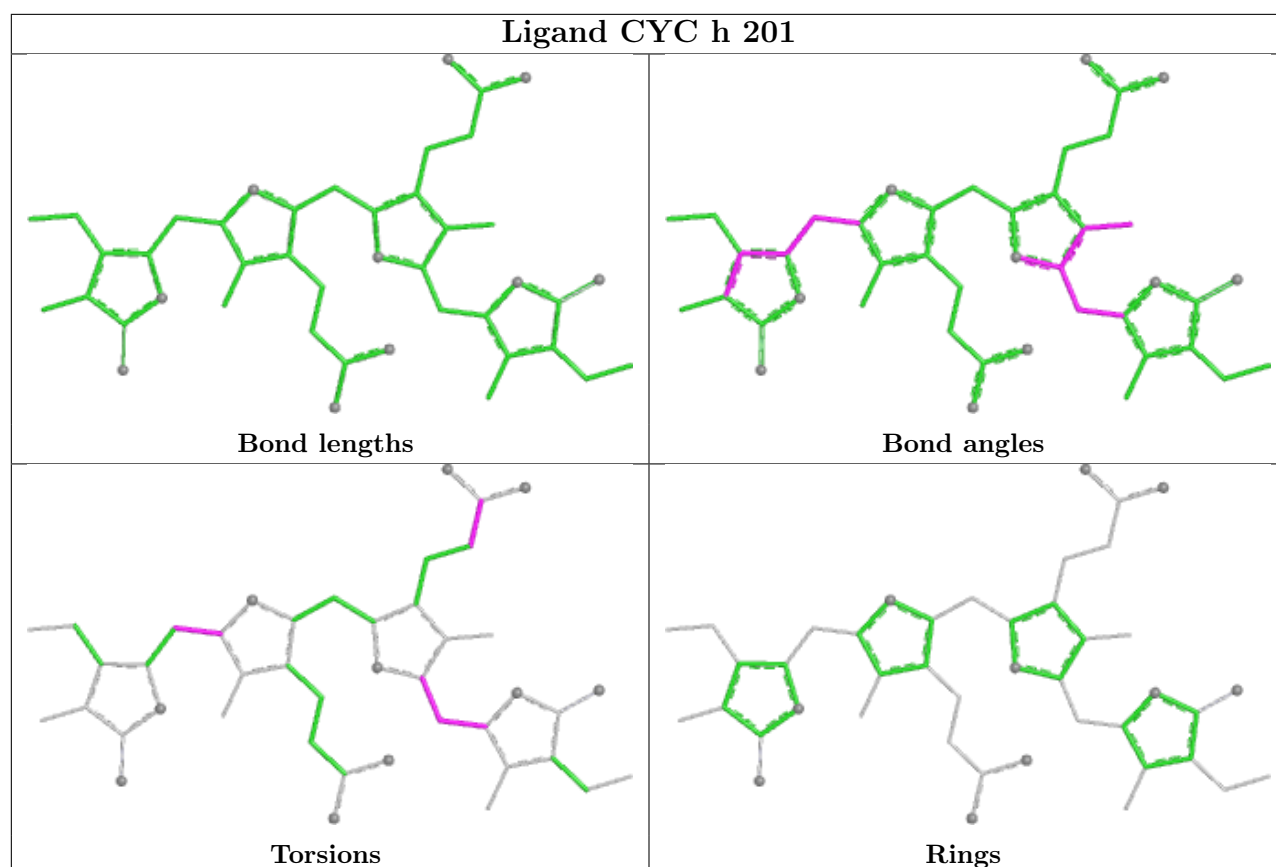
## Ligand CYC J 201

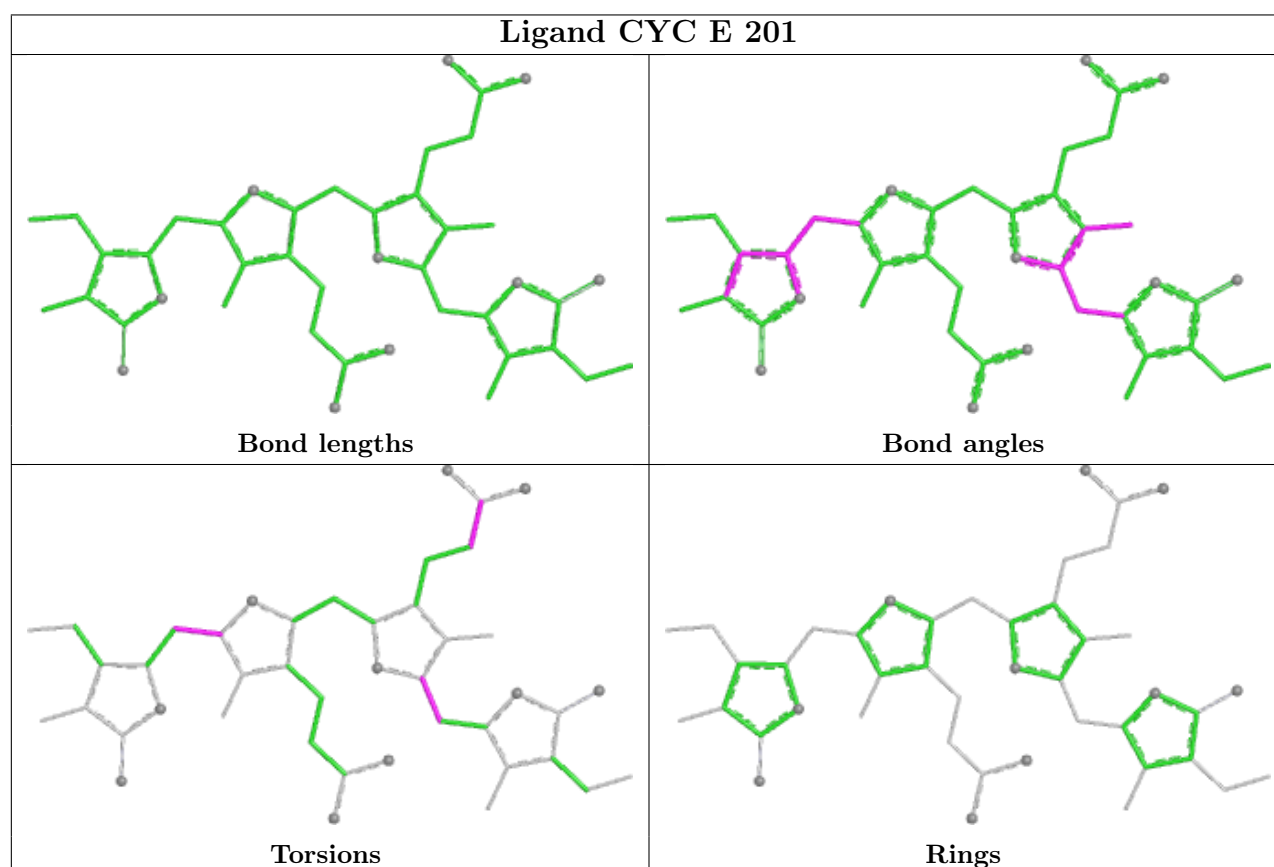
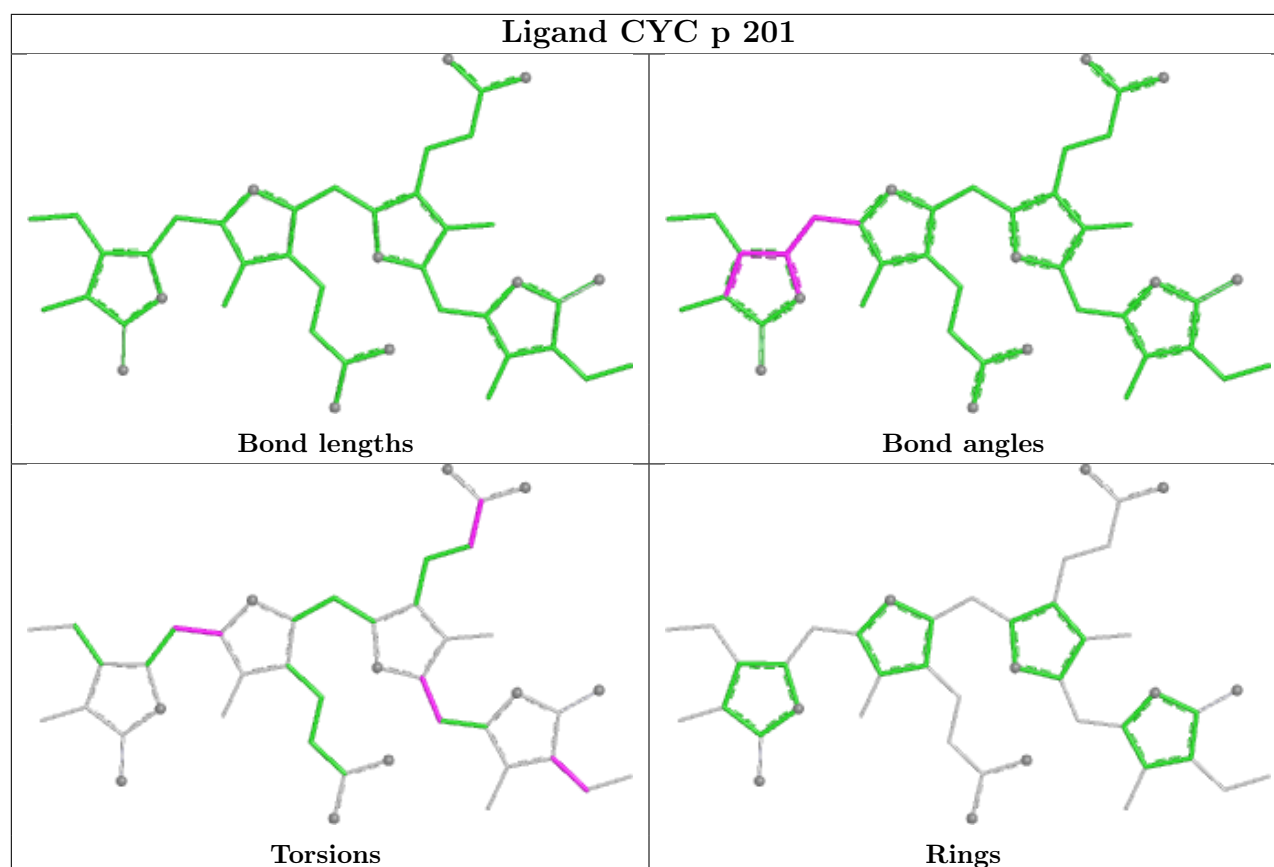


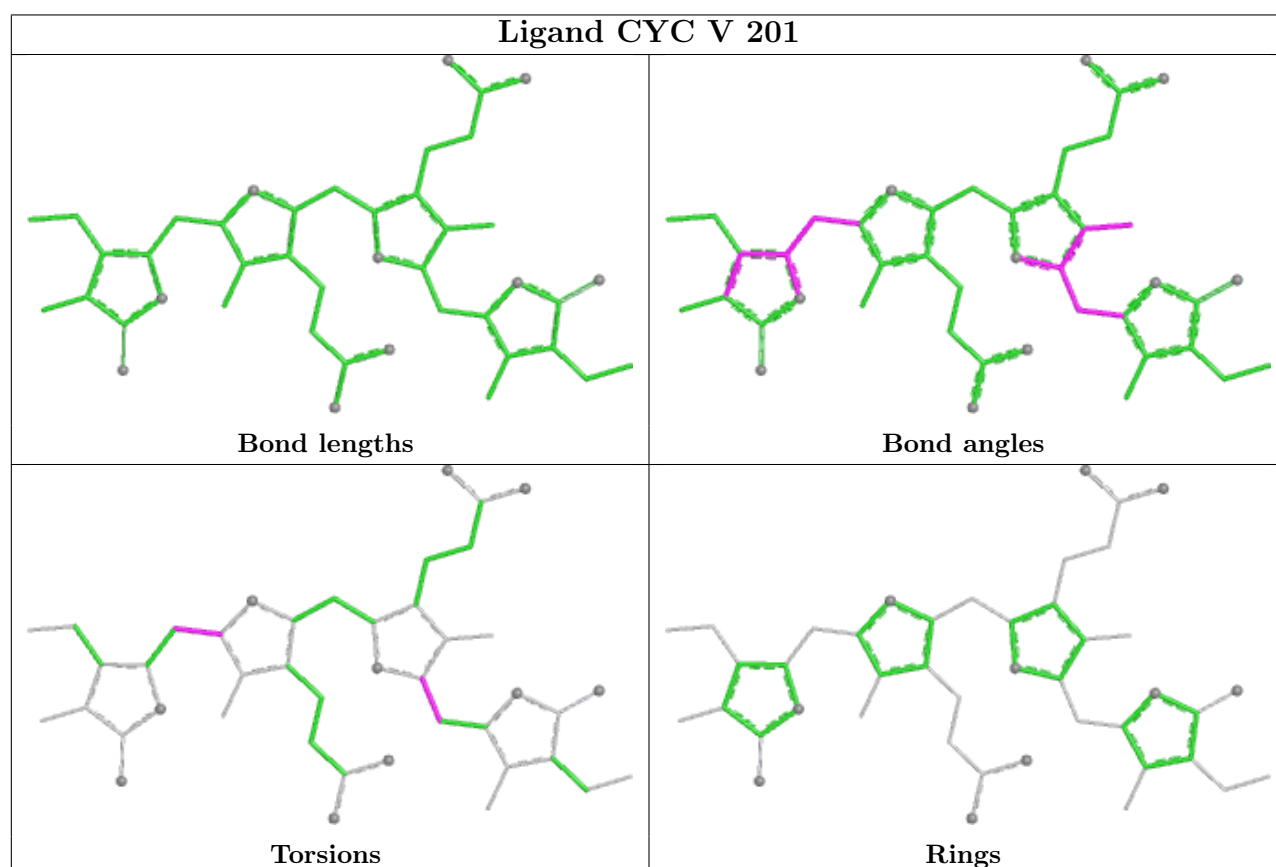
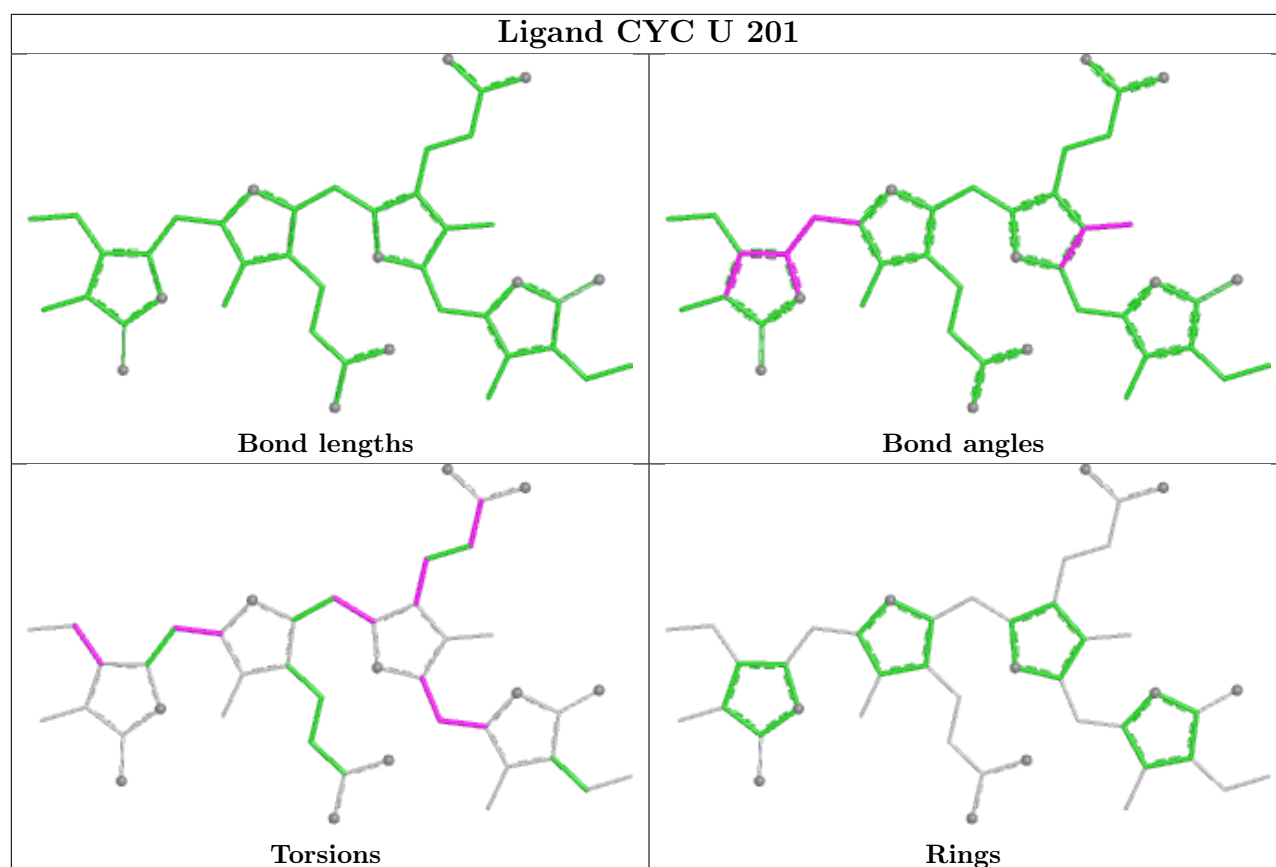




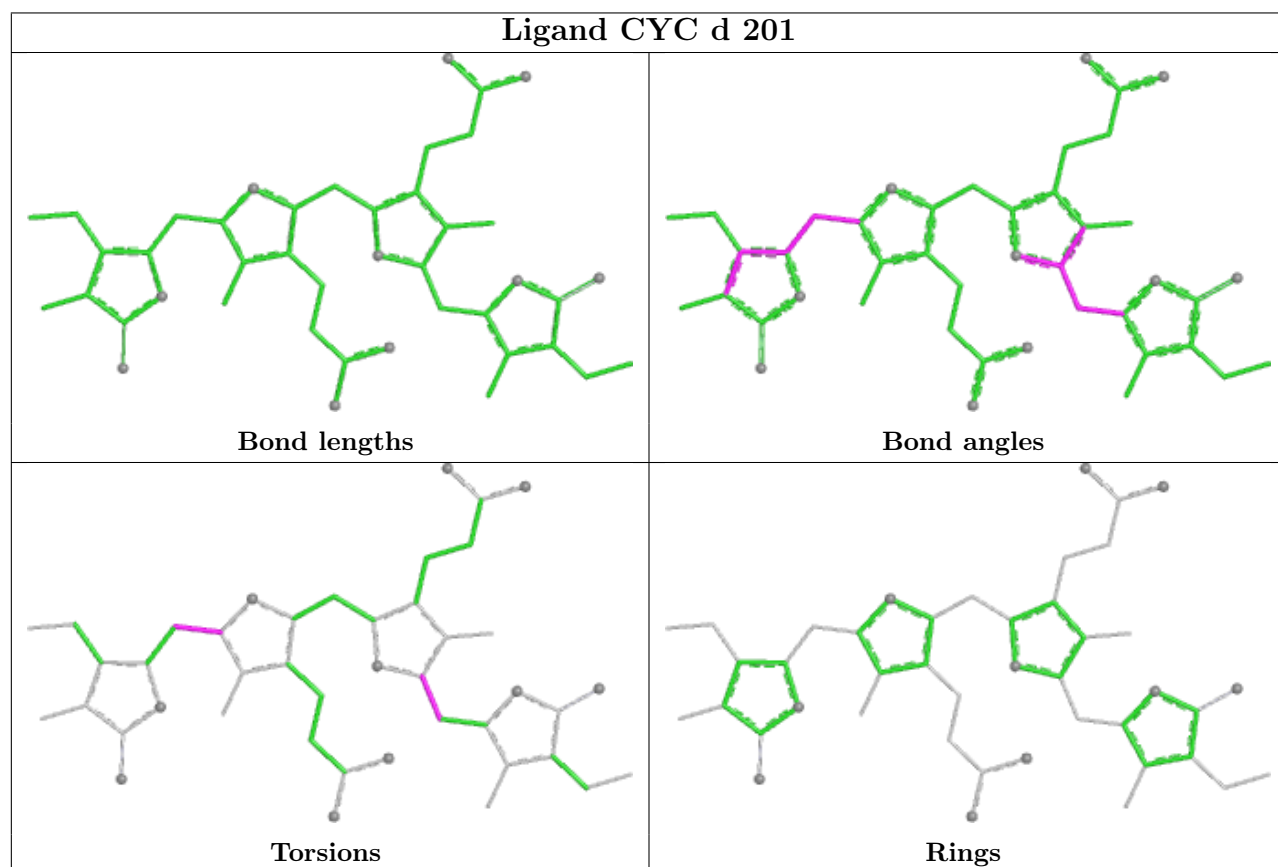
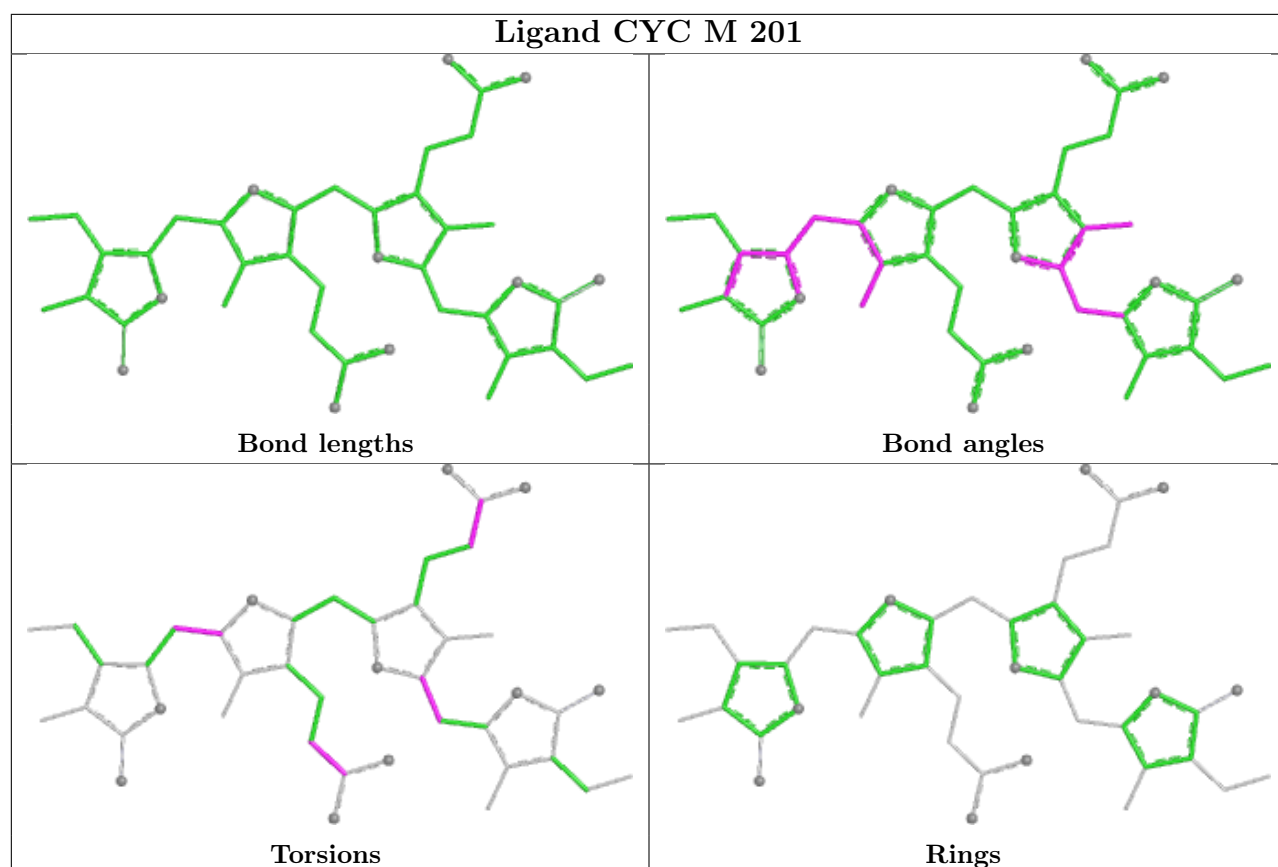


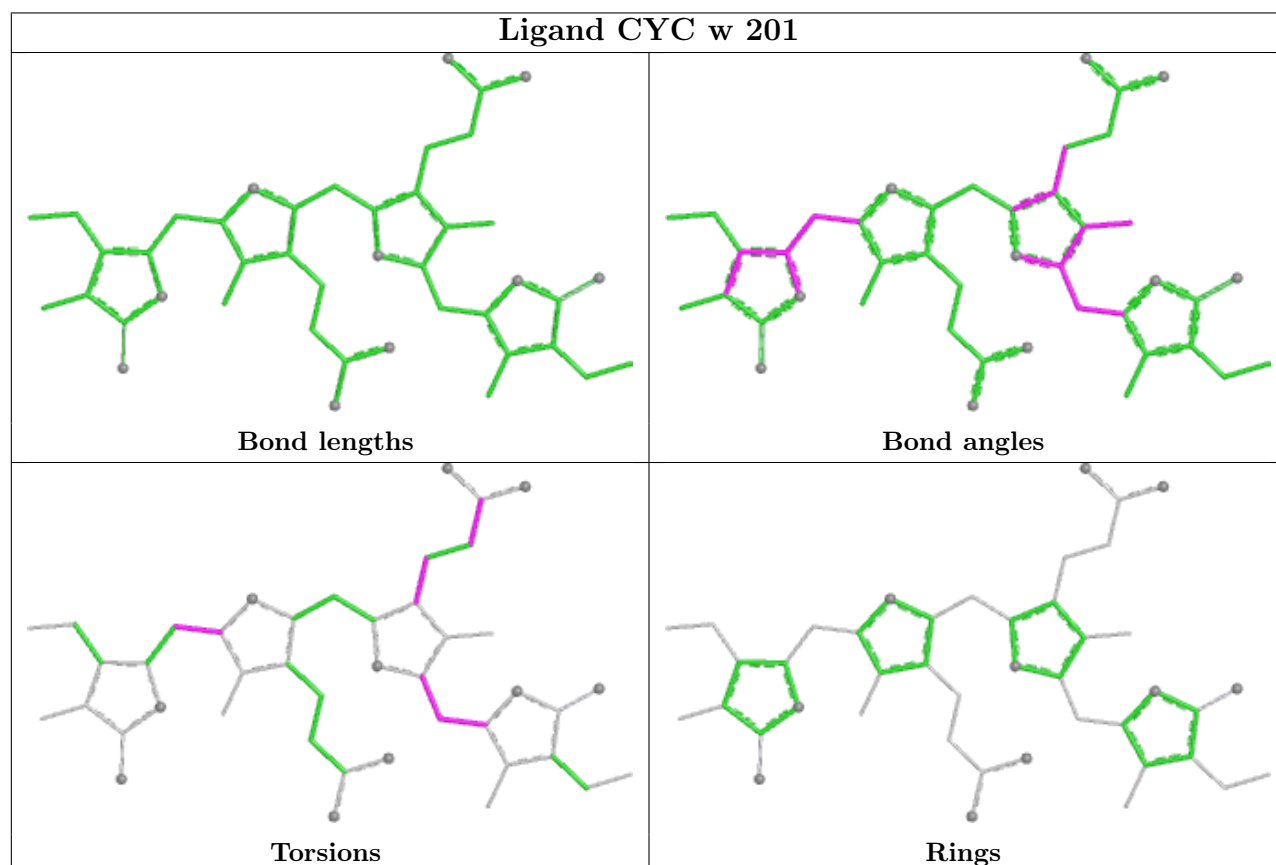
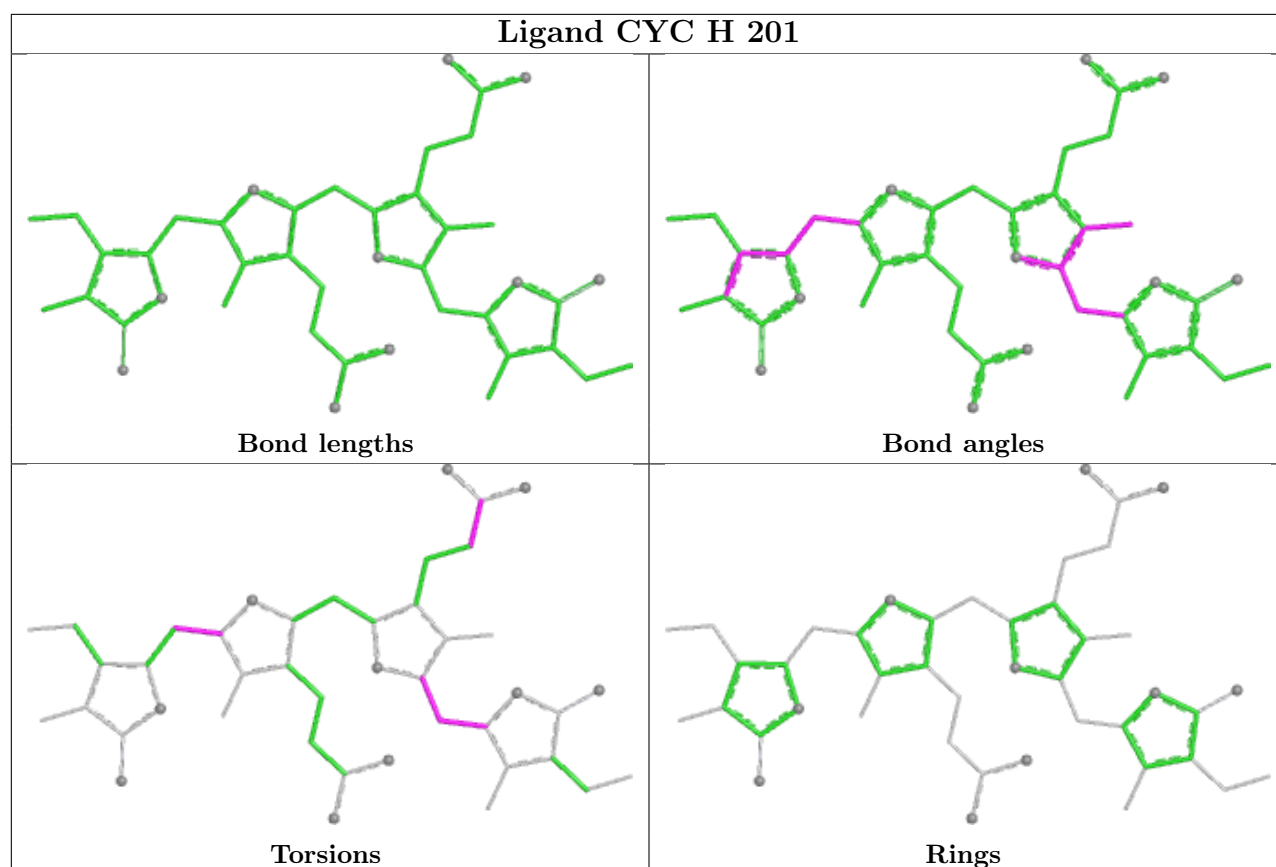




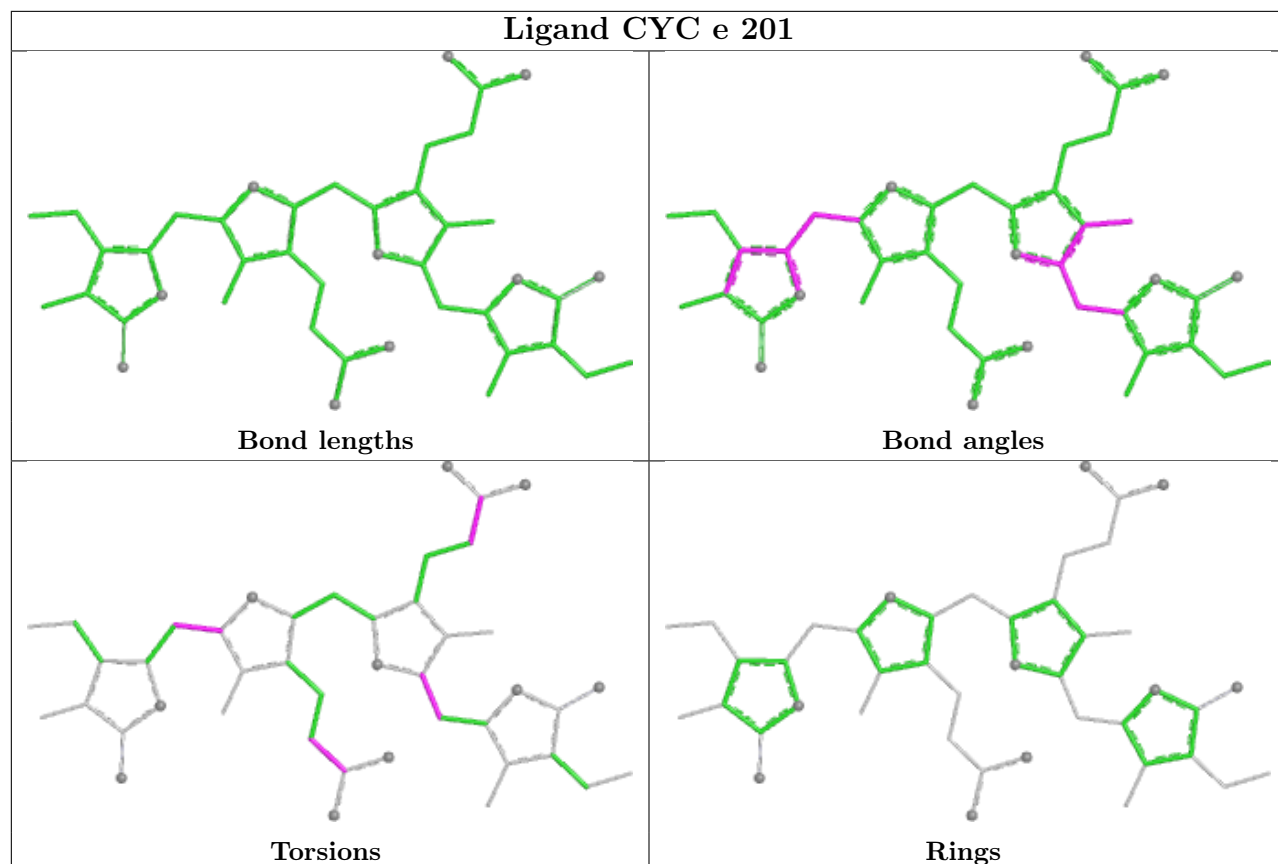




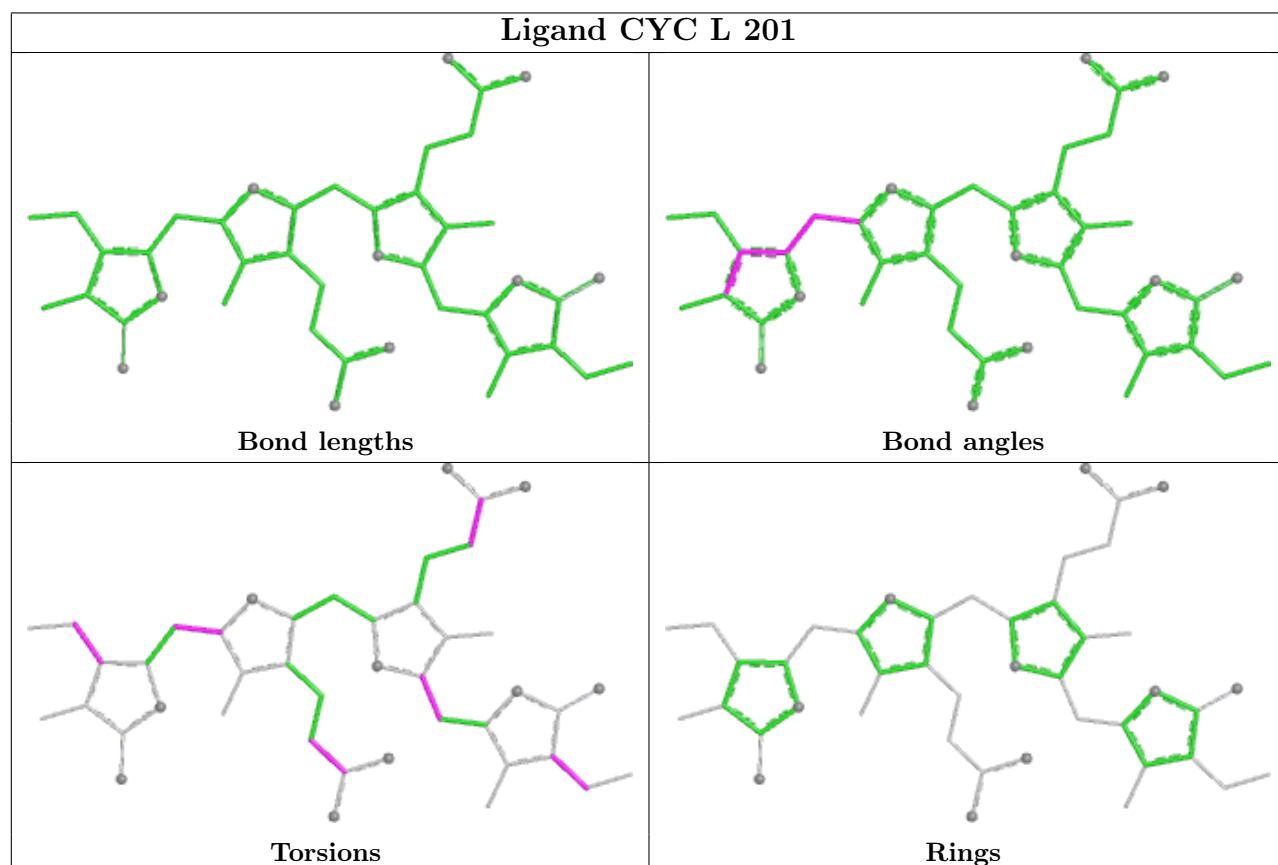


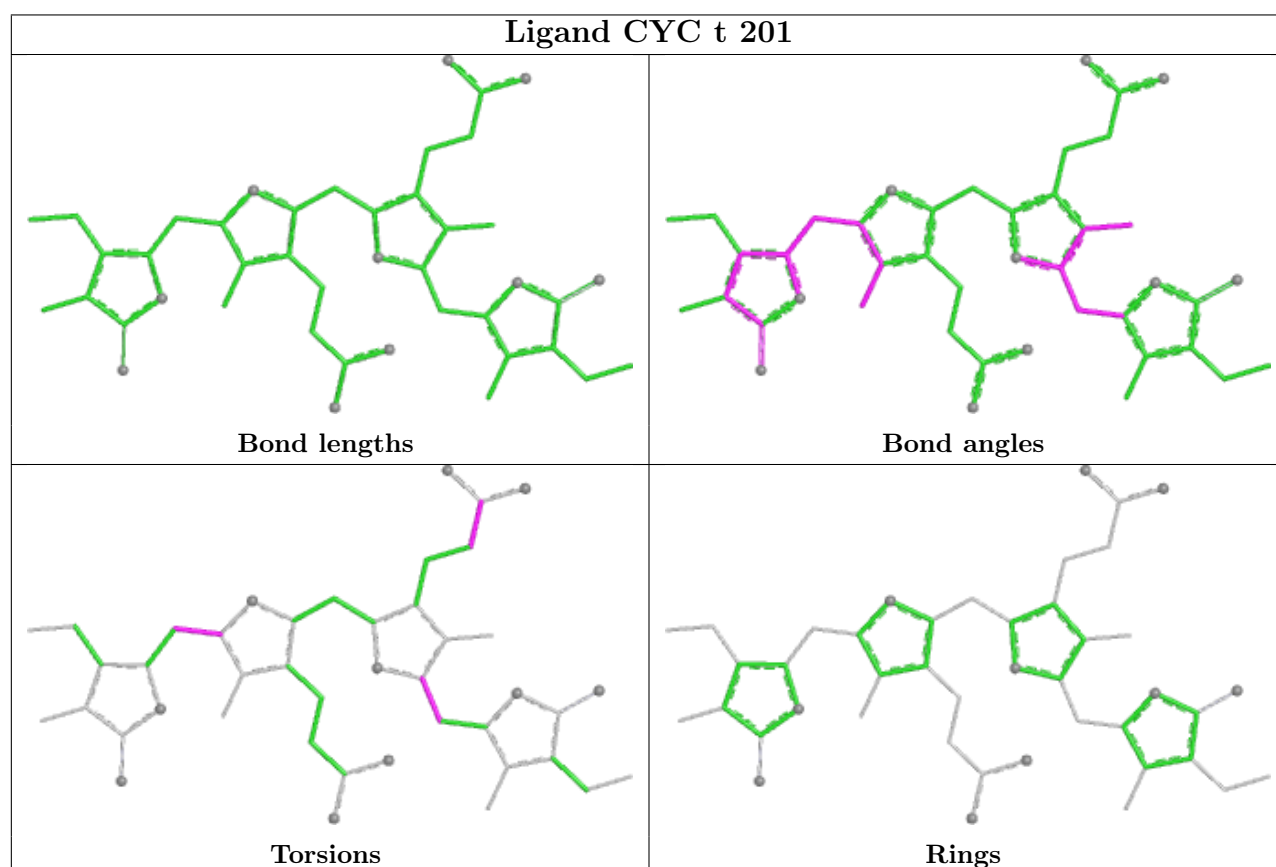
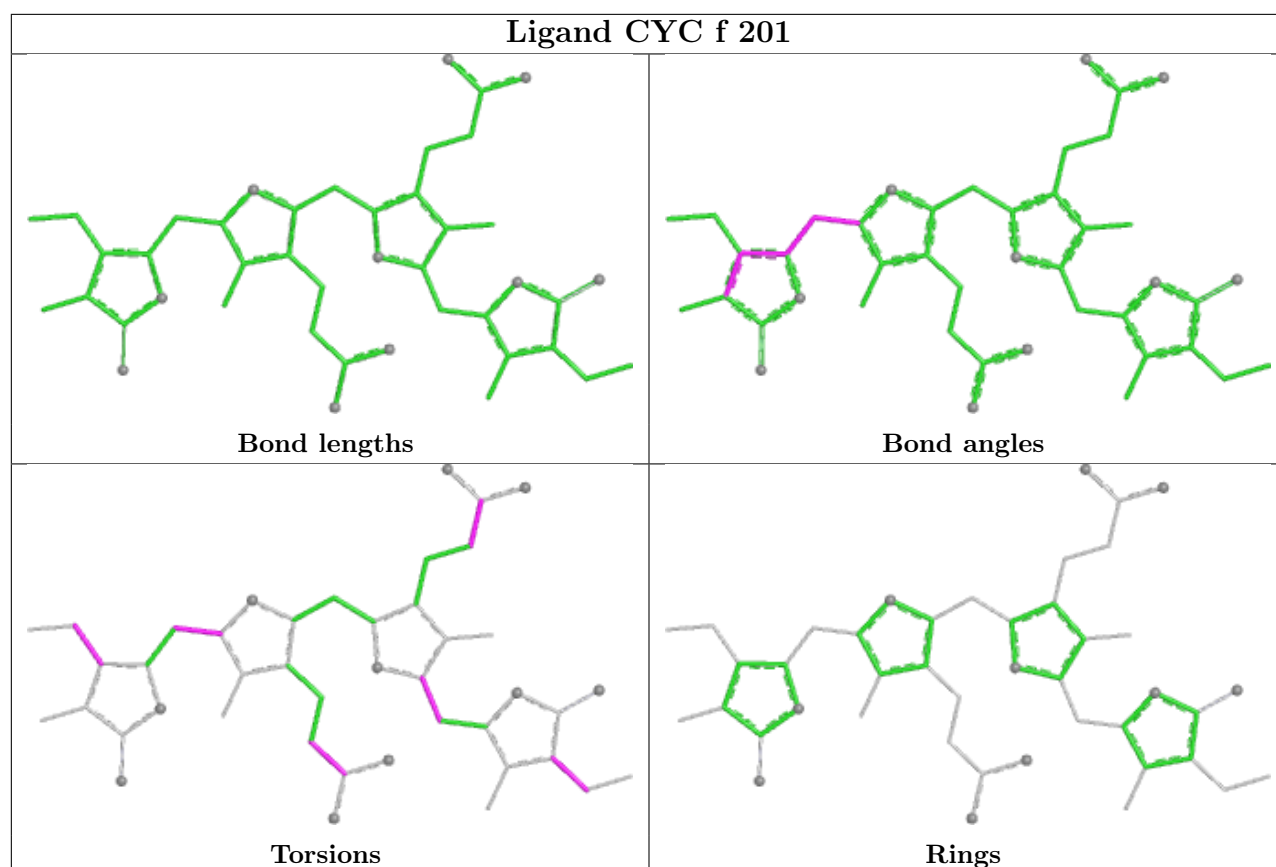


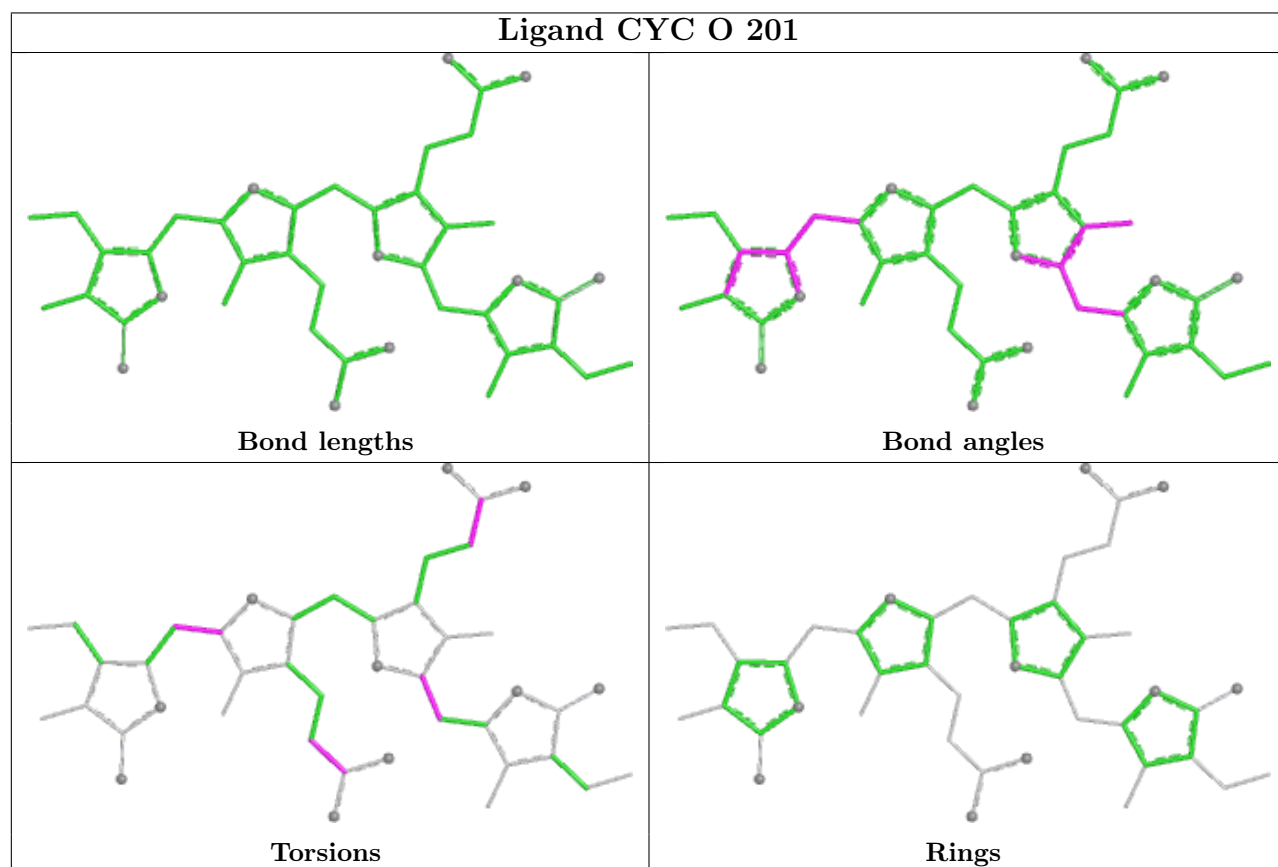
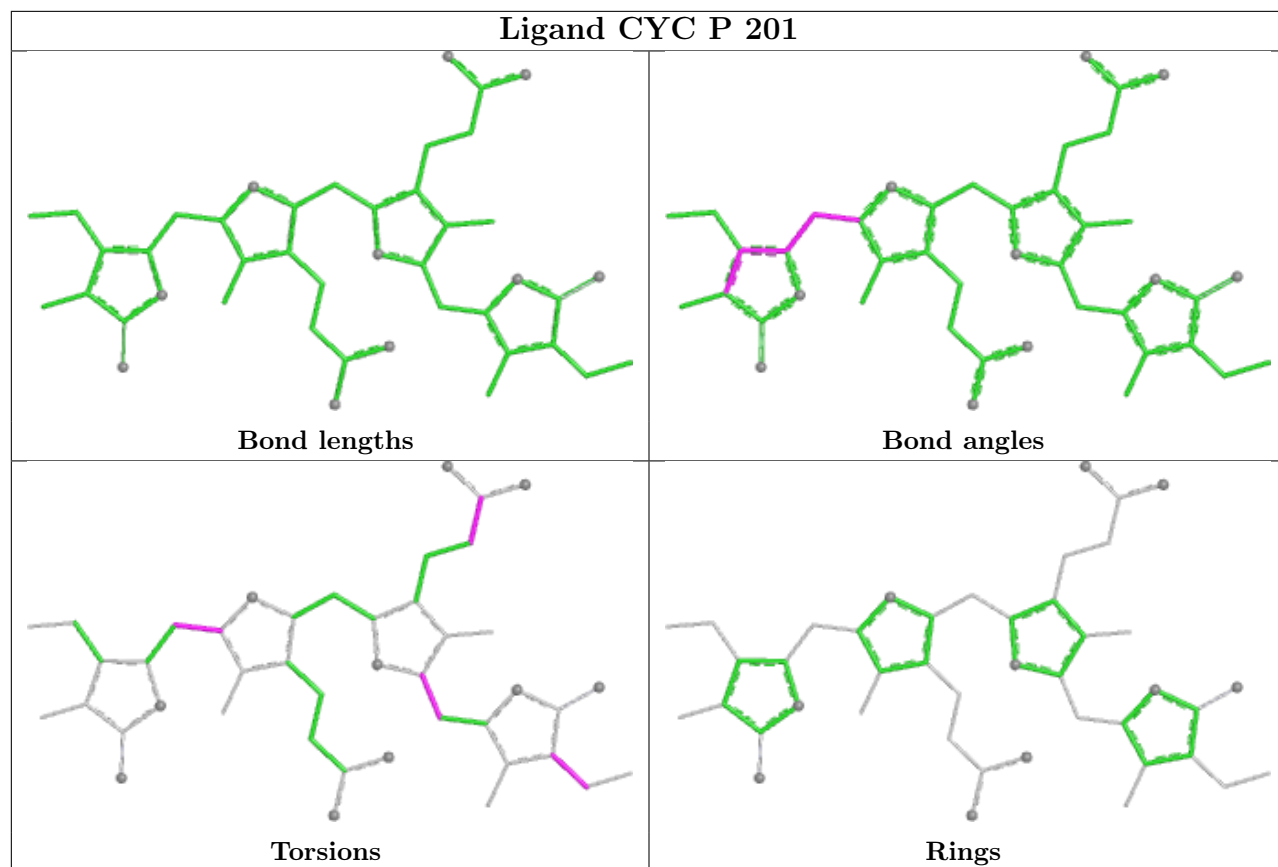
## Ligand CYC e 201

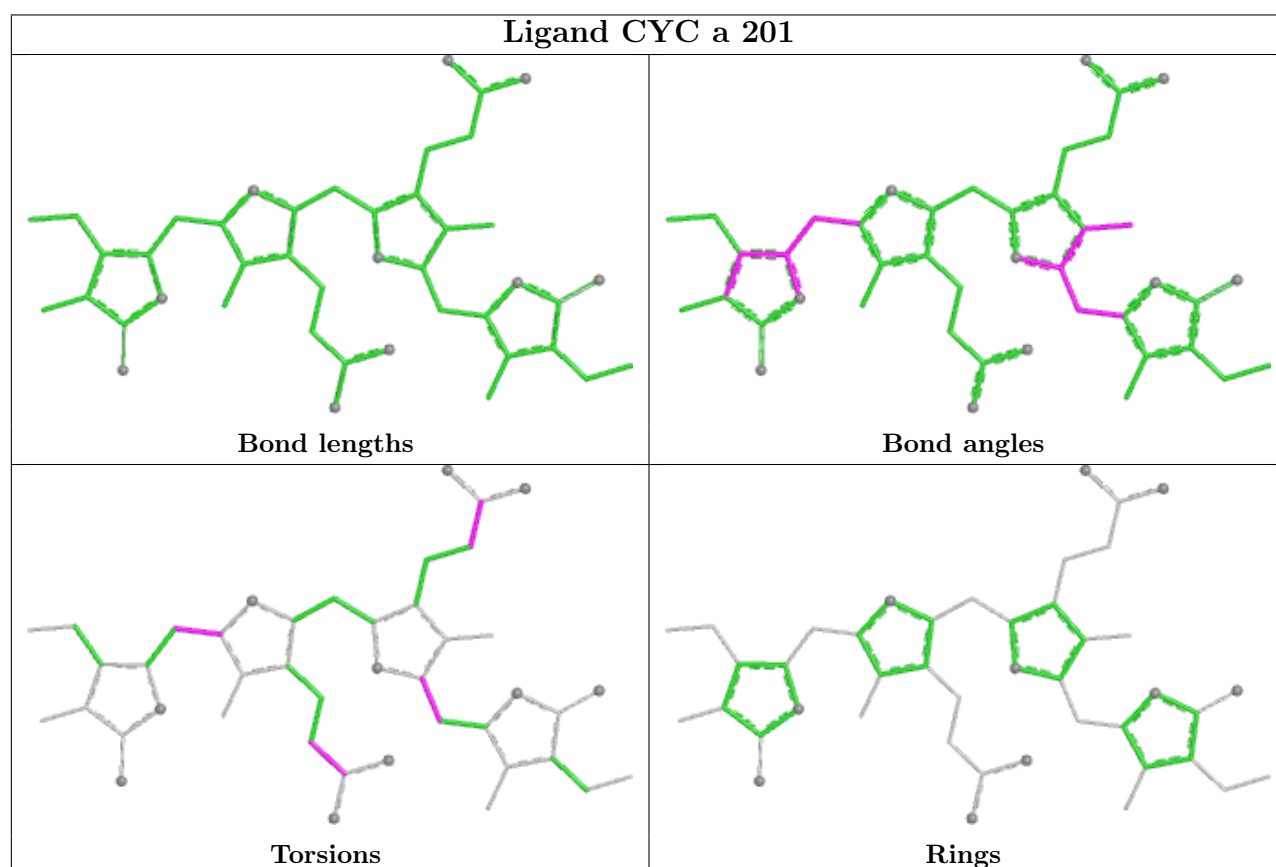
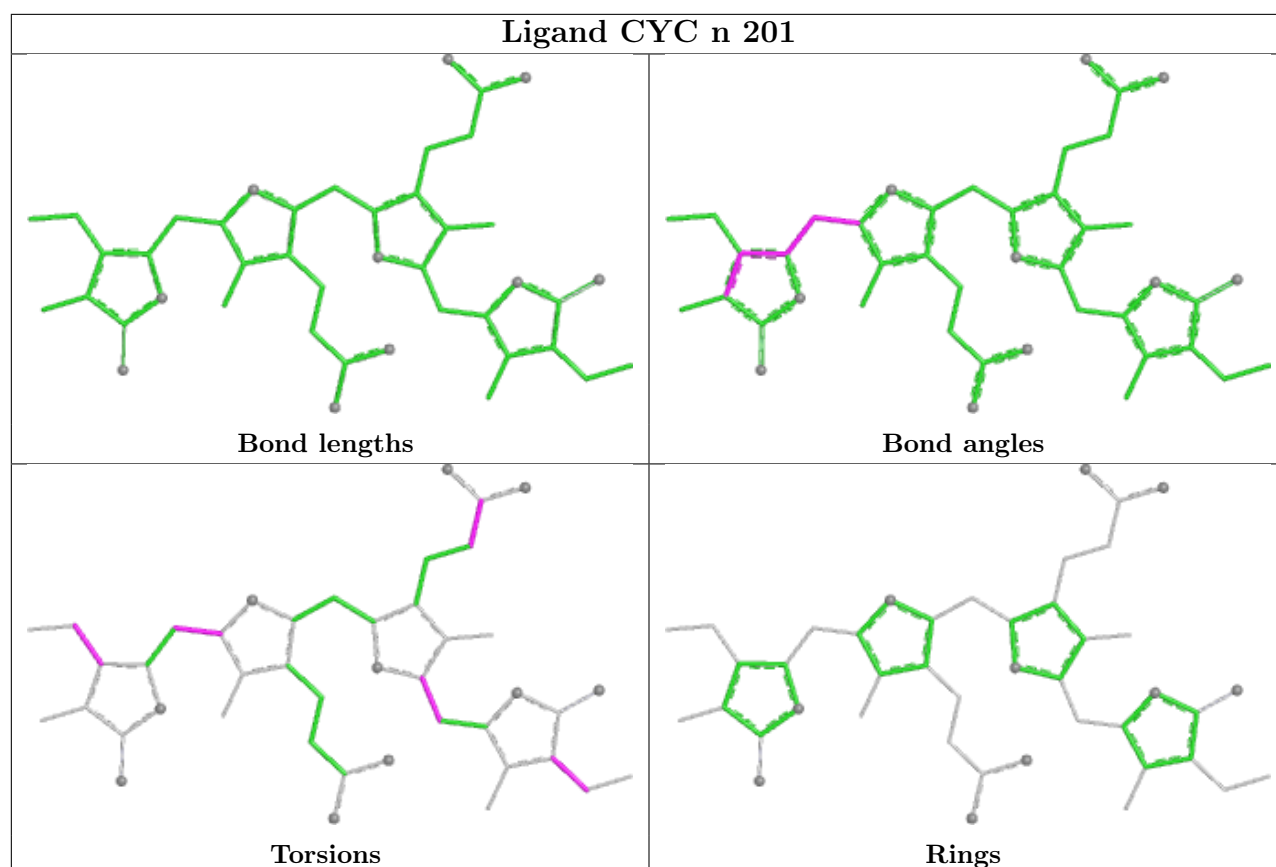


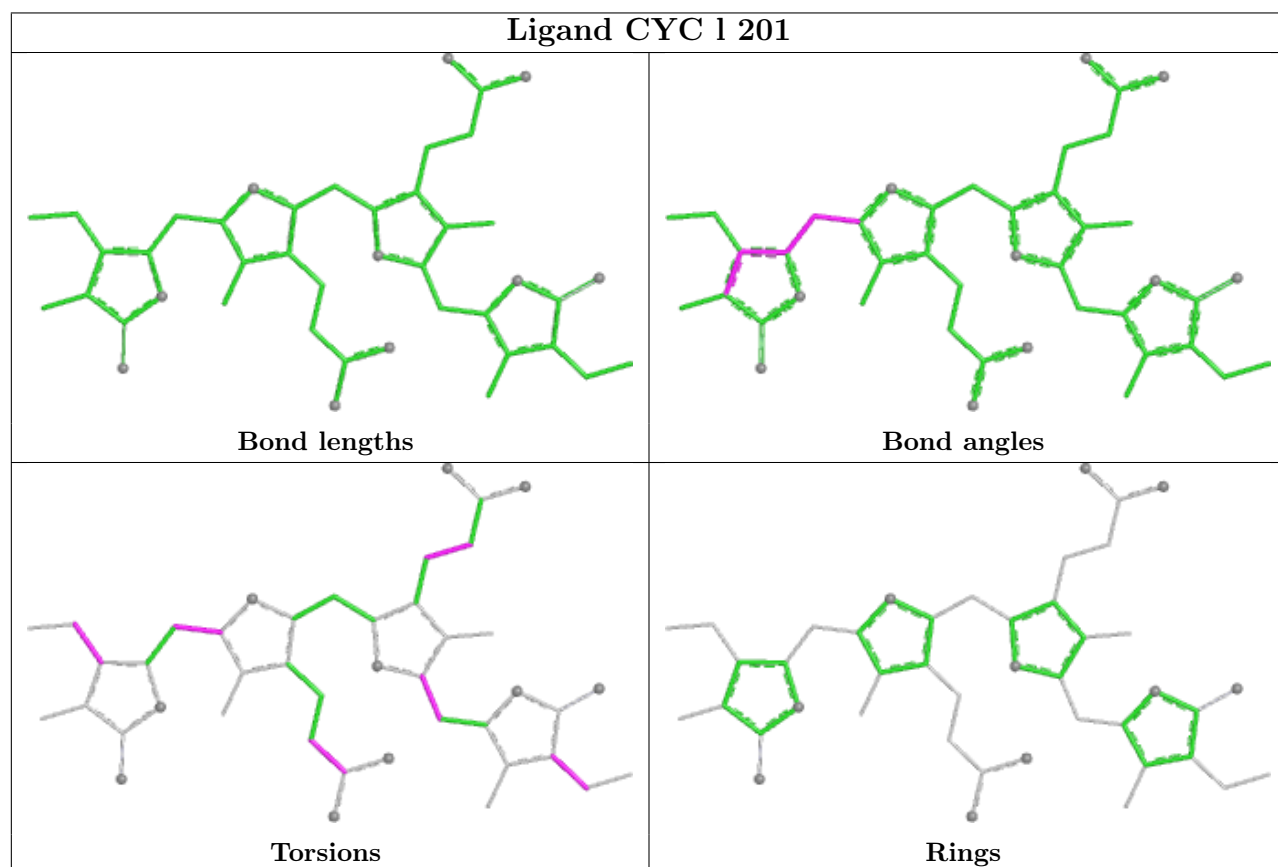
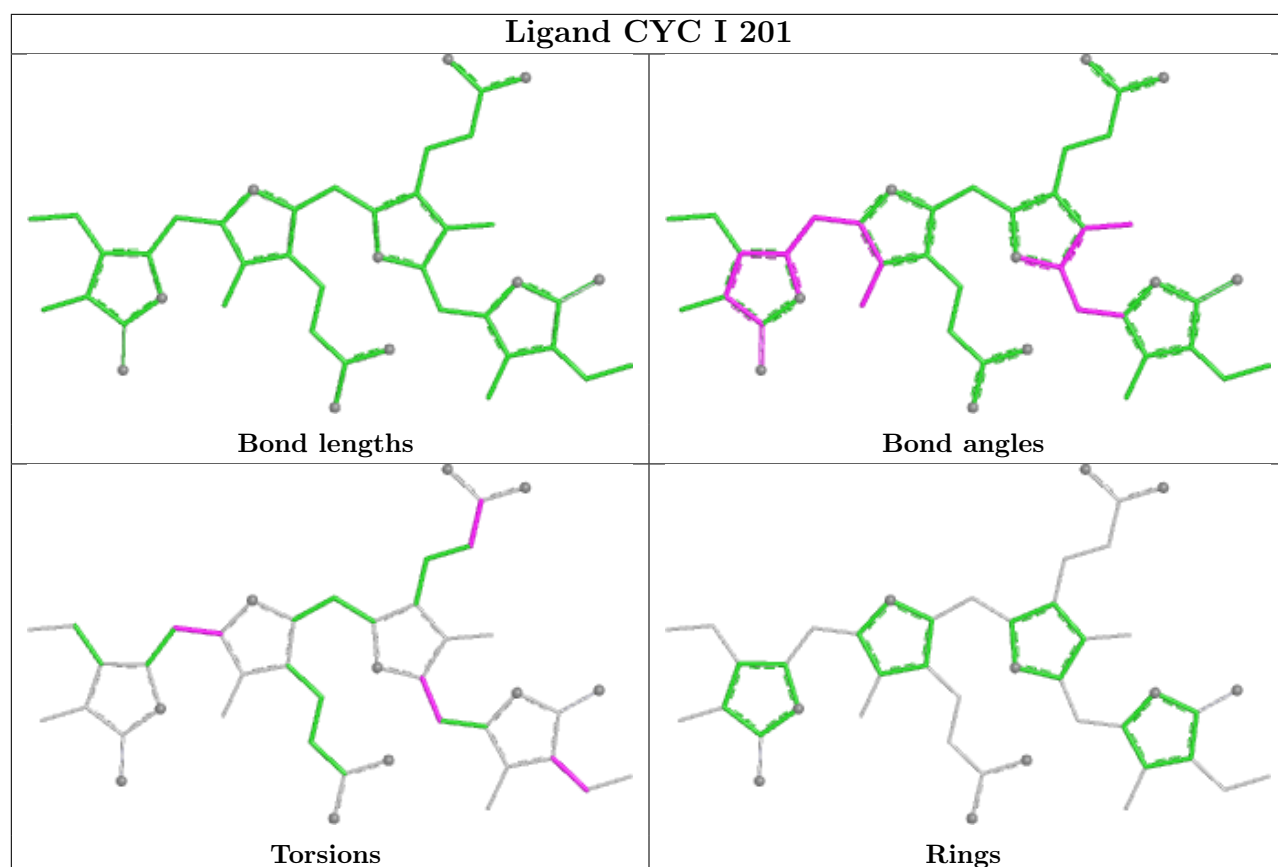
## Ligand CYC L 201

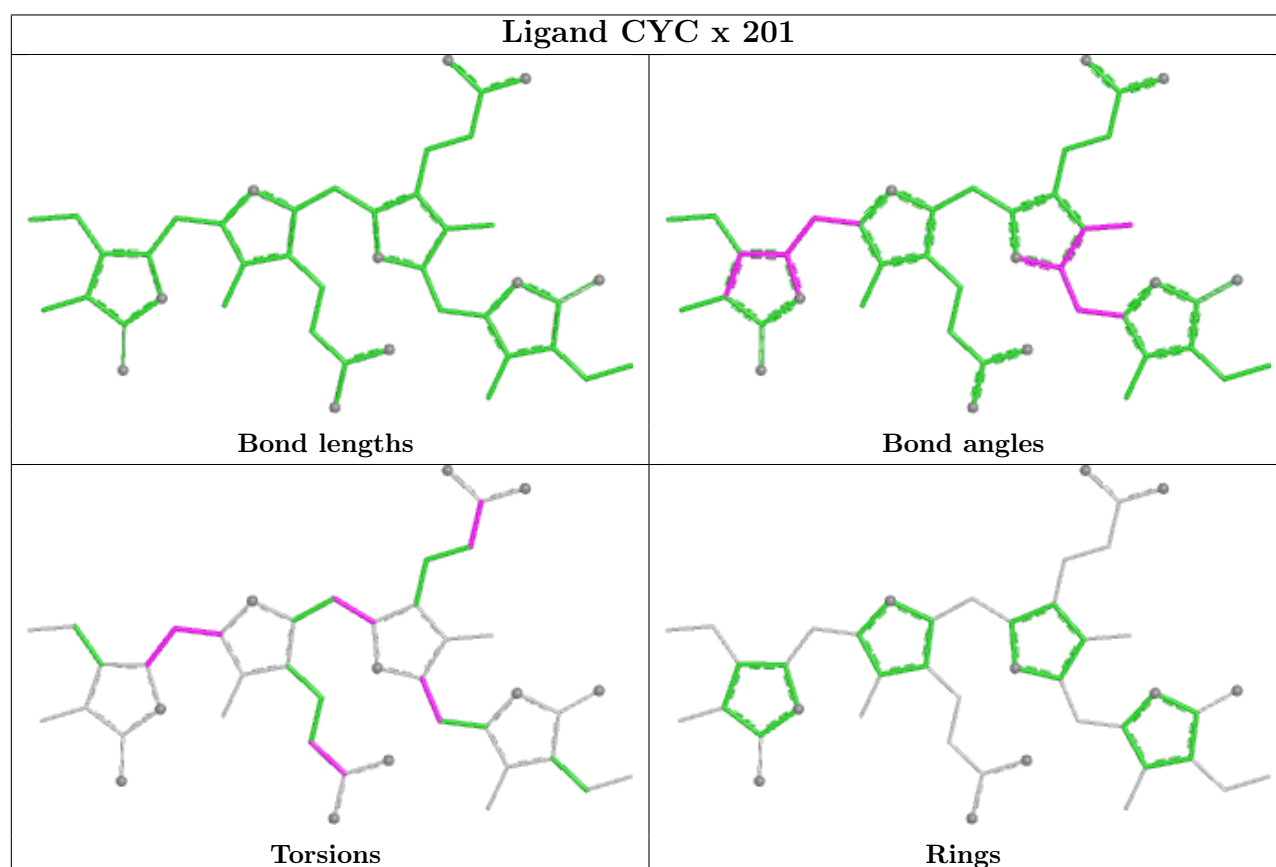
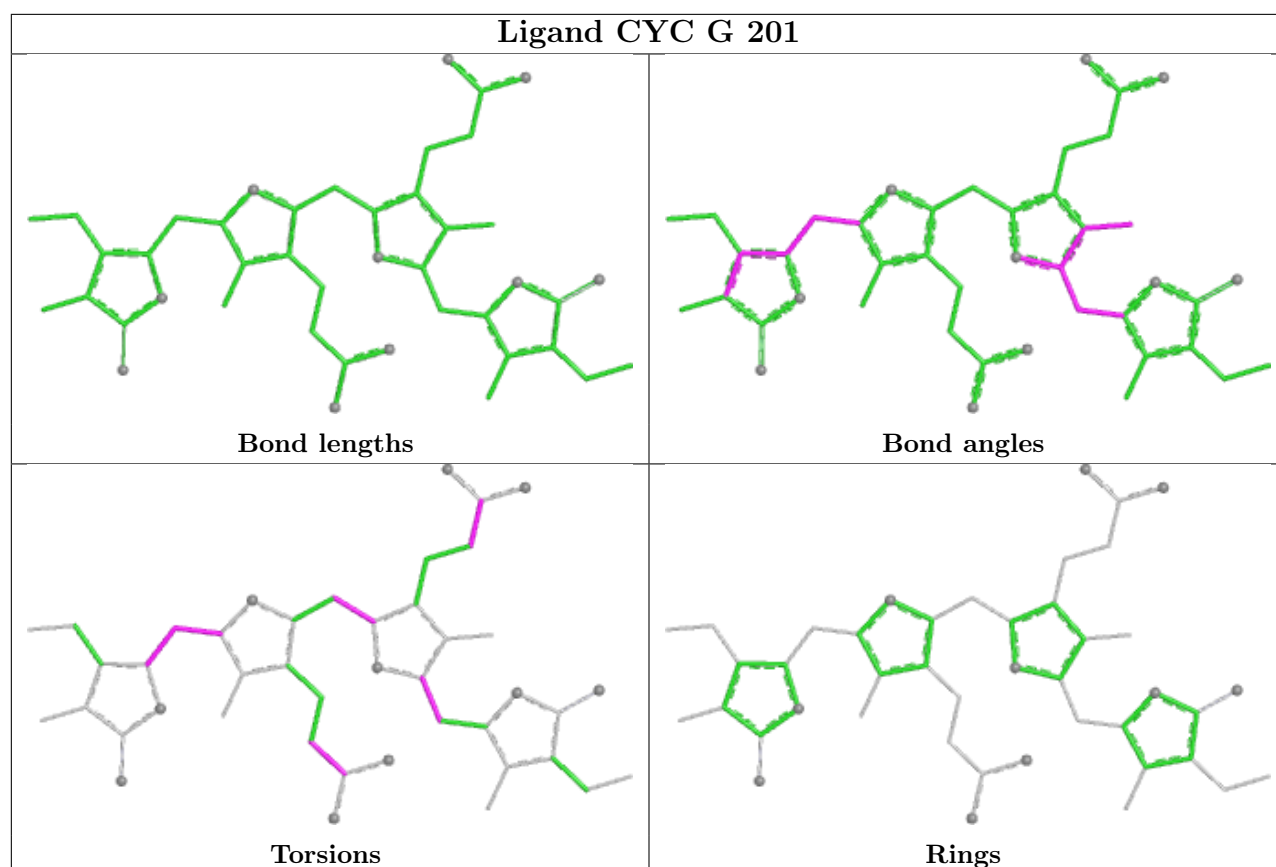




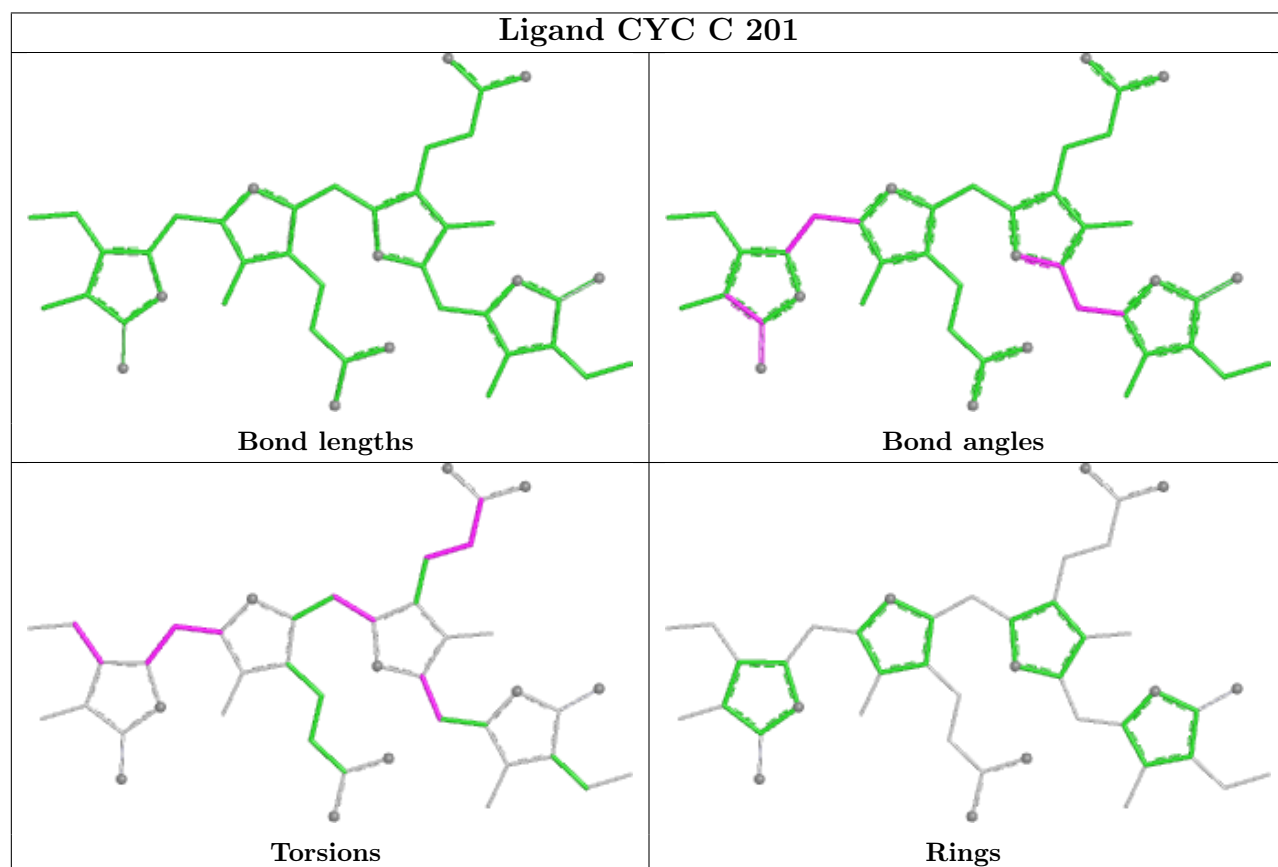
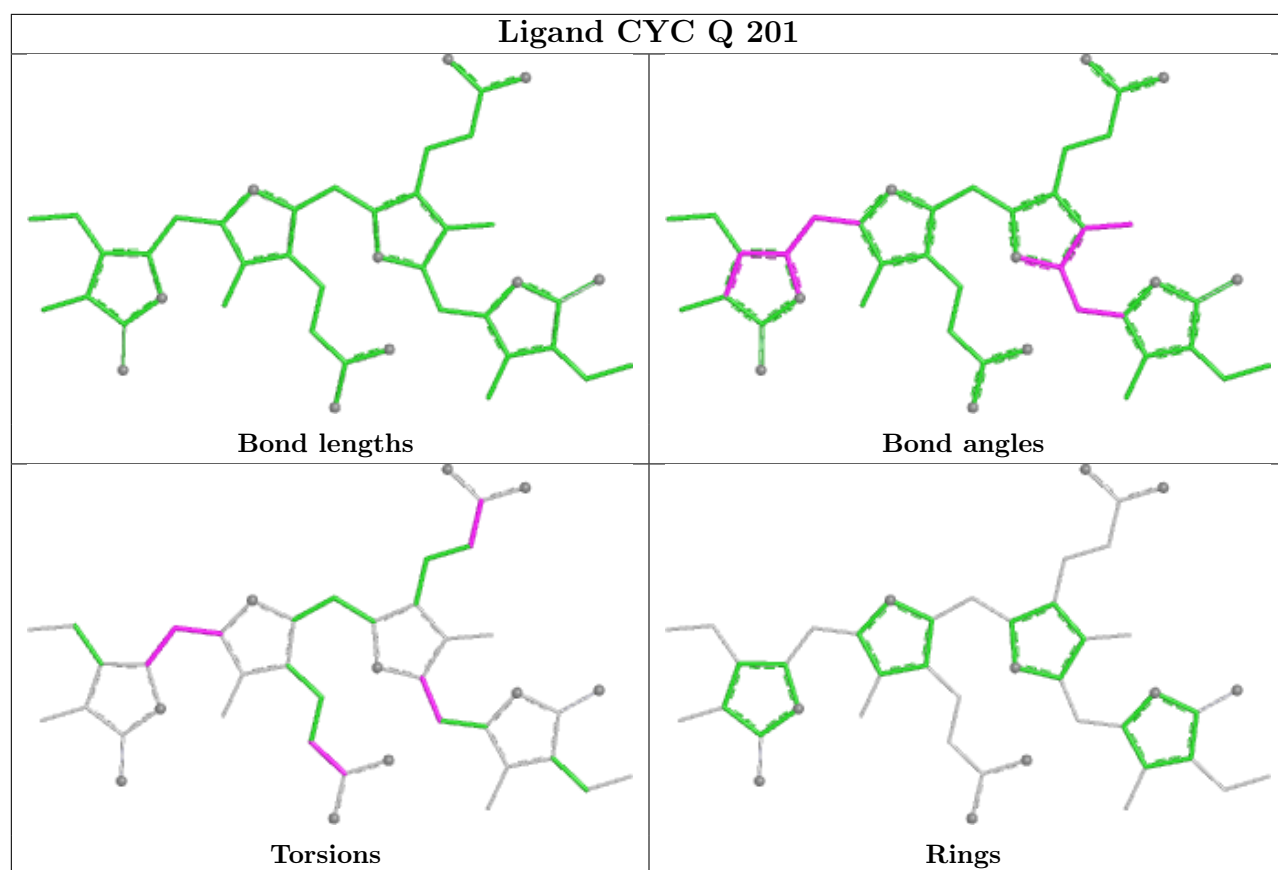


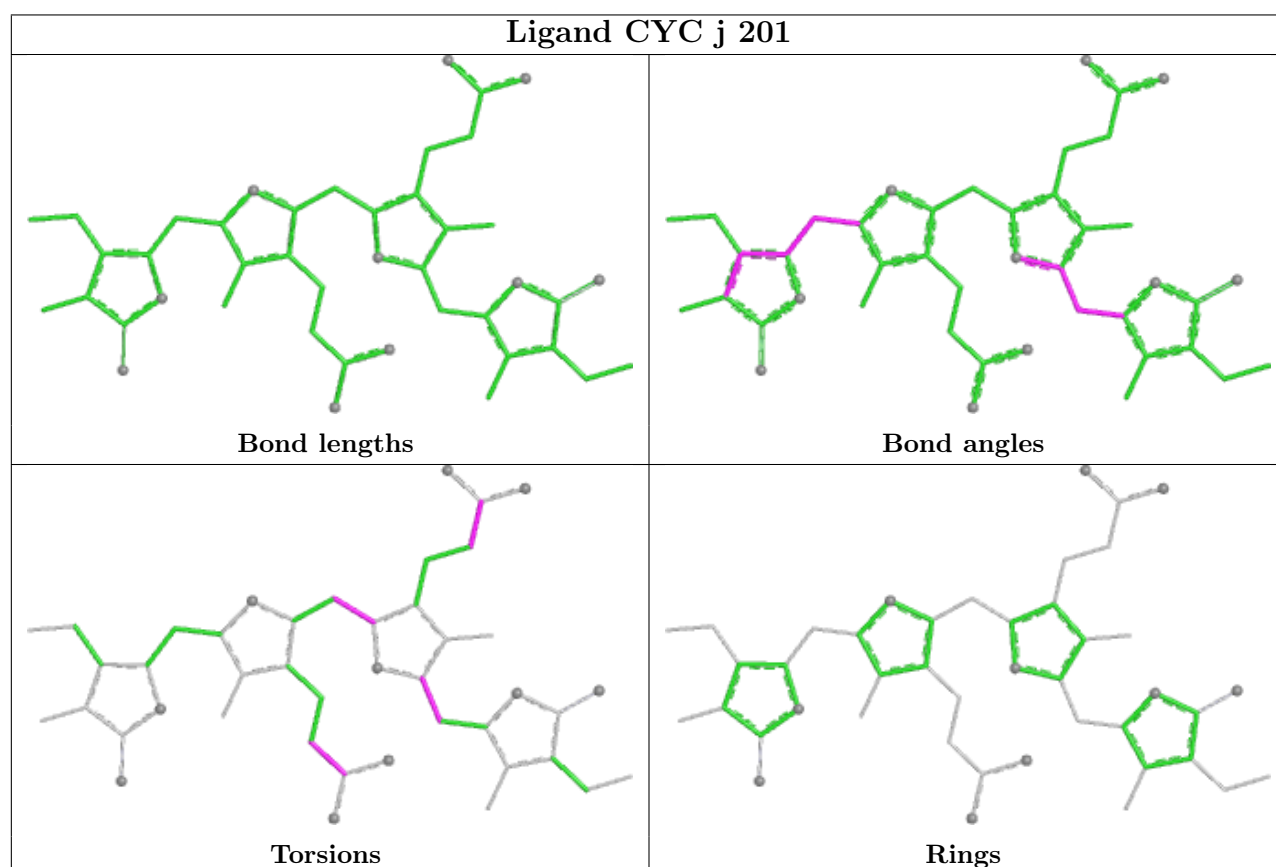
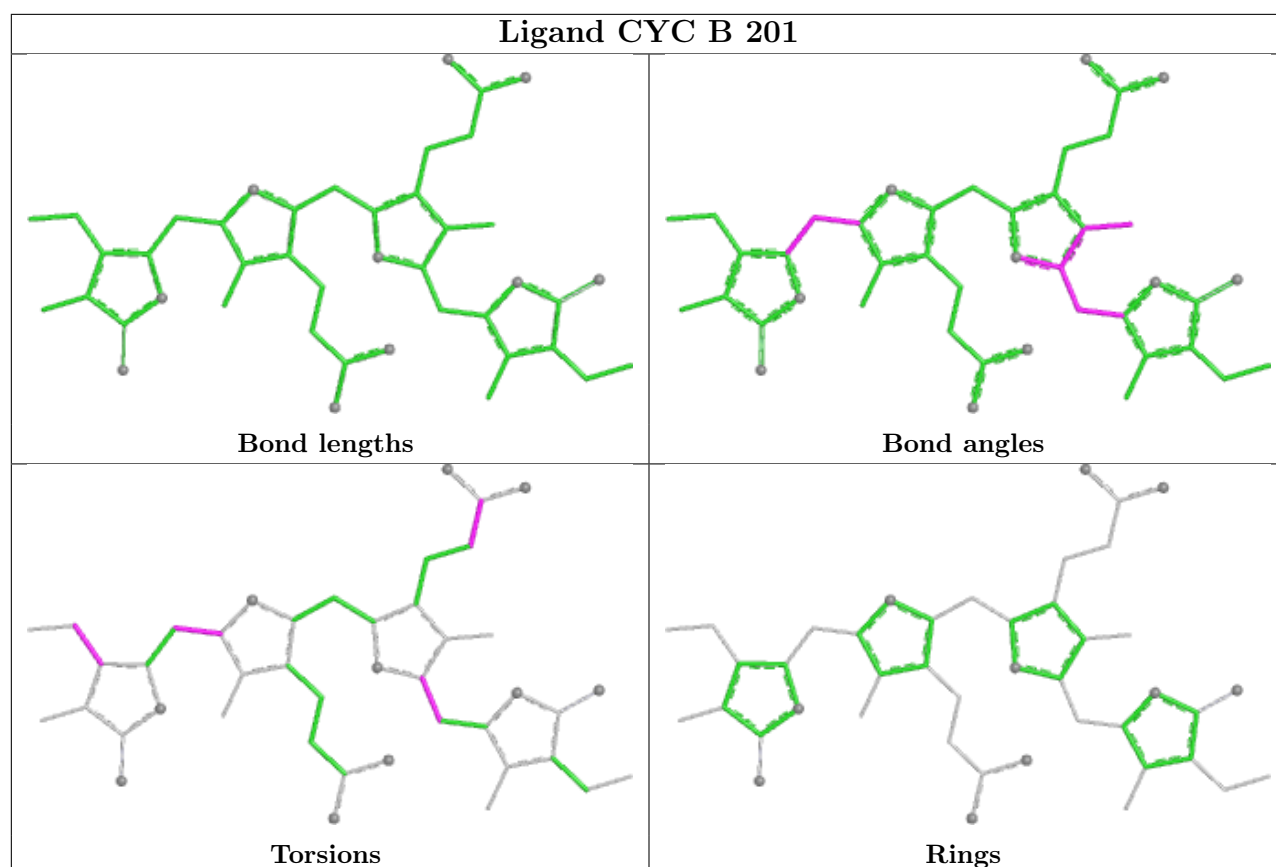


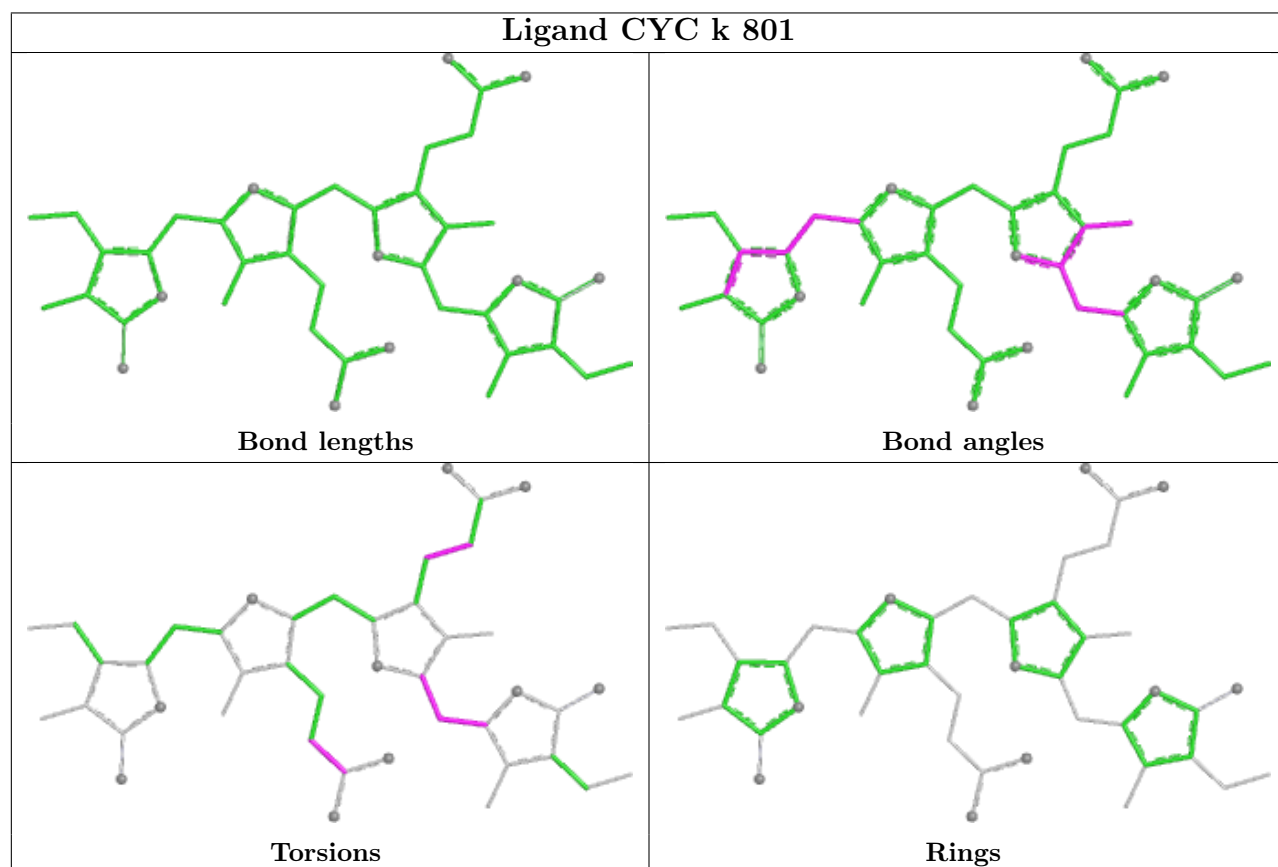
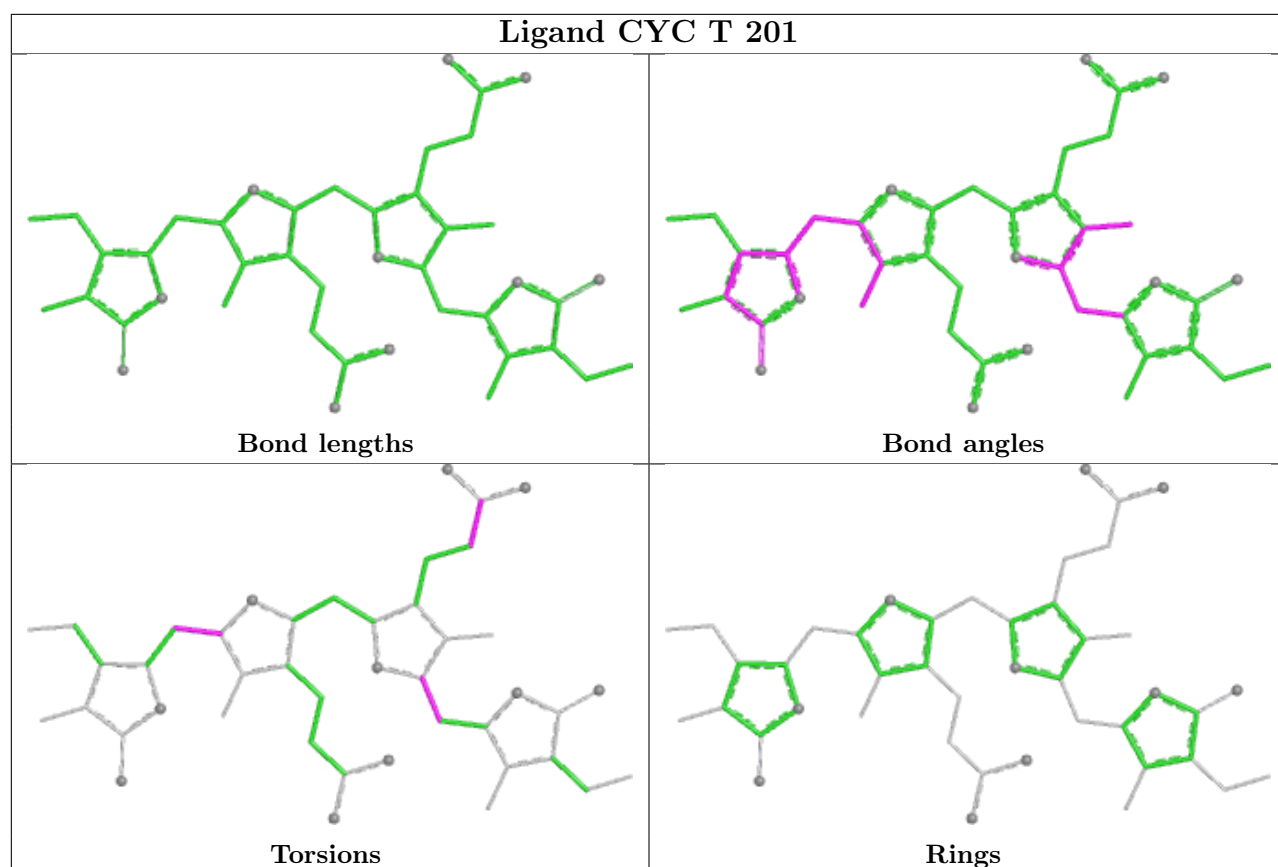


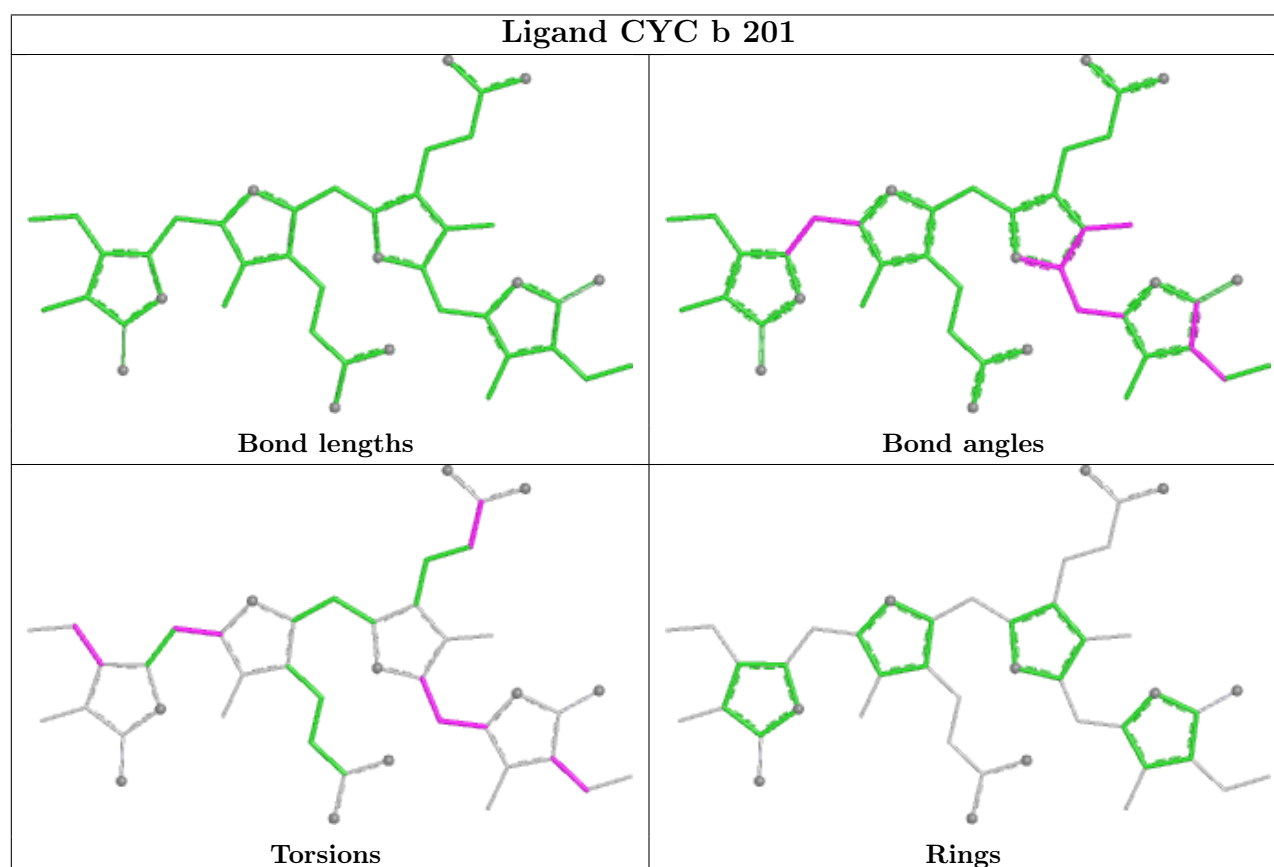
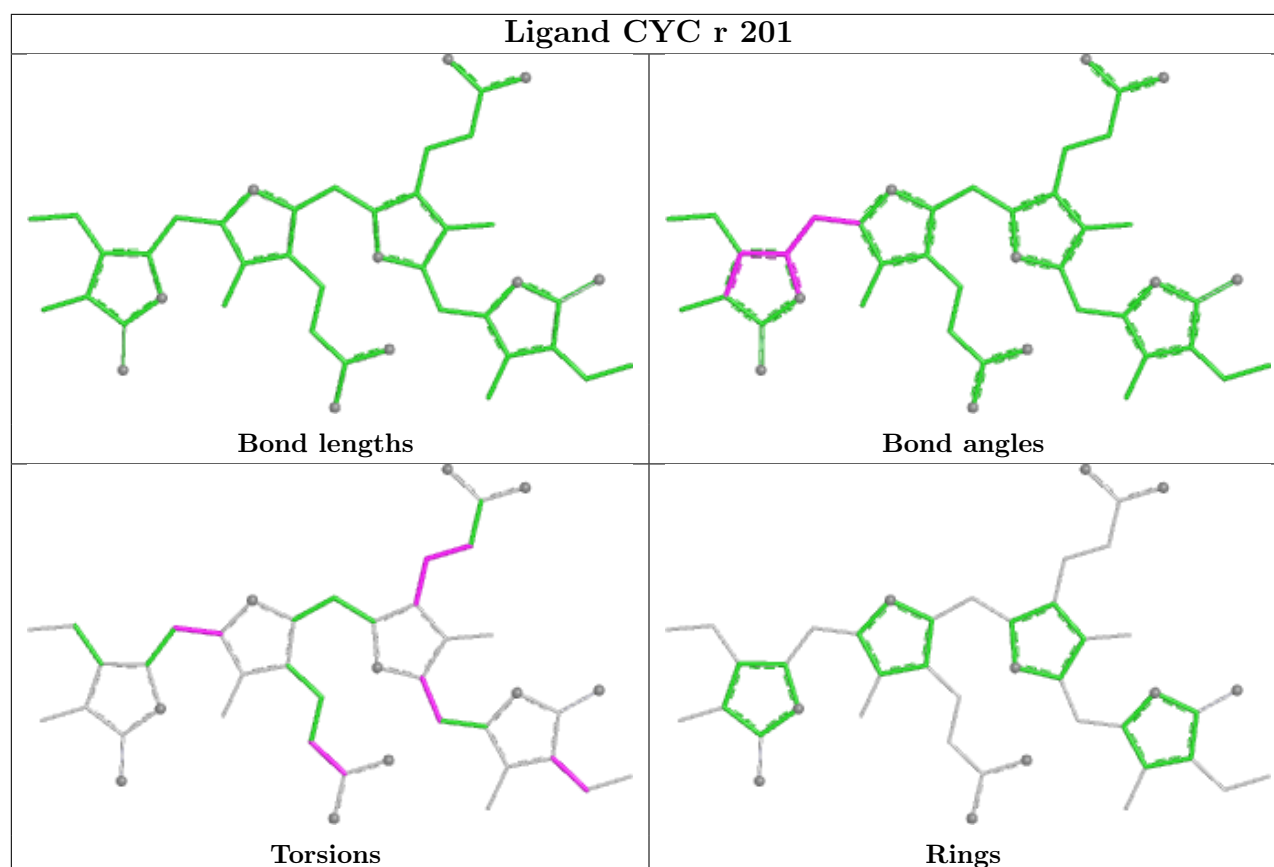


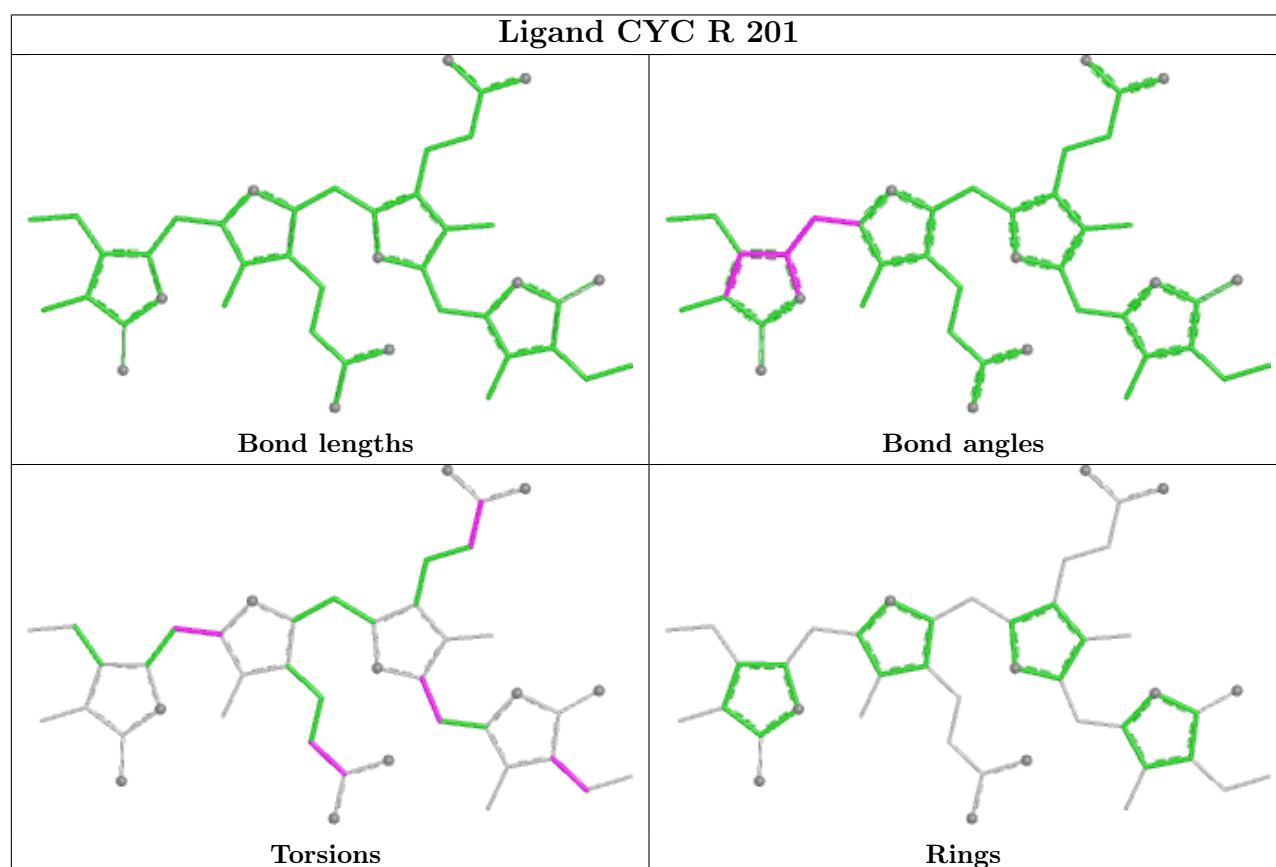
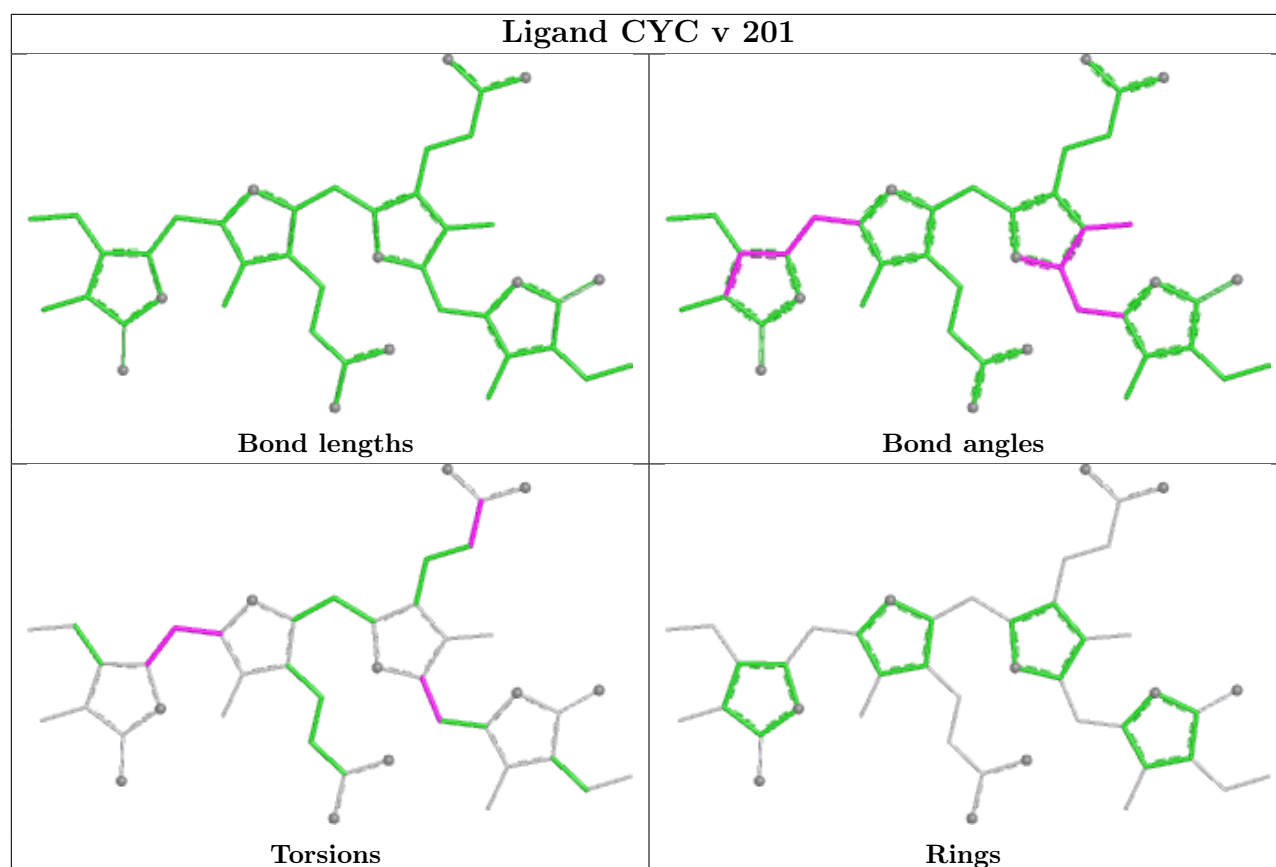


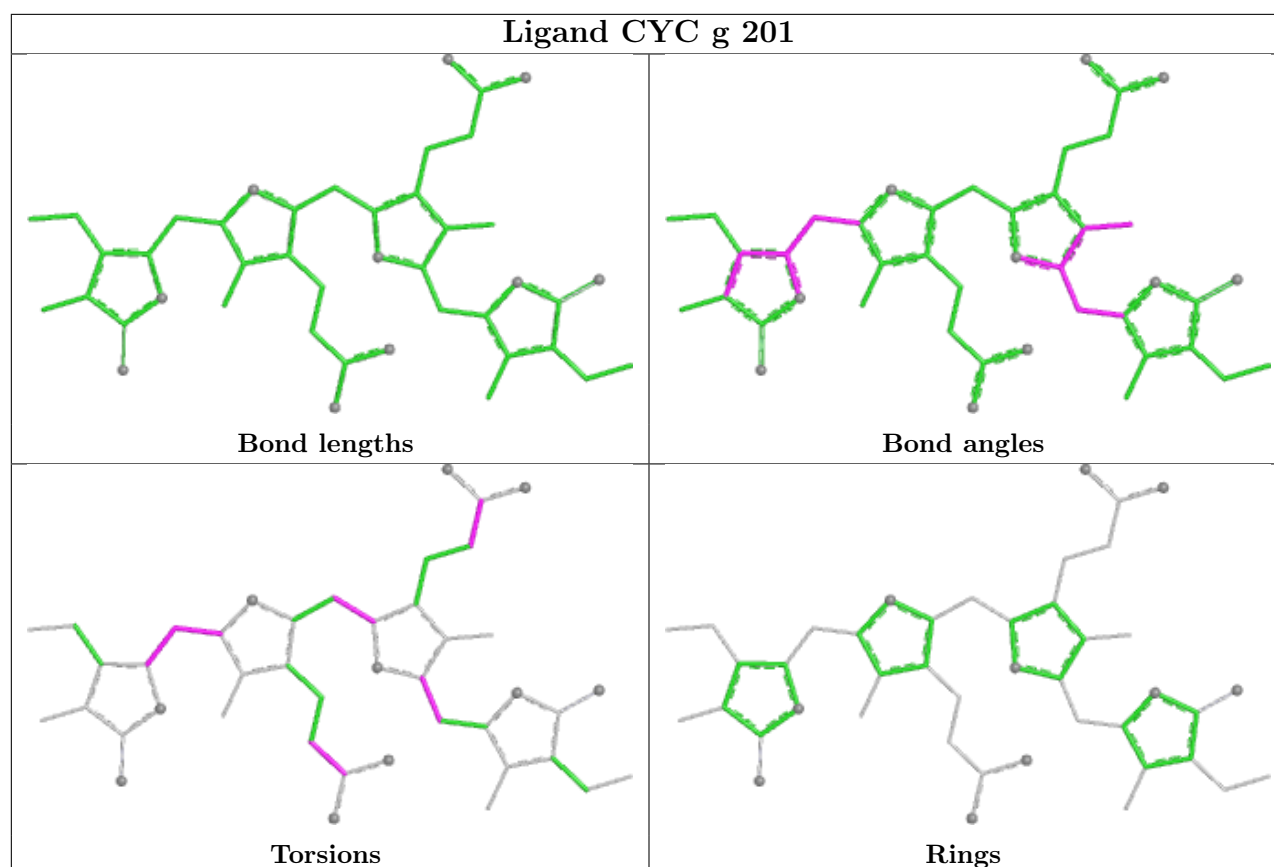












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

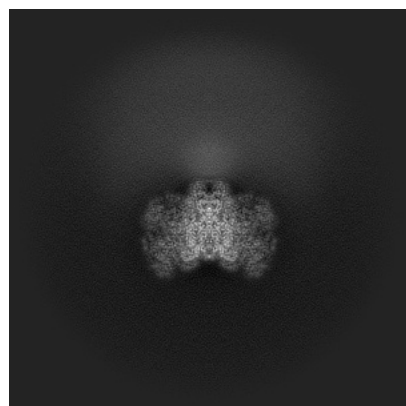
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52573. These allow visual inspection of the internal detail of the map and identification of artifacts.

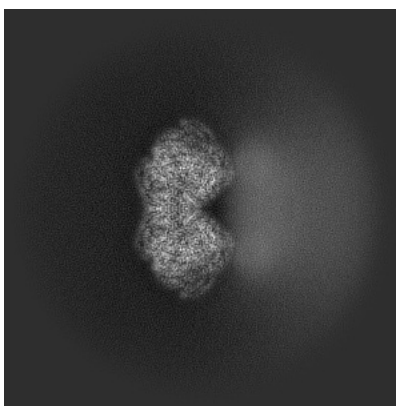
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

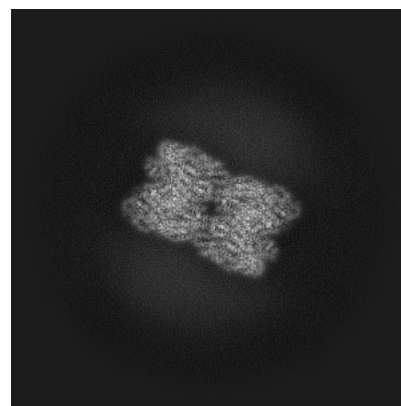
#### 6.1.1 Primary map



X

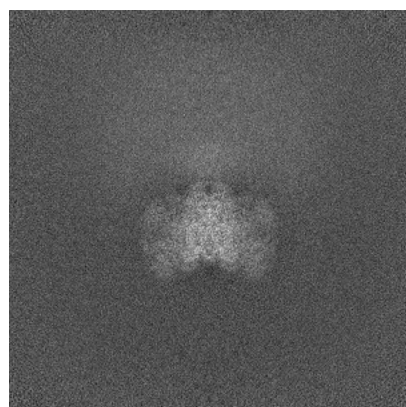


Y

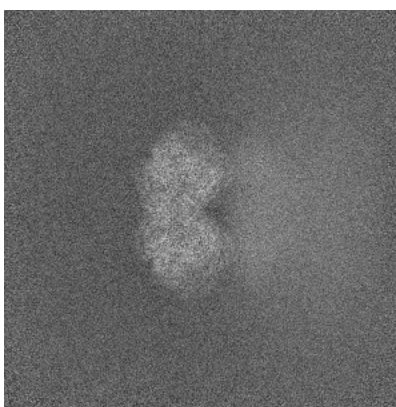


Z

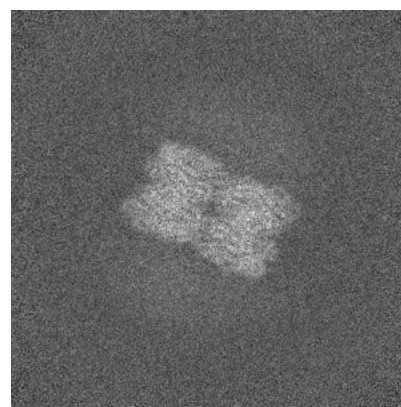
#### 6.1.2 Raw map



X



Y



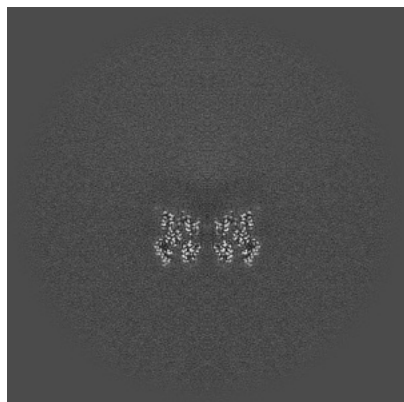
Z

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

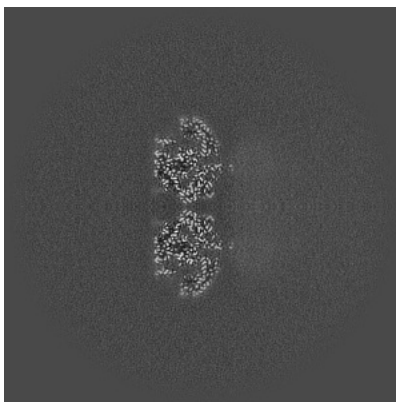


## 6.2 Central slices [i](#)

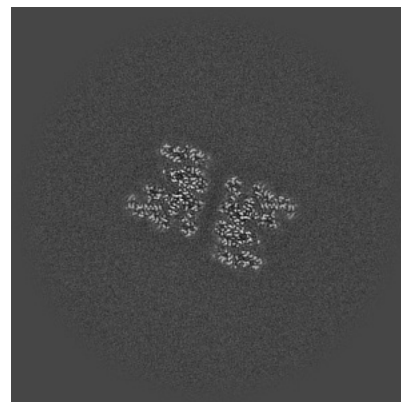
### 6.2.1 Primary map



X Index: 350

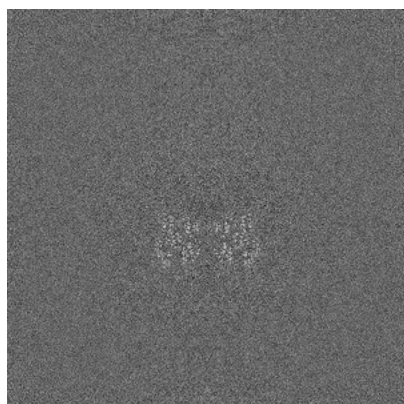


Y Index: 350

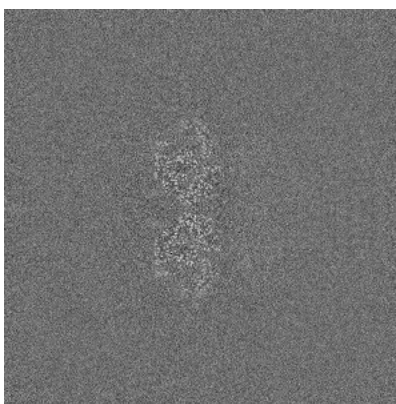


Z Index: 350

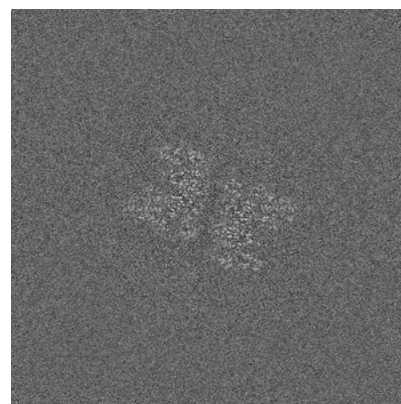
### 6.2.2 Raw map



X Index: 350



Y Index: 350



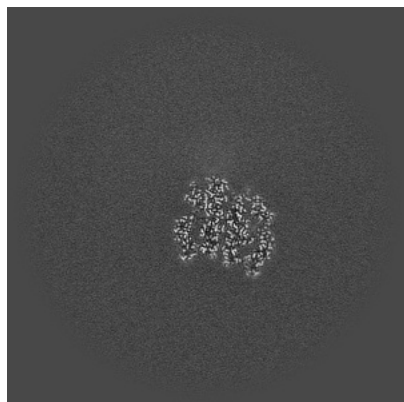
Z Index: 350

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

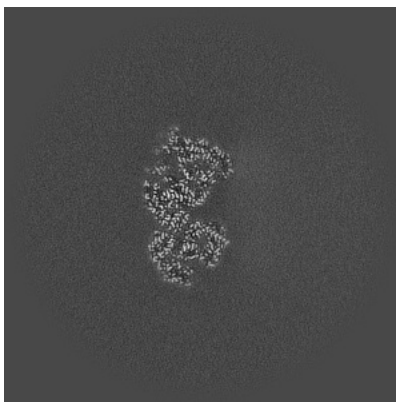


## 6.3 Largest variance slices [i](#)

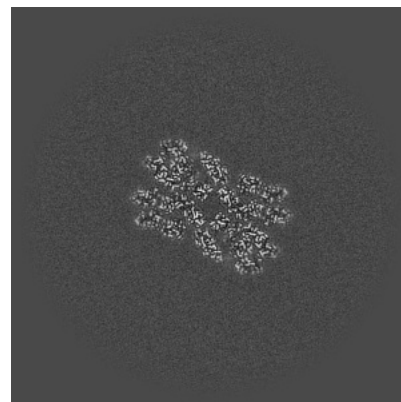
### 6.3.1 Primary map



X Index: 285

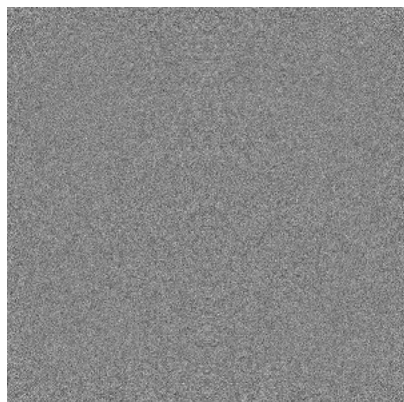


Y Index: 321

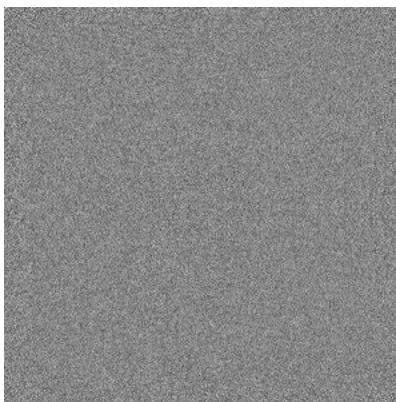


Z Index: 288

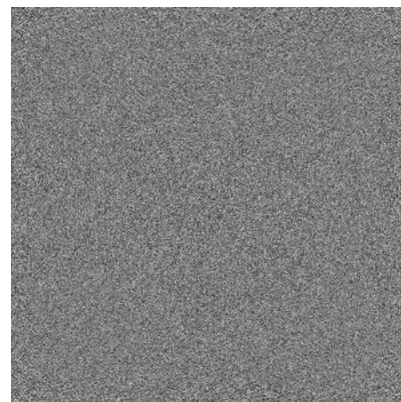
### 6.3.2 Raw map



X Index: 0



Y Index: 0

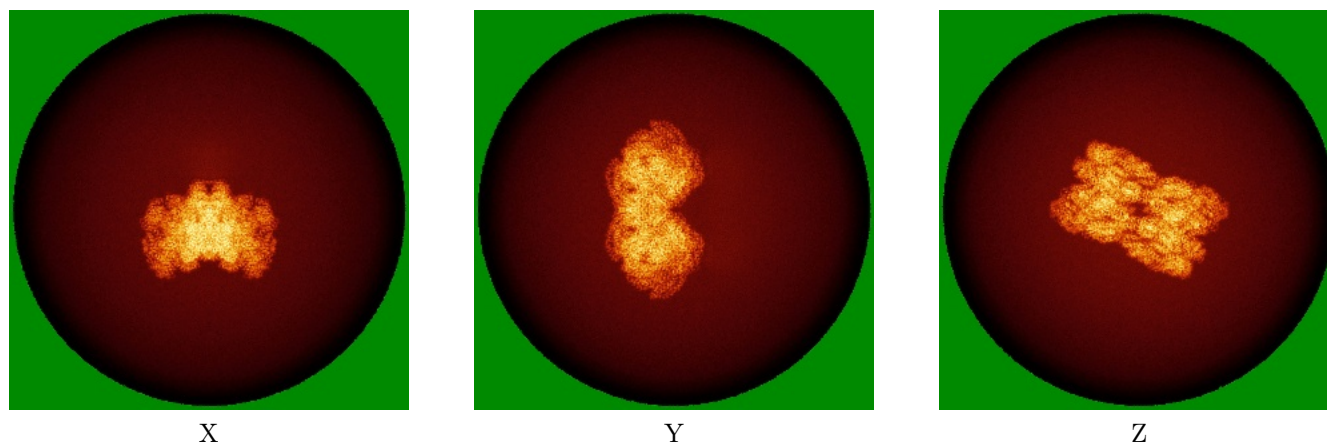


Z Index: 0

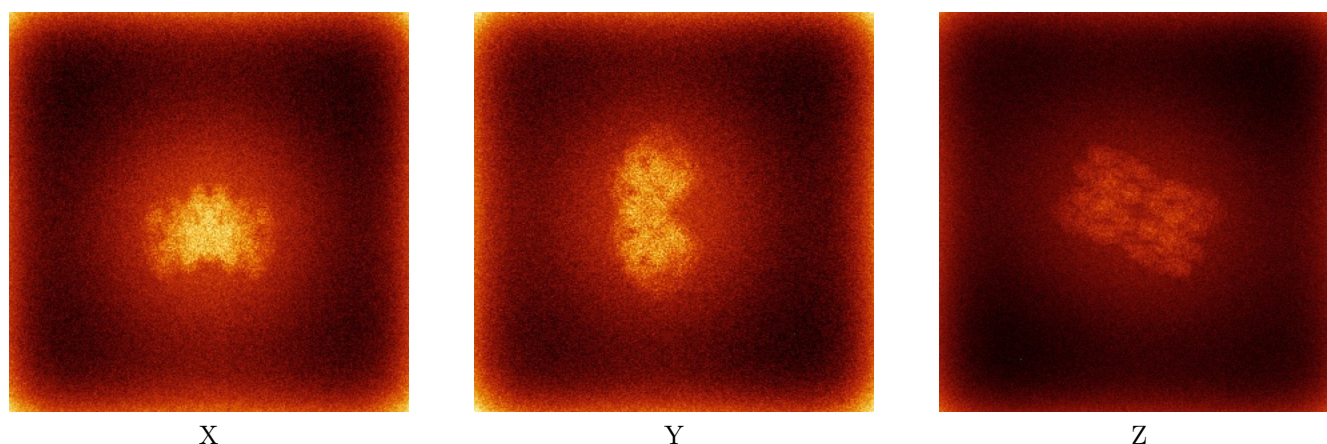
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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](#)

This section was not generated.

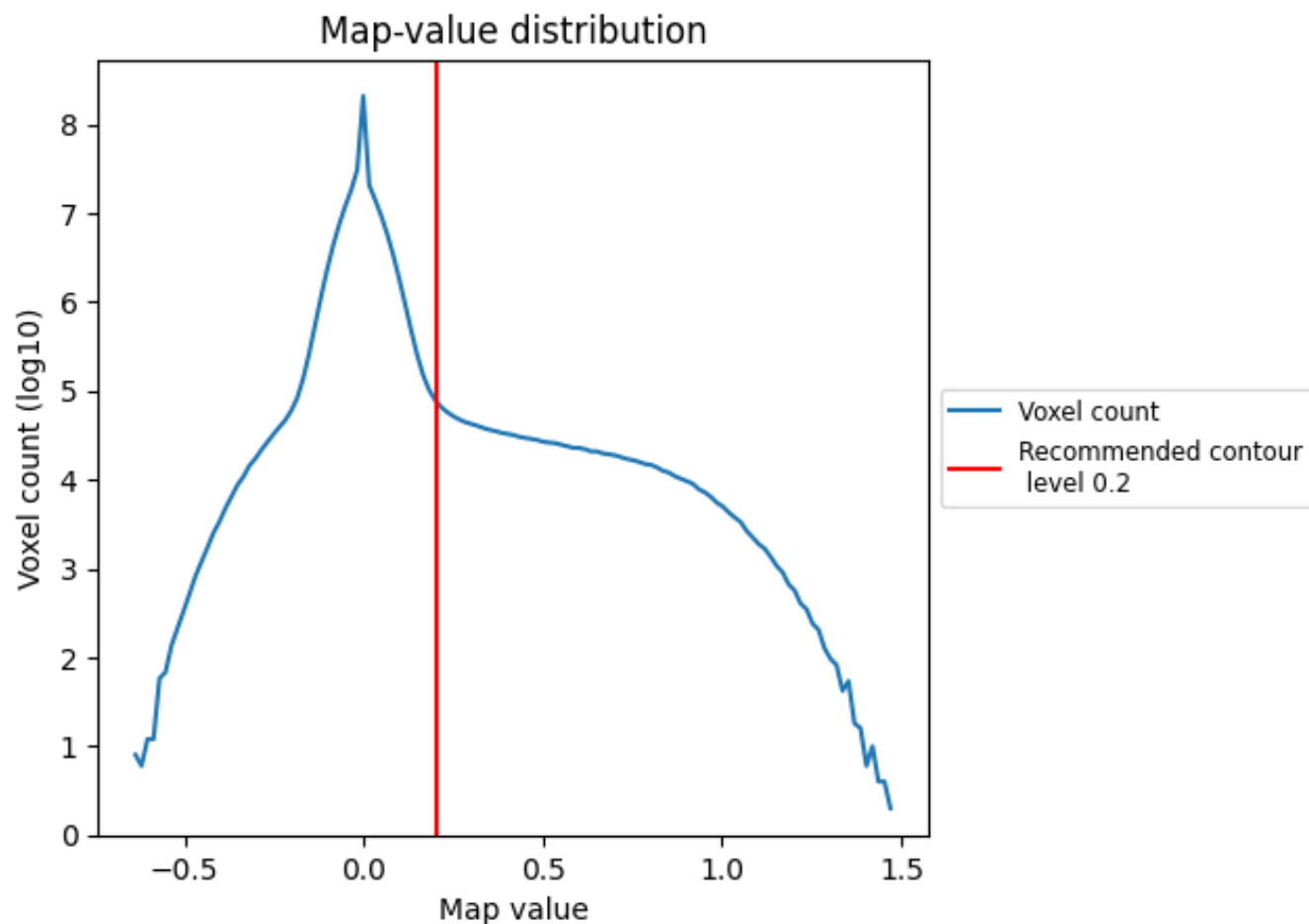
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

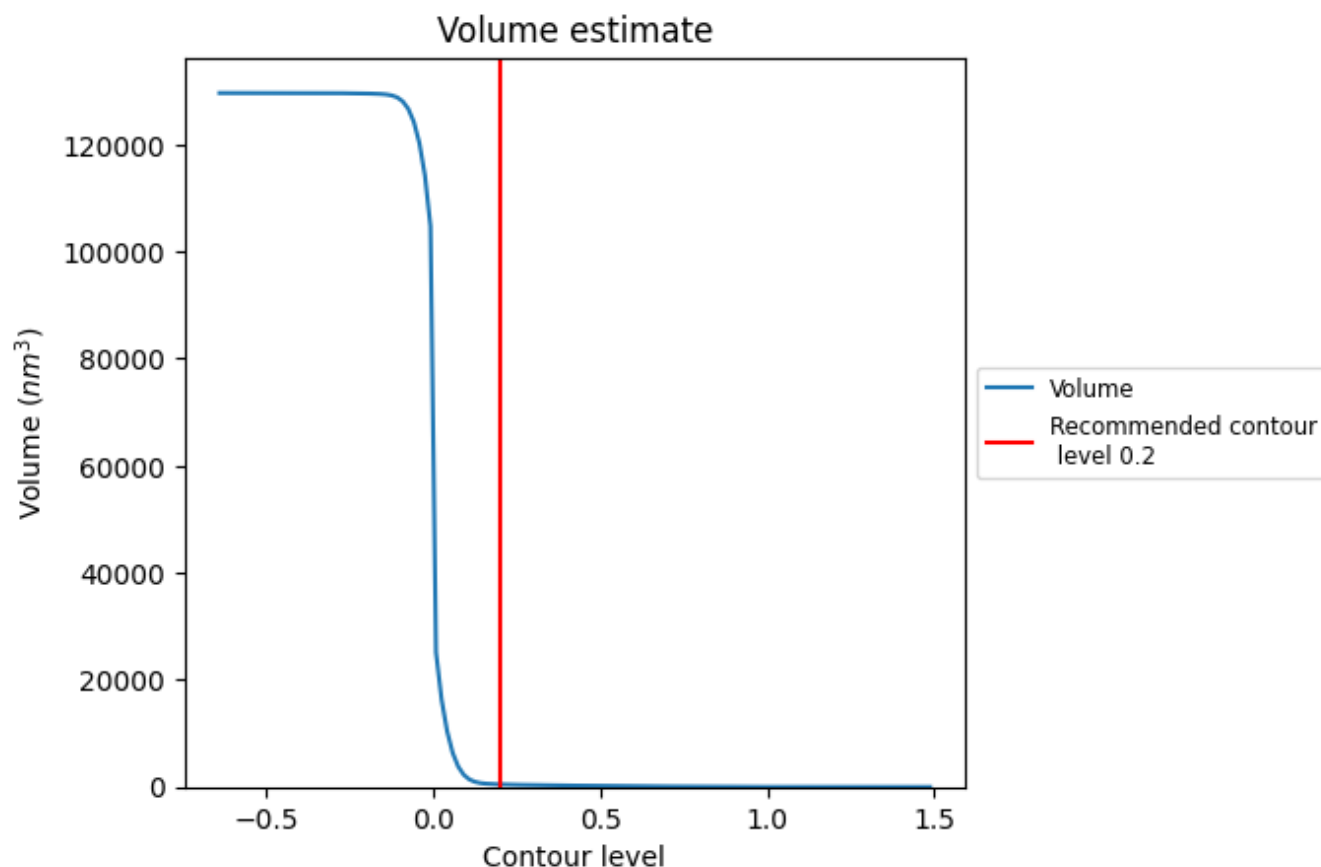
This section contains the results of statistical analysis of the map.

### 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.

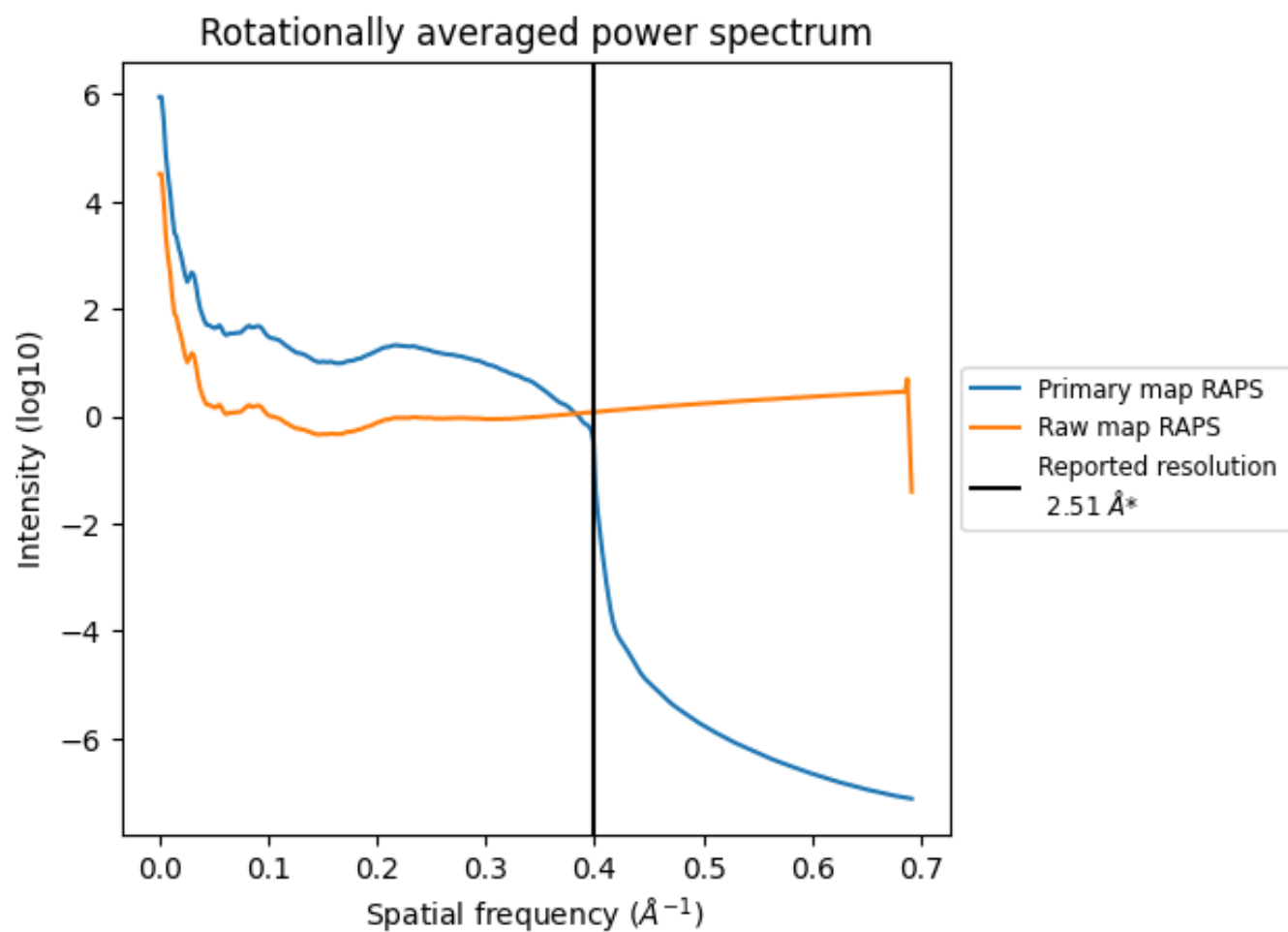
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 482 nm<sup>3</sup>; this corresponds to an approximate mass of 436 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 ⓘ

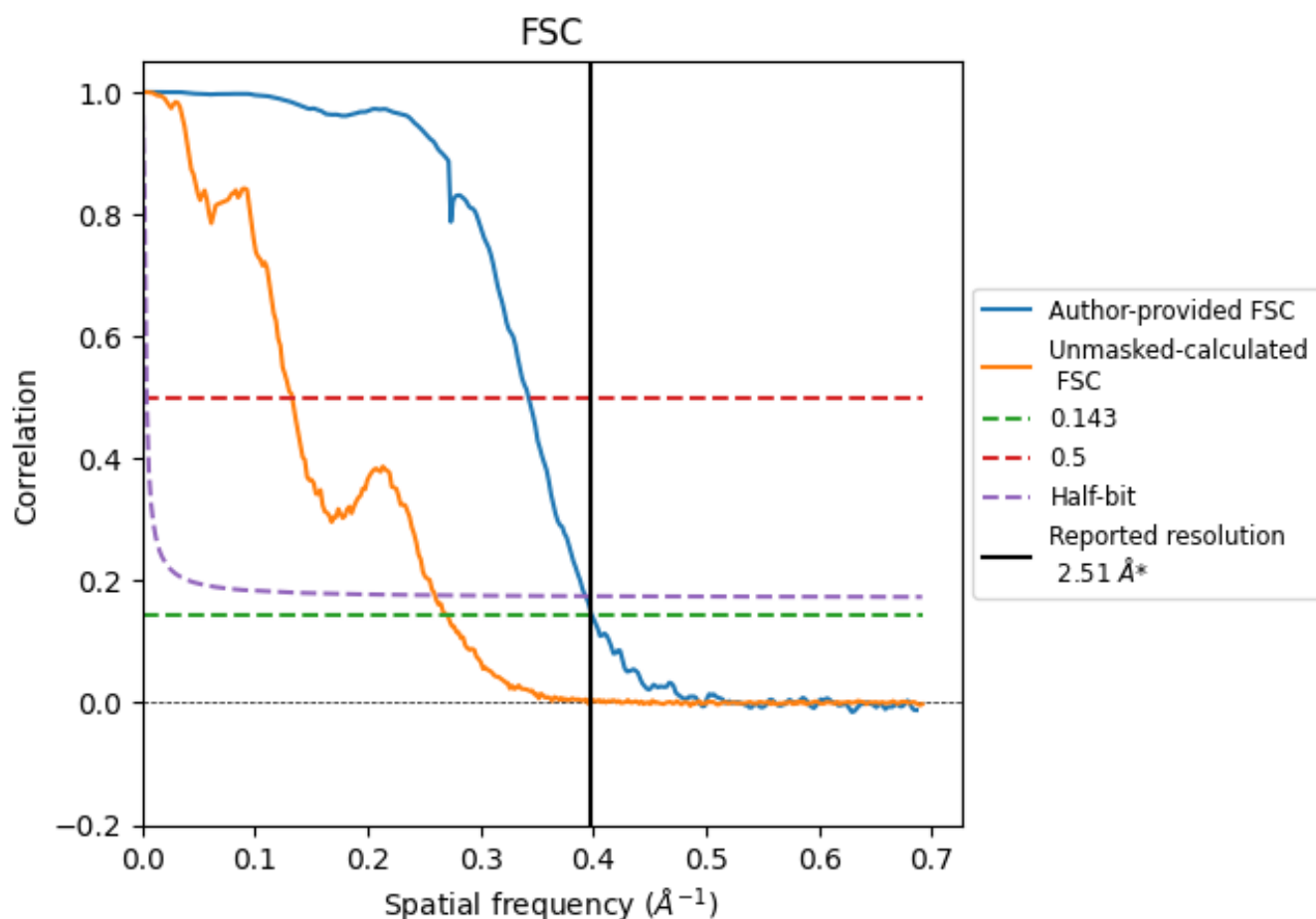


\*Reported resolution corresponds to spatial frequency of 0.398  $\text{\AA}^{-1}$

## 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 0.398  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

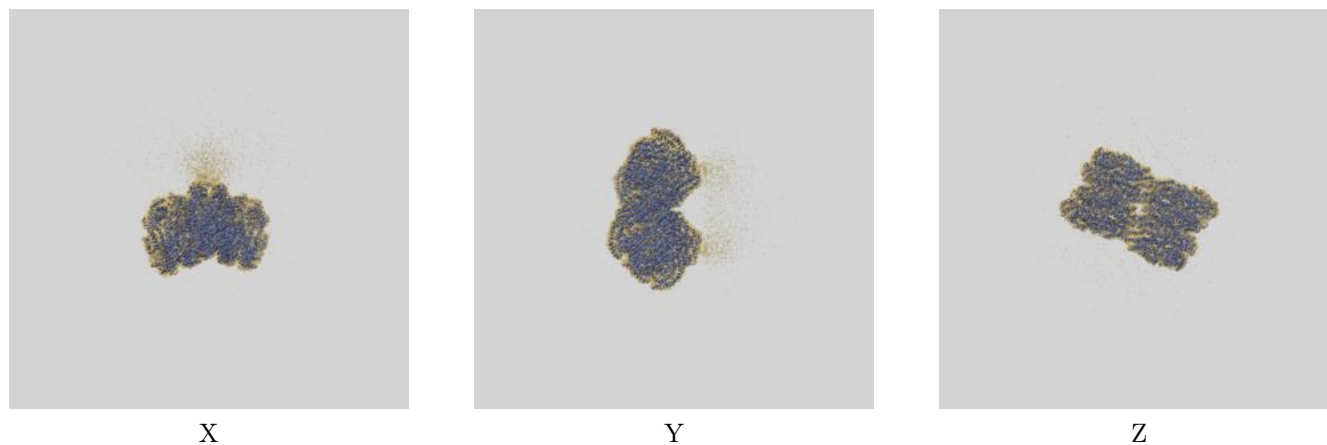
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.51	-	-
Author-provided FSC curve	2.51	2.92	2.54
Unmasked-calculated*	3.69	7.52	3.85

\*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 3.69 differs from the reported value 2.51 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52573 and PDB model 9I1R. Per-residue inclusion information can be found in section 3 on page 12.

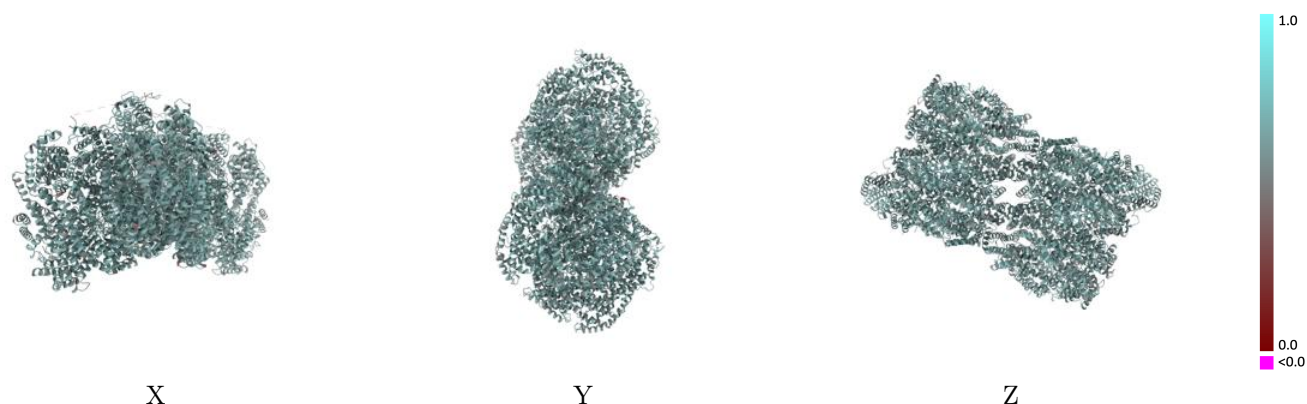
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.2 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](#)

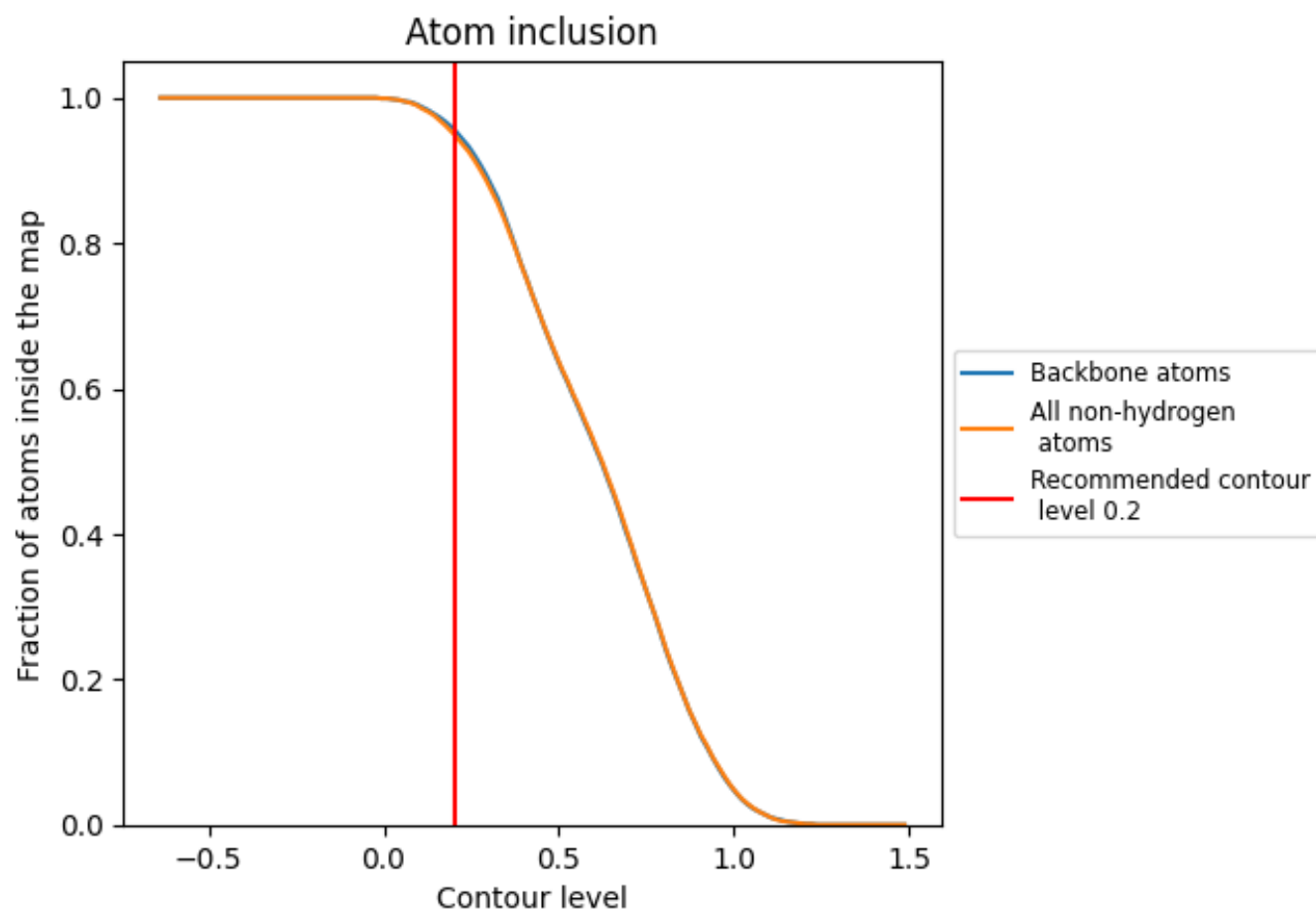


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.6220
A	 0.9310	 0.5950
B	 0.9590	 0.6180
C	 0.9400	 0.6170
D	 0.9660	 0.6340
E	 0.9490	 0.6190
F	 0.9550	 0.6060
G	 0.9410	 0.6070
H	 0.9690	 0.6330
I	 0.9600	 0.6370
J	 0.9560	 0.6350
K	 0.9570	 0.6340
L	 0.9350	 0.6090
M	 0.9530	 0.6320
N	 0.9470	 0.6070
O	 0.9430	 0.6110
P	 0.9550	 0.6110
Q	 0.9330	 0.5970
R	 0.9610	 0.6210
S	 0.9570	 0.6380
T	 0.9540	 0.6270
U	 0.9690	 0.6300
V	 0.9420	 0.6080
W	 0.9690	 0.6380
X	 0.9470	 0.6230
Y	 0.9630	 0.6400
a	 0.9340	 0.5950
b	 0.9560	 0.6170
c	 0.9390	 0.6170
d	 0.9670	 0.6340
e	 0.9480	 0.6220
f	 0.9590	 0.6060
g	 0.9410	 0.6090
h	 0.9690	 0.6350
i	 0.9580	 0.6380



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
j	 0.9590	 0.6360
k	 0.9570	 0.6340
l	 0.9370	 0.6090
m	 0.9550	 0.6340
n	 0.9520	 0.6090
o	 0.9420	 0.6110
p	 0.9570	 0.6120
q	 0.9310	 0.5960
r	 0.9600	 0.6210
s	 0.9640	 0.6420
t	 0.9540	 0.6270
u	 0.9680	 0.6290
v	 0.9410	 0.6040
w	 0.9690	 0.6360
x	 0.9460	 0.6220
y	 0.9640	 0.6400