



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:47 PM UTC

PDB ID : 8IMM / pdb_00008imm
EMDB ID : EMD-35569
Title : Rs2'I-Rs2'II, Rs1'I-Rs1'II, Rb'I-Rb'II cylinder in cyanobacterial phycobilisome from *Anthocerotibacter panamensis* (Cluster E)
Authors : Wang, C.H.; Yang, C.H.; Wu, H.Y.; Jiang, H.W.; Ho, M.C.; Ho, M.Y.
Deposited on : 2023-03-07
Resolution : 2.76 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

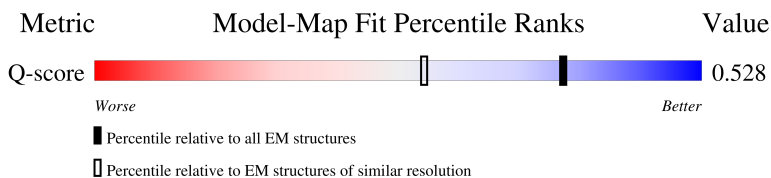
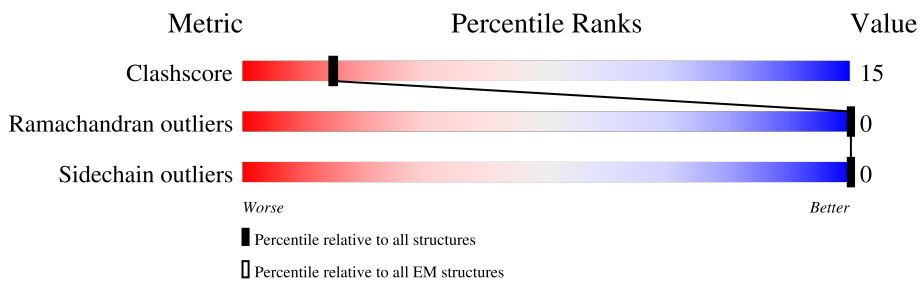
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.76 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.




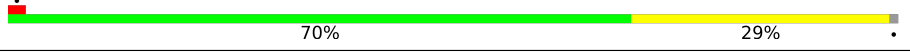

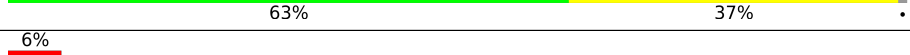
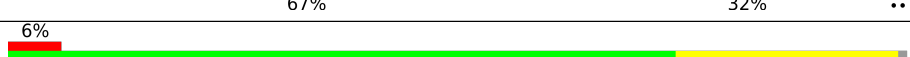
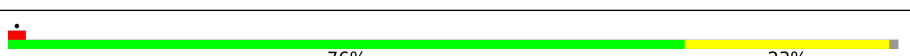












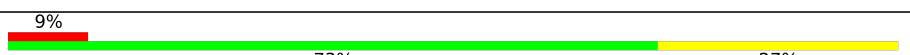
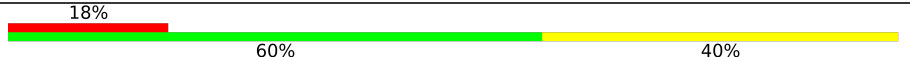





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10642 (2.26 - 3.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	3	531	<p>75% (green), 22% (yellow), 3% (grey), 0% (red)</p>
2	A	163	<p>68% (green), 31% (yellow), 1% (grey), 0% (red)</p>
2	B	163	<p>67% (green), 33% (yellow), 0% (grey), 7% (red)</p>
2	C	163	<p>67% (green), 33% (yellow), 0% (grey), 20% (red)</p>

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Mol	Chain	Length	Quality of chain
2	D	163	 74% 25%
2	E	163	 70% 29%
2	F	163	 74% 26%
2	N	163	 14% 63% 37%
2	O	163	 6% 67% 32%
2	P	163	 6% 75% 25%
2	Q	163	 76% 23%
2	R	163	 71% 29%
2	S	163	 77% 23%
2	a	163	 87% 56% 44%
2	b	163	 12% 67% 33%
2	c	163	 67% 57% 42%
2	d	163	 5% 74% 25%
2	e	163	 58% 64% 36%
2	f	163	 16% 67% 33%
3	G	172	 28% 71% 29%
3	H	172	 28% 62% 38%
3	I	172	 11% 62% 38%
3	J	172	 79% 21%
3	K	172	 73% 27%
3	L	172	 74% 26%
3	T	172	 9% 73% 27%
3	U	172	 18% 60% 40%
3	V	172	 5% 65% 35%
3	W	172	 82% 18%

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Mol	Chain	Length	Quality of chain
3	X	172	78% 22%
3	Y	172	78% 22%
3	g	172	87% 65% 35%
3	h	172	77% 63% 37%
3	i	172	70% 67% 33%
3	j	172	74% 26%
3	k	172	84% 16%
3	l	172	77% 23%
4	M	78	50% 51% 26% 23%
4	Z	78	29% 47% 29% 23%
4	m	78	71% 54% 35% 12%
5	4	252	23% 77% 22%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 55862 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 CpcJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	3	515	4129	2614	717	790	8	0	0

- Molecule 2 is a protein called CpcA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	162	1254	799	216	238	1	0	0
2	B	163	1262	804	217	239	2	0	0
2	C	162	1254	799	216	238	1	0	0
2	D	162	1254	799	216	238	1	0	0
2	E	162	1254	799	216	238	1	0	0
2	F	162	1254	799	216	238	1	0	0
2	N	162	1254	799	216	238	1	0	0
2	O	162	1254	799	216	238	1	0	0
2	P	162	1254	799	216	238	1	0	0
2	Q	162	1254	799	216	238	1	0	0
2	R	162	1254	799	216	238	1	0	0
2	S	162	1254	799	216	238	1	0	0
2	a	162	1254	799	216	238	1	0	0
2	b	163	1262	804	217	239	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	162	Total	C	N	O	S	0	0
			1254	799	216	238	1		
2	d	162	Total	C	N	O	S	0	0
			1254	799	216	238	1		
2	e	162	Total	C	N	O	S	0	0
			1254	799	216	238	1		
2	f	162	Total	C	N	O	S	0	0
			1254	799	216	238	1		

- Molecule 3 is a protein called CpcB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	H	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	I	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	J	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	K	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	L	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	T	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	U	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	V	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	W	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	X	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	Y	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	g	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	h	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	i	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	j	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	k	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		
3	l	172	Total	C	N	O	S	0	0
			1293	807	226	252	8		

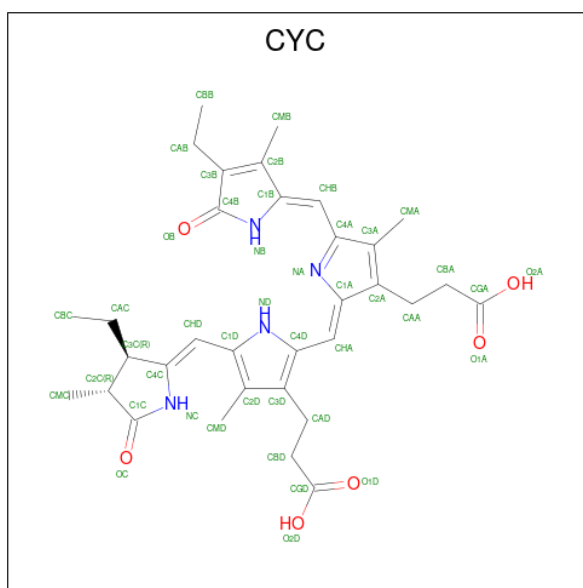
- Molecule 4 is a protein called CpcD.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	60	Total	C	N	O	S	0	0
			483	306	90	86	1		
4	Z	60	Total	C	N	O	S	0	0
			483	306	90	86	1		
4	m	69	Total	C	N	O	S	0	0
			546	345	101	99	1		

- Molecule 5 is a protein called CpcG.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	250	Total	C	N	O	S	0	0
			2037	1312	349	373	3		

- Molecule 6 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: $C_{33}H_{40}N_4O_6$) (labeled as "Ligand of Interest" by depositor).



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

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	R	1	Total 43	C 33	N 4	O 6	0
6	S	1	Total 43	C 33	N 4	O 6	0
6	T	1	Total 43	C 33	N 4	O 6	0
6	T	1	Total 43	C 33	N 4	O 6	0
6	U	1	Total 43	C 33	N 4	O 6	0
6	U	1	Total 43	C 33	N 4	O 6	0
6	V	1	Total 43	C 33	N 4	O 6	0
6	V	1	Total 43	C 33	N 4	O 6	0
6	W	1	Total 43	C 33	N 4	O 6	0
6	W	1	Total 43	C 33	N 4	O 6	0
6	X	1	Total 43	C 33	N 4	O 6	0
6	X	1	Total 43	C 33	N 4	O 6	0
6	Y	1	Total 43	C 33	N 4	O 6	0
6	Y	1	Total 43	C 33	N 4	O 6	0
6	4	1	Total 43	C 33	N 4	O 6	0
6	a	1	Total 43	C 33	N 4	O 6	0
6	b	1	Total 43	C 33	N 4	O 6	0
6	c	1	Total 43	C 33	N 4	O 6	0
6	d	1	Total 43	C 33	N 4	O 6	0
6	e	1	Total 43	C 33	N 4	O 6	0
6	f	1	Total 43	C 33	N 4	O 6	0

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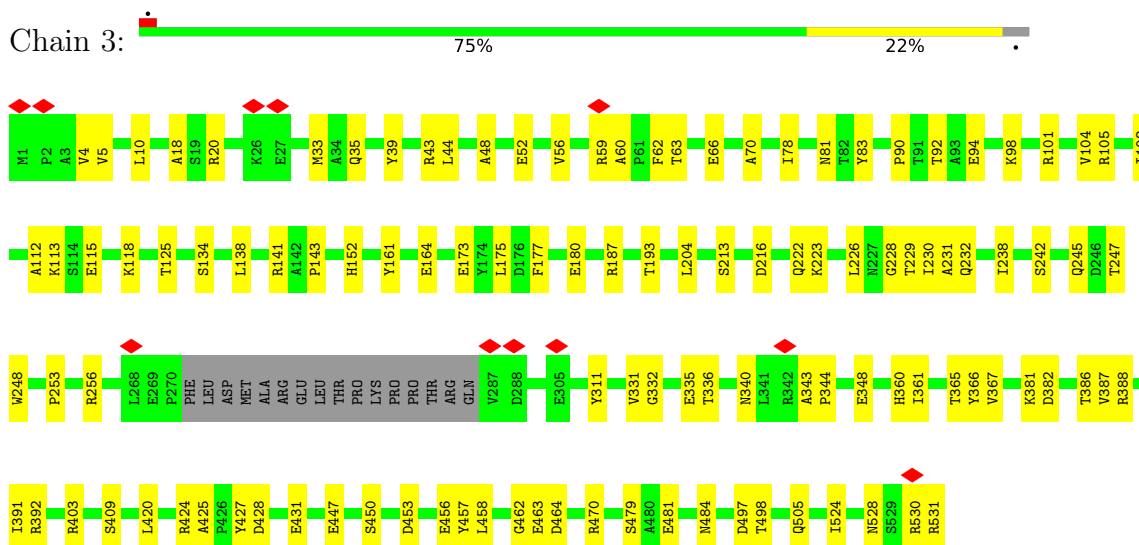
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	g	1	Total 43	33	4	6	0
6	g	1	Total 43	33	4	6	0
6	h	1	Total 43	33	4	6	0
6	h	1	Total 43	33	4	6	0
6	i	1	Total 43	33	4	6	0
6	j	1	Total 43	33	4	6	0
6	j	1	Total 43	33	4	6	0
6	k	1	Total 43	33	4	6	0
6	k	1	Total 43	33	4	6	0
6	l	1	Total 43	33	4	6	0
6	l	1	Total 43	33	4	6	0

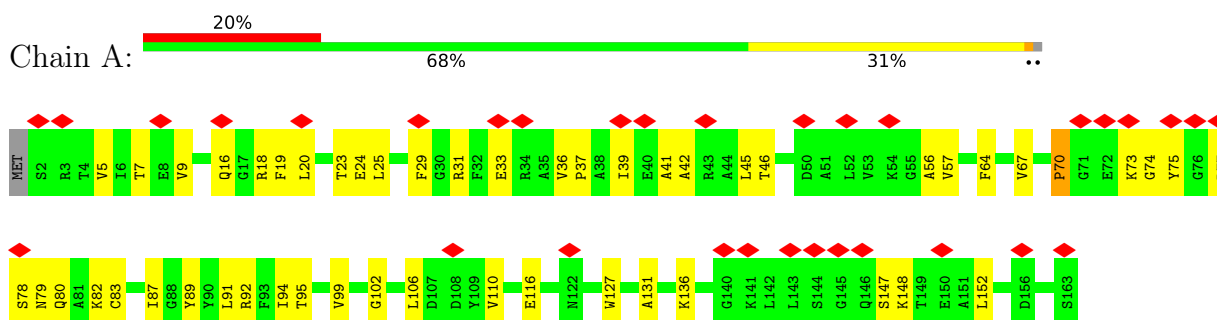
3 Residue-property plots [i](#)

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.

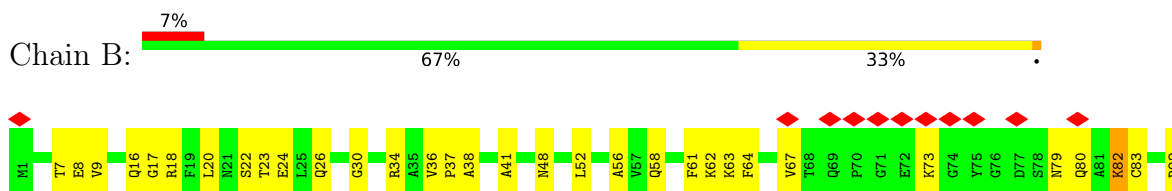
- Molecule 1: CpcJ



- Molecule 2: CpcA

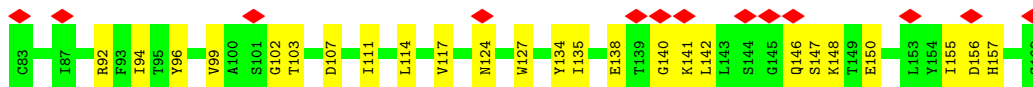
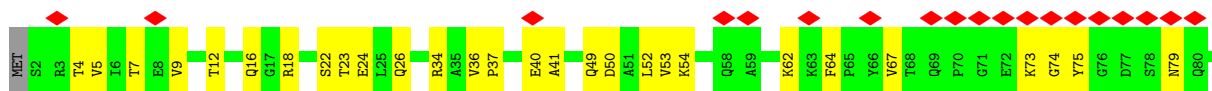


- Molecule 2: CpcA

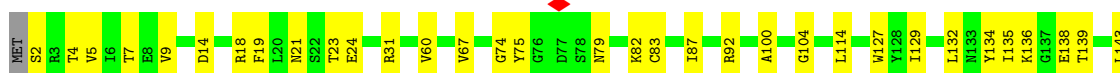




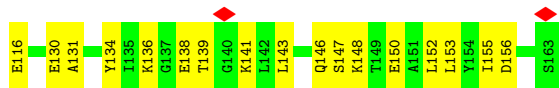
• Molecule 2: CpcA



• Molecule 2: CpcA



• Molecule 2: CpcA

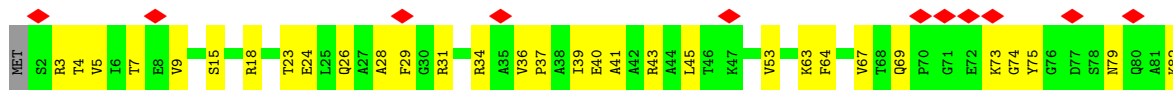


• Molecule 2: CpcA

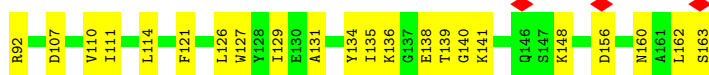
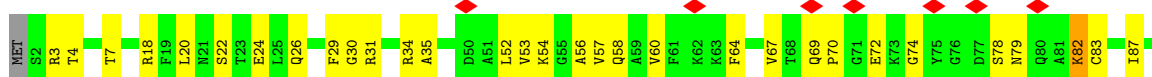


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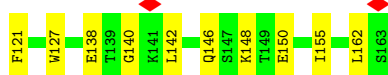
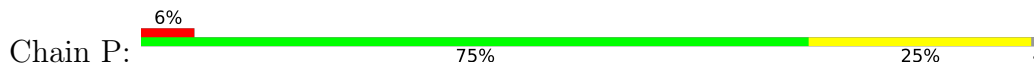




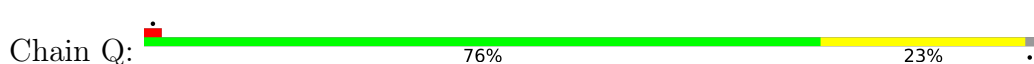
• Molecule 2: CpcA



• Molecule 2: CpcA

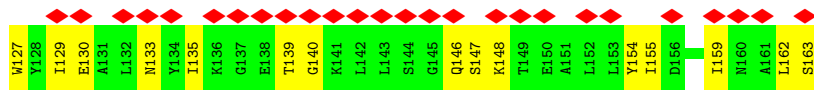


• Molecule 2: CpcA

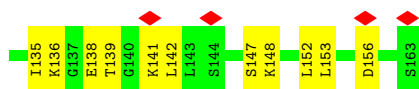
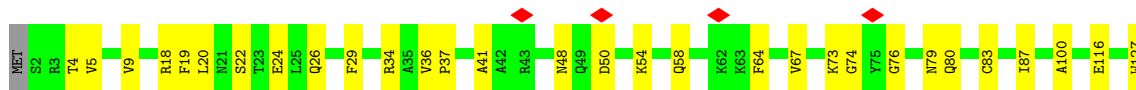
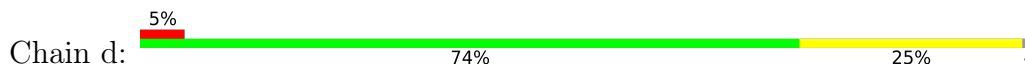


• Molecule 2: CpcA

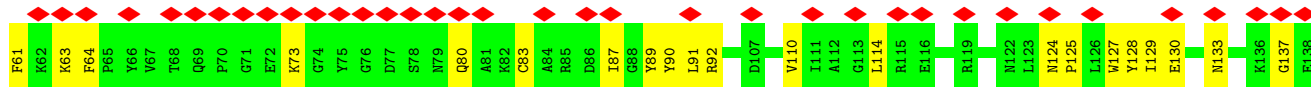
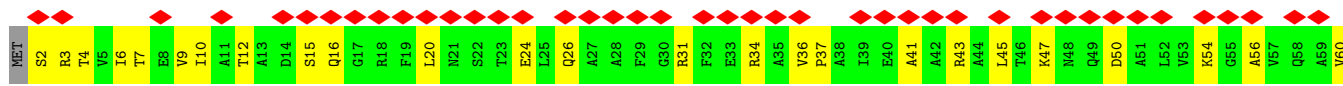




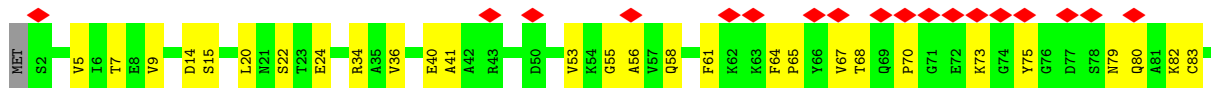
• Molecule 2: CpcA



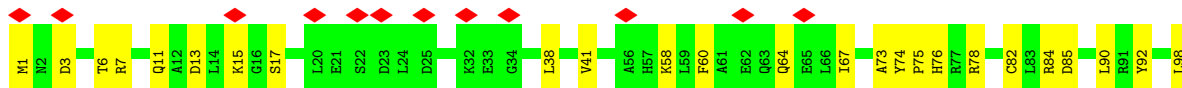
• Molecule 2: CpcA

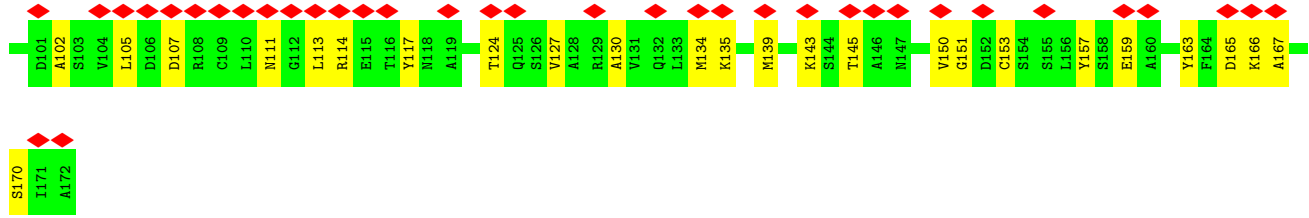


• Molecule 2: CpcA

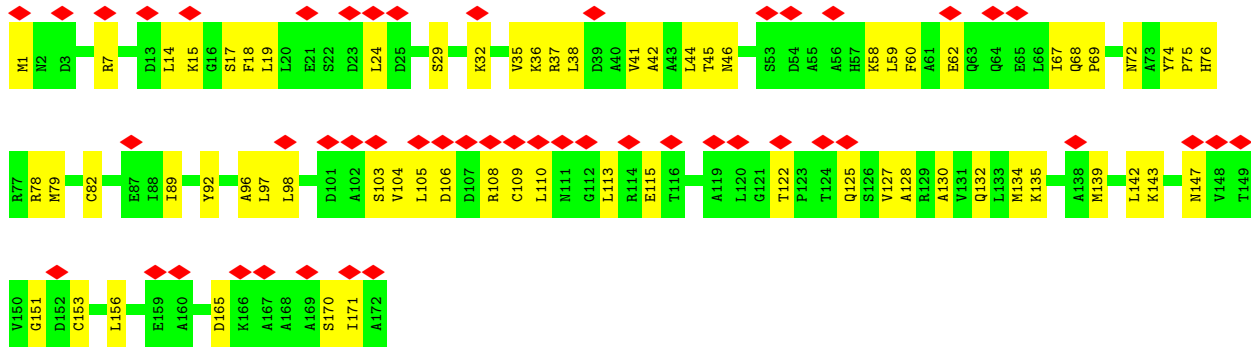


• Molecule 3: CpcB

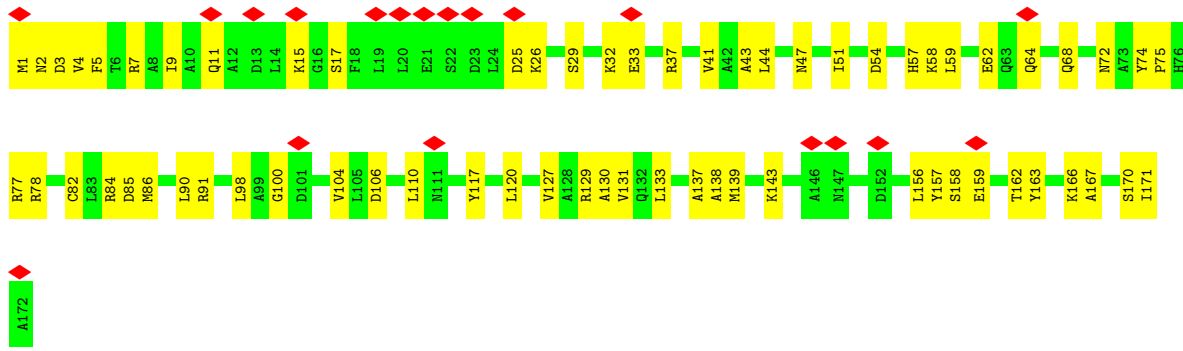




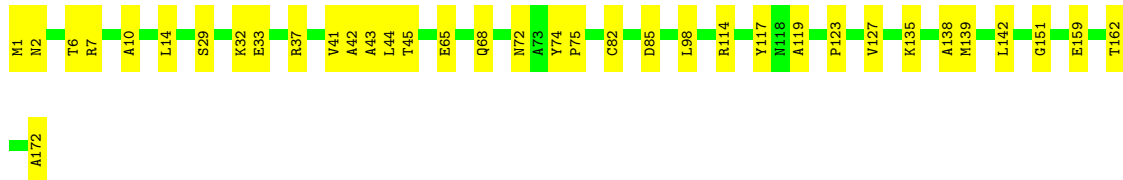
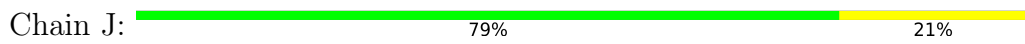
• Molecule 3: CpcB



• Molecule 3: CpcB

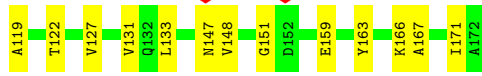


• Molecule 3: CpcB

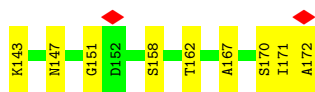
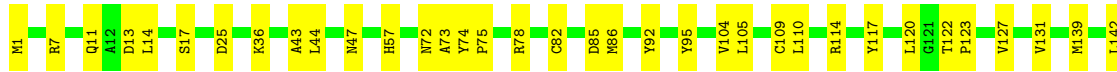


• Molecule 3: CpcB

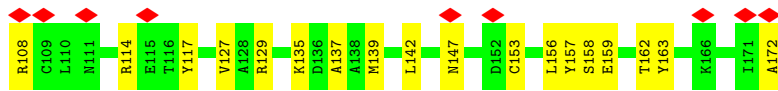
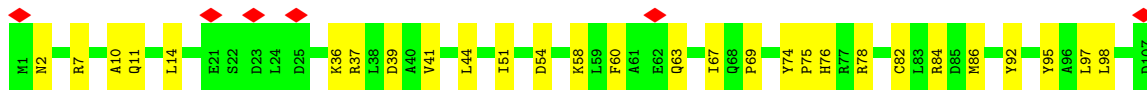
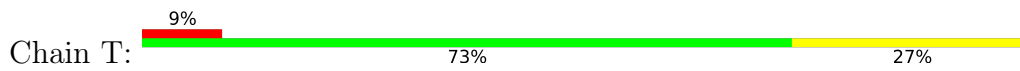




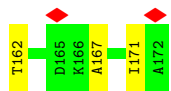
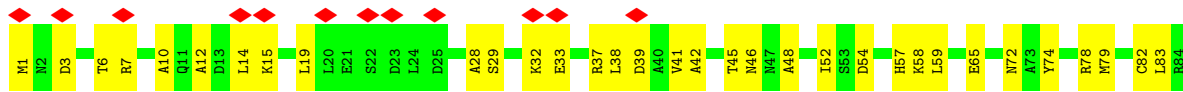
• Molecule 3: CpcB



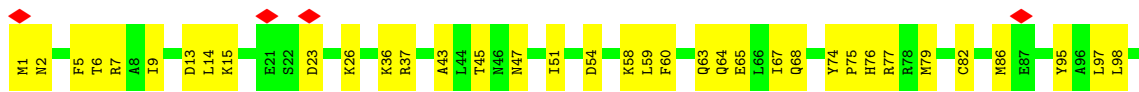
• Molecule 3: CpcB



• Molecule 3: CpcB

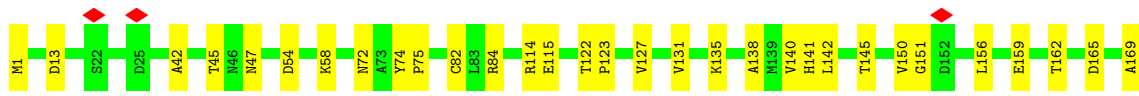
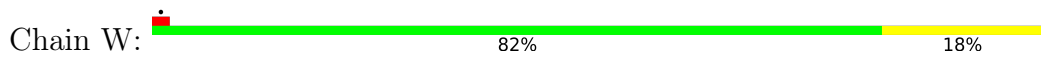


• Molecule 3: CpcB

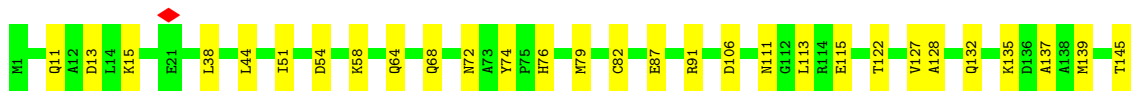
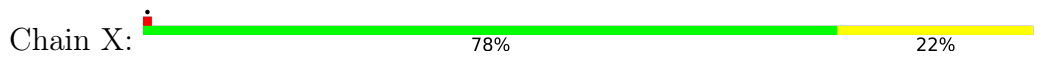




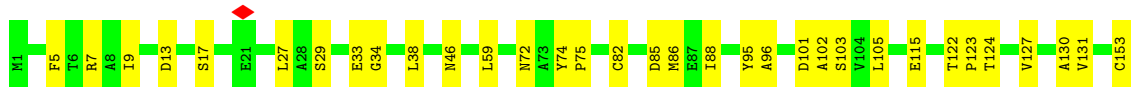
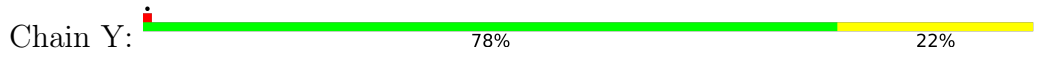
• Molecule 3: CpcB



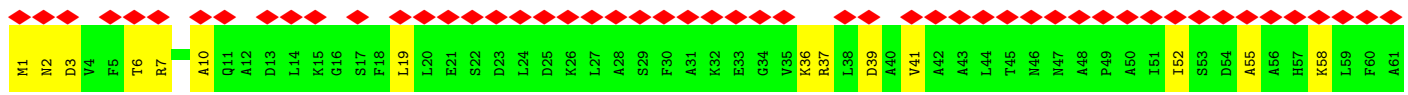
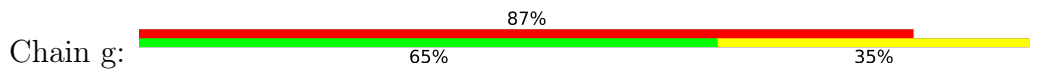
• Molecule 3: CpcB



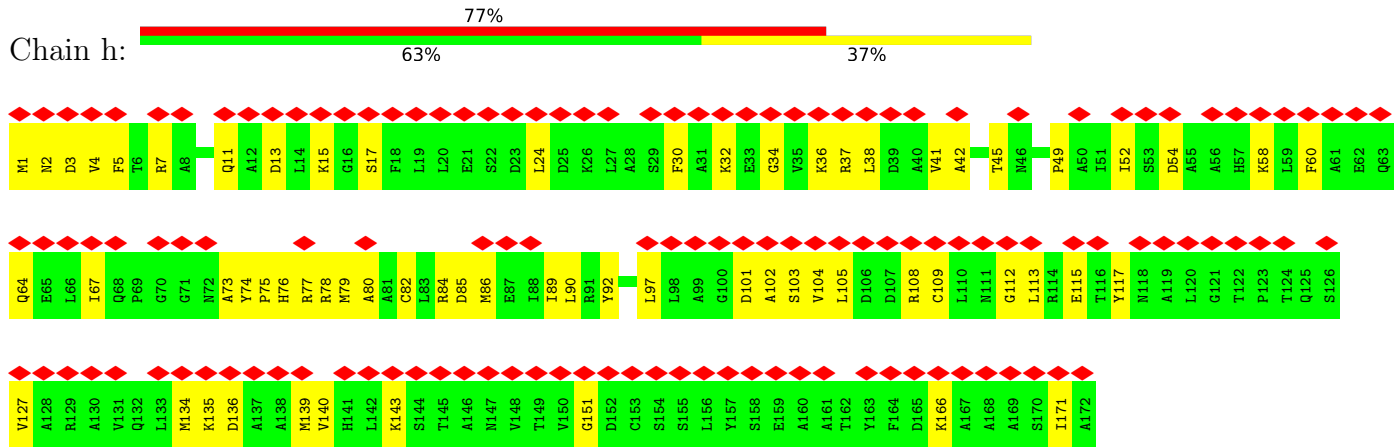
• Molecule 3: CpcB



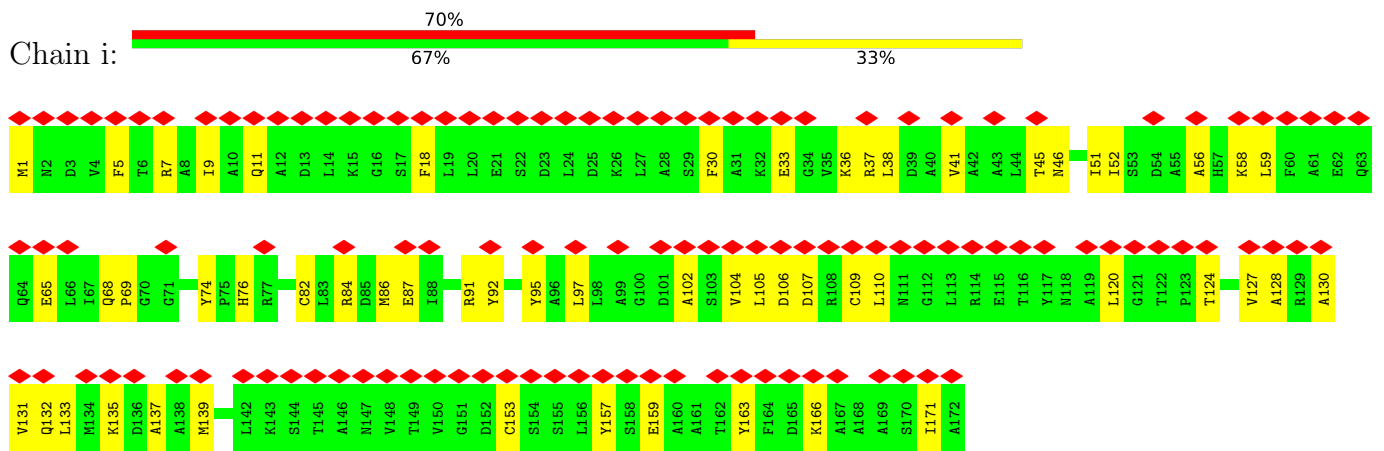
• Molecule 3: CpcB



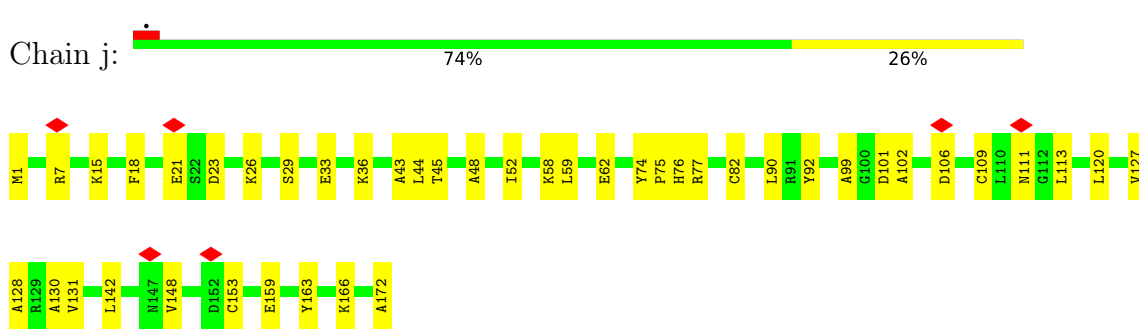
• Molecule 3: CpcB



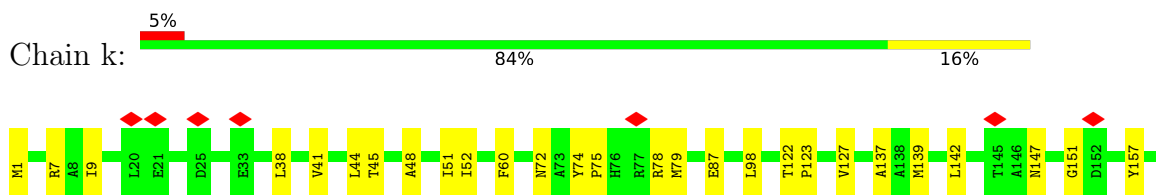
• Molecule 3: CpcB



• Molecule 3: CpcB

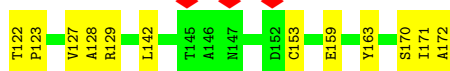
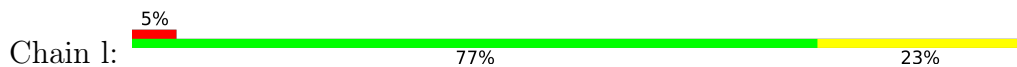


• Molecule 3: CpcB

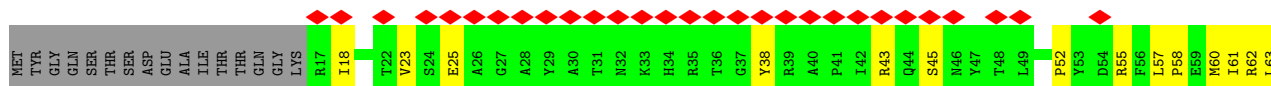




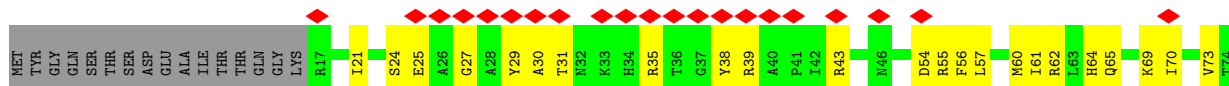
• Molecule 3: CpcB



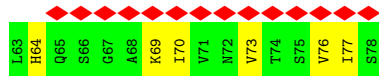
• Molecule 4: CpcD



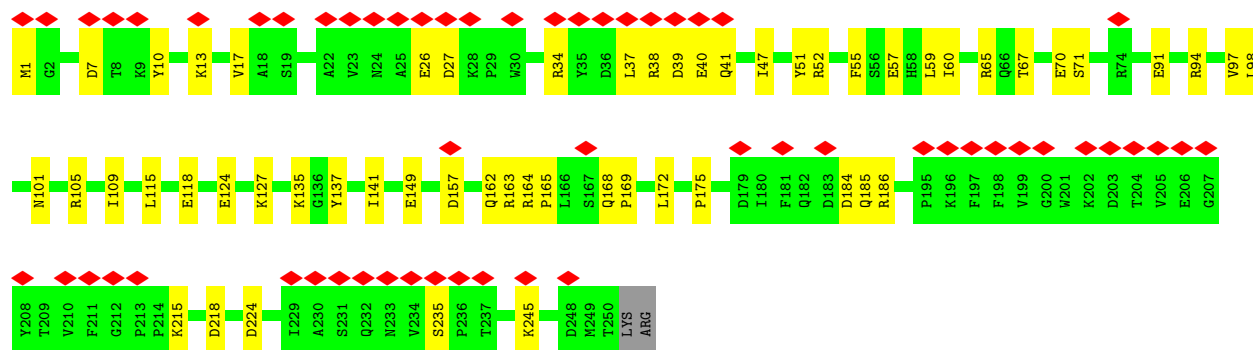
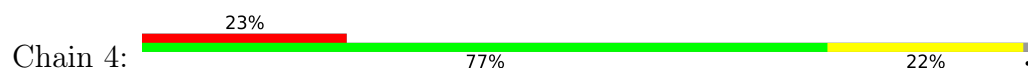
• Molecule 4: CpcD



• Molecule 4: CpcD



• Molecule 5: CpcG



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1109579	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	7.576	Depositor
Minimum map value	-0.226	Depositor
Average map value	0.065	Depositor
Map value standard deviation	0.123	Depositor
Recommended contour level	0.9	Depositor
Map size (\AA)	721.48, 721.48, 721.48	wwPDB
Map dimensions	680, 680, 680	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.061, 1.061, 1.061	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	3	0.49	0/4224	0.50	0/5713
2	A	0.29	0/1277	0.53	2/1729 (0.1%)
2	B	0.37	0/1285	0.49	1/1739 (0.1%)
2	C	0.27	0/1277	0.46	0/1729
2	D	0.40	0/1277	0.43	0/1729
2	E	0.32	0/1277	0.42	0/1729
2	F	0.41	0/1277	0.41	0/1729
2	N	0.26	0/1277	0.44	0/1729
2	O	0.37	0/1277	0.52	1/1729 (0.1%)
2	P	0.31	0/1277	0.45	0/1729
2	Q	0.43	0/1277	0.46	0/1729
2	R	0.33	0/1277	0.44	0/1729
2	S	0.41	0/1277	0.48	0/1729
2	a	0.24	0/1277	0.49	0/1729
2	b	0.33	0/1285	0.46	0/1739
2	c	0.22	0/1277	0.46	0/1729
2	d	0.35	0/1277	0.40	0/1729
2	e	0.25	0/1277	0.50	0/1729
2	f	0.32	0/1277	0.44	0/1729
3	G	0.22	0/1310	0.36	0/1772
3	H	0.23	0/1310	0.49	0/1772
3	I	0.30	0/1310	0.44	0/1772
3	J	0.42	0/1310	0.47	0/1772
3	K	0.39	0/1310	0.44	0/1772
3	L	0.46	0/1310	0.43	0/1772
3	T	0.26	0/1310	0.43	0/1772
3	U	0.26	0/1310	0.42	0/1772
3	V	0.32	0/1310	0.45	0/1772
3	W	0.41	0/1310	0.45	0/1772
3	X	0.43	0/1310	0.48	0/1772
3	Y	0.43	0/1310	0.41	0/1772
3	g	0.18	0/1310	0.41	0/1772

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	h	0.19	0/1310	0.43	0/1772
3	i	0.20	0/1310	0.42	0/1772
3	j	0.36	0/1310	0.44	0/1772
3	k	0.38	0/1310	0.42	0/1772
3	l	0.35	0/1310	0.41	0/1772
4	M	0.19	0/493	0.40	0/668
4	Z	0.25	0/493	0.58	1/668 (0.1%)
4	m	0.19	0/556	0.49	0/753
5	4	0.36	0/2091	0.48	0/2836
All	All	0.35	0/54439	0.45	5/73676 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	4	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	70	PRO	CA-N-CD	-9.88	98.17	112.00
2	B	82	LYS	CD-CE-NZ	-6.50	91.11	111.90
2	O	82	LYS	CB-CG-CD	6.18	125.52	111.30
2	A	70	PRO	N-CD-CG	-6.15	93.97	103.20
4	Z	39	ARG	CA-CB-CG	5.84	125.78	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	4	224	ASP	Peptide

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	3	4129	0	3997	99	0
2	A	1254	0	1253	45	0
2	B	1262	0	1265	46	0
2	C	1254	0	1255	42	0
2	D	1254	0	1255	38	0
2	E	1254	0	1255	39	0
2	F	1254	0	1255	33	0
2	N	1254	0	1255	58	0
2	O	1254	0	1255	51	0
2	P	1254	0	1255	35	0
2	Q	1254	0	1255	35	0
2	R	1254	0	1255	45	0
2	S	1254	0	1255	39	0
2	a	1254	0	1255	71	0
2	b	1262	0	1267	48	0
2	c	1254	0	1255	68	0
2	d	1254	0	1255	33	0
2	e	1254	0	1255	48	0
2	f	1254	0	1255	48	0
3	G	1293	0	1297	45	0
3	H	1293	0	1296	68	0
3	I	1293	0	1297	56	0
3	J	1293	0	1297	28	0
3	K	1293	0	1297	44	0
3	L	1293	0	1296	35	0
3	T	1293	0	1297	42	0
3	U	1293	0	1297	56	0
3	V	1293	0	1296	52	0
3	W	1293	0	1297	25	0
3	X	1293	0	1297	33	0
3	Y	1293	0	1297	32	0
3	g	1293	0	1297	63	0
3	h	1293	0	1297	60	0
3	i	1293	0	1297	53	0
3	j	1293	0	1297	41	0
3	k	1293	0	1297	23	0
3	l	1293	0	1297	33	0
4	M	483	0	493	18	0
4	Z	483	0	493	25	0
4	m	546	0	563	26	0
5	4	2037	0	2020	46	0
6	3	43	0	37	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	4	43	0	38	9	0
6	A	86	0	74	11	0
6	B	86	0	71	11	0
6	C	43	0	38	4	0
6	D	43	0	38	8	0
6	E	43	0	37	3	0
6	F	43	0	37	4	0
6	G	86	0	76	15	0
6	H	43	0	38	7	0
6	I	86	0	76	10	0
6	J	43	0	38	8	0
6	K	86	0	76	13	0
6	L	43	0	35	7	0
6	N	43	0	38	5	0
6	O	43	0	37	6	0
6	P	43	0	38	4	0
6	Q	43	0	38	6	0
6	R	43	0	38	9	0
6	S	43	0	38	7	0
6	T	86	0	76	12	0
6	U	86	0	76	8	0
6	V	86	0	75	10	0
6	W	86	0	76	9	0
6	X	86	0	76	14	0
6	Y	86	0	76	10	0
6	a	43	0	38	9	0
6	b	43	0	38	6	0
6	c	43	0	38	8	0
6	d	43	0	38	3	0
6	e	43	0	38	7	0
6	f	43	0	38	4	0
6	g	86	0	76	11	0
6	h	86	0	76	9	0
6	i	43	0	38	3	0
6	j	86	0	76	11	0
6	k	86	0	76	8	0
6	l	86	0	76	13	0
All	All	55862	0	55556	1667	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 15.

The worst 5 of 1667 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:O:79:ASN:HA	2:O:82:LYS:HE3	1.43	1.01
6:L:201:CYC:HMA3	6:L:201:CYC:HB	1.26	1.00
5:4:186:ARG:NH2	3:l:65:GLU:OE2	2.03	0.91
3:j:106:ASP:OD1	3:j:166:LYS:NZ	2.04	0.91
2:O:82:LYS:HZ3	6:O:200:CYC:HAD2	1.37	0.90

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	511/531 (96%)	492 (96%)	19 (4%)	0	100	100
2	A	160/163 (98%)	158 (99%)	2 (1%)	0	100	100
2	B	161/163 (99%)	159 (99%)	2 (1%)	0	100	100
2	C	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
2	D	160/163 (98%)	155 (97%)	5 (3%)	0	100	100
2	E	160/163 (98%)	154 (96%)	6 (4%)	0	100	100
2	F	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
2	N	160/163 (98%)	156 (98%)	4 (2%)	0	100	100
2	O	160/163 (98%)	159 (99%)	1 (1%)	0	100	100
2	P	160/163 (98%)	155 (97%)	5 (3%)	0	100	100
2	Q	160/163 (98%)	159 (99%)	1 (1%)	0	100	100
2	R	160/163 (98%)	157 (98%)	3 (2%)	0	100	100
2	S	160/163 (98%)	158 (99%)	2 (1%)	0	100	100
2	a	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
2	b	161/163 (99%)	160 (99%)	1 (1%)	0	100	100
2	c	160/163 (98%)	154 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	d	160/163 (98%)	153 (96%)	7 (4%)	0	100	100
2	e	160/163 (98%)	157 (98%)	3 (2%)	0	100	100
2	f	160/163 (98%)	159 (99%)	1 (1%)	0	100	100
3	G	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
3	H	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
3	I	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
3	J	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
3	K	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
3	L	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
3	T	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
3	U	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
3	V	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
3	W	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
3	X	170/172 (99%)	168 (99%)	2 (1%)	0	100	100
3	Y	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
3	g	170/172 (99%)	164 (96%)	6 (4%)	0	100	100
3	h	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
3	i	170/172 (99%)	168 (99%)	2 (1%)	0	100	100
3	j	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
3	k	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
3	l	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
4	M	58/78 (74%)	57 (98%)	1 (2%)	0	100	100
4	Z	58/78 (74%)	55 (95%)	3 (5%)	0	100	100
4	m	67/78 (86%)	61 (91%)	6 (9%)	0	100	100
5	4	248/252 (98%)	231 (93%)	17 (7%)	0	100	100
All	All	6884/7047 (98%)	6699 (97%)	185 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	430/445 (97%)	430 (100%)	0	100	100
2	A	128/129 (99%)	128 (100%)	0	100	100
2	B	129/129 (100%)	129 (100%)	0	100	100
2	C	128/129 (99%)	128 (100%)	0	100	100
2	D	128/129 (99%)	128 (100%)	0	100	100
2	E	128/129 (99%)	128 (100%)	0	100	100
2	F	128/129 (99%)	128 (100%)	0	100	100
2	N	128/129 (99%)	128 (100%)	0	100	100
2	O	128/129 (99%)	128 (100%)	0	100	100
2	P	128/129 (99%)	128 (100%)	0	100	100
2	Q	128/129 (99%)	128 (100%)	0	100	100
2	R	128/129 (99%)	128 (100%)	0	100	100
2	S	128/129 (99%)	128 (100%)	0	100	100
2	a	128/129 (99%)	128 (100%)	0	100	100
2	b	129/129 (100%)	129 (100%)	0	100	100
2	c	128/129 (99%)	128 (100%)	0	100	100
2	d	128/129 (99%)	128 (100%)	0	100	100
2	e	128/129 (99%)	128 (100%)	0	100	100
2	f	128/129 (99%)	128 (100%)	0	100	100
3	G	133/133 (100%)	133 (100%)	0	100	100
3	H	133/133 (100%)	133 (100%)	0	100	100
3	I	133/133 (100%)	133 (100%)	0	100	100
3	J	133/133 (100%)	133 (100%)	0	100	100
3	K	133/133 (100%)	133 (100%)	0	100	100
3	L	133/133 (100%)	133 (100%)	0	100	100
3	T	133/133 (100%)	133 (100%)	0	100	100
3	U	133/133 (100%)	133 (100%)	0	100	100
3	V	133/133 (100%)	133 (100%)	0	100	100
3	W	133/133 (100%)	133 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	X	133/133 (100%)	133 (100%)	0	100	100
3	Y	133/133 (100%)	133 (100%)	0	100	100
3	g	133/133 (100%)	133 (100%)	0	100	100
3	h	133/133 (100%)	133 (100%)	0	100	100
3	i	133/133 (100%)	133 (100%)	0	100	100
3	j	133/133 (100%)	133 (100%)	0	100	100
3	k	133/133 (100%)	133 (100%)	0	100	100
3	l	133/133 (100%)	133 (100%)	0	100	100
4	M	52/67 (78%)	52 (100%)	0	100	100
4	Z	52/67 (78%)	52 (100%)	0	100	100
4	m	59/67 (88%)	59 (100%)	0	100	100
5	4	220/222 (99%)	220 (100%)	0	100	100
All	All	5513/5584 (99%)	5513 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
3	W	11	GLN
4	m	14	GLN
5	4	75	ASN
3	l	118	ASN
3	h	147	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

54 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CYC	G	200	-	46,46,46	5.29	26 (56%)	63,67,67	3.90	17 (26%)
6	CYC	W	200	-	46,46,46	5.10	27 (58%)	63,67,67	4.34	18 (28%)
6	CYC	U	200	-	46,46,46	5.26	27 (58%)	63,67,67	3.91	19 (30%)
6	CYC	K	200	-	46,46,46	5.18	28 (60%)	63,67,67	4.29	21 (33%)
6	CYC	Q	200	-	46,46,46	5.08	28 (60%)	63,67,67	4.27	17 (26%)
6	CYC	S	200	-	46,46,46	5.18	27 (58%)	63,67,67	4.16	17 (26%)
6	CYC	W	201	-	46,46,46	5.25	27 (58%)	63,67,67	4.00	15 (23%)
6	CYC	f	200	-	46,46,46	5.23	27 (58%)	63,67,67	4.45	14 (22%)
6	CYC	4	301	-	46,46,46	5.31	27 (58%)	63,67,67	3.94	18 (28%)
6	CYC	c	200	-	46,46,46	5.31	26 (56%)	63,67,67	3.94	17 (26%)
6	CYC	N	200	-	46,46,46	5.25	27 (58%)	63,67,67	4.12	15 (23%)
6	CYC	A	201	-	46,46,46	5.21	27 (58%)	63,67,67	4.13	15 (23%)
6	CYC	Y	200	-	46,46,46	5.09	29 (63%)	63,67,67	4.29	23 (36%)
6	CYC	V	201	-	46,46,46	5.31	26 (56%)	63,67,67	4.11	15 (23%)
6	CYC	Y	201	-	46,46,46	5.18	27 (58%)	63,67,67	4.16	17 (26%)
6	CYC	e	200	-	46,46,46	5.26	26 (56%)	63,67,67	3.91	18 (28%)
6	CYC	H	200	-	46,46,46	5.22	26 (56%)	63,67,67	4.14	14 (22%)
6	CYC	V	200	-	46,46,46	5.20	26 (56%)	63,67,67	4.03	19 (30%)
6	CYC	j	200	-	46,46,46	5.18	27 (58%)	63,67,67	4.18	19 (30%)
6	CYC	X	200	-	46,46,46	5.12	28 (60%)	63,67,67	4.56	22 (34%)
6	CYC	j	201	-	46,46,46	5.25	27 (58%)	63,67,67	4.22	19 (30%)
6	CYC	l	200	-	46,46,46	5.12	27 (58%)	63,67,67	4.56	18 (28%)
6	CYC	T	200	-	46,46,46	5.29	25 (54%)	63,67,67	3.88	18 (28%)
6	CYC	3	601	-	46,46,46	5.13	28 (60%)	63,67,67	4.11	20 (31%)
6	CYC	X	201	-	46,46,46	5.20	25 (54%)	63,67,67	4.15	19 (30%)
6	CYC	g	200	-	46,46,46	5.34	25 (54%)	63,67,67	4.06	11 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CYC	C	200	-	46,46,46	5.26	27 (58%)	63,67,67	4.09	15 (23%)
6	CYC	T	201	-	46,46,46	5.29	25 (54%)	63,67,67	4.12	15 (23%)
6	CYC	E	200	-	46,46,46	5.17	27 (58%)	63,67,67	4.17	18 (28%)
6	CYC	h	200	-	46,46,46	5.27	26 (56%)	63,67,67	3.84	14 (22%)
6	CYC	k	201	-	46,46,46	5.21	27 (58%)	63,67,67	4.18	19 (30%)
6	CYC	B	200	-	46,46,46	5.32	27 (58%)	63,67,67	3.79	16 (25%)
6	CYC	L	201	-	46,46,46	5.26	26 (56%)	63,67,67	4.15	19 (30%)
6	CYC	G	201	-	46,46,46	5.27	26 (56%)	63,67,67	4.18	17 (26%)
6	CYC	a	200	-	46,46,46	5.29	26 (56%)	63,67,67	4.12	11 (17%)
6	CYC	k	200	-	46,46,46	5.20	26 (56%)	63,67,67	4.15	22 (34%)
6	CYC	D	200	-	46,46,46	5.15	27 (58%)	63,67,67	4.30	20 (31%)
6	CYC	l	201	-	46,46,46	5.26	26 (56%)	63,67,67	4.09	17 (26%)
6	CYC	U	201	-	46,46,46	5.26	27 (58%)	63,67,67	4.15	14 (22%)
6	CYC	d	200	-	46,46,46	5.17	26 (56%)	63,67,67	4.44	15 (23%)
6	CYC	R	200	-	46,46,46	5.23	26 (56%)	63,67,67	4.16	17 (26%)
6	CYC	B	201	-	46,46,46	5.30	26 (56%)	63,67,67	3.93	14 (22%)
6	CYC	g	201	-	46,46,46	5.31	26 (56%)	63,67,67	4.00	15 (23%)
6	CYC	b	200	-	46,46,46	5.22	27 (58%)	63,67,67	4.41	17 (26%)
6	CYC	A	200	-	46,46,46	5.25	26 (56%)	63,67,67	4.14	16 (25%)
6	CYC	I	200	-	46,46,46	5.18	26 (56%)	63,67,67	4.15	16 (25%)
6	CYC	h	201	-	46,46,46	5.35	26 (56%)	63,67,67	4.02	13 (20%)
6	CYC	i	201	-	46,46,46	5.30	26 (56%)	63,67,67	4.17	16 (25%)
6	CYC	K	201	-	46,46,46	5.26	25 (54%)	63,67,67	4.08	20 (31%)
6	CYC	F	200	-	46,46,46	5.19	26 (56%)	63,67,67	4.16	16 (25%)
6	CYC	O	200	-	46,46,46	5.26	26 (56%)	63,67,67	3.83	17 (26%)
6	CYC	P	200	-	46,46,46	5.24	27 (58%)	63,67,67	4.17	17 (26%)
6	CYC	I	201	-	46,46,46	5.23	26 (56%)	63,67,67	4.06	16 (25%)
6	CYC	J	200	-	46,46,46	5.15	26 (56%)	63,67,67	4.23	21 (33%)

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
6	CYC	G	200	-	-	9/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CYC	W	200	-	-	11/26/74/74	0/4/4/4
6	CYC	U	200	-	-	11/26/74/74	0/4/4/4
6	CYC	K	200	-	-	10/26/74/74	0/4/4/4
6	CYC	Q	200	-	-	17/26/74/74	0/4/4/4
6	CYC	S	200	-	-	13/26/74/74	0/4/4/4
6	CYC	W	201	-	-	15/26/74/74	0/4/4/4
6	CYC	f	200	-	-	14/26/74/74	0/4/4/4
6	CYC	4	301	-	-	11/26/74/74	0/4/4/4
6	CYC	c	200	-	-	11/26/74/74	0/4/4/4
6	CYC	N	200	-	-	15/26/74/74	0/4/4/4
6	CYC	A	201	-	-	11/26/74/74	0/4/4/4
6	CYC	Y	200	-	-	6/26/74/74	0/4/4/4
6	CYC	V	201	-	-	16/26/74/74	0/4/4/4
6	CYC	Y	201	-	-	16/26/74/74	0/4/4/4
6	CYC	e	200	-	-	13/26/74/74	0/4/4/4
6	CYC	H	200	-	-	14/26/74/74	0/4/4/4
6	CYC	V	200	-	-	13/26/74/74	0/4/4/4
6	CYC	j	200	-	-	11/26/74/74	0/4/4/4
6	CYC	X	200	-	-	10/26/74/74	0/4/4/4
6	CYC	j	201	-	-	14/26/74/74	0/4/4/4
6	CYC	l	200	-	-	11/26/74/74	0/4/4/4
6	CYC	T	200	-	-	12/26/74/74	0/4/4/4
6	CYC	3	601	-	-	6/26/74/74	0/4/4/4
6	CYC	X	201	-	-	16/26/74/74	0/4/4/4
6	CYC	g	200	-	-	9/26/74/74	0/4/4/4
6	CYC	C	200	-	-	12/26/74/74	0/4/4/4
6	CYC	T	201	-	-	19/26/74/74	0/4/4/4
6	CYC	E	200	-	-	12/26/74/74	0/4/4/4
6	CYC	h	200	-	-	10/26/74/74	0/4/4/4
6	CYC	k	201	-	-	10/26/74/74	0/4/4/4
6	CYC	B	200	-	-	8/26/74/74	0/4/4/4
6	CYC	L	201	-	-	15/26/74/74	0/4/4/4
6	CYC	G	201	-	-	16/26/74/74	0/4/4/4
6	CYC	a	200	-	-	21/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CYC	k	200	-	-	9/26/74/74	0/4/4/4
6	CYC	D	200	-	-	11/26/74/74	0/4/4/4
6	CYC	l	201	-	-	14/26/74/74	0/4/4/4
6	CYC	U	201	-	-	15/26/74/74	0/4/4/4
6	CYC	d	200	-	-	17/26/74/74	0/4/4/4
6	CYC	R	200	-	-	15/26/74/74	0/4/4/4
6	CYC	B	201	-	-	12/26/74/74	0/4/4/4
6	CYC	g	201	-	-	15/26/74/74	0/4/4/4
6	CYC	b	200	-	-	15/26/74/74	0/4/4/4
6	CYC	A	200	-	-	13/26/74/74	0/4/4/4
6	CYC	I	200	-	-	12/26/74/74	0/4/4/4
6	CYC	h	201	-	-	13/26/74/74	0/4/4/4
6	CYC	i	201	-	-	12/26/74/74	0/4/4/4
6	CYC	K	201	-	-	14/26/74/74	0/4/4/4
6	CYC	F	200	-	-	16/26/74/74	0/4/4/4
6	CYC	O	200	-	-	19/26/74/74	0/4/4/4
6	CYC	P	200	-	-	13/26/74/74	0/4/4/4
6	CYC	I	201	-	-	14/26/74/74	0/4/4/4
6	CYC	J	200	-	-	10/26/74/74	0/4/4/4

The worst 5 of 1430 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	g	201	CYC	C2C-C1C	13.70	1.64	1.52
6	h	201	CYC	C2C-C1C	13.56	1.64	1.52
6	O	200	CYC	C2C-C1C	13.50	1.64	1.52
6	A	200	CYC	C2C-C1C	13.40	1.64	1.52
6	T	201	CYC	C2C-C1C	13.25	1.63	1.52

The worst 5 of 918 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	W	200	CYC	OC-C1C-C2C	-23.94	107.14	126.17
6	l	200	CYC	OC-C1C-C2C	-23.46	107.52	126.17
6	K	200	CYC	OC-C1C-C2C	-23.08	107.82	126.17
6	j	200	CYC	OC-C1C-C2C	-22.81	108.03	126.17
6	3	601	CYC	OC-C1C-C2C	-22.56	108.23	126.17

There are no chirality outliers.

5 of 697 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	3	601	CYC	NA-C4A-CHB-C1B
6	3	601	CYC	C3A-C4A-CHB-C1B
6	3	601	CYC	NC-C4C-CHD-C1D
6	A	200	CYC	NA-C1A-CHA-C4D
6	A	200	CYC	C2A-C1A-CHA-C4D

There are no ring outliers.

54 monomers are involved in 307 short contacts:

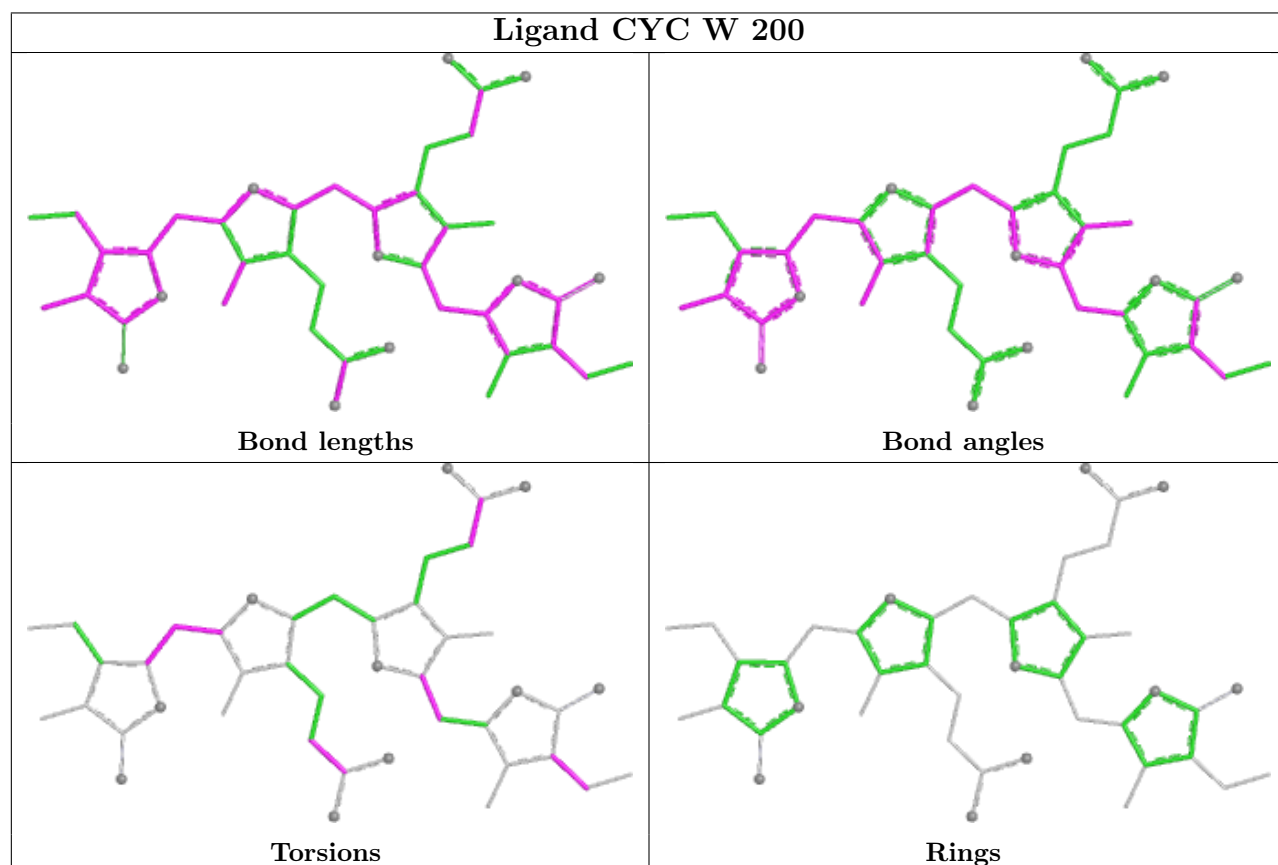
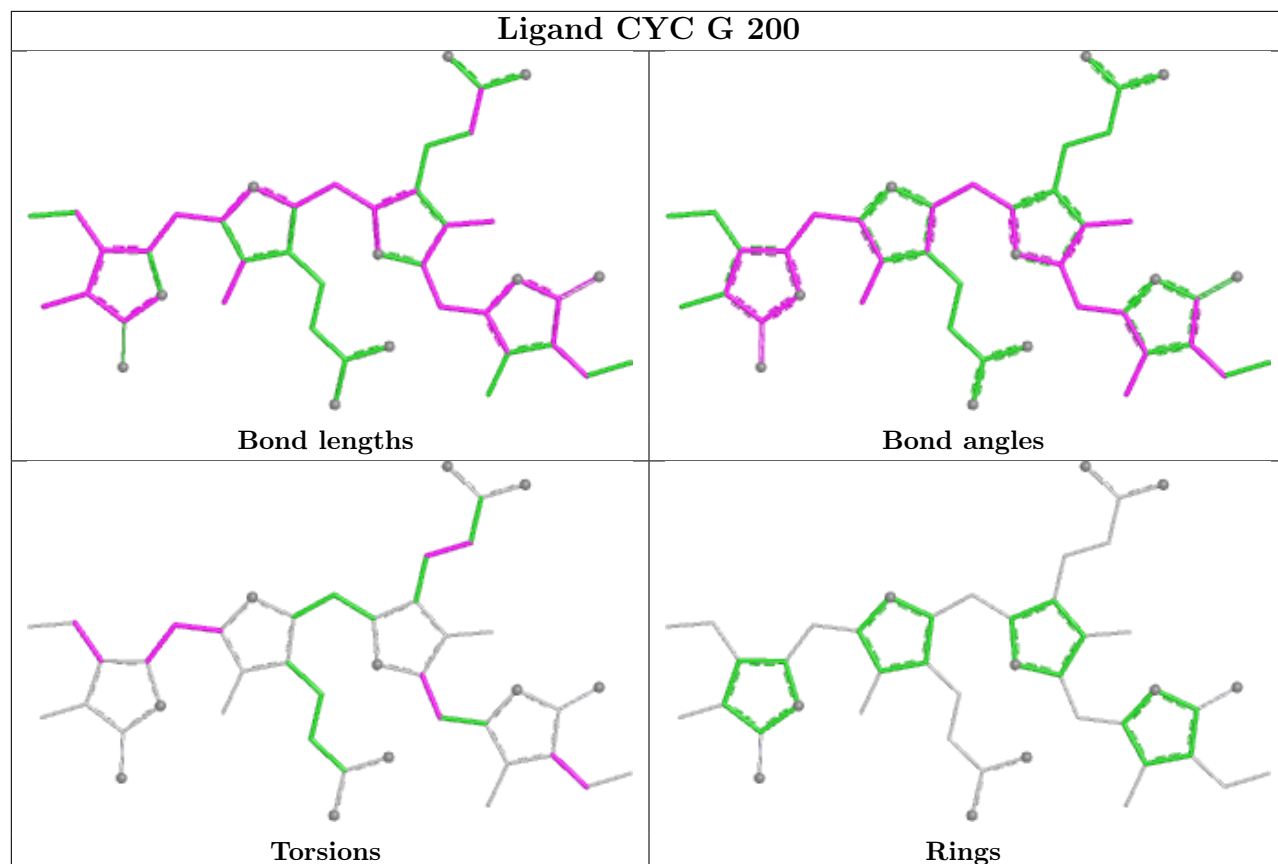
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	200	CYC	9	0
6	W	200	CYC	5	0
6	U	200	CYC	5	0
6	K	200	CYC	7	0
6	Q	200	CYC	6	0
6	S	200	CYC	7	0
6	W	201	CYC	4	0
6	f	200	CYC	4	0
6	4	301	CYC	9	0
6	c	200	CYC	8	0
6	N	200	CYC	5	0
6	A	201	CYC	4	0
6	Y	200	CYC	6	0
6	V	201	CYC	6	0
6	Y	201	CYC	4	0
6	e	200	CYC	7	0
6	H	200	CYC	7	0
6	V	200	CYC	4	0
6	j	200	CYC	8	0
6	X	200	CYC	7	0
6	j	201	CYC	3	0
6	l	200	CYC	4	0
6	T	200	CYC	9	0
6	3	601	CYC	5	0
6	X	201	CYC	7	0
6	g	200	CYC	4	0
6	C	200	CYC	4	0
6	T	201	CYC	3	0
6	E	200	CYC	3	0
6	h	200	CYC	7	0

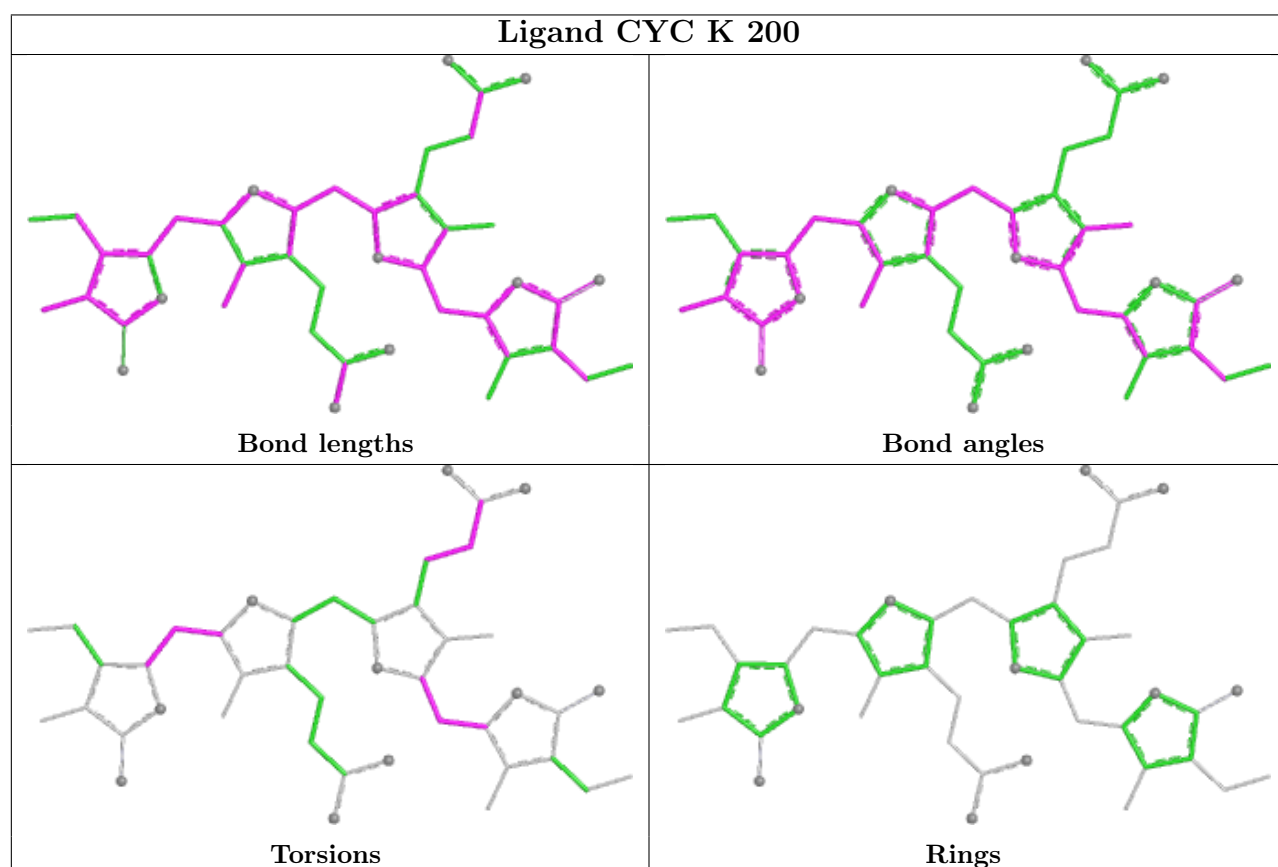
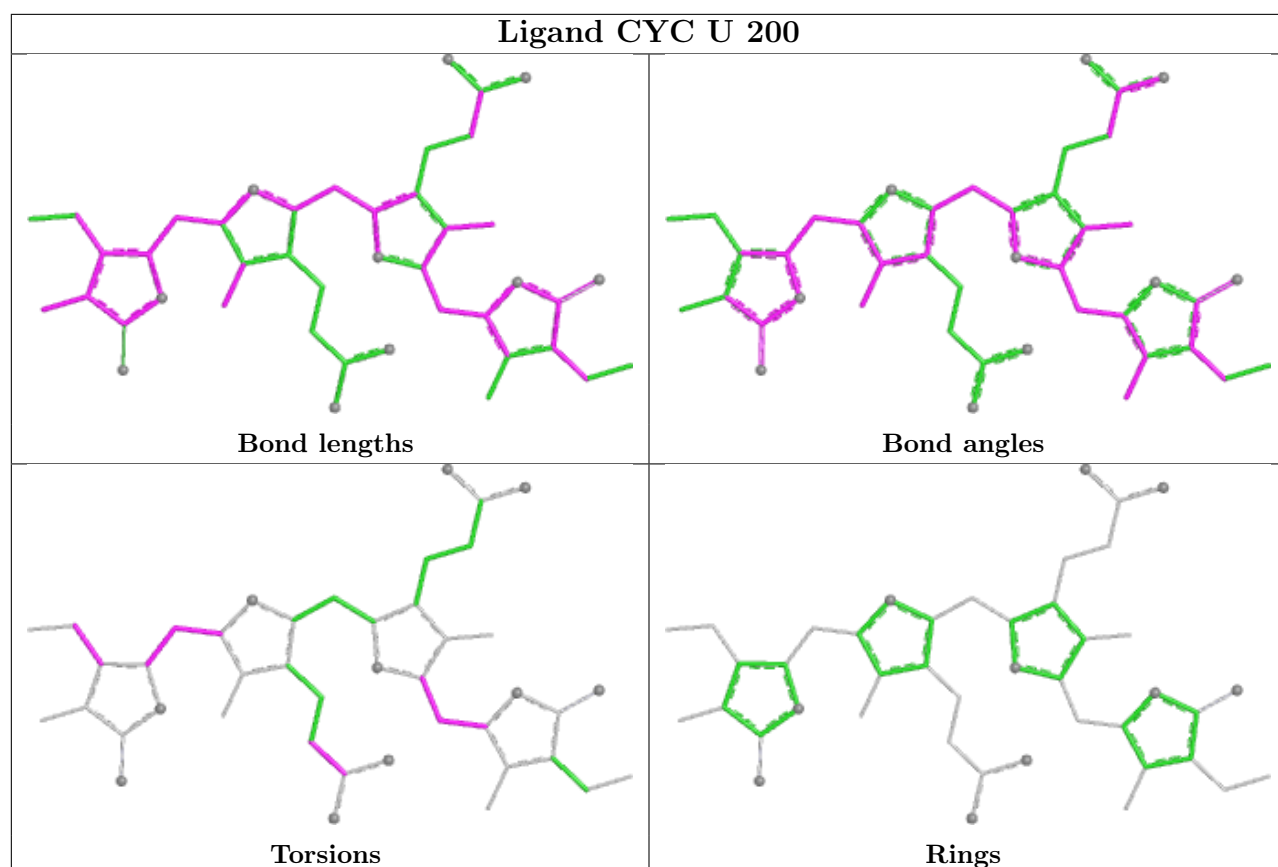
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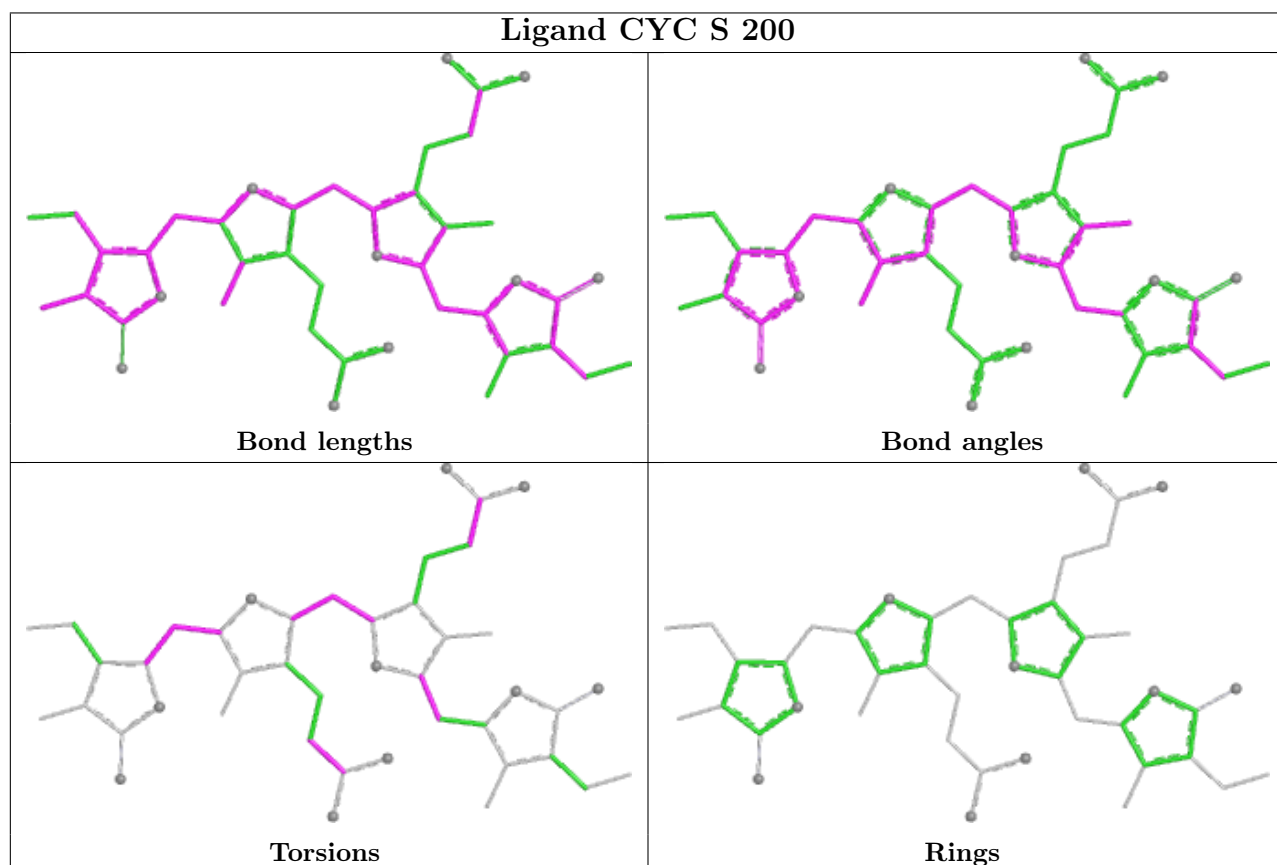
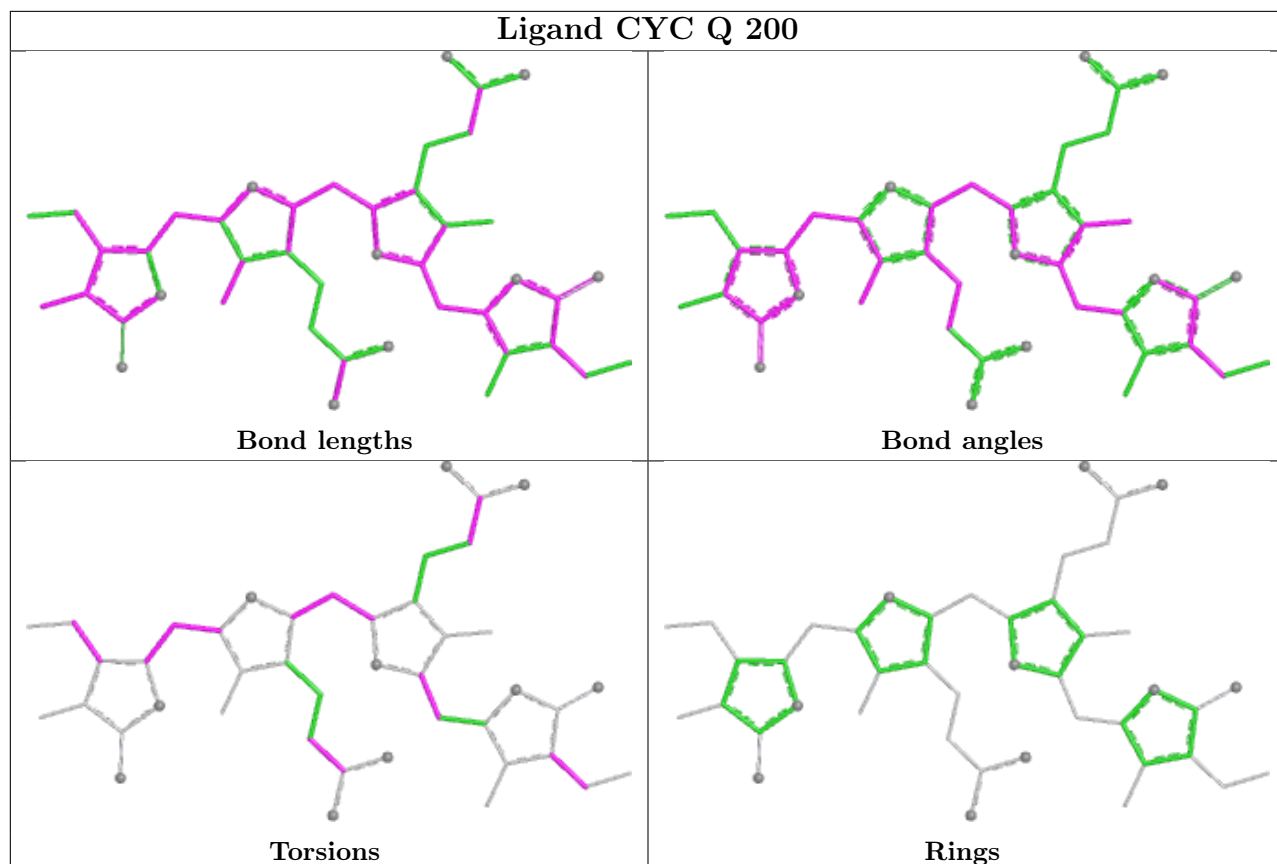
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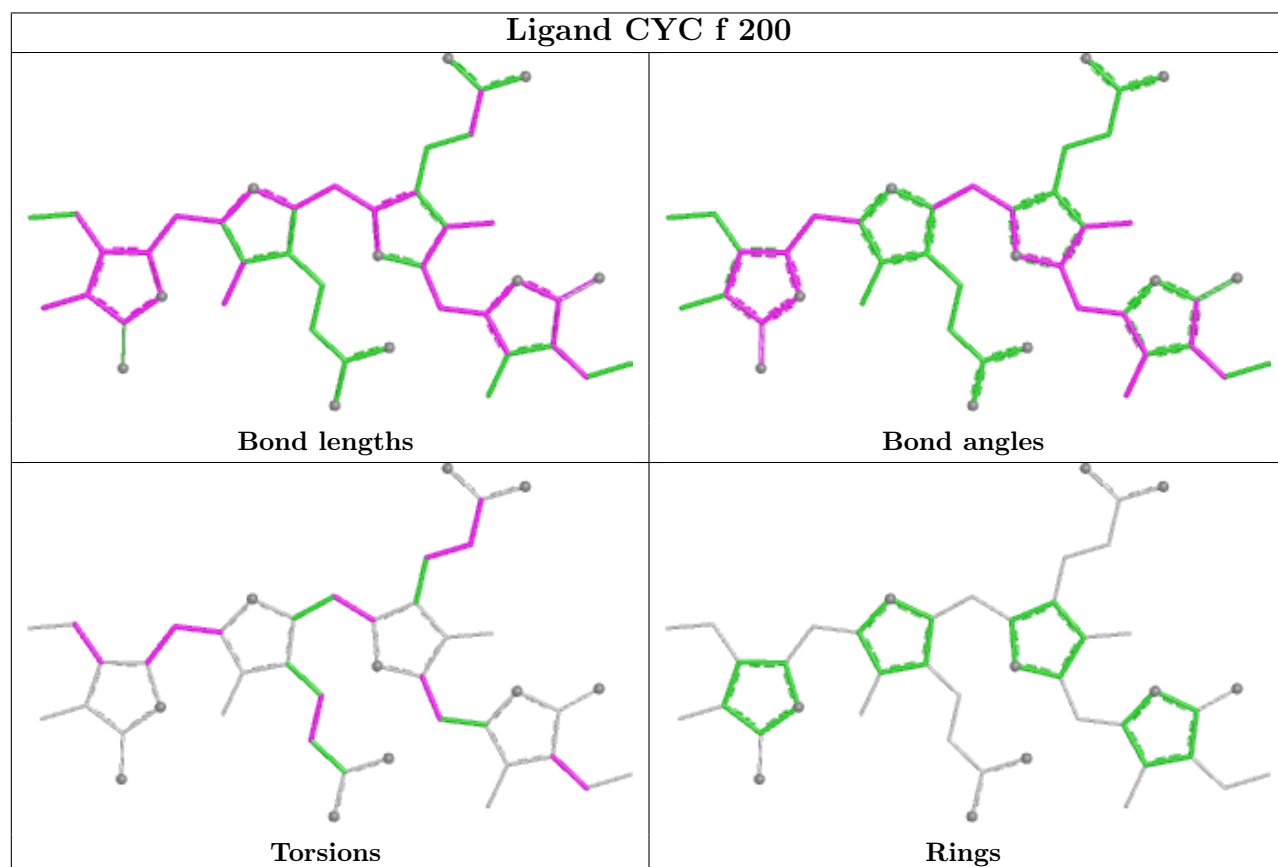
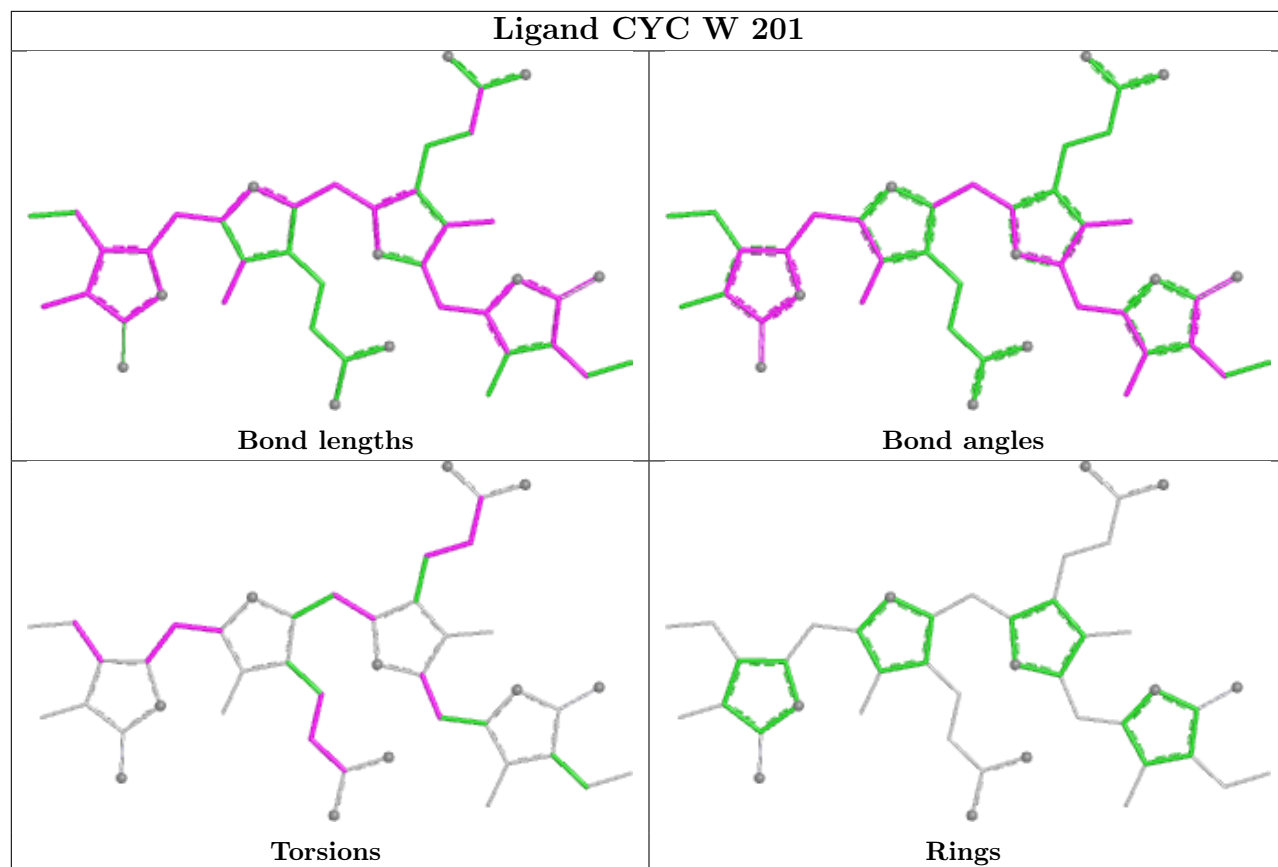
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	k	201	CYC	3	0
6	B	200	CYC	9	0
6	L	201	CYC	7	0
6	G	201	CYC	6	0
6	a	200	CYC	9	0
6	k	200	CYC	5	0
6	D	200	CYC	8	0
6	l	201	CYC	9	0
6	U	201	CYC	3	0
6	d	200	CYC	3	0
6	R	200	CYC	9	0
6	B	201	CYC	2	0
6	g	201	CYC	7	0
6	b	200	CYC	6	0
6	A	200	CYC	7	0
6	I	200	CYC	7	0
6	h	201	CYC	2	0
6	i	201	CYC	3	0
6	K	201	CYC	6	0
6	F	200	CYC	4	0
6	O	200	CYC	6	0
6	P	200	CYC	4	0
6	I	201	CYC	3	0
6	J	200	CYC	8	0

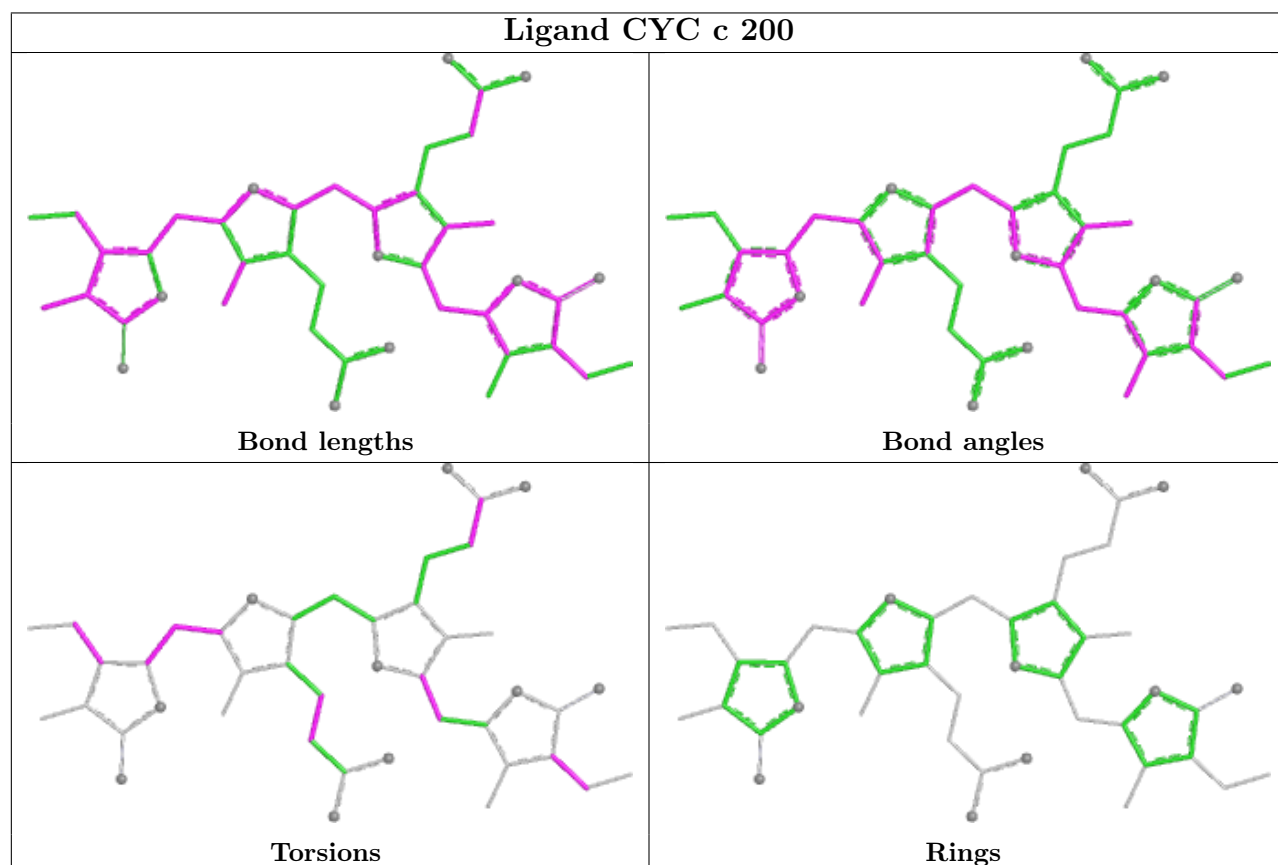
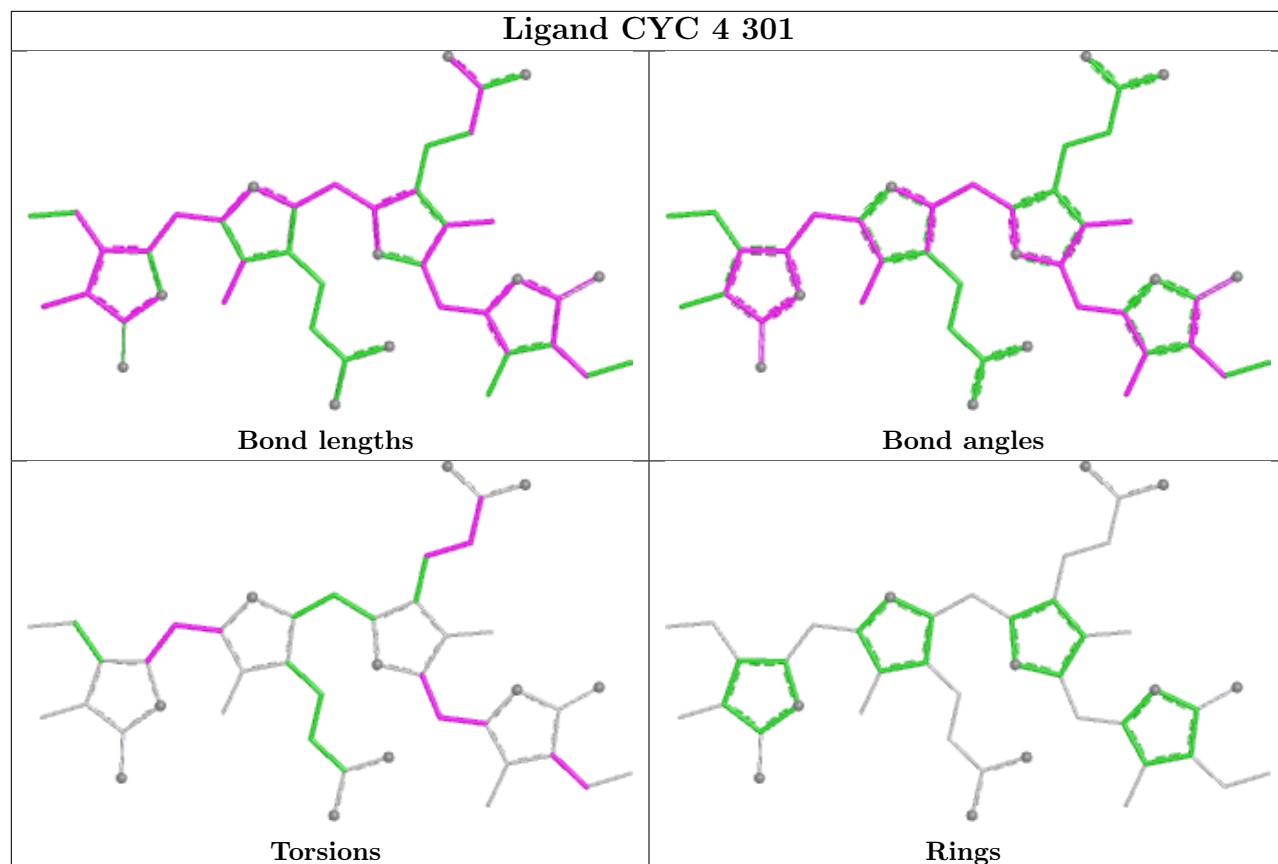
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

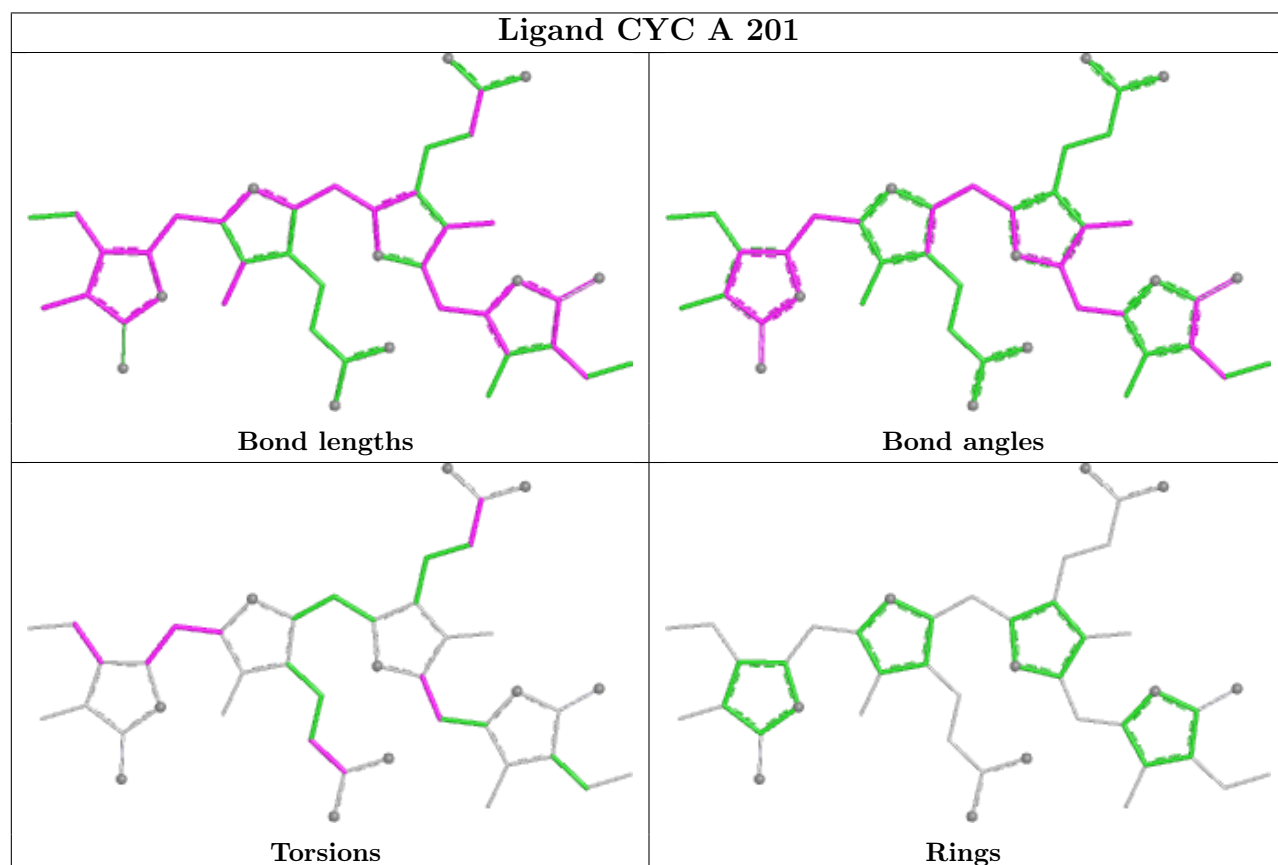
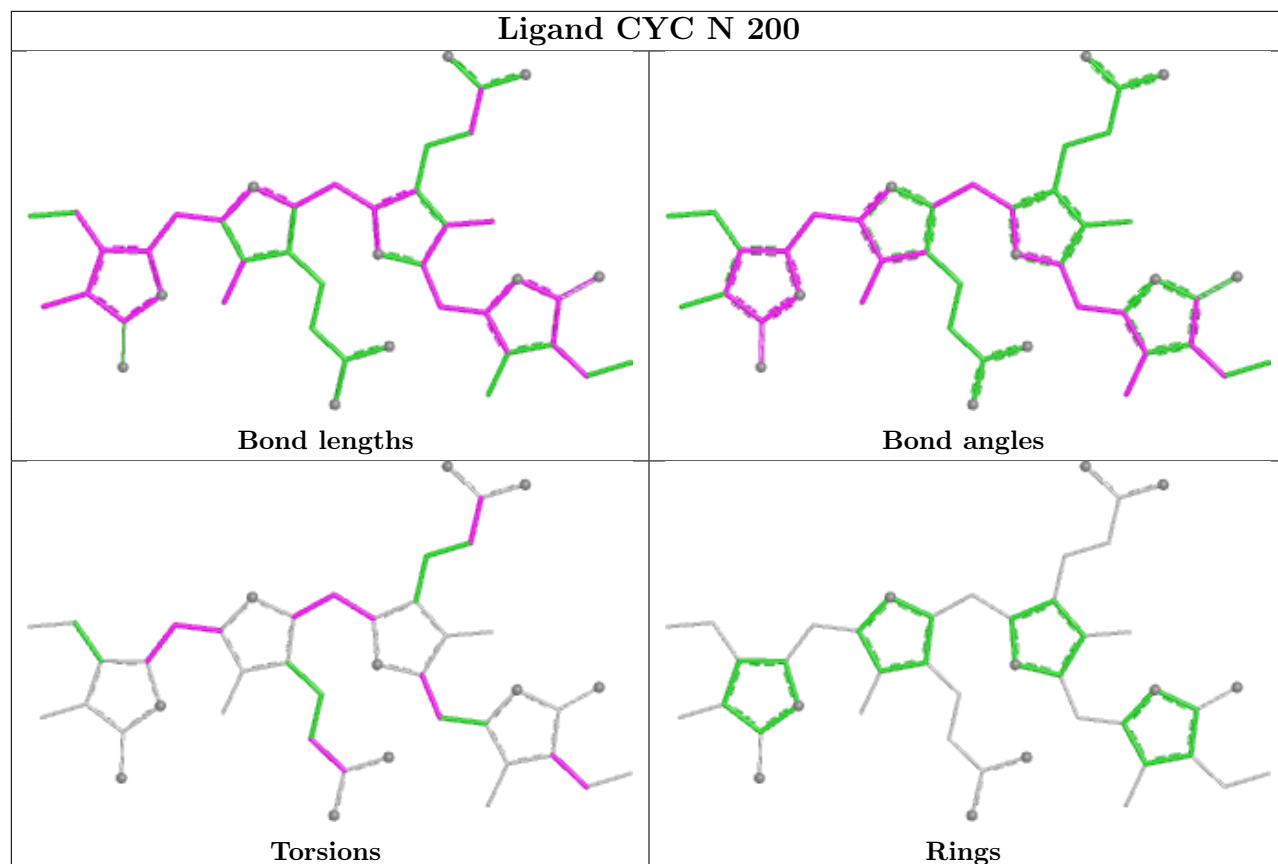


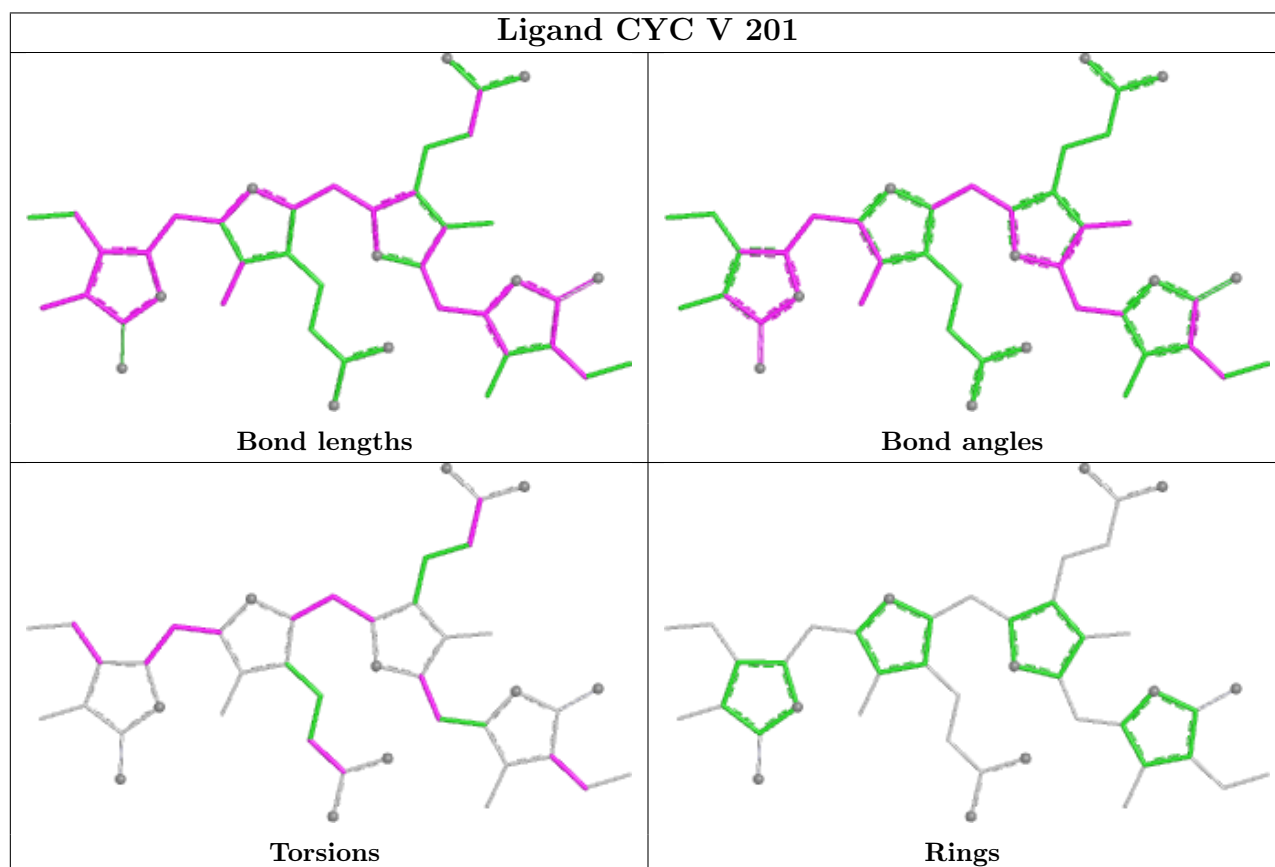
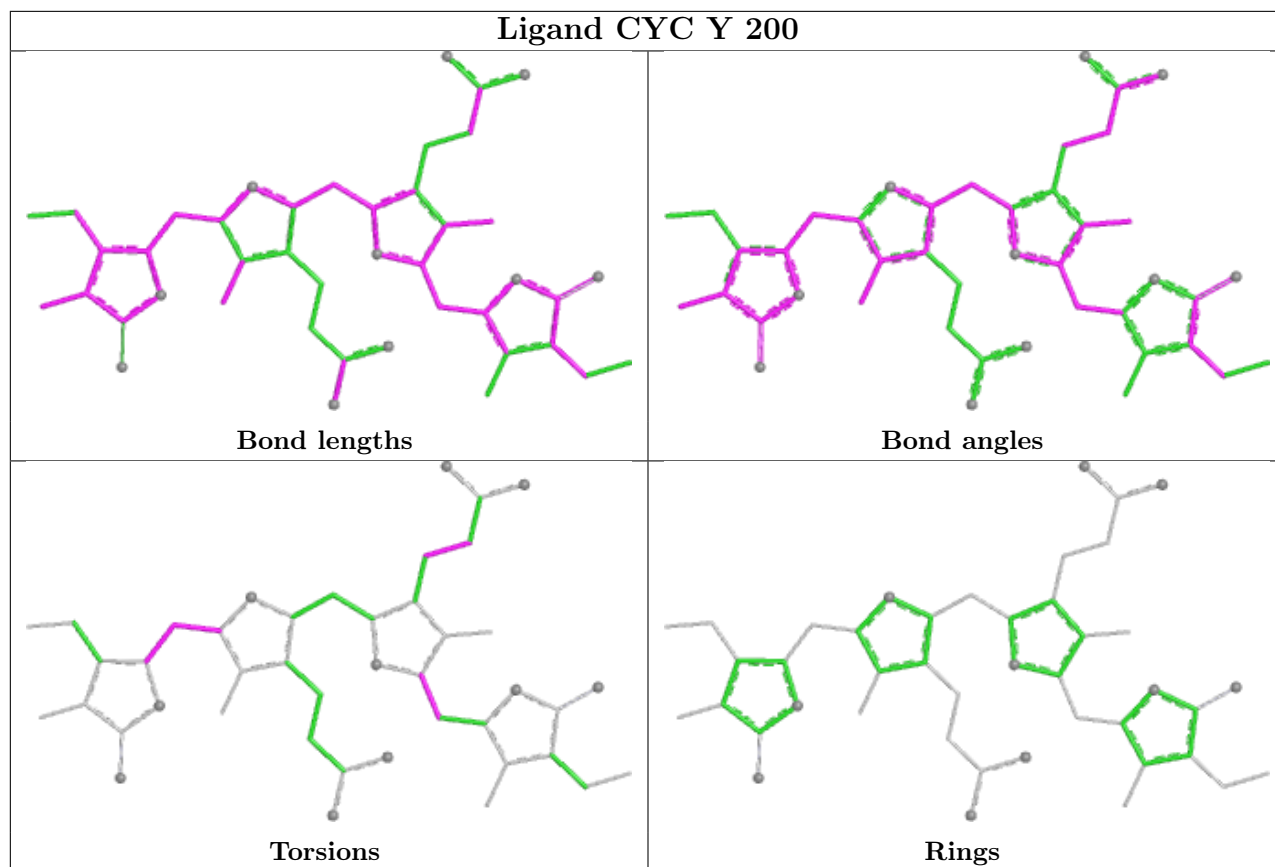


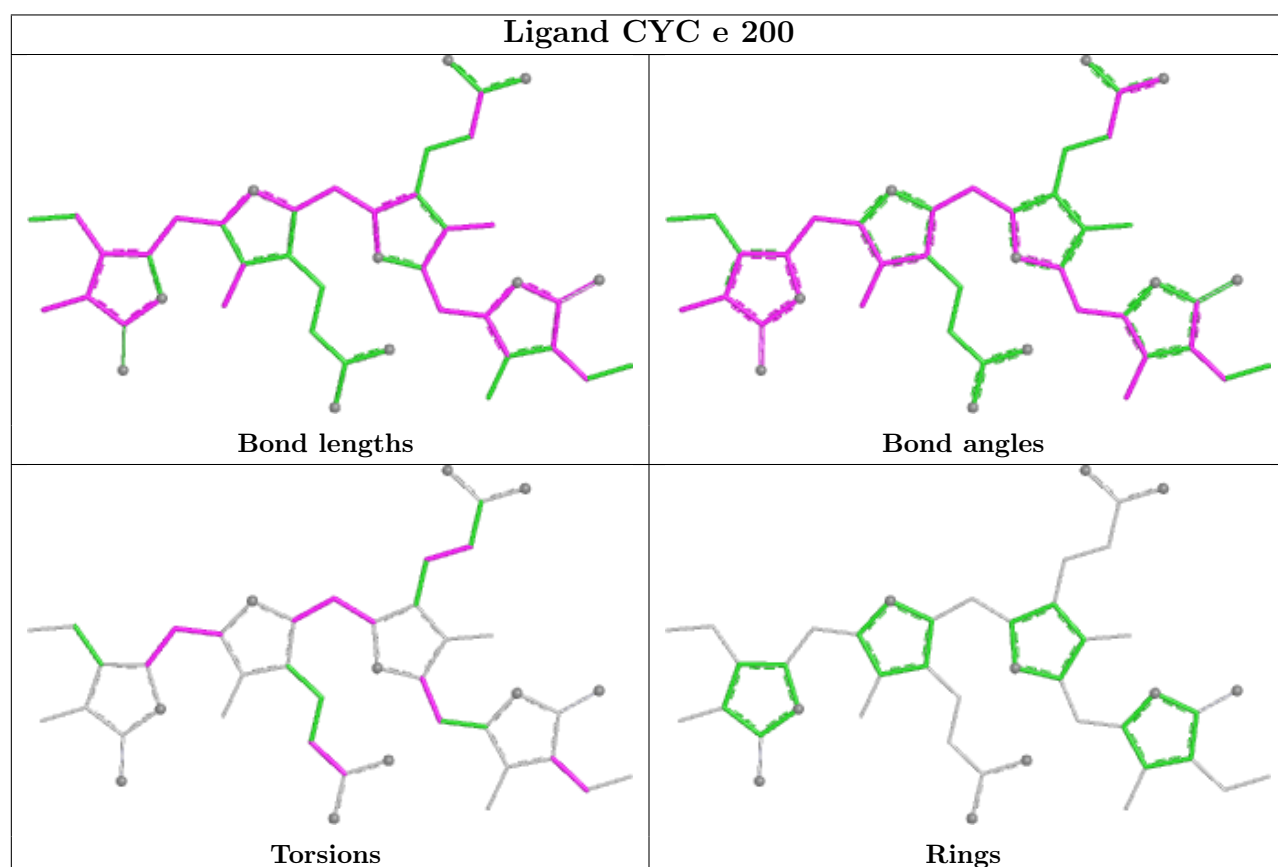
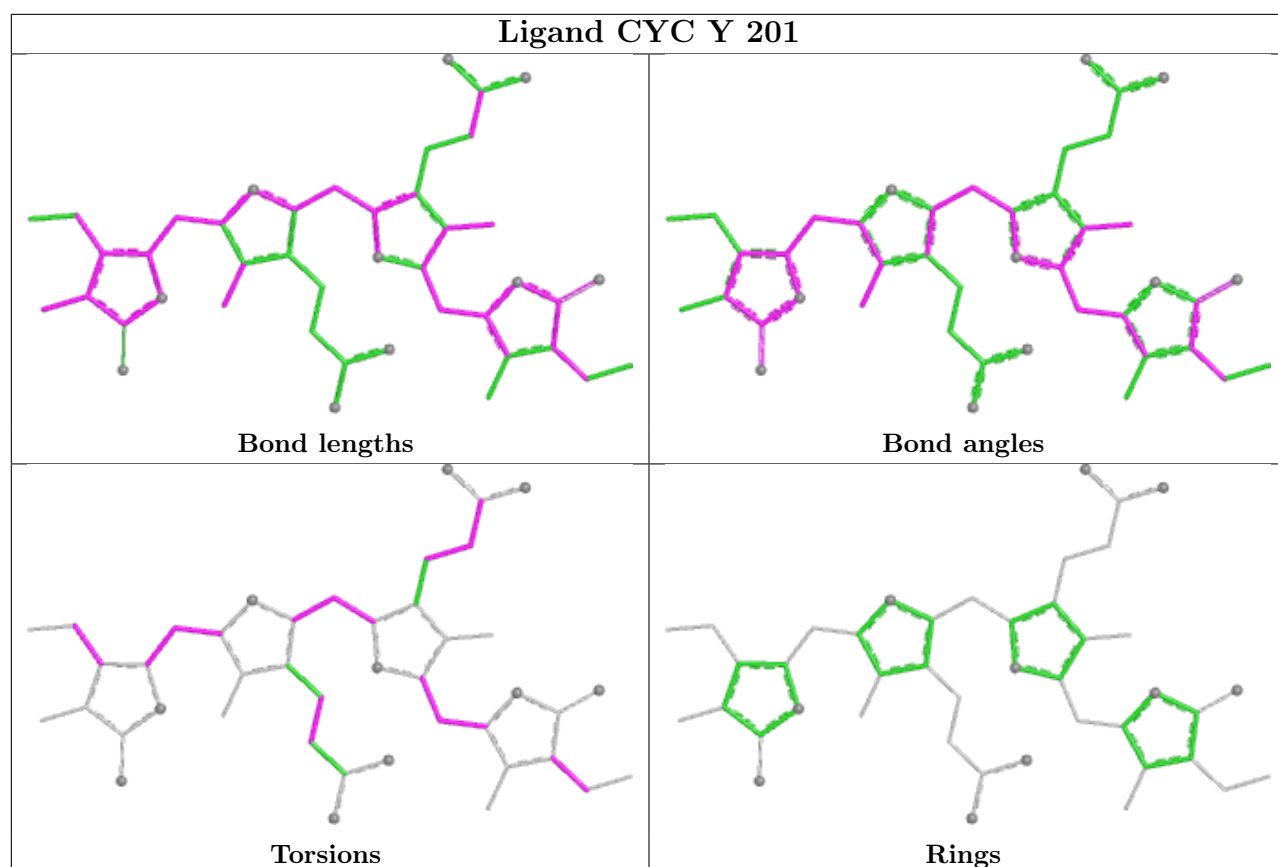


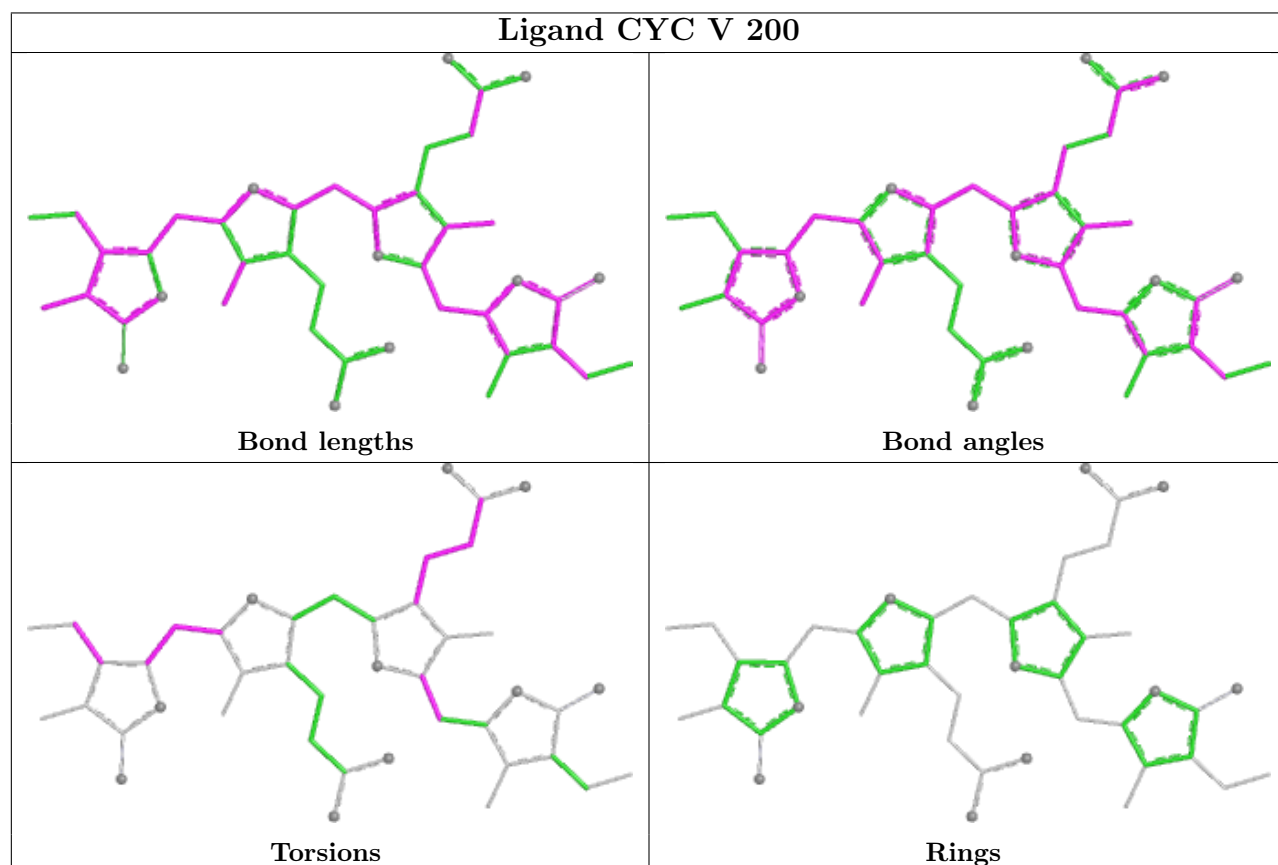
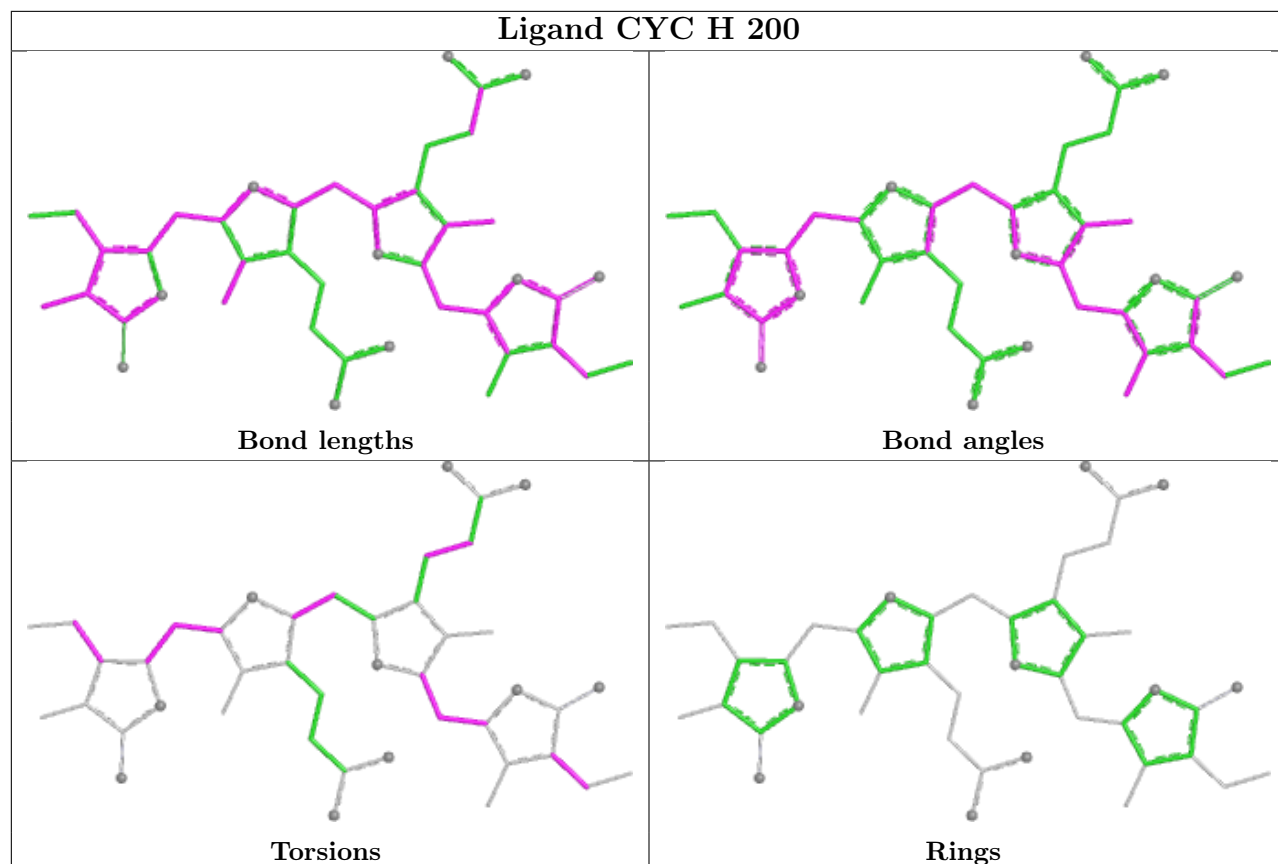


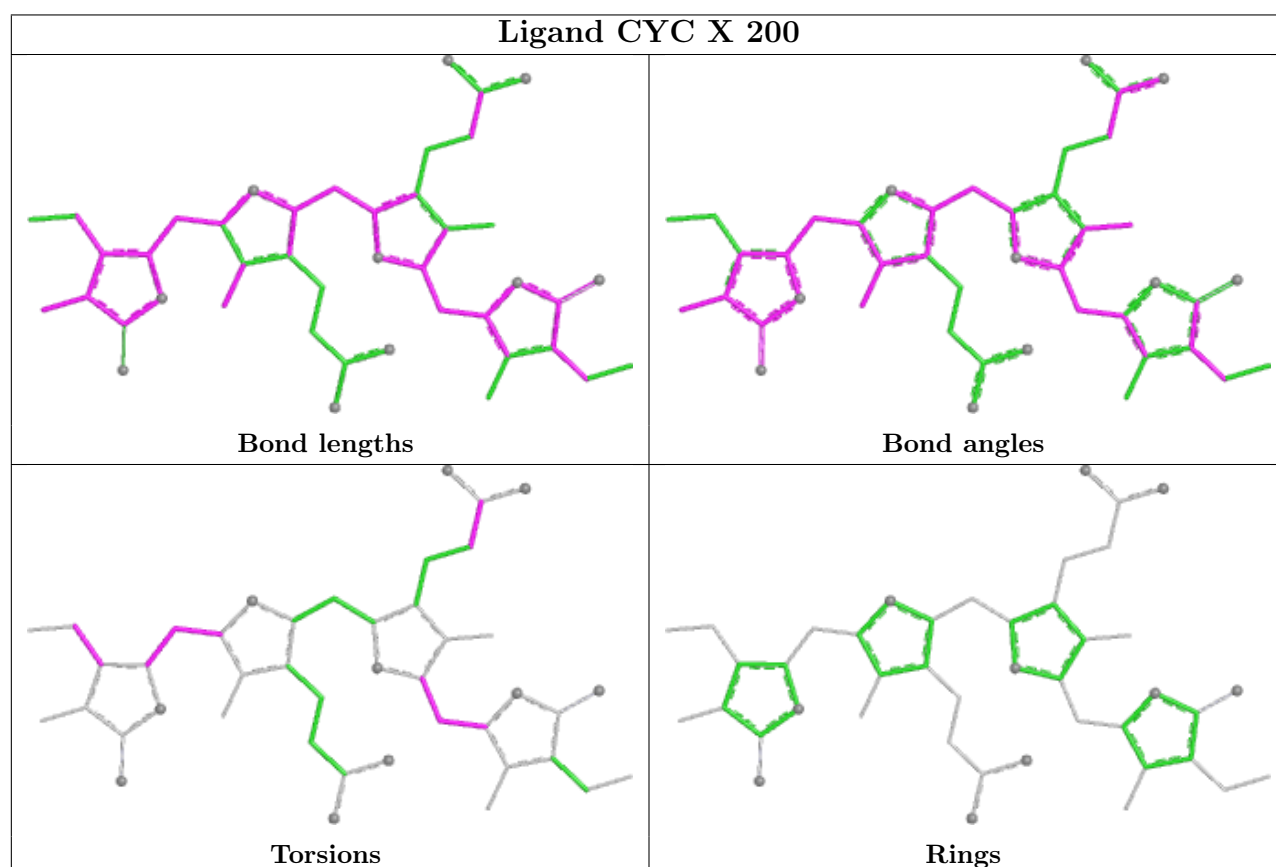
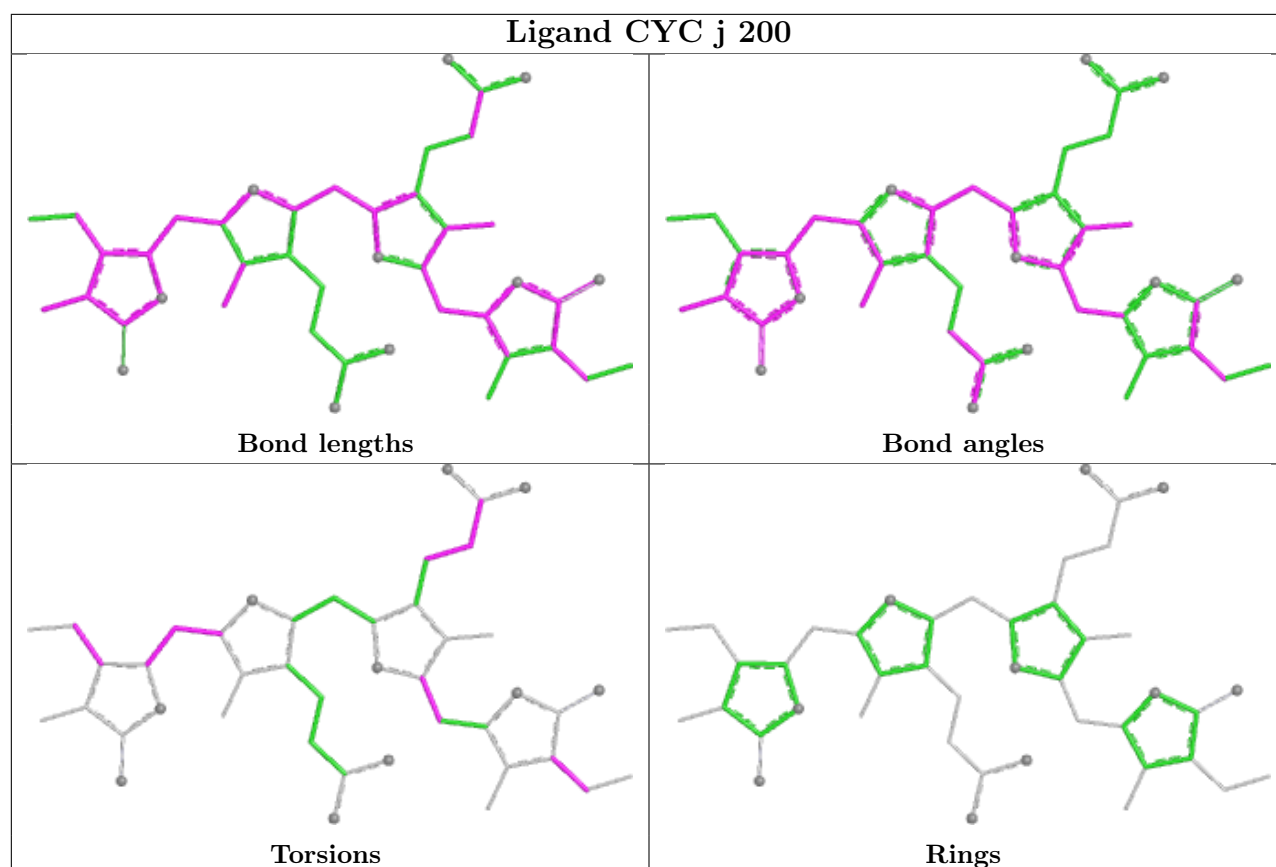


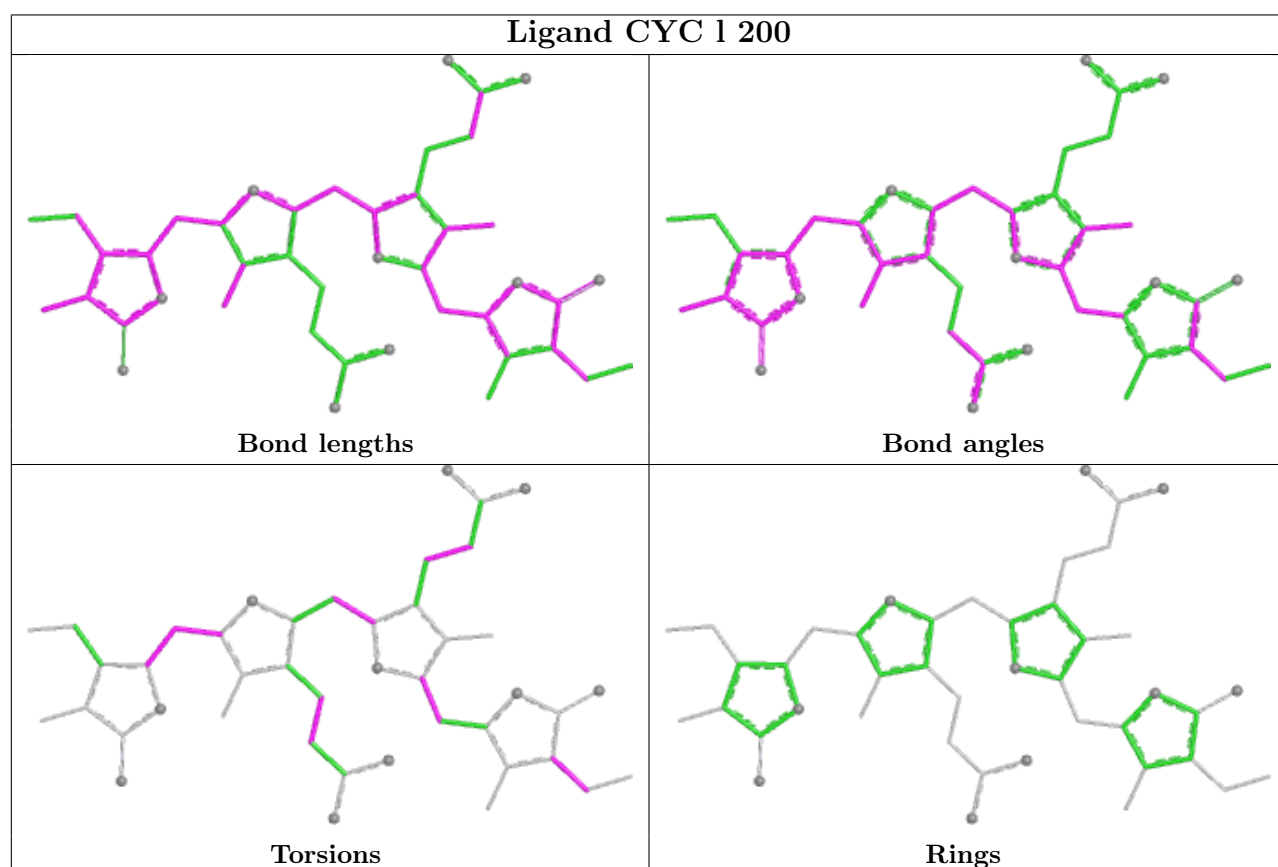
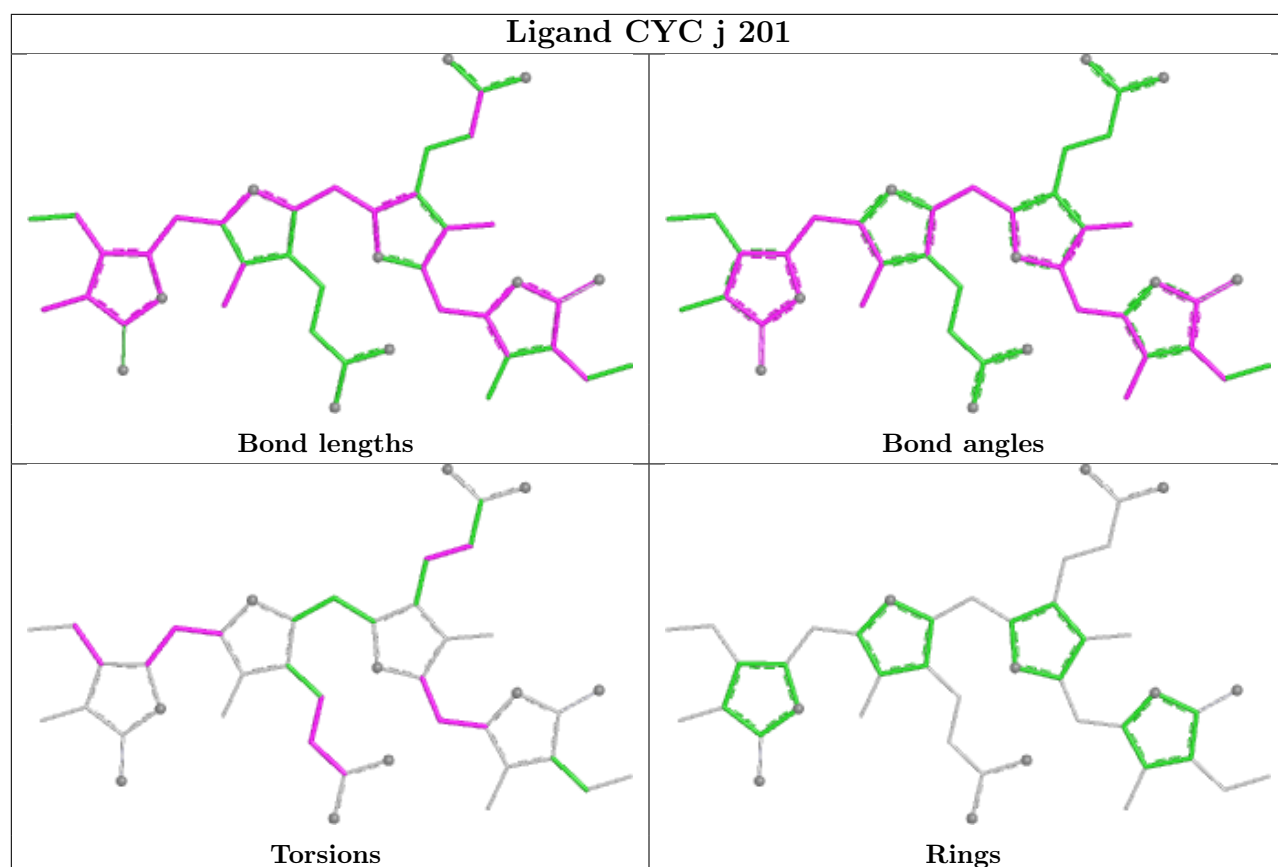


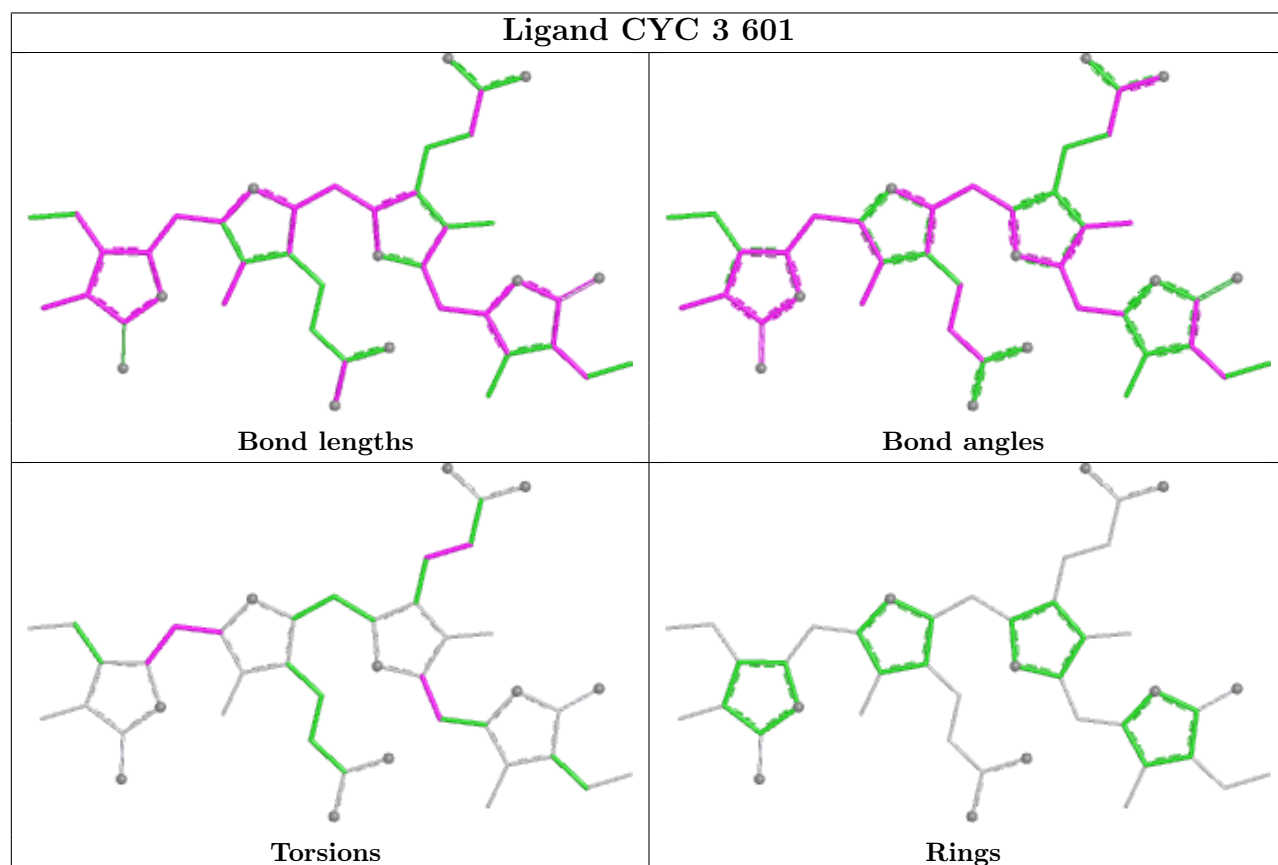
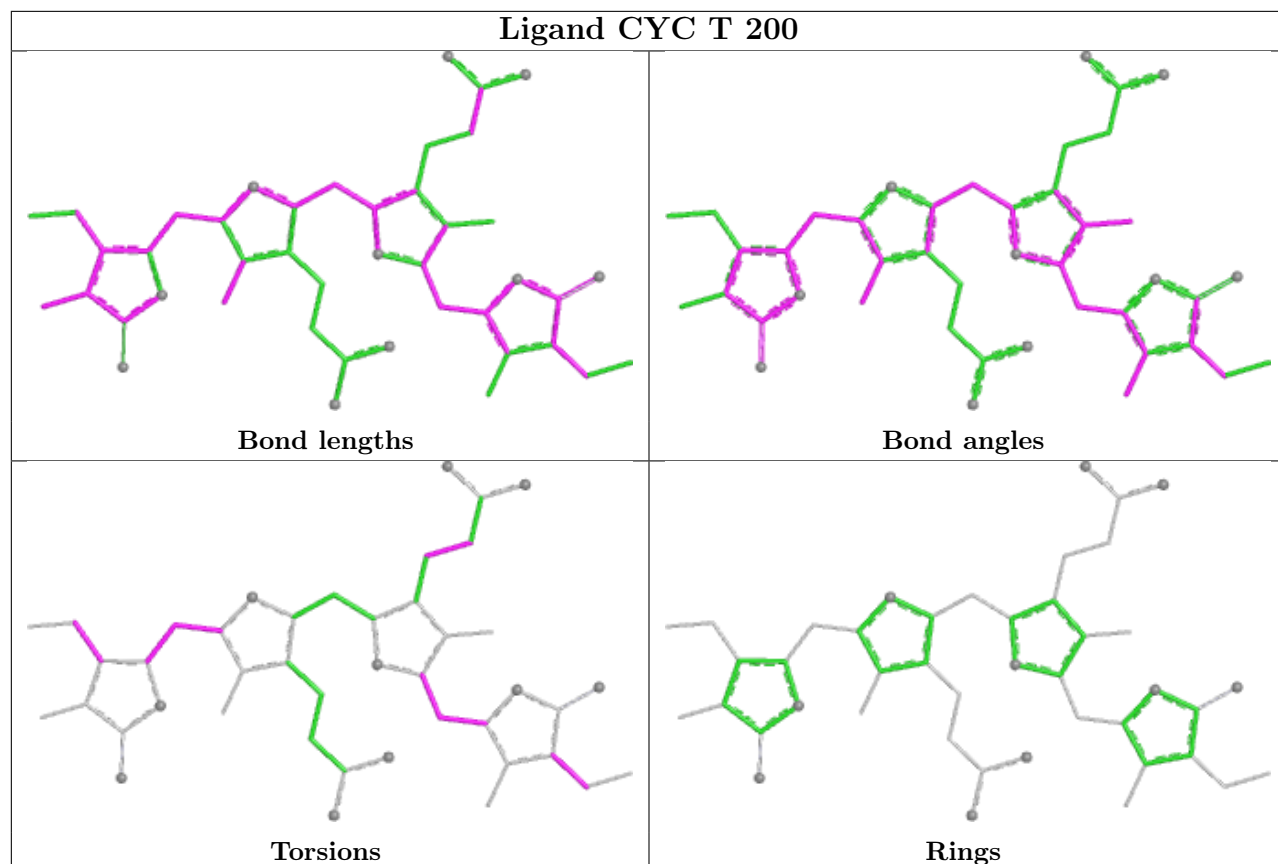


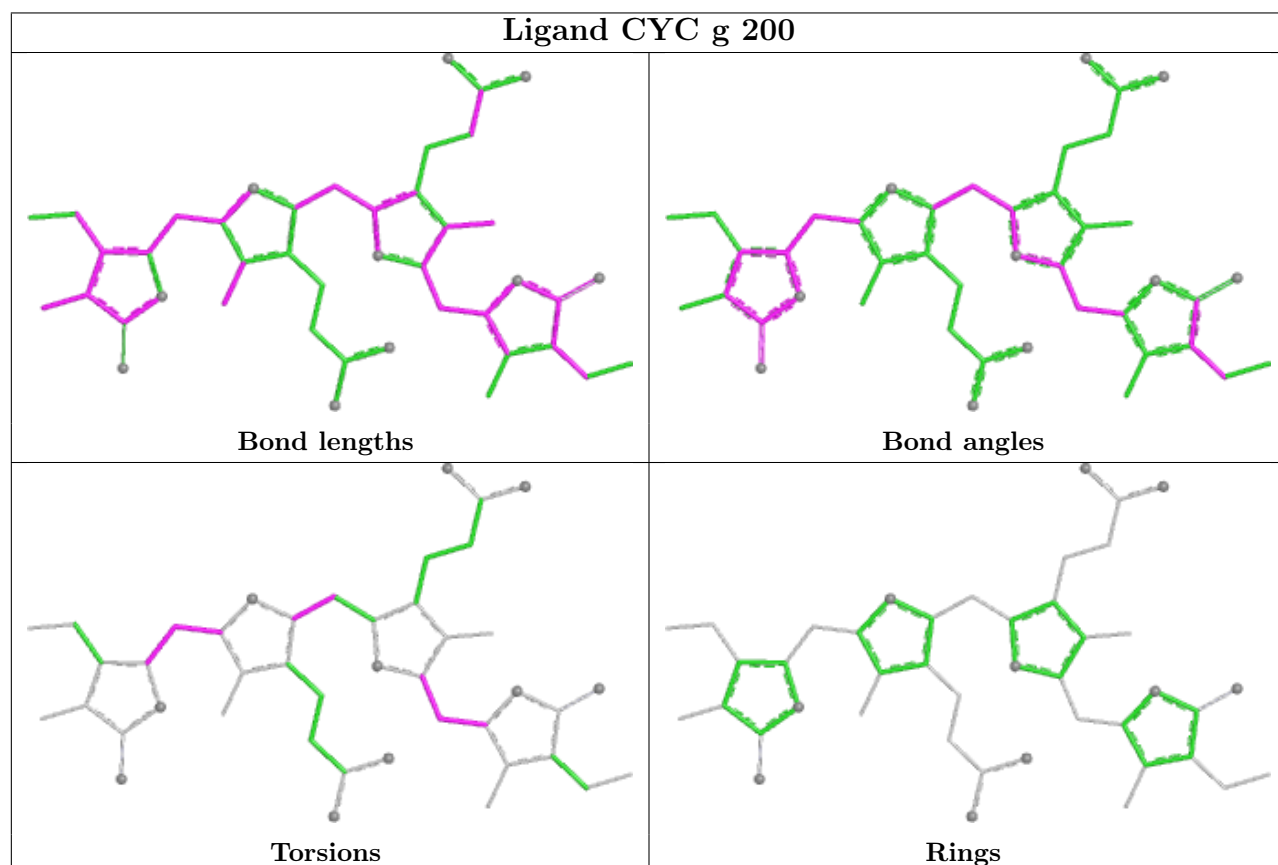
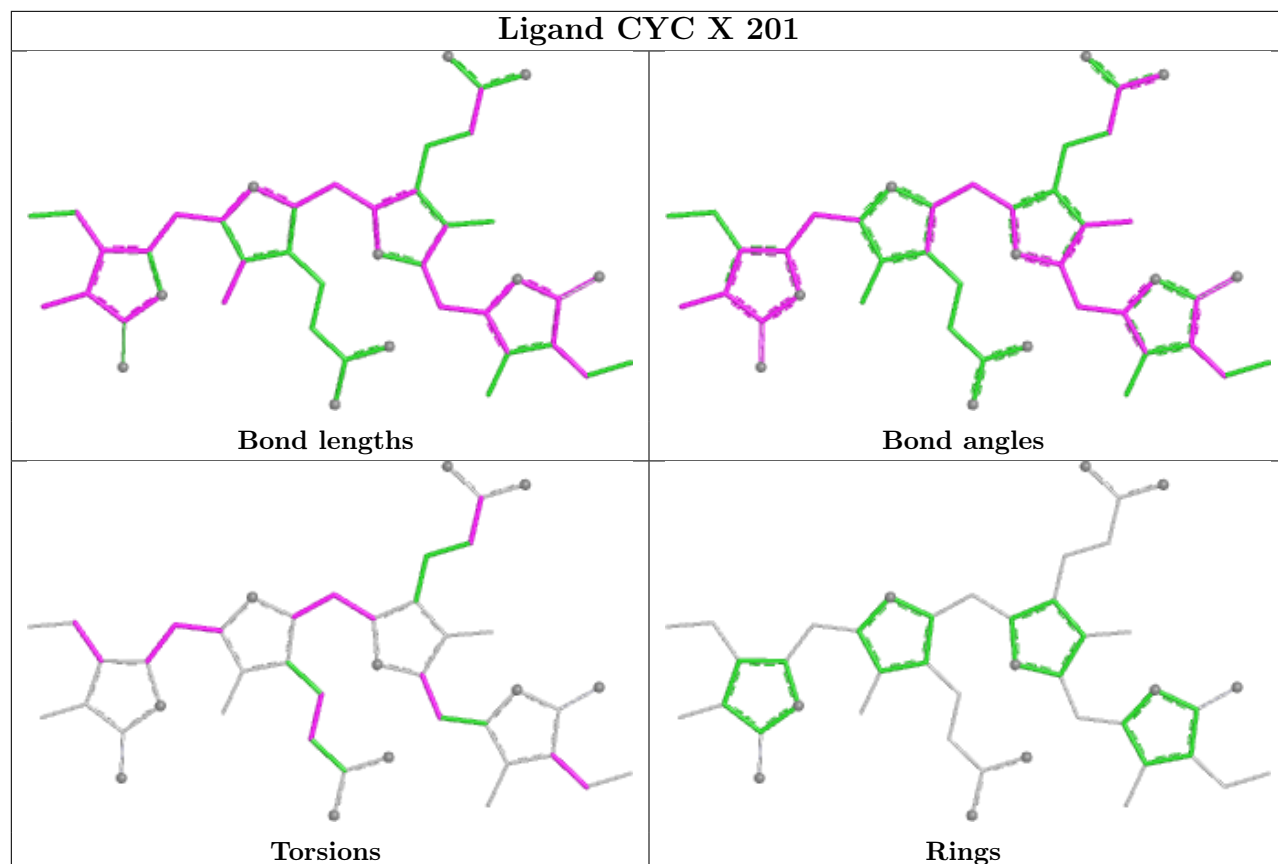


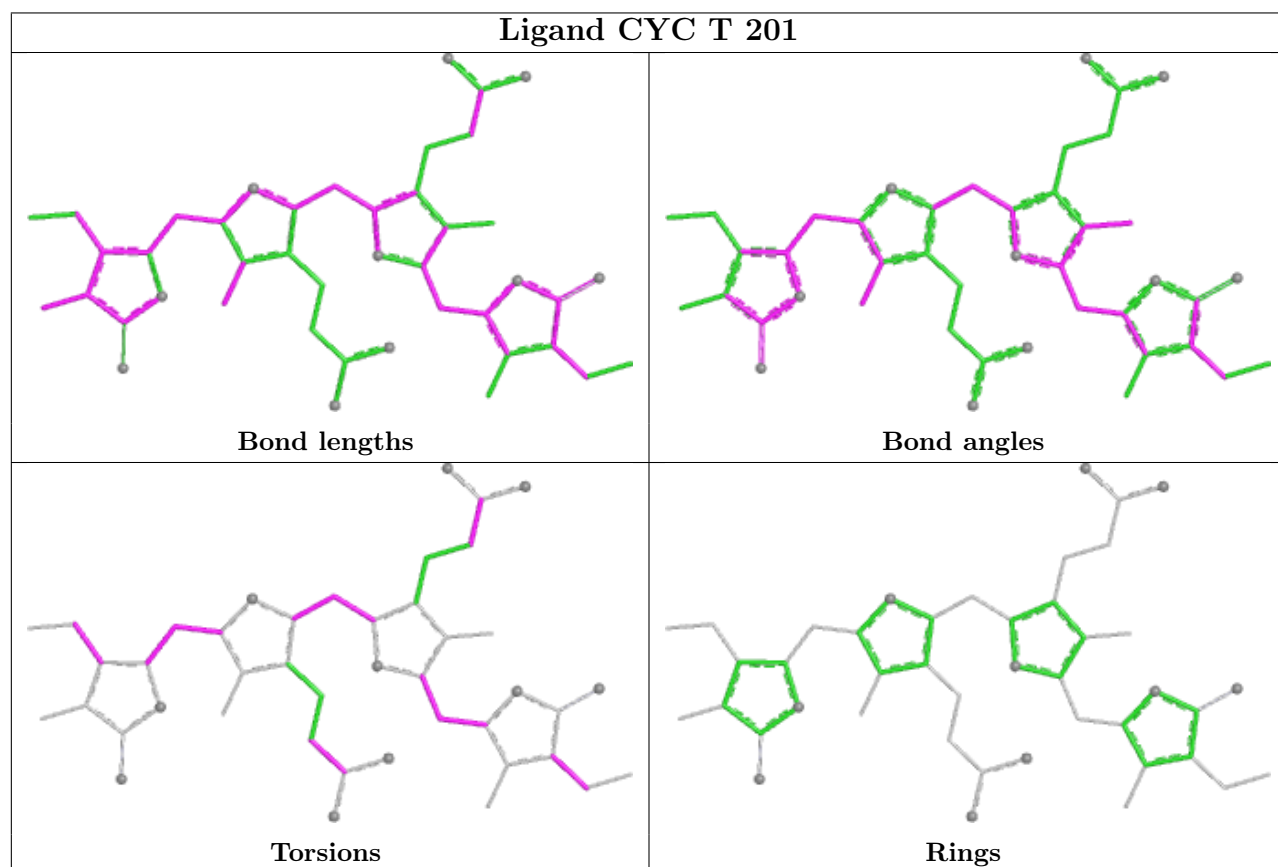
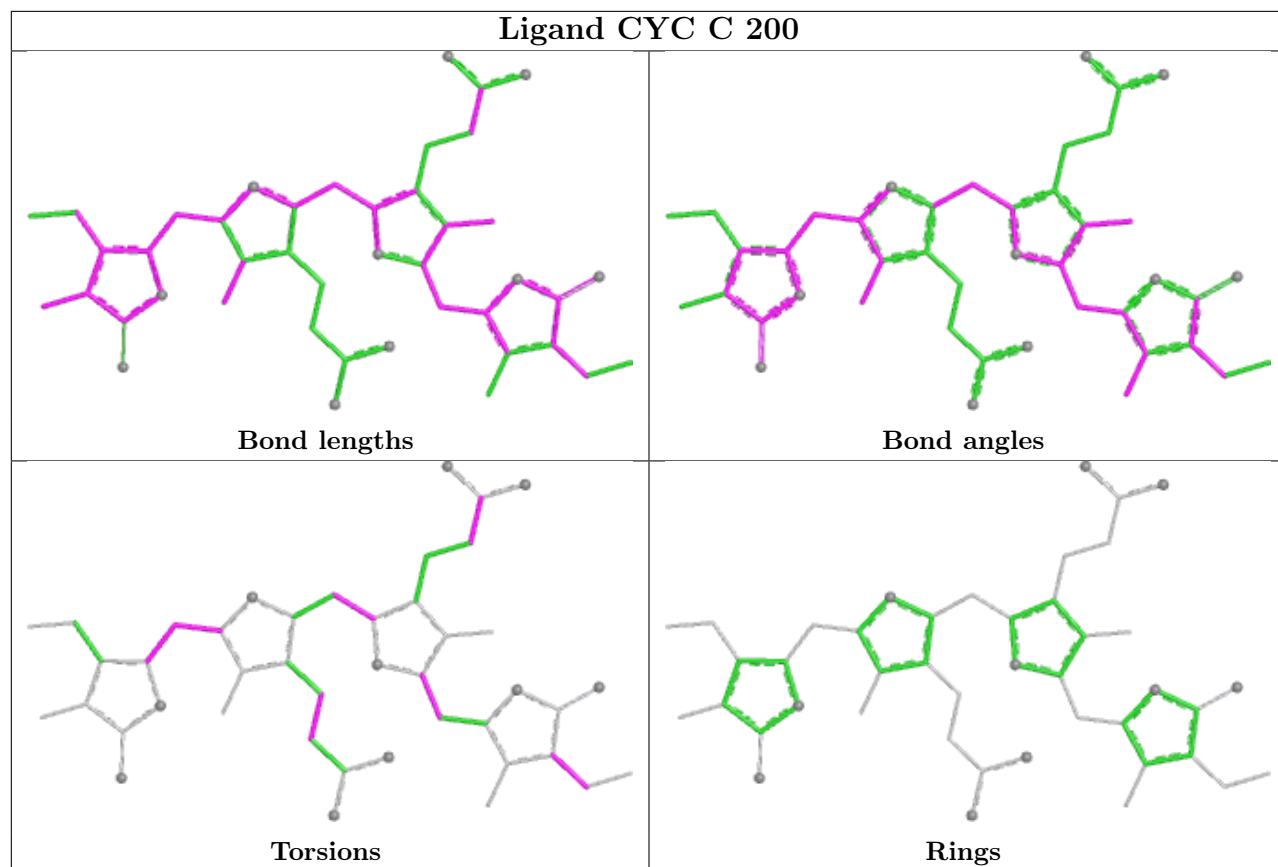


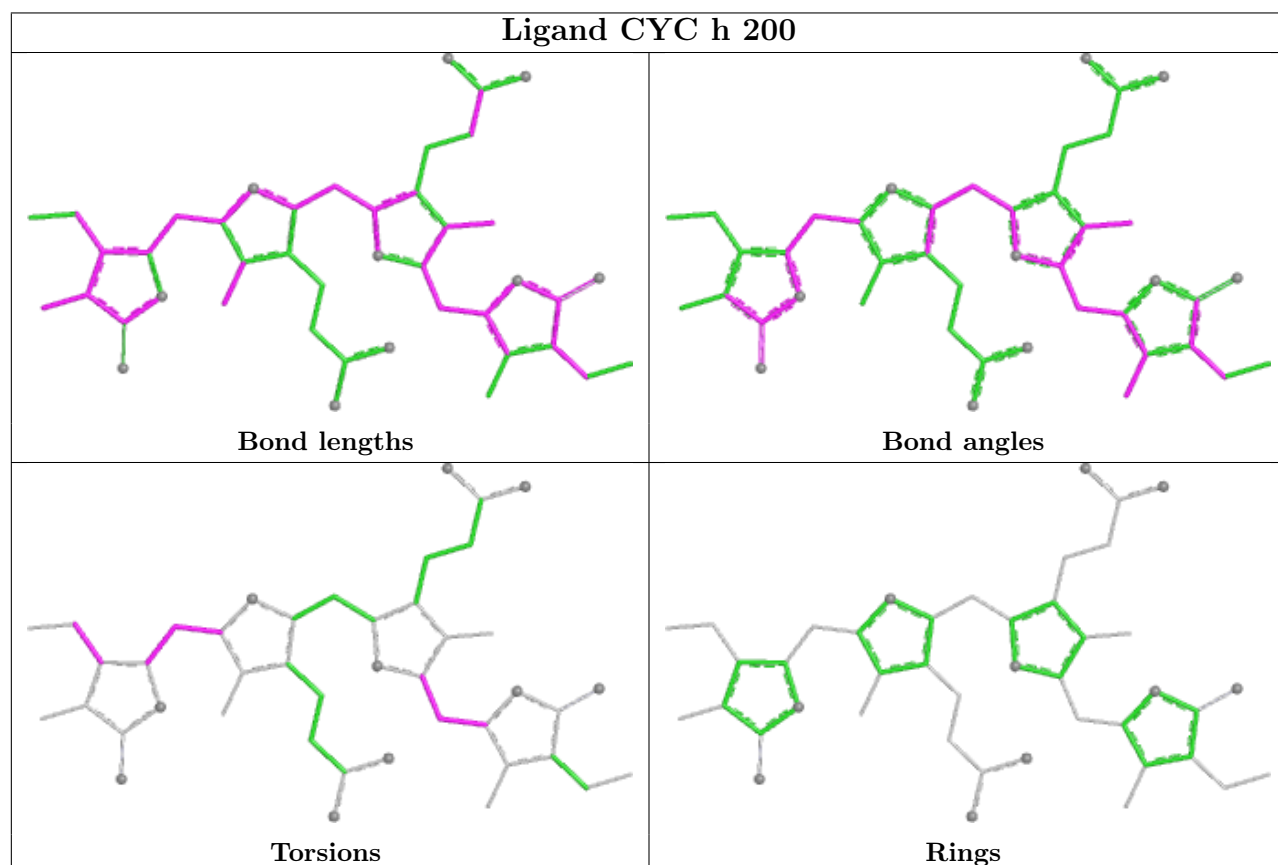
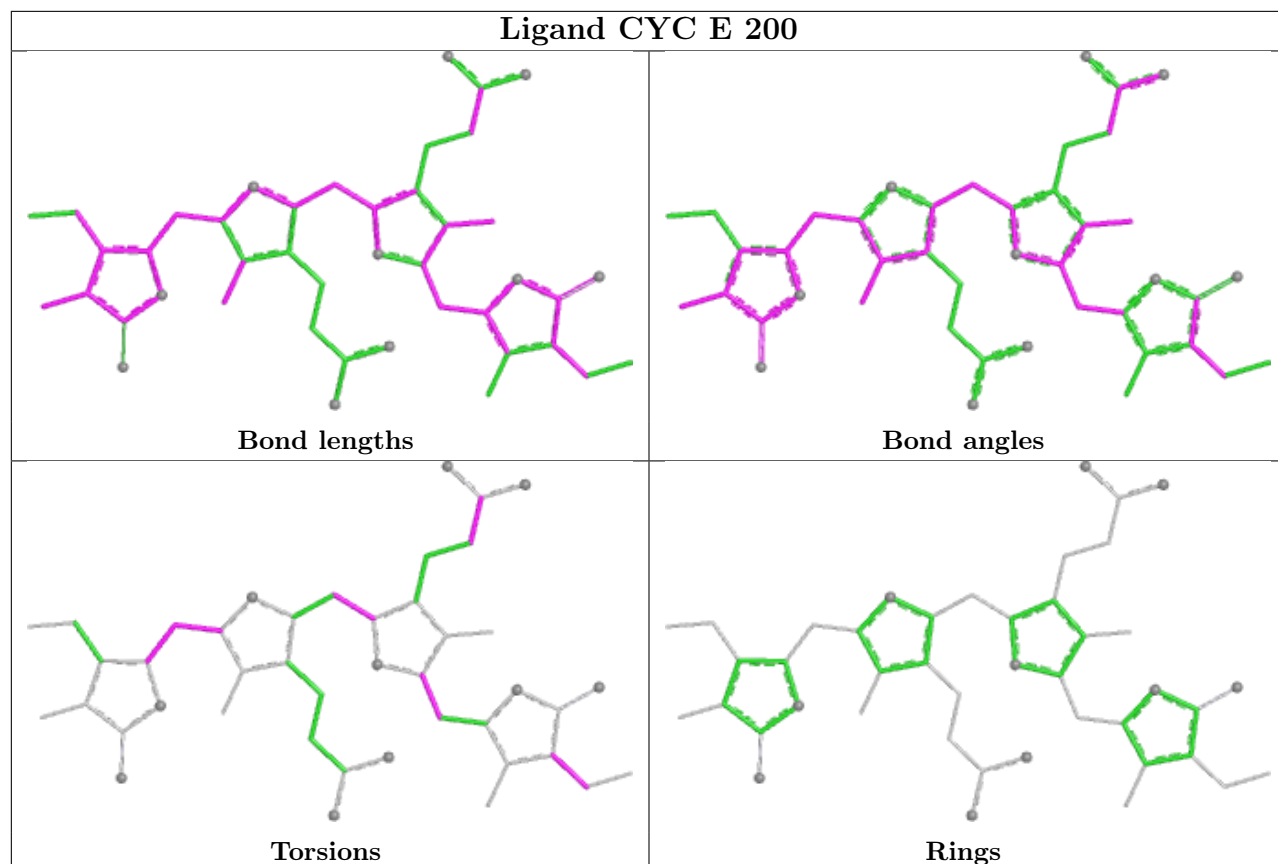


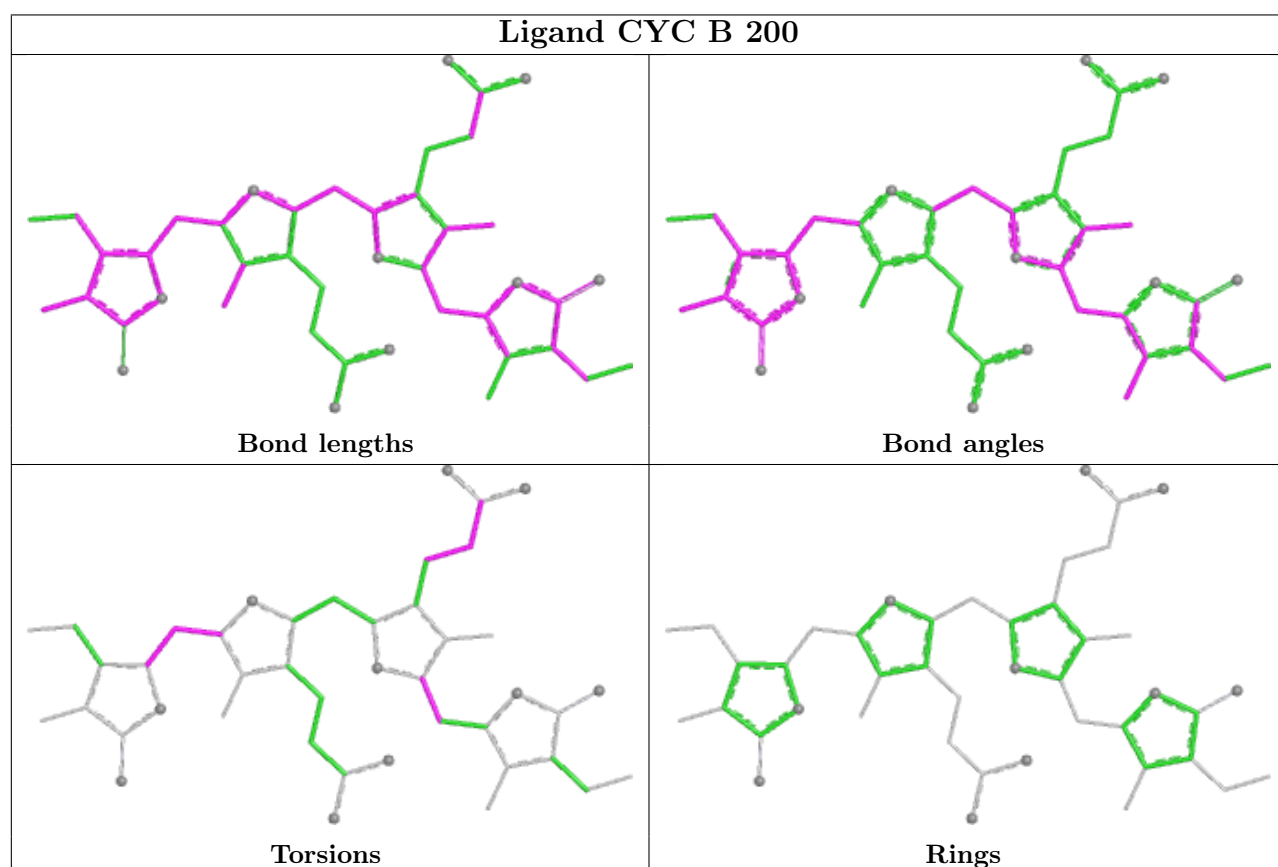
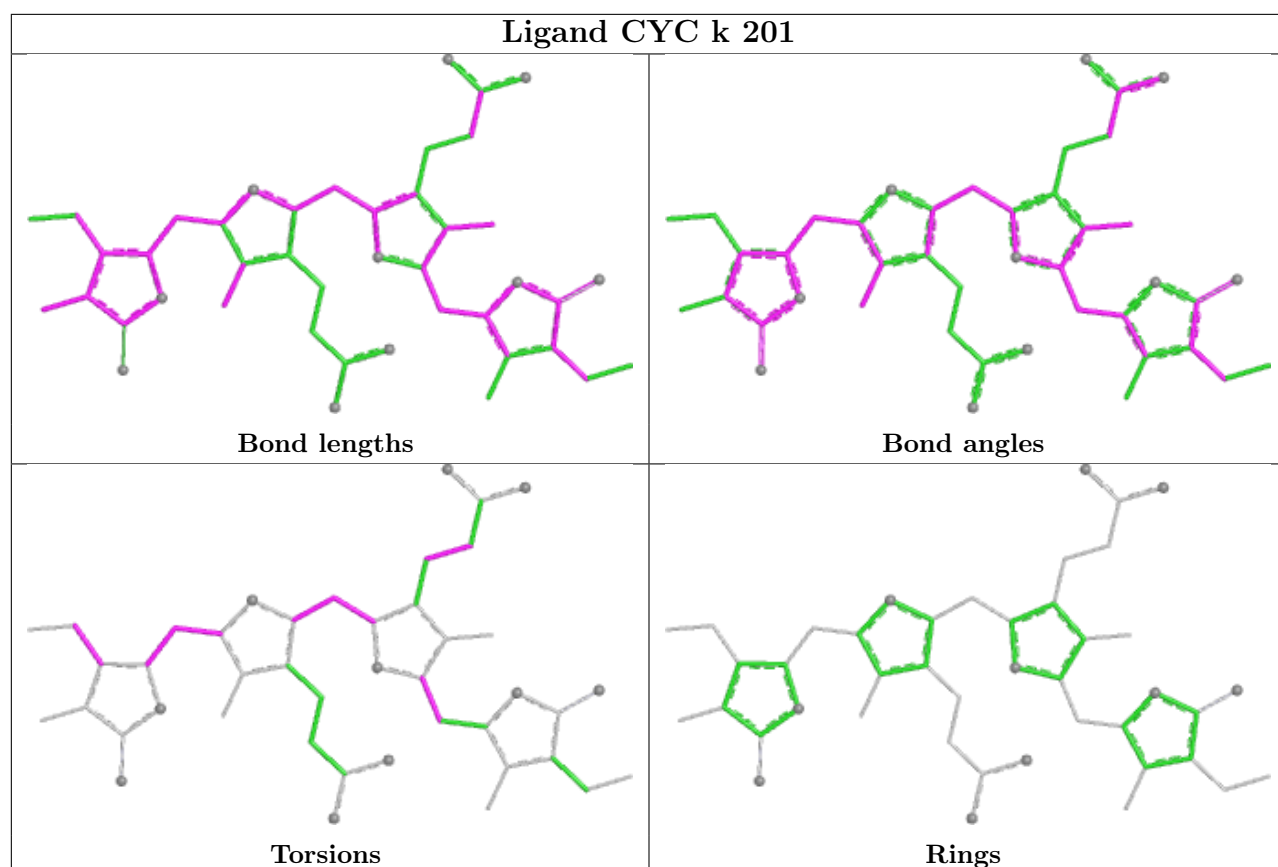


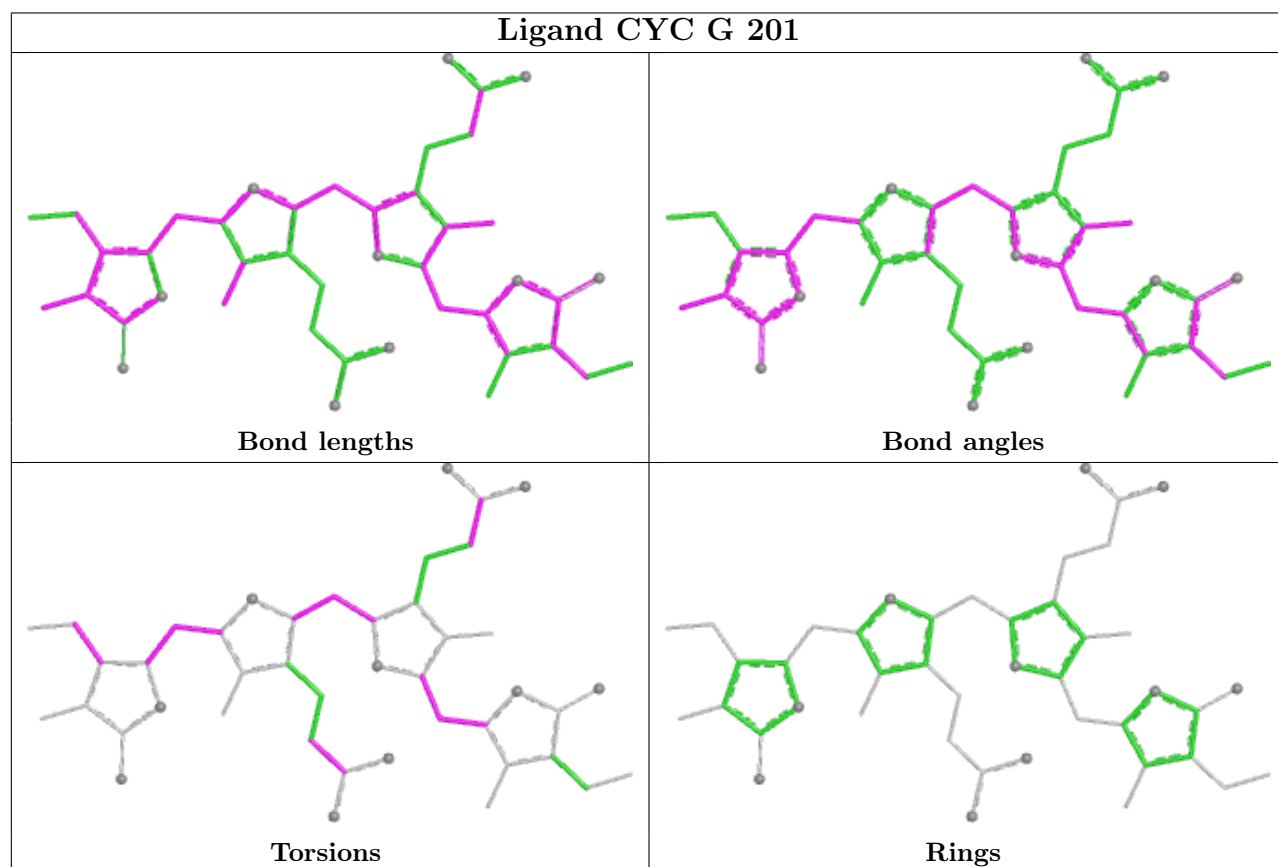
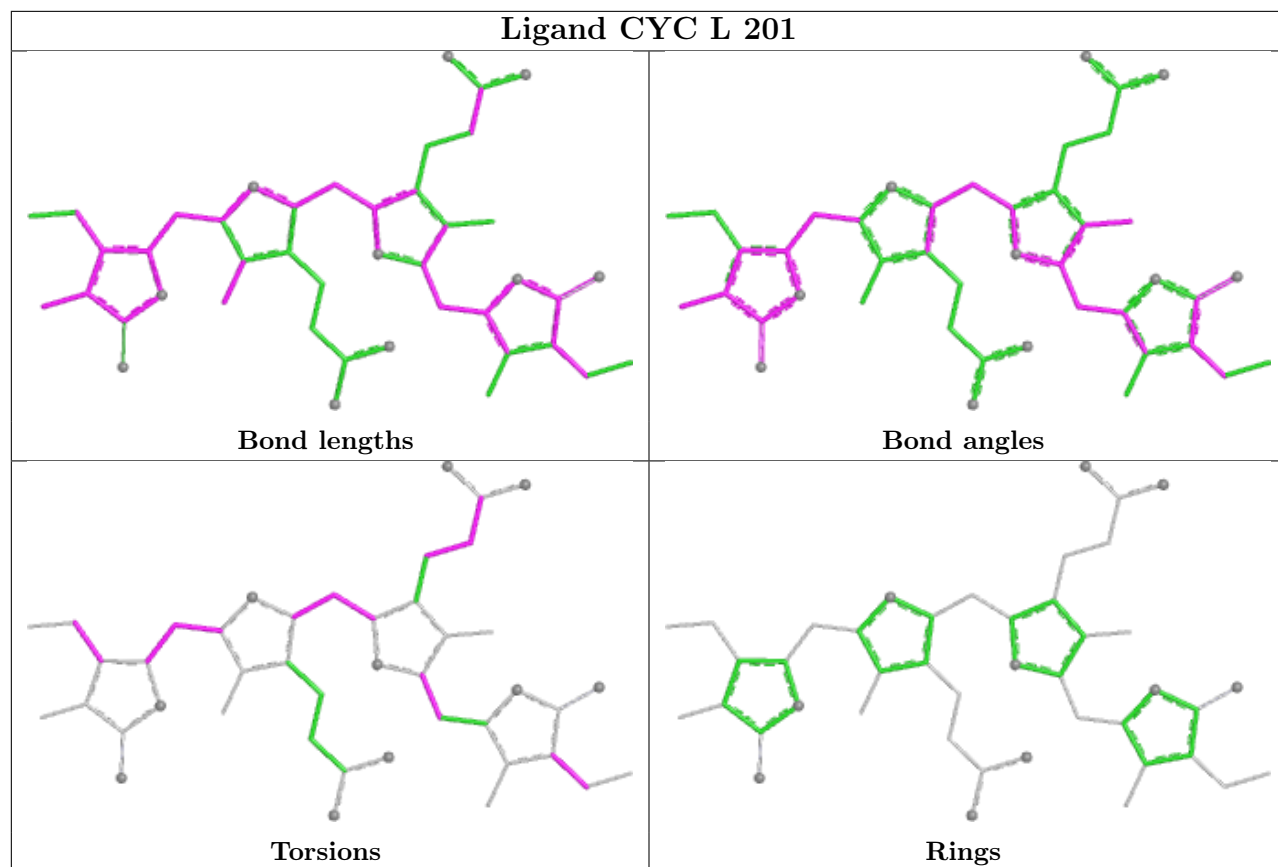


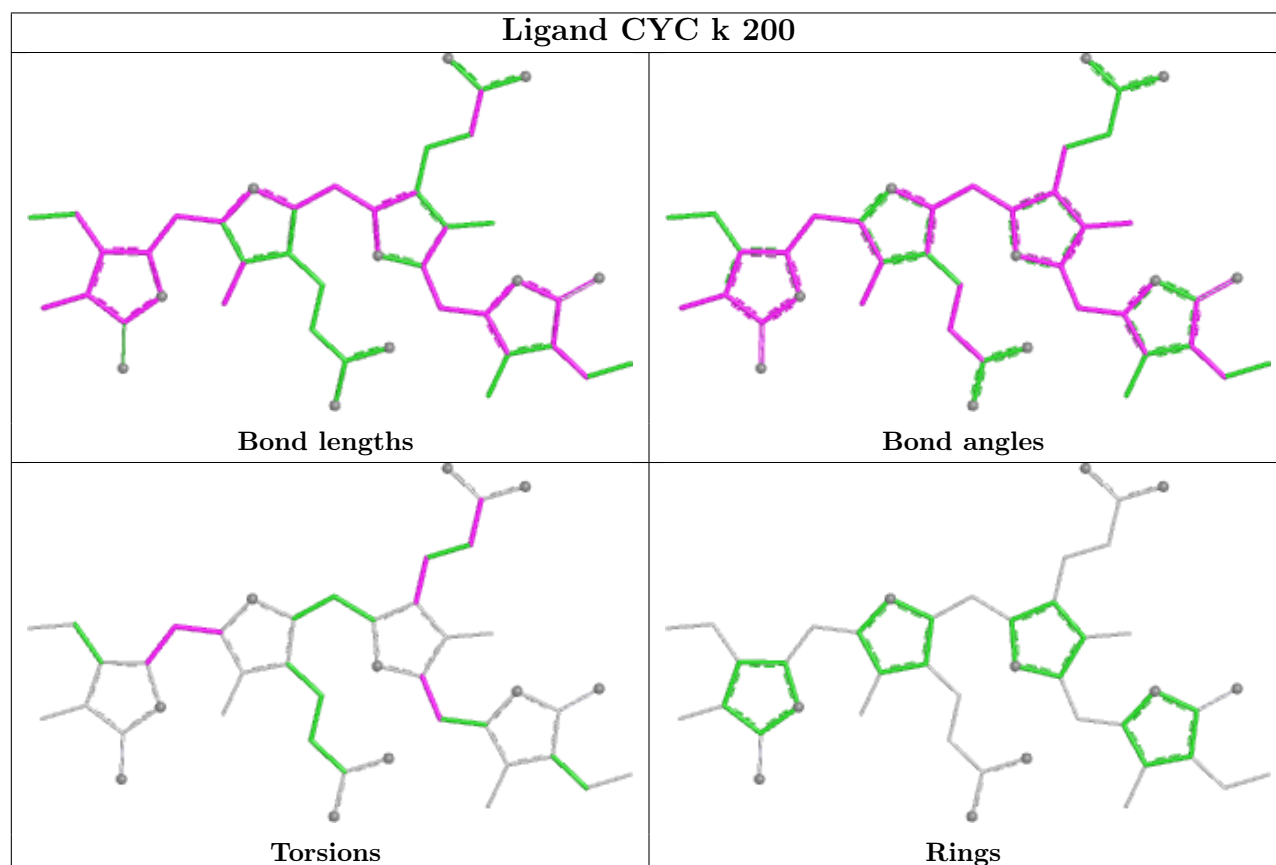
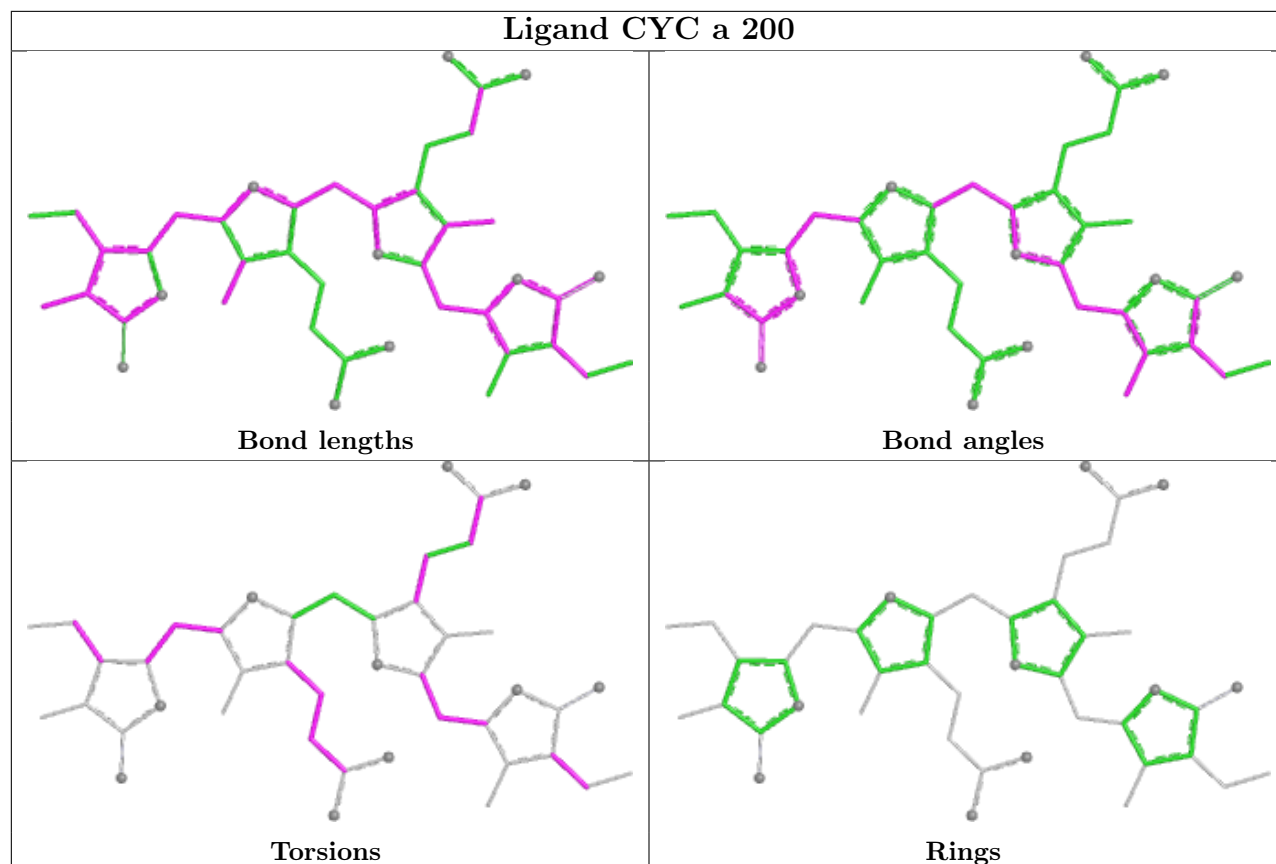


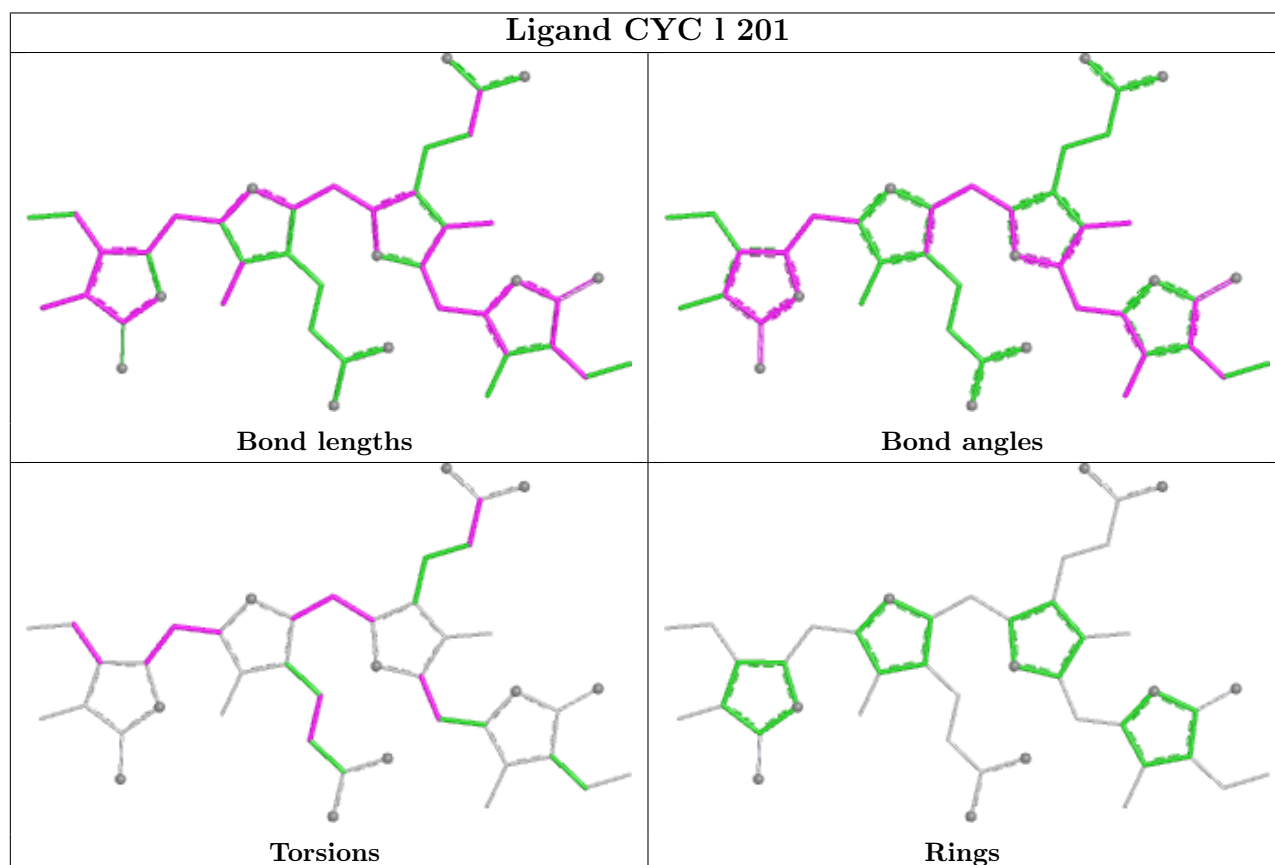
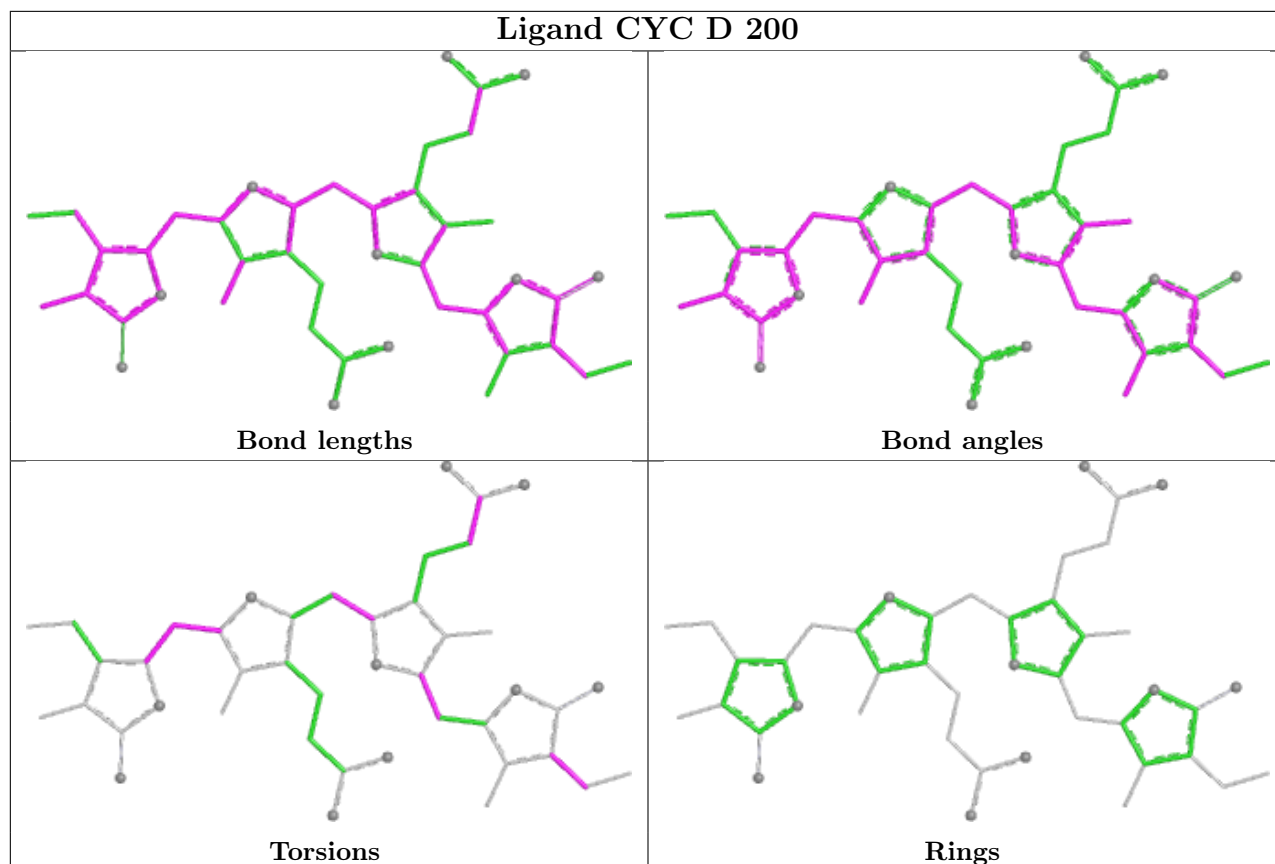


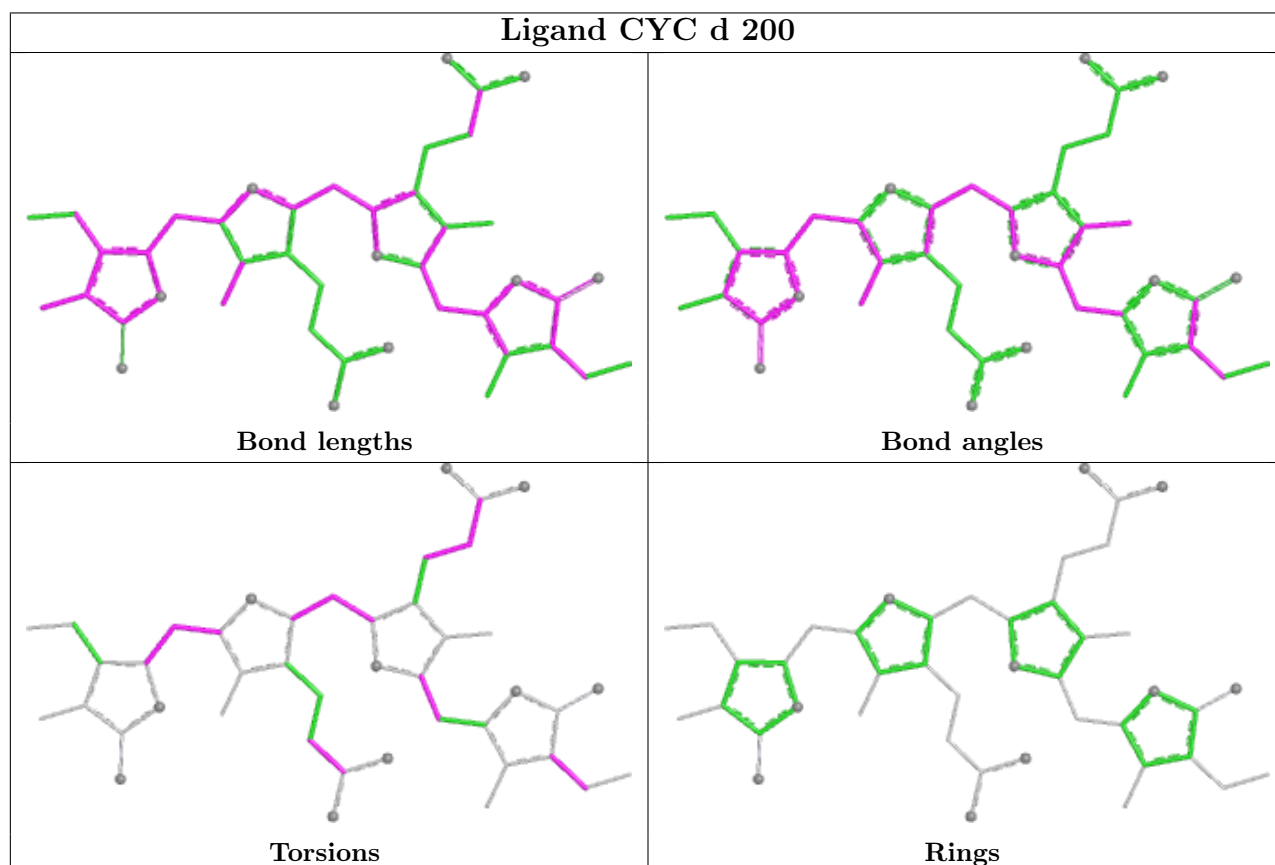
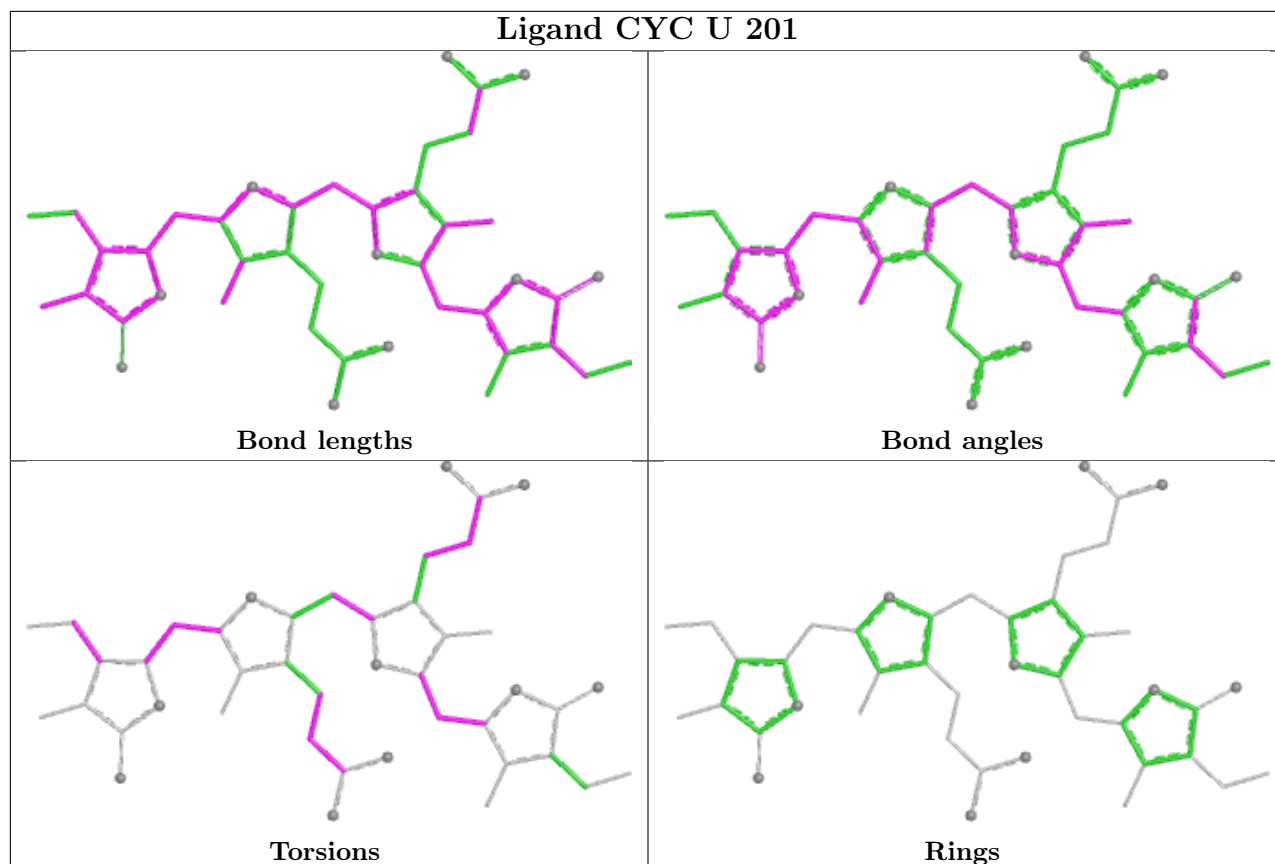


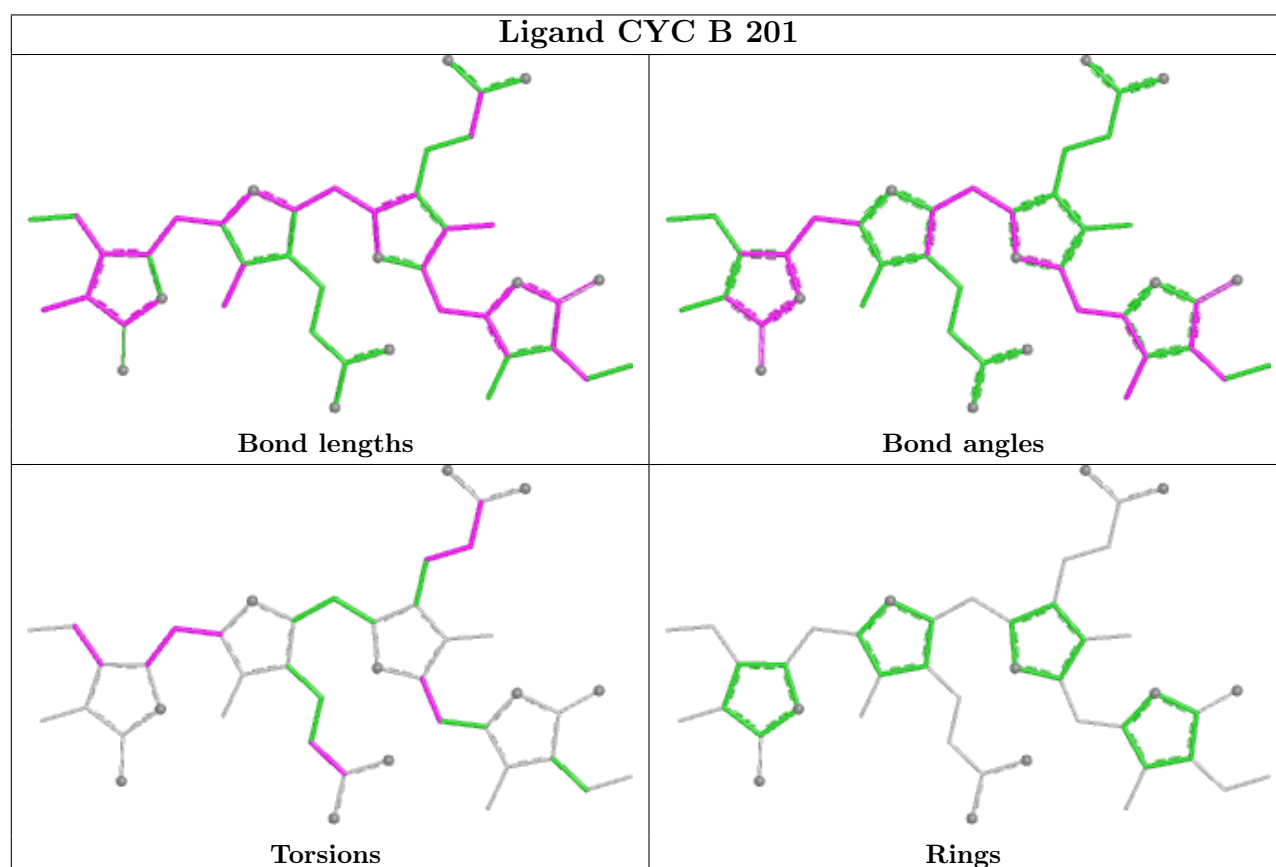
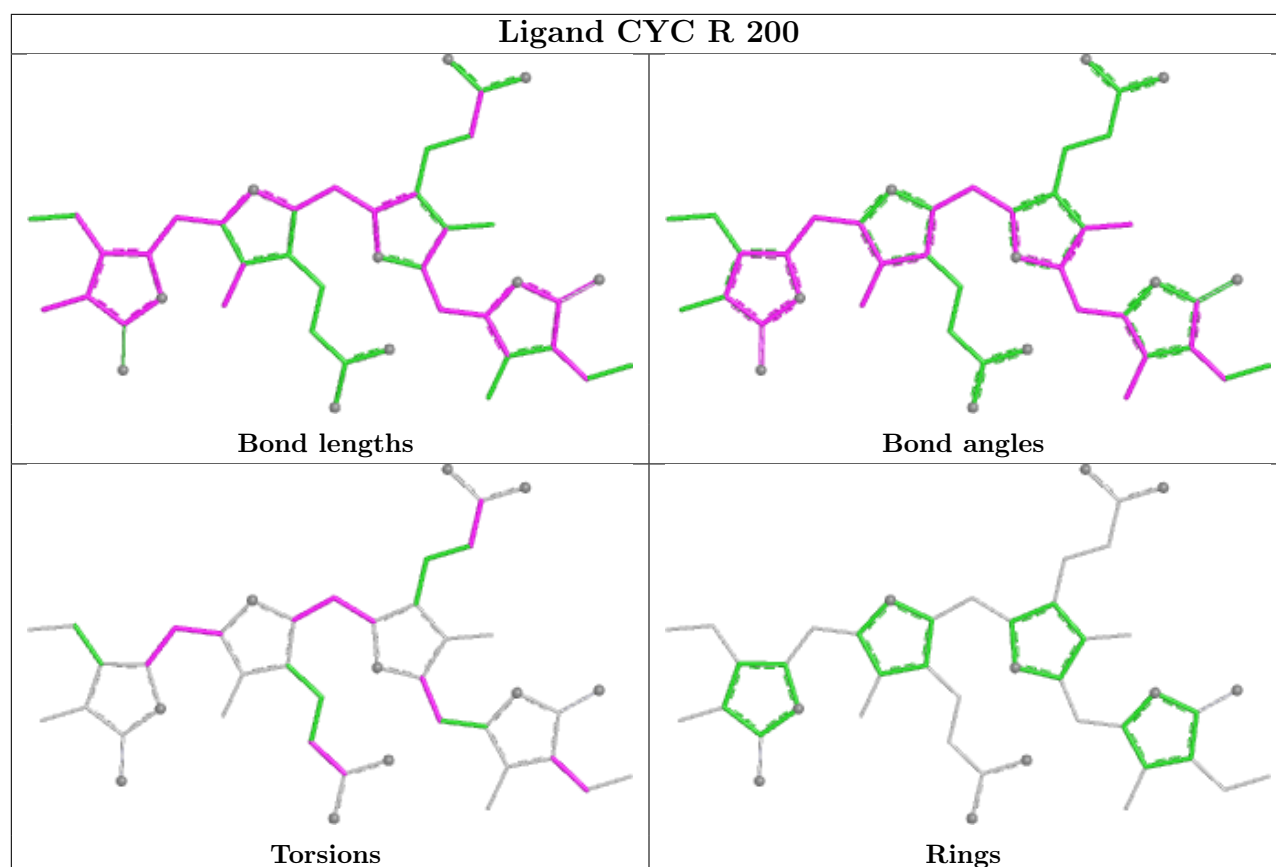


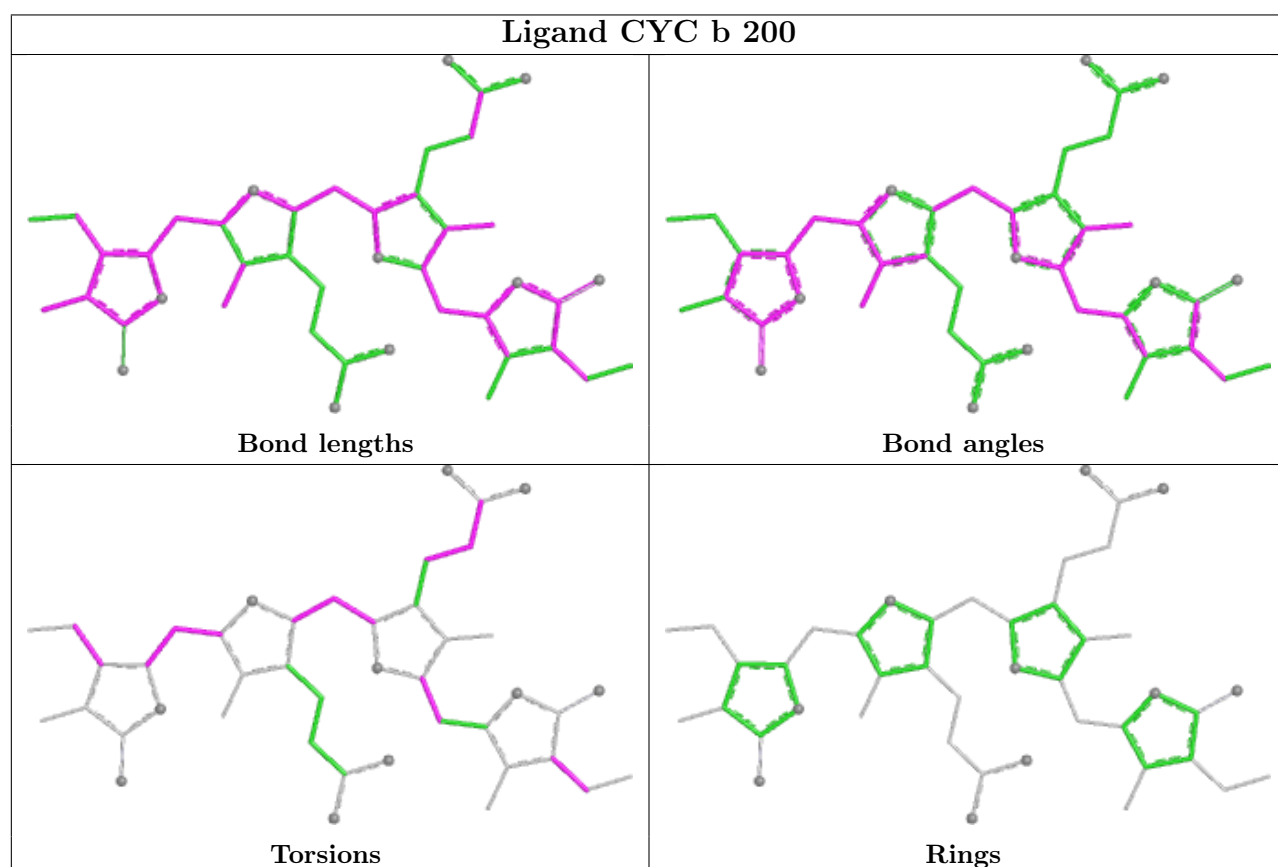
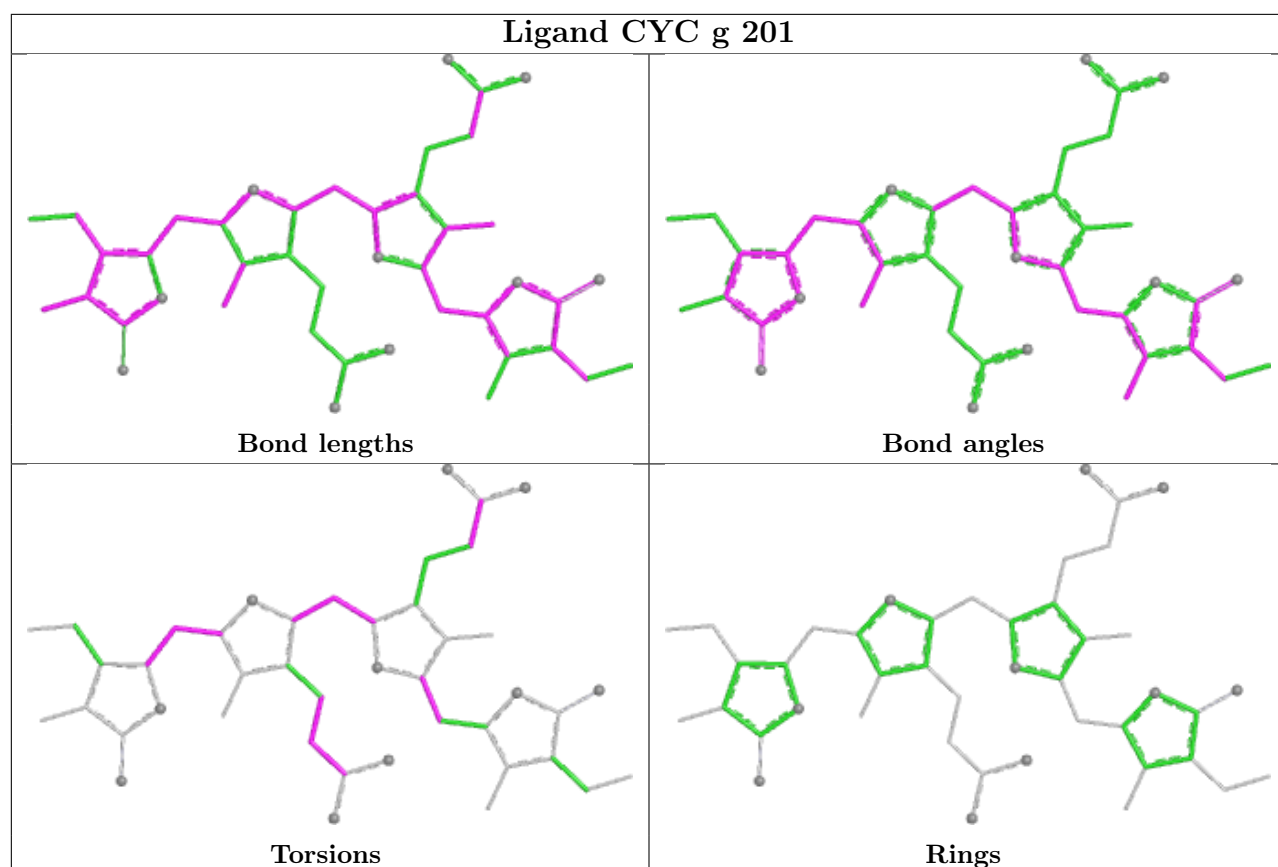


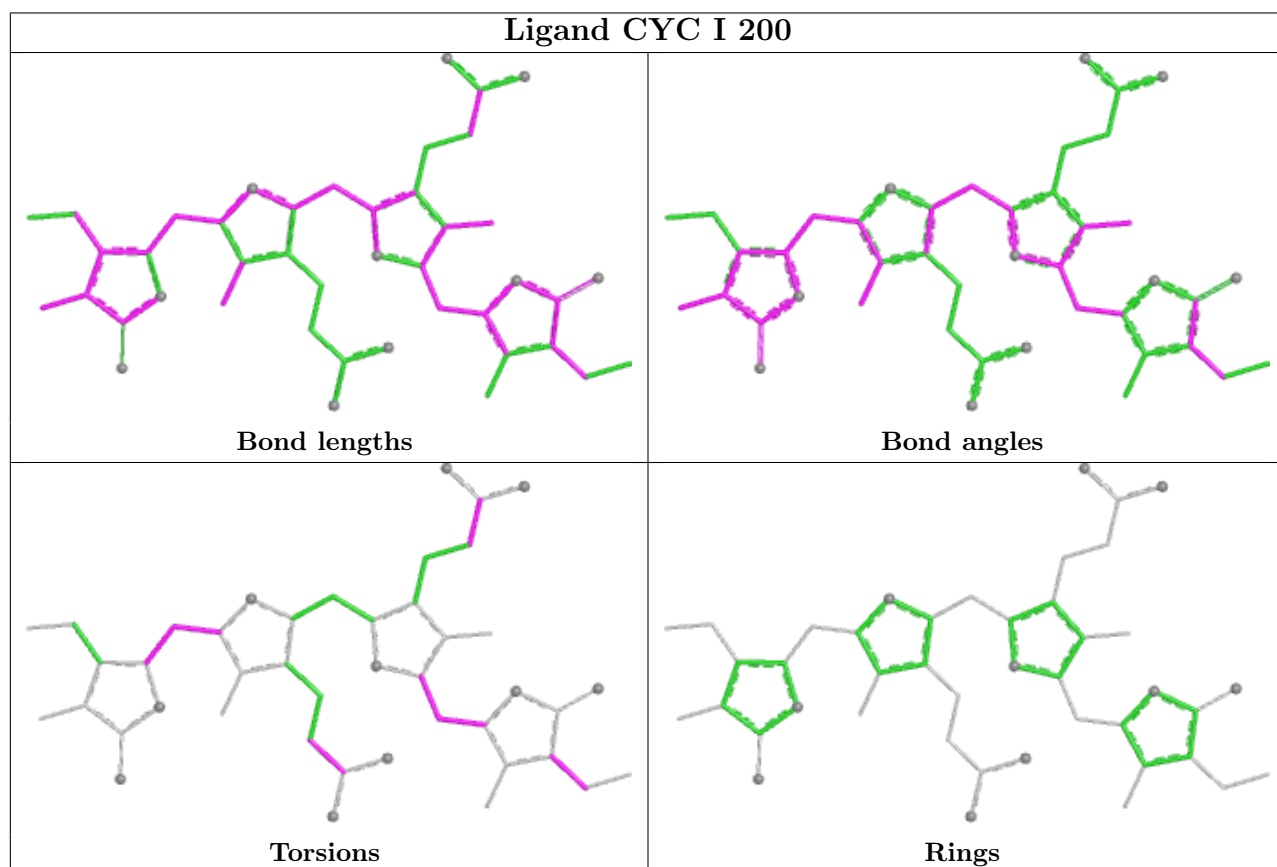
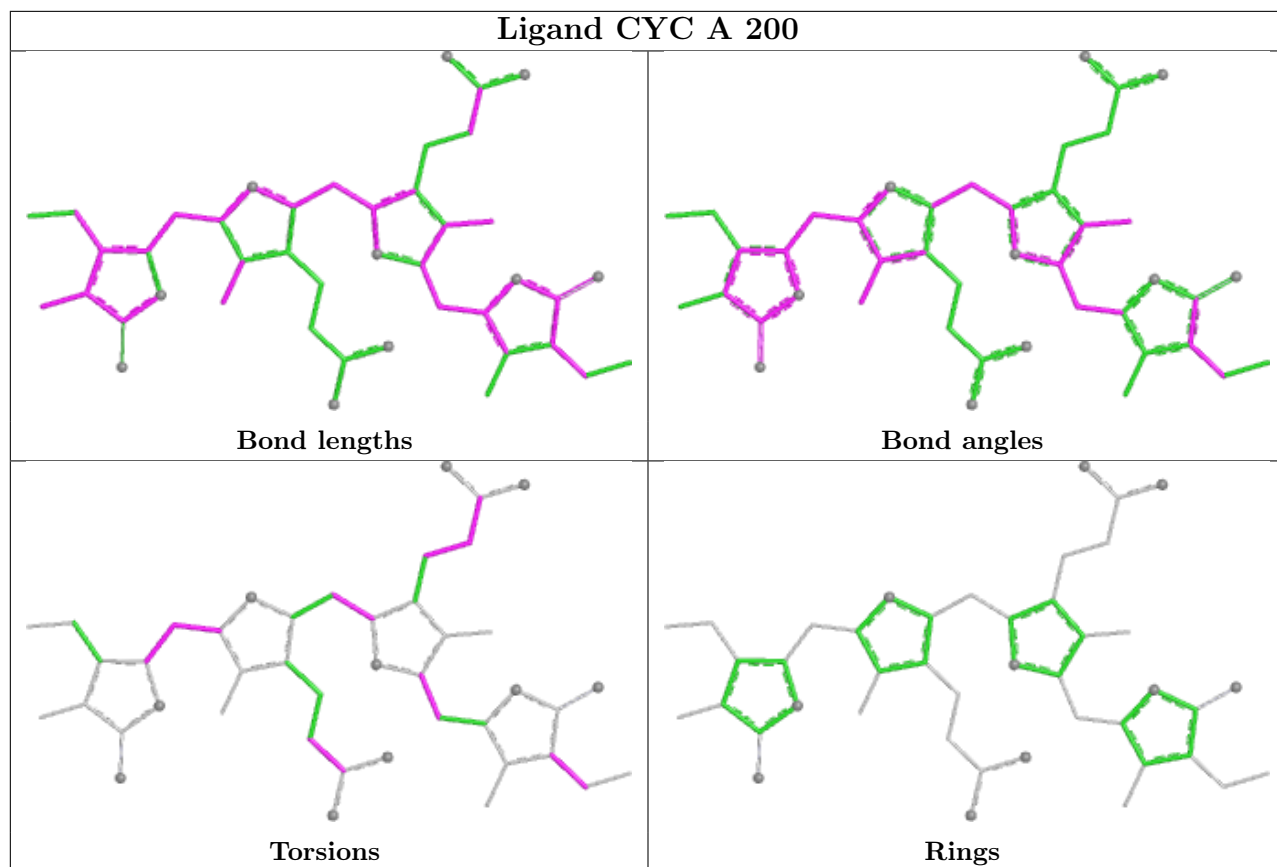


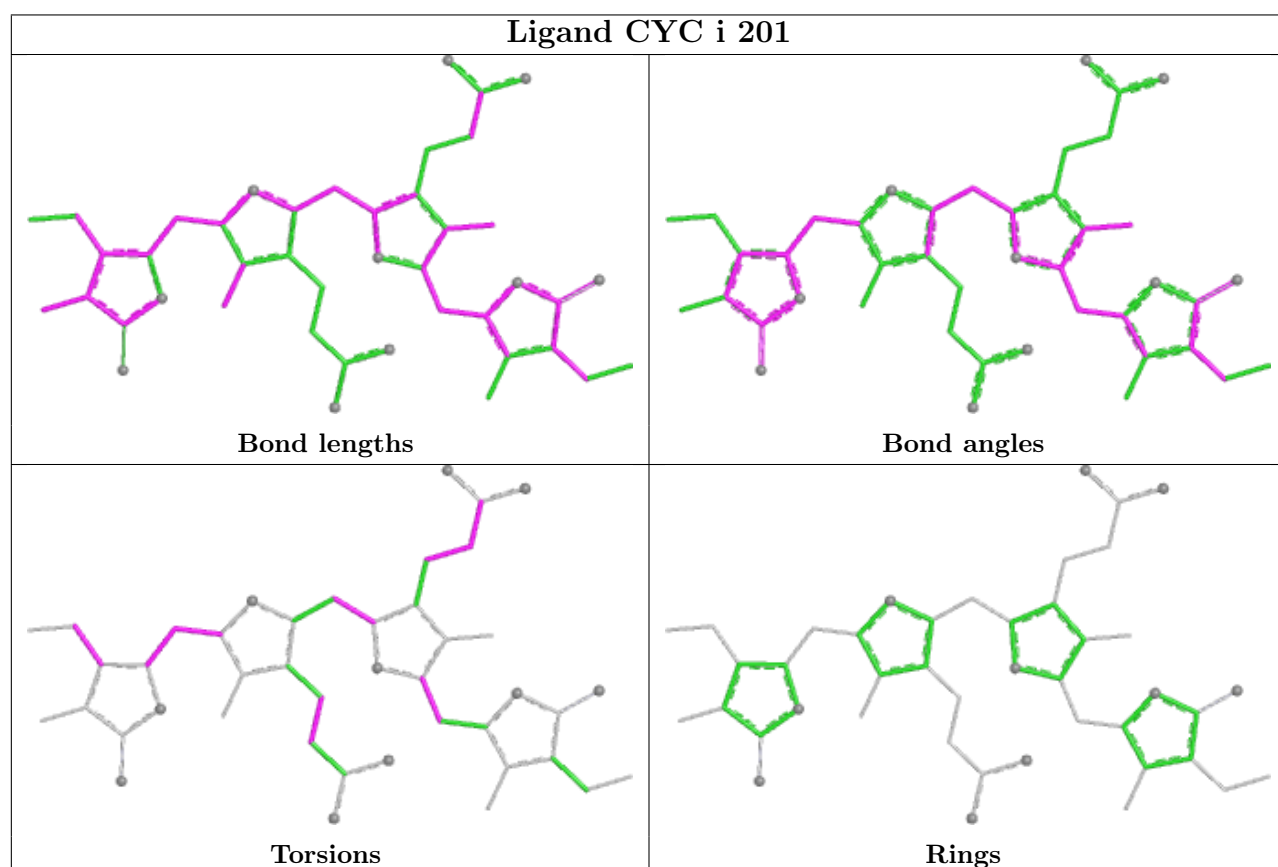
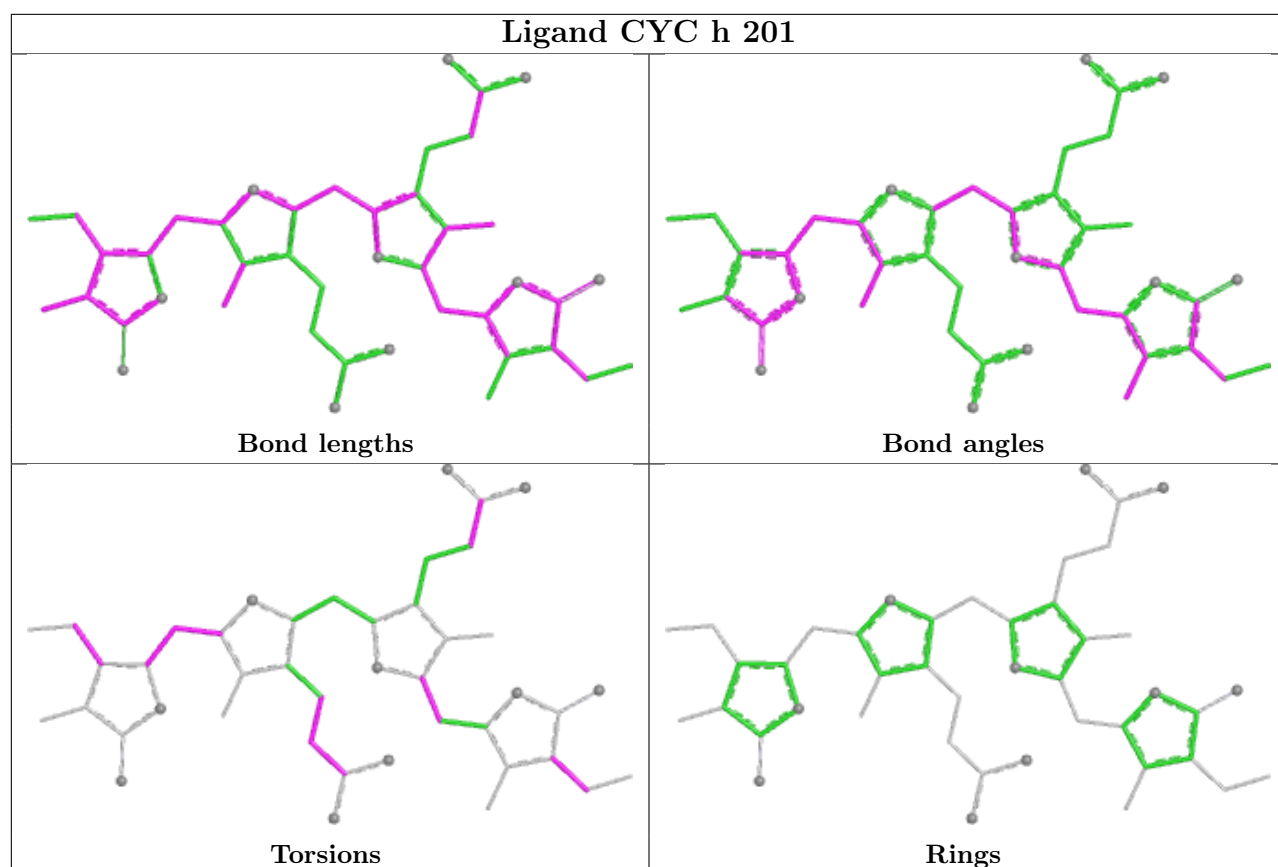


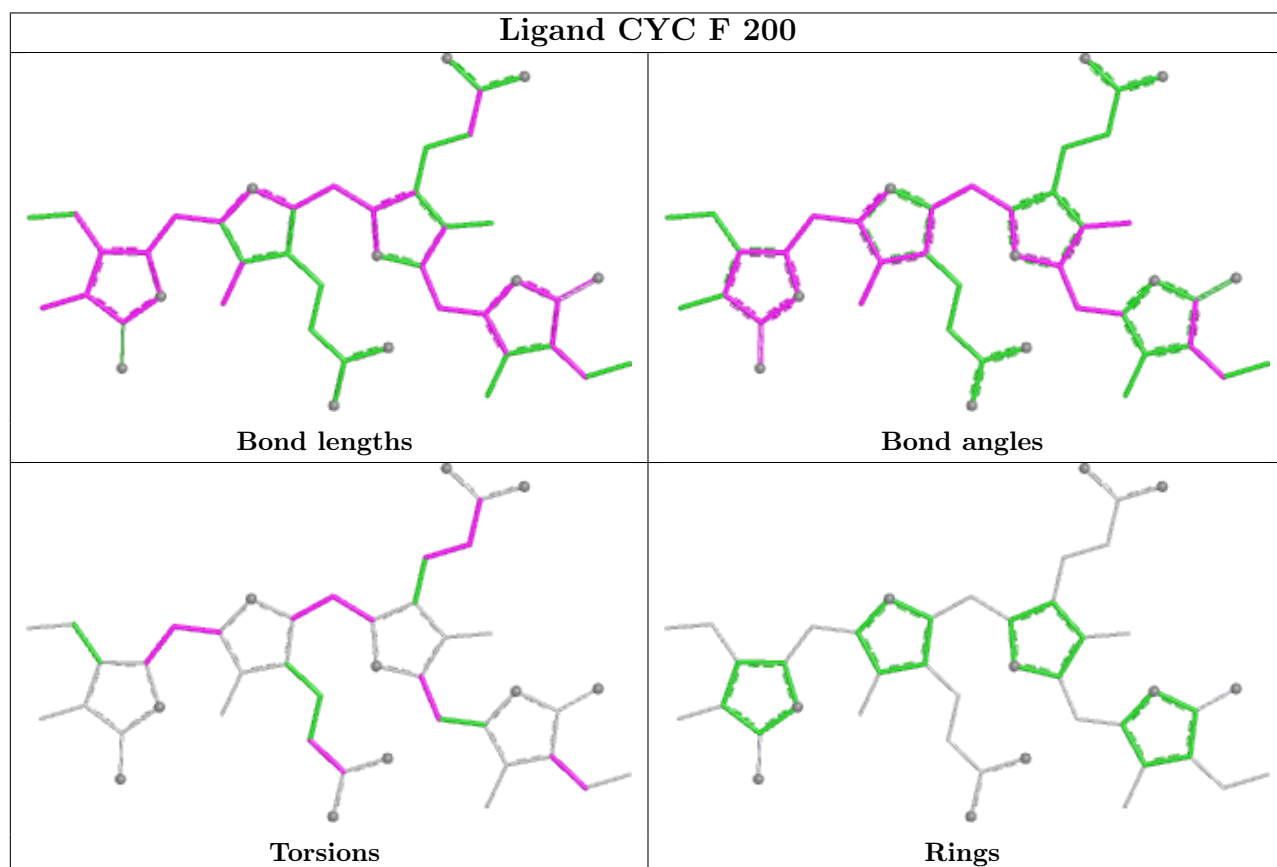
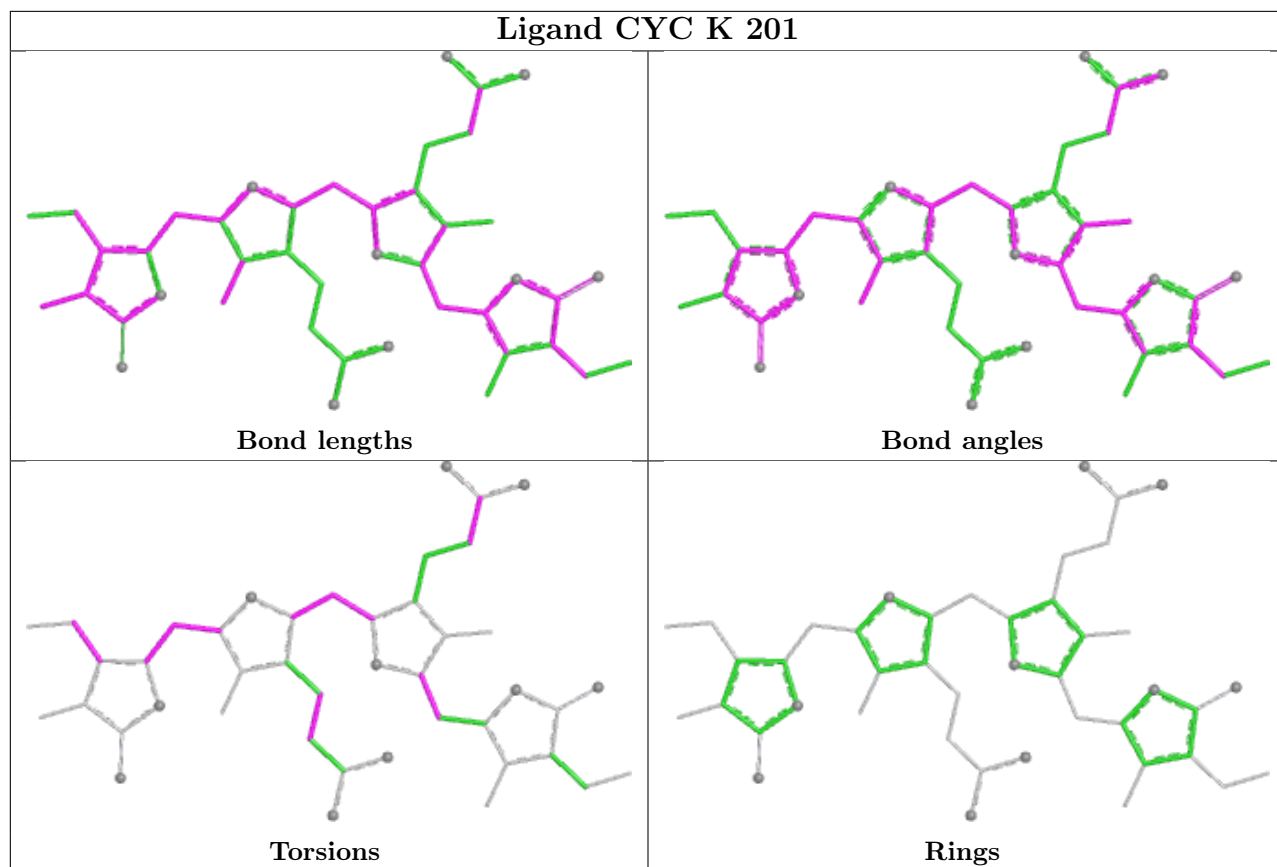


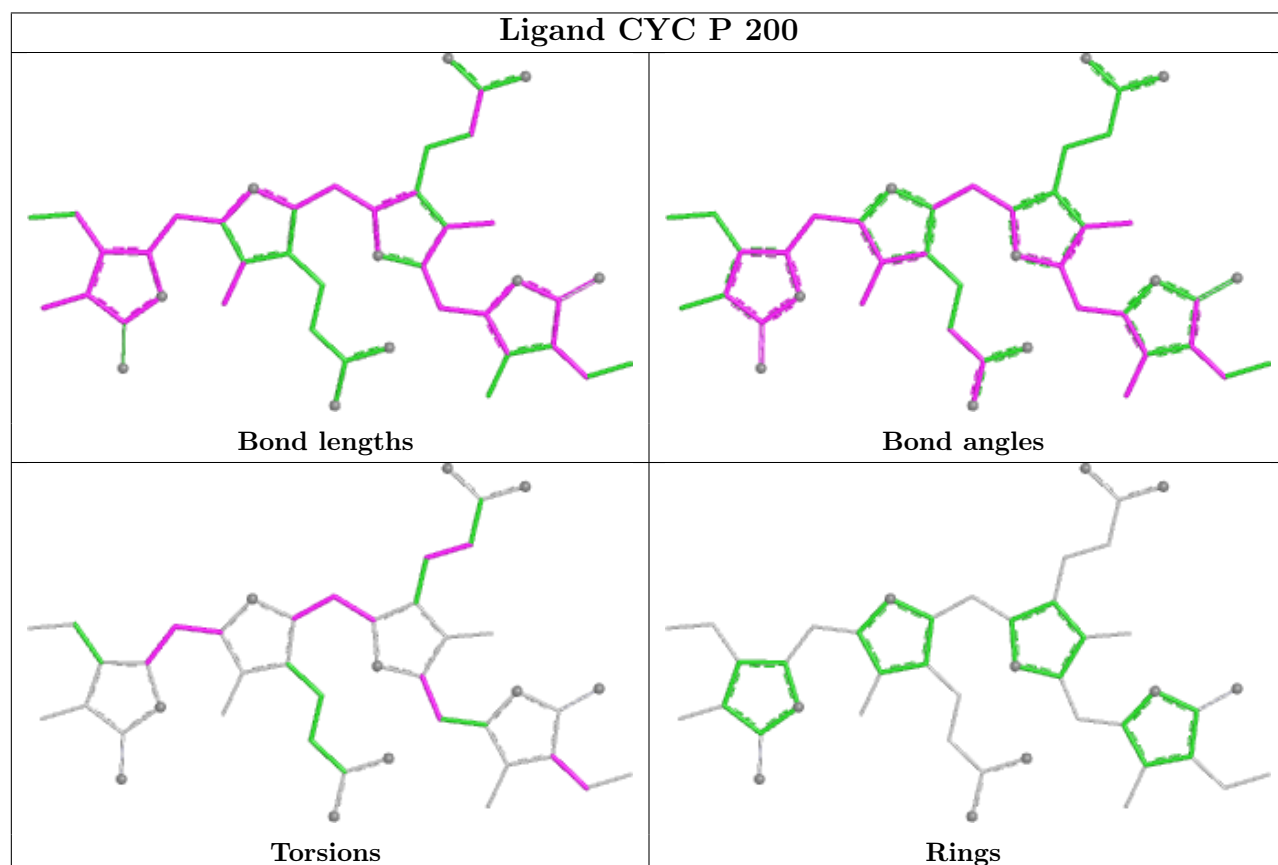
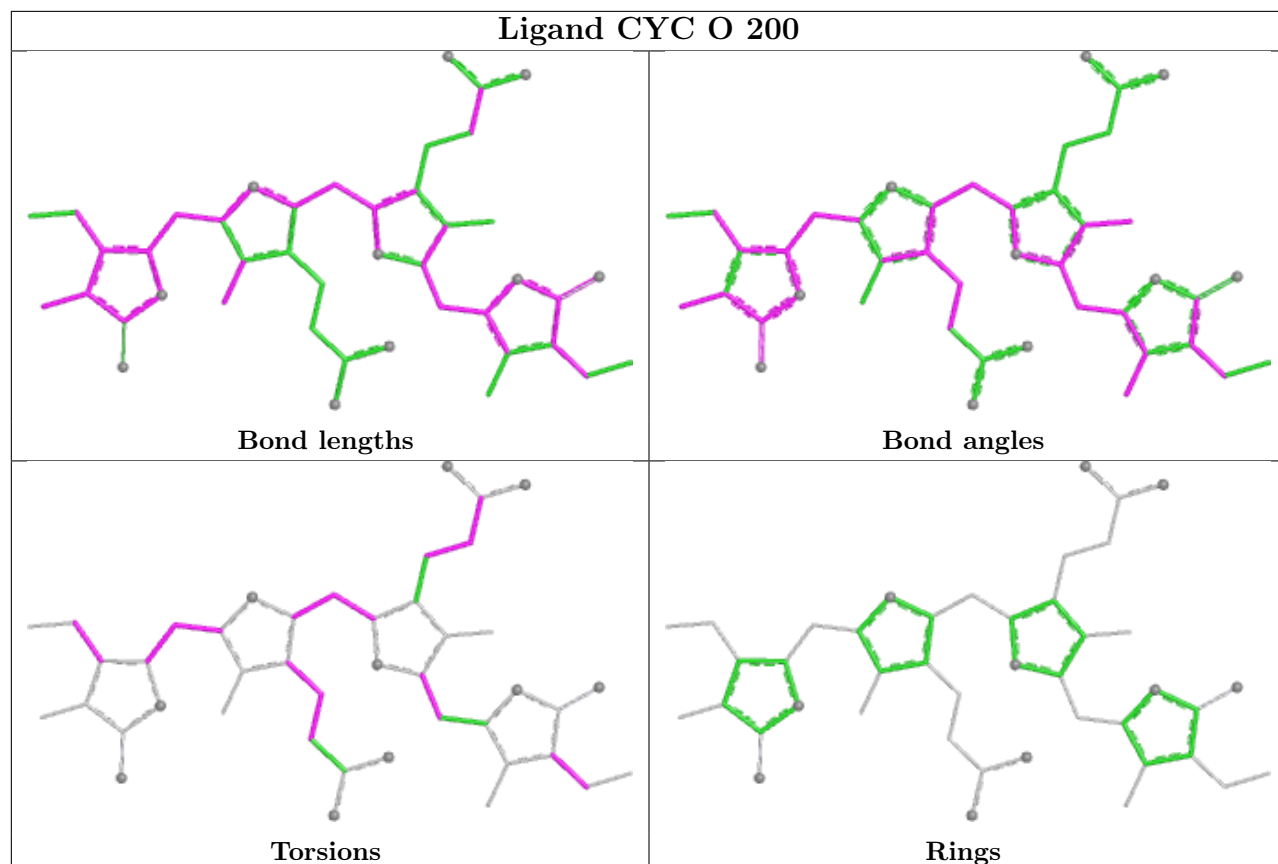


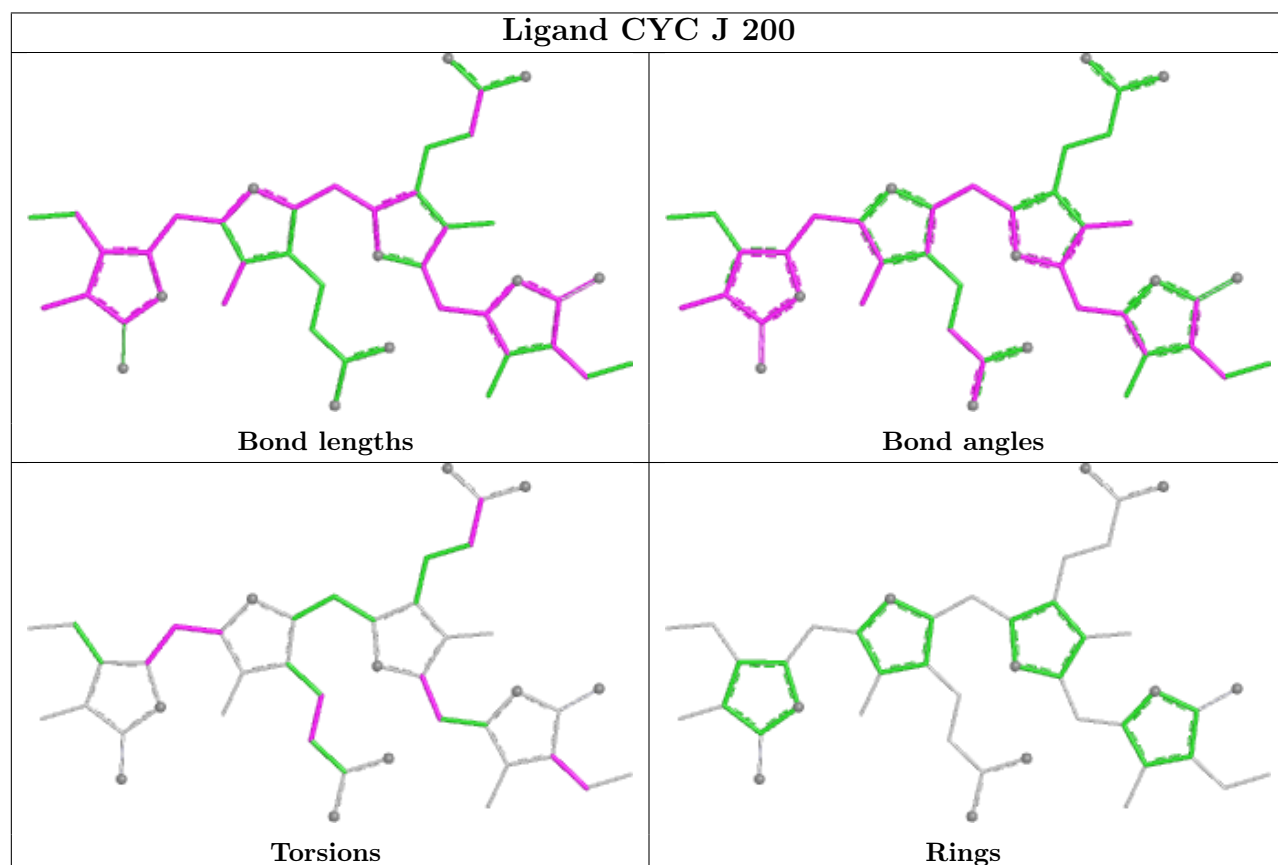
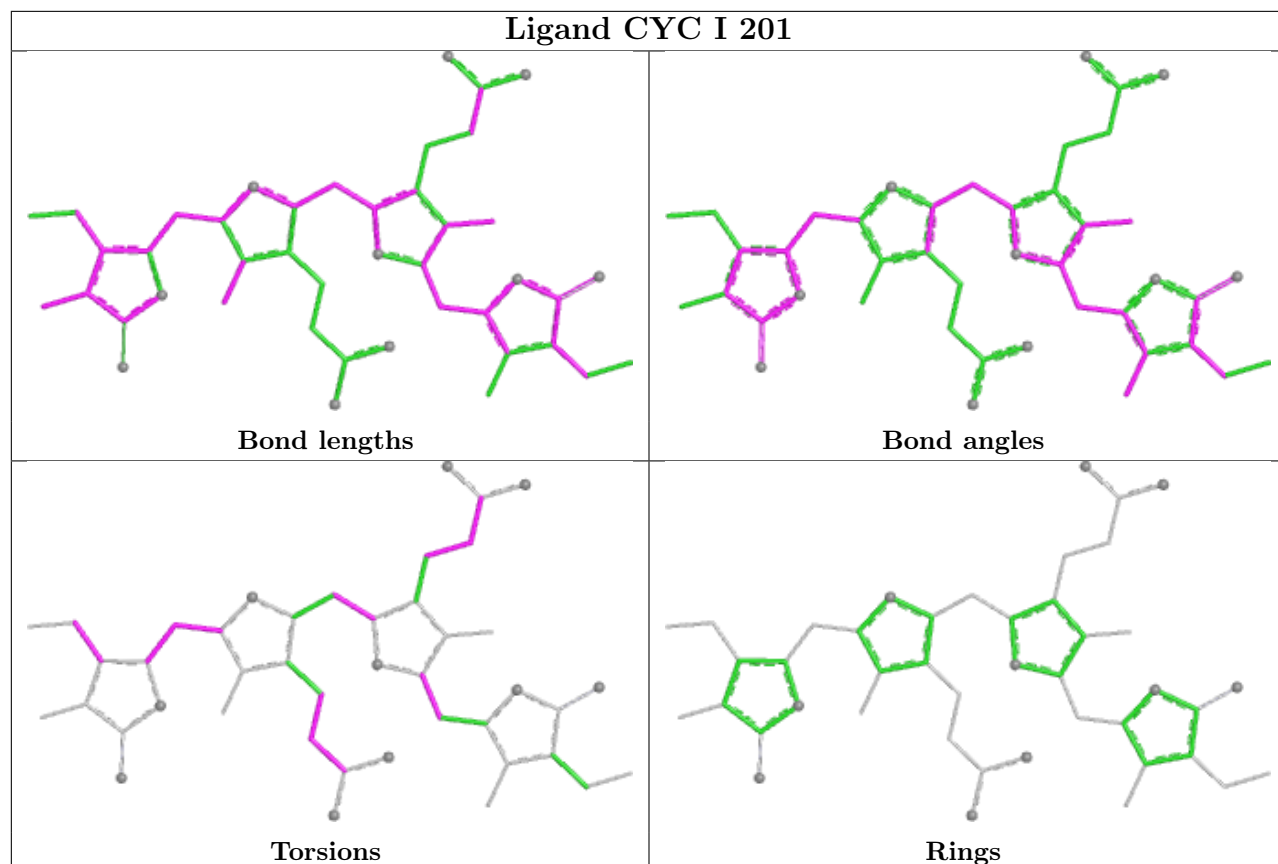












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

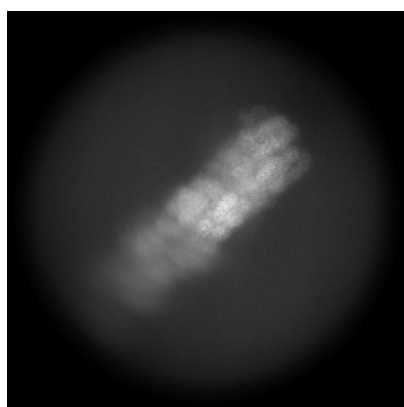
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35569. These allow visual inspection of the internal detail of the map and identification of artifacts.

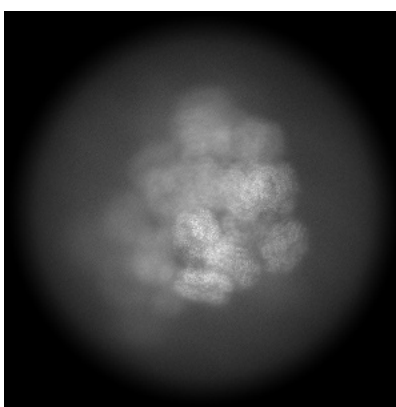
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

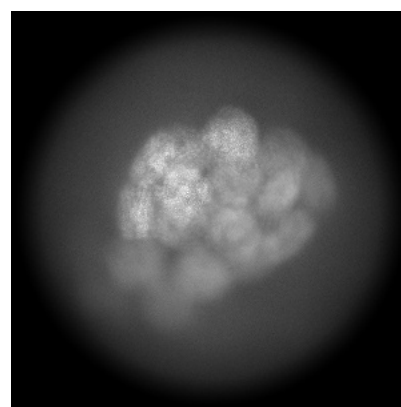
6.1.1 Primary map



X



Y

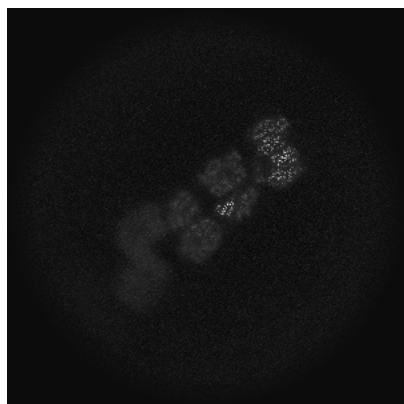


Z

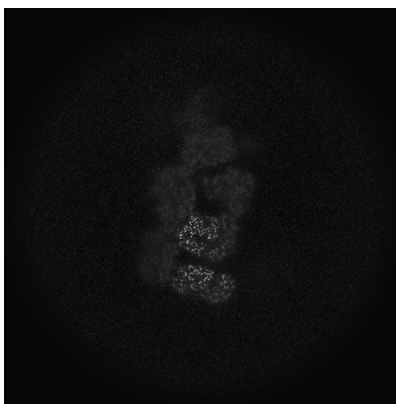
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

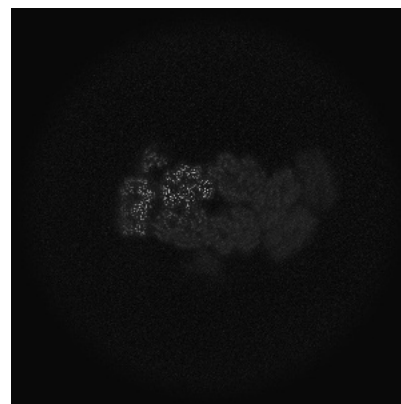
6.2.1 Primary map



X Index: 340



Y Index: 340

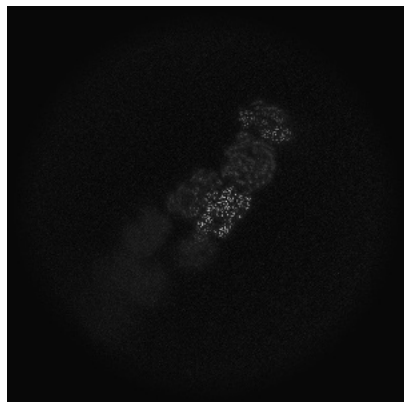


Z Index: 340

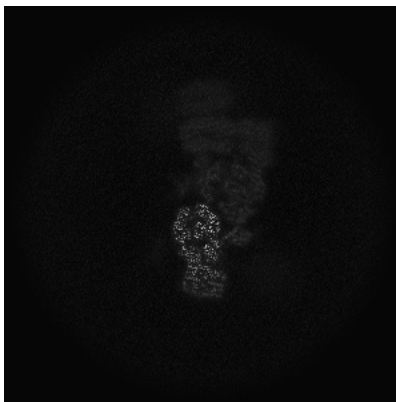
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

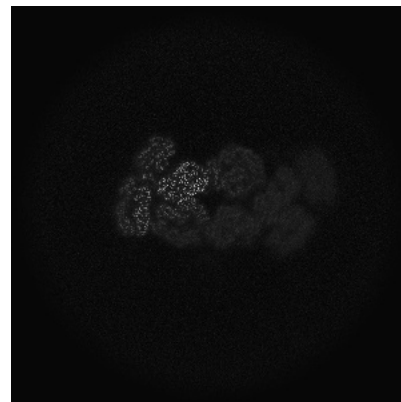
6.3.1 Primary map



X Index: 299



Y Index: 369

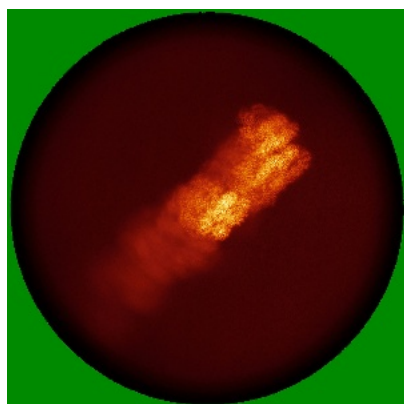


Z Index: 352

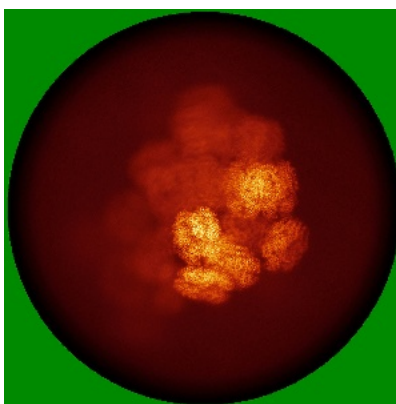
The images above show the largest variance slices of the map in three orthogonal directions.

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

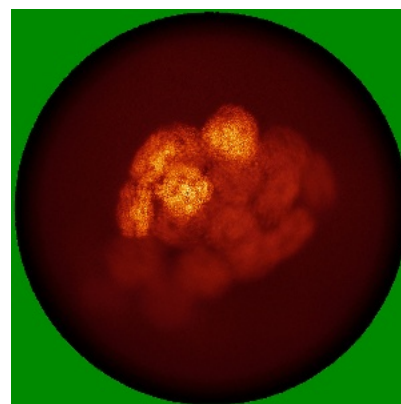
6.4.1 Primary map



X



Y

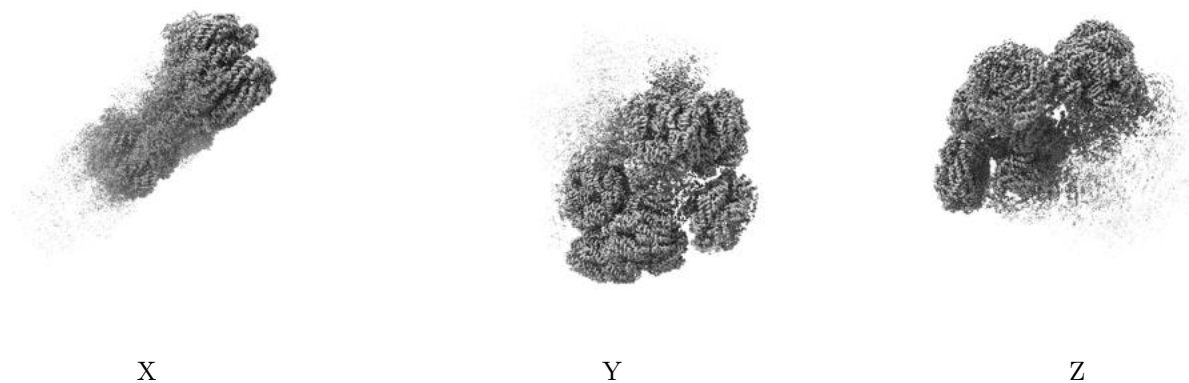


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

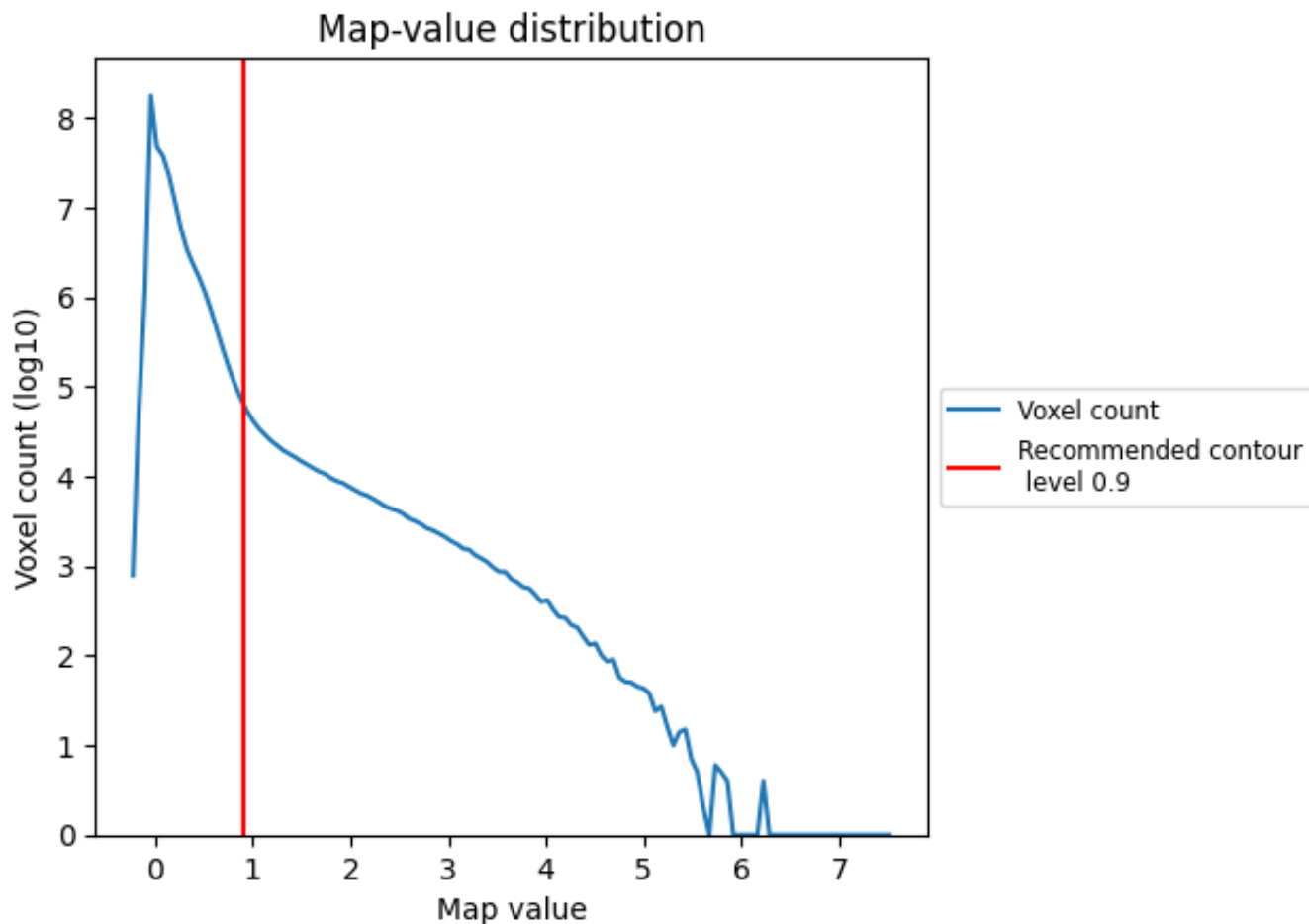
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

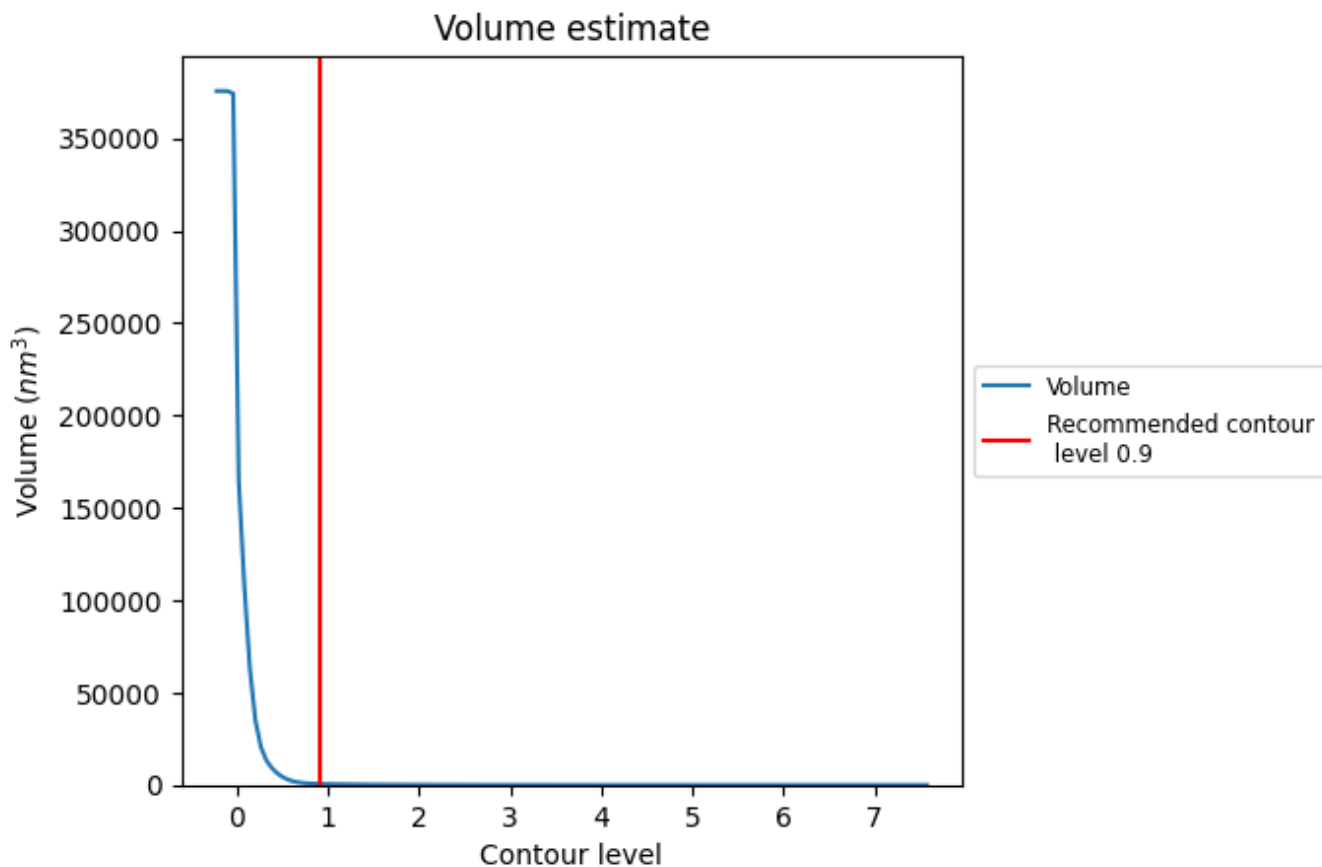
This section contains the results of statistical analysis of the map.

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.

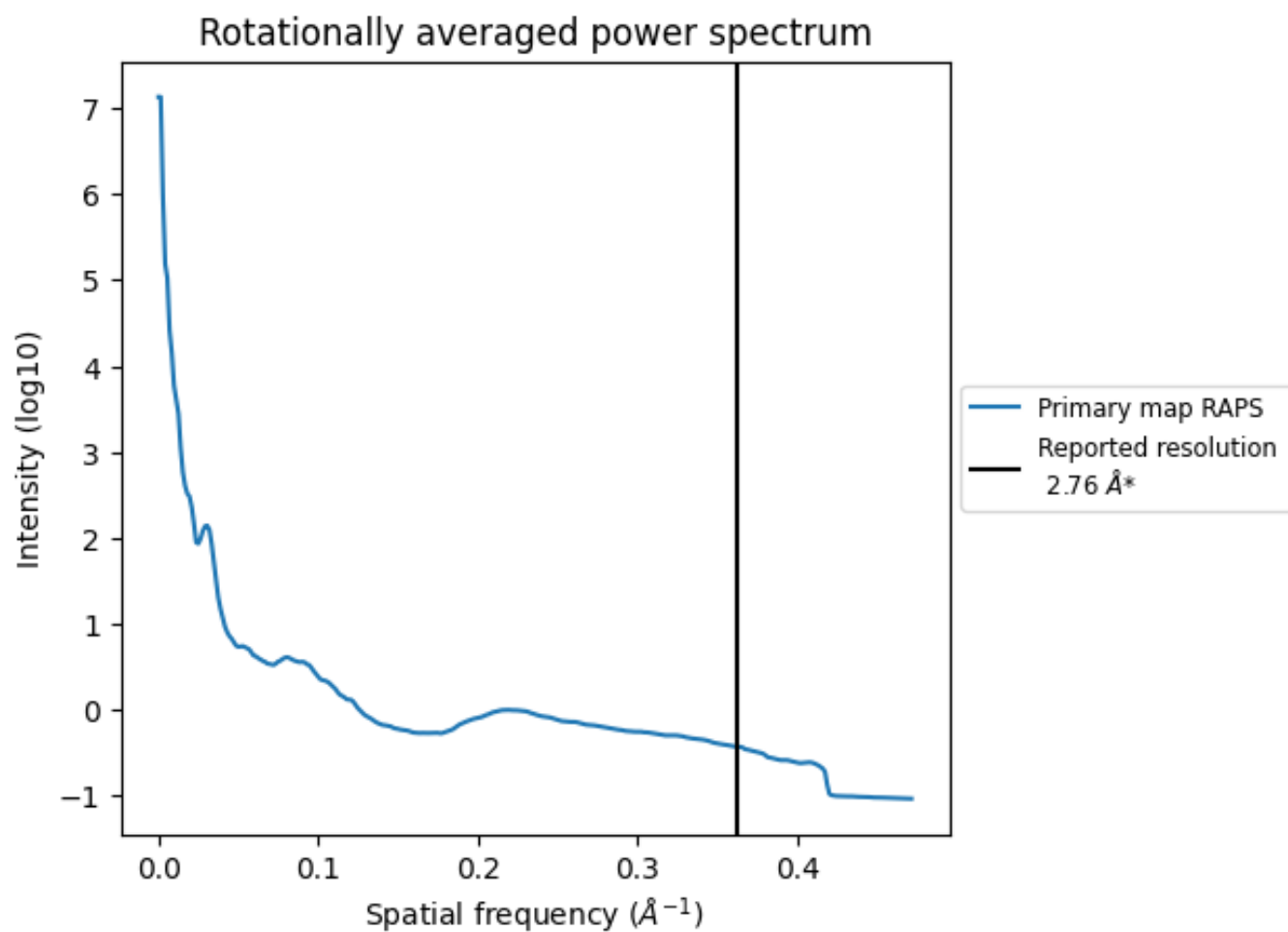
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 588 nm^3 ; this corresponds to an approximate mass of 531 kDa.

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

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.362 \AA^{-1}

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

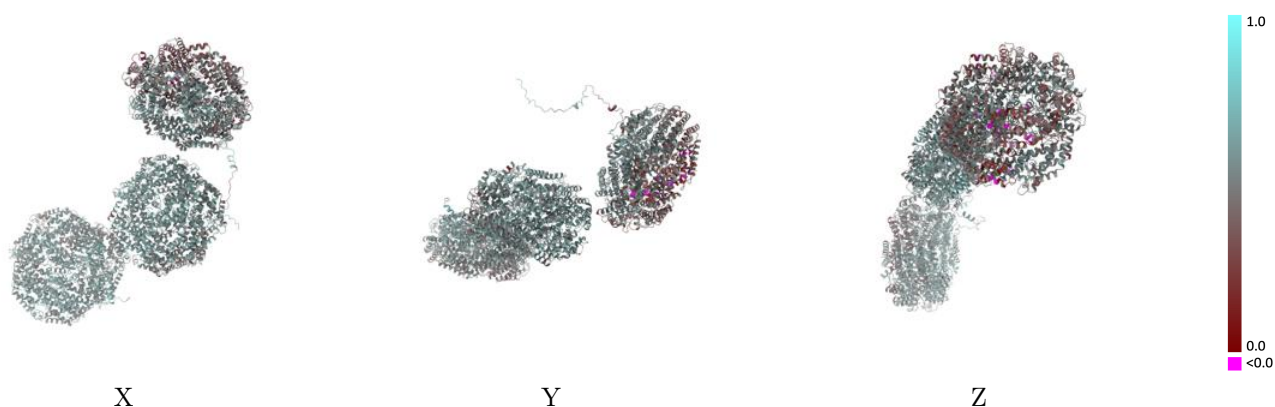
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35569 and PDB model 8IMM. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

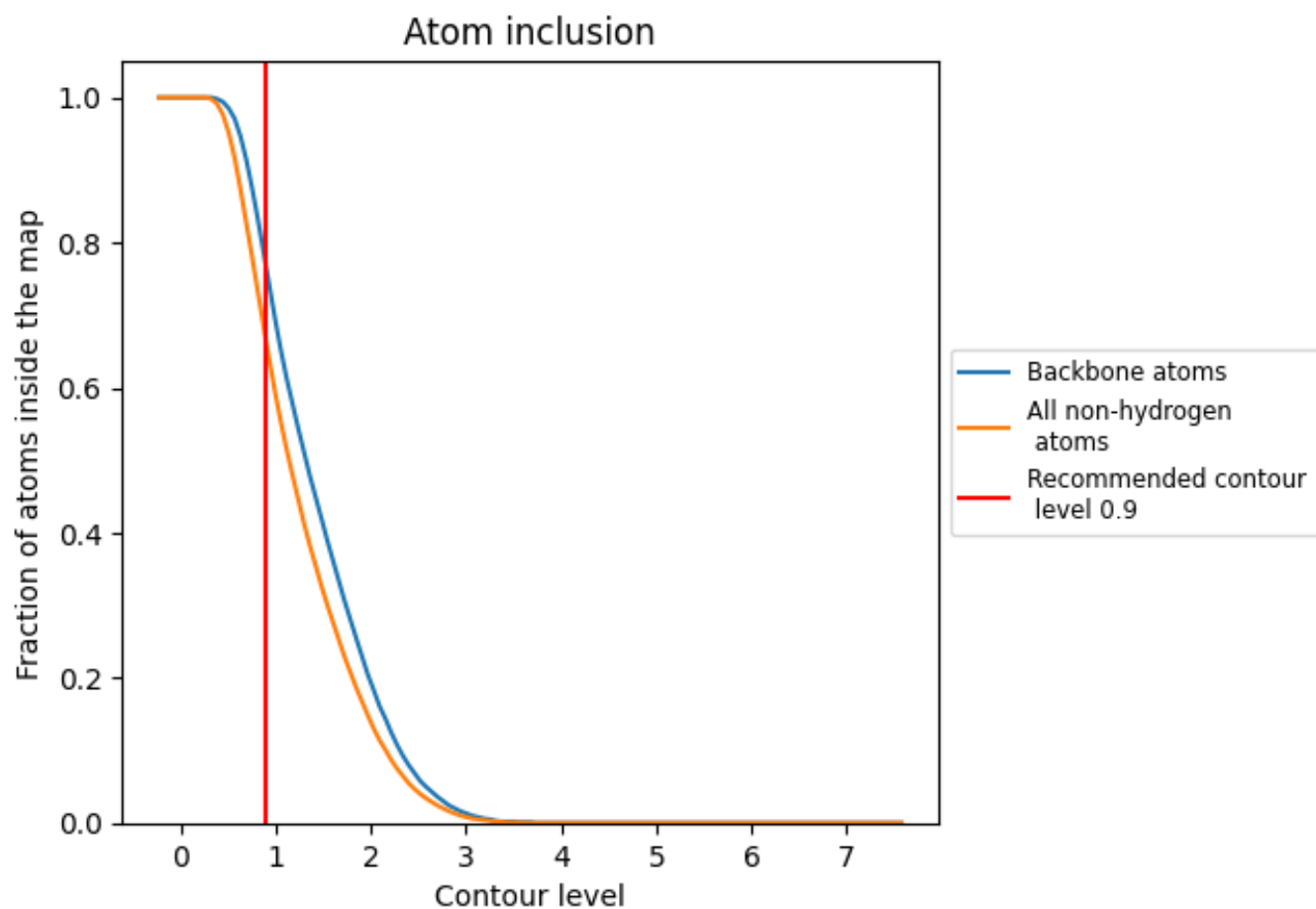


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 66% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6620	 0.5280
3	 0.8870	 0.6100
4	 0.6300	 0.5370
A	 0.5970	 0.5060
B	 0.7250	 0.5400
C	 0.6000	 0.5250
D	 0.8520	 0.5790
E	 0.7550	 0.5570
F	 0.8670	 0.5870
G	 0.5260	 0.4890
H	 0.5190	 0.4630
I	 0.7060	 0.5340
J	 0.8690	 0.5890
K	 0.8230	 0.5730
L	 0.8760	 0.5900
M	 0.3030	 0.4740
N	 0.6060	 0.5220
O	 0.7520	 0.5500
P	 0.7050	 0.5550
Q	 0.8640	 0.5930
R	 0.7740	 0.5750
S	 0.8610	 0.5780
T	 0.6950	 0.5490
U	 0.5950	 0.5010
V	 0.7480	 0.5660
W	 0.8170	 0.5790
X	 0.8530	 0.5850
Y	 0.8730	 0.6010
Z	 0.4810	 0.5080
a	 0.1740	 0.3190
b	 0.6550	 0.5240
c	 0.3160	 0.4270
d	 0.7030	 0.5360
e	 0.3740	 0.4530
f	 0.6030	 0.5120



Continued on next page...

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Chain	Atom inclusion	Q-score
g	 0.1710	 0.3440
h	 0.2730	 0.4030
i	 0.2890	 0.4100
j	 0.7240	 0.5480
k	 0.7400	 0.5510
l	 0.7010	 0.5390
m	 0.1720	 0.3410