



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 19, 2024 – 01:04 AM EDT

PDB ID : 4H0M  
Title : X-Ray Crystal Structure of Phycocyanin from *Synechococcus elongatus* sp.  
PCC 7942  
Authors : Marx, A.; Adir, N.  
Deposited on : 2012-09-09  
Resolution : 2.20 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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:

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

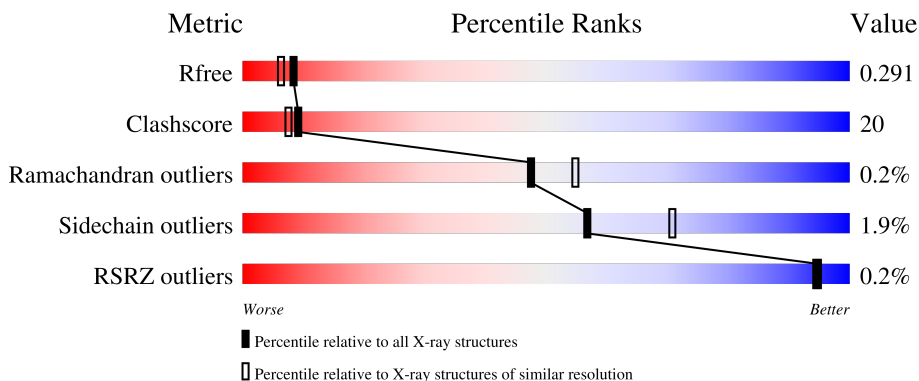
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	163	69% (green), 31% (yellow), . (grey)
1	C	163	70% (green), 28% (yellow), .. (grey)
1	E	163	78% (green), 20% (yellow), .. (grey)
1	G	163	72% (green), 26% (yellow), .. (grey)
1	I	163	78% (green), 21% (yellow), . (grey)

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Mol	Chain	Length	Quality of chain
1	K	163	79% 20% ..
1	M	163	69% 28% ..
1	O	163	79% 18% ..
1	Q	163	75% 23% ..
1	S	163	74% 25% ..
1	U	163	81% 18% .
1	W	163	74% 26% .
2	B	173	66% 31% ...
2	D	173	67% 31% ..
2	F	173	68% 30% ..
2	H	173	71% 27% ..
2	J	173	69% 28% ..
2	L	173	69% 29% ..
2	N	173	60% 38% ..
2	P	173	69% 27% ..
2	R	173	64% 32% ...
2	T	173	69% 27% ..
2	V	173	67% 29% ...
2	X	173	72% 26% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MEN	J	72	-	-	X	-
2	MEN	N	72	-	-	X	-
2	MEN	T	72	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 32152 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called C-phycoerythrin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	162	1213	766	204	242	1	0	0	0
1	C	162	1213	766	204	242	1	0	0	0
1	E	162	1213	766	204	242	1	0	0	0
1	G	162	1213	766	204	242	1	0	0	0
1	I	162	1213	766	204	242	1	0	0	0
1	K	162	1213	766	204	242	1	0	0	0
1	M	162	1213	766	204	242	1	0	0	0
1	O	162	1213	766	204	242	1	0	0	0
1	Q	162	1213	766	204	242	1	0	0	0
1	S	162	1213	766	204	242	1	0	0	0
1	U	162	1213	766	204	242	1	0	0	0
1	W	162	1213	766	204	242	1	0	0	0

- Molecule 2 is a protein called C-phycoerythrin beta chain.

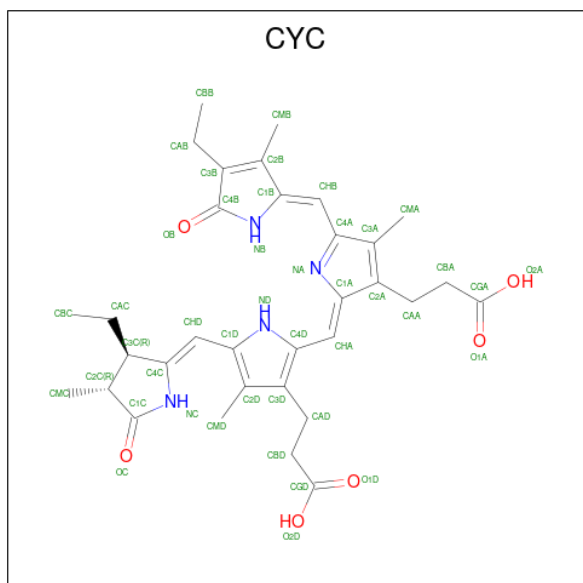
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	172	1273	789	228	250	6	0	0	0
2	D	172	1273	789	228	250	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	H	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	J	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	L	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	N	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	P	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	R	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	T	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	V	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0
2	X	172	Total 1273	C 789	N 228	O 250	S 6	0	0	0

- Molecule 3 is PHYCOCYANOBILIN (three-letter code: CYC) (formula:  $C_{33}H_{40}N_4O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	Total 43	C 33	N 4	O 6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	B	1	43	33	4	6	0	0
3	B	1	43	33	4	6	0	0
3	C	1	43	33	4	6	0	0
3	D	1	43	33	4	6	0	0
3	D	1	43	33	4	6	0	0
3	E	1	43	33	4	6	0	0
3	F	1	43	33	4	6	0	0
3	F	1	43	33	4	6	0	0
3	G	1	43	33	4	6	0	0
3	H	1	43	33	4	6	0	0
3	H	1	43	33	4	6	0	0
3	I	1	43	33	4	6	0	0
3	J	1	43	33	4	6	0	0
3	J	1	43	33	4	6	0	0
3	K	1	43	33	4	6	0	0
3	L	1	43	33	4	6	0	0
3	L	1	43	33	4	6	0	0
3	M	1	43	33	4	6	0	0
3	N	1	43	33	4	6	0	0
3	N	1	43	33	4	6	0	0
3	O	1	43	33	4	6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	P	1	Total	C	N	O	0	0
			43	33	4	6		
3	P	1	Total	C	N	O	0	0
			43	33	4	6		
3	Q	1	Total	C	N	O	0	0
			43	33	4	6		
3	R	1	Total	C	N	O	0	0
			43	33	4	6		
3	R	1	Total	C	N	O	0	0
			43	33	4	6		
3	S	1	Total	C	N	O	0	0
			43	33	4	6		
3	T	1	Total	C	N	O	0	0
			43	33	4	6		
3	T	1	Total	C	N	O	0	0
			43	33	4	6		
3	U	1	Total	C	N	O	0	0
			43	33	4	6		
3	V	1	Total	C	N	O	0	0
			43	33	4	6		
3	V	1	Total	C	N	O	0	0
			43	33	4	6		
3	W	1	Total	C	N	O	0	0
			43	33	4	6		
3	X	1	Total	C	N	O	0	0
			43	33	4	6		
3	X	1	Total	C	N	O	0	0
			43	33	4	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	41	Total	O	0	0
			41	41		
4	B	41	Total	O	0	0
			41	41		
4	C	31	Total	O	0	0
			31	31		
4	D	38	Total	O	0	0
			38	38		
4	E	46	Total	O	0	0
			46	46		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	19	Total O 19 19	0	0
4	G	30	Total O 30 30	0	0
4	H	17	Total O 17 17	0	0
4	I	34	Total O 34 34	0	0
4	J	25	Total O 25 25	0	0
4	K	33	Total O 33 33	0	0
4	L	20	Total O 20 20	0	0
4	M	37	Total O 37 37	0	0
4	N	23	Total O 23 23	0	0
4	O	35	Total O 35 35	0	0
4	P	27	Total O 27 27	0	0
4	Q	38	Total O 38 38	0	0
4	R	25	Total O 25 25	0	0
4	S	47	Total O 47 47	0	0
4	T	21	Total O 21 21	0	0
4	U	41	Total O 41 41	0	0
4	V	31	Total O 31 31	0	0
4	W	40	Total O 40 40	0	0
4	X	32	Total O 32 32	0	0

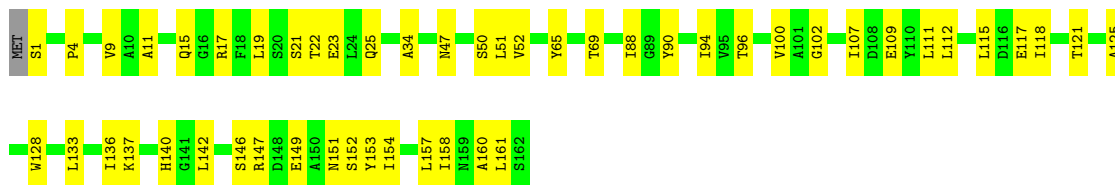


### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

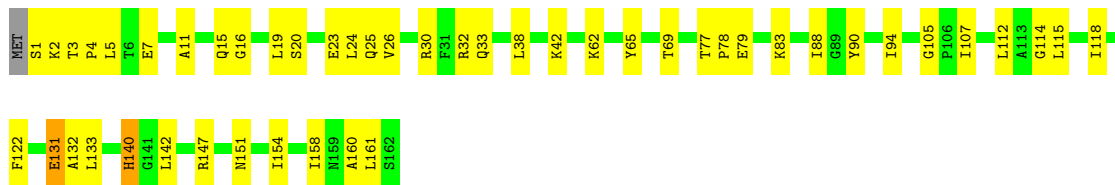
- Molecule 1: C-phycoerythrin alpha chain

Chain A: 




- Molecule 1: C-phycoerythrin alpha chain

Chain C: 



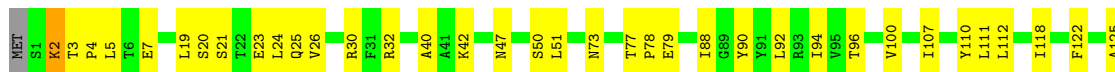
- Molecule 1: C-phycoerythrin alpha chain

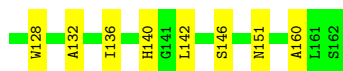
Chain E: 



- Molecule 1: C-phycoerythrin alpha chain

Chain G: 

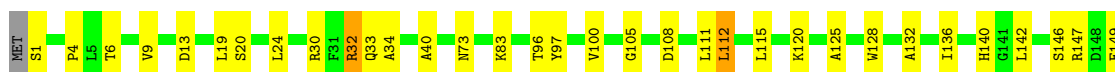
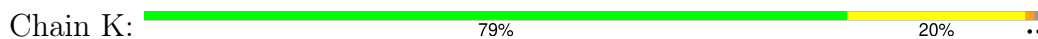




- Molecule 1: C-phyco cyanin alpha chain



- Molecule 1: C-phyco cyanin alpha chain



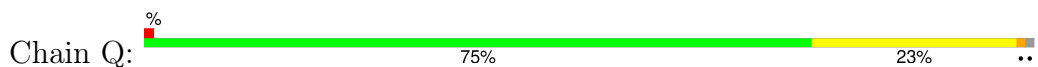
- Molecule 1: C-phyco cyanin alpha chain



- Molecule 1: C-phyco cyanin alpha chain



- Molecule 1: C-phyco cyanin alpha chain





- Molecule 1: C-phyco cyanin alpha chain

Chain S: 74% 25%



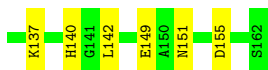
- Molecule 1: C-phyco cyanin alpha chain

Chain U: 81% 18%



- Molecule 1: C-phyco cyanin alpha chain

Chain W: 74% 26%



- Molecule 2: C-phyco cyanin beta chain

Chain B: 66% 31%



- Molecule 2: C-phyco cyanin beta chain

Chain D: 67% 31%





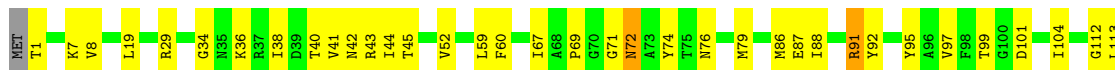
- Molecule 2: C-phycoyanin beta chain



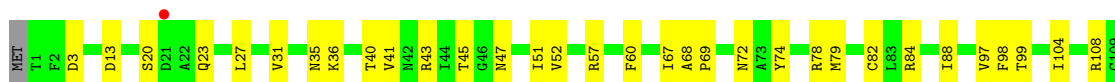
- Molecule 2: C-phycoyanin beta chain



- Molecule 2: C-phycoyanin beta chain

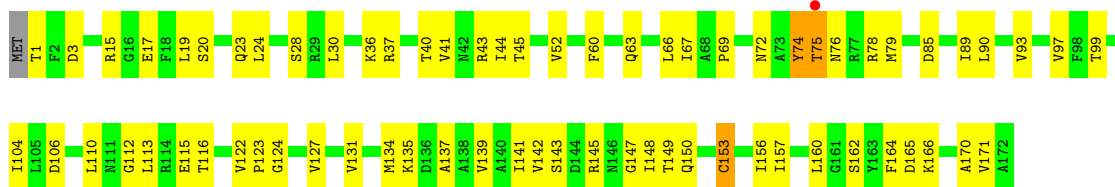


- Molecule 2: C-phycoyanin beta chain



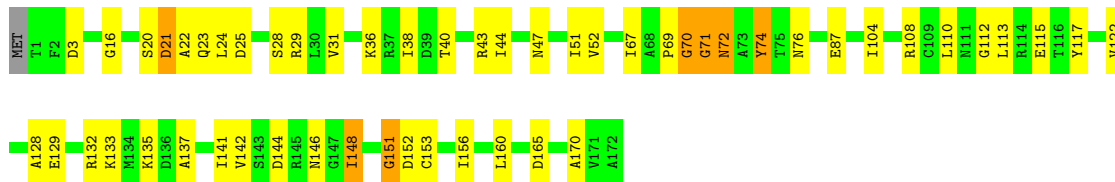
- Molecule 2: C-phycoyanin beta chain





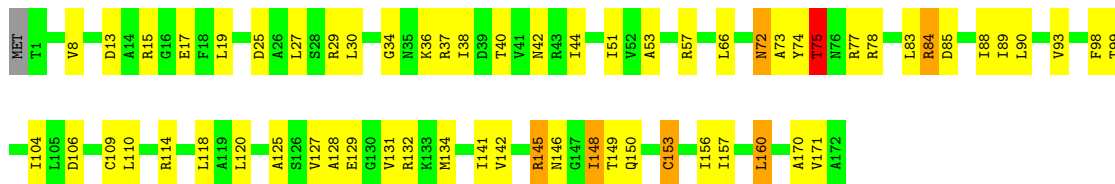
- Molecule 2: C-phycoyanin beta chain

Chain P: 69% 27%



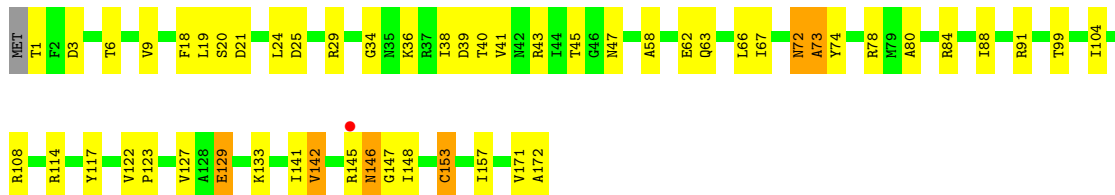
- Molecule 2: C-phycoyanin beta chain

Chain R: 64% 32%



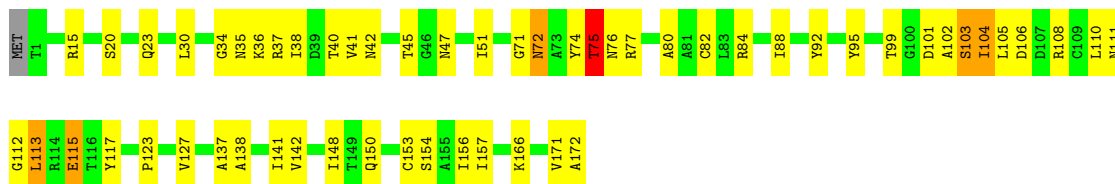
- Molecule 2: C-phycoyanin beta chain

Chain T: 69% 27%



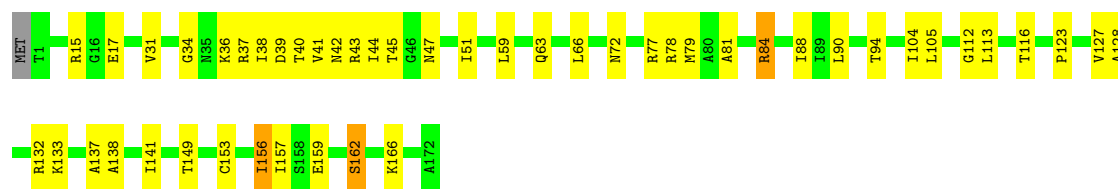
- Molecule 2: C-phycoyanin beta chain

Chain V: 67% 29%



- Molecule 2: C-phycoyanin beta chain

Chain X:  72% 26% ..



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.84Å 113.52Å 184.44Å 90.00° 89.97° 90.00°	Depositor
Resolution (Å)	40.00 – 2.20 36.89 – 2.20	Depositor EDS
% Data completeness (in resolution range)	87.4 (40.00-2.20) 87.3 (36.89-2.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.79 (at 2.20Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.242 , 0.295 0.238 , 0.291	Depositor DCC
$R_{free}$ test set	9751 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.6	Xtrriage
Anisotropy	0.133	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 1.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.447 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	32152	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.2934e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.67	1/1237 (0.1%)	0.61	0/1681
1	C	0.79	0/1237	0.70	1/1681 (0.1%)
1	E	0.78	3/1237 (0.2%)	0.59	0/1681
1	G	0.68	0/1237	0.62	0/1681
1	I	0.81	3/1237 (0.2%)	0.61	0/1681
1	K	0.66	0/1237	0.62	1/1681 (0.1%)
1	M	0.64	1/1237 (0.1%)	0.63	1/1681 (0.1%)
1	O	0.68	1/1237 (0.1%)	0.62	1/1681 (0.1%)
1	Q	0.66	0/1237	0.66	1/1681 (0.1%)
1	S	0.84	0/1237	0.64	1/1681 (0.1%)
1	U	0.61	0/1237	0.57	0/1681
1	W	0.67	2/1237 (0.2%)	0.63	1/1681 (0.1%)
2	B	0.88	4/1276 (0.3%)	0.76	2/1724 (0.1%)
2	D	0.75	4/1276 (0.3%)	0.67	2/1724 (0.1%)
2	F	0.78	1/1276 (0.1%)	0.66	1/1724 (0.1%)
2	H	0.78	3/1276 (0.2%)	0.65	1/1724 (0.1%)
2	J	0.94	3/1276 (0.2%)	0.67	0/1724
2	L	0.86	2/1276 (0.2%)	0.71	0/1724
2	N	0.88	2/1276 (0.2%)	0.66	0/1724
2	P	0.87	4/1276 (0.3%)	0.75	2/1724 (0.1%)
2	R	0.91	2/1276 (0.2%)	0.74	3/1724 (0.2%)
2	T	0.82	4/1276 (0.3%)	0.74	3/1724 (0.2%)
2	V	0.72	2/1276 (0.2%)	0.66	0/1724
2	X	0.80	0/1276	0.73	1/1724 (0.1%)
All	All	0.78	42/30156 (0.1%)	0.67	22/40860 (0.1%)

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	153	CYS	CB-SG	-17.54	1.52	1.82
2	N	153	CYS	CB-SG	-16.53	1.54	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	153	CYS	CB-SG	-13.73	1.58	1.82
2	H	153	CYS	CB-SG	-11.14	1.63	1.82
2	L	153	CYS	CB-SG	-7.89	1.68	1.82

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	140	HIS	CB-CA-C	-11.58	87.23	110.40
2	P	74	TYR	C-N-CA	-7.38	103.24	121.70
2	T	153	CYS	CA-CB-SG	6.94	126.50	114.00
1	K	111	LEU	CA-CB-CG	6.75	130.82	115.30
2	P	74	TYR	O-C-N	-6.42	112.42	122.70

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	1213	0	1182	39	0
1	C	1213	0	1183	48	0
1	E	1213	0	1183	31	0
1	G	1213	0	1183	41	0
1	I	1213	0	1183	33	0
1	K	1213	0	1183	35	0
1	M	1213	0	1183	46	0
1	O	1213	0	1183	36	0
1	Q	1213	0	1183	44	0
1	S	1213	0	1183	48	0
1	U	1213	0	1183	37	0
1	W	1213	0	1183	40	0
2	B	1273	0	1275	74	0
2	D	1273	0	1275	62	0
2	F	1273	0	1276	71	0
2	H	1273	0	1275	62	0
2	J	1273	0	1276	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	1273	0	1275	56	0
2	N	1273	0	1275	100	0
2	P	1273	0	1275	65	0
2	R	1273	0	1274	60	0
2	T	1273	0	1274	56	0
2	V	1273	0	1276	59	0
2	X	1273	0	1275	47	0
3	A	43	0	37	5	0
3	B	86	0	71	19	0
3	C	43	0	37	6	0
3	D	86	0	74	18	0
3	E	43	0	37	4	0
3	F	86	0	74	13	0
3	G	43	0	37	5	0
3	H	86	0	73	8	0
3	I	43	0	37	7	0
3	J	86	0	76	16	0
3	K	43	0	37	5	0
3	L	86	0	74	13	0
3	M	43	0	37	2	0
3	N	86	0	74	11	0
3	O	43	0	37	4	0
3	P	86	0	73	16	0
3	Q	43	0	37	3	0
3	R	86	0	74	9	0
3	S	43	0	37	4	0
3	T	86	0	71	17	0
3	U	43	0	37	4	0
3	V	86	0	75	18	0
3	W	43	0	37	5	0
3	X	86	0	72	10	0
4	A	41	0	0	2	0
4	B	41	0	0	2	0
4	C	31	0	0	1	0
4	D	38	0	0	3	0
4	E	46	0	0	3	0
4	F	19	0	0	1	0
4	G	30	0	0	3	0
4	H	17	0	0	3	0
4	I	34	0	0	3	0
4	J	25	0	0	2	0
4	K	33	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	20	0	0	0	0
4	M	37	0	0	0	0
4	N	23	0	0	3	0
4	O	35	0	0	5	0
4	P	27	0	0	1	0
4	Q	38	0	0	4	0
4	R	25	0	0	2	0
4	S	47	0	0	2	0
4	T	21	0	0	2	0
4	U	41	0	0	1	0
4	V	31	0	0	0	0
4	W	40	0	0	4	0
4	X	32	0	0	1	0
All	All	32152	0	30821	1235	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 20.

The worst 5 of 1235 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:153:CYS:SG	3:F:202:CYC:HAC2	1.28	1.66
2:D:153:CYS:SG	3:D:202:CYC:HAC2	1.12	1.62
2:J:153:CYS:SG	3:J:202:CYC:HAC2	1.38	1.59
2:V:153:CYS:SG	3:V:202:CYC:HAC2	1.60	1.40
2:N:72:MEN:CE2	2:N:123:PRO:HD2	1.52	1.39

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
1	C	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
1	E	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
1	G	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
1	I	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
1	K	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
1	M	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
1	O	160/163 (98%)	155 (97%)	5 (3%)	0	100	100
1	Q	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
1	S	160/163 (98%)	158 (99%)	2 (1%)	0	100	100
1	U	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
1	W	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
2	B	169/173 (98%)	166 (98%)	2 (1%)	1 (1%)	25	26
2	D	169/173 (98%)	161 (95%)	8 (5%)	0	100	100
2	F	169/173 (98%)	165 (98%)	2 (1%)	2 (1%)	13	10
2	H	169/173 (98%)	165 (98%)	4 (2%)	0	100	100
2	J	169/173 (98%)	166 (98%)	2 (1%)	1 (1%)	25	26
2	L	169/173 (98%)	166 (98%)	3 (2%)	0	100	100
2	N	169/173 (98%)	164 (97%)	5 (3%)	0	100	100
2	P	169/173 (98%)	160 (95%)	8 (5%)	1 (1%)	25	26
2	R	169/173 (98%)	165 (98%)	4 (2%)	0	100	100
2	T	169/173 (98%)	166 (98%)	2 (1%)	1 (1%)	25	26
2	V	169/173 (98%)	164 (97%)	2 (1%)	3 (2%)	8	5
2	X	169/173 (98%)	166 (98%)	3 (2%)	0	100	100
All	All	3948/4032 (98%)	3832 (97%)	107 (3%)	9 (0%)	47	55

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	74	TYR
2	V	103	SER
2	V	104	ILE
2	P	71	GLY
2	V	75	THR

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	122/123 (99%)	121 (99%)	1 (1%)	81	90
1	C	122/123 (99%)	120 (98%)	2 (2%)	62	76
1	E	122/123 (99%)	120 (98%)	2 (2%)	62	76
1	G	122/123 (99%)	120 (98%)	2 (2%)	62	76
1	I	122/123 (99%)	121 (99%)	1 (1%)	81	90
1	K	122/123 (99%)	120 (98%)	2 (2%)	62	76
1	M	122/123 (99%)	119 (98%)	3 (2%)	47	60
1	O	122/123 (99%)	119 (98%)	3 (2%)	47	60
1	Q	122/123 (99%)	119 (98%)	3 (2%)	47	60
1	S	122/123 (99%)	119 (98%)	3 (2%)	47	60
1	U	122/123 (99%)	121 (99%)	1 (1%)	81	90
1	W	122/123 (99%)	122 (100%)	0	100	100
2	B	127/128 (99%)	123 (97%)	4 (3%)	40	51
2	D	127/128 (99%)	125 (98%)	2 (2%)	62	76
2	F	127/128 (99%)	125 (98%)	2 (2%)	62	76
2	H	127/128 (99%)	125 (98%)	2 (2%)	62	76
2	J	127/128 (99%)	124 (98%)	3 (2%)	49	62
2	L	127/128 (99%)	127 (100%)	0	100	100
2	N	127/128 (99%)	125 (98%)	2 (2%)	62	76
2	P	127/128 (99%)	124 (98%)	3 (2%)	49	62
2	R	127/128 (99%)	119 (94%)	8 (6%)	18	20
2	T	127/128 (99%)	125 (98%)	2 (2%)	62	76
2	V	127/128 (99%)	123 (97%)	4 (3%)	40	51
2	X	127/128 (99%)	124 (98%)	3 (2%)	49	62
All	All	2988/3012 (99%)	2930 (98%)	58 (2%)	57	71

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	36	SER
2	X	84	ARG
1	Q	33	GLN
2	V	115	GLU
2	T	145	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	15	GLN
2	R	150	GLN
1	O	33	GLN
1	Q	15	GLN
2	T	63	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](#)

12 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	J	72	2	7,8,9	1.49	1 (14%)	4,9,11	1.87	2 (50%)
2	MEN	F	72	2	7,8,9	0.97	0	4,9,11	0.45	0
2	MEN	H	72	2	7,8,9	1.44	1 (14%)	4,9,11	0.60	0
2	MEN	L	72	2	7,8,9	0.52	0	4,9,11	0.53	0
2	MEN	P	72	2	7,8,9	1.80	3 (42%)	4,9,11	1.22	1 (25%)
2	MEN	T	72	2	7,8,9	1.22	0	4,9,11	1.46	1 (25%)
2	MEN	X	72	2	7,8,9	0.84	0	4,9,11	0.81	0
2	MEN	D	72	2	7,8,9	0.99	0	4,9,11	0.55	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	0.47	0	4,9,11	0.53	0
2	MEN	R	72	2	7,8,9	4.42	2 (28%)	4,9,11	2.77	3 (75%)
2	MEN	B	72	2	7,8,9	1.23	1 (14%)	4,9,11	0.50	0
2	MEN	V	72	2	7,8,9	3.42	4 (57%)	4,9,11	2.79	2 (50%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	J	72	2	-	0/7/8/10	-
2	MEN	F	72	2	-	4/7/8/10	-
2	MEN	H	72	2	-	4/7/8/10	-
2	MEN	L	72	2	-	6/7/8/10	-
2	MEN	P	72	2	-	4/7/8/10	-
2	MEN	T	72	2	-	4/7/8/10	-
2	MEN	X	72	2	-	2/7/8/10	-
2	MEN	D	72	2	-	4/7/8/10	-
2	MEN	N	72	2	-	4/7/8/10	-
2	MEN	R	72	2	-	4/7/8/10	-
2	MEN	B	72	2	-	2/7/8/10	-
2	MEN	V	72	2	-	3/7/8/10	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	72	MEN	CE2-ND2	-10.40	1.27	1.45
2	V	72	MEN	CB-CG	-5.52	1.39	1.51
2	V	72	MEN	CB-CA	-5.47	1.42	1.53
2	R	72	MEN	CG-ND2	-4.44	1.14	1.34
2	H	72	MEN	CB-CG	3.51	1.59	1.51

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	72	MEN	CB-CG-ND2	-4.76	109.32	115.53
2	R	72	MEN	OD1-CG-CB	-4.06	115.59	121.54
2	R	72	MEN	CB-CG-ND2	3.03	119.48	115.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	72	MEN	CE2-ND2-CG	-2.85	100.94	121.92
2	P	72	MEN	CE2-ND2-CG	2.44	139.90	121.92

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	72	MEN	CB-CG-ND2-CE2
2	B	72	MEN	OD1-CG-ND2-CE2
2	D	72	MEN	CB-CG-ND2-CE2
2	D	72	MEN	OD1-CG-ND2-CE2
2	F	72	MEN	O-C-CA-CB

There are no ring outliers.

10 monomers are involved in 55 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	72	MEN	11	0
2	L	72	MEN	1	0
2	P	72	MEN	1	0
2	T	72	MEN	14	0
2	X	72	MEN	1	0
2	D	72	MEN	2	0
2	N	72	MEN	22	0
2	R	72	MEN	1	0
2	B	72	MEN	1	0
2	V	72	MEN	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

36 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the



expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	CYC	P	202	2	42,46,46	2.87	13 (30%)	52,67,67	3.70	24 (46%)
3	CYC	N	201	2	42,46,46	2.28	14 (33%)	52,67,67	3.48	24 (46%)
3	CYC	D	201	2	42,46,46	2.23	11 (26%)	52,67,67	3.57	21 (40%)
3	CYC	R	201	2	42,46,46	2.25	11 (26%)	52,67,67	3.44	22 (42%)
3	CYC	V	202	2	42,46,46	2.82	14 (33%)	52,67,67	3.87	22 (42%)
3	CYC	L	202	2	42,46,46	2.55	15 (35%)	52,67,67	3.86	26 (50%)
3	CYC	E	201	1	42,46,46	2.16	13 (30%)	52,67,67	3.40	21 (40%)
3	CYC	N	202	2	42,46,46	3.19	17 (40%)	52,67,67	3.58	27 (51%)
3	CYC	J	202	2	42,46,46	2.66	15 (35%)	52,67,67	4.04	24 (46%)
3	CYC	Q	201	1	42,46,46	2.24	15 (35%)	52,67,67	3.43	23 (44%)
3	CYC	X	202	2	42,46,46	3.25	17 (40%)	52,67,67	4.36	28 (53%)
3	CYC	H	202	2	42,46,46	2.22	12 (28%)	52,67,67	3.87	24 (46%)
3	CYC	F	202	2	42,46,46	2.61	15 (35%)	52,67,67	3.95	25 (48%)
3	CYC	F	201	2	42,46,46	2.20	12 (28%)	52,67,67	3.41	19 (36%)
3	CYC	C	201	1	42,46,46	2.20	12 (28%)	52,67,67	3.42	22 (42%)
3	CYC	G	201	1	42,46,46	2.22	15 (35%)	52,67,67	3.46	23 (44%)
3	CYC	T	202	2	42,46,46	3.76	15 (35%)	52,67,67	4.15	25 (48%)
3	CYC	B	201	2	42,46,46	2.36	13 (30%)	52,67,67	3.50	21 (40%)
3	CYC	K	201	1	42,46,46	2.18	13 (30%)	52,67,67	3.42	21 (40%)
3	CYC	A	201	1	42,46,46	2.12	14 (33%)	52,67,67	3.53	24 (46%)
3	CYC	P	201	2	42,46,46	2.19	11 (26%)	52,67,67	3.56	23 (44%)
3	CYC	I	201	1	42,46,46	2.27	15 (35%)	52,67,67	3.46	22 (42%)
3	CYC	L	201	-	42,46,46	2.38	15 (35%)	52,67,67	3.46	23 (44%)
3	CYC	H	201	2	42,46,46	2.27	15 (35%)	52,67,67	3.55	23 (44%)
3	CYC	X	201	2	42,46,46	2.29	12 (28%)	52,67,67	3.52	22 (42%)
3	CYC	B	202	2	42,46,46	3.27	15 (35%)	52,67,67	4.10	26 (50%)
3	CYC	D	202	2	42,46,46	4.07	14 (33%)	52,67,67	4.46	26 (50%)
3	CYC	R	202	2	42,46,46	2.19	13 (30%)	52,67,67	3.58	24 (46%)
3	CYC	M	201	1	42,46,46	2.27	13 (30%)	52,67,67	3.47	24 (46%)
3	CYC	O	201	1	42,46,46	2.20	14 (33%)	52,67,67	3.34	21 (40%)
3	CYC	J	201	2	42,46,46	2.25	13 (30%)	52,67,67	3.55	22 (42%)
3	CYC	T	201	2	42,46,46	2.17	11 (26%)	52,67,67	3.43	21 (40%)
3	CYC	S	201	1	42,46,46	2.16	12 (28%)	52,67,67	3.43	22 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	CYC	W	201	1	42,46,46	2.21	14 (33%)	52,67,67	3.48	21 (40%)
3	CYC	V	201	-	42,46,46	2.28	11 (26%)	52,67,67	3.48	22 (42%)
3	CYC	U	201	1	42,46,46	2.15	14 (33%)	52,67,67	3.47	20 (38%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CYC	P	202	2	-	6/25/74/74	0/4/4/4
3	CYC	N	201	2	-	10/25/74/74	0/4/4/4
3	CYC	D	201	2	-	8/25/74/74	0/4/4/4
3	CYC	R	201	2	-	8/25/74/74	0/4/4/4
3	CYC	V	202	2	-	6/25/74/74	0/4/4/4
3	CYC	L	202	2	-	7/25/74/74	0/4/4/4
3	CYC	E	201	1	-	11/25/74/74	0/4/4/4
3	CYC	N	202	2	-	9/25/74/74	0/4/4/4
3	CYC	J	202	2	-	7/25/74/74	0/4/4/4
3	CYC	Q	201	1	-	9/25/74/74	0/4/4/4
3	CYC	X	202	2	-	7/25/74/74	0/4/4/4
3	CYC	H	202	2	-	6/25/74/74	0/4/4/4
3	CYC	F	202	2	-	7/25/74/74	0/4/4/4
3	CYC	F	201	2	-	10/25/74/74	0/4/4/4
3	CYC	C	201	1	-	10/25/74/74	0/4/4/4
3	CYC	G	201	1	-	11/25/74/74	0/4/4/4
3	CYC	T	202	2	-	9/25/74/74	0/4/4/4
3	CYC	B	201	2	-	6/25/74/74	0/4/4/4
3	CYC	K	201	1	-	12/25/74/74	0/4/4/4
3	CYC	A	201	1	-	10/25/74/74	0/4/4/4
3	CYC	P	201	2	-	6/25/74/74	0/4/4/4
3	CYC	I	201	1	-	10/25/74/74	0/4/4/4
3	CYC	L	201	-	-	9/25/74/74	0/4/4/4
3	CYC	H	201	2	-	9/25/74/74	0/4/4/4
3	CYC	X	201	2	-	8/25/74/74	0/4/4/4
3	CYC	B	202	2	-	8/25/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CYC	D	202	2	-	9/25/74/74	0/4/4/4
3	CYC	R	202	2	-	6/25/74/74	0/4/4/4
3	CYC	M	201	1	-	7/25/74/74	0/4/4/4
3	CYC	O	201	1	-	12/25/74/74	0/4/4/4
3	CYC	J	201	2	-	8/25/74/74	0/4/4/4
3	CYC	T	201	2	-	7/25/74/74	0/4/4/4
3	CYC	S	201	1	-	10/25/74/74	0/4/4/4
3	CYC	W	201	1	-	13/25/74/74	0/4/4/4
3	CYC	V	201	-	-	7/25/74/74	0/4/4/4
3	CYC	U	201	1	-	9/25/74/74	0/4/4/4

The worst 5 of 488 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	202	CYC	CBD-CGD	-20.80	1.02	1.50
3	T	202	CYC	CBD-CGD	-18.88	1.06	1.50
3	B	202	CYC	CBD-CGD	-14.28	1.17	1.50
3	X	202	CYC	CBD-CGD	-14.04	1.18	1.50
3	P	202	CYC	CBD-CGD	-12.54	1.21	1.50

The worst 5 of 828 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	202	CYC	CAD-CBD-CGD	15.53	155.68	113.83
3	D	202	CYC	C3B-C4B-NB	13.57	117.59	106.77
3	L	201	CYC	C3B-C4B-NB	13.37	117.43	106.77
3	P	202	CYC	C3B-C4B-NB	13.28	117.36	106.77
3	W	201	CYC	C3B-C4B-NB	13.25	117.34	106.77

There are no chirality outliers.

5 of 307 torsion outliers are listed below:

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

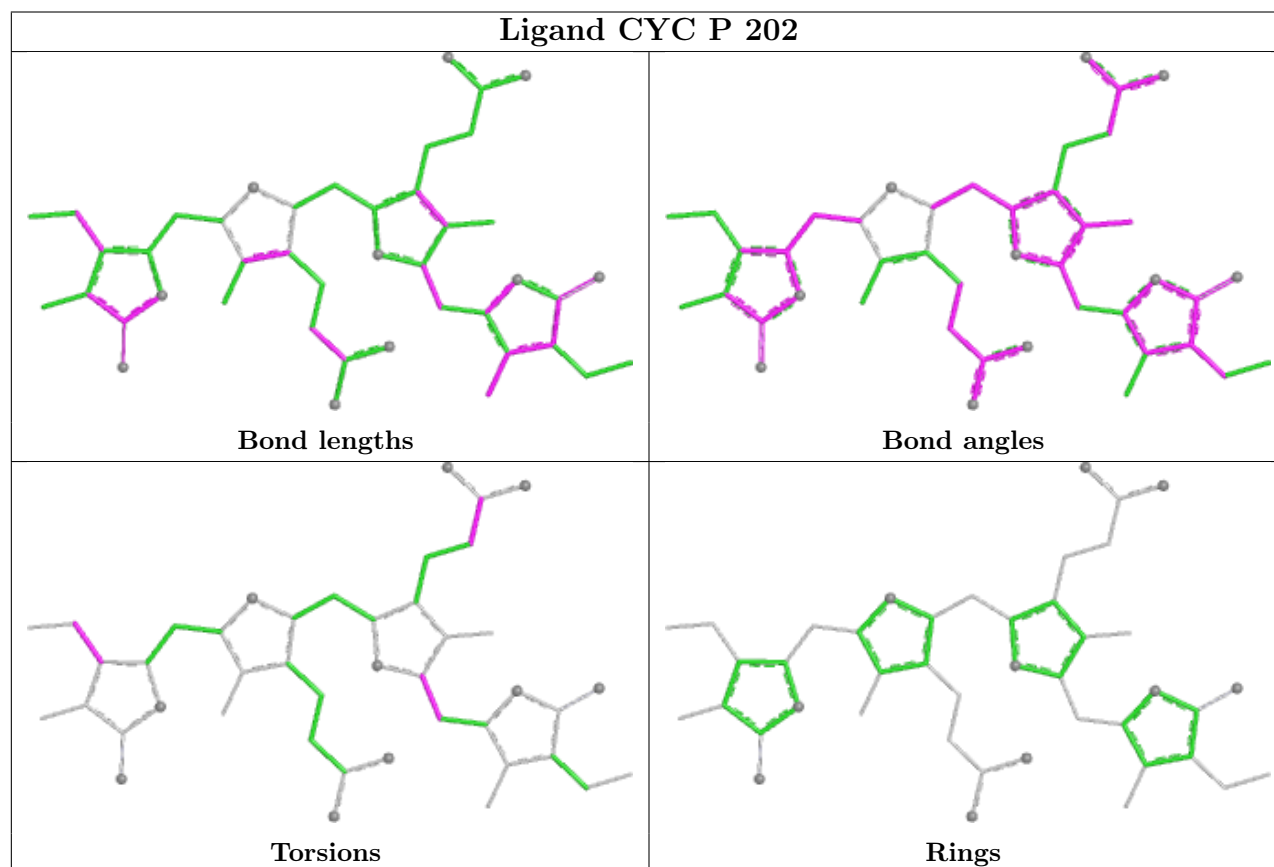
There are no ring outliers.

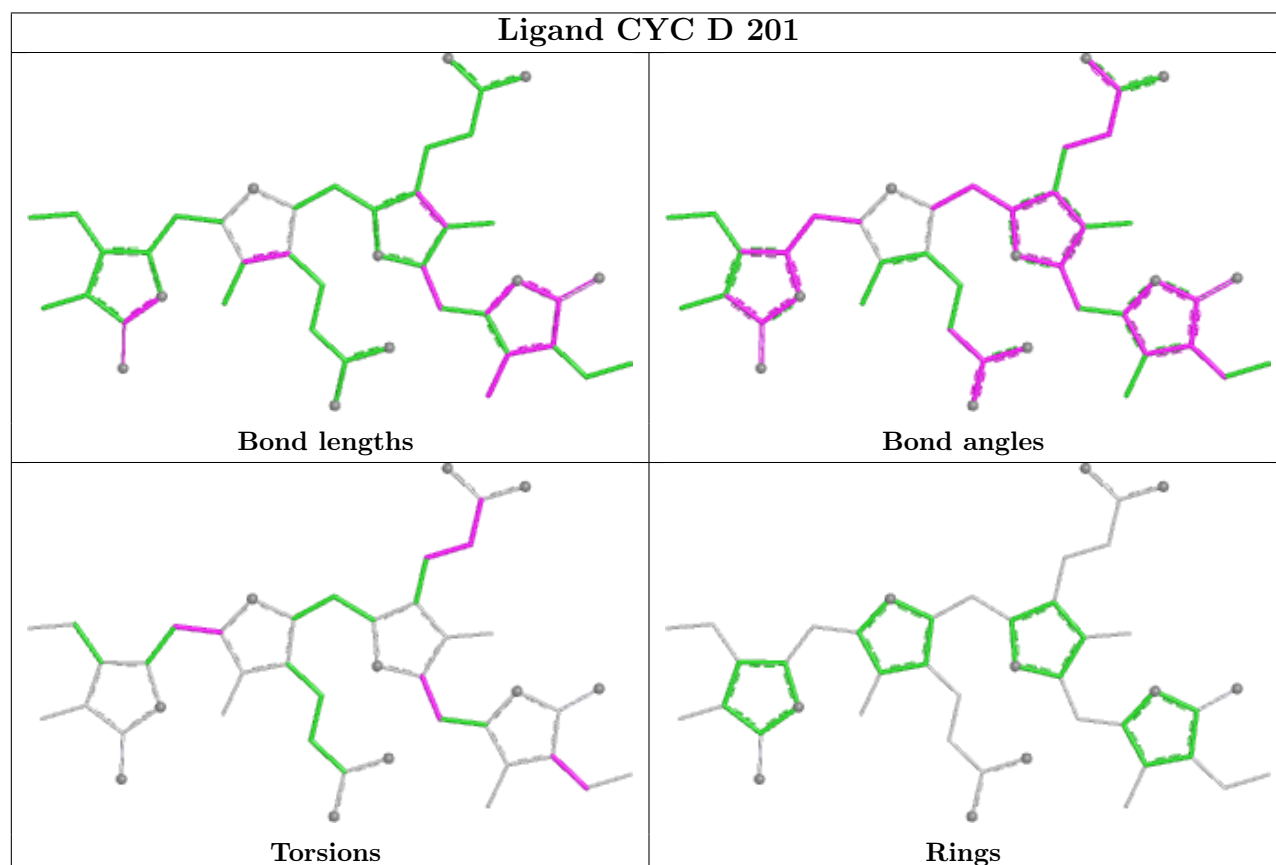
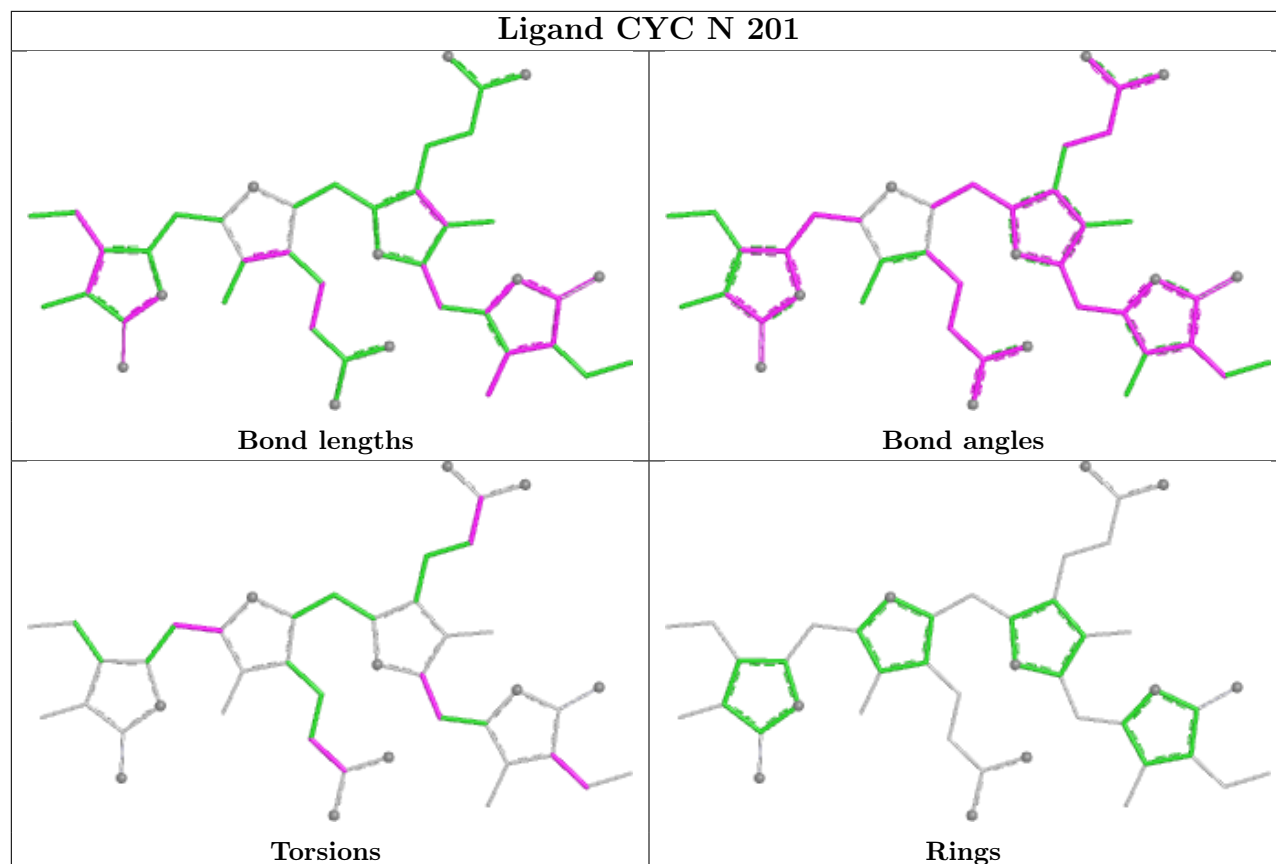
36 monomers are involved in 222 short contacts:

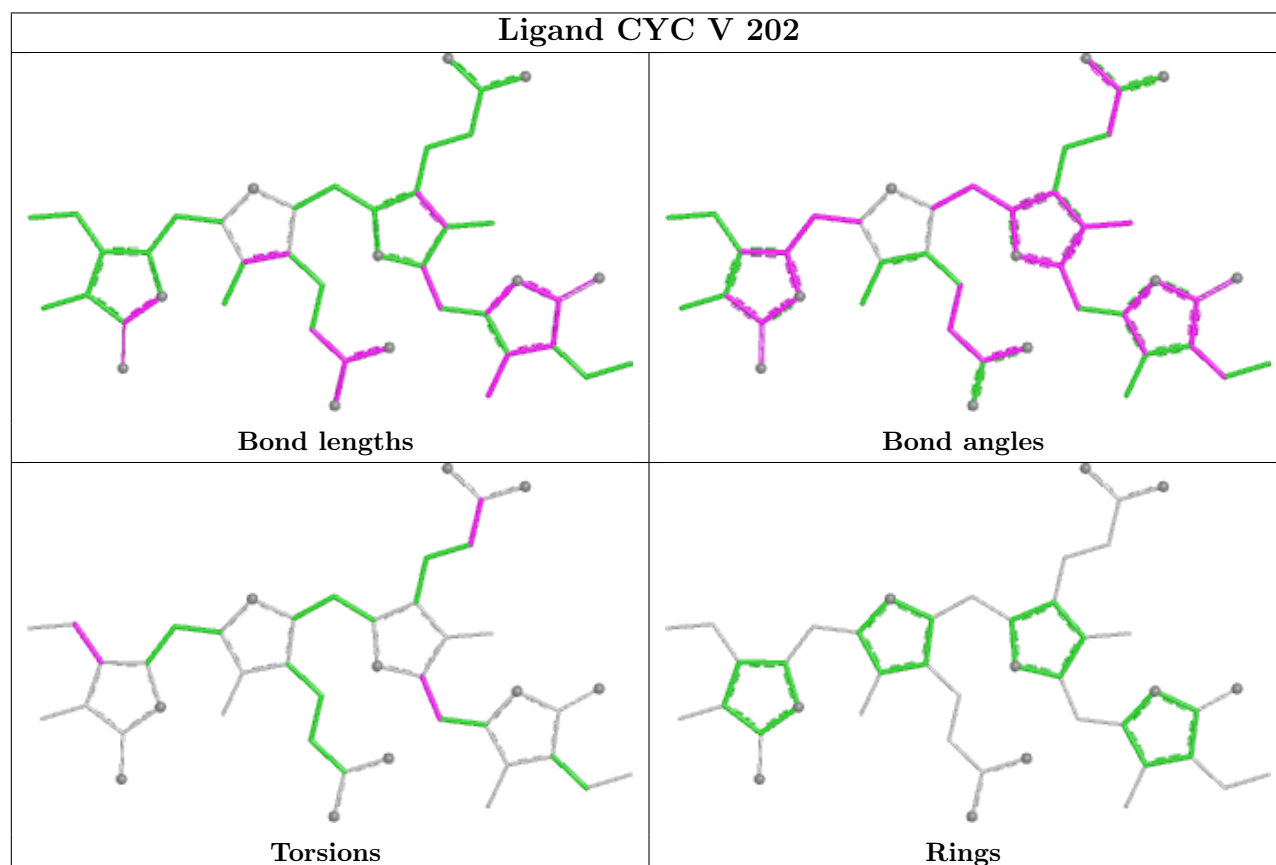
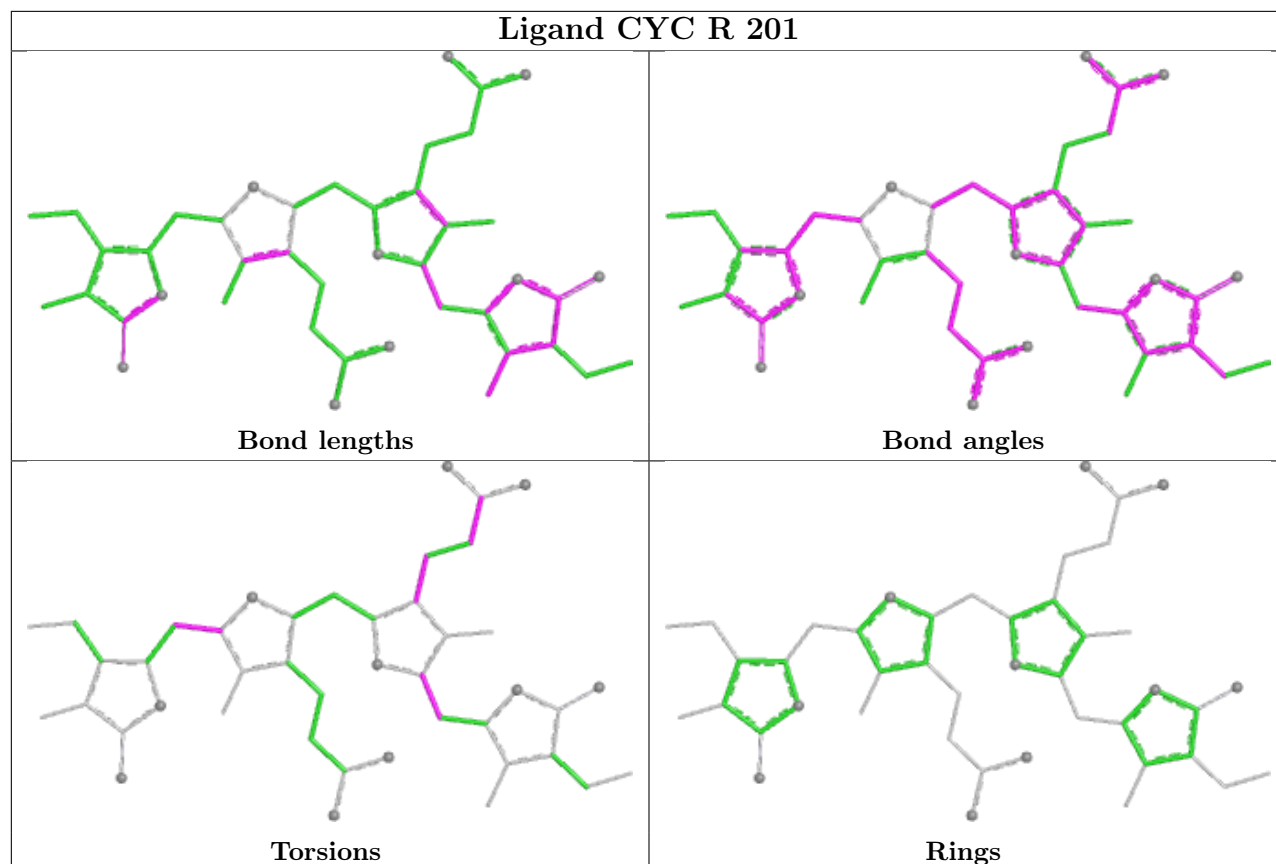
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	202	CYC	14	0
3	N	201	CYC	6	0
3	D	201	CYC	3	0
3	R	201	CYC	3	0
3	V	202	CYC	11	0
3	L	202	CYC	7	0
3	E	201	CYC	4	0
3	N	202	CYC	5	0
3	J	202	CYC	8	0
3	Q	201	CYC	3	0
3	X	202	CYC	7	0
3	H	202	CYC	4	0
3	F	202	CYC	11	0
3	F	201	CYC	2	0
3	C	201	CYC	6	0
3	G	201	CYC	5	0
3	T	202	CYC	4	0
3	B	201	CYC	6	0
3	K	201	CYC	5	0
3	A	201	CYC	5	0
3	P	201	CYC	2	0
3	I	201	CYC	7	0
3	L	201	CYC	6	0
3	H	201	CYC	4	0
3	X	201	CYC	3	0
3	B	202	CYC	13	0
3	D	202	CYC	15	0
3	R	202	CYC	6	0
3	M	201	CYC	2	0
3	O	201	CYC	4	0
3	J	201	CYC	8	0
3	T	201	CYC	13	0
3	S	201	CYC	4	0
3	W	201	CYC	5	0
3	V	201	CYC	7	0
3	U	201	CYC	4	0

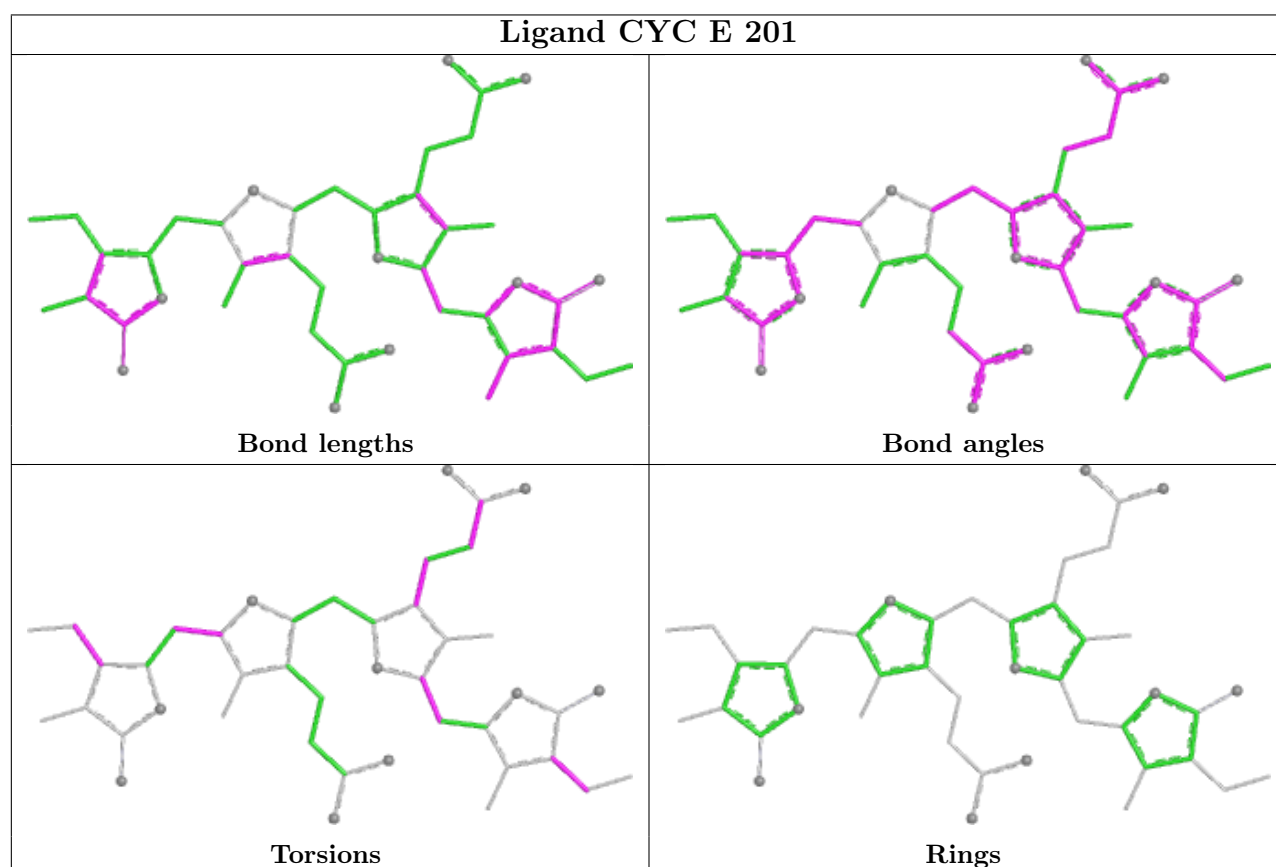
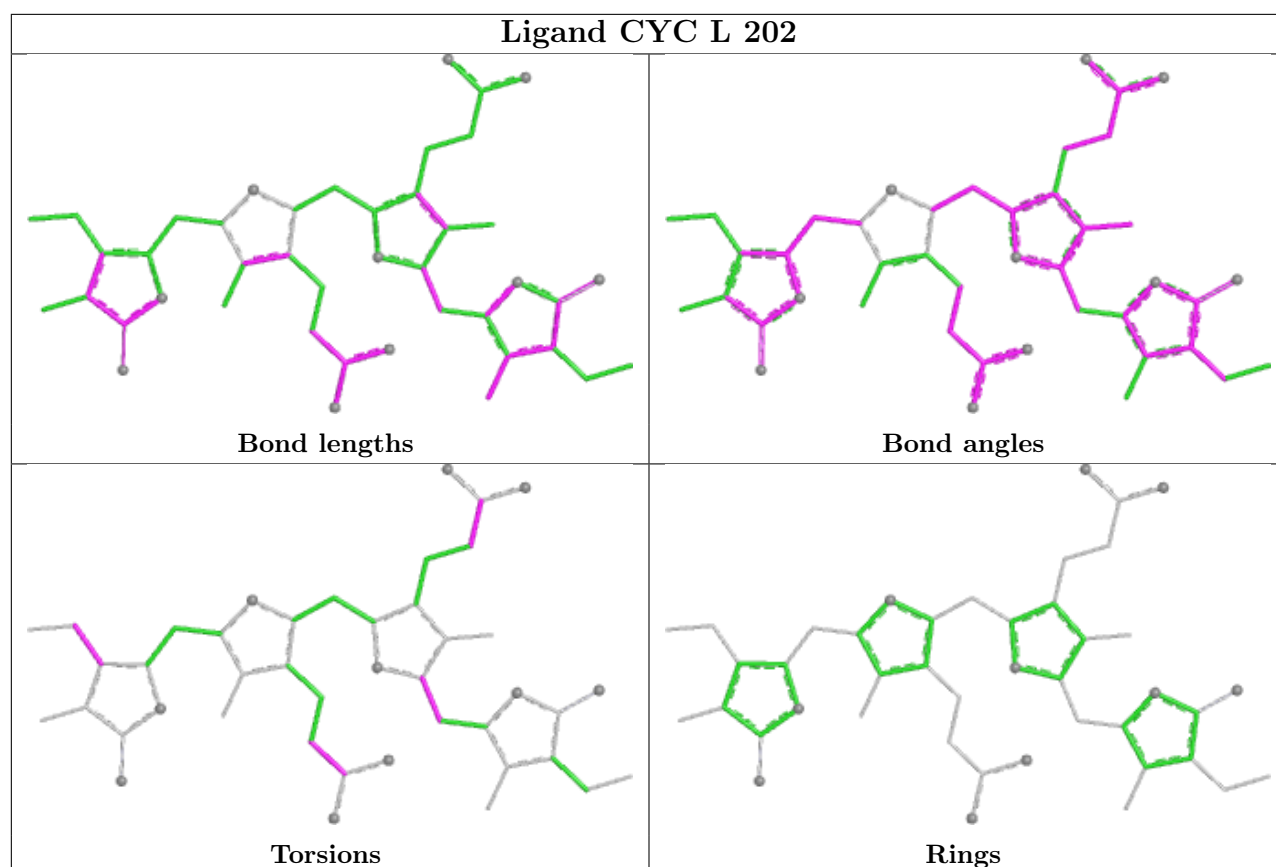
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

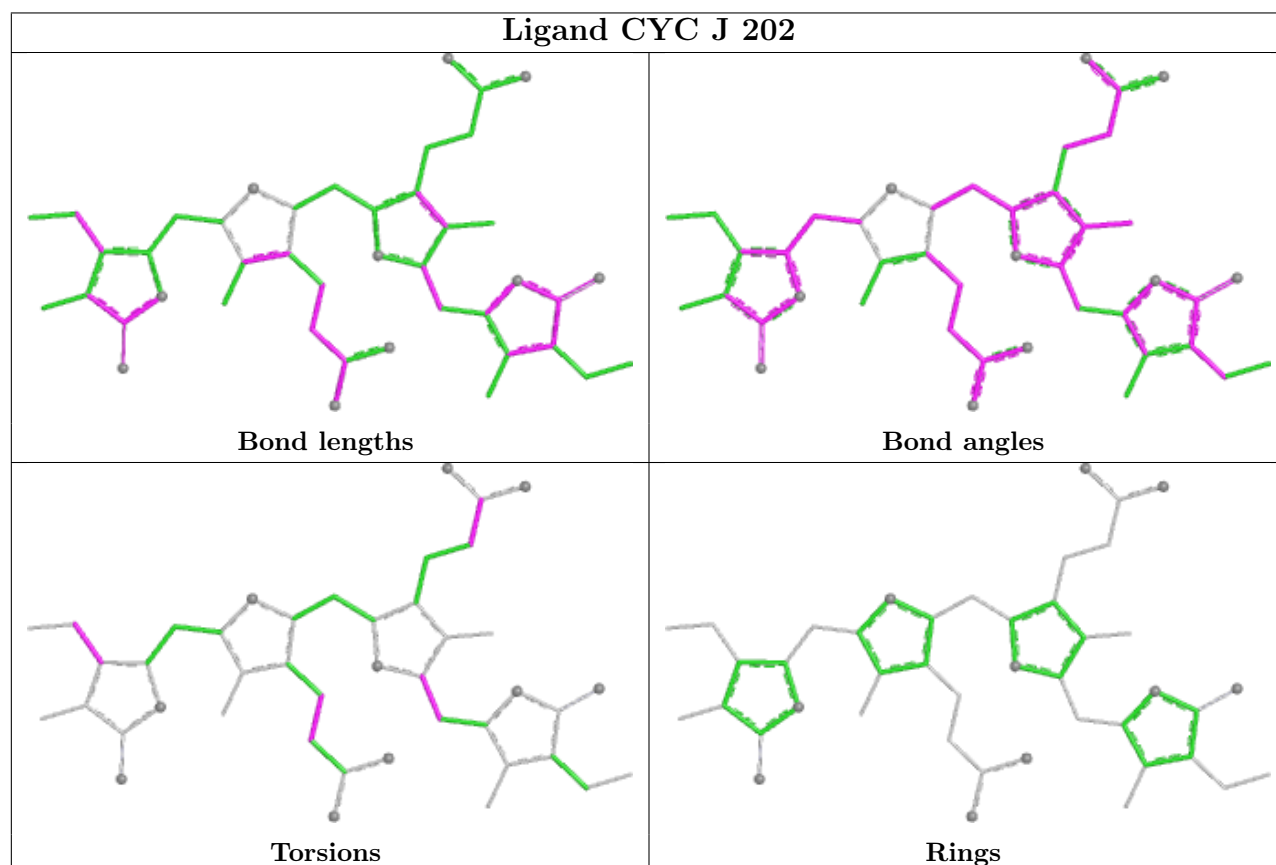
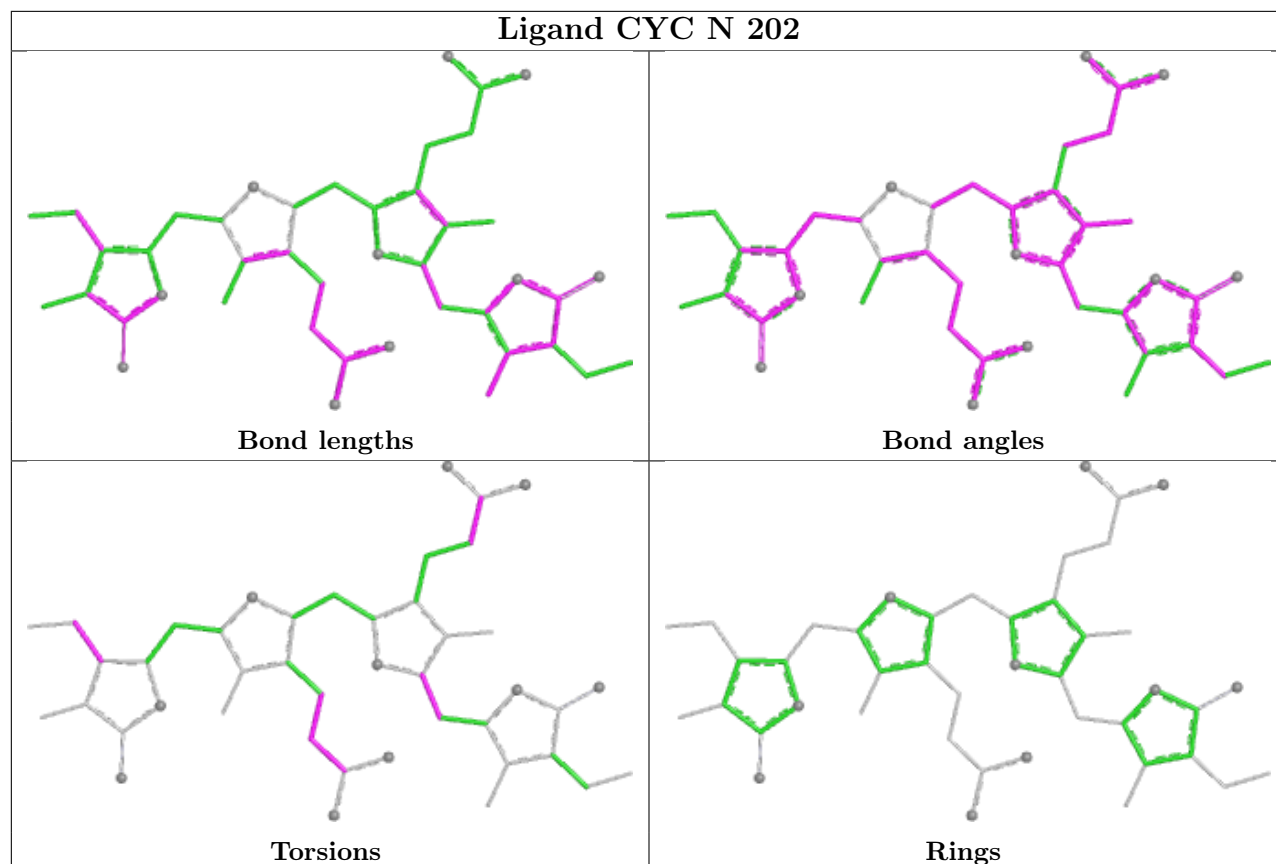


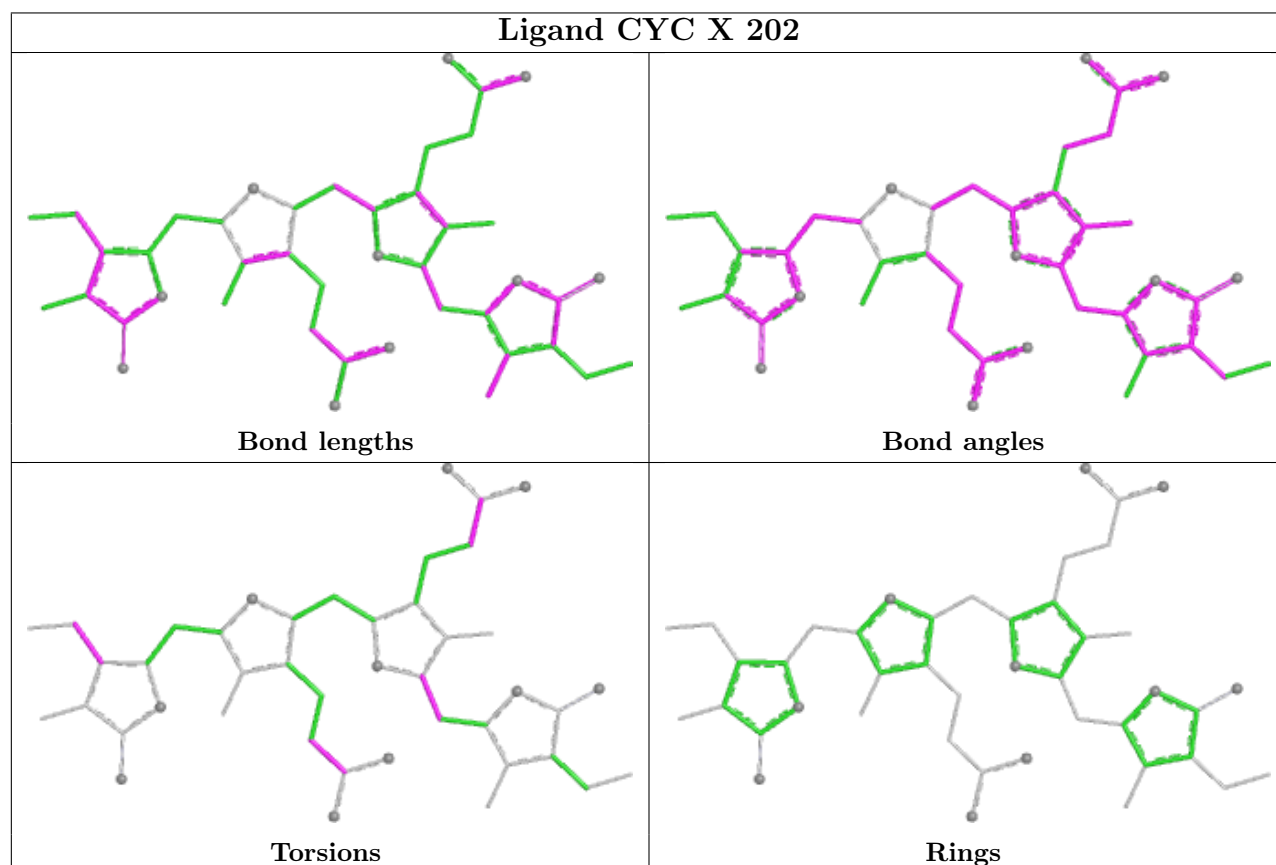
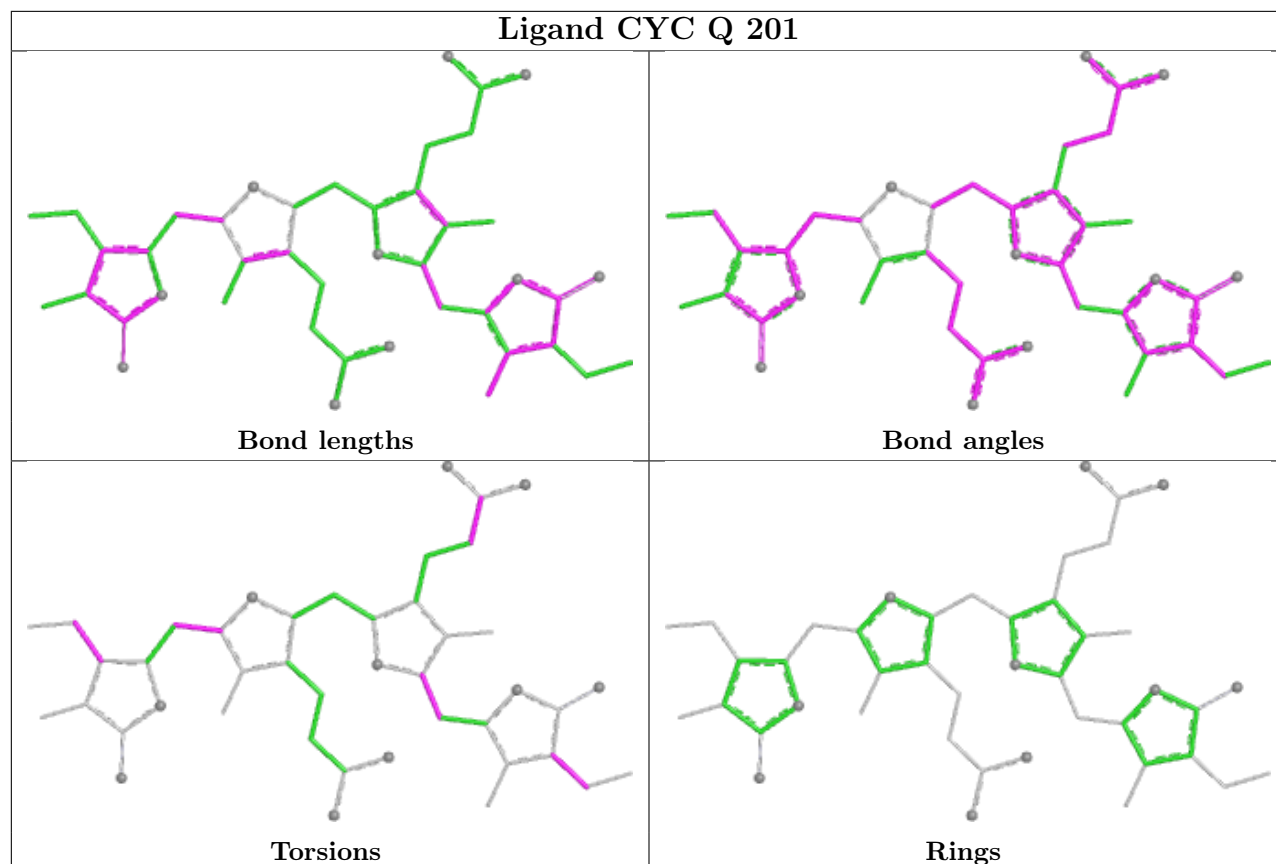


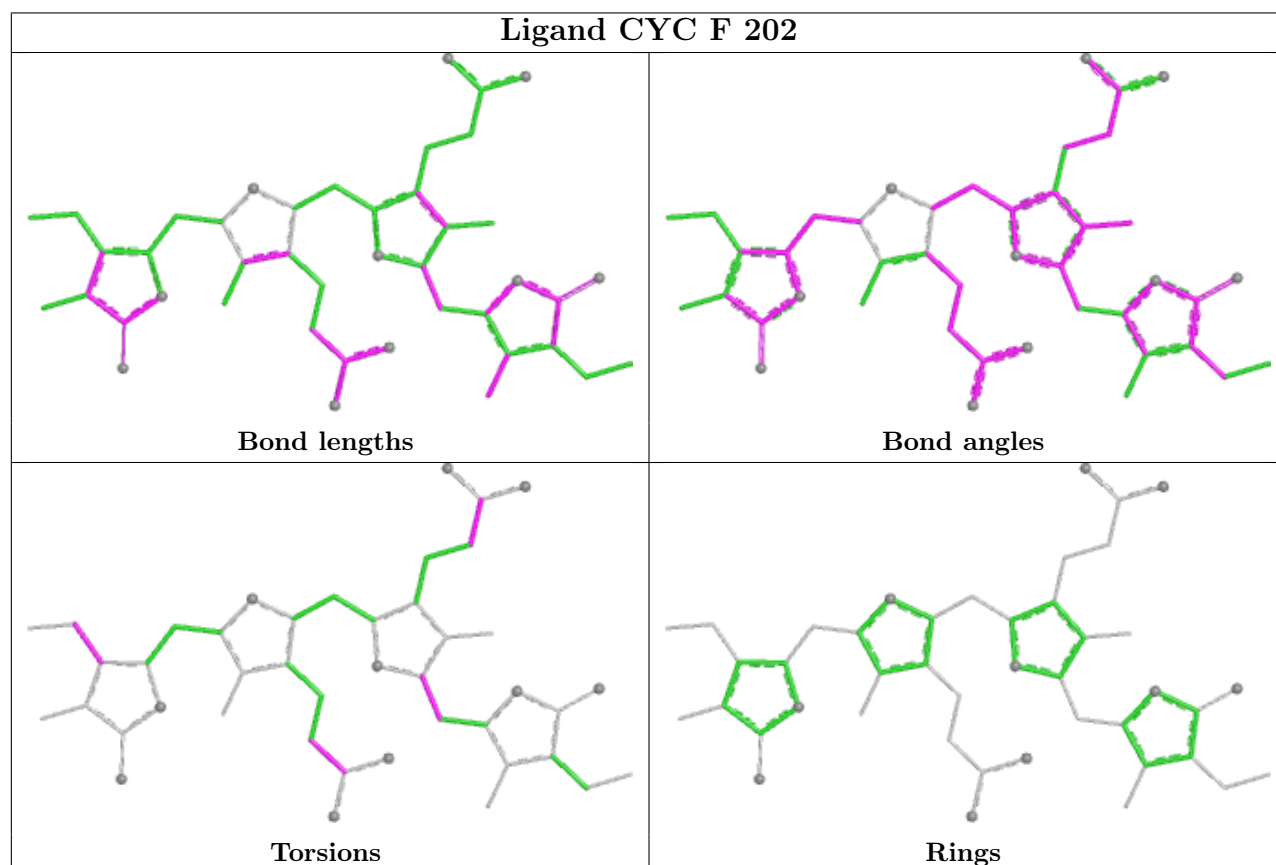
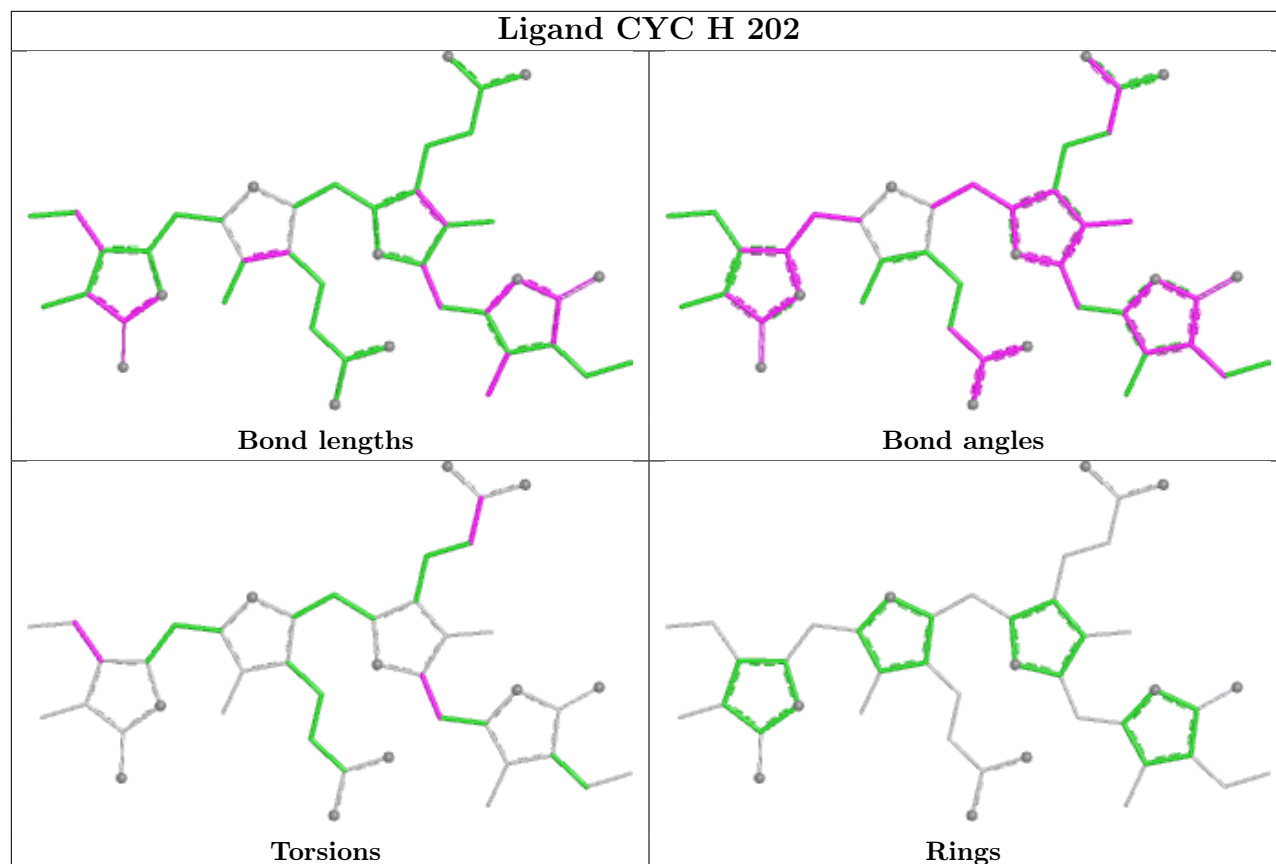


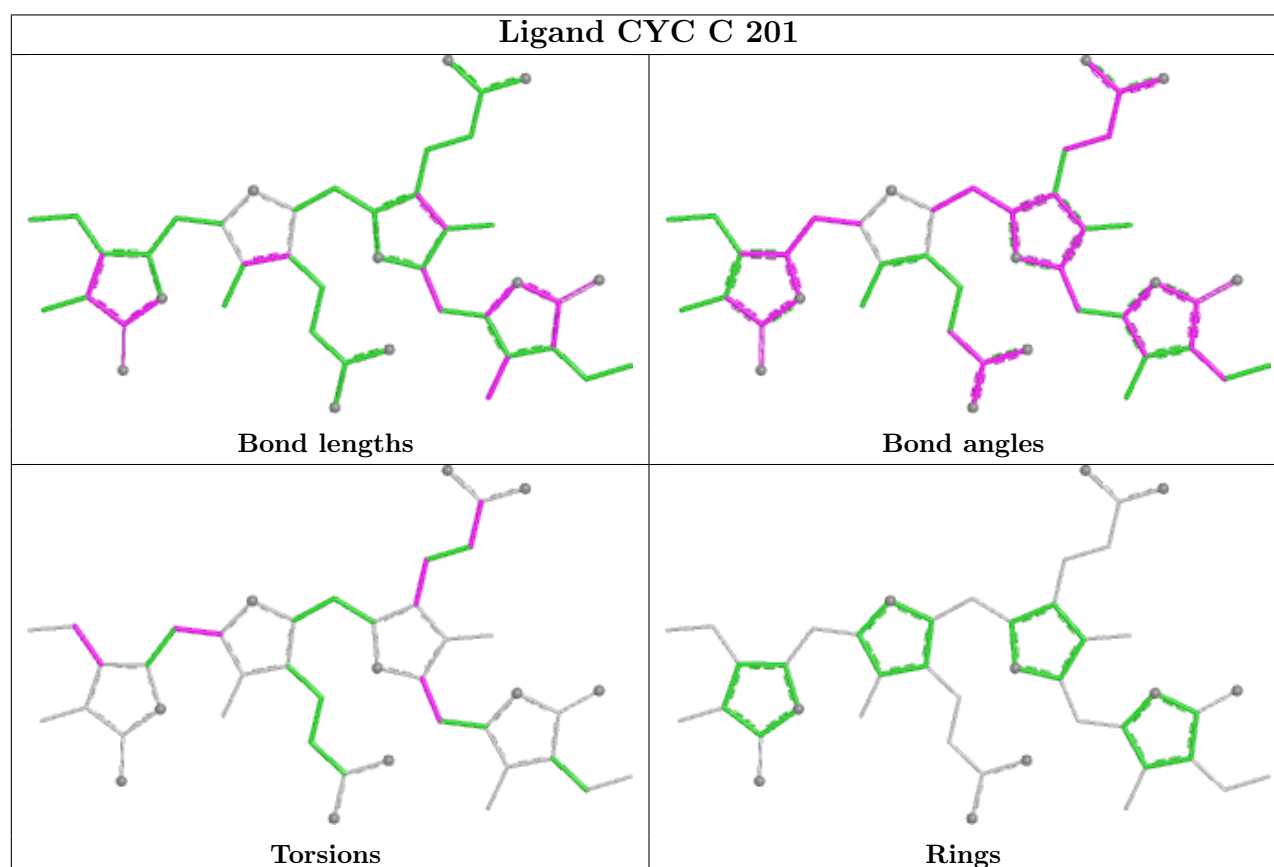
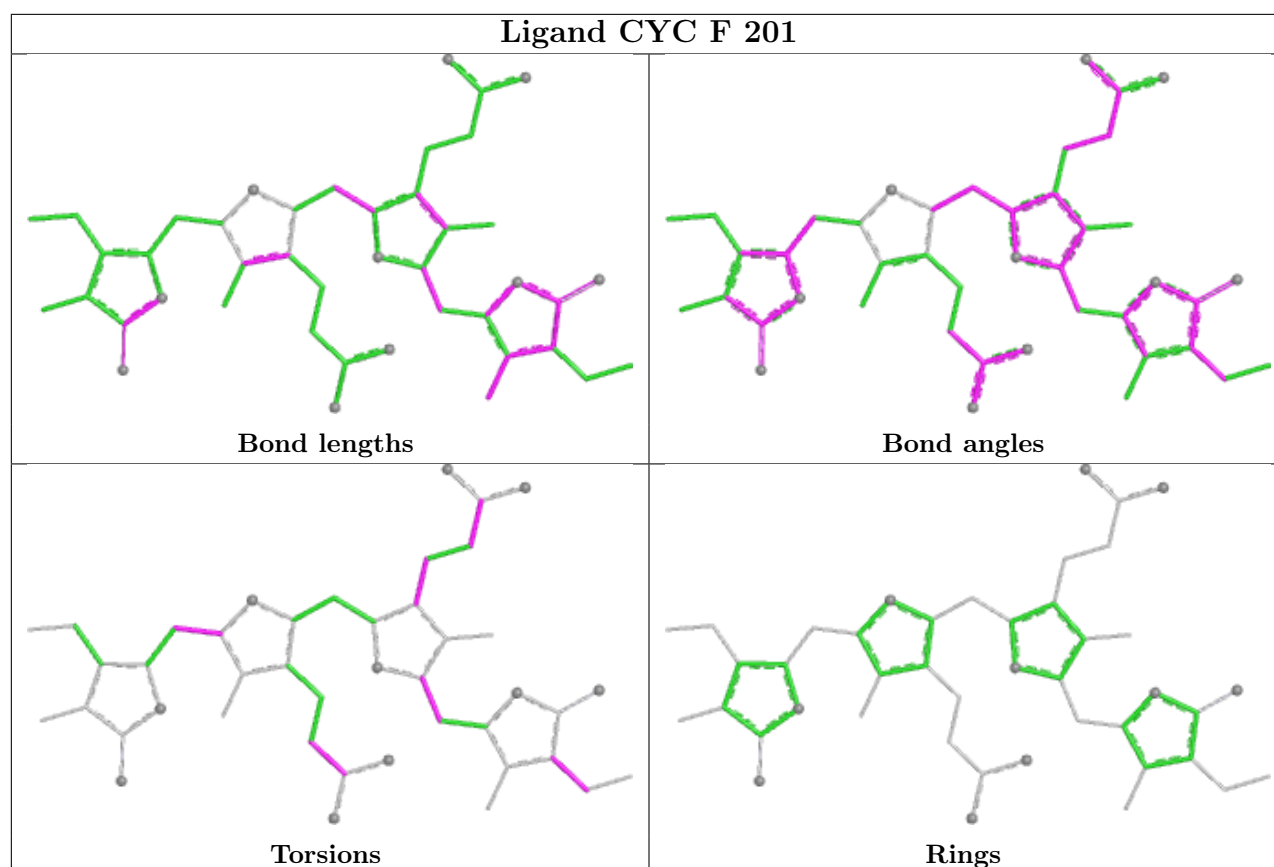


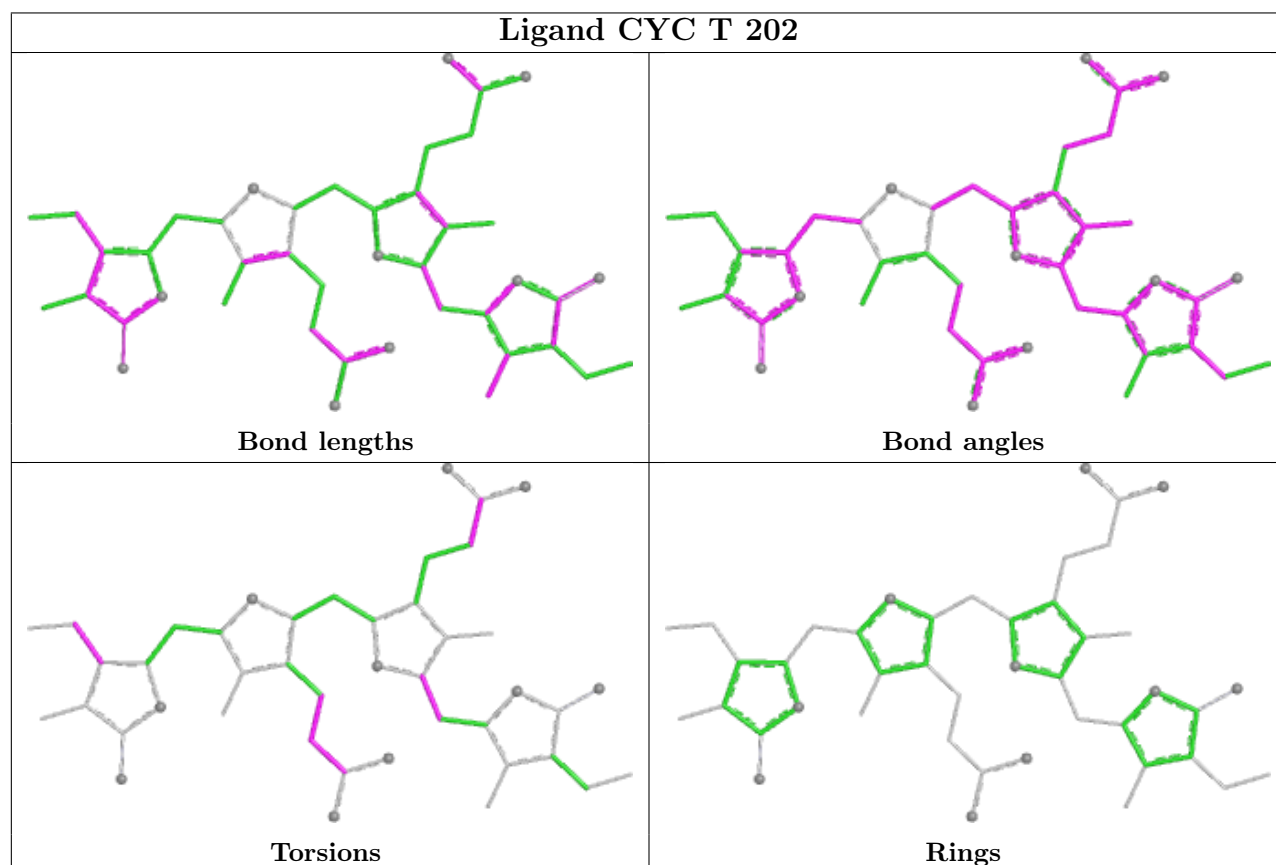
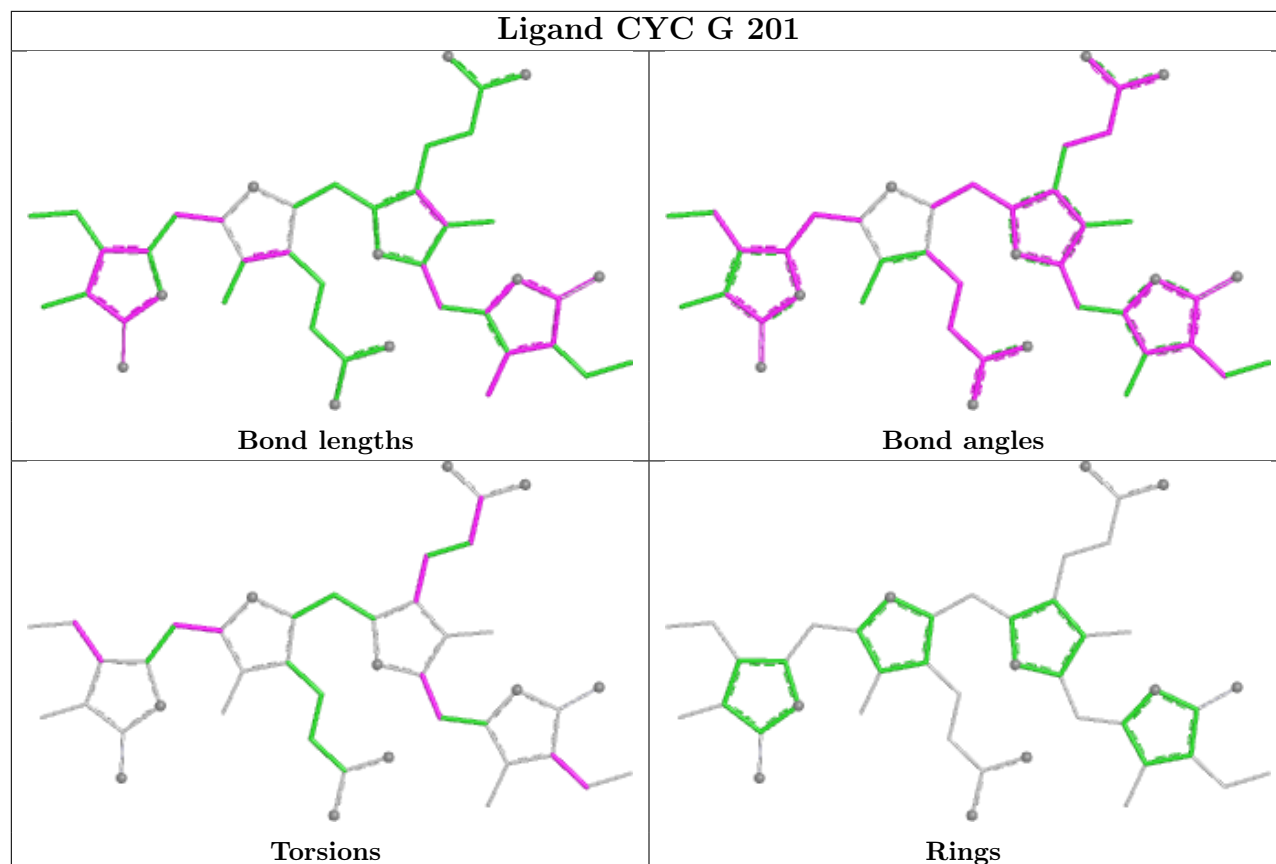


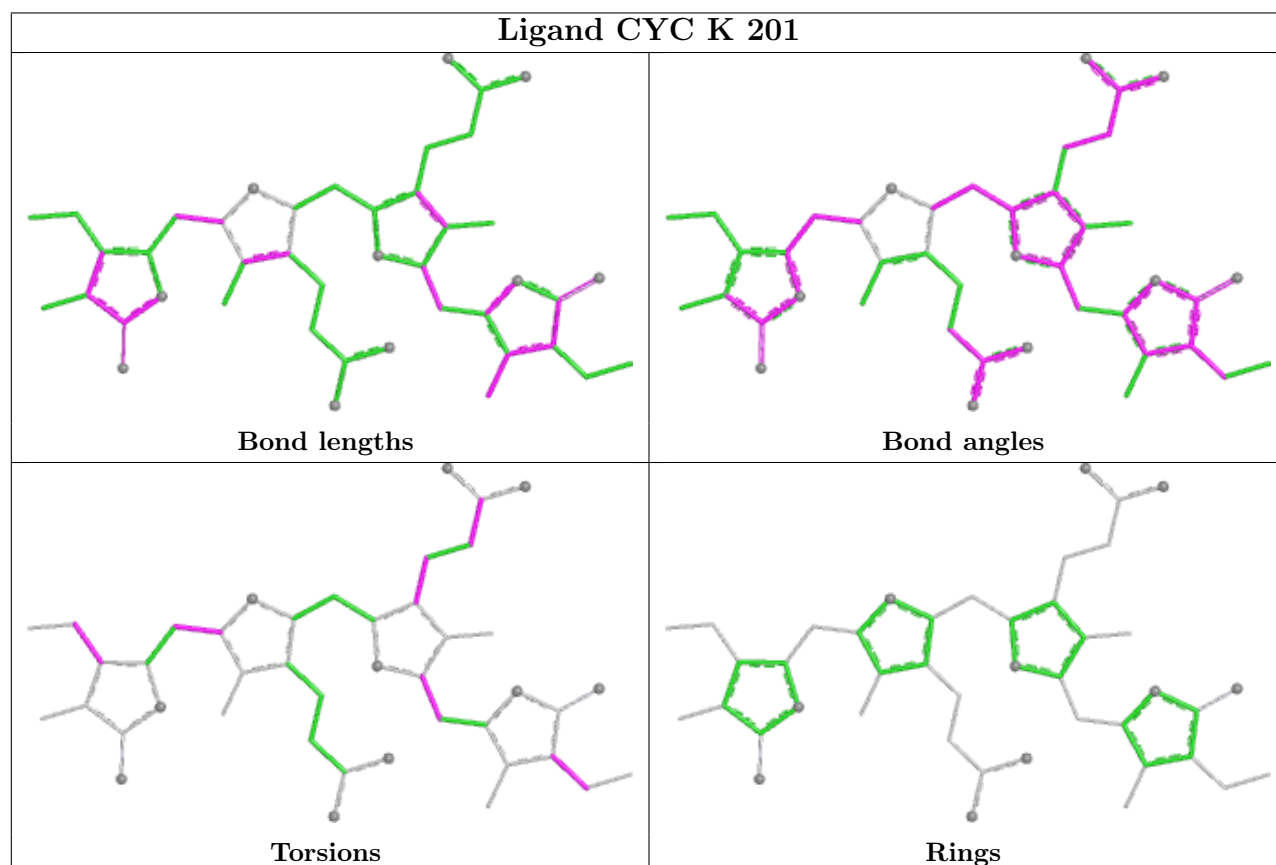
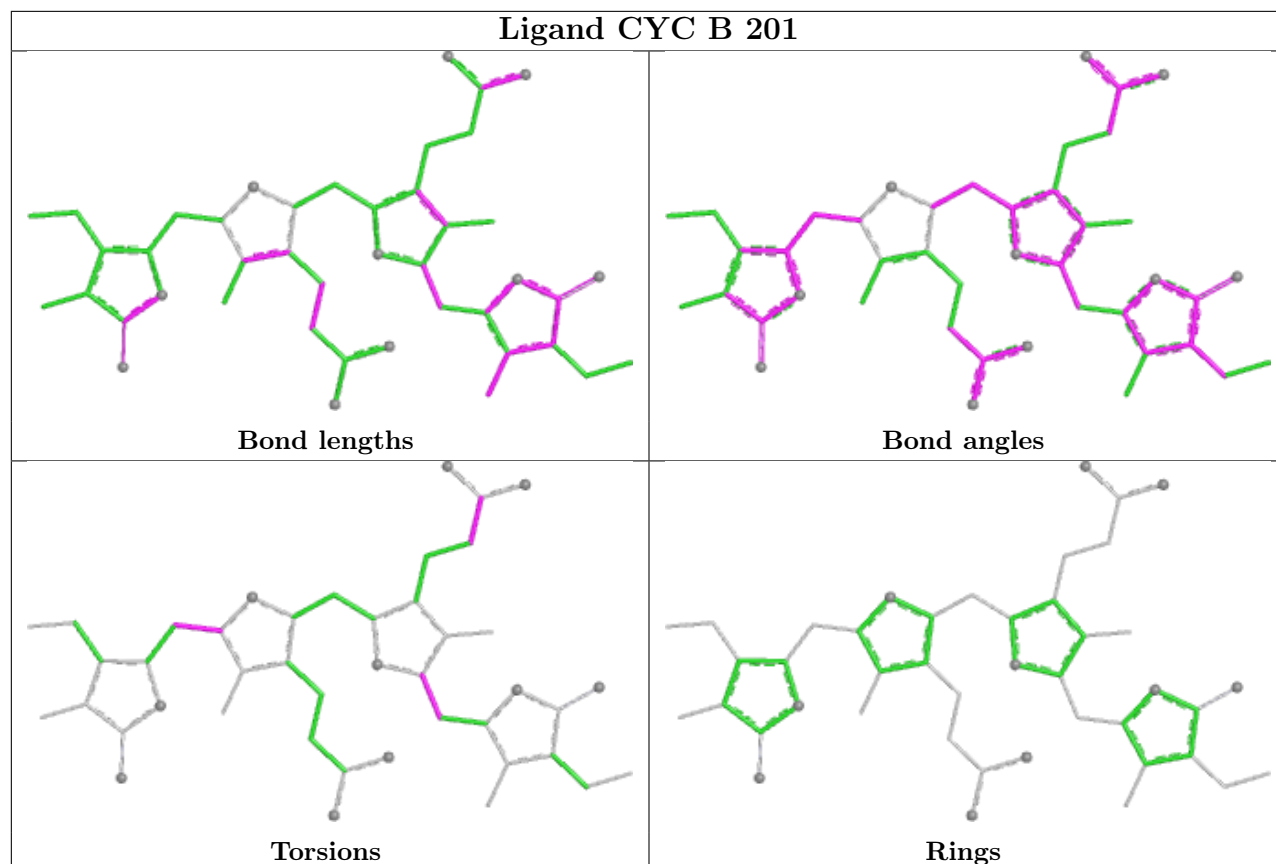


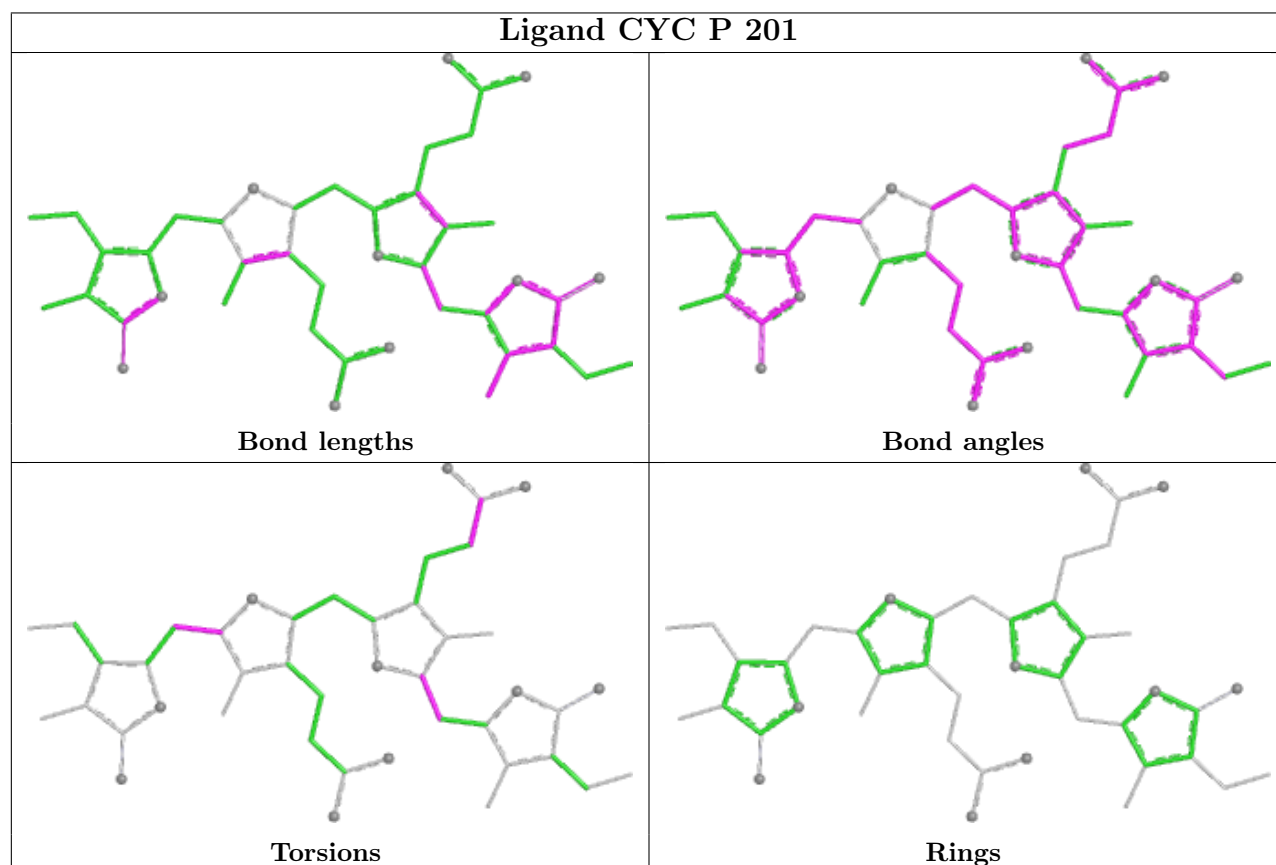
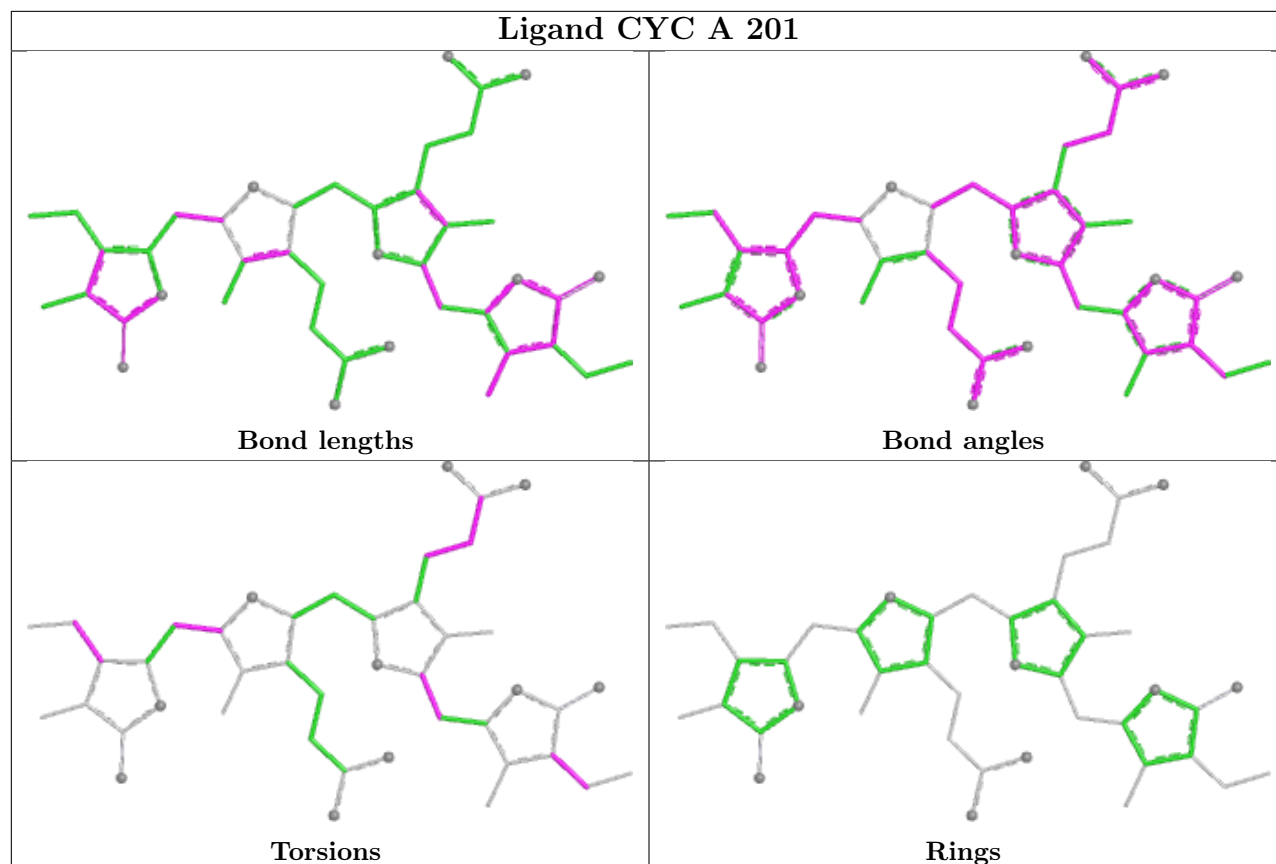


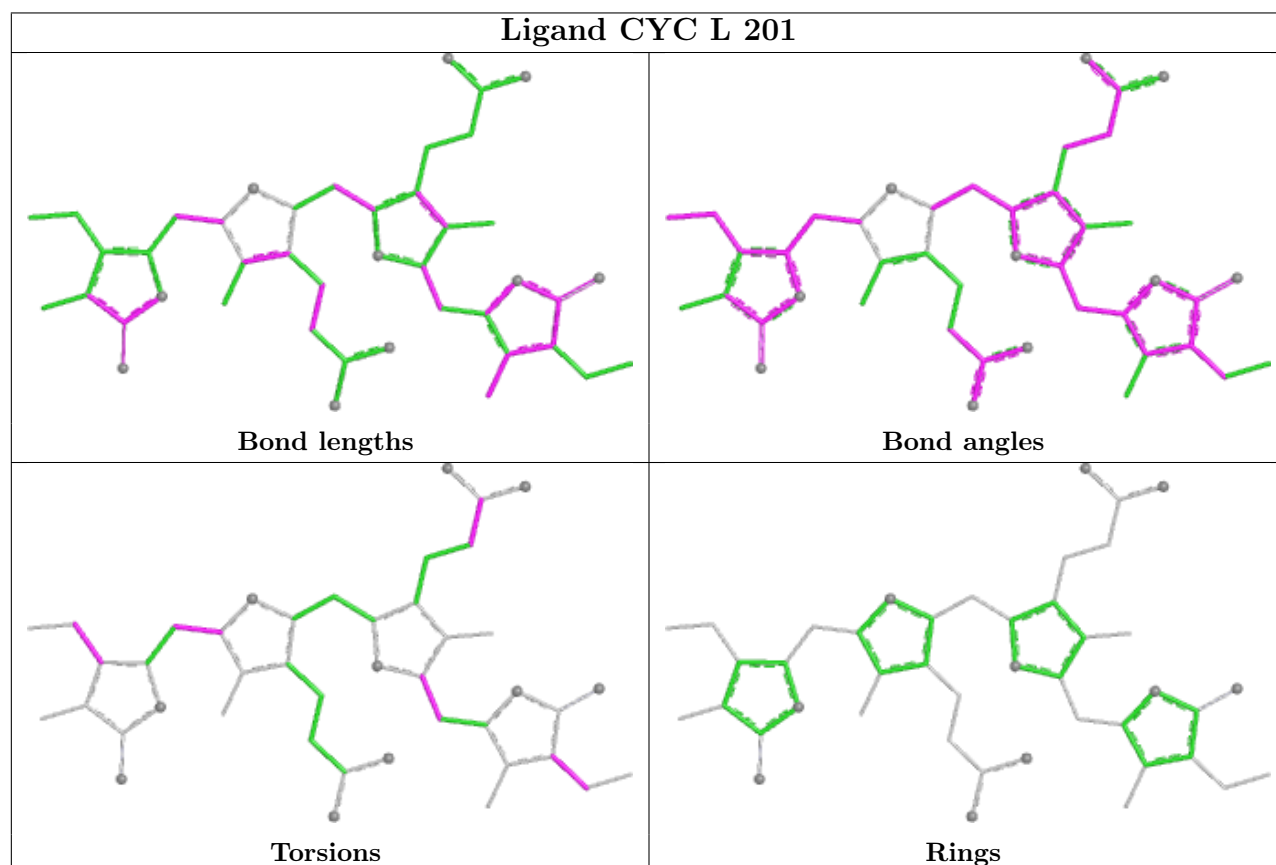
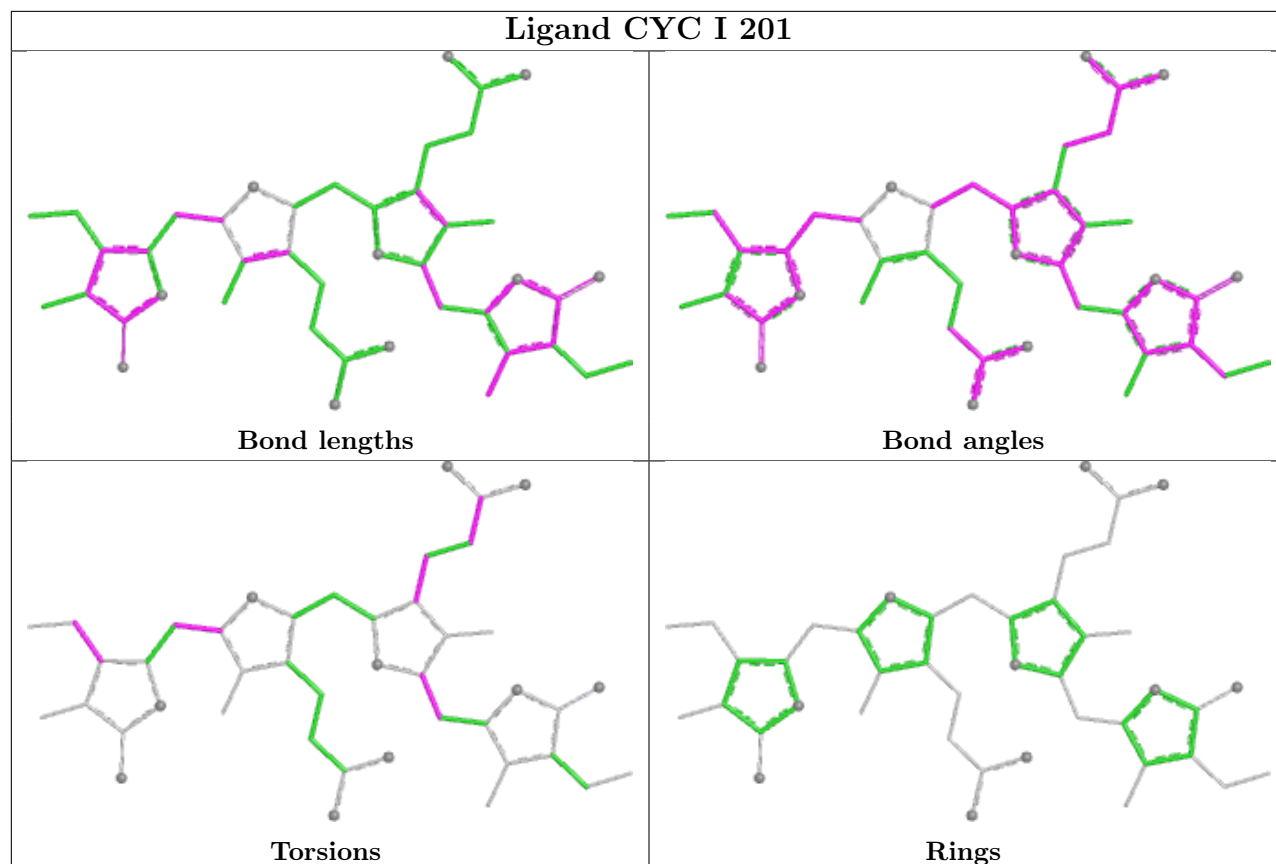




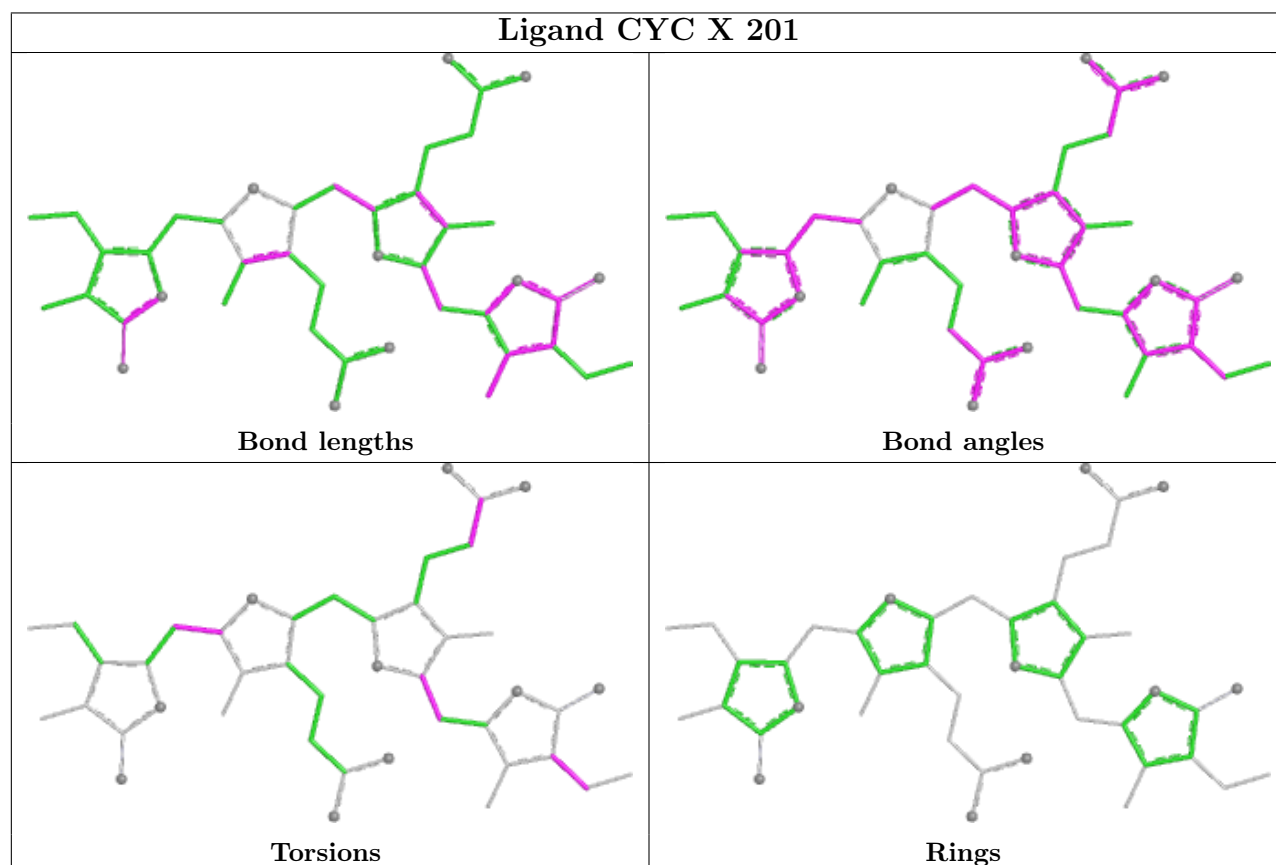
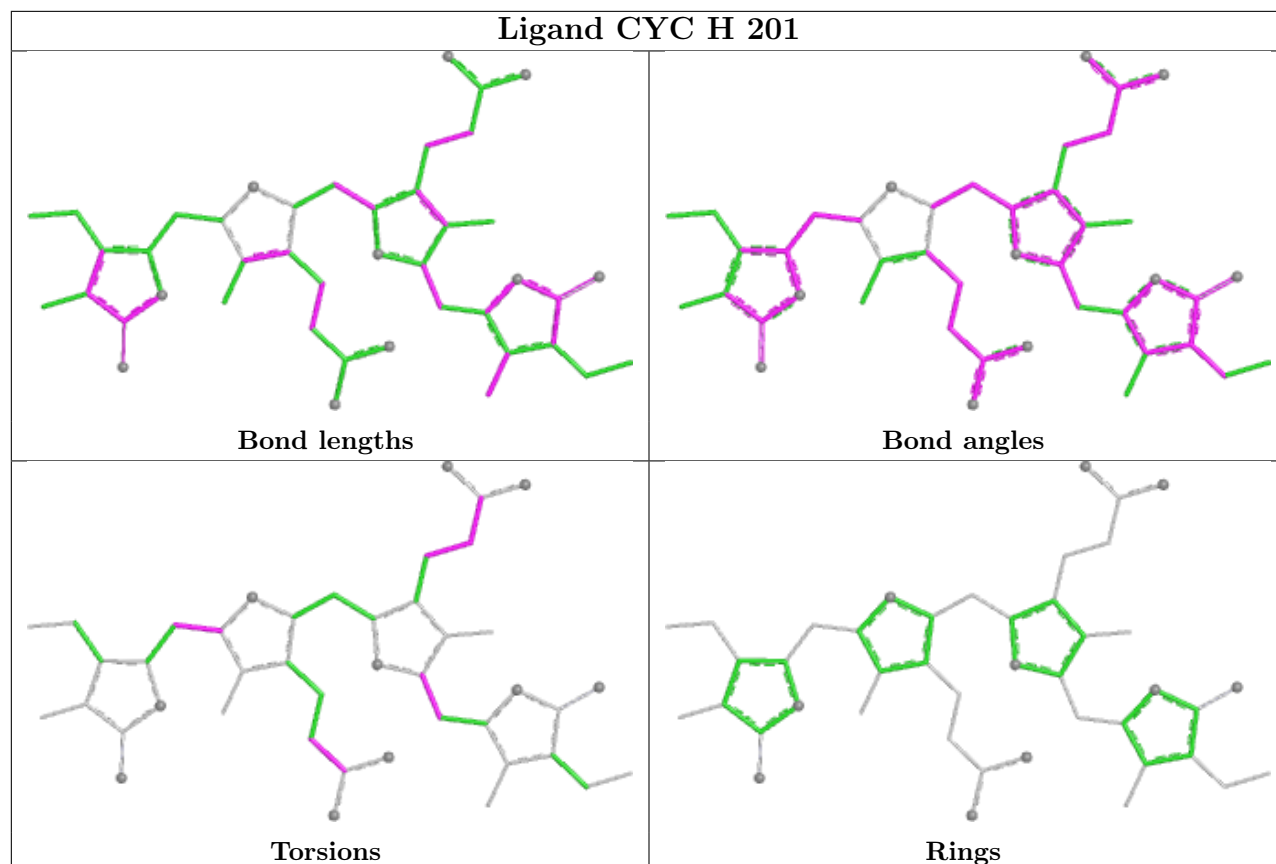


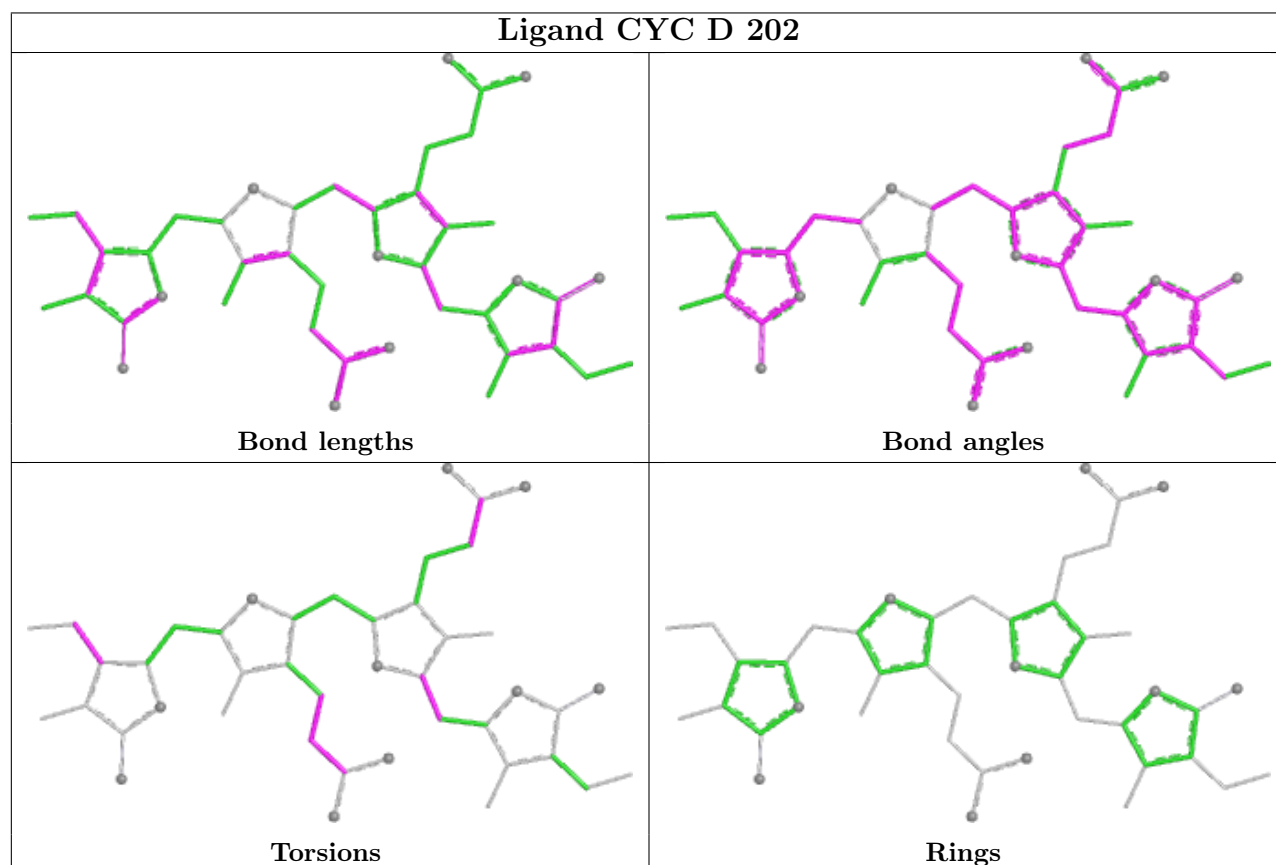
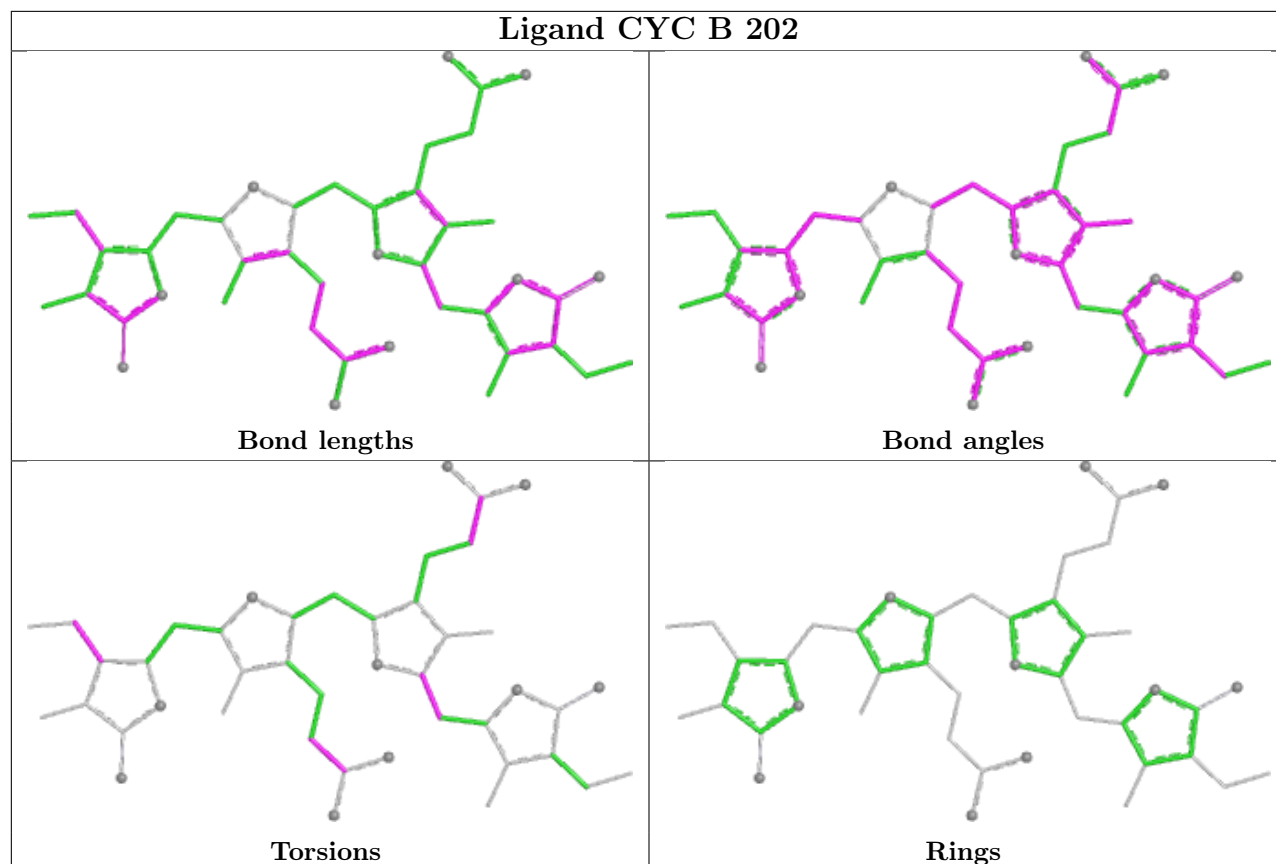


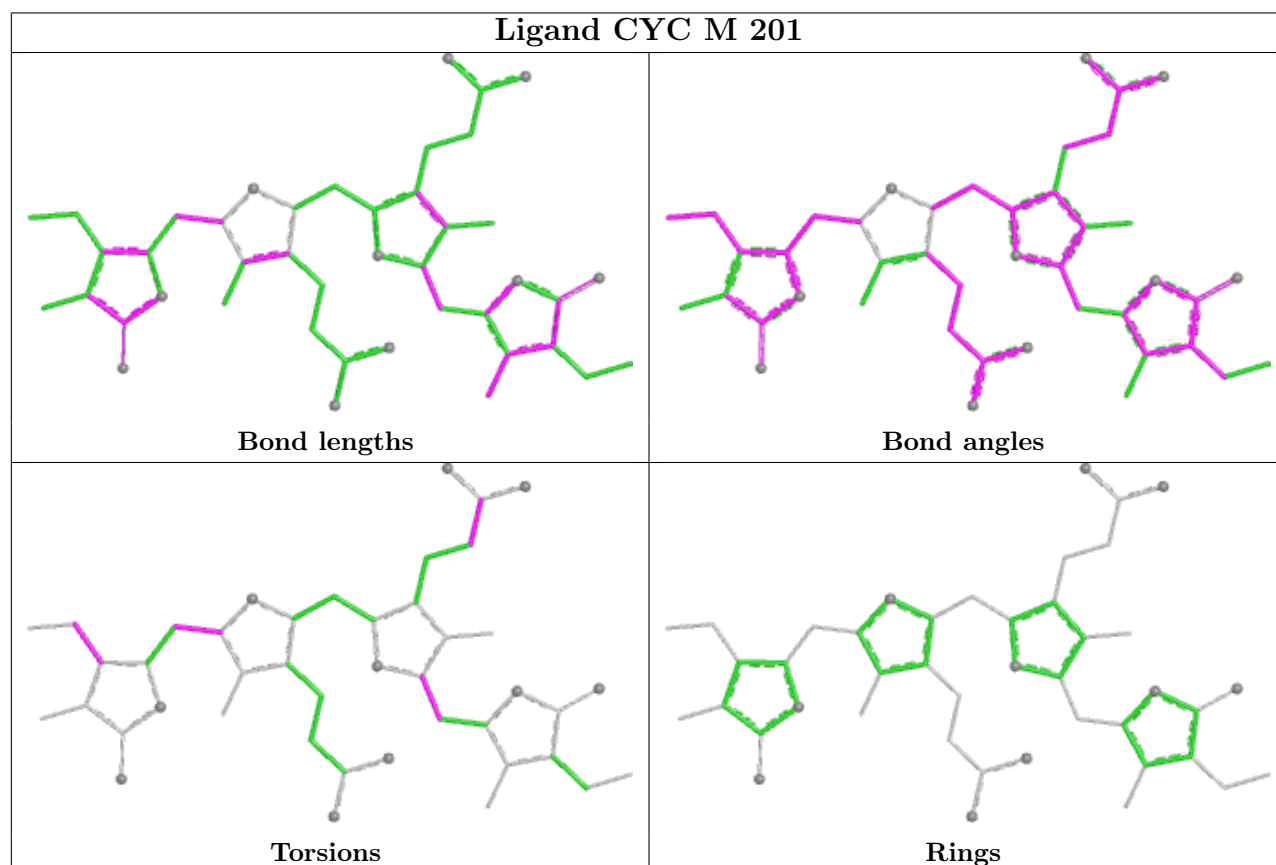
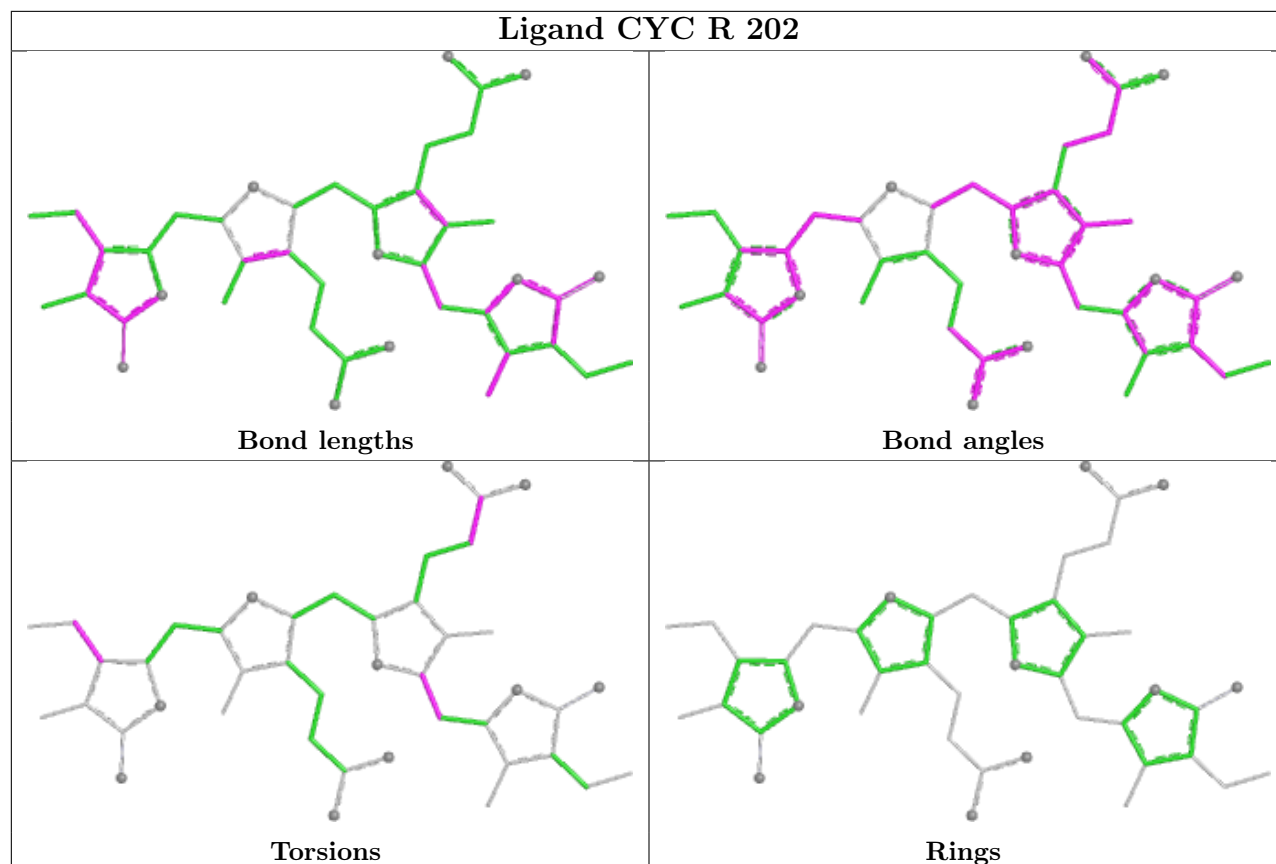


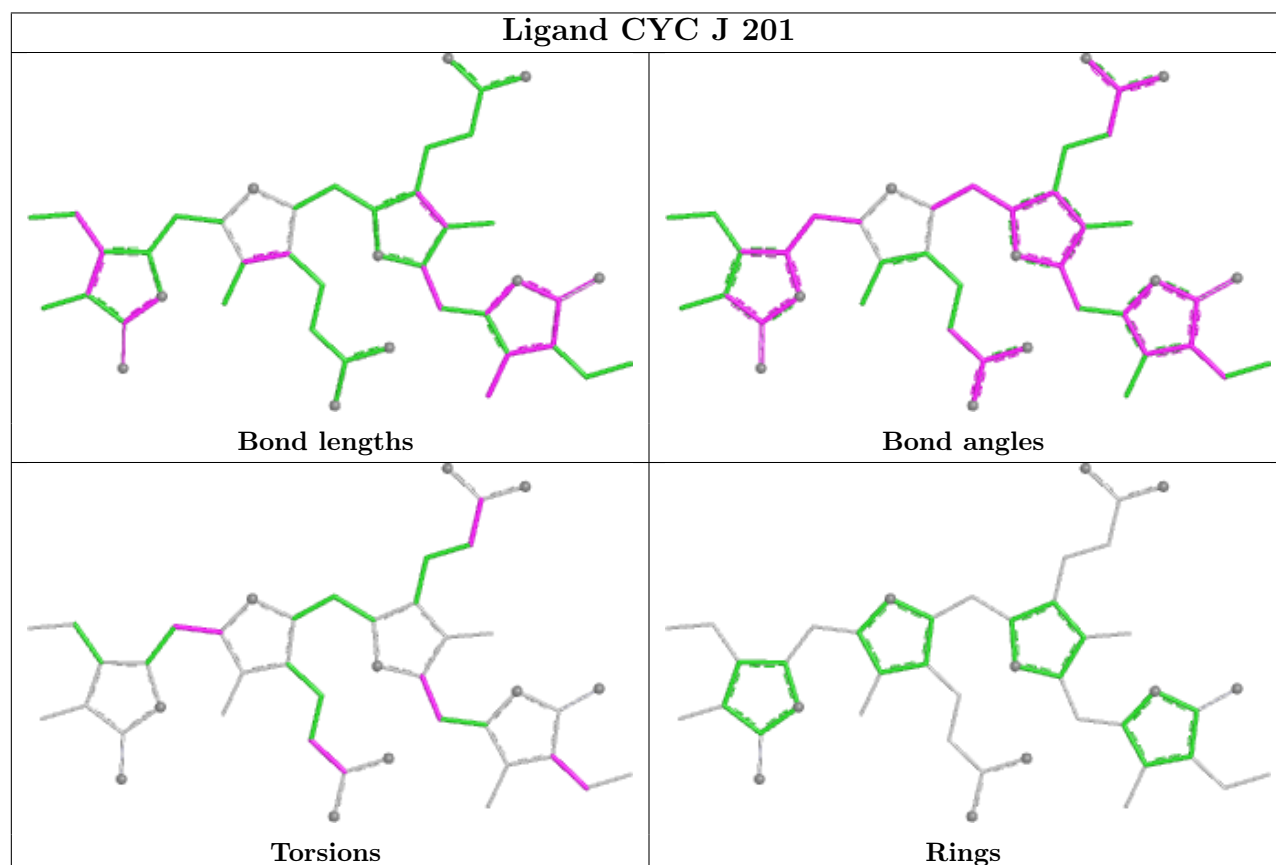
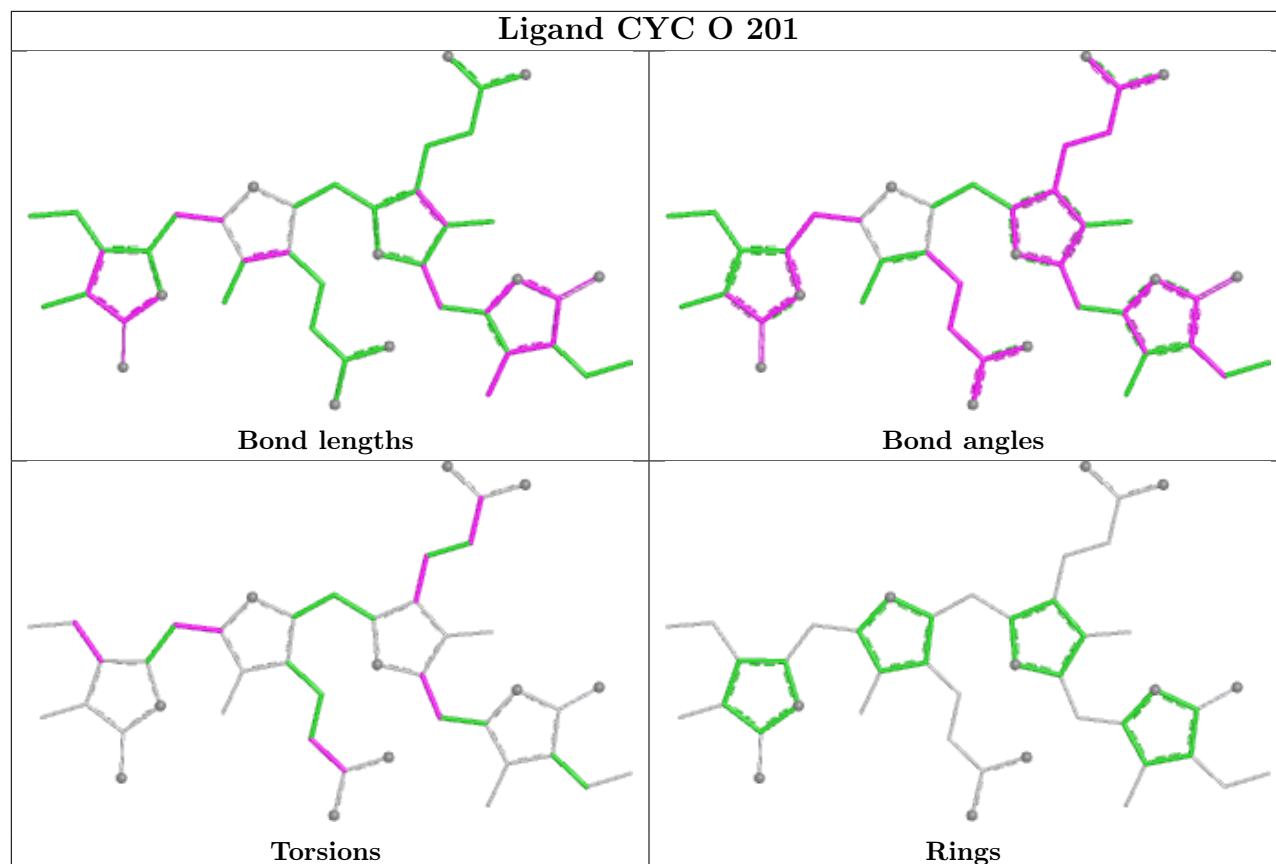


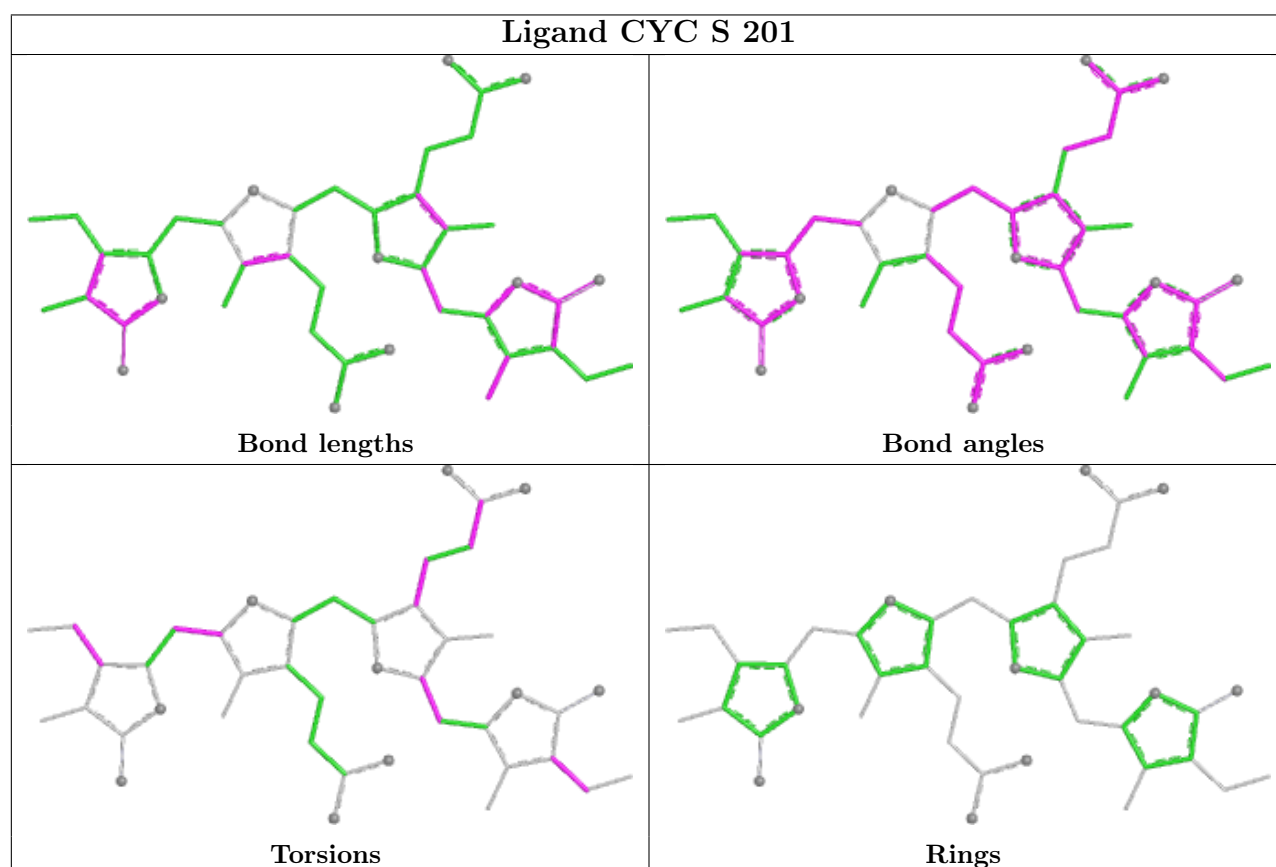
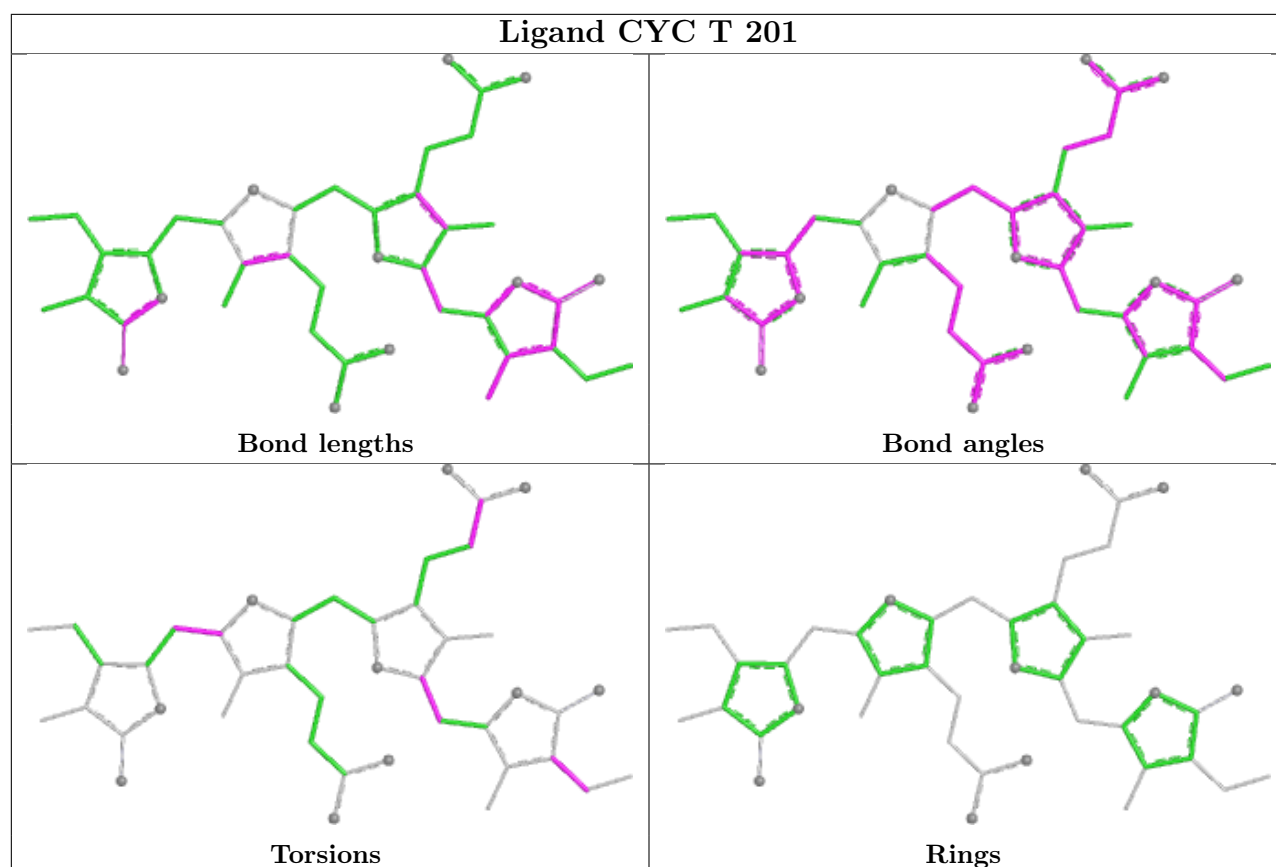


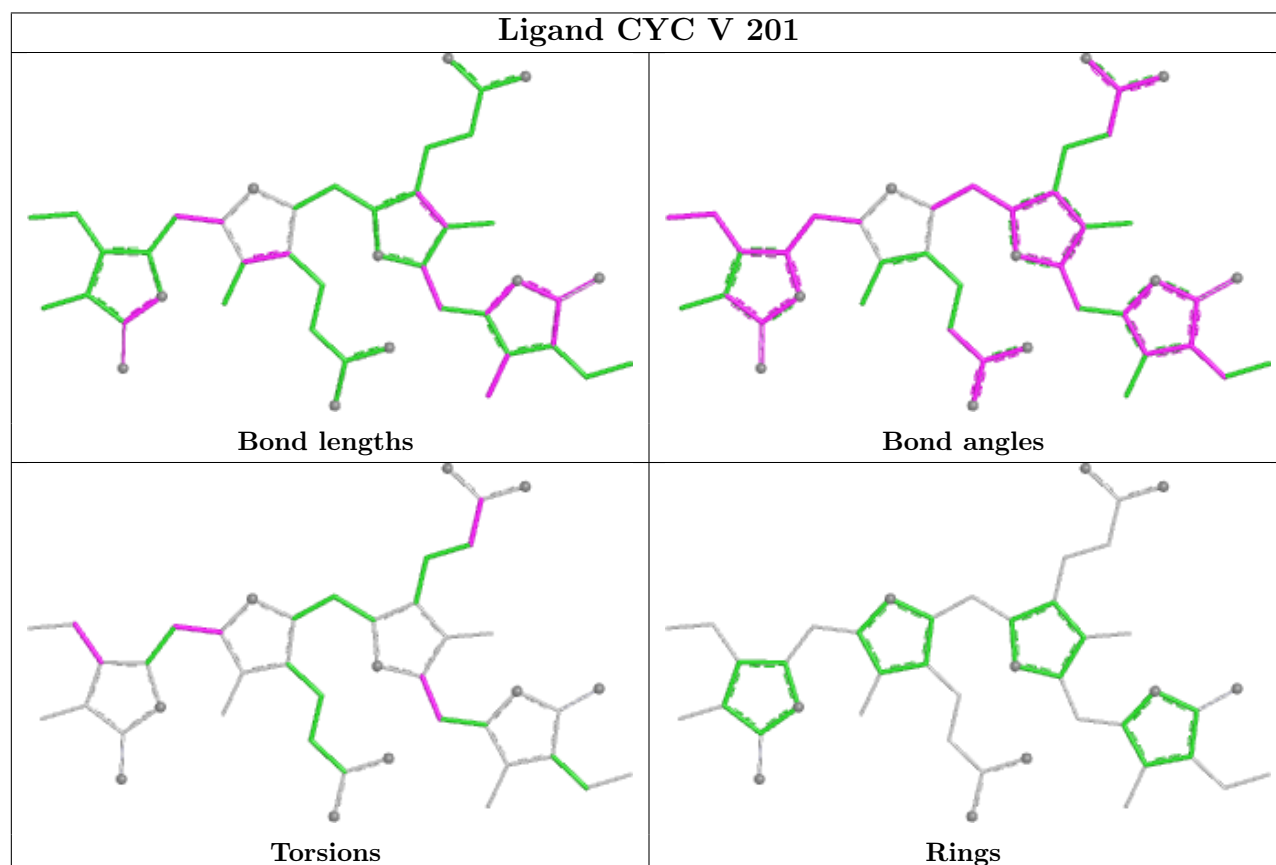
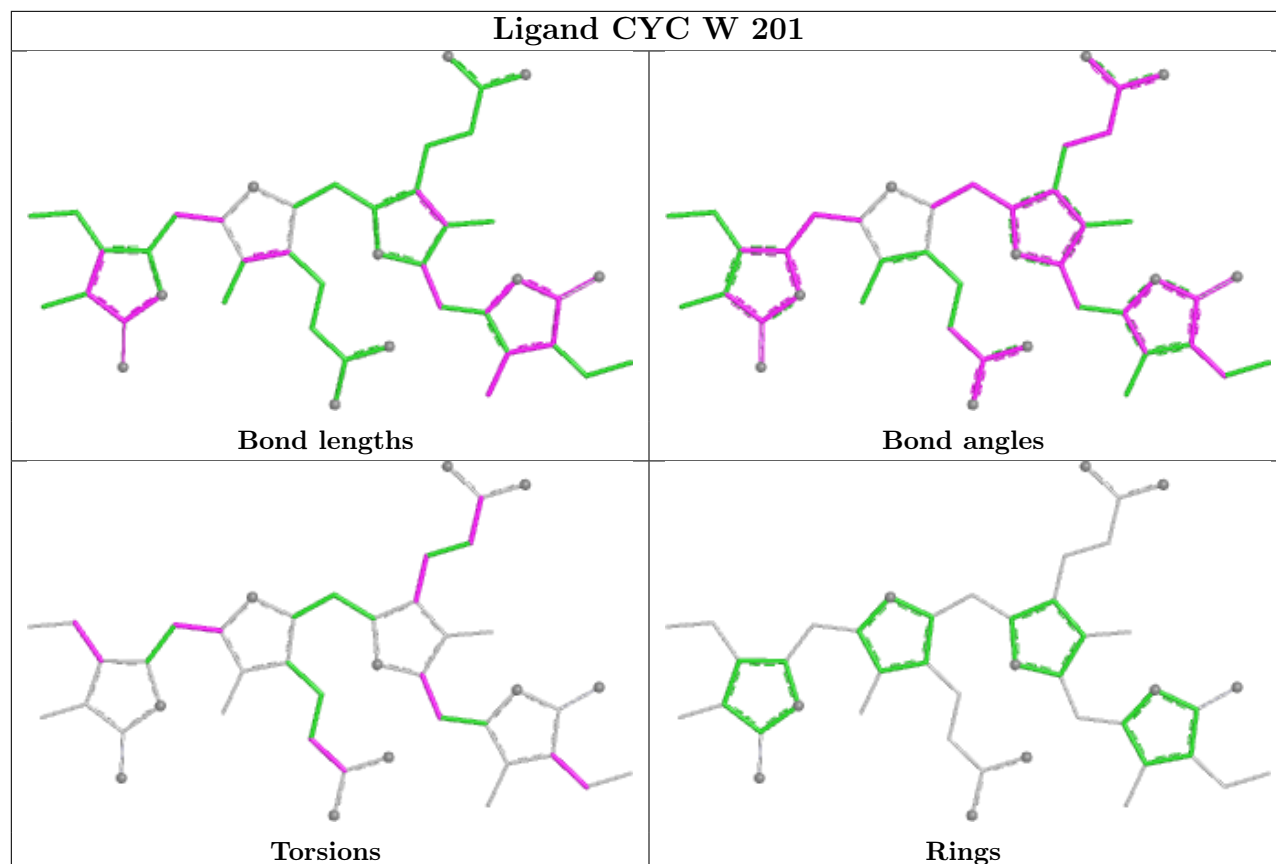


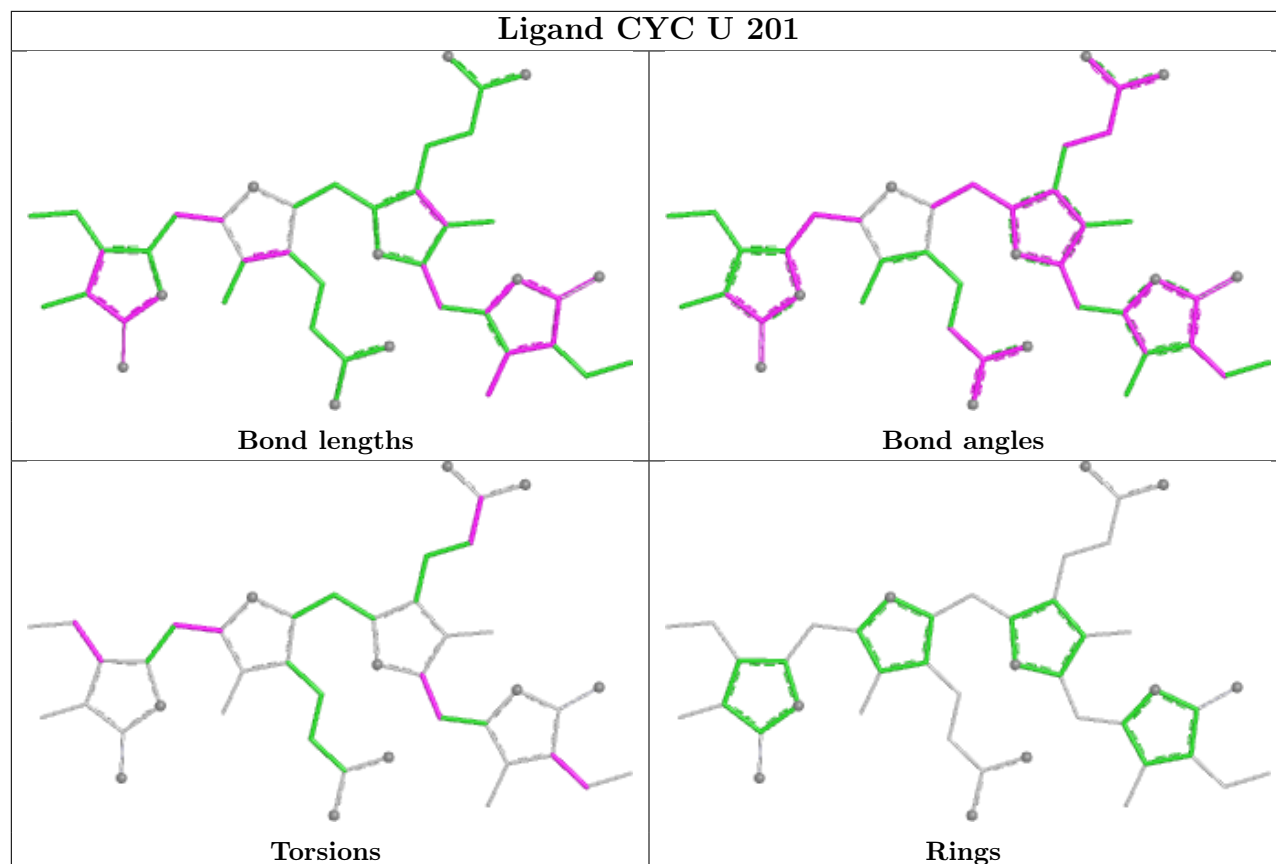












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	162/163 (99%)	-0.47	0 100 100	3, 11, 25, 35	0
1	C	162/163 (99%)	-0.41	0 100 100	5, 14, 27, 56	0
1	E	162/163 (99%)	-0.41	0 100 100	5, 12, 26, 57	0
1	G	162/163 (99%)	-0.39	0 100 100	5, 14, 29, 40	0
1	I	162/163 (99%)	-0.44	0 100 100	3, 12, 28, 55	0
1	K	162/163 (99%)	-0.40	0 100 100	3, 13, 27, 65	0
1	M	162/163 (99%)	-0.38	0 100 100	6, 13, 30, 51	0
1	O	162/163 (99%)	-0.42	0 100 100	4, 13, 25, 37	0
1	Q	162/163 (99%)	-0.36	1 (0%) 89 88	4, 13, 30, 65	0
1	S	162/163 (99%)	-0.43	0 100 100	3, 12, 23, 38	0
1	U	162/163 (99%)	-0.47	0 100 100	3, 12, 21, 30	0
1	W	162/163 (99%)	-0.35	0 100 100	4, 14, 28, 41	0
2	B	171/173 (98%)	-0.30	1 (0%) 89 88	3, 14, 31, 53	0
2	D	171/173 (98%)	-0.33	0 100 100	4, 14, 30, 55	0
2	F	171/173 (98%)	-0.25	1 (0%) 89 88	5, 16, 34, 48	0
2	H	171/173 (98%)	-0.30	0 100 100	7, 18, 36, 53	0
2	J	171/173 (98%)	-0.19	0 100 100	6, 16, 36, 50	0
2	L	171/173 (98%)	-0.26	2 (1%) 79 77	5, 16, 35, 51	0
2	N	171/173 (98%)	-0.29	1 (0%) 89 88	5, 15, 35, 54	0
2	P	171/173 (98%)	-0.29	0 100 100	6, 15, 34, 61	0
2	R	171/173 (98%)	-0.25	0 100 100	6, 17, 40, 53	0
2	T	171/173 (98%)	-0.30	1 (0%) 89 88	5, 16, 34, 51	0
2	V	171/173 (98%)	-0.36	0 100 100	5, 13, 29, 45	0
2	X	171/173 (98%)	-0.34	0 100 100	5, 14, 33, 43	0

*Continued on next page...*



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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
All	All	3996/4032 (99%)	-0.35	7 (0%) 95 94	3, 14, 33, 65	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	21	ASP	2.9
2	T	145	ARG	2.8
2	B	153	CYS	2.8
2	F	172	ALA	2.7
2	N	75	THR	2.3

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MEN	H	72	9/10	0.75	0.18	20,20,32,32	0
2	MEN	J	72	9/10	0.81	0.21	15,19,27,29	0
2	MEN	L	72	9/10	0.84	0.21	20,20,23,30	0
2	MEN	N	72	9/10	0.84	0.26	15,19,24,24	0
2	MEN	R	72	9/10	0.85	0.15	15,19,28,28	0
2	MEN	V	72	9/10	0.85	0.17	20,21,27,27	0
2	MEN	F	72	9/10	0.86	0.19	26,28,35,37	0
2	MEN	P	72	9/10	0.88	0.17	20,20,31,34	0
2	MEN	T	72	9/10	0.90	0.15	20,20,30,30	0
2	MEN	X	72	9/10	0.91	0.18	19,21,23,23	0
2	MEN	D	72	9/10	0.93	0.12	18,19,25,28	0
2	MEN	B	72	9/10	0.94	0.14	15,19,20,20	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

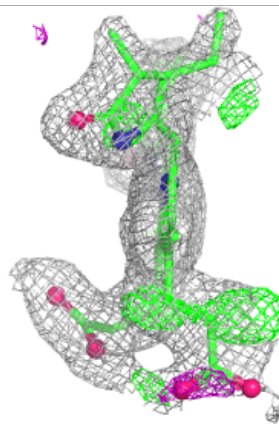
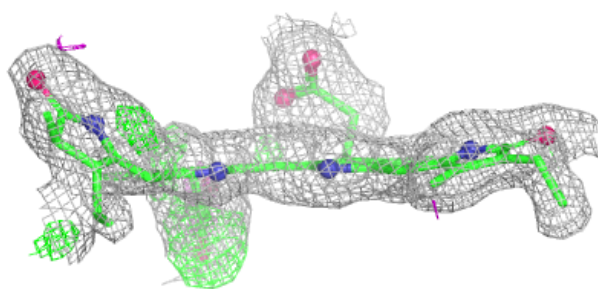
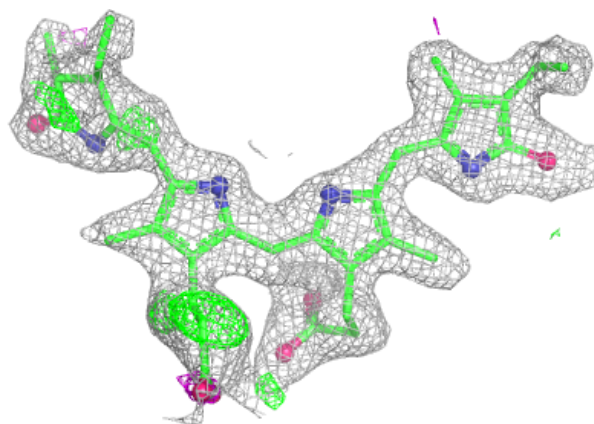
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	CYC	R	202	43/43	0.85	0.19	9,20,32,39	0
3	CYC	T	201	43/43	0.89	0.16	15,19,26,29	0
3	CYC	D	202	43/43	0.90	0.15	4,17,31,39	0
3	CYC	V	202	43/43	0.90	0.16	7,17,32,41	0
3	CYC	X	202	43/43	0.90	0.17	6,18,29,40	0
3	CYC	N	202	43/43	0.91	0.14	4,17,31,38	0
3	CYC	P	202	43/43	0.91	0.15	5,16,33,41	0
3	CYC	A	201	43/43	0.91	0.15	5,11,18,23	0
3	CYC	H	202	43/43	0.91	0.14	4,15,32,41	0
3	CYC	T	202	43/43	0.91	0.15	7,18,32,39	0
3	CYC	J	202	43/43	0.91	0.13	4,13,34,45	0
3	CYC	M	201	43/43	0.91	0.15	7,12,17,23	0
3	CYC	R	201	43/43	0.92	0.14	16,18,24,25	0
3	CYC	F	202	43/43	0.92	0.15	4,21,35,43	0
3	CYC	J	201	43/43	0.92	0.14	6,19,24,27	0
3	CYC	H	201	43/43	0.93	0.14	14,18,22,24	0
3	CYC	P	201	43/43	0.93	0.14	8,17,25,26	0
3	CYC	D	201	43/43	0.93	0.13	11,14,19,22	0
3	CYC	B	201	43/43	0.93	0.13	8,14,25,27	0
3	CYC	F	201	43/43	0.93	0.13	13,18,22,25	0
3	CYC	K	201	43/43	0.93	0.12	2,10,16,20	0
3	CYC	L	201	43/43	0.93	0.15	6,16,25,31	0
3	CYC	U	201	43/43	0.93	0.13	6,9,14,17	0
3	CYC	L	202	43/43	0.93	0.14	2,18,35,46	0
3	CYC	B	202	43/43	0.93	0.16	5,15,31,40	0
3	CYC	I	201	43/43	0.94	0.12	5,10,13,15	0
3	CYC	N	201	43/43	0.94	0.13	8,17,28,32	0
3	CYC	E	201	43/43	0.94	0.12	3,9,13,15	0
3	CYC	V	201	43/43	0.94	0.14	3,11,20,23	0
3	CYC	O	201	43/43	0.94	0.12	5,11,14,20	0
3	CYC	W	201	43/43	0.94	0.12	7,12,16,18	0
3	CYC	X	201	43/43	0.94	0.12	8,15,18,22	0
3	CYC	S	201	43/43	0.94	0.13	3,7,12,16	0
3	CYC	G	201	43/43	0.95	0.11	5,15,18,18	0
3	CYC	C	201	43/43	0.95	0.11	5,10,15,21	0
3	CYC	Q	201	43/43	0.96	0.10	5,10,13,14	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

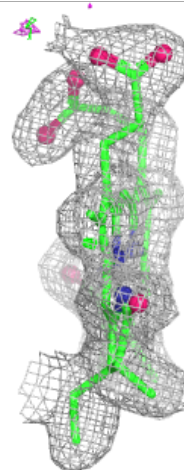
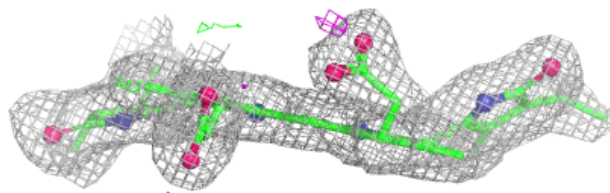
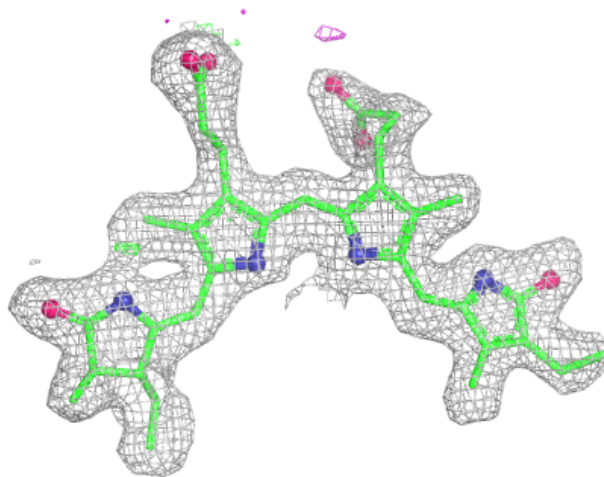
**Electron density around CYC R 202:**

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



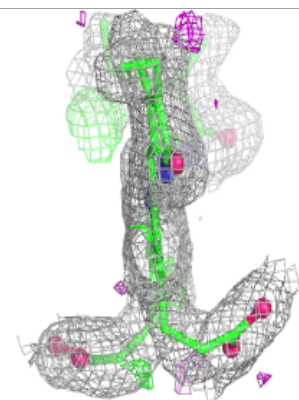
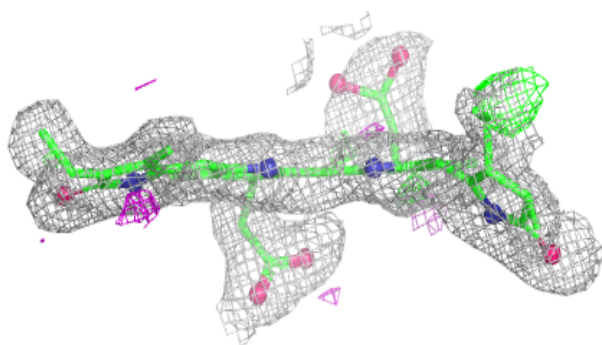
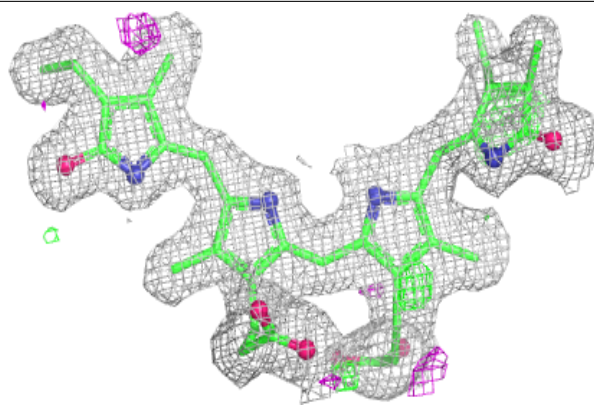
**Electron density around CYC T 201:**

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

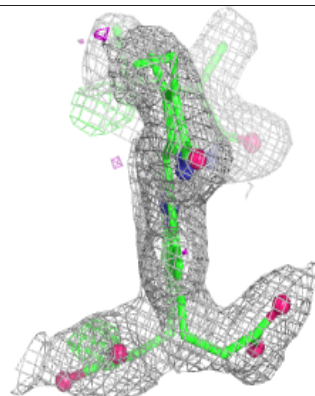
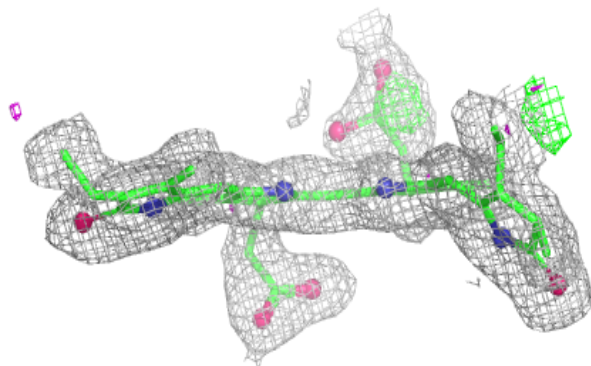
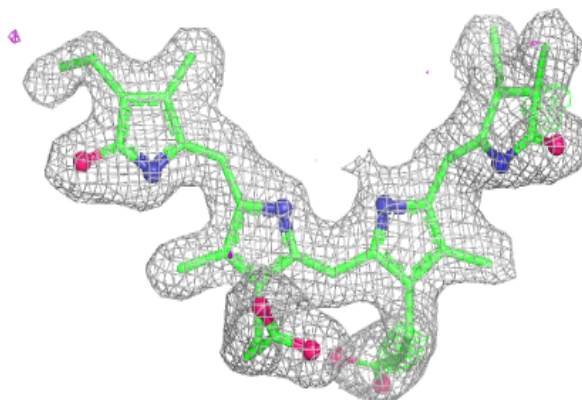


**Electron density around CYC D 202:**

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

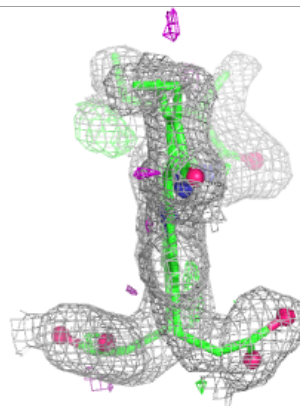
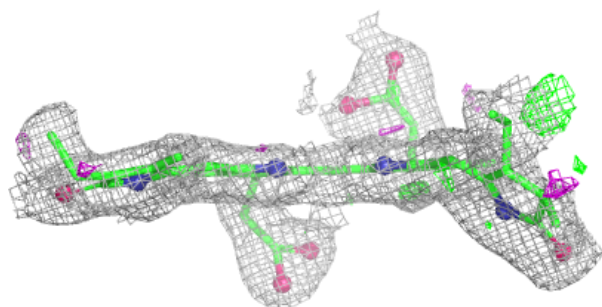
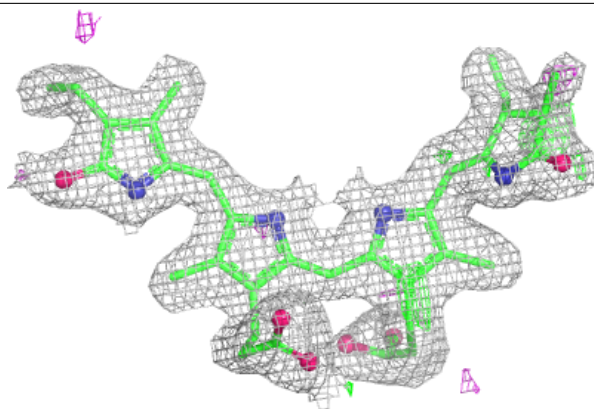
**Electron density around CYC V 202:**

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

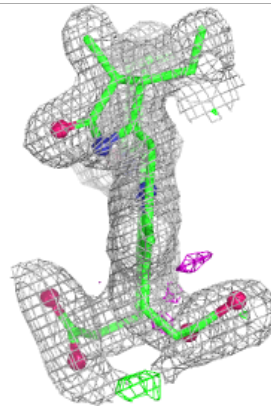
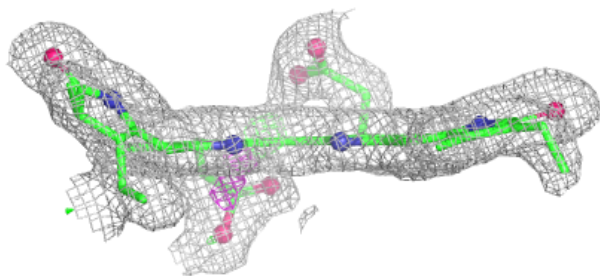
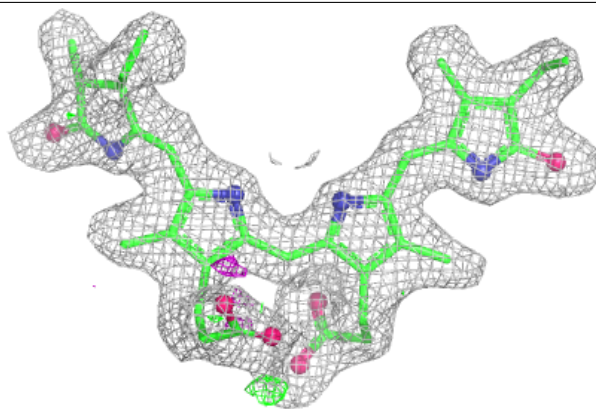


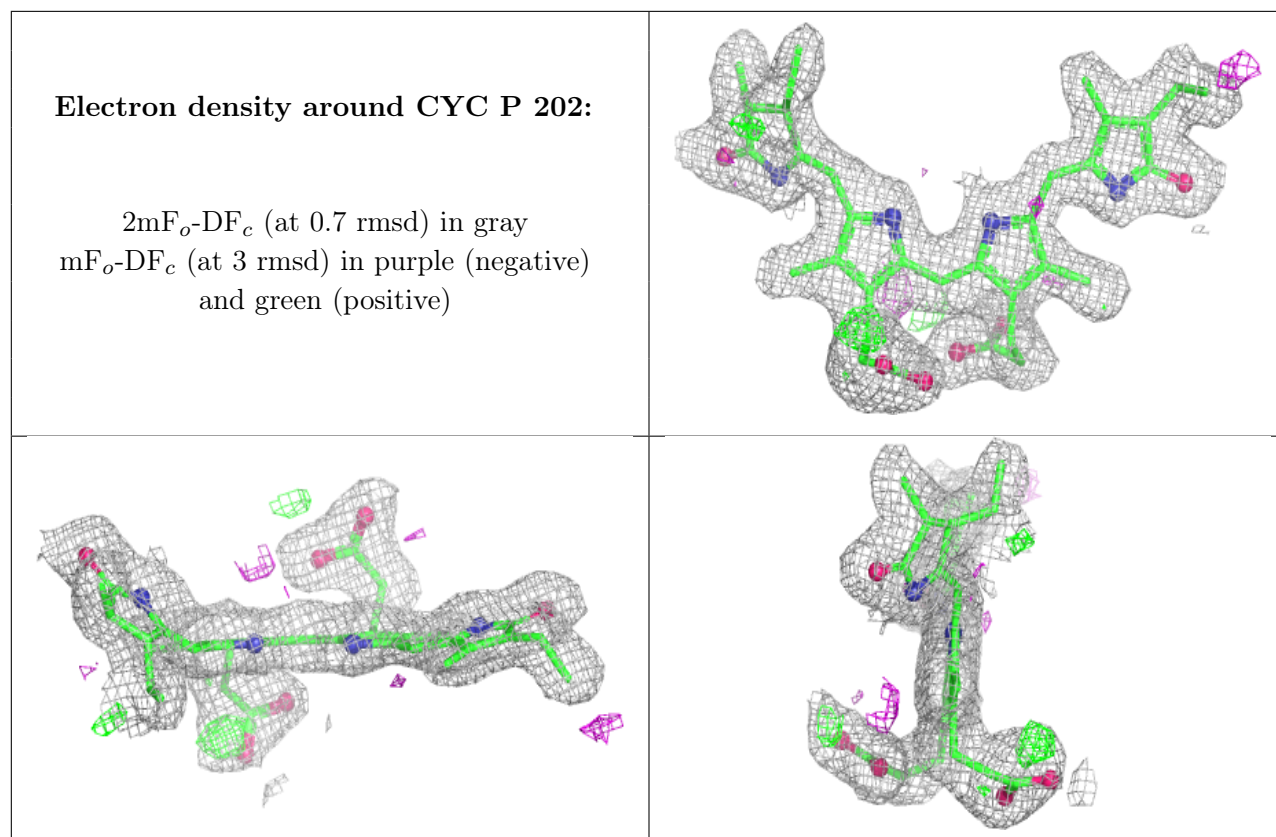
**Electron density around CYC X 202:**

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

**Electron density around CYC N 202:**

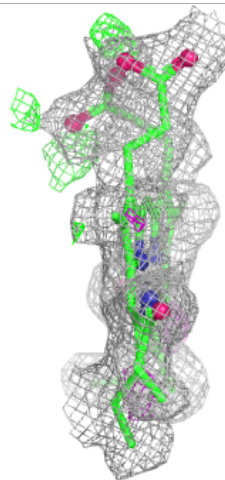
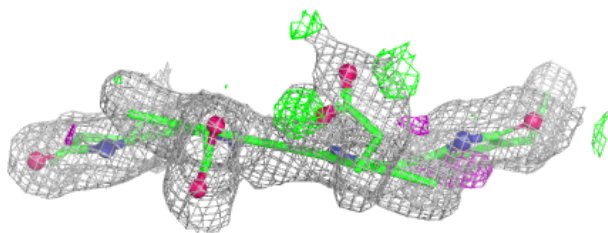
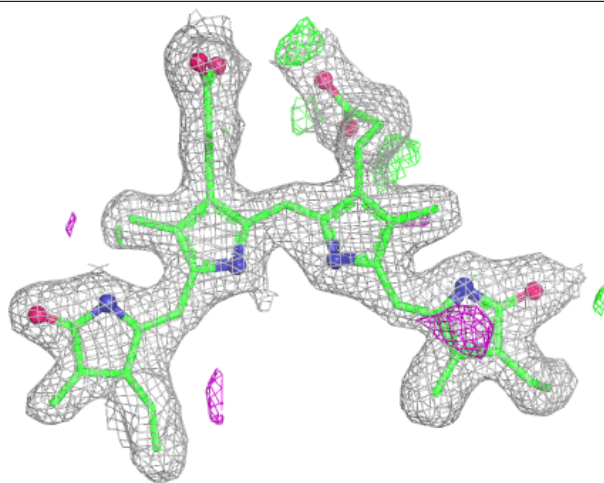
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around CYC A 201:**

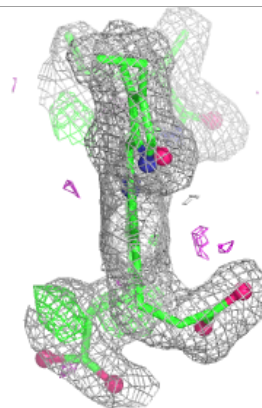
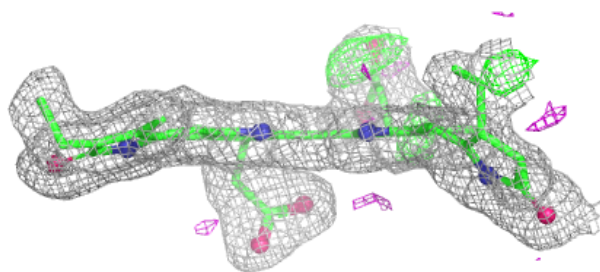
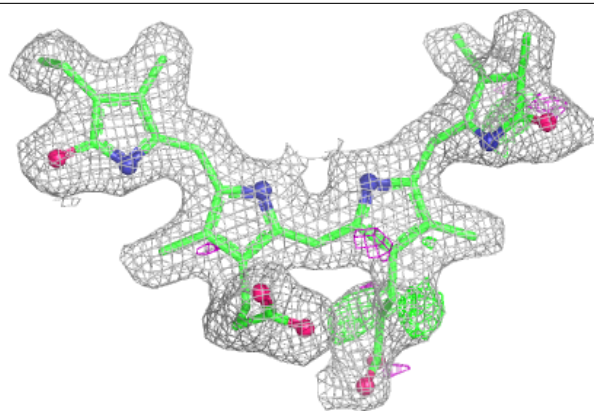
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



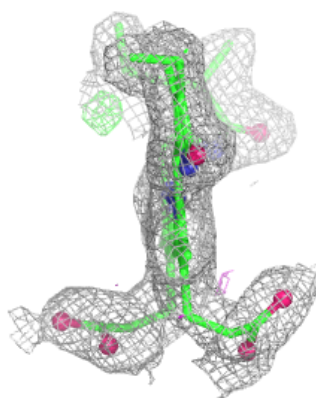
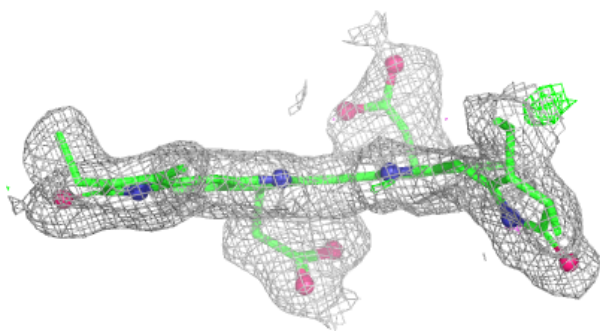
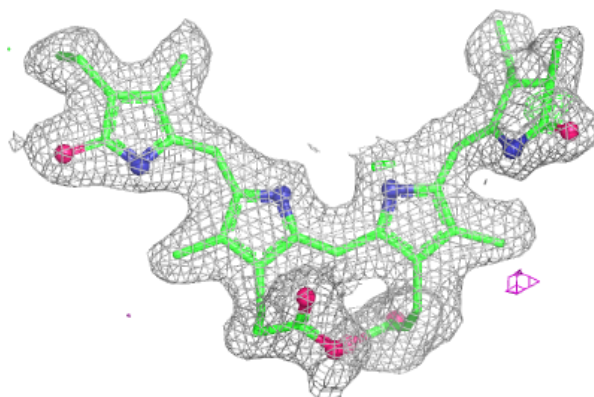


**Electron density around CYC H 202:**

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

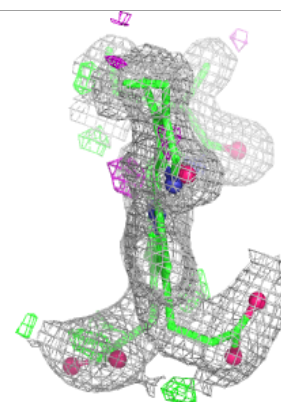
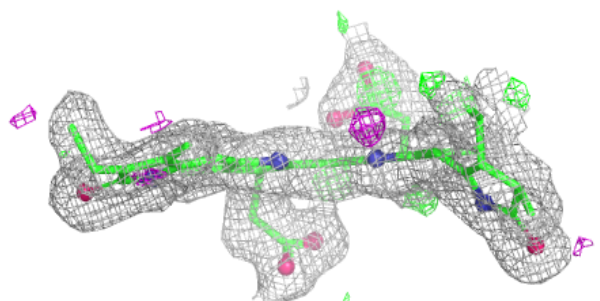
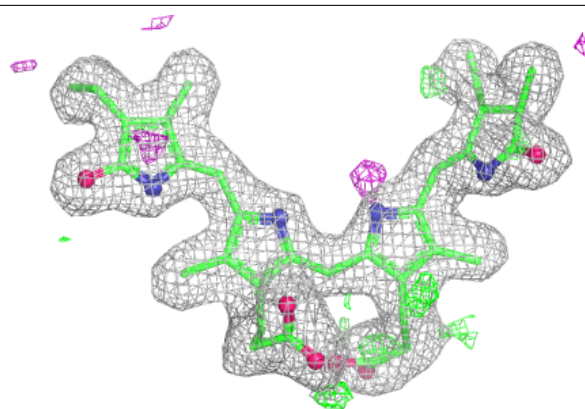
**Electron density around CYC T 202:**

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

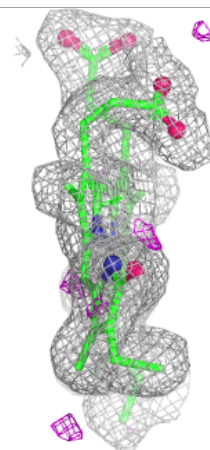
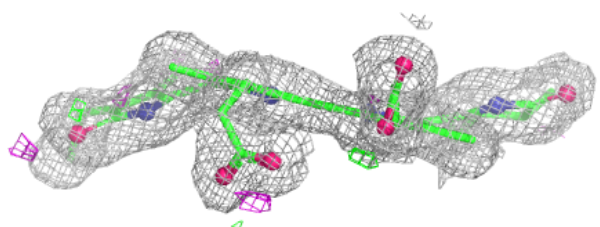
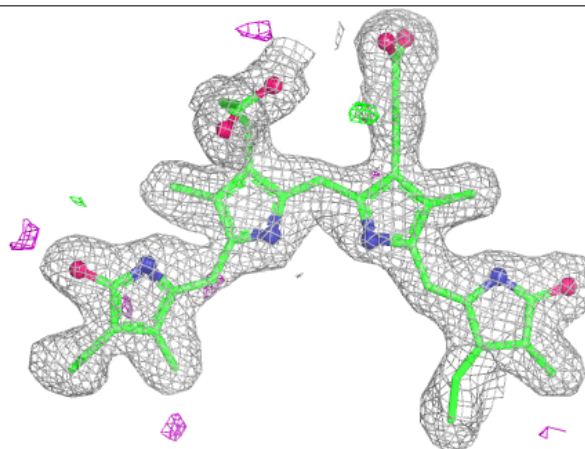


**Electron density around CYC J 202:**

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

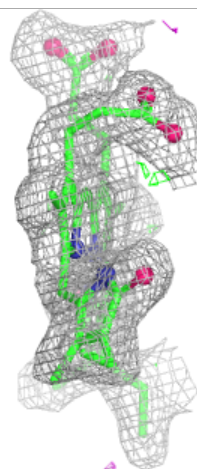
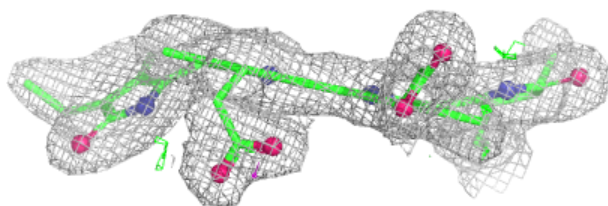
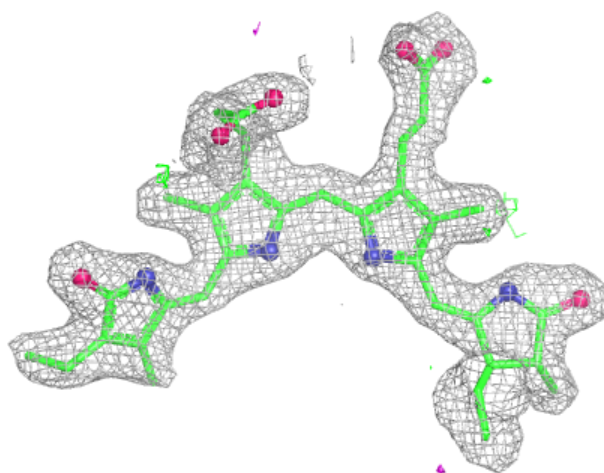
**Electron density around CYC M 201:**

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



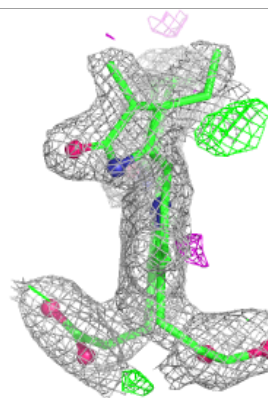
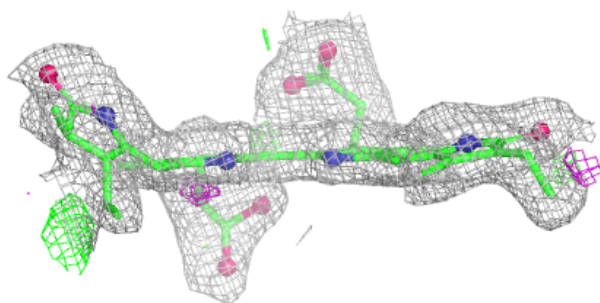
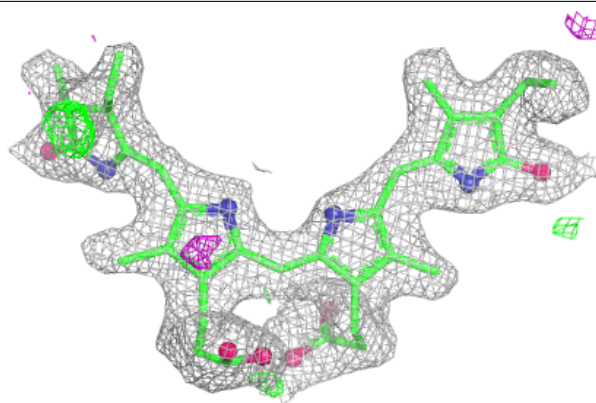
**Electron density around CYC R 201:**

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

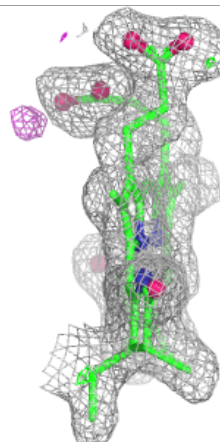
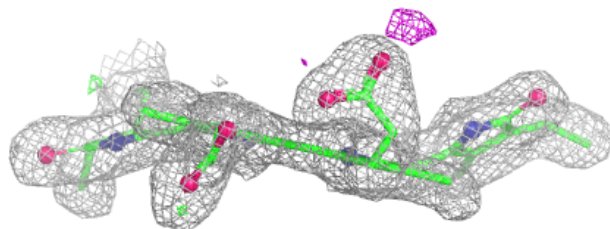
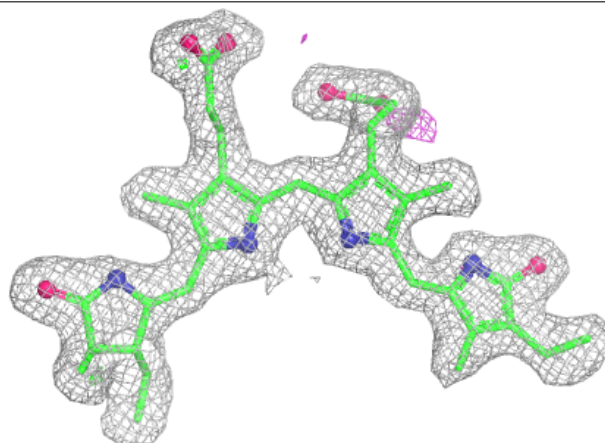


**Electron density around CYC F 202:**

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

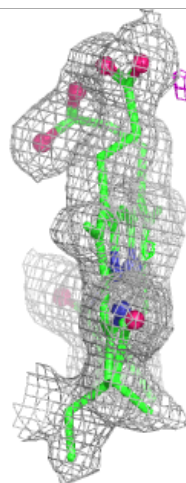
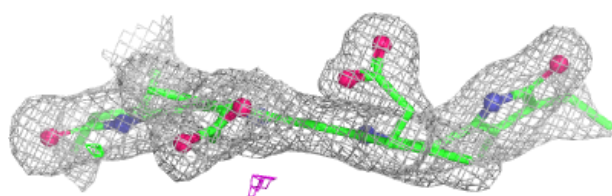
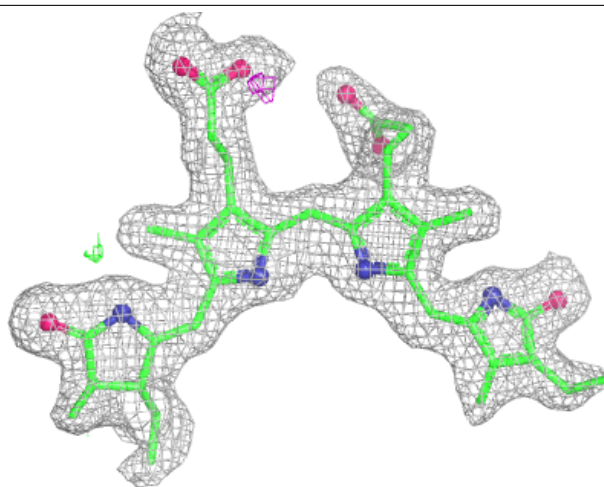
**Electron density around CYC J 201:**

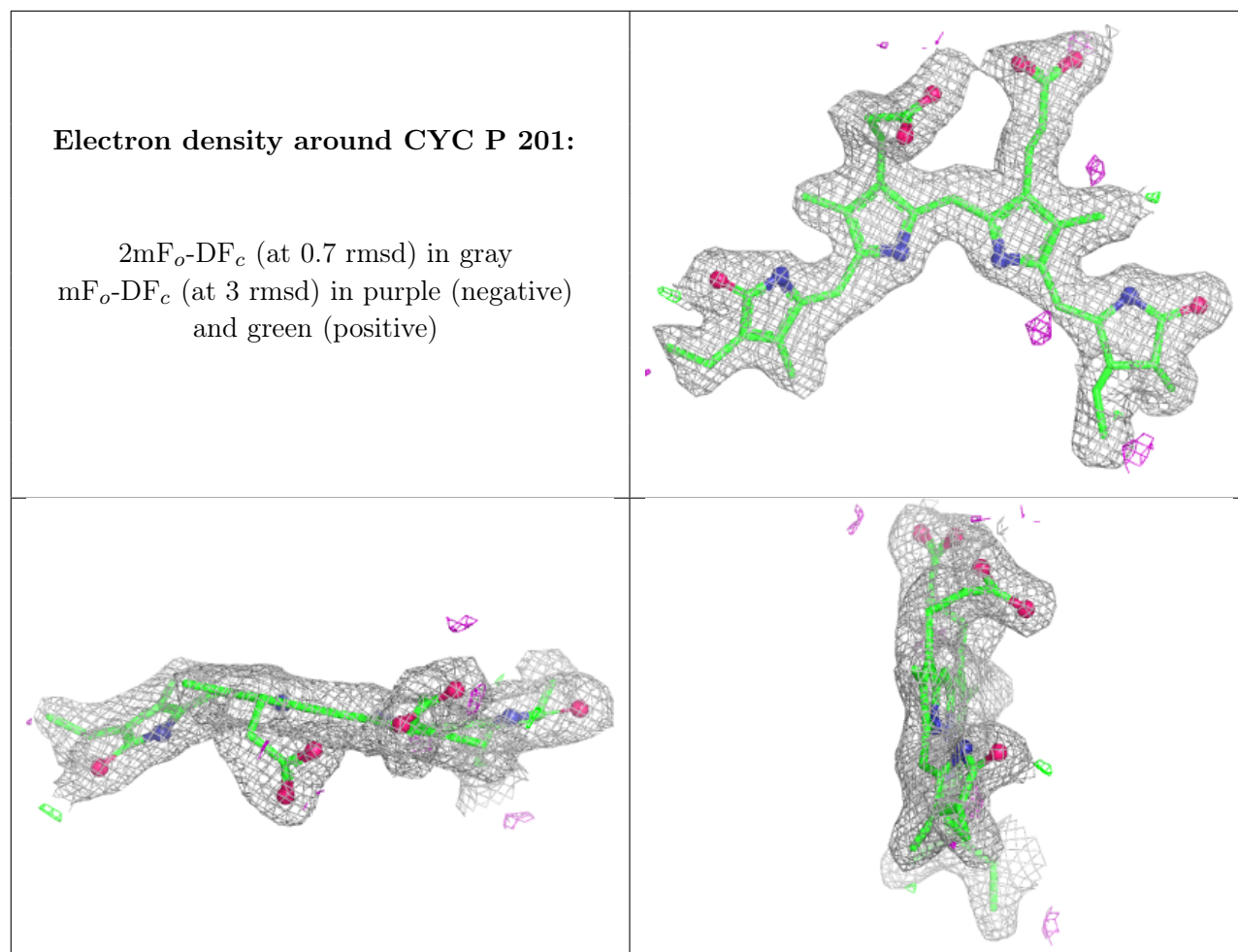
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

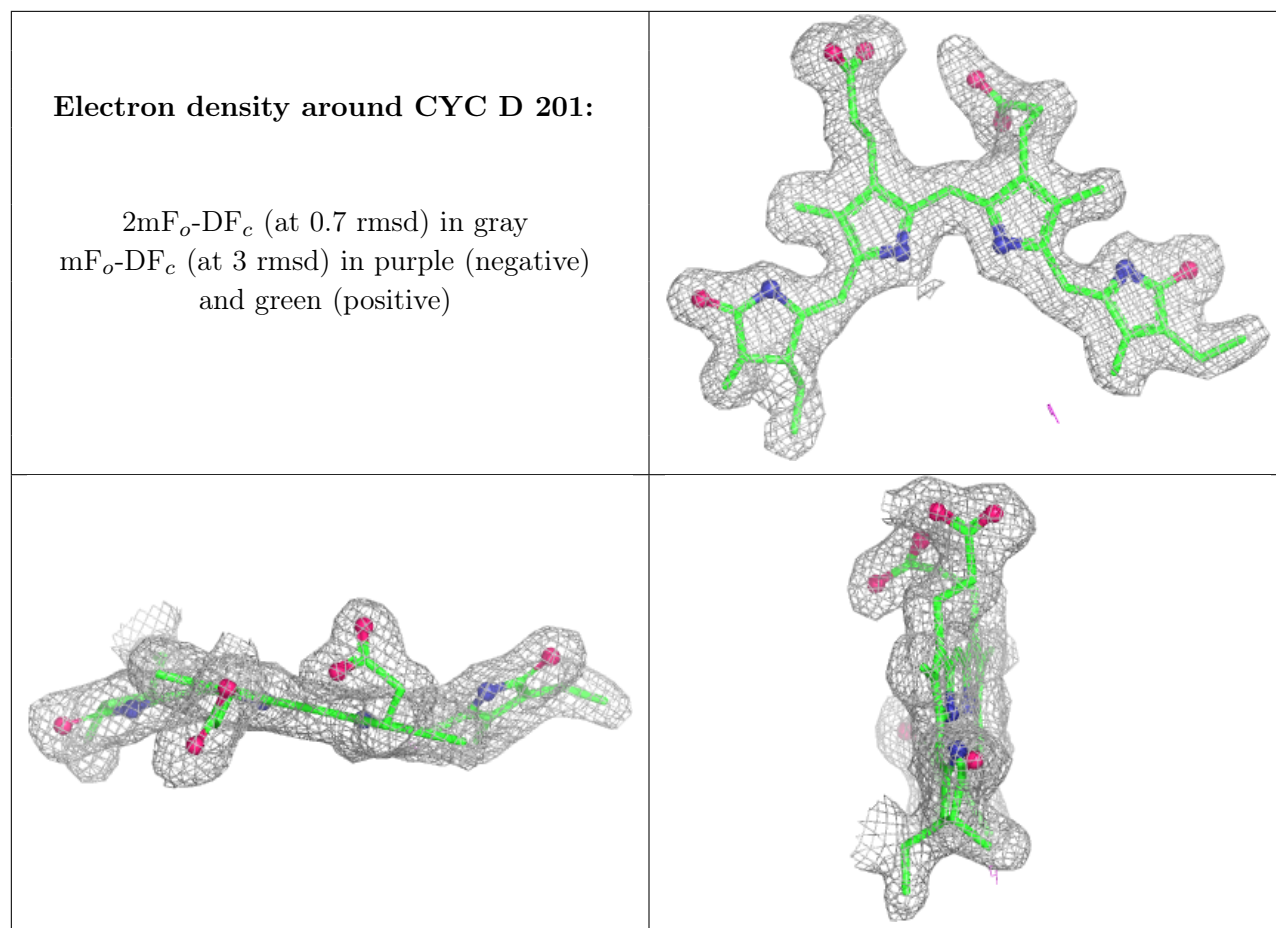


**Electron density around CYC H 201:**

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

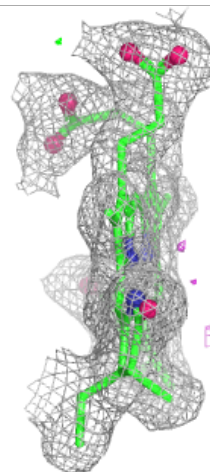
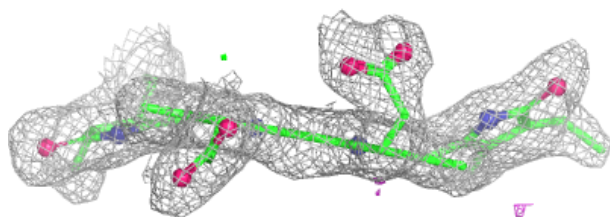
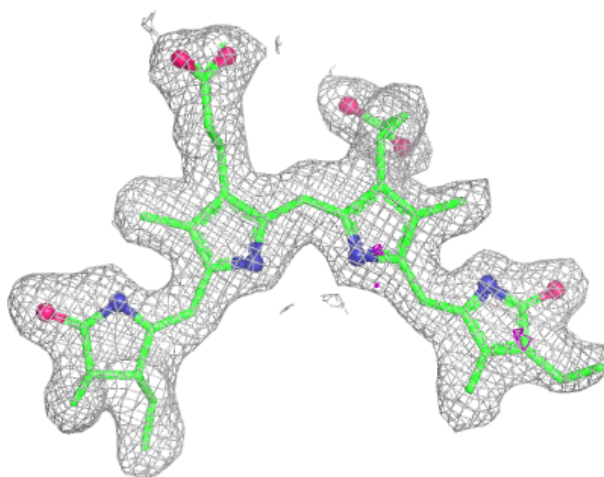






**Electron density around CYC B 201:**

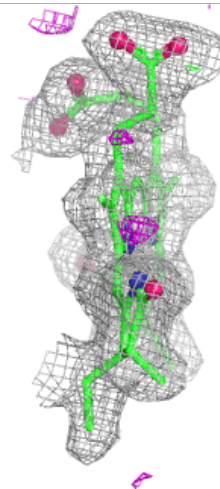
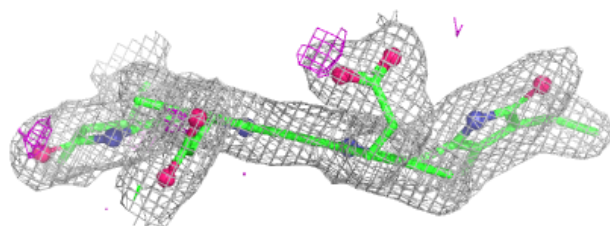
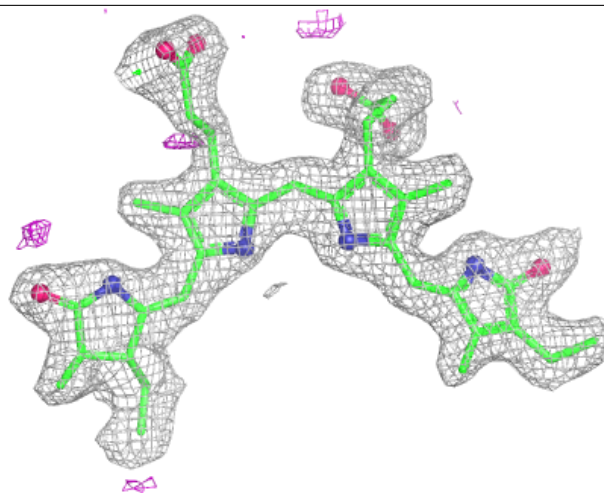
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





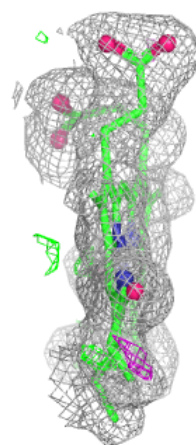
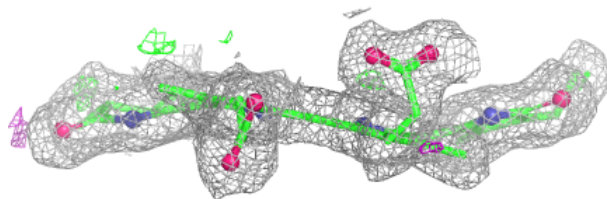
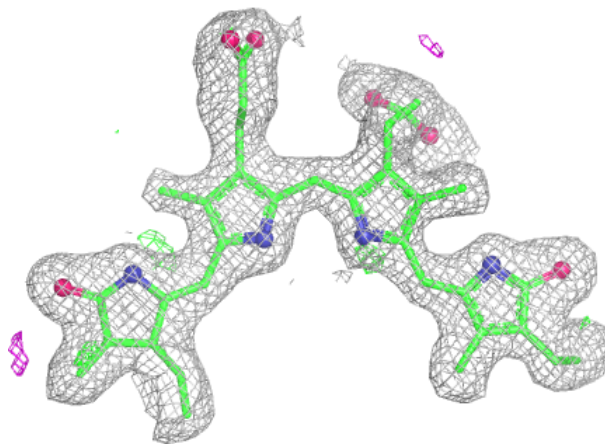
**Electron density around CYC F 201:**

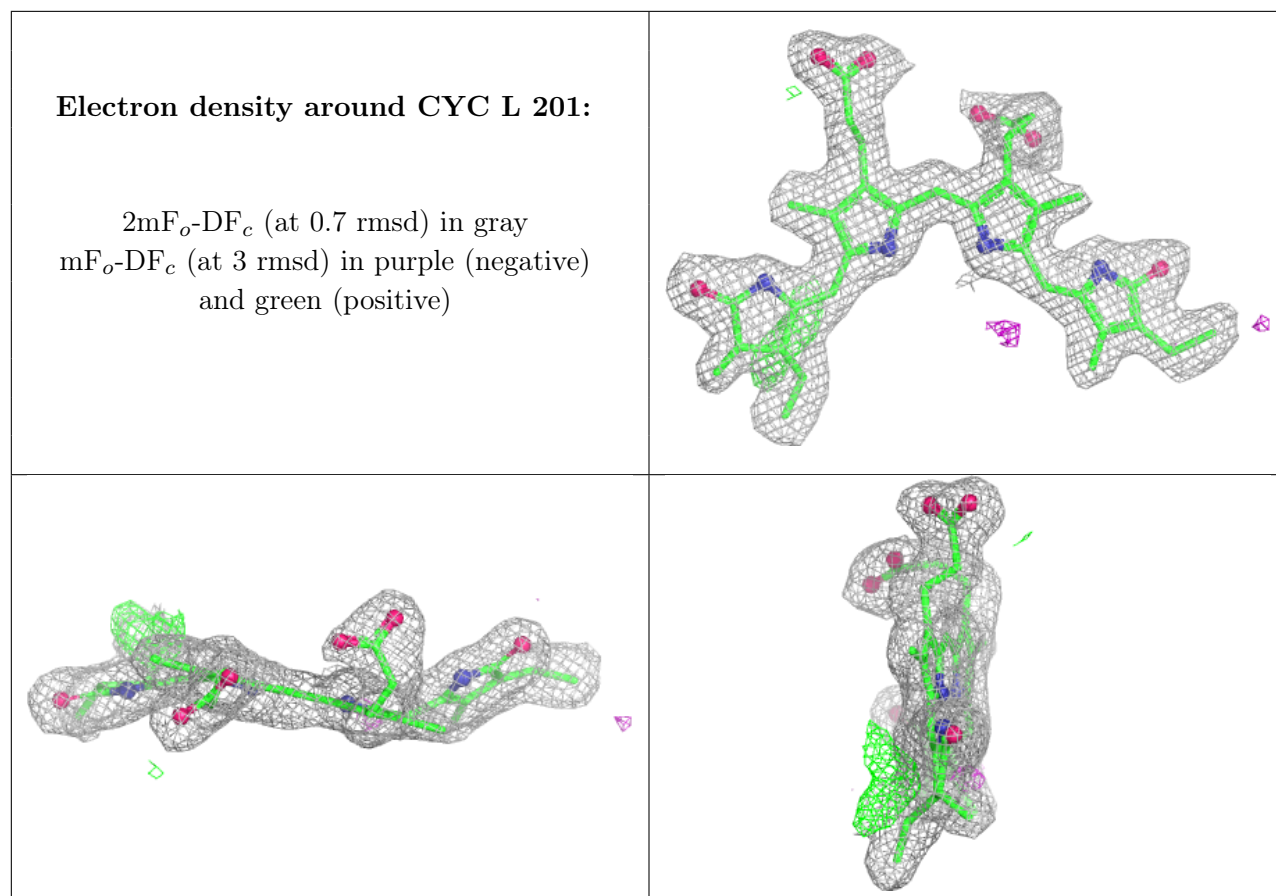
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CYC K 201:**

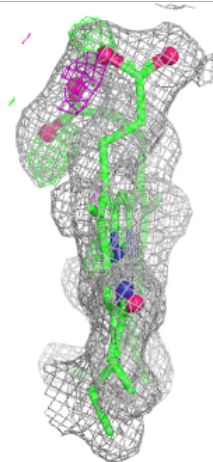
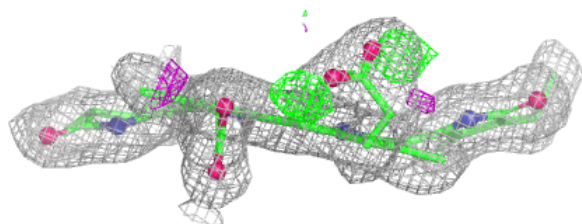
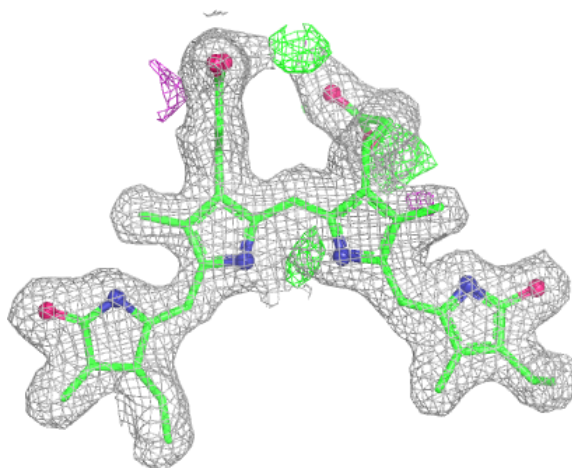
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





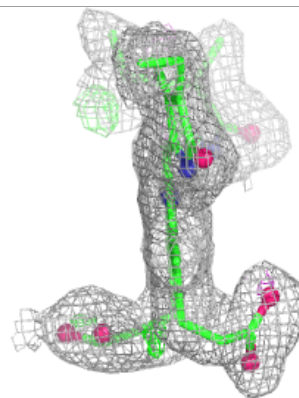
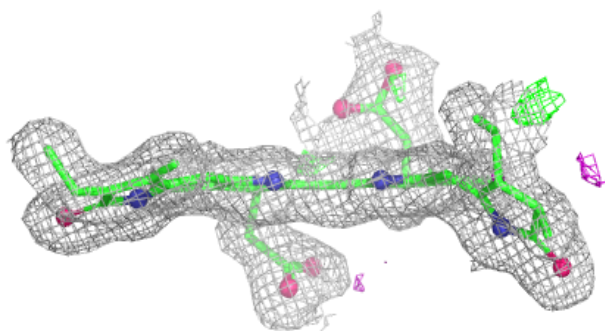
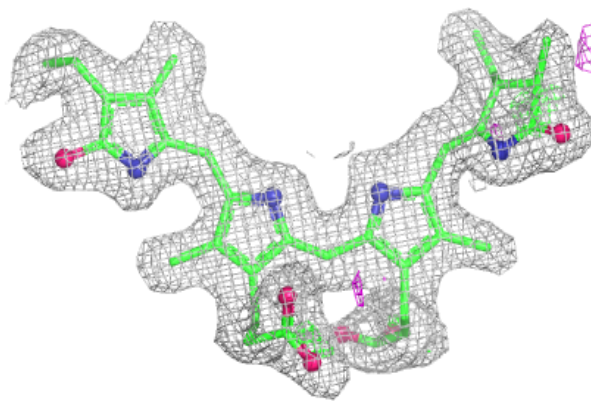
**Electron density around CYC U 201:**

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

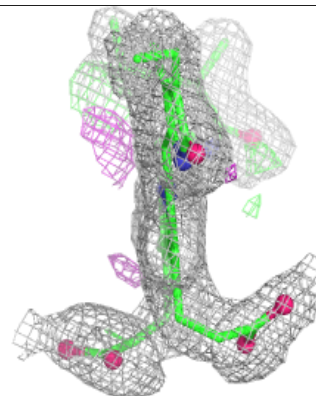
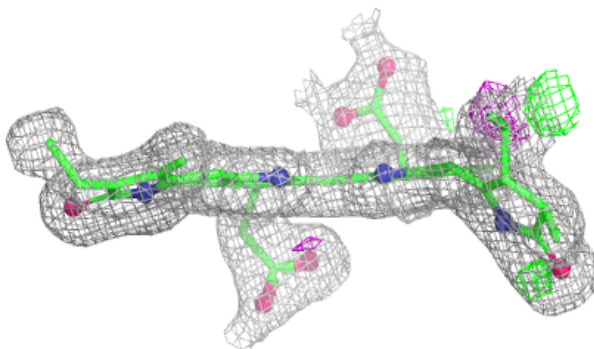
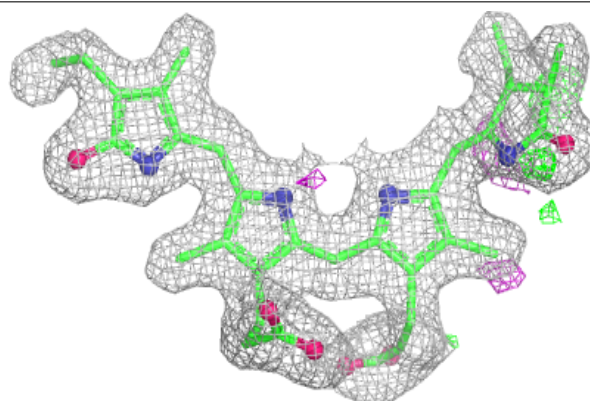


**Electron density around CYC L 202:**

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

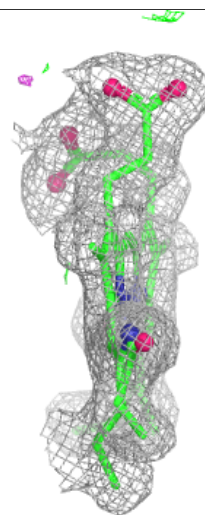
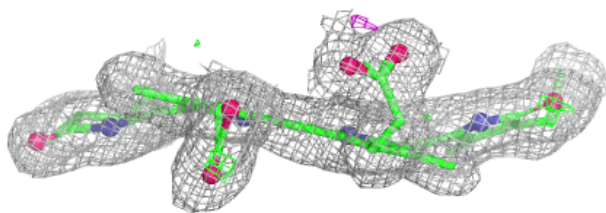
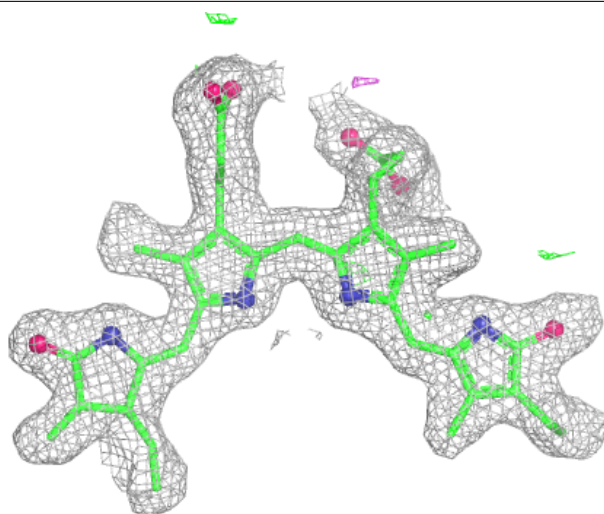
**Electron density around CYC B 202:**

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



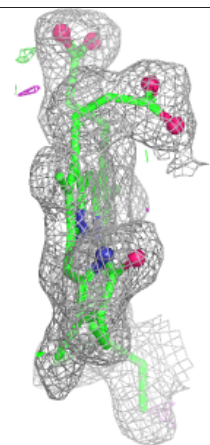
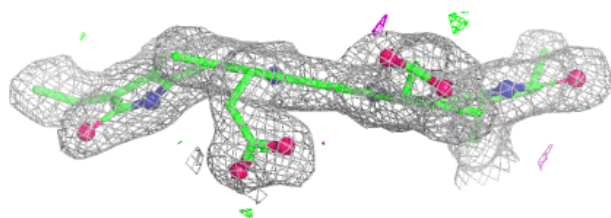
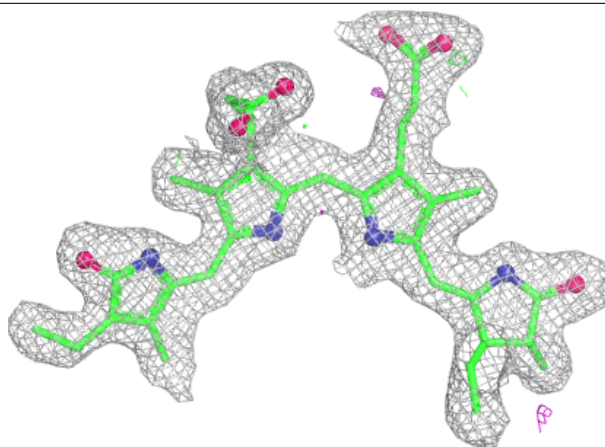
**Electron density around CYC I 201:**

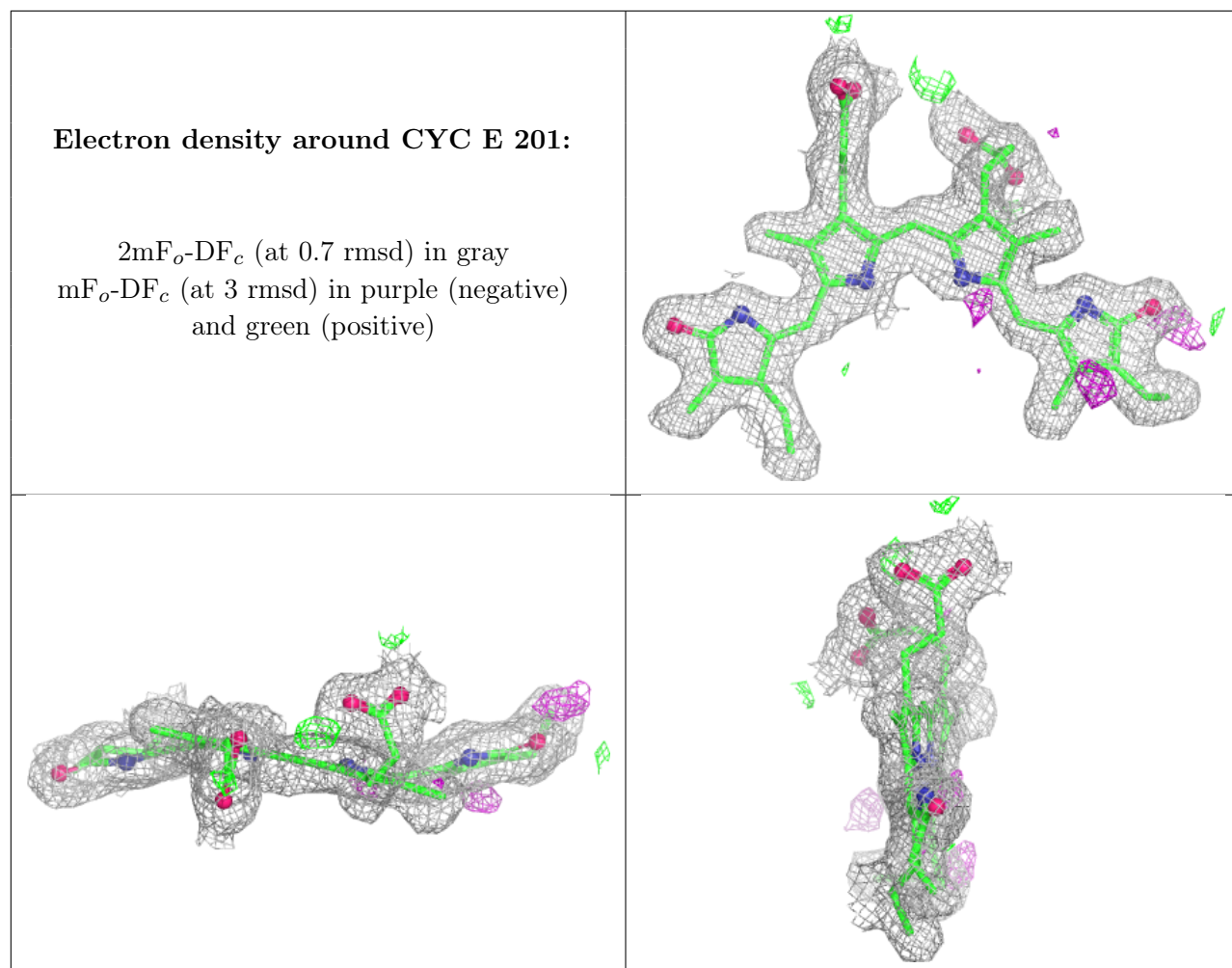
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CYC N 201:**

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

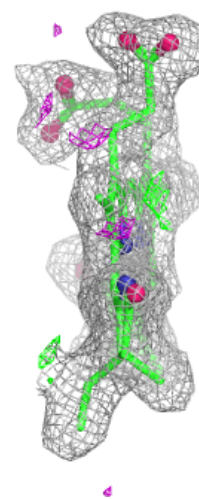
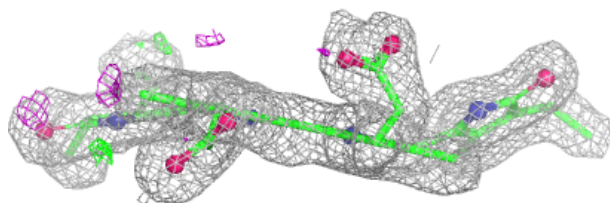
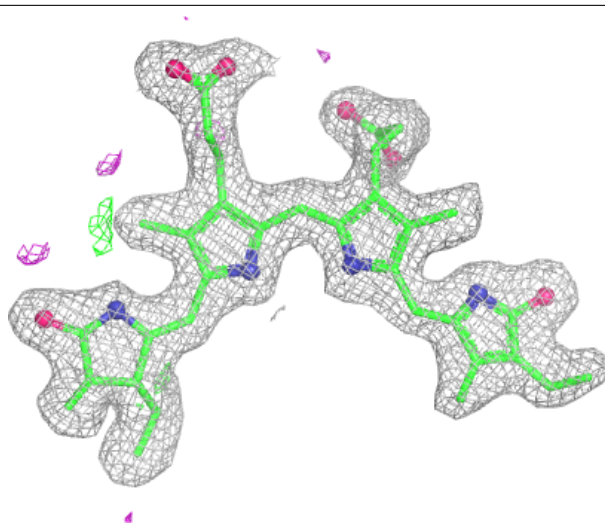






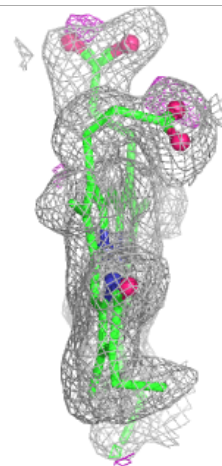
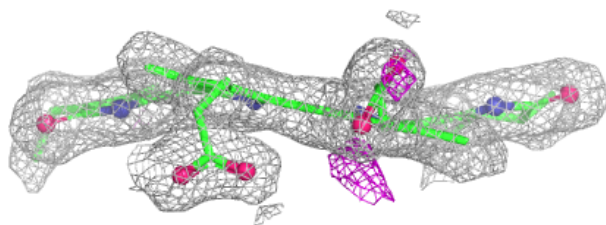
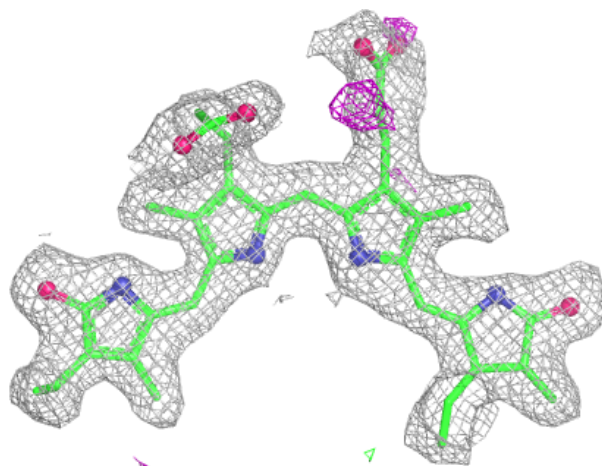
**Electron density around CYC V 201:**

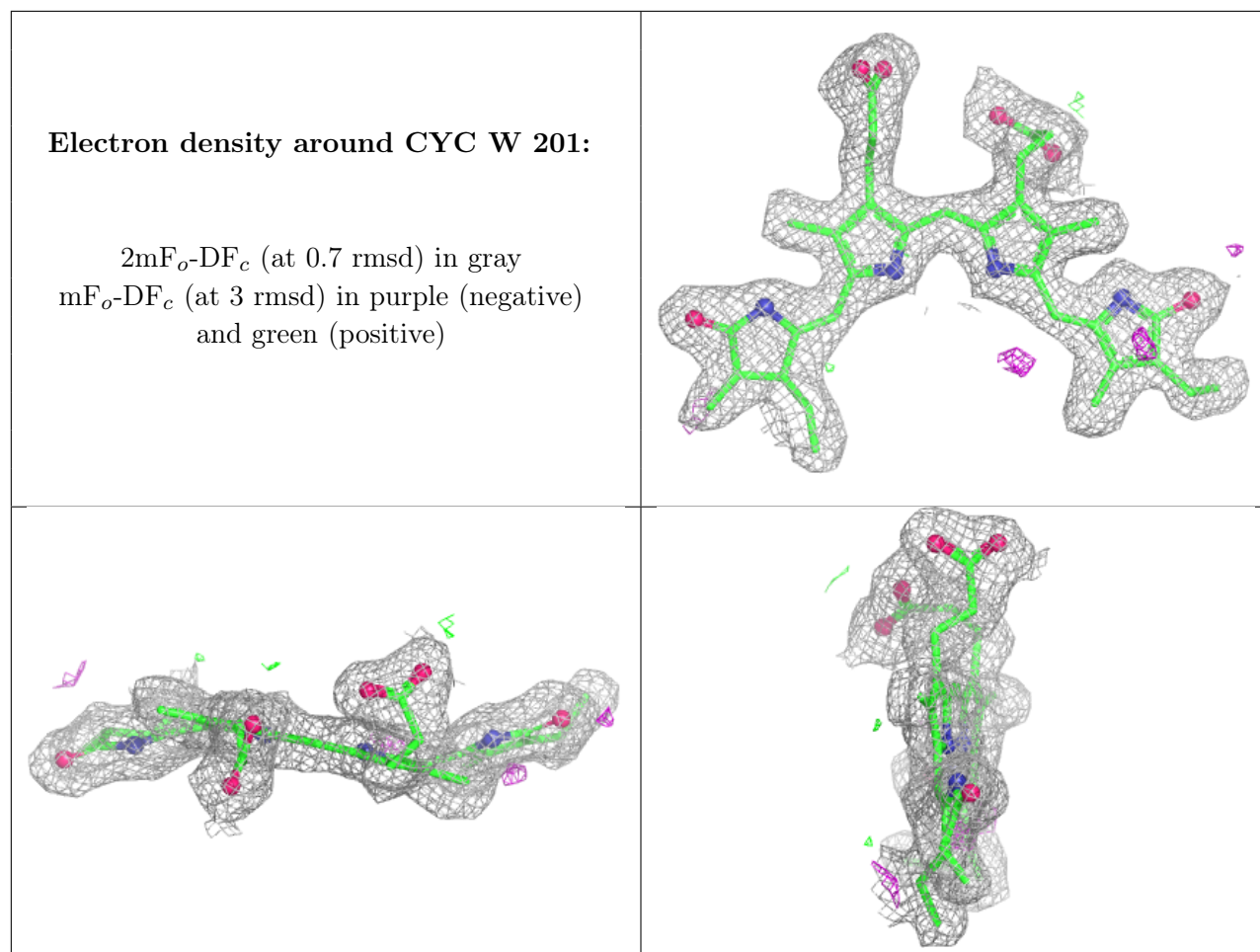
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

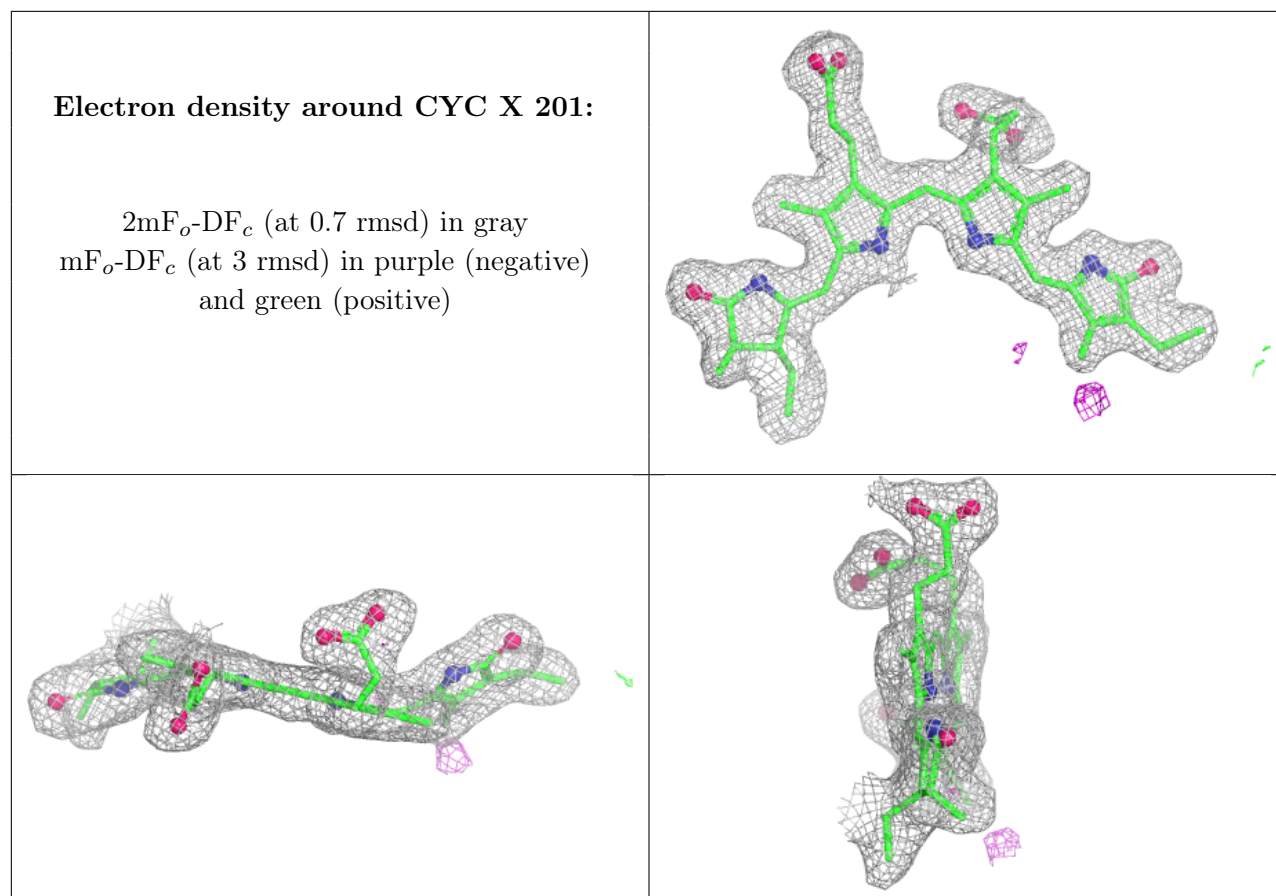


**Electron density around CYC O 201:**

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

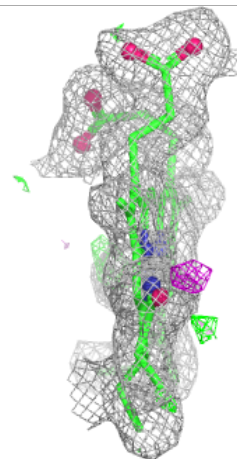
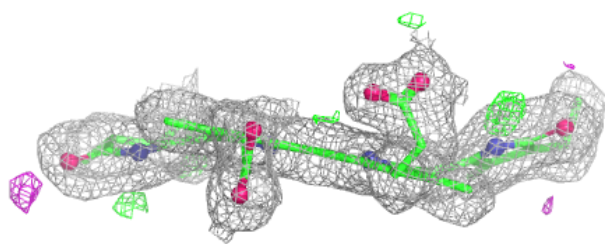
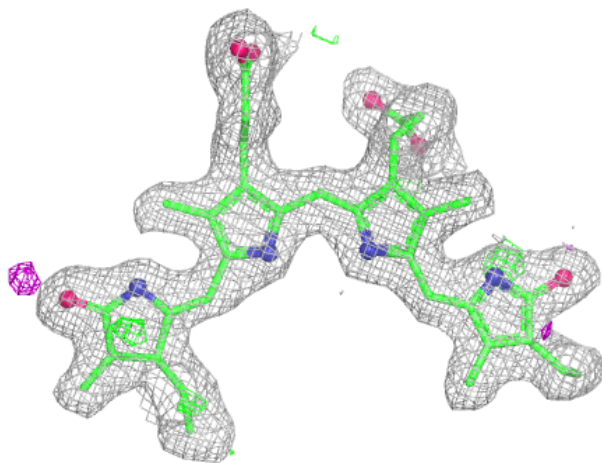






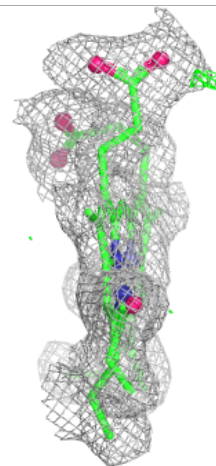
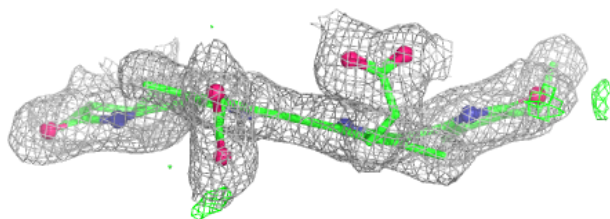
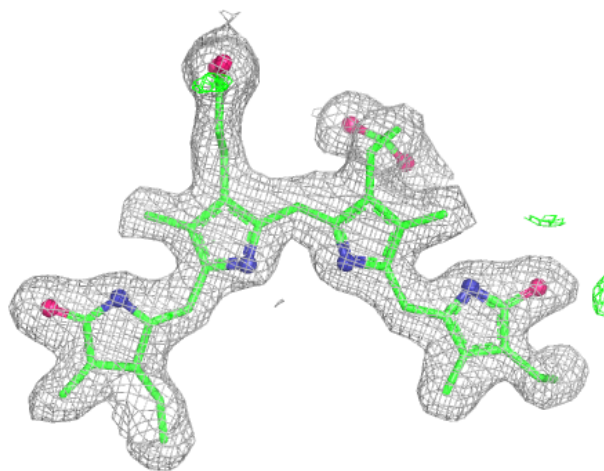
**Electron density around CYC S 201:**

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



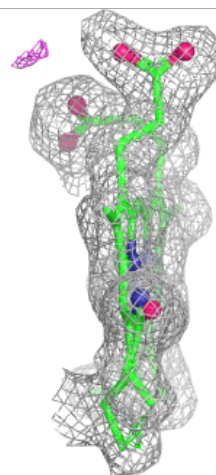
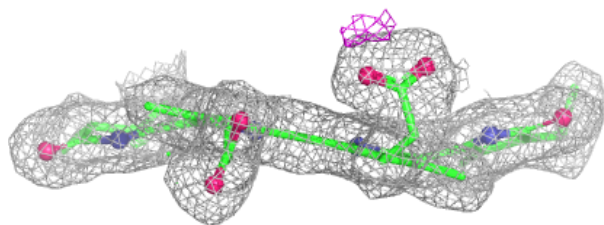
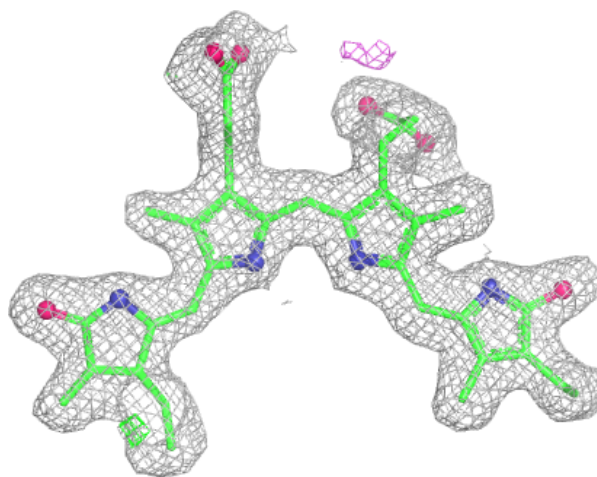
**Electron density around CYC G 201:**

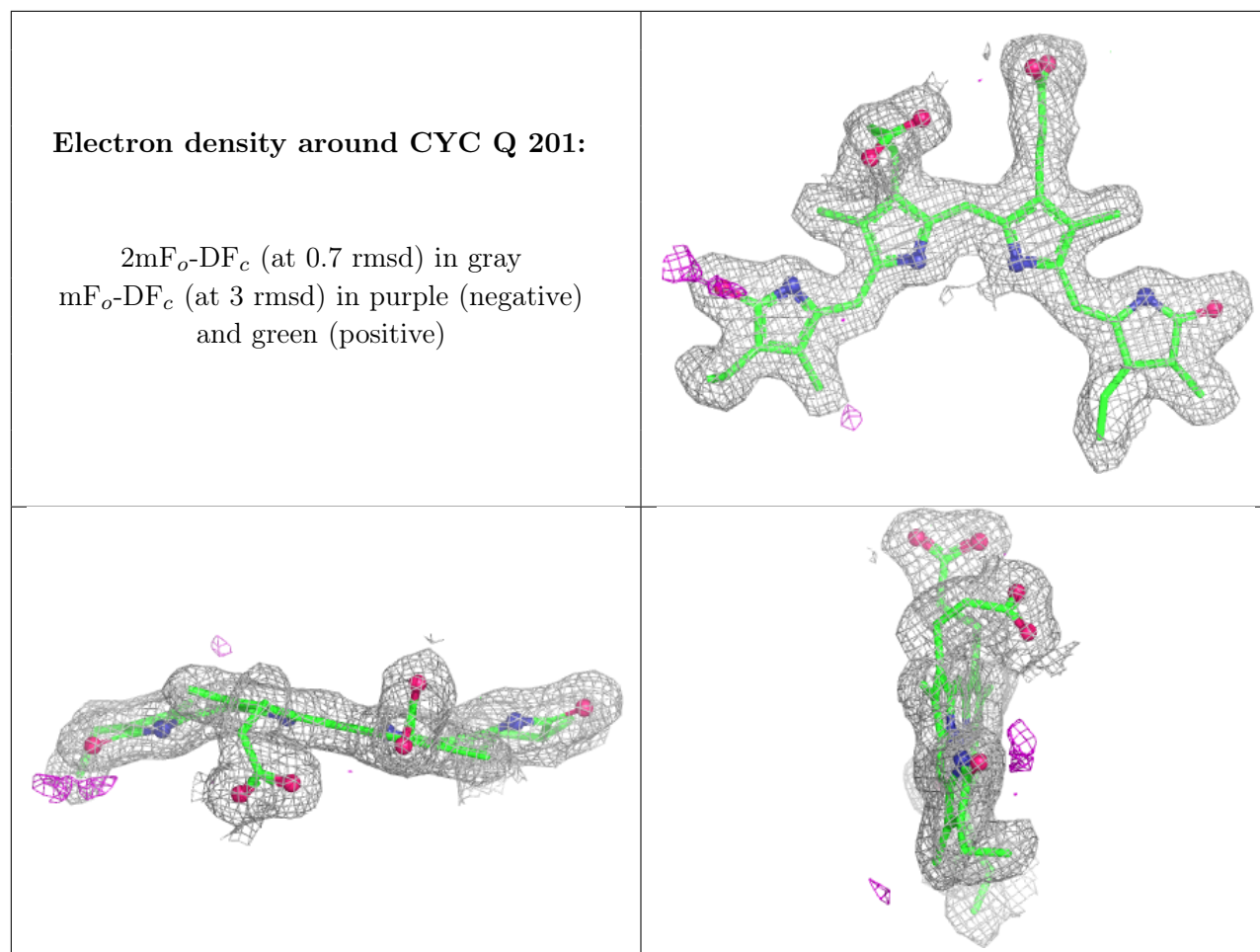
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CYC C 201:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.