



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:43 PM UTC

PDB ID : 8IMI / pdb_00008imi
EMDB ID : EMD-35565
Title : A1-A2, A3-A4, B'1-B'2, C'1-C'2 cylinder in cyanobacterial phycobilisome from
Anthocerotibacter panamensis (Cluster A)
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 : 2.59 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:

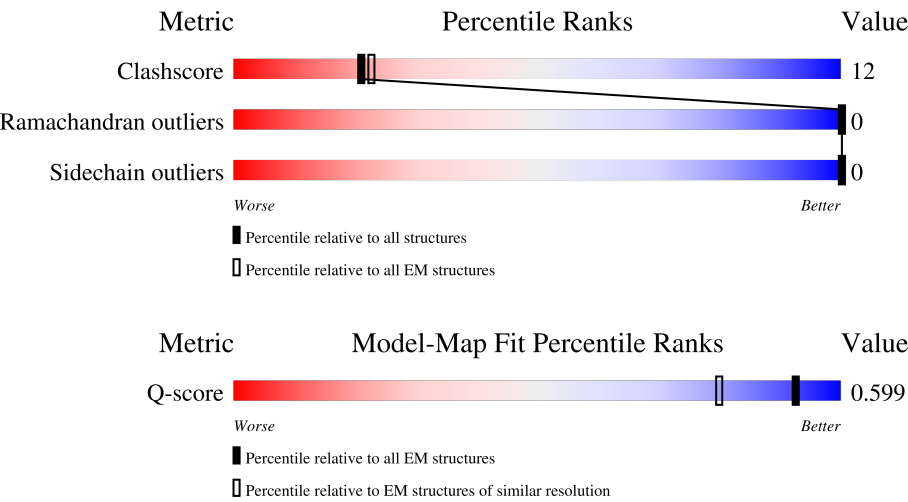
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.59 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	7741 (2.09 - 3.09)

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

Mol	Chain	Length	Quality of chain
1	0	1136	8% 72% 20% 8%
2	A	161	50% 69% 30% .
2	B	161	69% 30% .
2	C	161	91% 63% 37% .

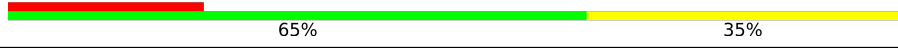
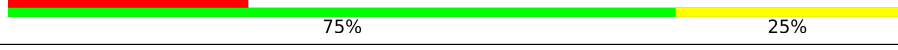
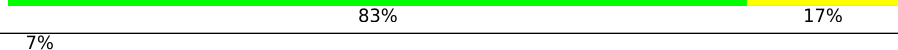
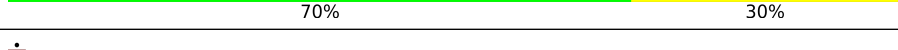
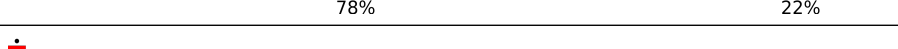
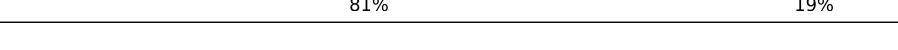
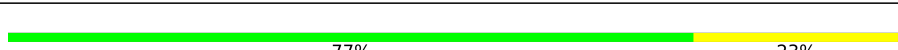
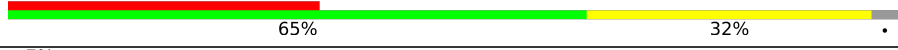
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Mol	Chain	Length	Quality of chain
2	D	161	
2	E	161	
2	N	161	
2	O	161	
2	P	161	
2	Q	161	
2	R	161	
2	S	161	
2	a	161	
2	b	161	
2	c	161	
2	d	161	
2	e	161	
2	f	161	
2	n	161	
2	o	161	
2	p	161	
2	q	161	
2	r	161	
2	s	161	
3	G	161	
4	H	162	
4	I	162	
4	J	162	
4	K	162	

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Mol	Chain	Length	Quality of chain
4	L	162	
4	T	162	
4	U	162	
4	V	162	
4	W	162	
4	X	162	
4	Y	162	
4	g	162	
4	h	162	
4	i	162	
4	j	162	
4	k	162	
4	l	162	
4	t	162	
4	u	162	
4	v	162	
4	w	162	
4	x	162	
4	y	162	
5	M	68	
5	Z	68	
5	m	68	
5	z	68	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 69970 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 ApcE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	1045	Total	C	N	O	S	0	0
			8344	5311	1451	1565	17		

- Molecule 2 is a protein called ApcA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	B	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	C	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	D	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	E	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	N	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	O	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	P	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	Q	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	R	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	S	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	a	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	b	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	c	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	d	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	e	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	f	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	n	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	o	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	p	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	q	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	r	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		
2	s	160	Total	C	N	O	S	0	0
			1218	766	211	237	4		

- Molecule 3 is a protein called ApcB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	161	Total	C	N	O	S	0	0
			1242	794	211	232	5		

- Molecule 4 is a protein called ApcB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	I	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	J	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	K	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	L	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	T	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	U	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	V	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	W	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	X	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	Y	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	g	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	h	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	i	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	j	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	k	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	l	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	t	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	u	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	v	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	w	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	x	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		
4	y	162	Total	C	N	O	S	0	0
			1230	774	205	245	6		

- Molecule 5 is a protein called ApcC2.

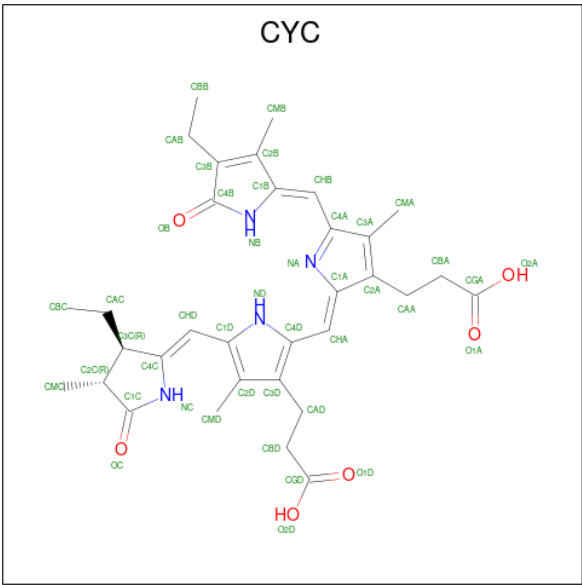
Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	57	Total	C	N	O	S	0	0
			474	307	86	80	1		
5	Z	66	Total	C	N	O	S	0	0
			532	343	97	91	1		
5	m	66	Total	C	N	O	S	0	0
			532	343	97	91	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	z	58	Total	C	N	O	S	0	0
			478	309	87	81	1		

- Molecule 6 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: C₃₃H₄₀N₄O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
6	0	1	Total	C	N	O	0
			43	33	4	6	
6	0	1	Total	C	N	O	0
			43	33	4	6	
6	0	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	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	G	1	Total	C	N	O	0
			43	33	4	6	
6	H	1	Total	C	N	O	0
			43	33	4	6	

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Mol	Chain	Residues	Atoms				AltConf
6	I	1	Total 43	C 33	N 4	O 6	0
6	J	1	Total 43	C 33	N 4	O 6	0
6	L	1	Total 43	C 33	N 4	O 6	0
6	N	1	Total 43	C 33	N 4	O 6	0
6	O	1	Total 43	C 33	N 4	O 6	0
6	P	1	Total 43	C 33	N 4	O 6	0
6	Q	1	Total 43	C 33	N 4	O 6	0
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	V	1	Total 43	C 33	N 4	O 6	0
6	W	1	Total 43	C 33	N 4	O 6	0
6	Y	1	Total 43	C 33	N 4	O 6	0
6	Z	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
6	h	1	Total 43	C 33	N 4	O 6	0

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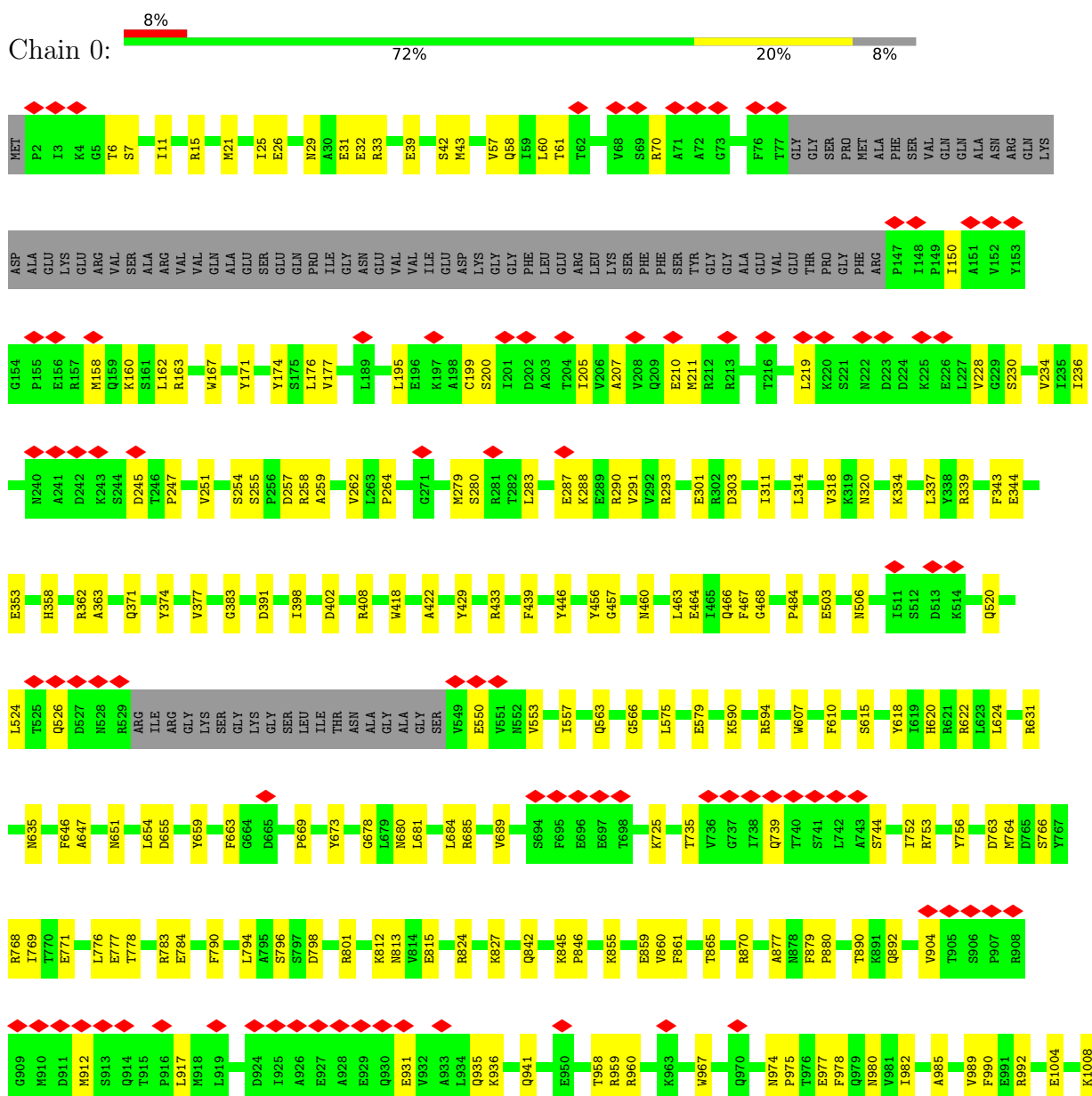
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Mol	Chain	Residues	Atoms				AltConf
6	i	1	Total 43	C 33	N 4	O 6	0
6	j	1	Total 43	C 33	N 4	O 6	0
6	k	1	Total 43	C 33	N 4	O 6	0
6	l	1	Total 43	C 33	N 4	O 6	0
6	m	1	Total 43	C 33	N 4	O 6	0
6	n	1	Total 43	C 33	N 4	O 6	0
6	o	1	Total 43	C 33	N 4	O 6	0
6	p	1	Total 43	C 33	N 4	O 6	0
6	q	1	Total 43	C 33	N 4	O 6	0
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	u	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	x	1	Total 43	C 33	N 4	O 6	0
6	y	1	Total 43	C 33	N 4	O 6	0

3 Residue-property plots

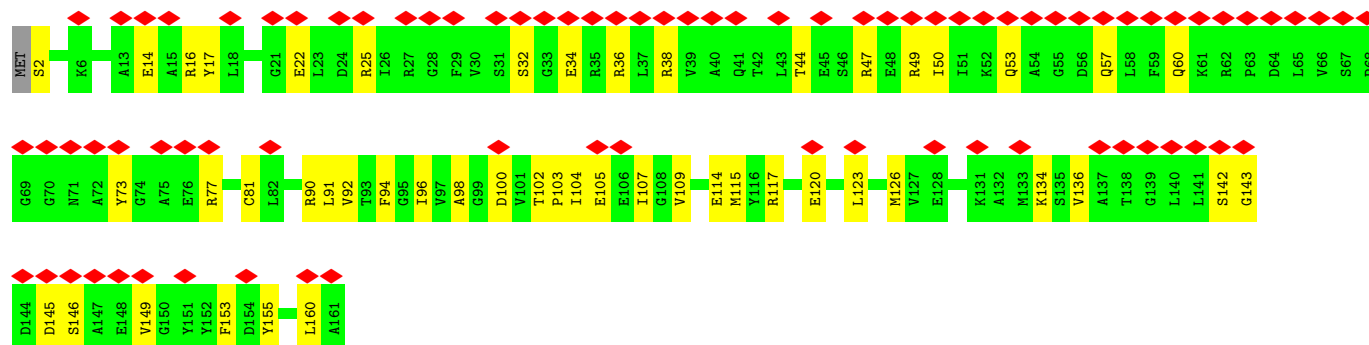
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: ApcE

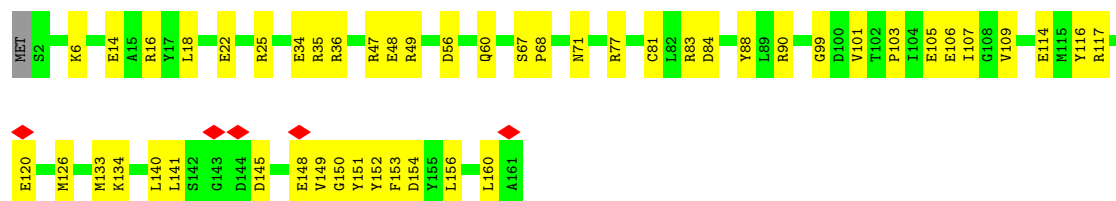




• Molecule 2: ApcA2



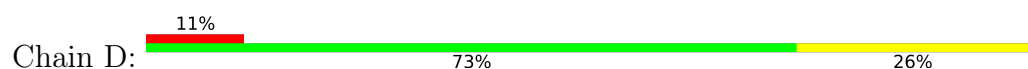
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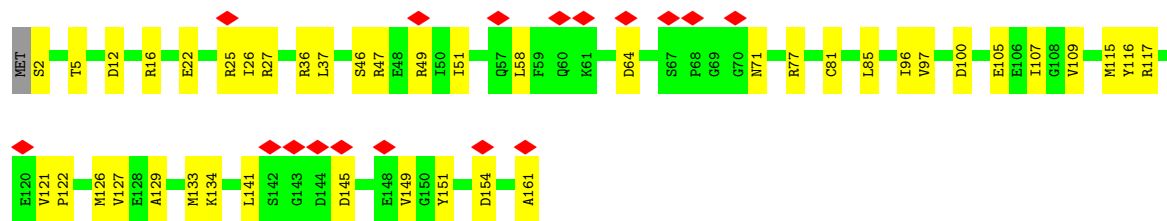


• Molecule 2: ApcA2

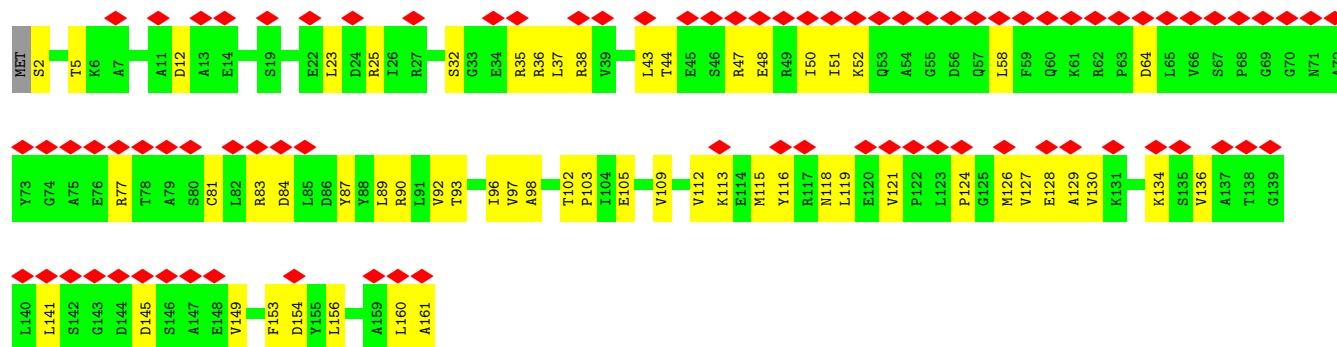


• Molecule 2: ApcA2

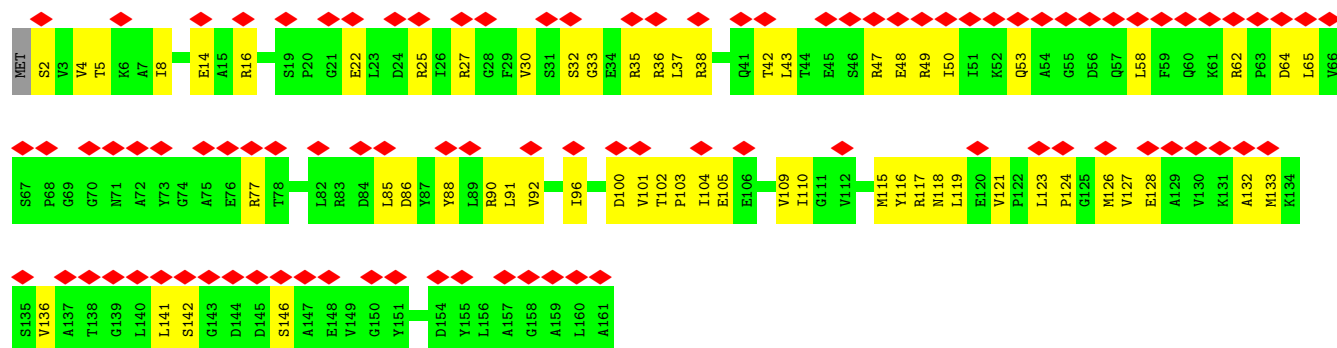




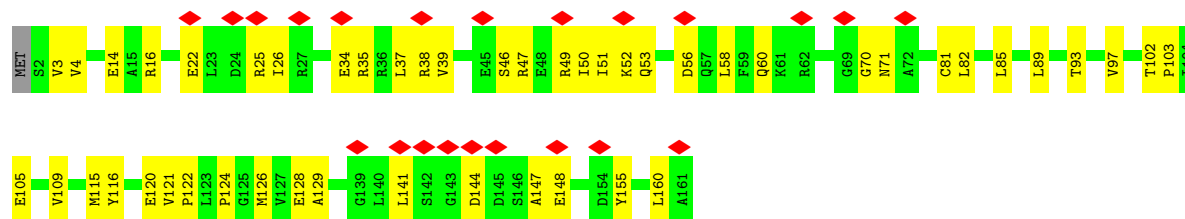
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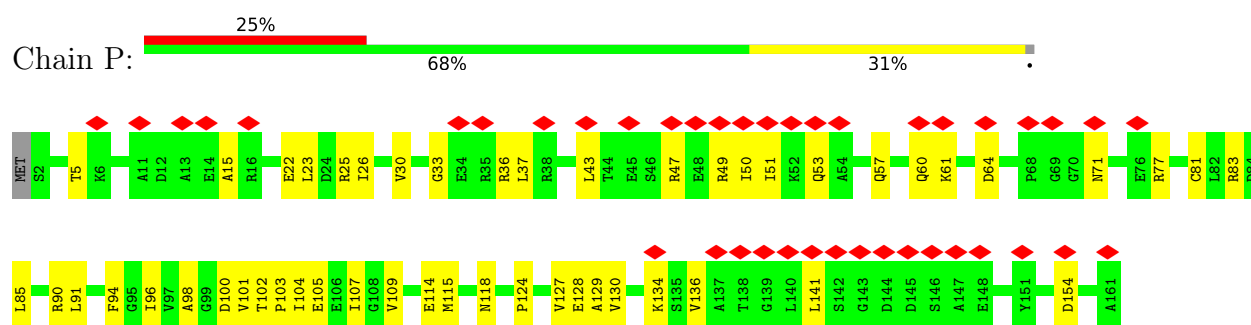


• Molecule 2: ApcA2

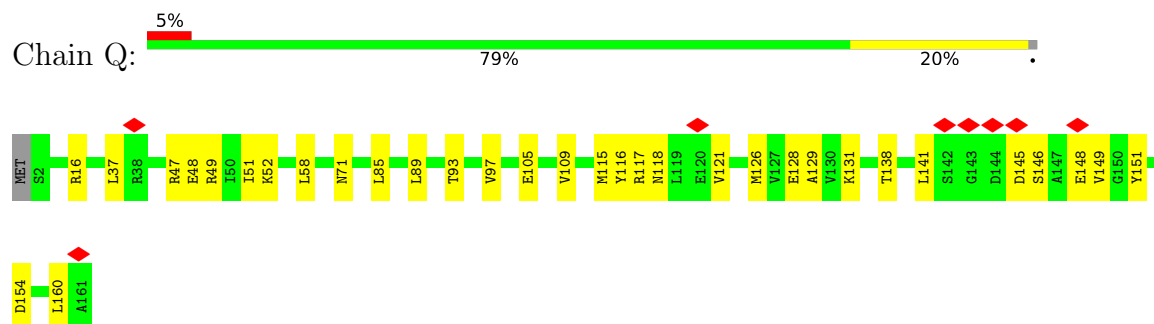


• Molecule 2: ApcA2

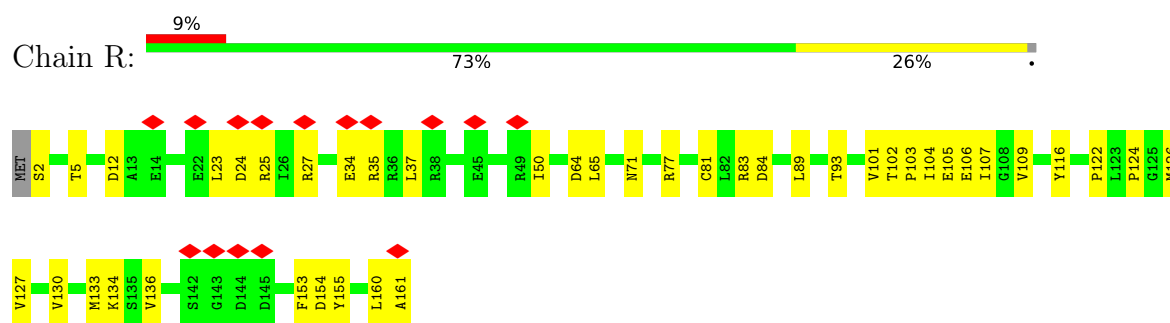




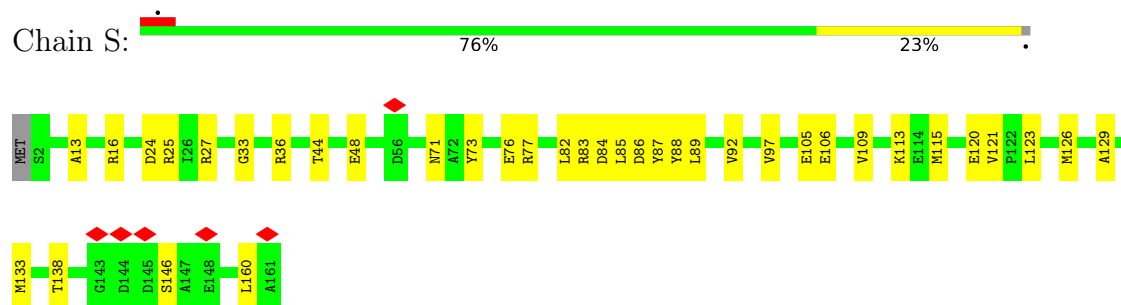
- Molecule 2: ApcA2



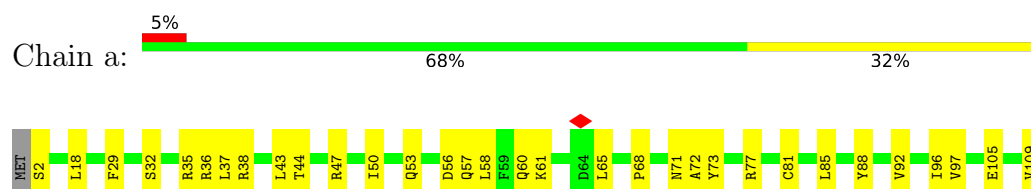
- Molecule 2: ApcA2

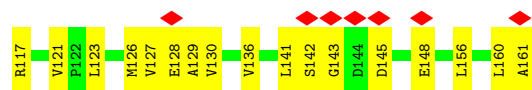


- Molecule 2: ApcA2

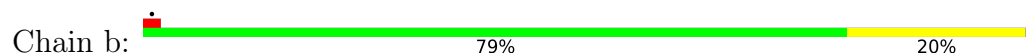


- Molecule 2: ApcA2

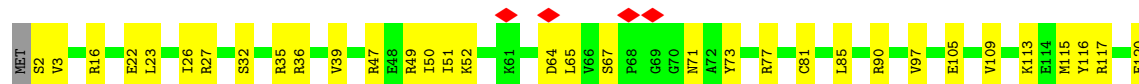




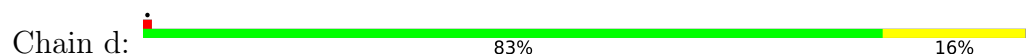
• Molecule 2: ApcA2



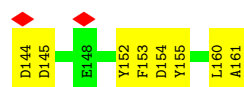
• Molecule 2: ApcA2



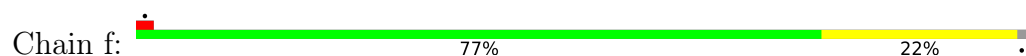
• Molecule 2: ApcA2

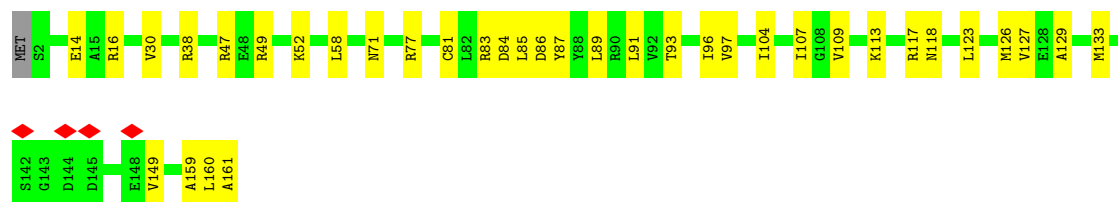


• Molecule 2: ApcA2

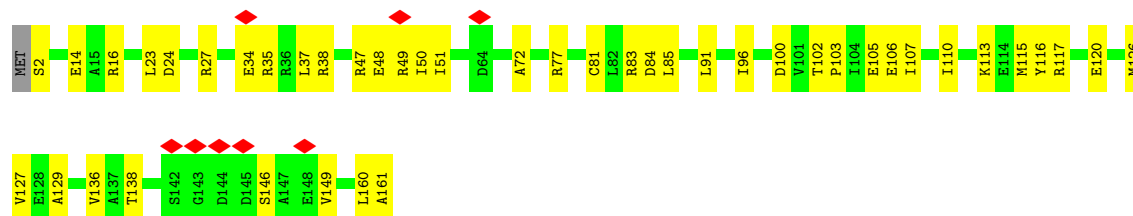


• Molecule 2: ApcA2

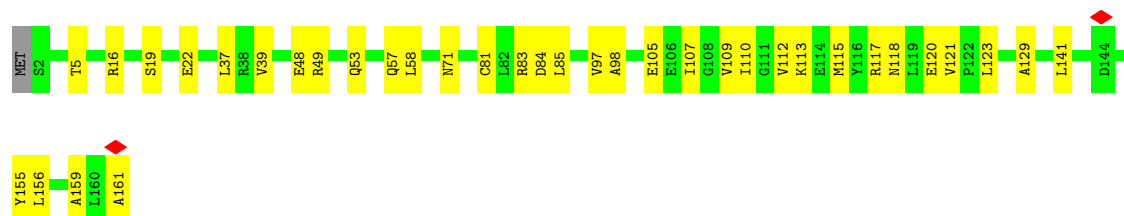
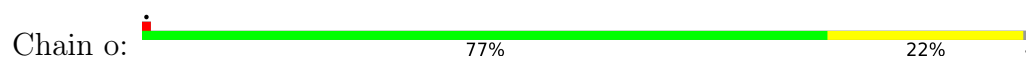




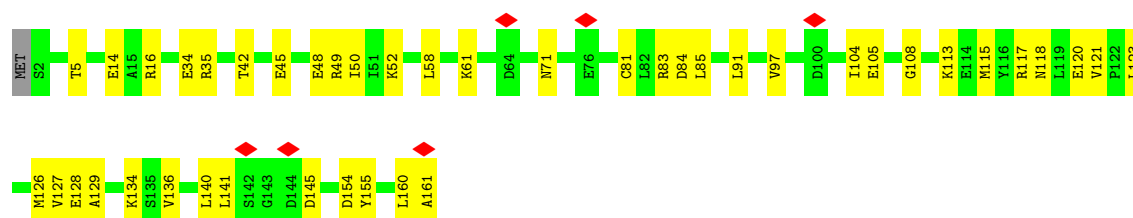
• Molecule 2: ApcA2



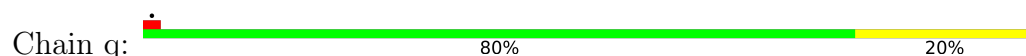
• Molecule 2: ApcA2



• Molecule 2: ApcA2

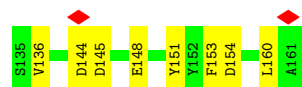
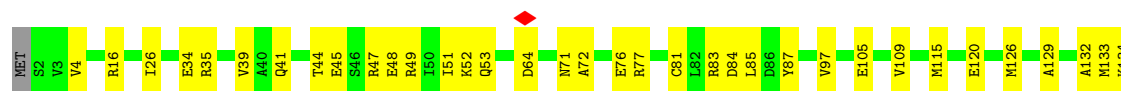


• Molecule 2: ApcA2

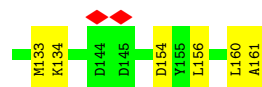
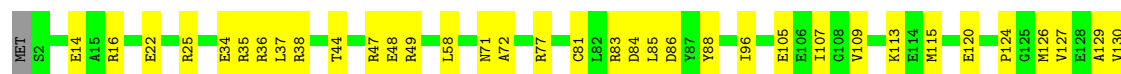




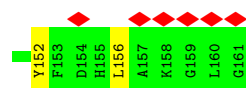
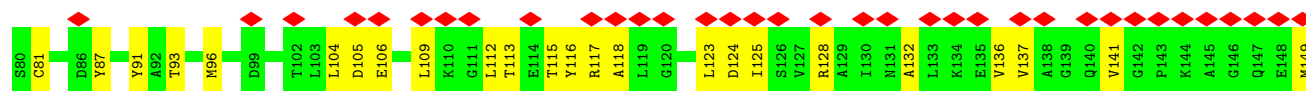
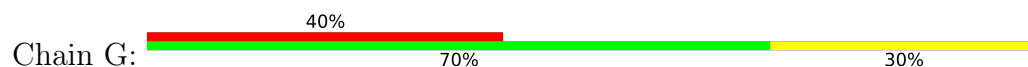
• Molecule 2: ApcA2



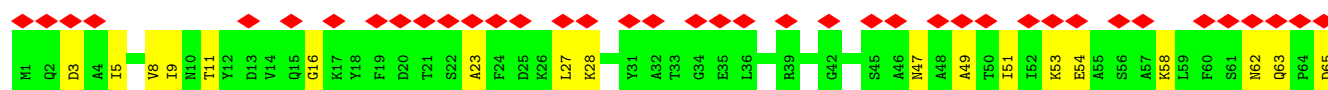
• Molecule 2: ApcA2

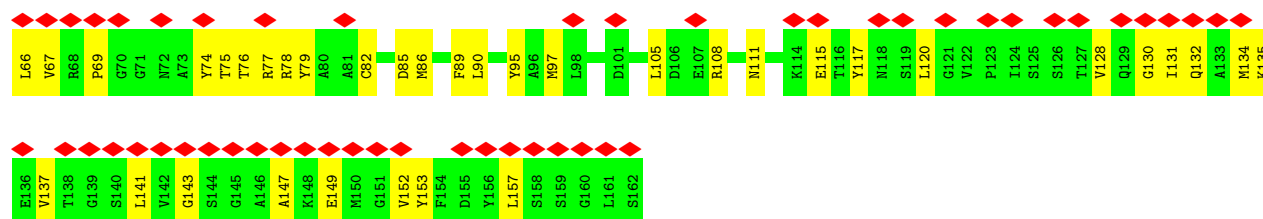


• Molecule 3: ApcB3

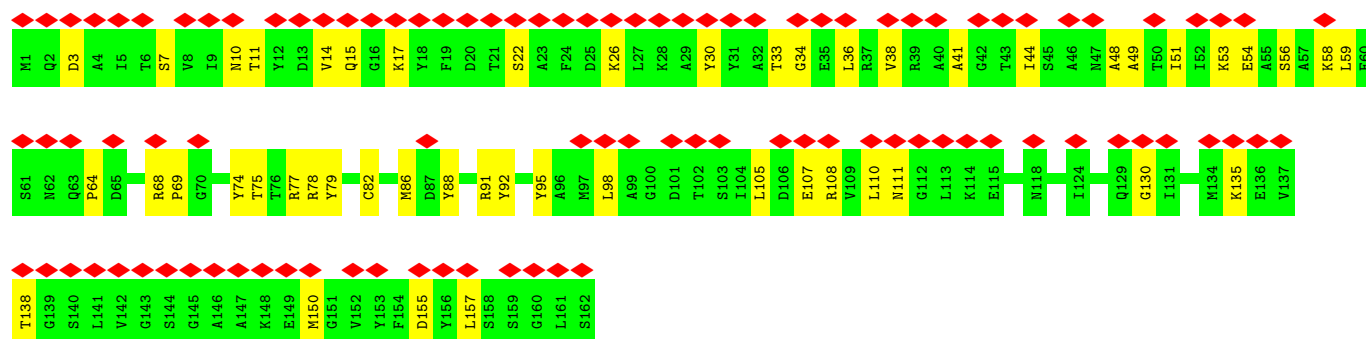


• Molecule 4: ApcB2

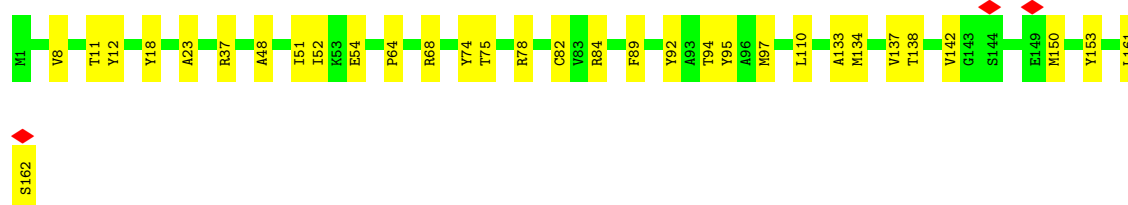
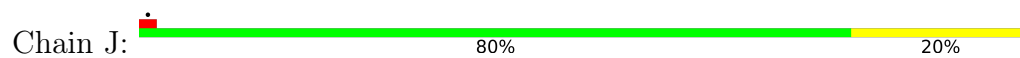




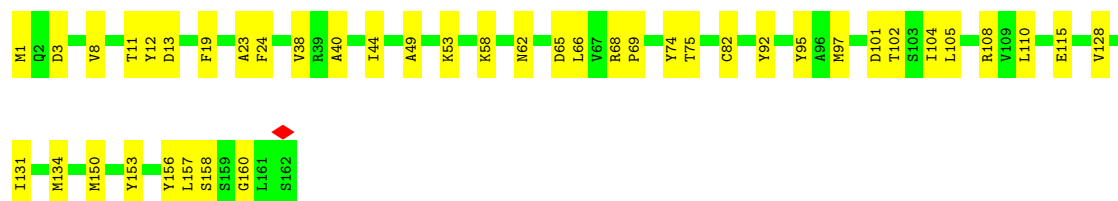
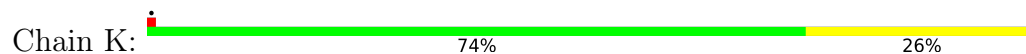
• Molecule 4: ApcB2



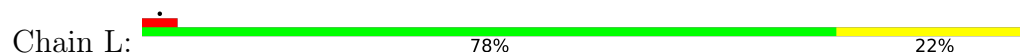
• Molecule 4: ApcB2



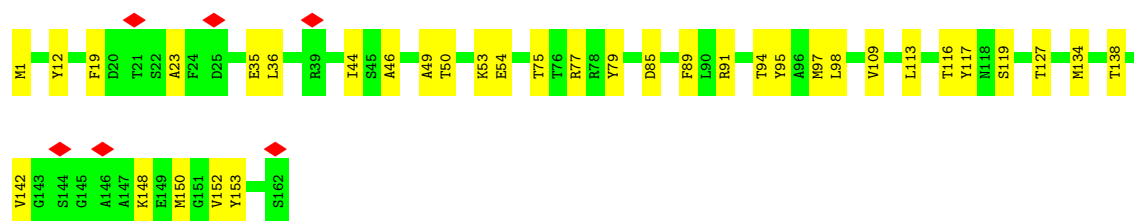
• Molecule 4: ApcB2



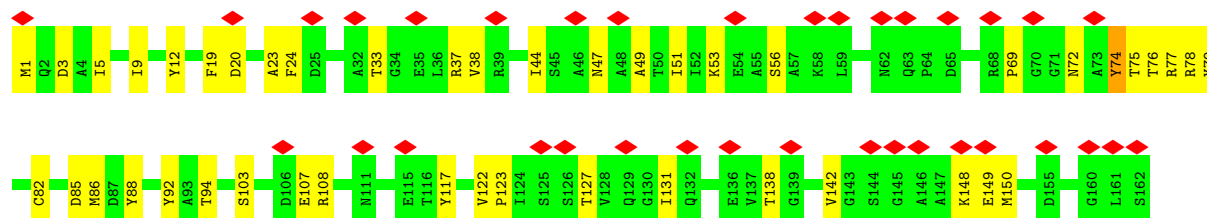
• Molecule 4: ApcB2



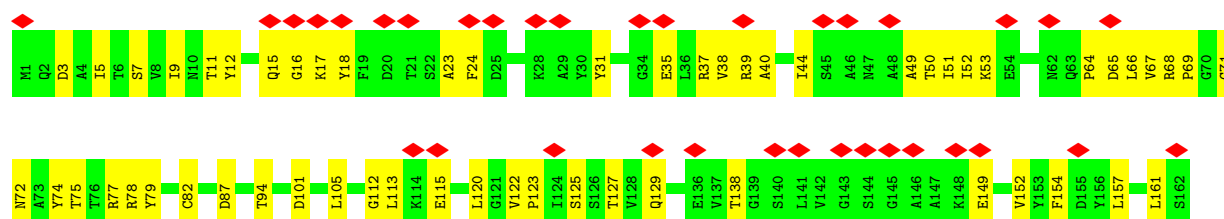
• Molecule 4: ApcB2



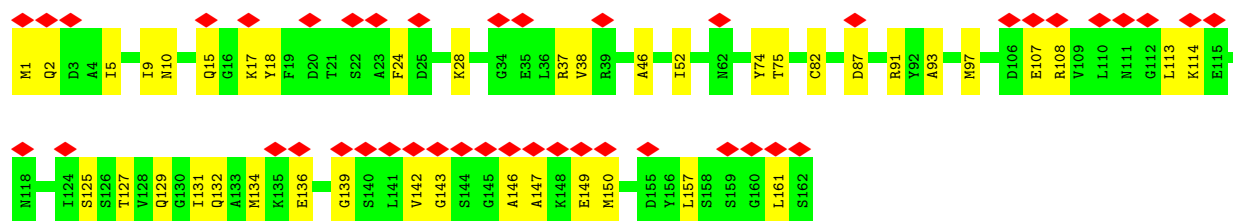
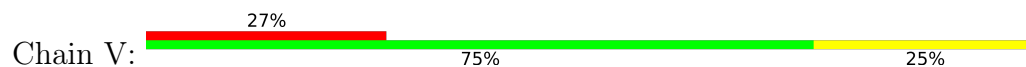
• Molecule 4: ApcB2



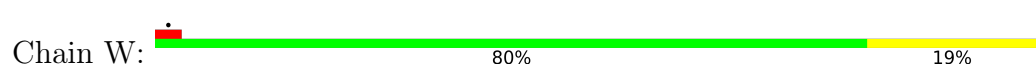
• Molecule 4: ApcB2



• Molecule 4: ApcB2



• Molecule 4: ApcB2



• Molecule 4: ApcB2

Chain X:  81% 19%



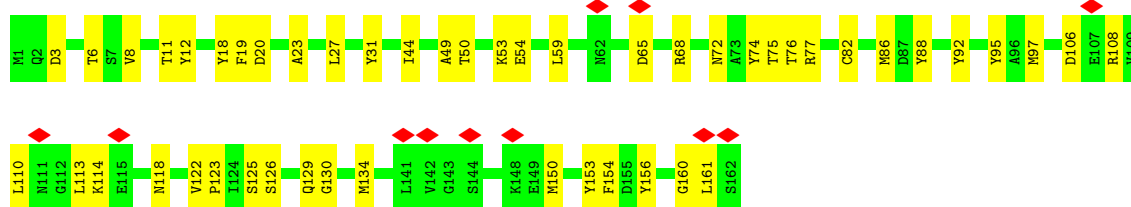
• Molecule 4: ApcB2

Chain Y:  83% 17%



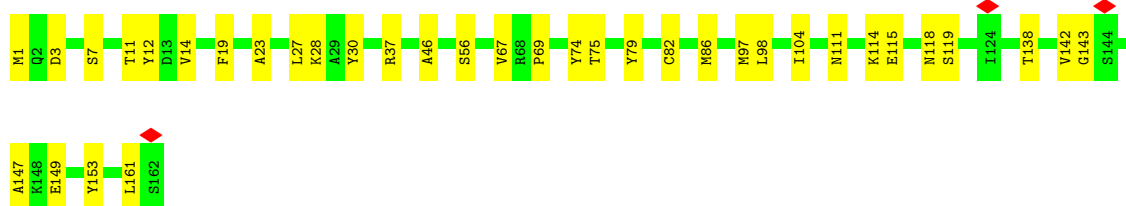
• Molecule 4: ApcB2

Chain g:  7% 70% 30%



• Molecule 4: ApcB2

Chain h:  78% 22%



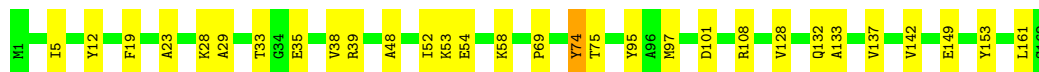
• Molecule 4: ApcB2

Chain i:  81% 19%



• Molecule 4: ApcB2

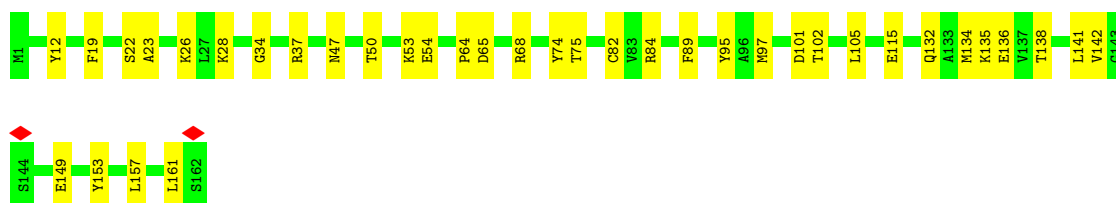
Chain j:  81% 18%



• Molecule 4: ApcB2

Chain k:  81% 19%

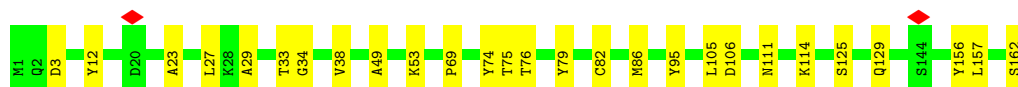
• Molecule 4: ApcB2

Chain l:  77% 23%

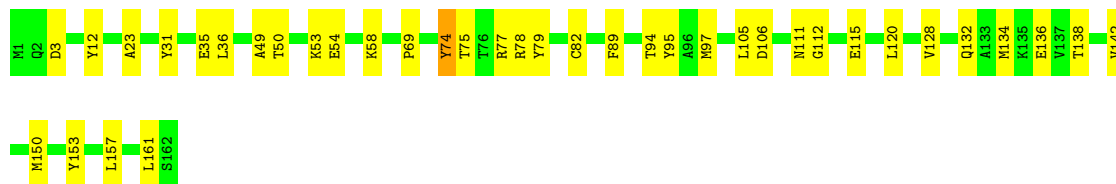
• Molecule 4: ApcB2

Chain t:  75% 25%

• Molecule 4: ApcB2

Chain u:  83% 17%

• Molecule 4: ApcB2

Chain v:  77% 23%

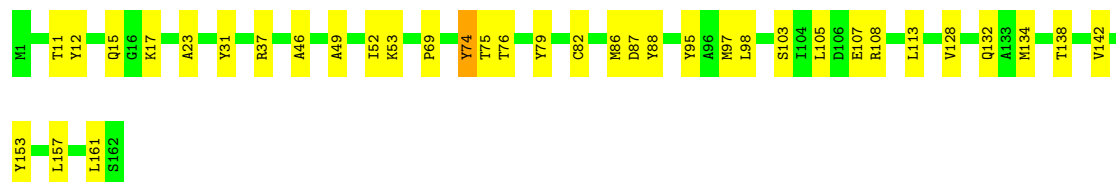
• Molecule 4: ApcB2

Chain w:  80% 20%



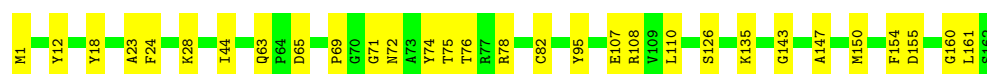
• Molecule 4: ApcB2

Chain x: 78% 22%



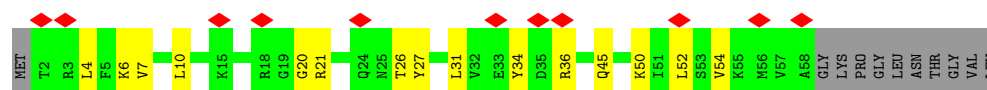
• Molecule 4: ApcB2

Chain y: 81% 19%



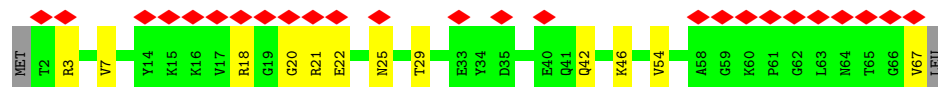
• Molecule 5: ApcC2

Chain M: 16% 62% 22% 16%



• Molecule 5: ApcC2

Chain Z: 37% 79% 18%



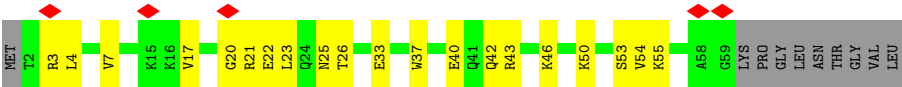
• Molecule 5: ApcC2

Chain m: 35% 65% 32%



• Molecule 5: ApcC2

Chain z: 7% 56% 29% 15%



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)	3000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.176	Depositor
Minimum map value	-0.348	Depositor
Average map value	0.054	Depositor
Map value standard deviation	0.116	Depositor
Recommended contour level	1	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	1.061, 1.061, 1.061	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.26	0/8527	0.46	0/11545
2	A	0.19	0/1235	0.46	0/1668
2	B	0.22	0/1235	0.43	0/1668
2	C	0.18	0/1235	0.48	0/1668
2	D	0.21	0/1235	0.43	0/1668
2	E	0.19	0/1235	0.48	0/1668
2	N	0.20	0/1235	0.48	0/1668
2	O	0.19	0/1235	0.43	0/1668
2	P	0.18	0/1235	0.44	0/1668
2	Q	0.21	0/1235	0.41	0/1668
2	R	0.20	0/1235	0.46	0/1668
2	S	0.21	0/1235	0.43	0/1668
2	a	0.23	0/1235	0.46	0/1668
2	b	0.23	0/1235	0.43	0/1668
2	c	0.22	0/1235	0.46	0/1668
2	d	0.23	0/1235	0.45	0/1668
2	e	0.22	0/1235	0.47	0/1668
2	f	0.24	0/1235	0.45	0/1668
2	n	0.24	0/1235	0.42	0/1668
2	o	0.23	0/1235	0.44	0/1668
2	p	0.22	0/1235	0.45	0/1668
2	q	0.25	0/1235	0.47	0/1668
2	r	0.22	0/1235	0.40	0/1668
2	s	0.25	0/1235	0.44	0/1668
3	G	0.16	0/1263	0.42	0/1709
4	H	0.17	0/1249	0.43	0/1688
4	I	0.17	0/1249	0.42	0/1688
4	J	0.23	0/1249	0.43	0/1688
4	K	0.23	0/1249	0.45	0/1688
4	L	0.22	0/1249	0.44	0/1688
4	T	0.18	0/1249	0.41	0/1688
4	U	0.18	0/1249	0.43	0/1688

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	V	0.18	0/1249	0.43	0/1688
4	W	0.24	0/1249	0.43	0/1688
4	X	0.23	0/1249	0.41	0/1688
4	Y	0.22	0/1249	0.40	0/1688
4	g	0.21	0/1249	0.44	0/1688
4	h	0.22	0/1249	0.46	0/1688
4	i	0.21	0/1249	0.43	0/1688
4	j	0.27	0/1249	0.49	0/1688
4	k	0.26	0/1249	0.49	0/1688
4	l	0.26	0/1249	0.48	0/1688
4	t	0.24	0/1249	0.43	0/1688
4	u	0.22	0/1249	0.41	0/1688
4	v	0.26	0/1249	0.47	0/1688
4	w	0.26	0/1249	0.43	0/1688
4	x	0.26	0/1249	0.48	0/1688
4	y	0.25	0/1249	0.42	0/1688
5	M	0.17	0/482	0.37	0/644
5	Z	0.13	0/541	0.35	0/724
5	m	0.20	0/541	0.51	0/724
5	z	0.22	0/486	0.45	0/649
All	All	0.22	0/68972	0.44	0/93183

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
4	T	0	1
4	W	0	1
4	j	0	1
4	k	0	1
4	v	0	1
4	x	0	1
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	T	74	TYR	Peptide
4	W	74	TYR	Peptide
4	j	74	TYR	Peptide
4	k	74	TYR	Peptide
4	v	74	TYR	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	8344	0	8320	172	0
2	A	1218	0	1229	42	0
2	B	1218	0	1229	39	0
2	C	1218	0	1229	55	0
2	D	1218	0	1229	42	0
2	E	1218	0	1229	53	0
2	N	1218	0	1229	55	0
2	O	1218	0	1229	36	0
2	P	1218	0	1229	40	0
2	Q	1218	0	1229	22	0
2	R	1218	0	1229	32	0
2	S	1218	0	1229	31	0
2	a	1218	0	1229	35	0
2	b	1218	0	1229	32	0
2	c	1218	0	1229	41	0
2	d	1218	0	1229	21	0
2	e	1218	0	1229	32	0
2	f	1218	0	1229	31	0
2	n	1218	0	1229	36	0
2	o	1218	0	1229	35	0
2	p	1218	0	1229	37	0
2	q	1218	0	1229	26	0
2	r	1218	0	1229	32	0
2	s	1218	0	1229	34	0
3	G	1242	0	1263	41	0
4	H	1230	0	1219	51	0
4	I	1230	0	1219	41	0
4	J	1230	0	1218	23	0
4	K	1230	0	1219	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	1230	0	1219	24	0
4	T	1230	0	1219	44	0
4	U	1230	0	1219	53	0
4	V	1230	0	1219	30	0
4	W	1230	0	1219	27	0
4	X	1230	0	1219	21	0
4	Y	1230	0	1219	20	0
4	g	1230	0	1219	45	0
4	h	1230	0	1219	29	0
4	i	1230	0	1219	25	0
4	j	1230	0	1219	25	0
4	k	1230	0	1219	24	0
4	l	1230	0	1219	27	0
4	t	1230	0	1219	29	0
4	u	1230	0	1219	25	0
4	v	1230	0	1219	26	0
4	w	1230	0	1219	28	0
4	x	1230	0	1219	30	0
4	y	1230	0	1219	24	0
5	M	474	0	501	19	0
5	Z	532	0	563	10	0
5	m	532	0	563	25	0
5	z	478	0	504	18	0
6	O	129	0	113	17	0
6	A	43	0	38	3	0
6	B	43	0	38	6	0
6	C	43	0	38	6	0
6	D	43	0	38	5	0
6	E	43	0	38	6	0
6	G	43	0	38	7	0
6	H	43	0	38	5	0
6	I	43	0	38	3	0
6	J	43	0	36	5	0
6	L	43	0	38	3	0
6	N	43	0	38	8	0
6	O	43	0	38	6	0
6	P	43	0	38	7	0
6	Q	43	0	38	5	0
6	R	43	0	38	6	0
6	S	43	0	38	4	0
6	T	43	0	38	4	0
6	V	43	0	38	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	W	43	0	38	6	0
6	Y	43	0	38	5	0
6	Z	43	0	38	7	0
6	a	43	0	38	7	0
6	b	43	0	38	6	0
6	c	43	0	38	7	0
6	d	43	0	38	5	0
6	e	43	0	38	3	0
6	f	43	0	38	8	0
6	h	43	0	38	6	0
6	i	43	0	38	3	0
6	j	43	0	38	2	0
6	k	43	0	38	5	0
6	l	43	0	38	6	0
6	m	43	0	38	5	0
6	n	43	0	38	6	0
6	o	43	0	38	5	0
6	p	43	0	38	6	0
6	q	43	0	38	5	0
6	r	43	0	38	7	0
6	s	43	0	38	5	0
6	t	43	0	38	11	0
6	u	43	0	38	3	0
6	v	43	0	38	5	0
6	w	43	0	38	3	0
6	x	43	0	38	7	0
6	y	43	0	38	6	0
All	All	69970	0	69838	1665	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 12.

The worst 5 of 1665 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)
4:W:103:SER:O	4:W:107:GLU:HB2	1.61	0.99
6:b:200:CYC:HMD1	6:b:200:CYC:HC	1.29	0.97
2:B:117:ARG:O	4:K:53:LYS:NZ	2.01	0.94
6:W:200:CYC:HMD1	6:W:200:CYC:HC	1.34	0.92
4:v:58:LYS:NZ	4:v:136:GLU:OE1	2.07	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	1039/1136 (92%)	1011 (97%)	28 (3%)	0	100	100
2	A	158/161 (98%)	152 (96%)	6 (4%)	0	100	100
2	B	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	C	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	D	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	E	158/161 (98%)	153 (97%)	5 (3%)	0	100	100
2	N	158/161 (98%)	153 (97%)	5 (3%)	0	100	100
2	O	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	P	158/161 (98%)	154 (98%)	4 (2%)	0	100	100
2	Q	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	R	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	S	158/161 (98%)	158 (100%)	0	0	100	100
2	a	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	b	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	c	158/161 (98%)	158 (100%)	0	0	100	100
2	d	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	e	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
2	f	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	n	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	o	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
2	p	158/161 (98%)	157 (99%)	1 (1%)	0	100	100
2	q	158/161 (98%)	157 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	r	158/161 (98%)	154 (98%)	4 (2%)	0	100	100
2	s	158/161 (98%)	156 (99%)	2 (1%)	0	100	100
3	G	159/161 (99%)	158 (99%)	1 (1%)	0	100	100
4	H	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
4	I	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	J	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
4	K	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
4	L	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	T	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
4	U	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	V	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	W	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	X	160/162 (99%)	159 (99%)	1 (1%)	0	100	100
4	Y	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
4	g	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
4	h	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	i	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	j	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	k	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
4	l	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	t	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
4	u	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
4	v	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	w	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
4	x	160/162 (99%)	157 (98%)	3 (2%)	0	100	100
4	y	160/162 (99%)	158 (99%)	2 (1%)	0	100	100
5	M	55/68 (81%)	54 (98%)	1 (2%)	0	100	100
5	Z	64/68 (94%)	63 (98%)	1 (2%)	0	100	100
5	m	64/68 (94%)	58 (91%)	6 (9%)	0	100	100
5	z	56/68 (82%)	53 (95%)	3 (5%)	0	100	100
All	All	8751/8998 (97%)	8598 (98%)	153 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	892/962 (93%)	892 (100%)	0	100	100
2	A	127/128 (99%)	127 (100%)	0	100	100
2	B	127/128 (99%)	127 (100%)	0	100	100
2	C	127/128 (99%)	127 (100%)	0	100	100
2	D	127/128 (99%)	127 (100%)	0	100	100
2	E	127/128 (99%)	127 (100%)	0	100	100
2	N	127/128 (99%)	127 (100%)	0	100	100
2	O	127/128 (99%)	127 (100%)	0	100	100
2	P	127/128 (99%)	127 (100%)	0	100	100
2	Q	127/128 (99%)	127 (100%)	0	100	100
2	R	127/128 (99%)	127 (100%)	0	100	100
2	S	127/128 (99%)	127 (100%)	0	100	100
2	a	127/128 (99%)	127 (100%)	0	100	100
2	b	127/128 (99%)	127 (100%)	0	100	100
2	c	127/128 (99%)	127 (100%)	0	100	100
2	d	127/128 (99%)	127 (100%)	0	100	100
2	e	127/128 (99%)	127 (100%)	0	100	100
2	f	127/128 (99%)	127 (100%)	0	100	100
2	n	127/128 (99%)	127 (100%)	0	100	100
2	o	127/128 (99%)	127 (100%)	0	100	100
2	p	127/128 (99%)	127 (100%)	0	100	100
2	q	127/128 (99%)	127 (100%)	0	100	100
2	r	127/128 (99%)	127 (100%)	0	100	100
2	s	127/128 (99%)	127 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	124/124 (100%)	124 (100%)	0	100	100
4	H	128/128 (100%)	128 (100%)	0	100	100
4	I	128/128 (100%)	128 (100%)	0	100	100
4	J	128/128 (100%)	128 (100%)	0	100	100
4	K	128/128 (100%)	128 (100%)	0	100	100
4	L	128/128 (100%)	128 (100%)	0	100	100
4	T	128/128 (100%)	128 (100%)	0	100	100
4	U	128/128 (100%)	128 (100%)	0	100	100
4	V	128/128 (100%)	128 (100%)	0	100	100
4	W	128/128 (100%)	128 (100%)	0	100	100
4	X	128/128 (100%)	128 (100%)	0	100	100
4	Y	128/128 (100%)	128 (100%)	0	100	100
4	g	128/128 (100%)	128 (100%)	0	100	100
4	h	128/128 (100%)	128 (100%)	0	100	100
4	i	128/128 (100%)	128 (100%)	0	100	100
4	j	128/128 (100%)	128 (100%)	0	100	100
4	k	128/128 (100%)	128 (100%)	0	100	100
4	l	128/128 (100%)	128 (100%)	0	100	100
4	t	128/128 (100%)	128 (100%)	0	100	100
4	u	128/128 (100%)	128 (100%)	0	100	100
4	v	128/128 (100%)	128 (100%)	0	100	100
4	w	128/128 (100%)	128 (100%)	0	100	100
4	x	128/128 (100%)	128 (100%)	0	100	100
4	y	128/128 (100%)	128 (100%)	0	100	100
5	M	50/58 (86%)	50 (100%)	0	100	100
5	Z	56/58 (97%)	56 (100%)	0	100	100
5	m	56/58 (97%)	56 (100%)	0	100	100
5	z	50/58 (86%)	50 (100%)	0	100	100
All	All	7093/7206 (98%)	7093 (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 68

such sidechains are listed below:

Mol	Chain	Res	Type
2	q	118	ASN
4	t	62	ASN
4	y	62	ASN
4	K	62	ASN
4	J	132	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](#)

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 [i](#)

48 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	CYC	P	200	-	46,46,46	5.32	26 (56%)	63,67,67	3.99	16 (25%)
6	CYC	G	200	-	46,46,46	5.31	26 (56%)	63,67,67	4.00	15 (23%)
6	CYC	a	200	-	46,46,46	5.30	26 (56%)	63,67,67	3.96	18 (28%)
6	CYC	o	200	-	46,46,46	5.24	27 (58%)	63,67,67	4.19	19 (30%)
6	CYC	p	200	-	46,46,46	5.27	27 (58%)	63,67,67	3.93	21 (33%)
6	CYC	t	200	-	46,46,46	5.23	26 (56%)	63,67,67	4.01	17 (26%)
6	CYC	S	200	-	46,46,46	5.26	27 (58%)	63,67,67	4.13	17 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CYC	N	200	-	46,46,46	5.28	26 (56%)	63,67,67	4.14	16 (25%)
6	CYC	n	200	-	46,46,46	5.25	27 (58%)	63,67,67	4.08	17 (26%)
6	CYC	q	200	-	46,46,46	5.25	27 (58%)	63,67,67	4.01	16 (25%)
6	CYC	0	1203	-	46,46,46	5.26	25 (54%)	63,67,67	3.96	18 (28%)
6	CYC	u	200	-	46,46,46	5.26	26 (56%)	63,67,67	4.03	18 (28%)
6	CYC	c	200	-	46,46,46	5.29	26 (56%)	63,67,67	4.08	19 (30%)
6	CYC	A	200	-	46,46,46	5.29	26 (56%)	63,67,67	3.97	16 (25%)
6	CYC	y	200	-	46,46,46	5.23	28 (60%)	63,67,67	3.84	17 (26%)
6	CYC	r	200	-	46,46,46	5.26	27 (58%)	63,67,67	3.93	18 (28%)
6	CYC	j	200	-	46,46,46	5.33	28 (60%)	63,67,67	3.99	19 (30%)
6	CYC	b	200	-	46,46,46	5.28	27 (58%)	63,67,67	3.91	17 (26%)
6	CYC	k	200	-	46,46,46	5.26	26 (56%)	63,67,67	3.82	17 (26%)
6	CYC	x	200	-	46,46,46	5.25	25 (54%)	63,67,67	3.76	19 (30%)
6	CYC	W	200	-	46,46,46	5.24	27 (58%)	63,67,67	3.93	18 (28%)
6	CYC	i	200	-	46,46,46	5.22	26 (56%)	63,67,67	3.99	16 (25%)
6	CYC	B	200	-	46,46,46	5.27	27 (58%)	63,67,67	3.95	16 (25%)
6	CYC	D	200	-	46,46,46	5.28	26 (56%)	63,67,67	4.05	20 (31%)
6	CYC	I	200	-	46,46,46	5.28	26 (56%)	63,67,67	4.07	15 (23%)
6	CYC	h	200	-	46,46,46	5.26	27 (58%)	63,67,67	3.86	19 (30%)
6	CYC	s	200	-	46,46,46	5.20	28 (60%)	63,67,67	4.22	17 (26%)
6	CYC	w	200	-	46,46,46	5.28	29 (63%)	63,67,67	4.02	21 (33%)
6	CYC	Q	200	-	46,46,46	5.24	27 (58%)	63,67,67	4.20	18 (28%)
6	CYC	f	200	-	46,46,46	5.26	27 (58%)	63,67,67	4.01	20 (31%)
6	CYC	v	200	-	46,46,46	5.18	26 (56%)	63,67,67	4.01	20 (31%)
6	CYC	J	200	-	46,46,46	5.26	27 (58%)	63,67,67	3.80	19 (30%)
6	CYC	Y	200	-	46,46,46	5.24	25 (54%)	63,67,67	4.00	19 (30%)
6	CYC	e	200	-	46,46,46	5.30	27 (58%)	63,67,67	3.96	18 (28%)
6	CYC	V	200	-	46,46,46	5.24	26 (56%)	63,67,67	4.06	18 (28%)
6	CYC	0	1202	-	46,46,46	5.22	26 (56%)	63,67,67	3.93	18 (28%)
6	CYC	C	200	-	46,46,46	5.29	26 (56%)	63,67,67	3.97	13 (20%)
6	CYC	H	200	-	46,46,46	5.31	26 (56%)	63,67,67	4.06	16 (25%)
6	CYC	R	200	-	46,46,46	5.25	26 (56%)	63,67,67	4.00	18 (28%)
6	CYC	m	200	-	46,46,46	5.29	26 (56%)	63,67,67	4.02	19 (30%)
6	CYC	l	200	-	46,46,46	5.28	27 (58%)	63,67,67	3.85	18 (28%)
6	CYC	E	200	-	46,46,46	5.36	25 (54%)	63,67,67	3.87	15 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CYC	Z	200	-	46,46,46	5.31	26 (56%)	63,67,67	3.96	15 (23%)
6	CYC	0	1201	-	46,46,46	5.31	25 (54%)	63,67,67	3.97	20 (31%)
6	CYC	O	200	-	46,46,46	5.31	27 (58%)	63,67,67	4.12	20 (31%)
6	CYC	L	200	-	46,46,46	5.31	27 (58%)	63,67,67	3.98	23 (36%)
6	CYC	T	200	-	46,46,46	5.28	26 (56%)	63,67,67	3.85	17 (26%)
6	CYC	d	200	-	46,46,46	5.23	27 (58%)	63,67,67	3.96	19 (30%)

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	P	200	-	-	8/26/74/74	0/4/4/4
6	CYC	G	200	-	-	7/26/74/74	0/4/4/4
6	CYC	a	200	-	-	7/26/74/74	0/4/4/4
6	CYC	o	200	-	-	10/26/74/74	0/4/4/4
6	CYC	p	200	-	-	9/26/74/74	0/4/4/4
6	CYC	t	200	-	-	11/26/74/74	0/4/4/4
6	CYC	S	200	-	-	10/26/74/74	0/4/4/4
6	CYC	N	200	-	-	19/26/74/74	0/4/4/4
6	CYC	n	200	-	-	11/26/74/74	0/4/4/4
6	CYC	q	200	-	-	8/26/74/74	0/4/4/4
6	CYC	0	1203	-	-	11/26/74/74	0/4/4/4
6	CYC	u	200	-	-	5/26/74/74	0/4/4/4
6	CYC	c	200	-	-	8/26/74/74	0/4/4/4
6	CYC	A	200	-	-	8/26/74/74	0/4/4/4
6	CYC	y	200	-	-	11/26/74/74	0/4/4/4
6	CYC	r	200	-	-	6/26/74/74	0/4/4/4
6	CYC	j	200	-	-	8/26/74/74	0/4/4/4
6	CYC	b	200	-	-	8/26/74/74	0/4/4/4
6	CYC	k	200	-	-	7/26/74/74	0/4/4/4
6	CYC	x	200	-	-	7/26/74/74	0/4/4/4
6	CYC	W	200	-	-	7/26/74/74	0/4/4/4
6	CYC	i	200	-	-	9/26/74/74	0/4/4/4
6	CYC	B	200	-	-	7/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CYC	D	200	-	-	9/26/74/74	0/4/4/4
6	CYC	I	200	-	-	10/26/74/74	0/4/4/4
6	CYC	h	200	-	-	10/26/74/74	0/4/4/4
6	CYC	s	200	-	-	6/26/74/74	0/4/4/4
6	CYC	w	200	-	-	8/26/74/74	0/4/4/4
6	CYC	Q	200	-	-	7/26/74/74	0/4/4/4
6	CYC	f	200	-	-	6/26/74/74	0/4/4/4
6	CYC	v	200	-	-	10/26/74/74	0/4/4/4
6	CYC	J	200	-	-	9/26/74/74	0/4/4/4
6	CYC	Y	200	-	-	8/26/74/74	0/4/4/4
6	CYC	e	200	-	-	10/26/74/74	0/4/4/4
6	CYC	V	200	-	-	14/26/74/74	0/4/4/4
6	CYC	0	1202	-	-	7/26/74/74	0/4/4/4
6	CYC	C	200	-	-	15/26/74/74	0/4/4/4
6	CYC	H	200	-	-	10/26/74/74	0/4/4/4
6	CYC	R	200	-	-	9/26/74/74	0/4/4/4
6	CYC	m	200	-	-	9/26/74/74	0/4/4/4
6	CYC	l	200	-	-	10/26/74/74	0/4/4/4
6	CYC	E	200	-	-	12/26/74/74	0/4/4/4
6	CYC	Z	200	-	-	7/26/74/74	0/4/4/4
6	CYC	0	1201	-	-	12/26/74/74	0/4/4/4
6	CYC	O	200	-	-	9/26/74/74	0/4/4/4
6	CYC	L	200	-	-	9/26/74/74	0/4/4/4
6	CYC	T	200	-	-	14/26/74/74	0/4/4/4
6	CYC	d	200	-	-	10/26/74/74	0/4/4/4

The worst 5 of 1270 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	j	200	CYC	C2C-C1C	14.02	1.64	1.52
6	L	200	CYC	C2C-C1C	13.52	1.64	1.52
6	k	200	CYC	C2C-C1C	13.42	1.64	1.52
6	w	200	CYC	C2C-C1C	13.27	1.63	1.52
6	l	200	CYC	C2C-C1C	13.26	1.63	1.52

The worst 5 of 855 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	s	200	CYC	OC-C1C-C2C	-22.01	108.67	126.17
6	Q	200	CYC	OC-C1C-C2C	-21.48	109.09	126.17
6	Y	200	CYC	OC-C1C-C2C	-21.28	109.26	126.17
6	A	200	CYC	OC-C1C-C2C	-21.13	109.37	126.17
6	u	200	CYC	OC-C1C-C2C	-20.92	109.54	126.17

There are no chirality outliers.

5 of 442 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	0	1201	CYC	C4B-C3B-CAB-CBB
6	0	1201	CYC	C2C-C3C-CAC-CBC
6	0	1201	CYC	NC-C4C-CHD-C1D
6	0	1202	CYC	NC-C4C-CHD-C1D
6	0	1203	CYC	NC-C4C-CHD-C1D

There are no ring outliers.

48 monomers are involved in 260 short contacts:

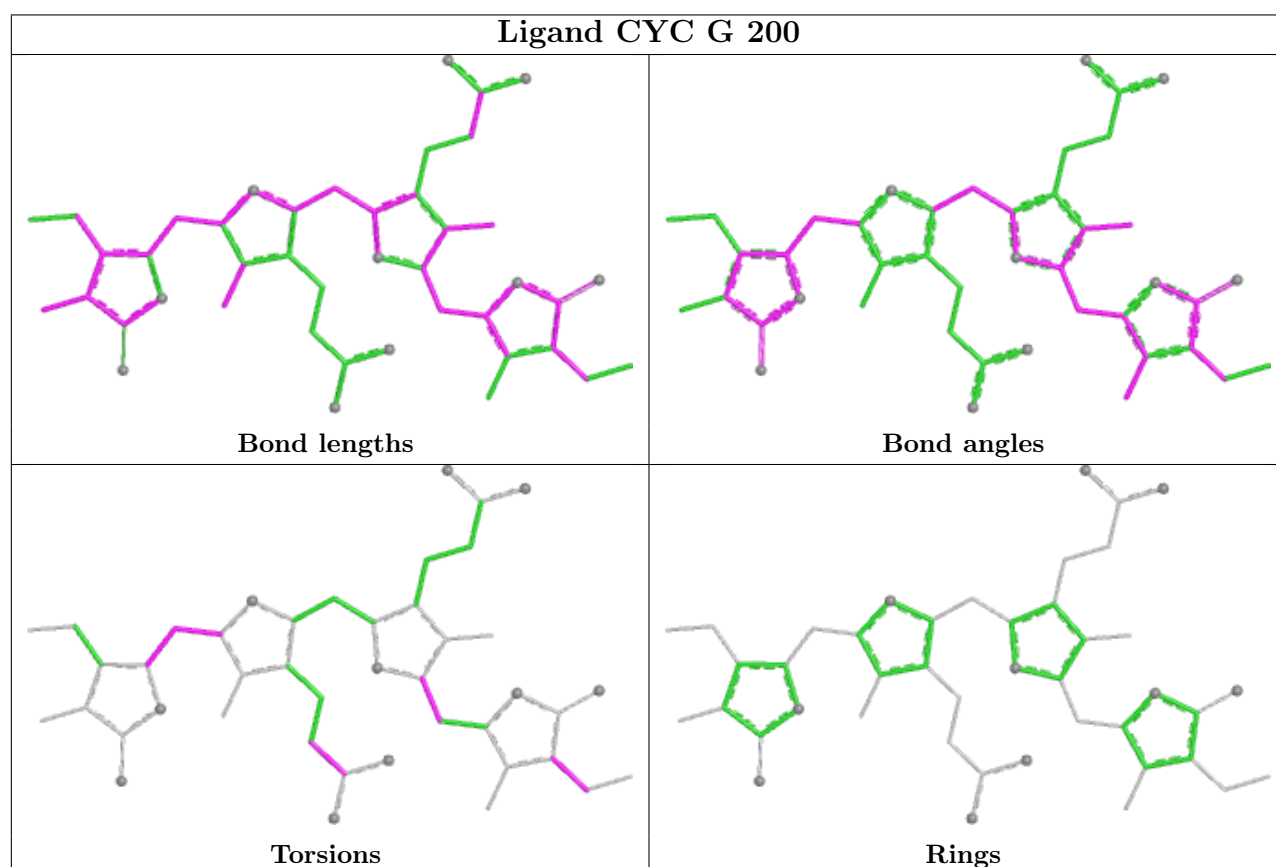
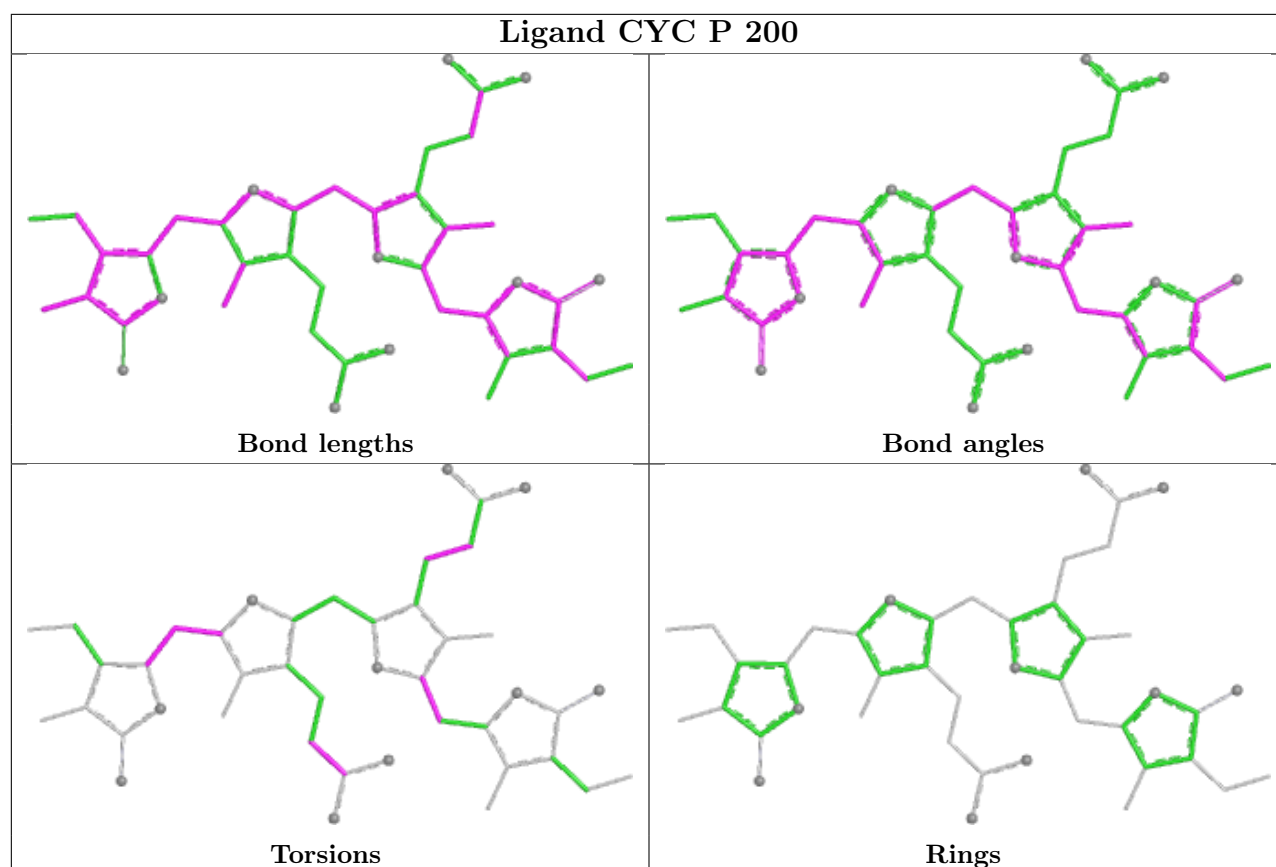
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	P	200	CYC	7	0
6	G	200	CYC	7	0
6	a	200	CYC	7	0
6	o	200	CYC	5	0
6	p	200	CYC	6	0
6	t	200	CYC	11	0
6	S	200	CYC	4	0
6	N	200	CYC	8	0
6	n	200	CYC	6	0
6	q	200	CYC	5	0
6	0	1203	CYC	6	0
6	u	200	CYC	3	0
6	c	200	CYC	7	0
6	A	200	CYC	3	0
6	y	200	CYC	6	0
6	r	200	CYC	7	0
6	j	200	CYC	2	0
6	b	200	CYC	6	0
6	k	200	CYC	5	0
6	x	200	CYC	7	0
6	W	200	CYC	6	0
6	i	200	CYC	3	0

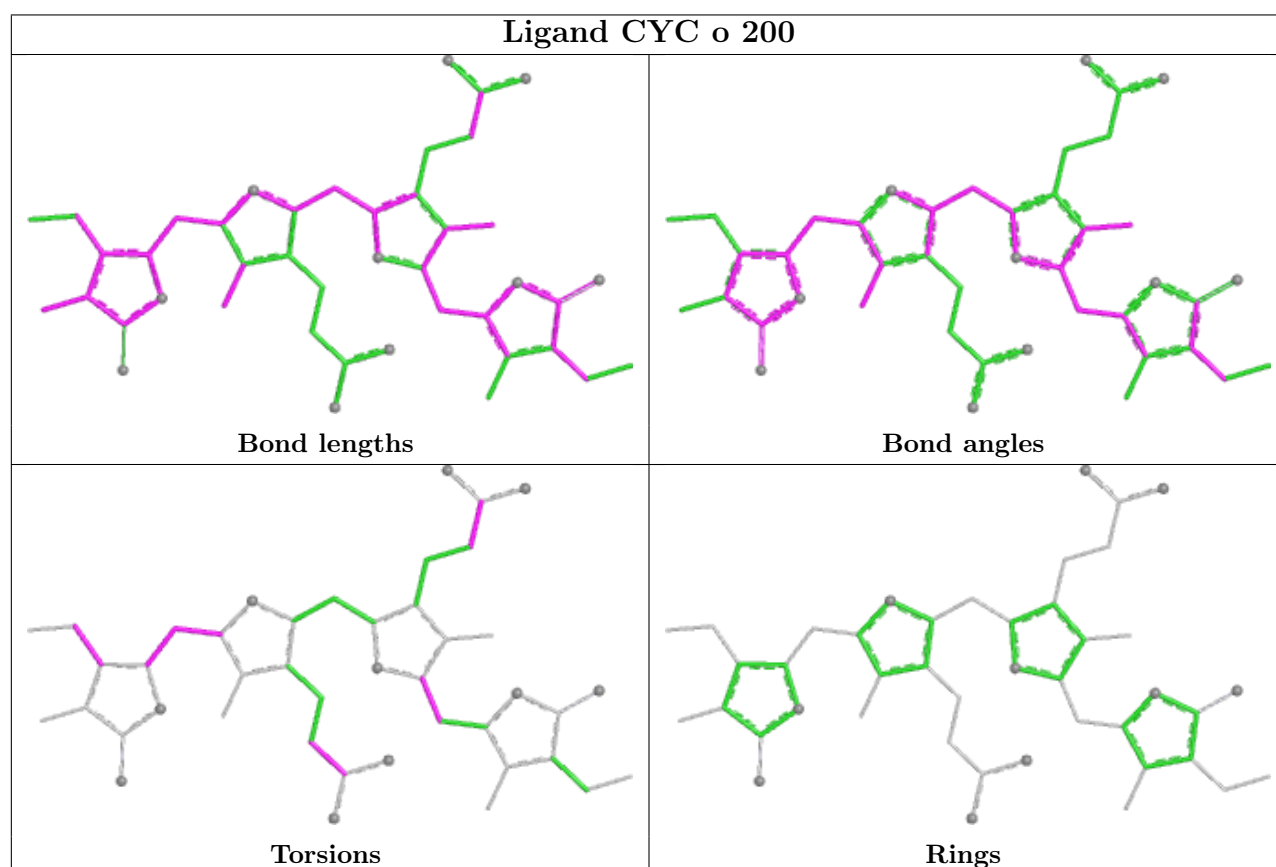
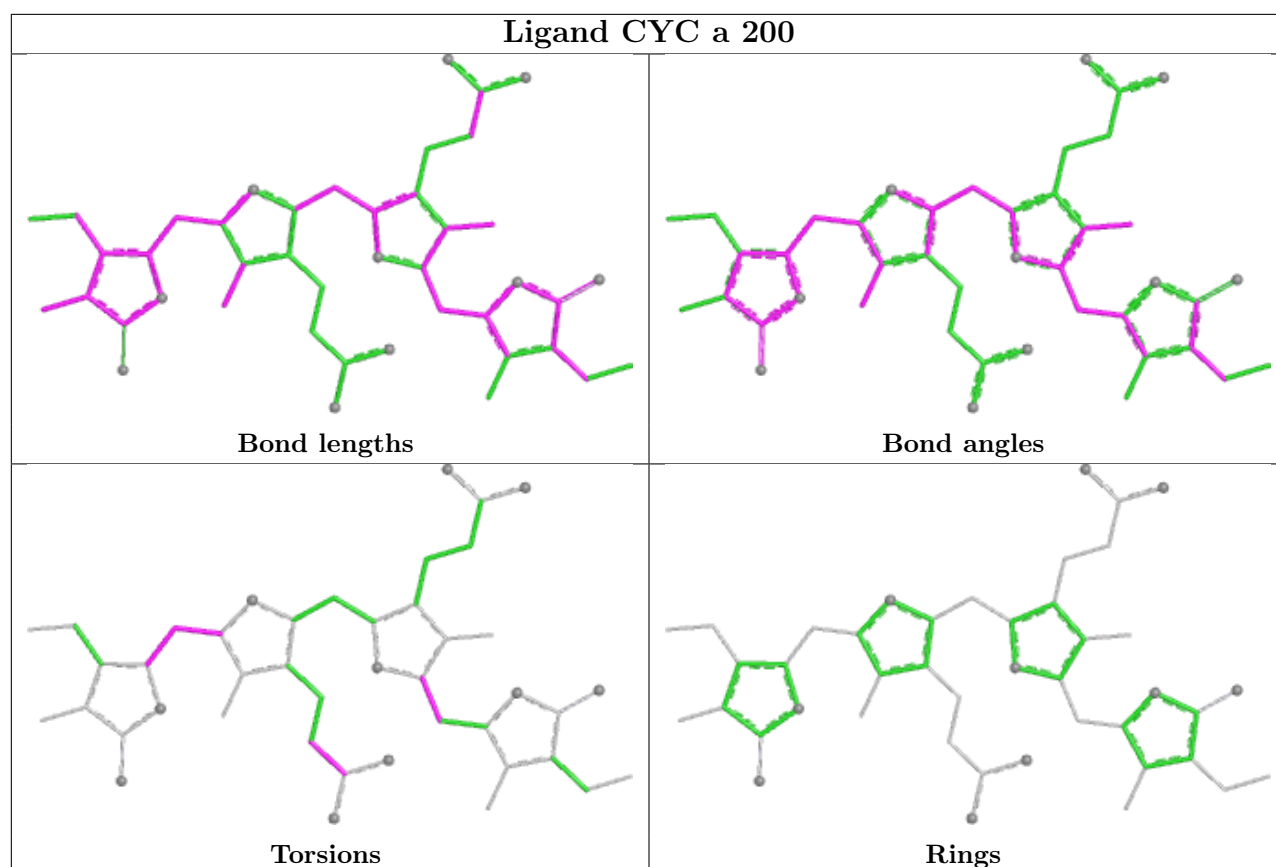
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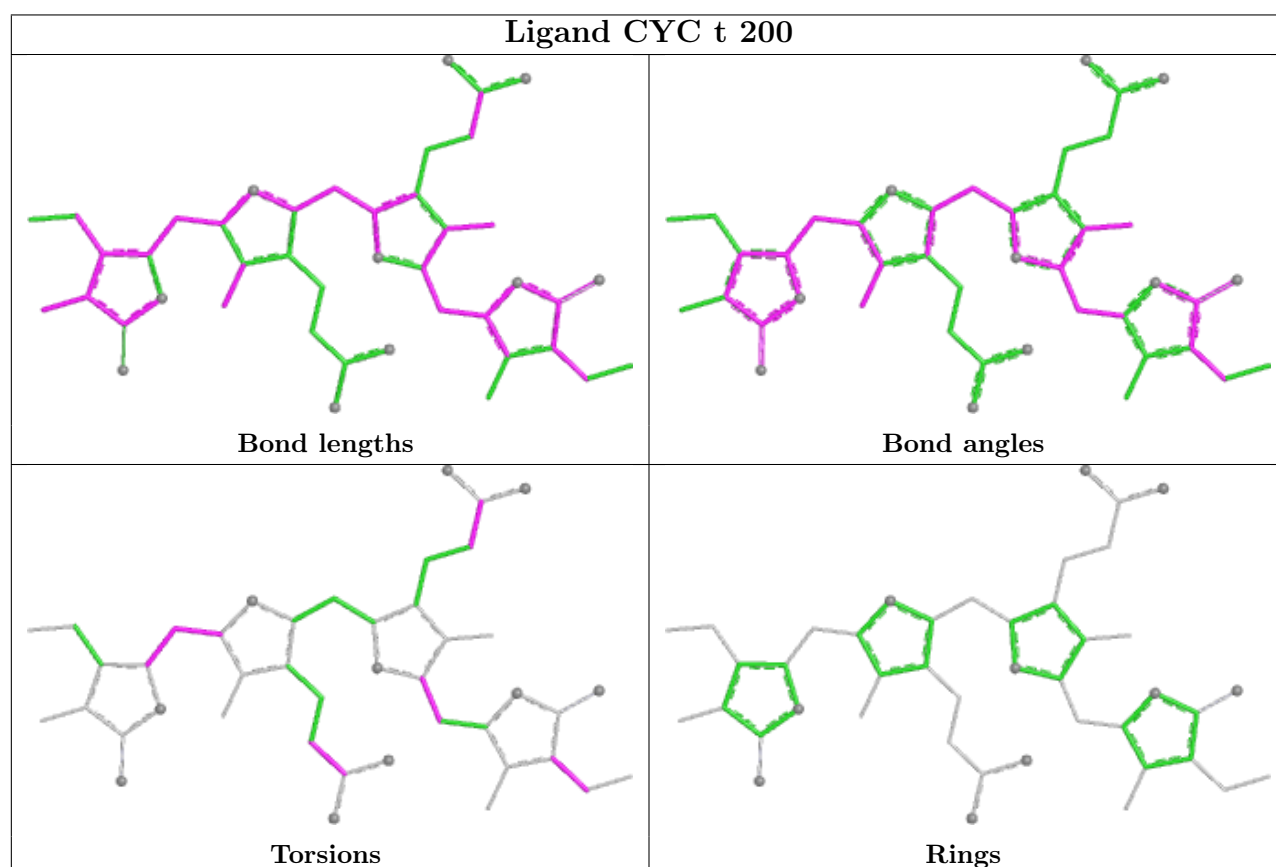
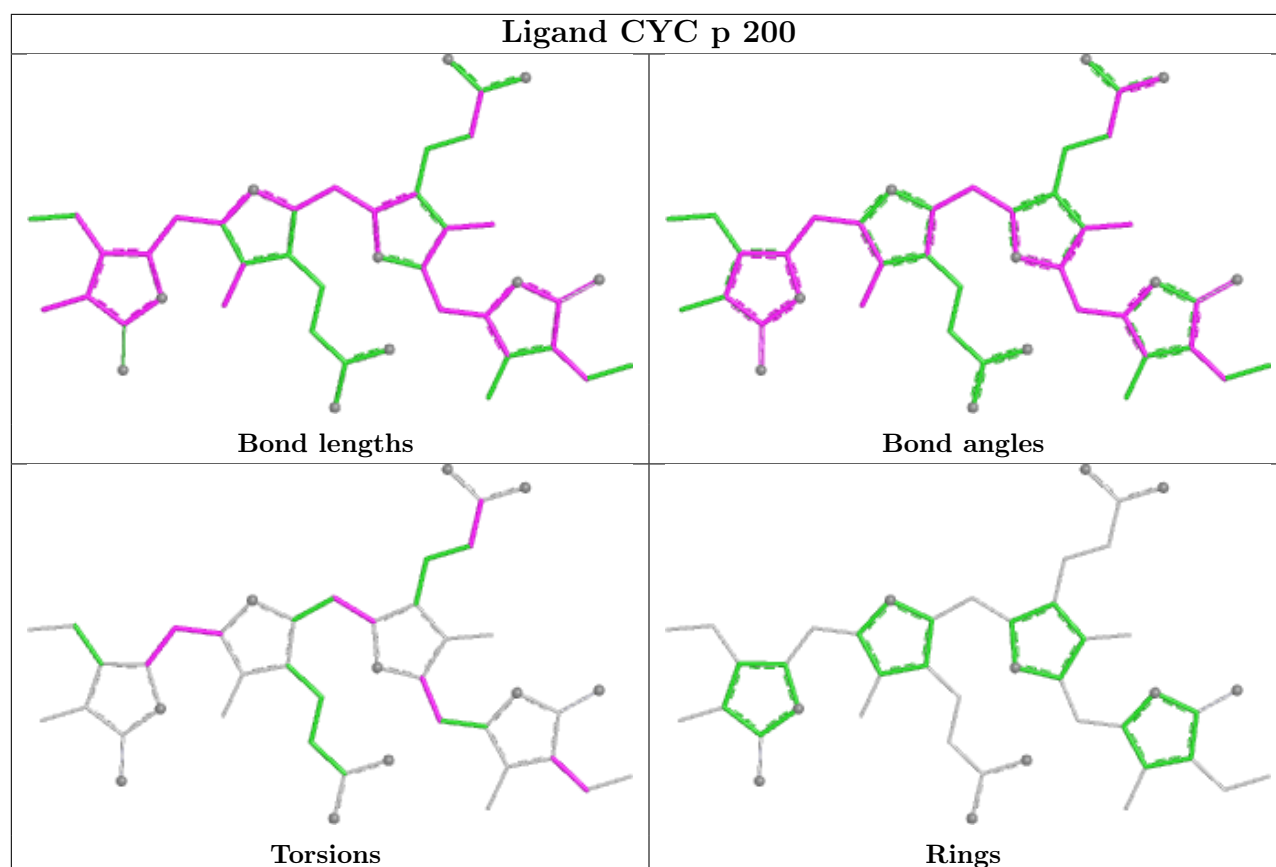
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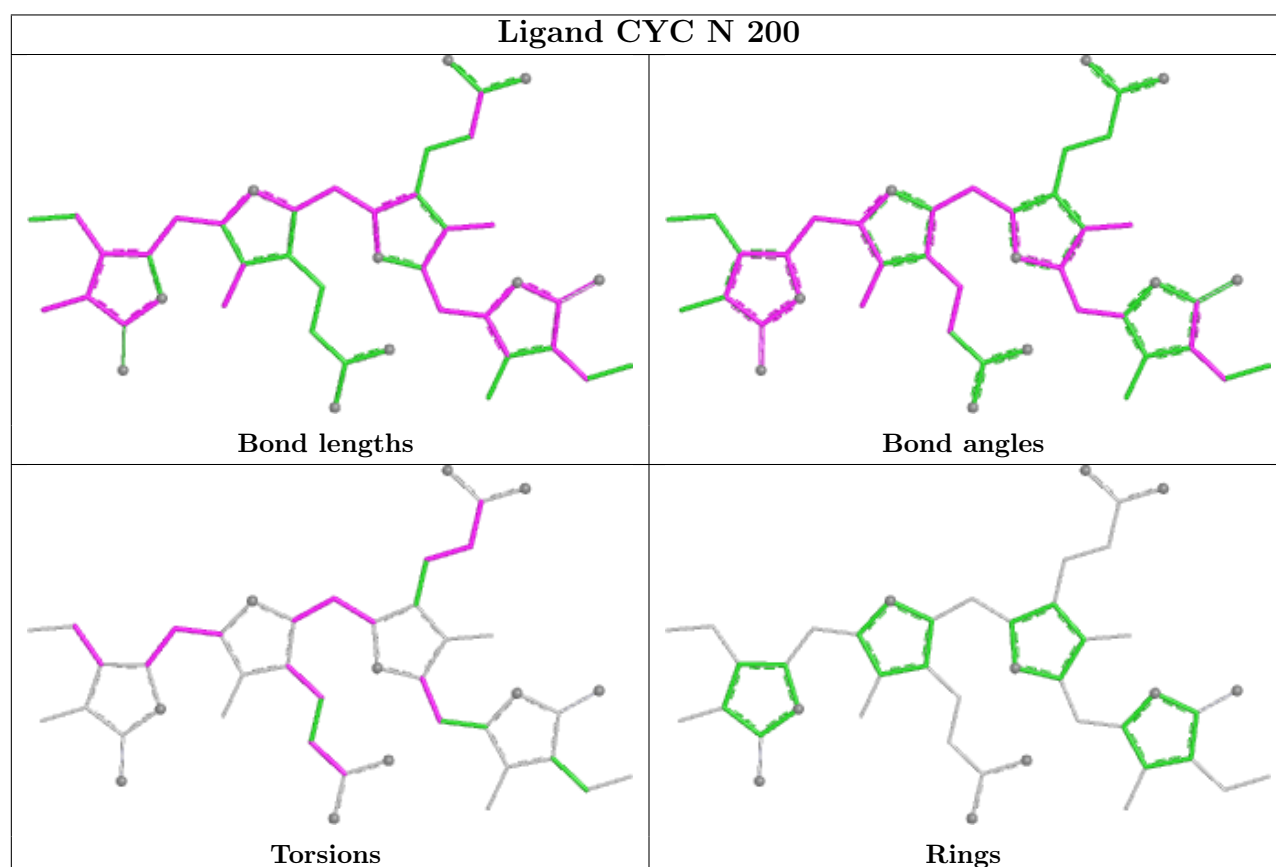
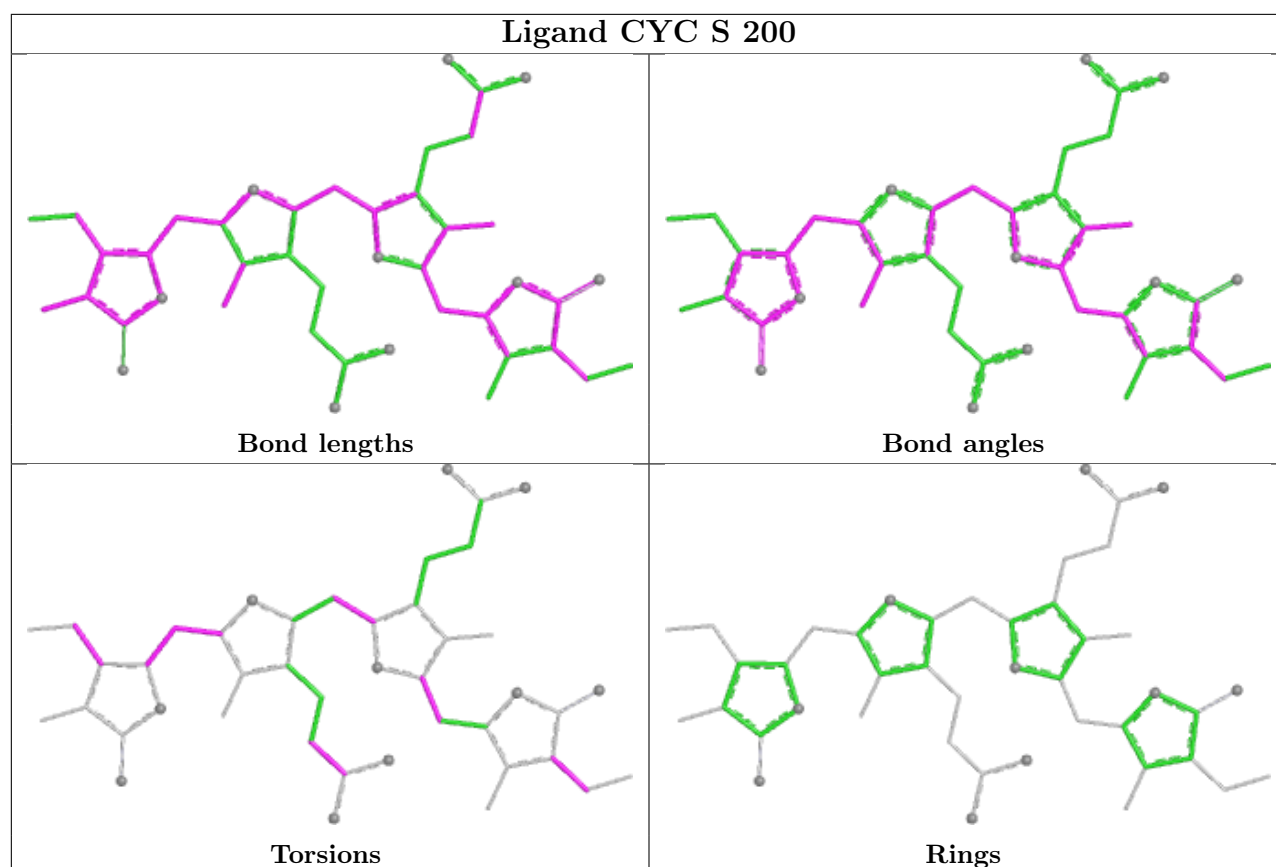
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	200	CYC	6	0
6	D	200	CYC	5	0
6	I	200	CYC	3	0
6	h	200	CYC	6	0
6	s	200	CYC	5	0
6	w	200	CYC	3	0
6	Q	200	CYC	5	0
6	f	200	CYC	8	0
6	v	200	CYC	5	0
6	J	200	CYC	5	0
6	Y	200	CYC	5	0
6	e	200	CYC	3	0
6	V	200	CYC	4	0
6	0	1202	CYC	6	0
6	C	200	CYC	6	0
6	H	200	CYC	5	0
6	R	200	CYC	6	0
6	m	200	CYC	5	0
6	l	200	CYC	6	0
6	E	200	CYC	6	0
6	Z	200	CYC	7	0
6	0	1201	CYC	5	0
6	O	200	CYC	6	0
6	L	200	CYC	3	0
6	T	200	CYC	4	0
6	d	200	CYC	5	0

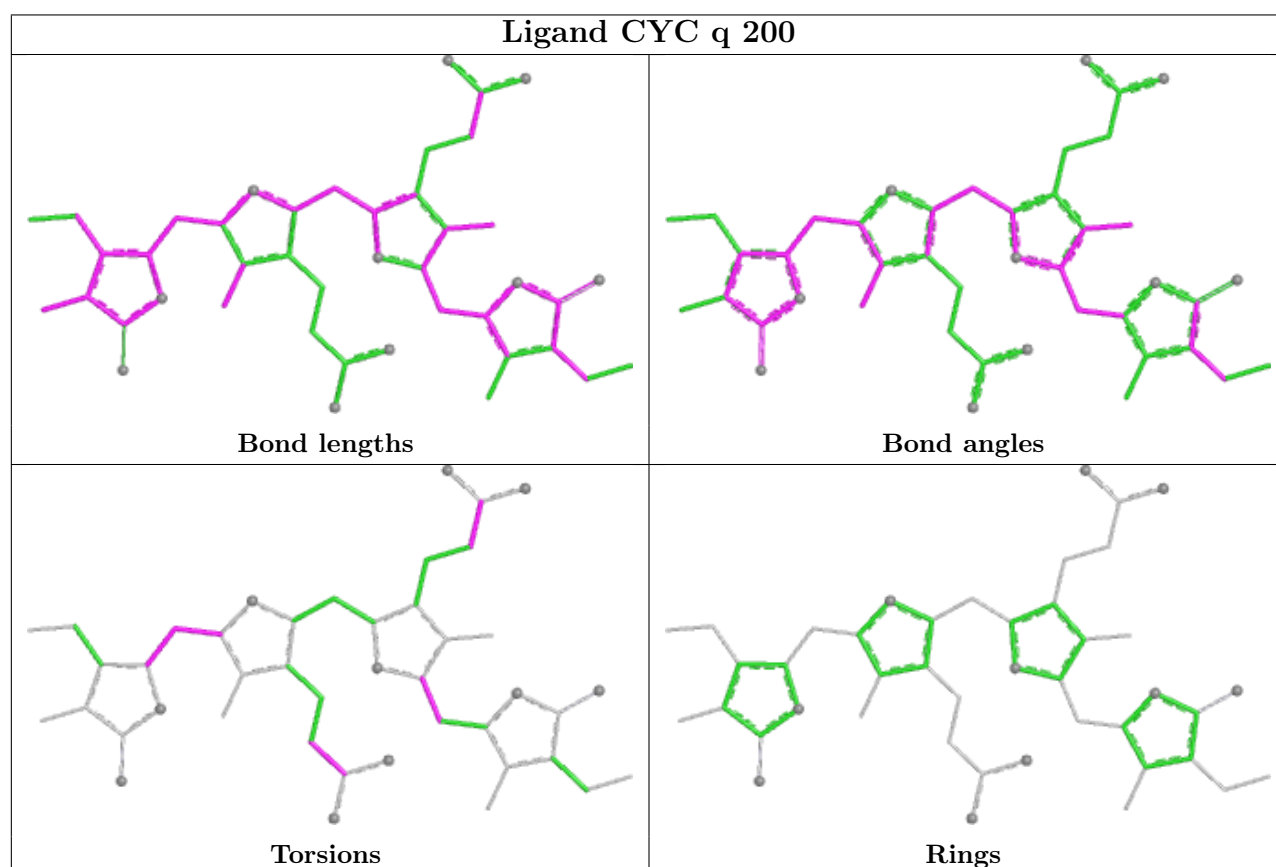
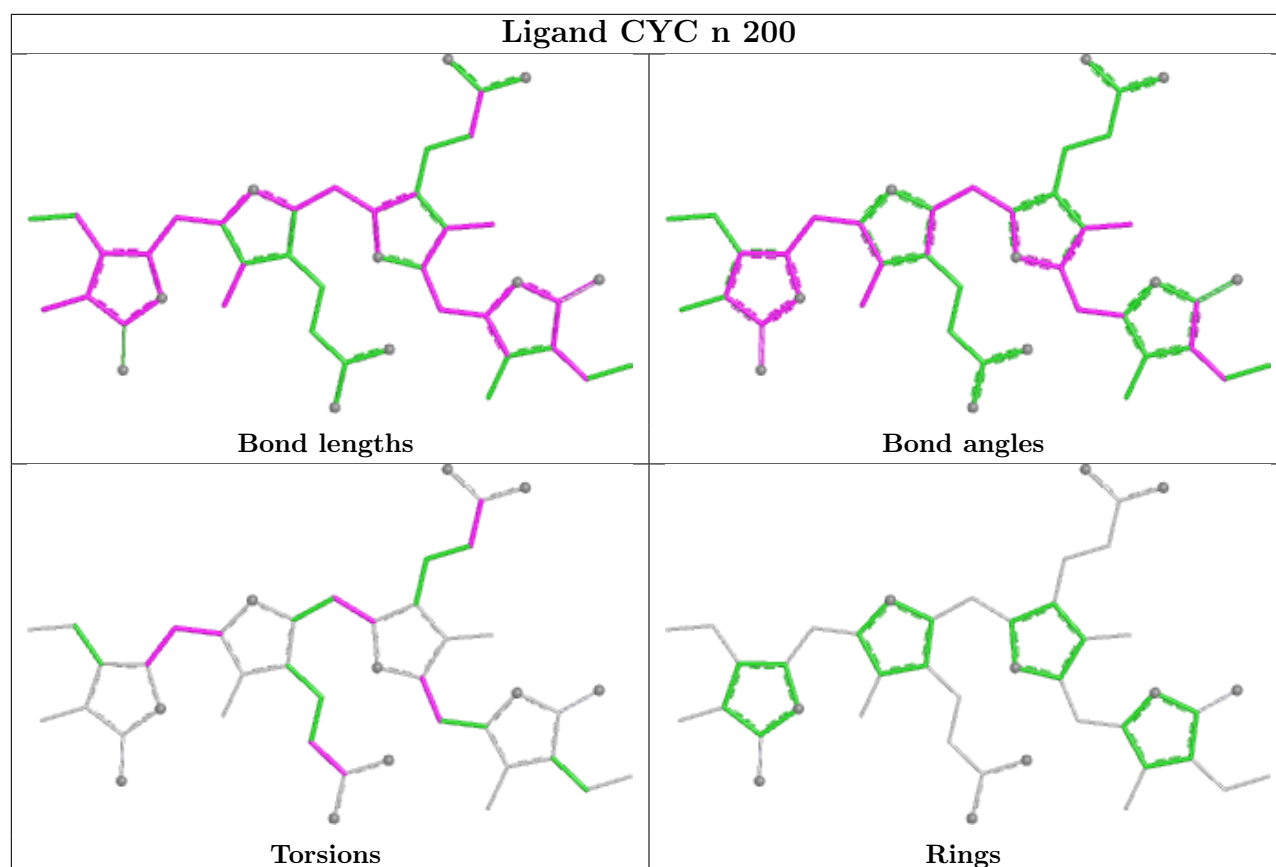
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

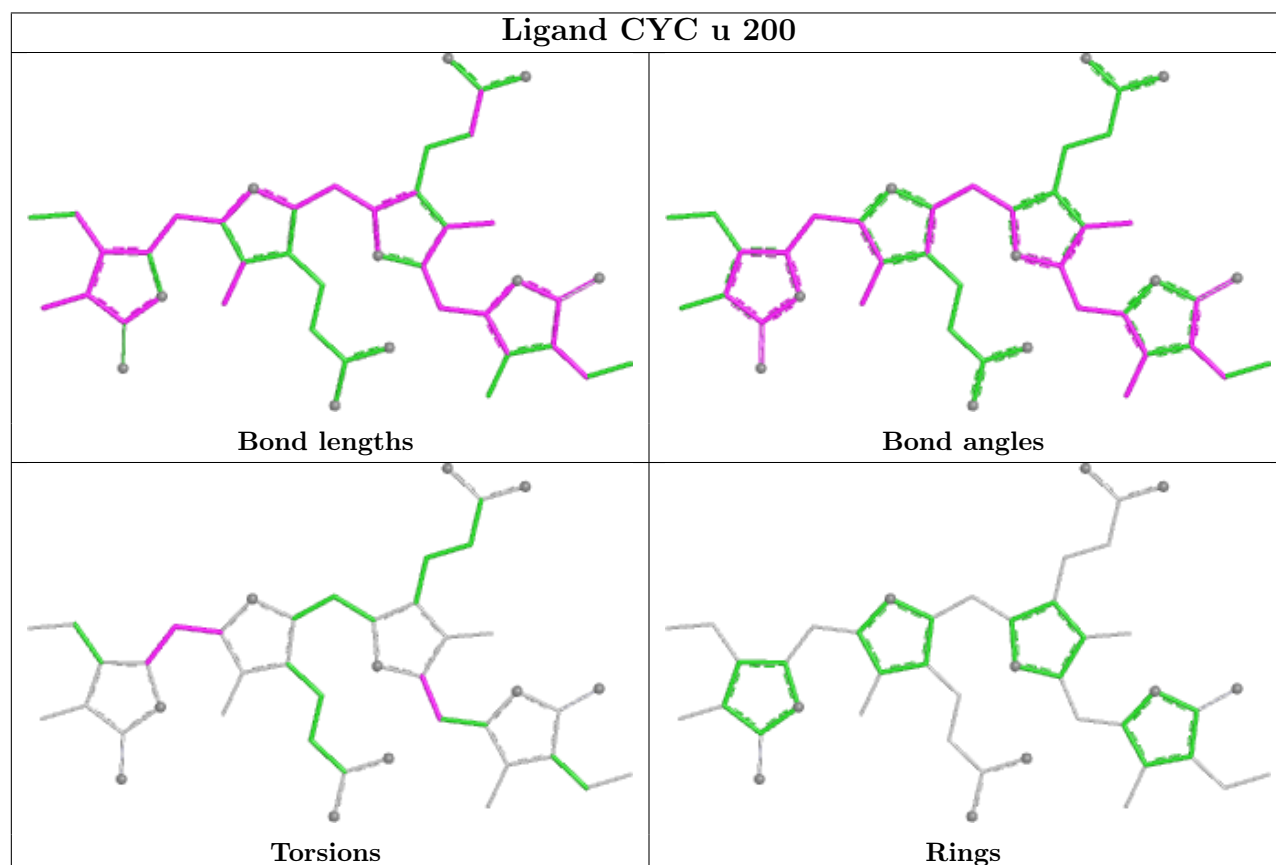
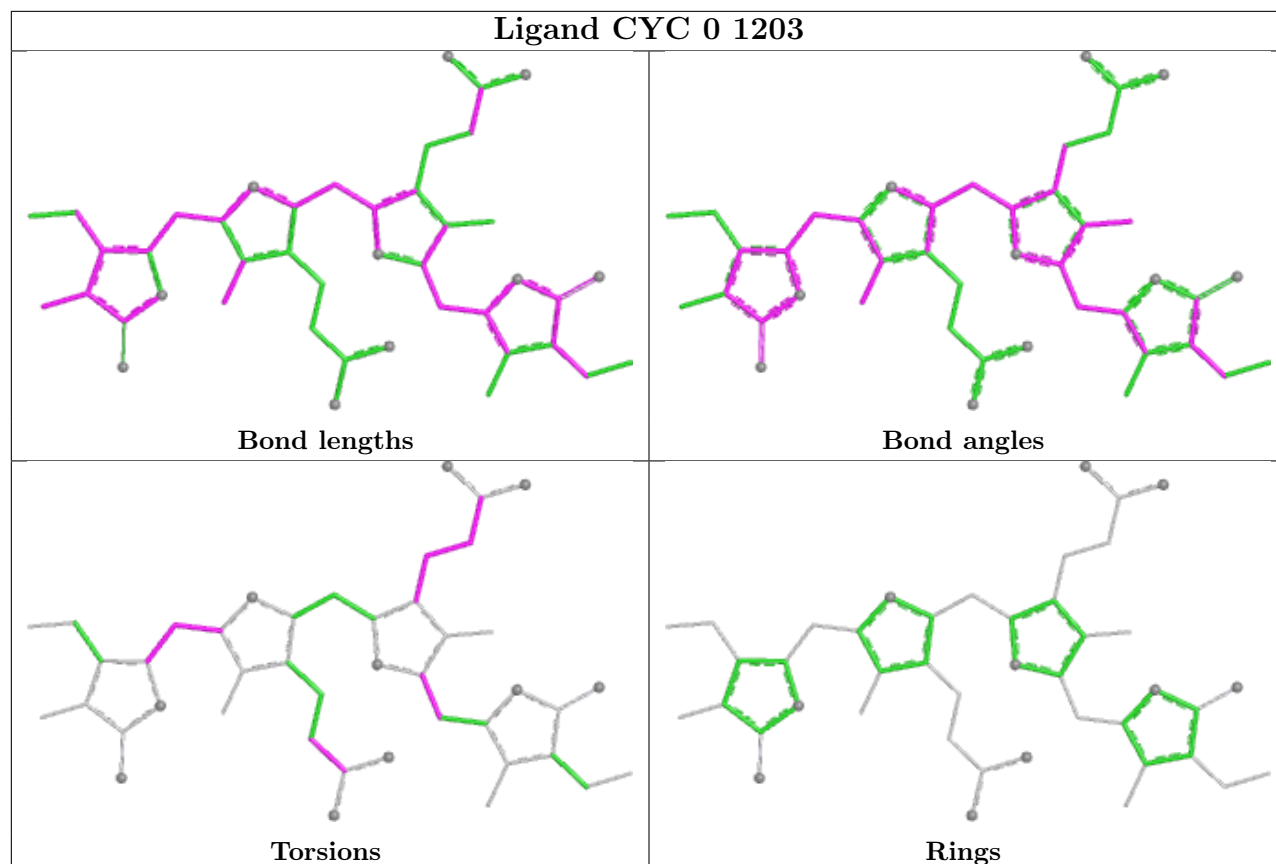


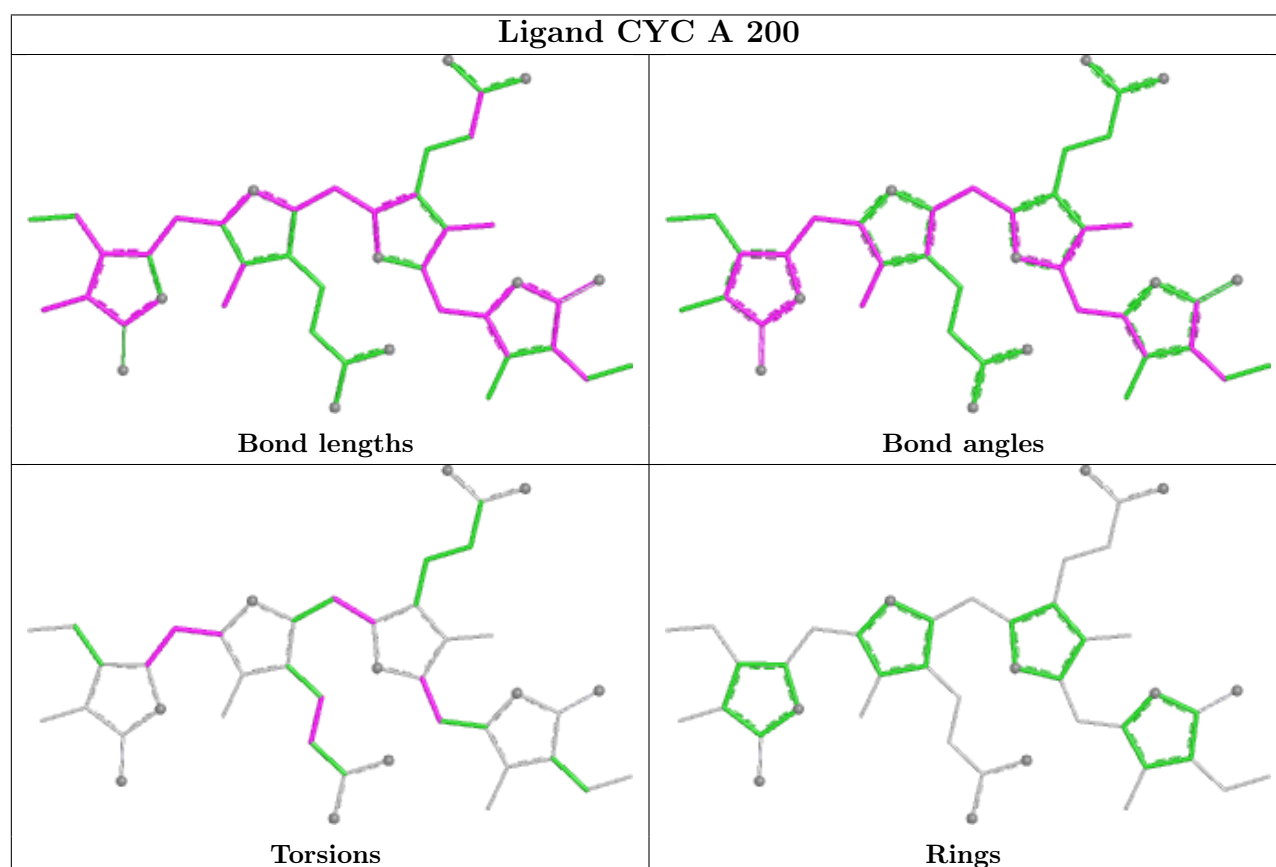
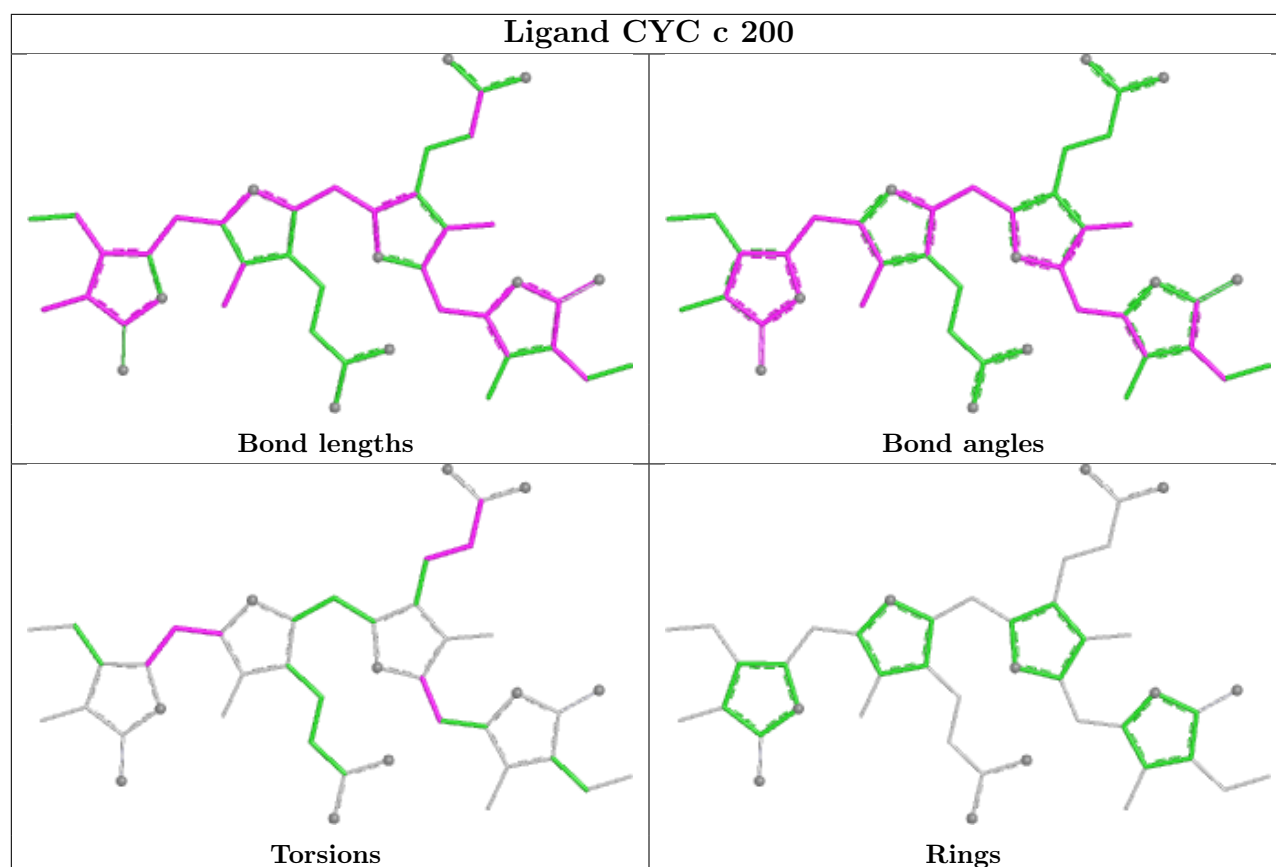


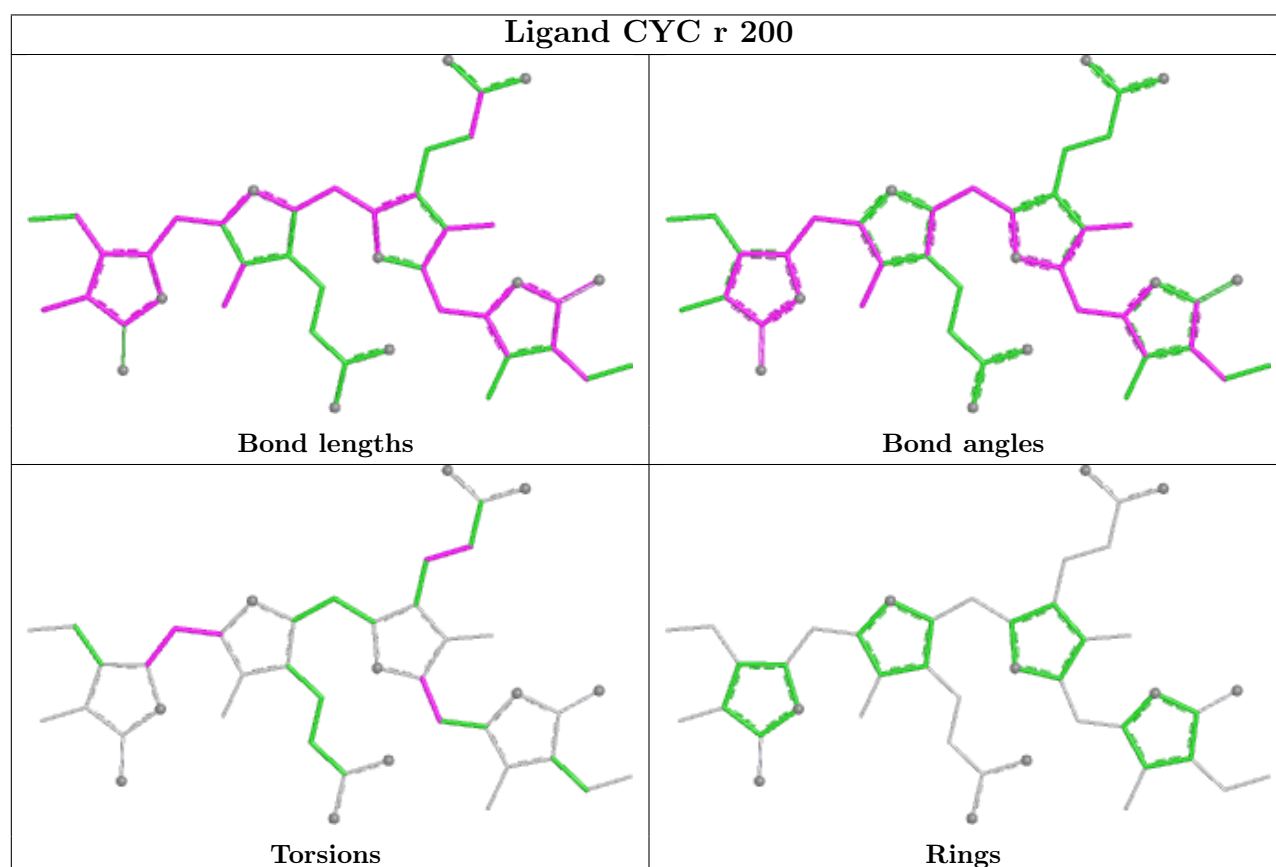
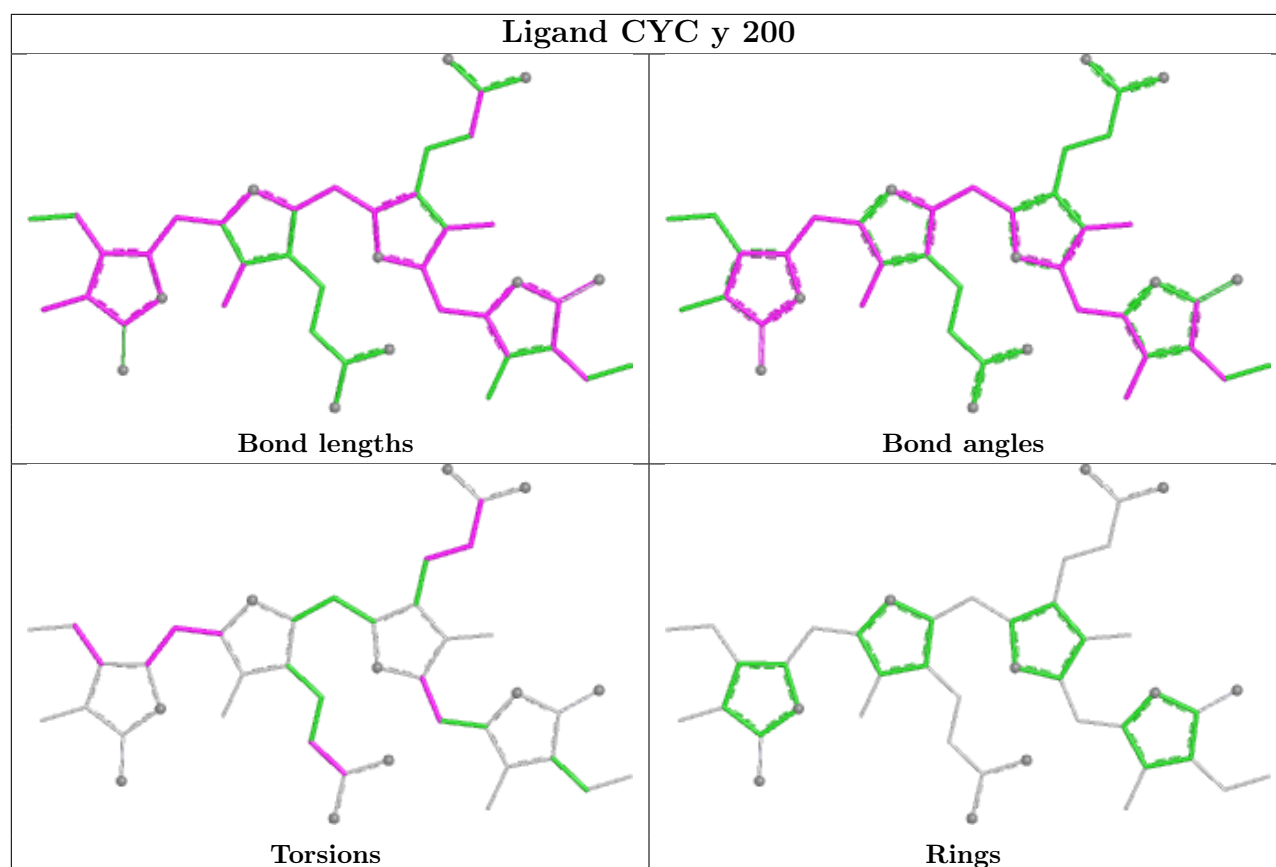


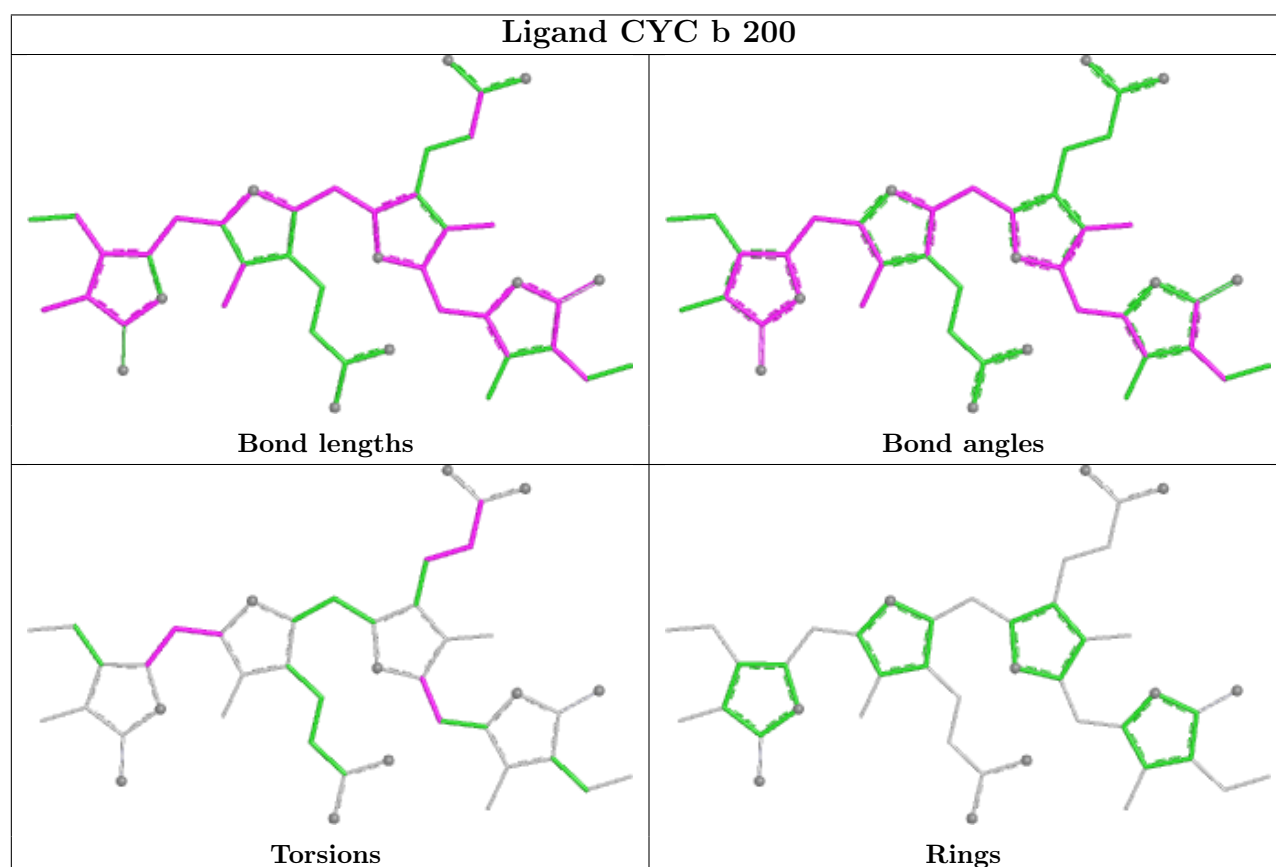
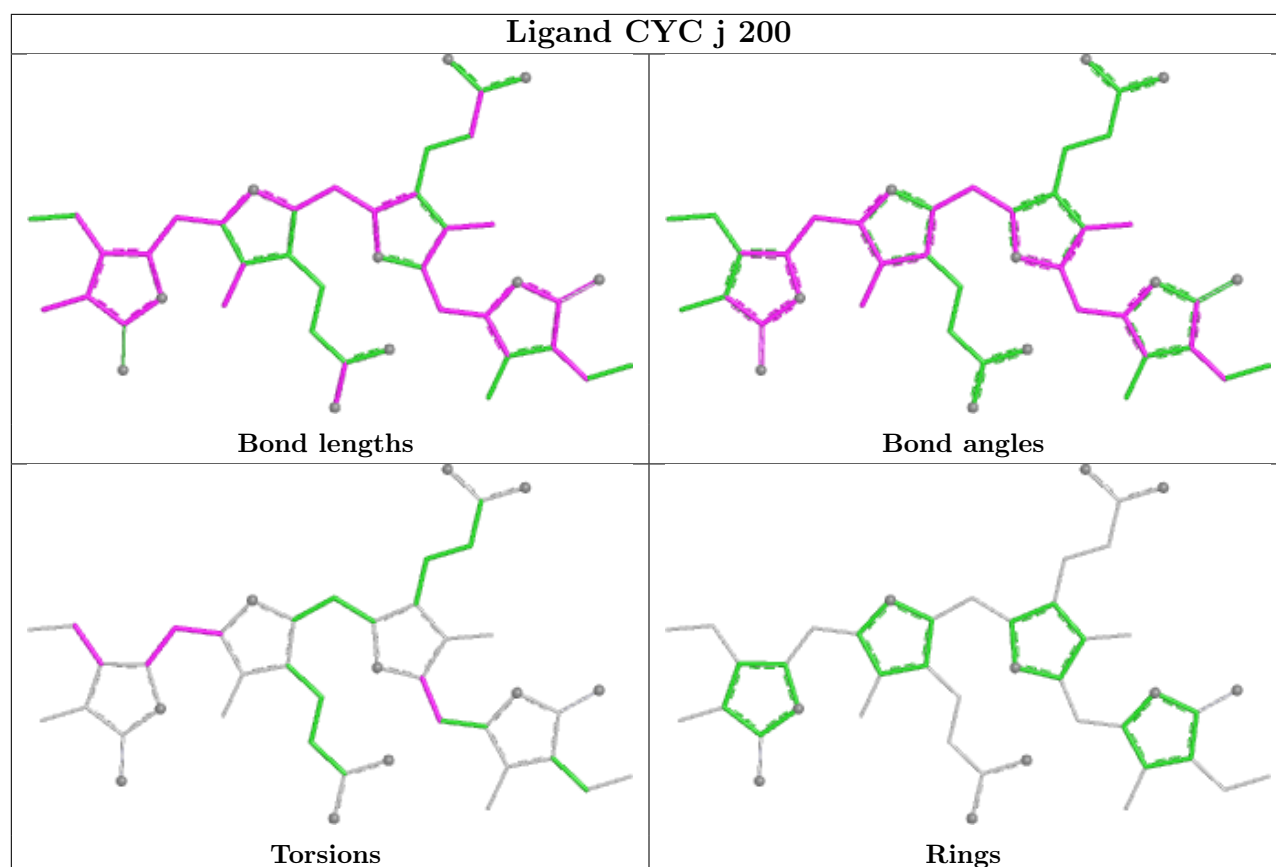


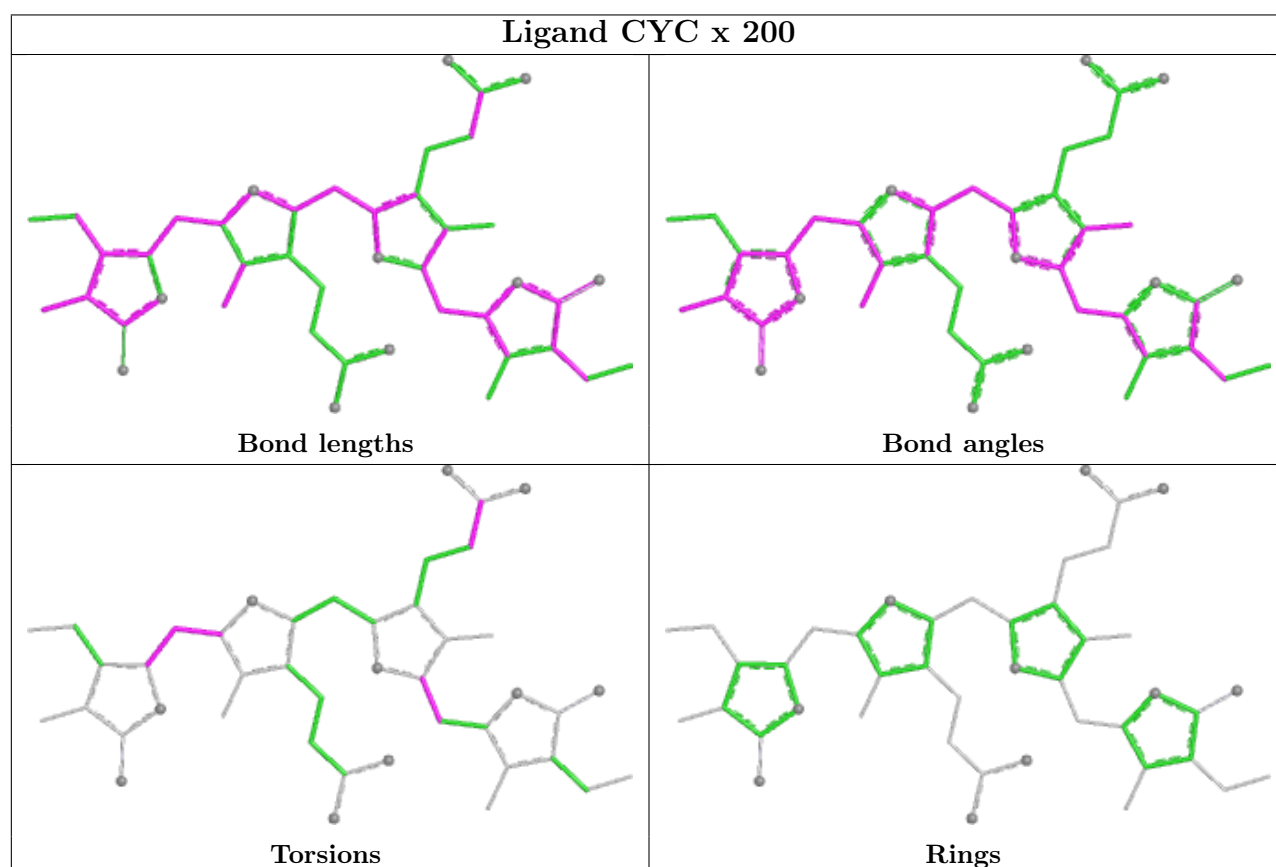
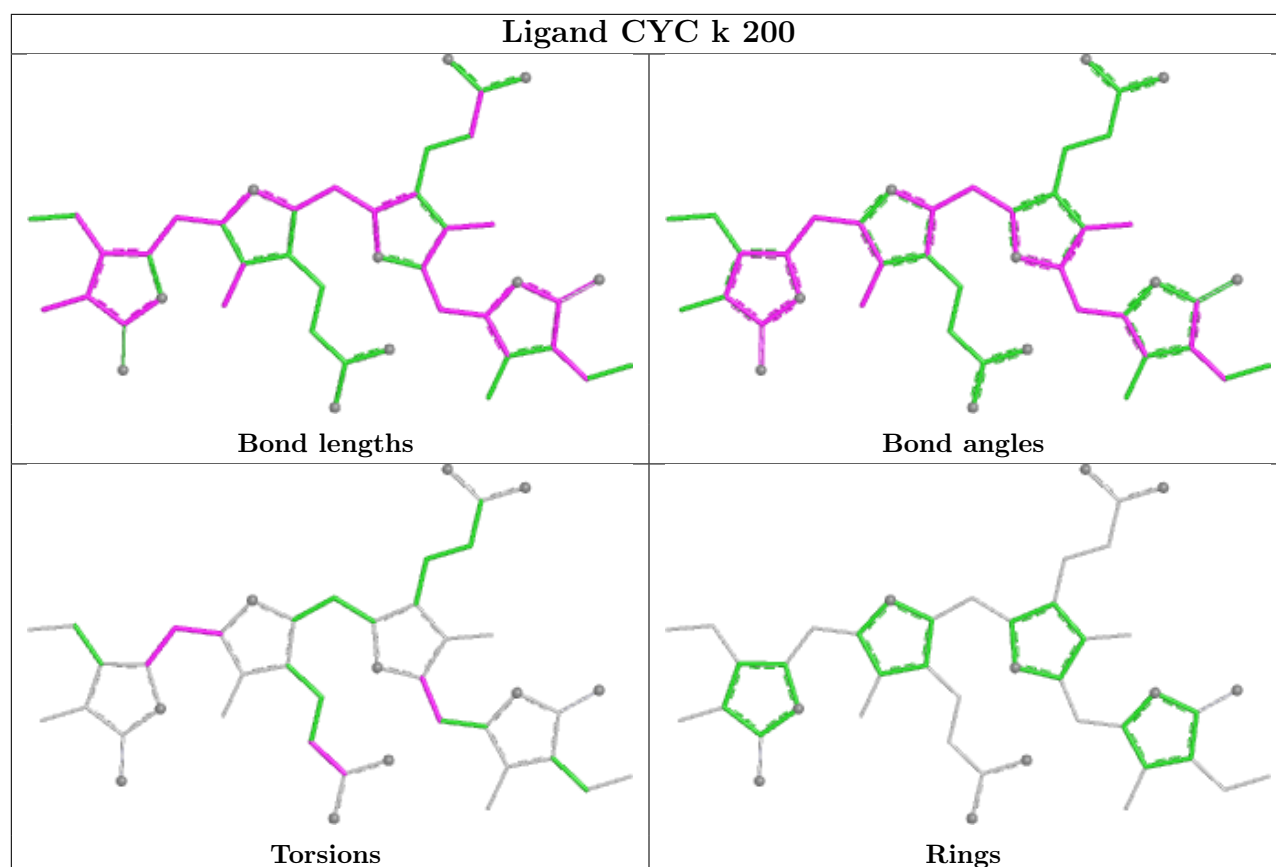


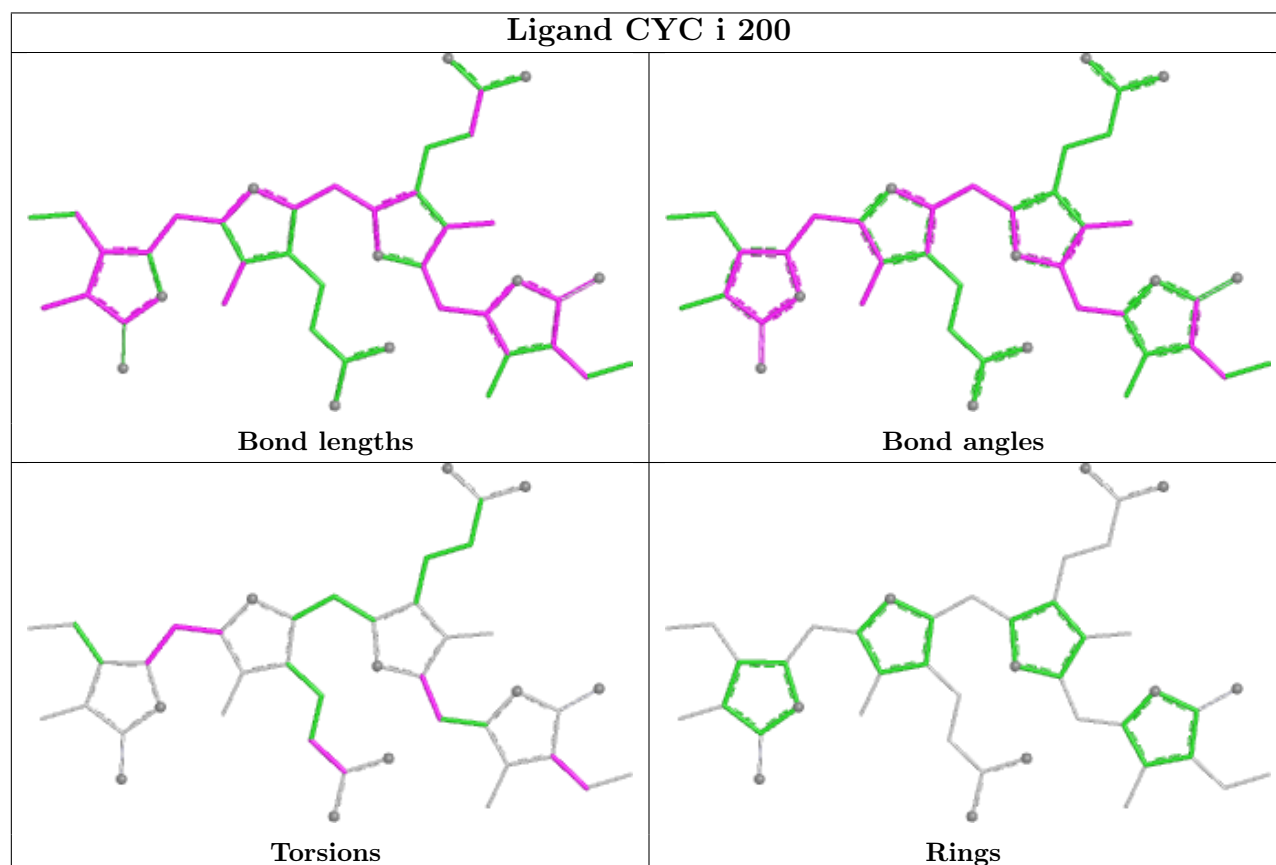
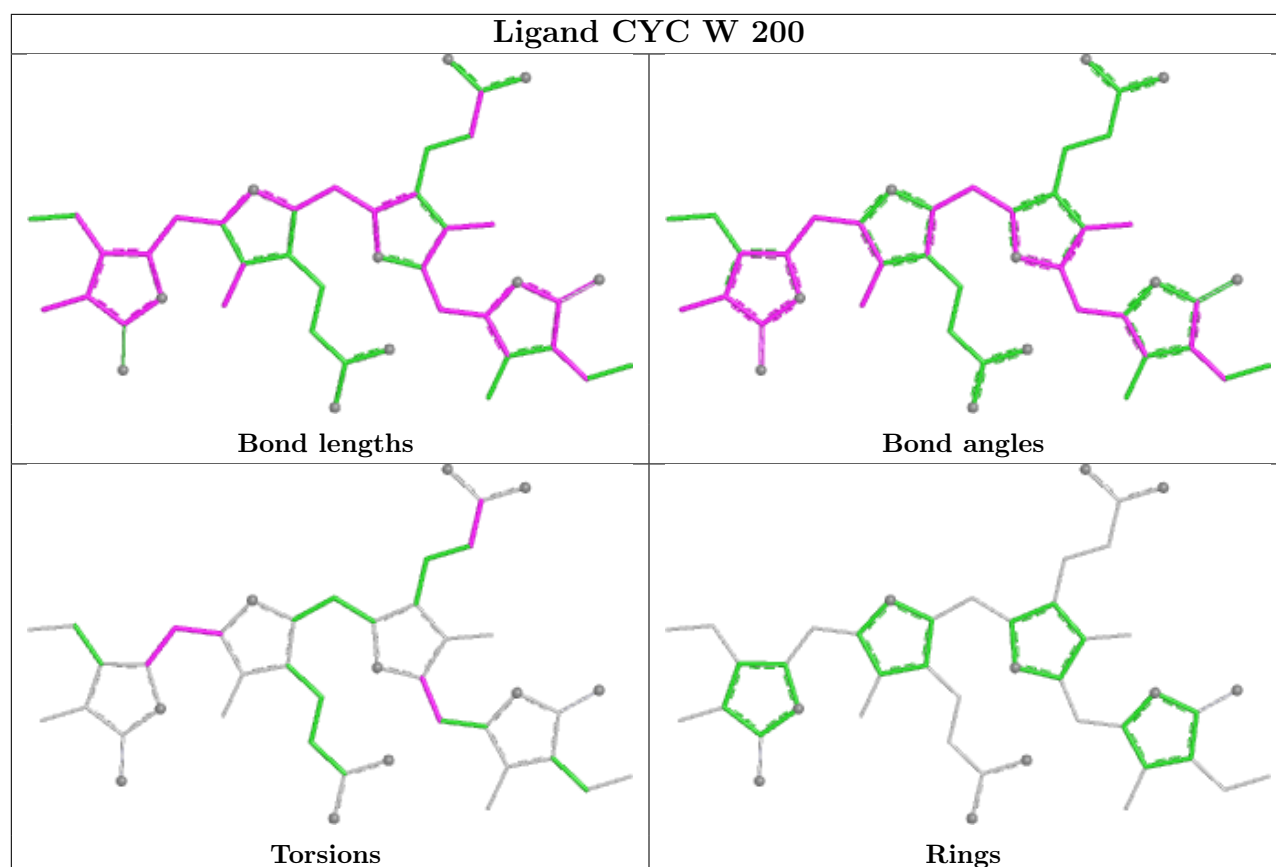


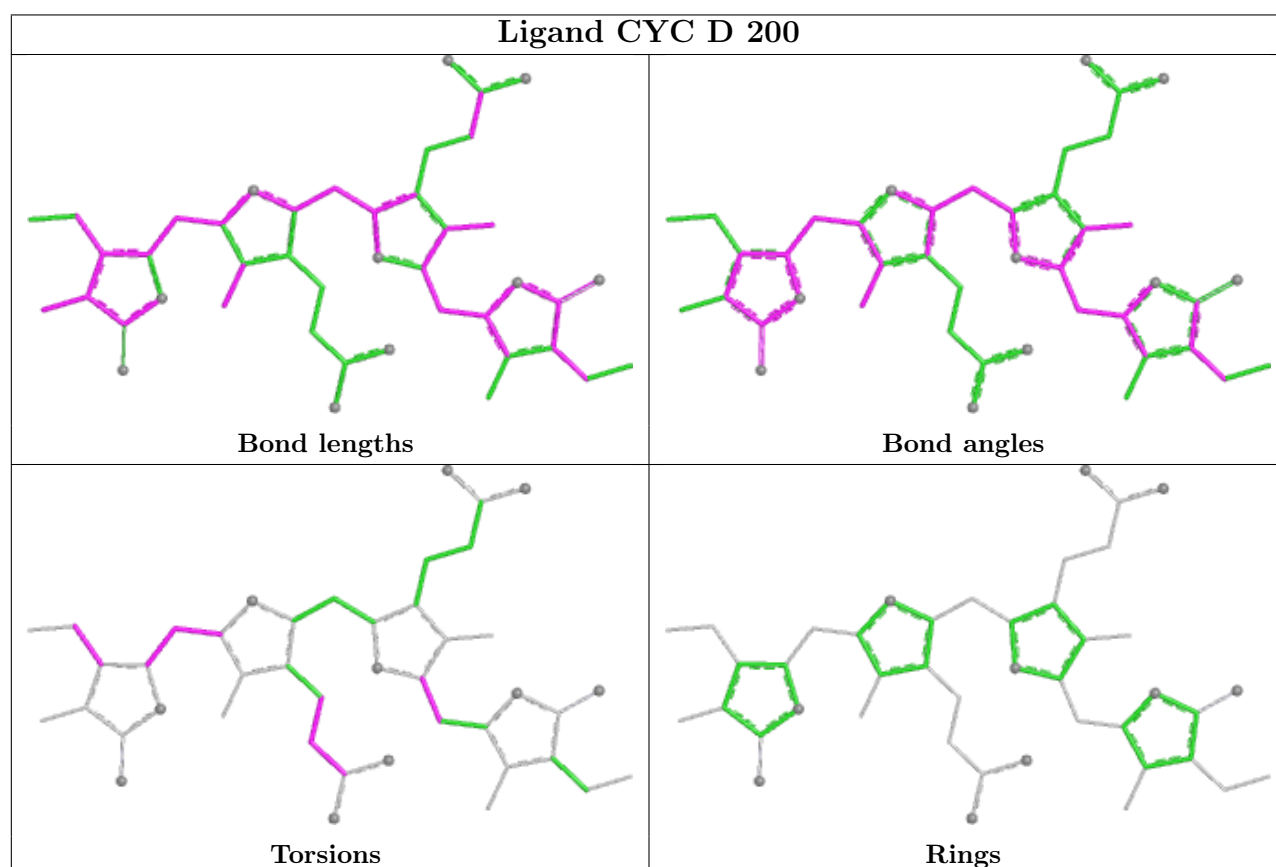
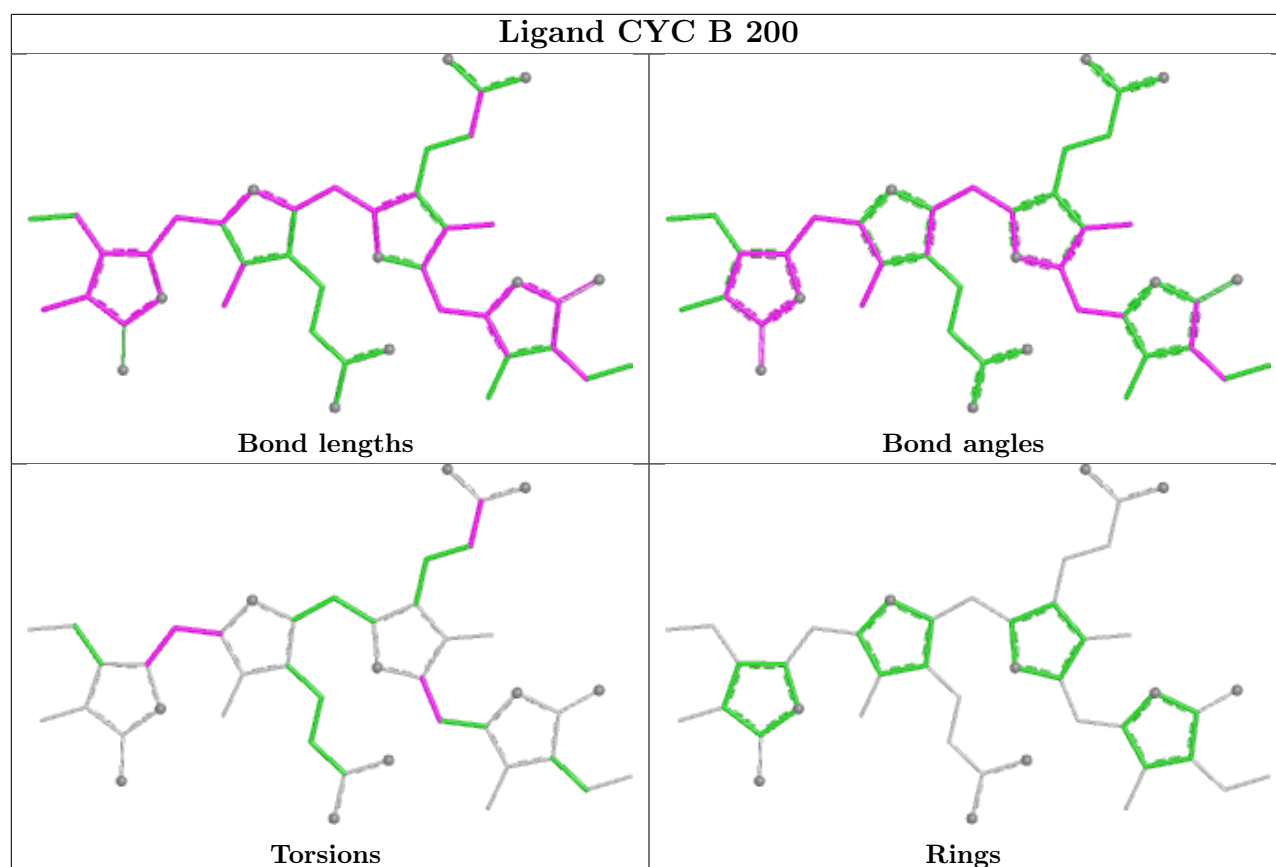




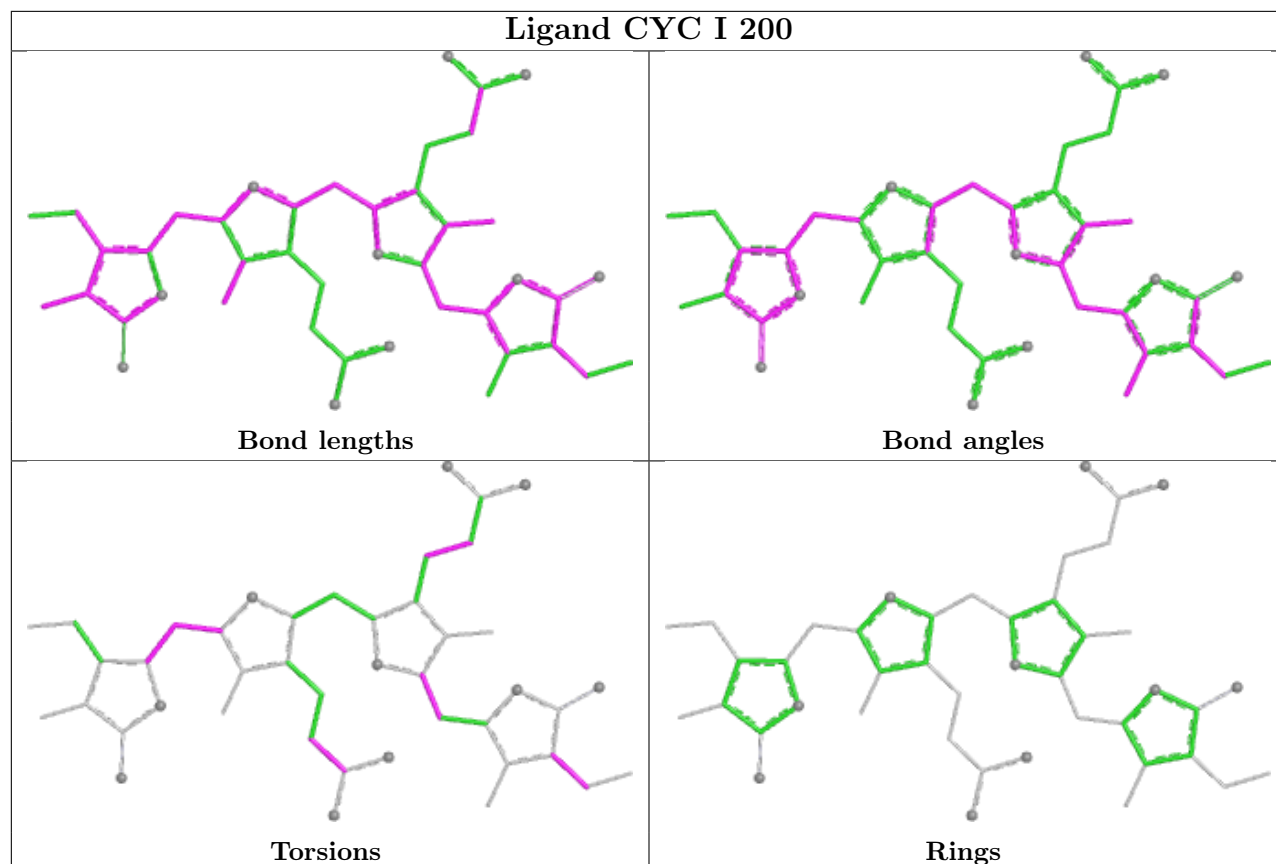




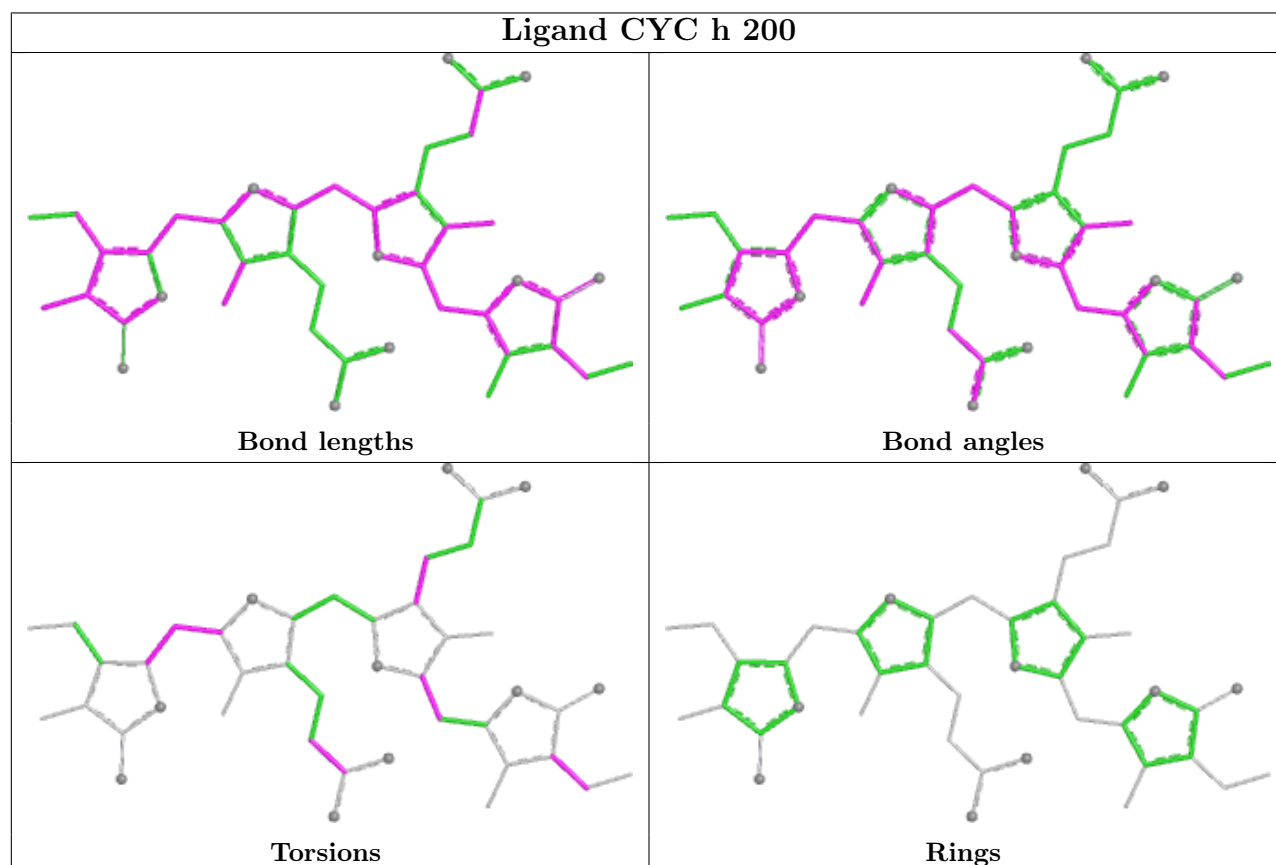


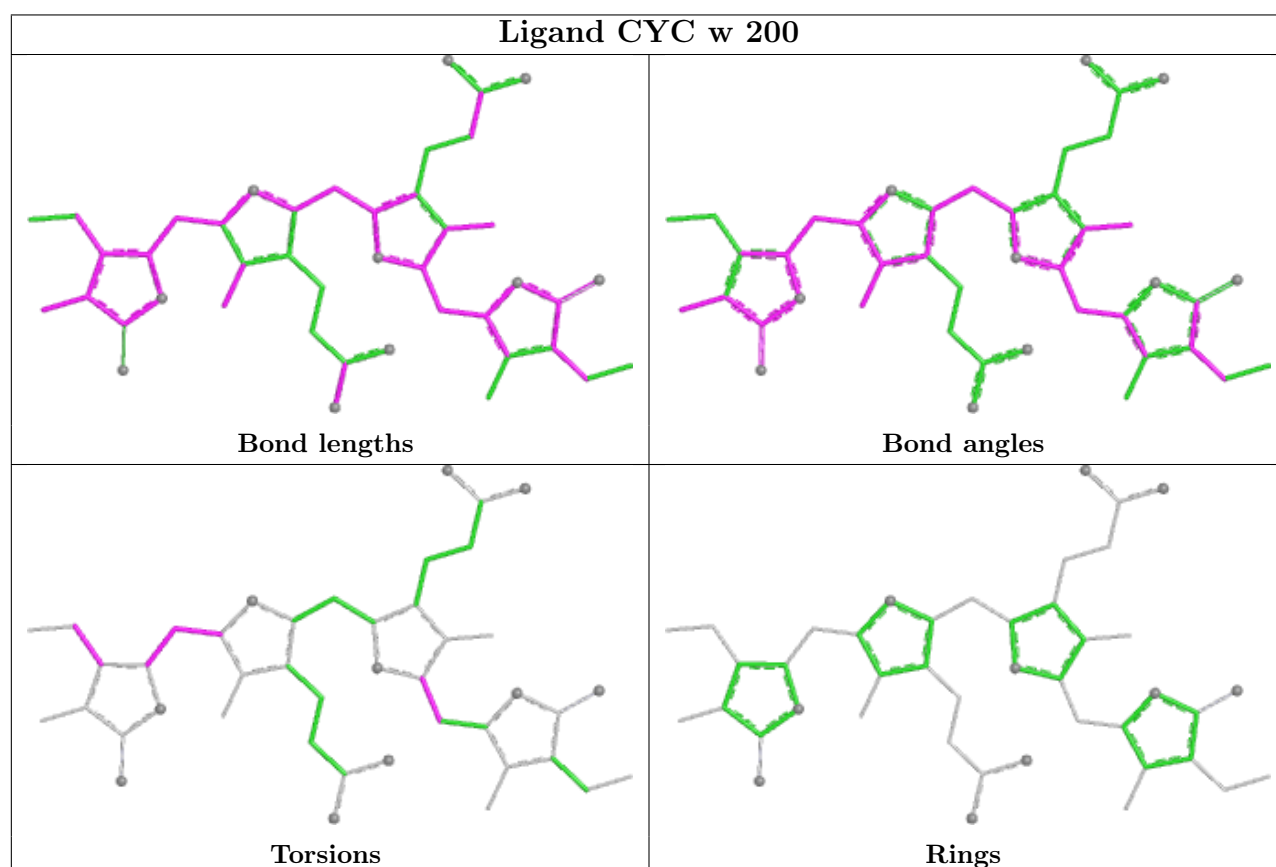
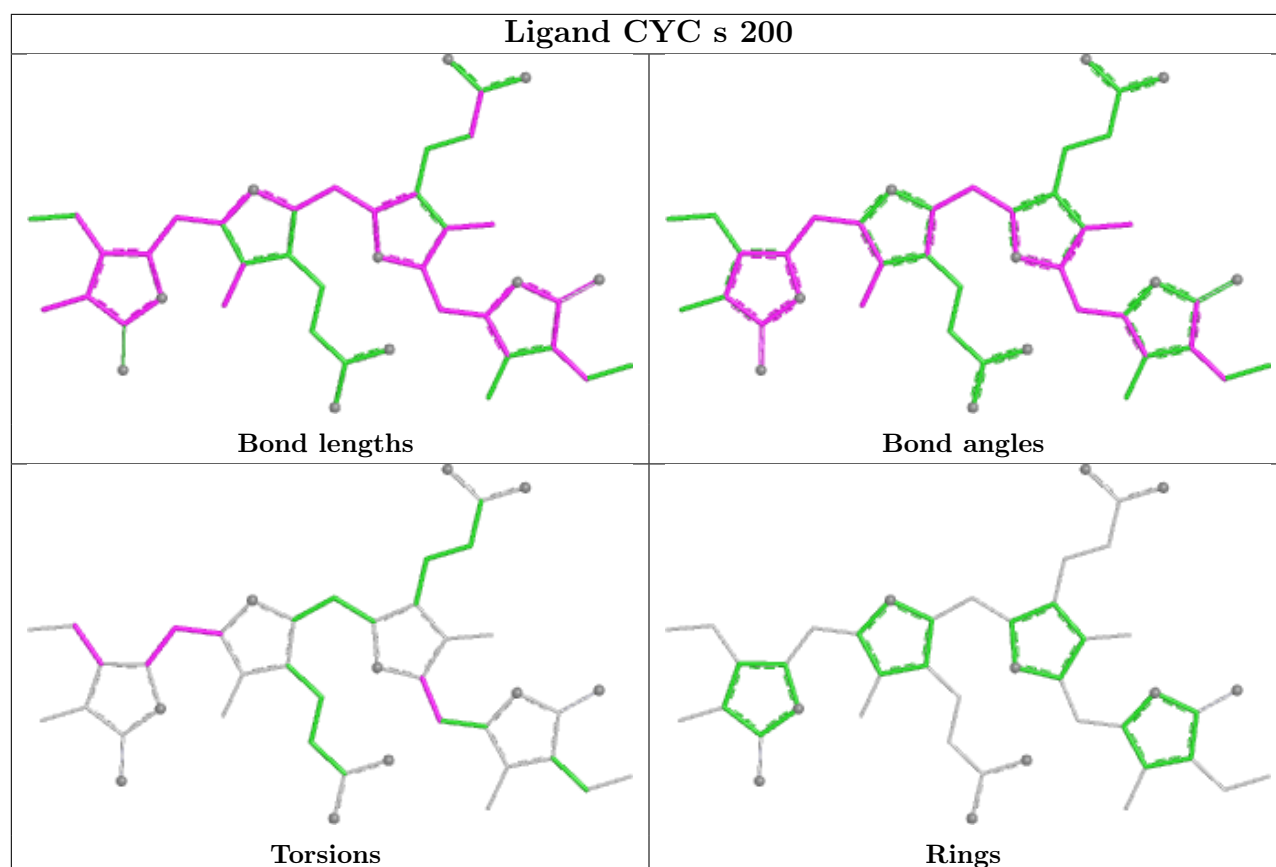


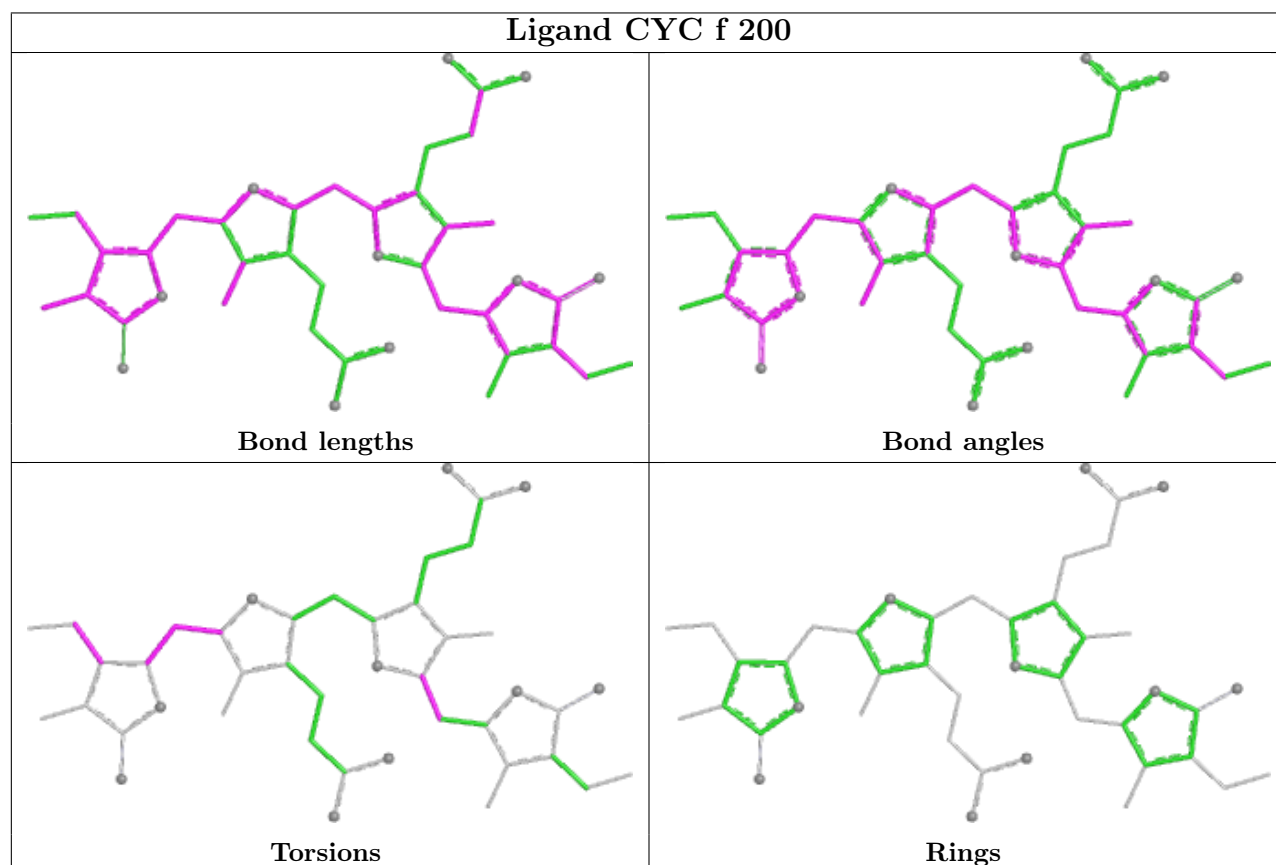
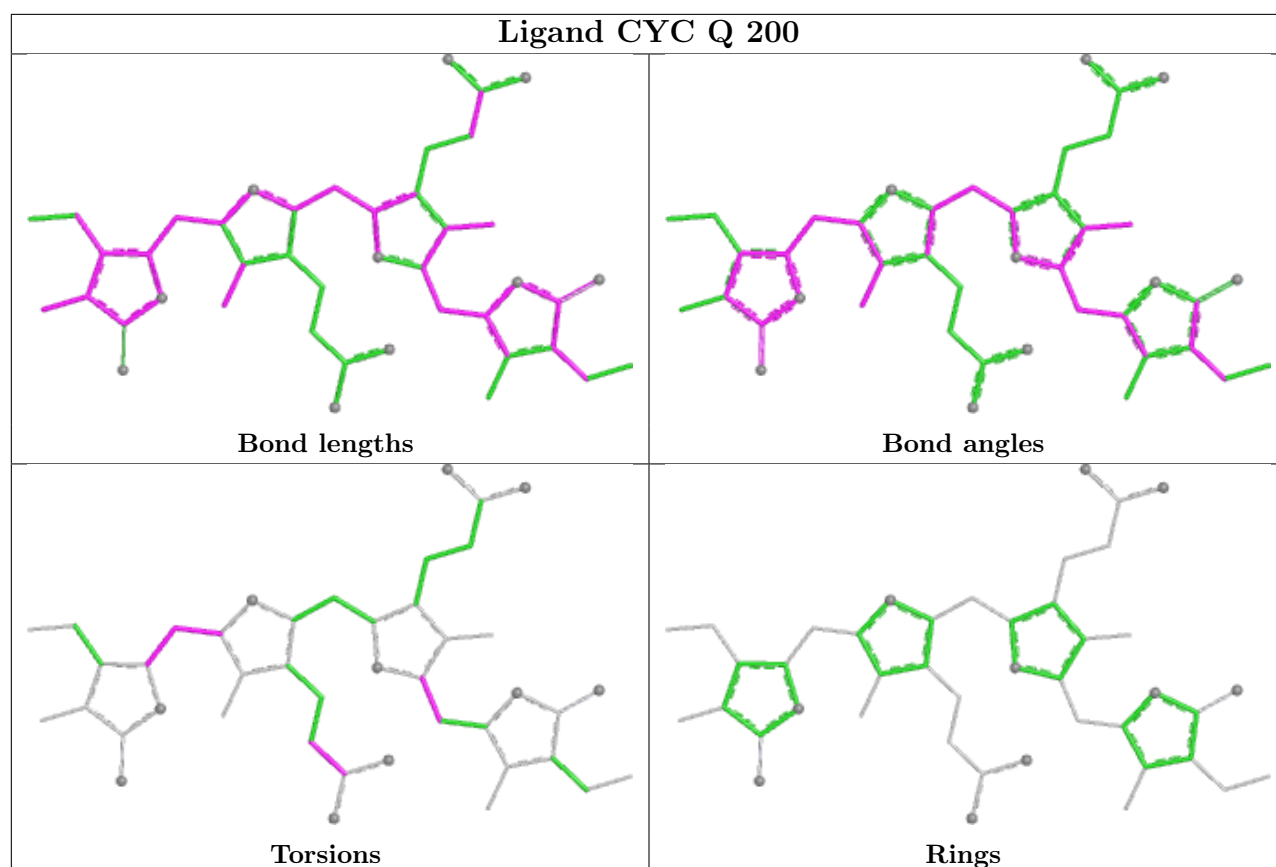
Ligand CYC I 200

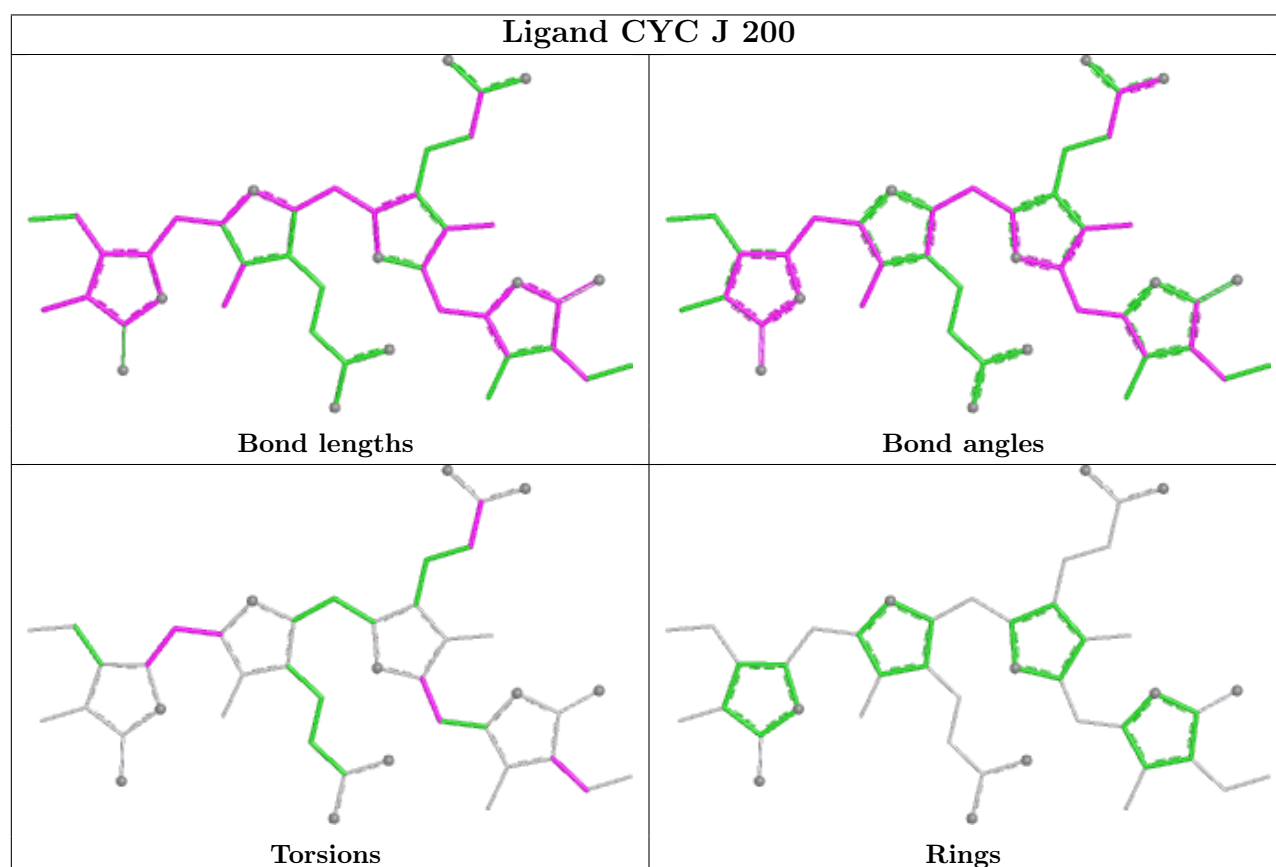
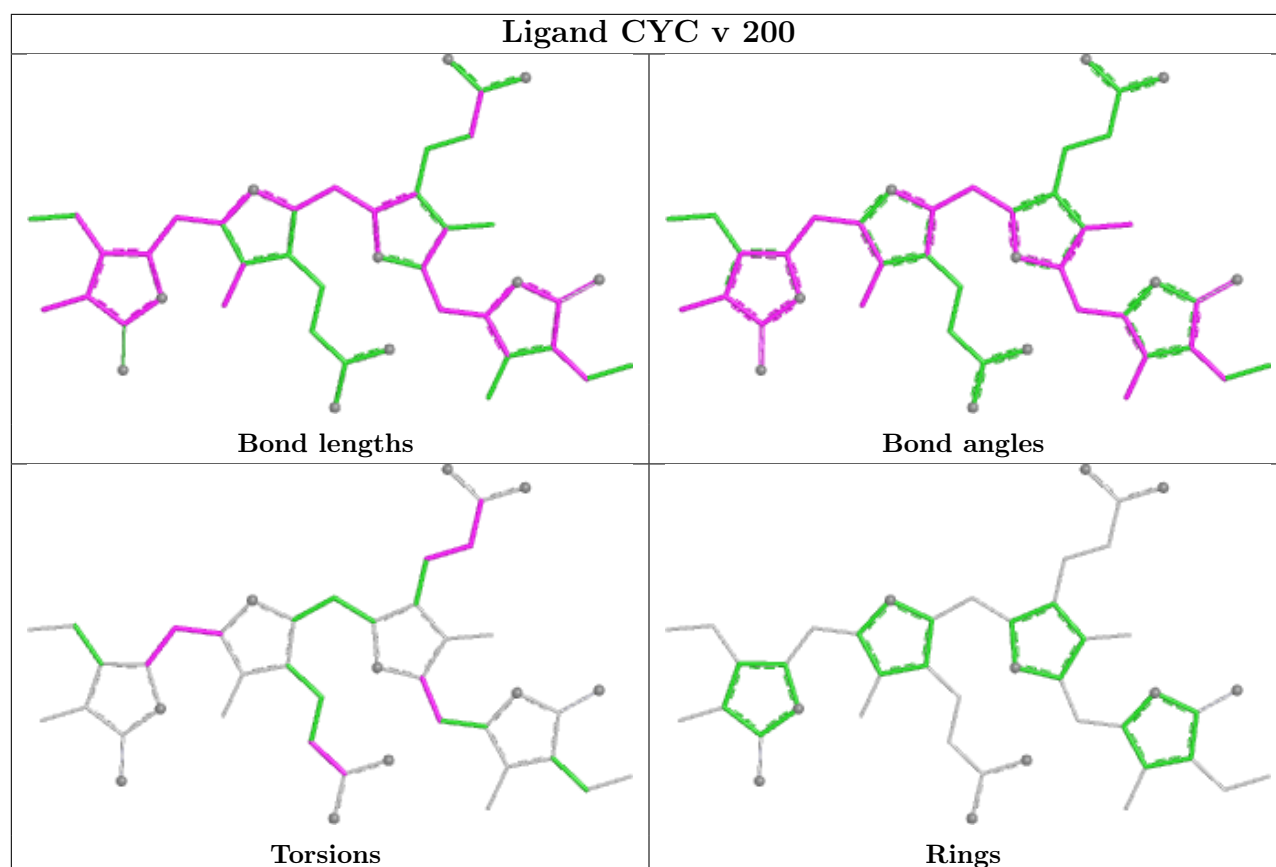


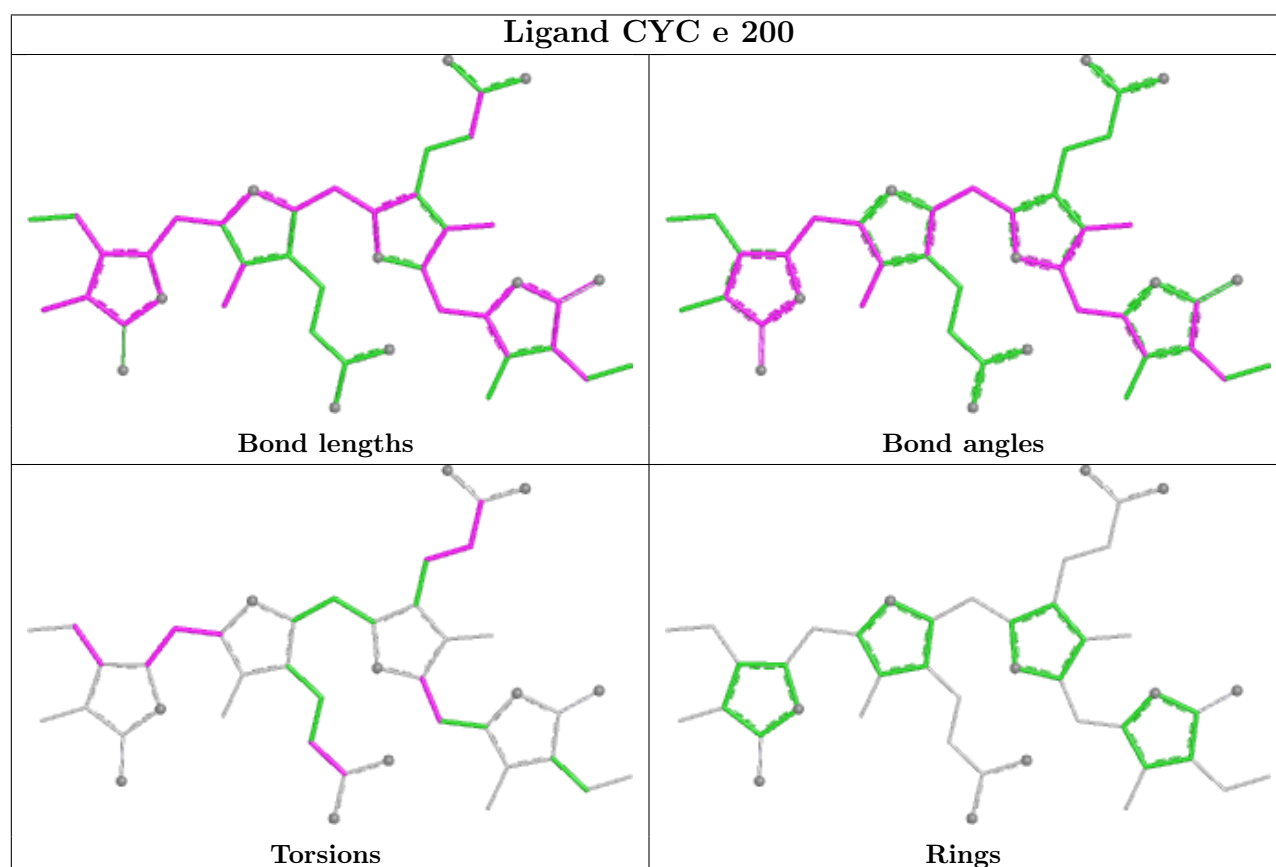
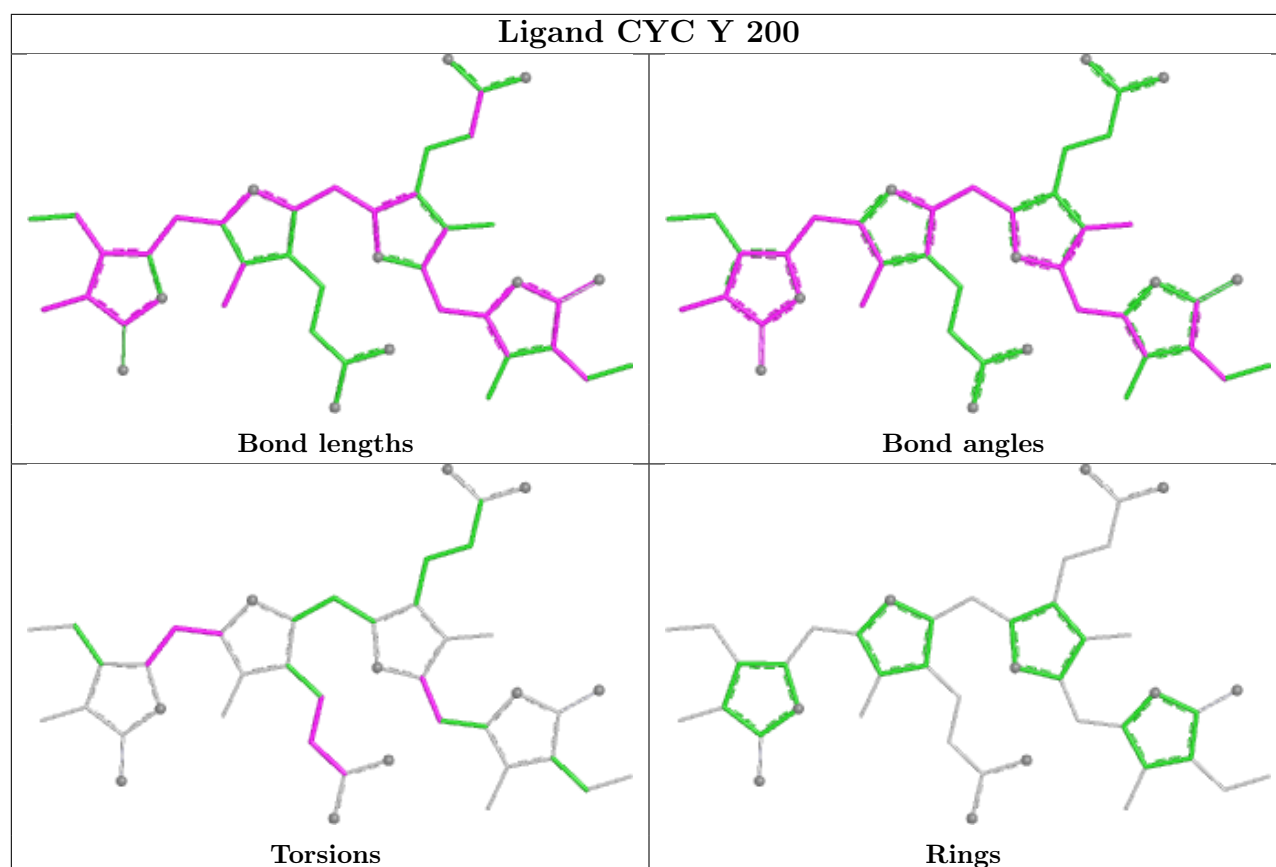
Ligand CYC h 200

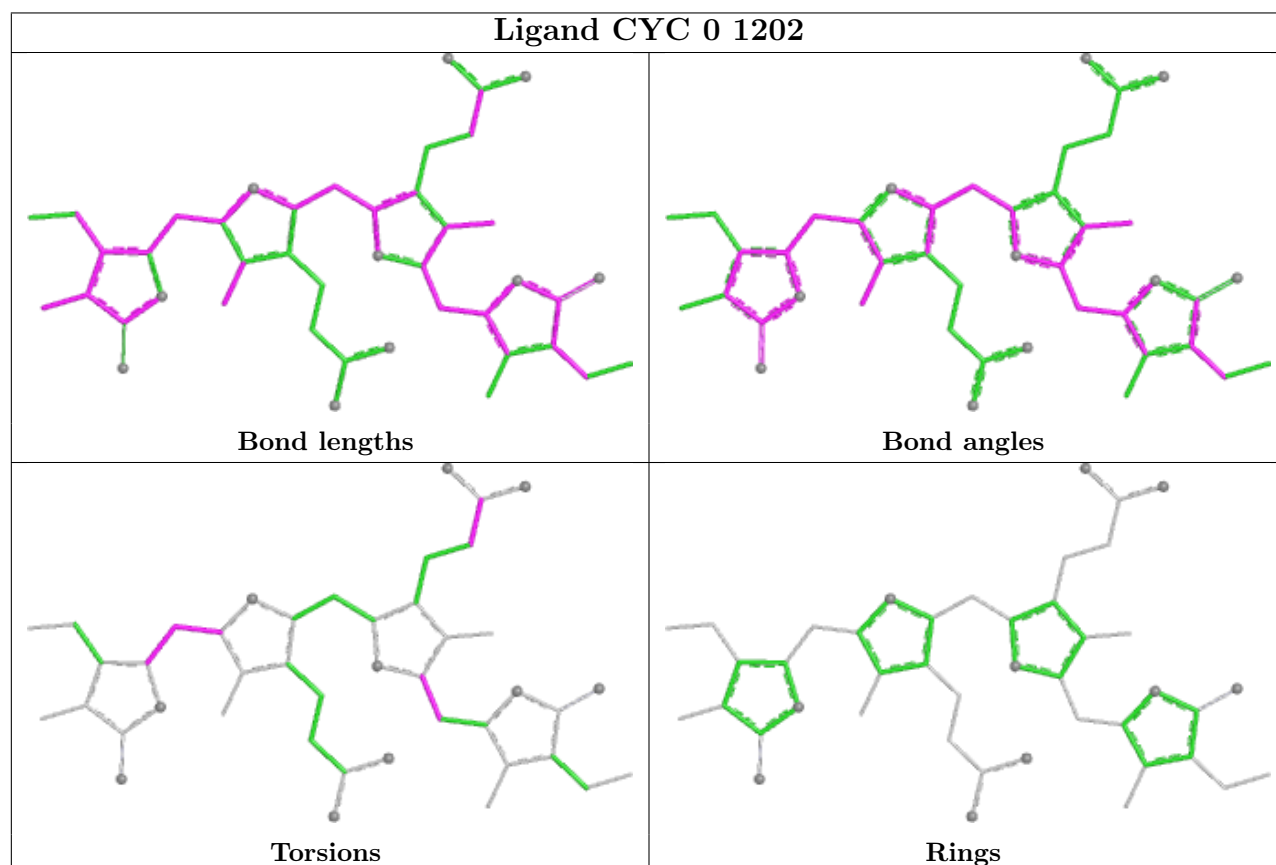
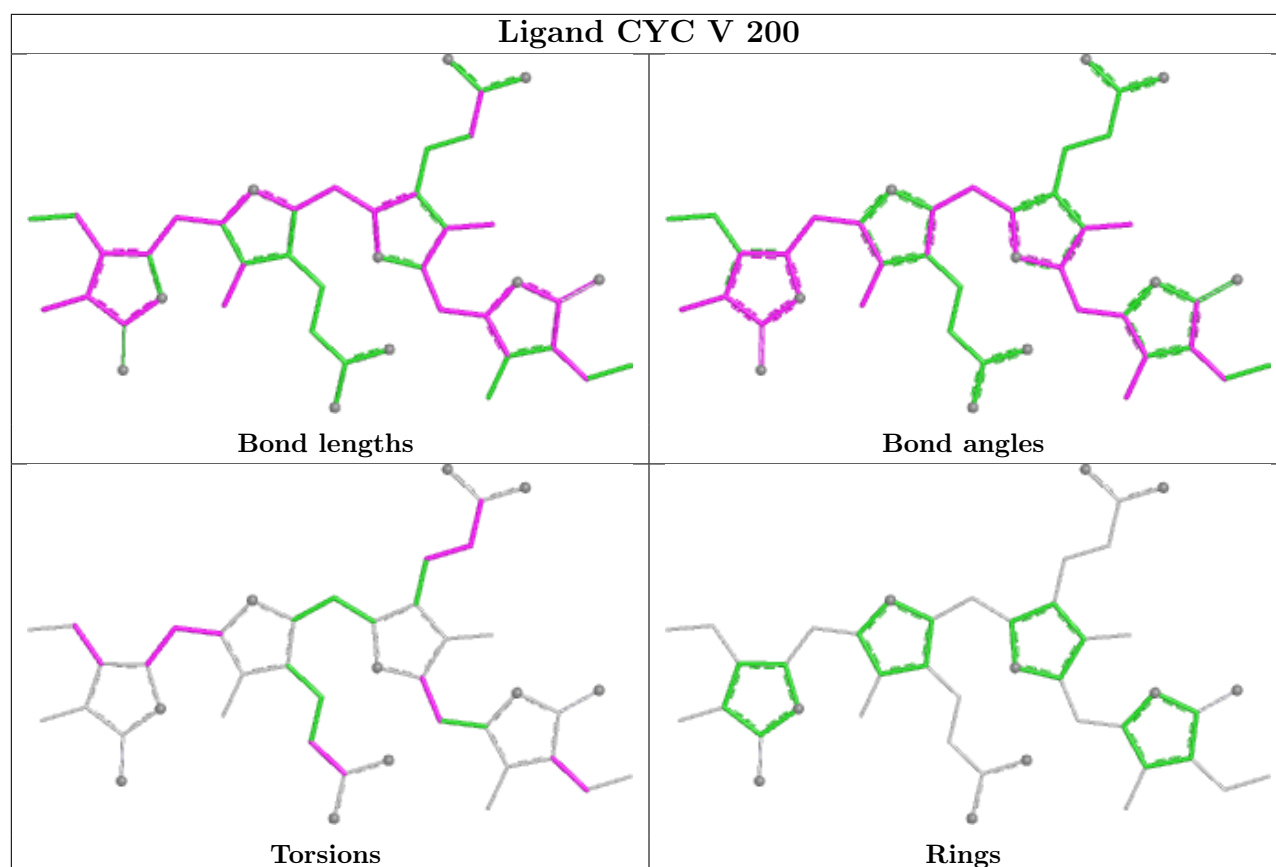


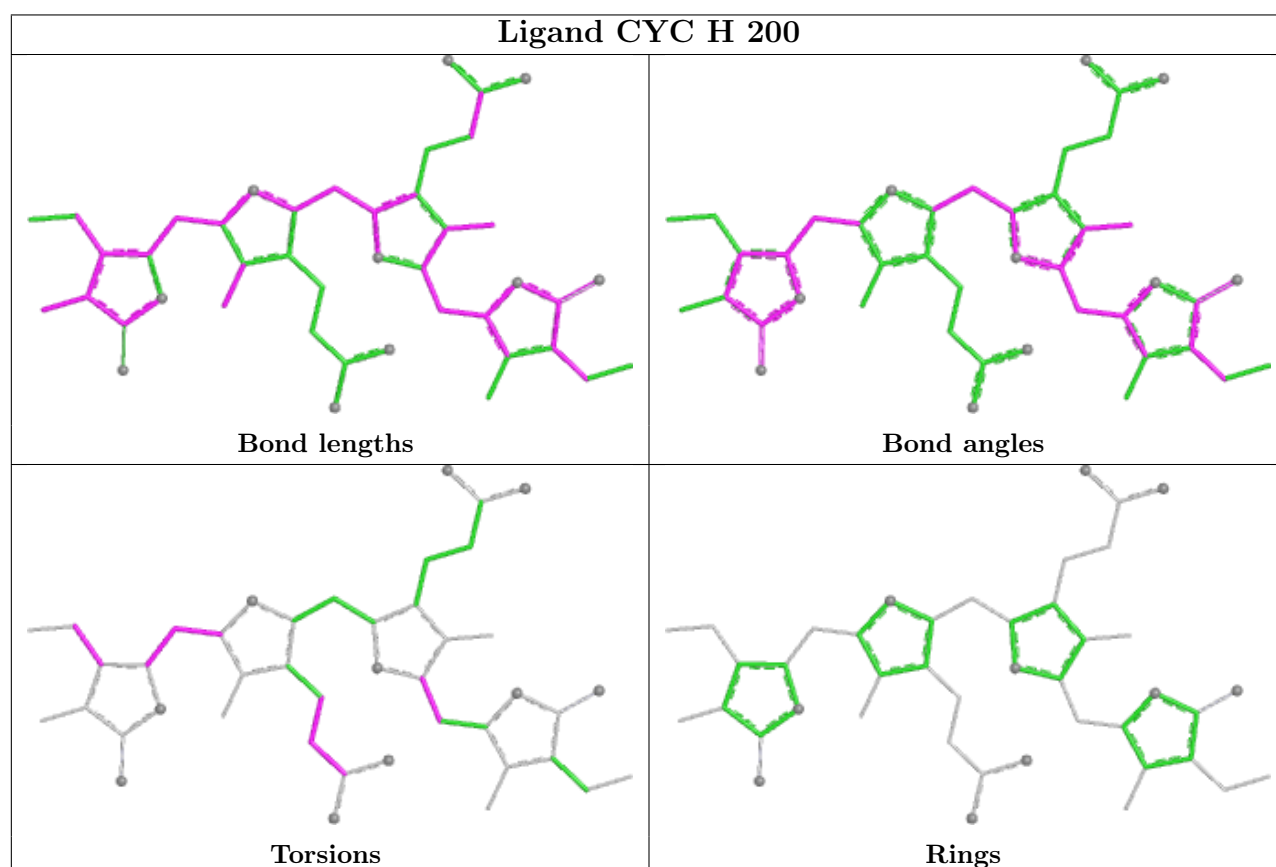
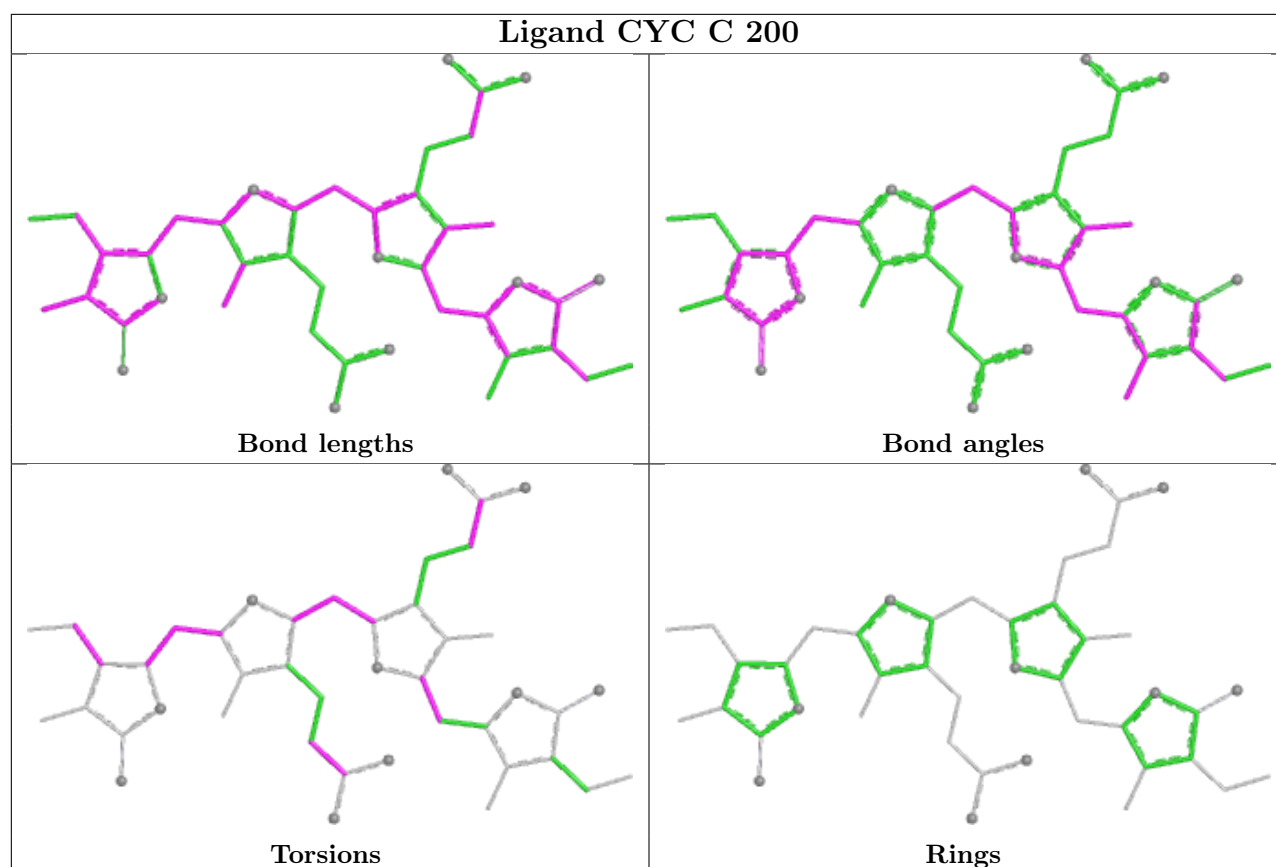


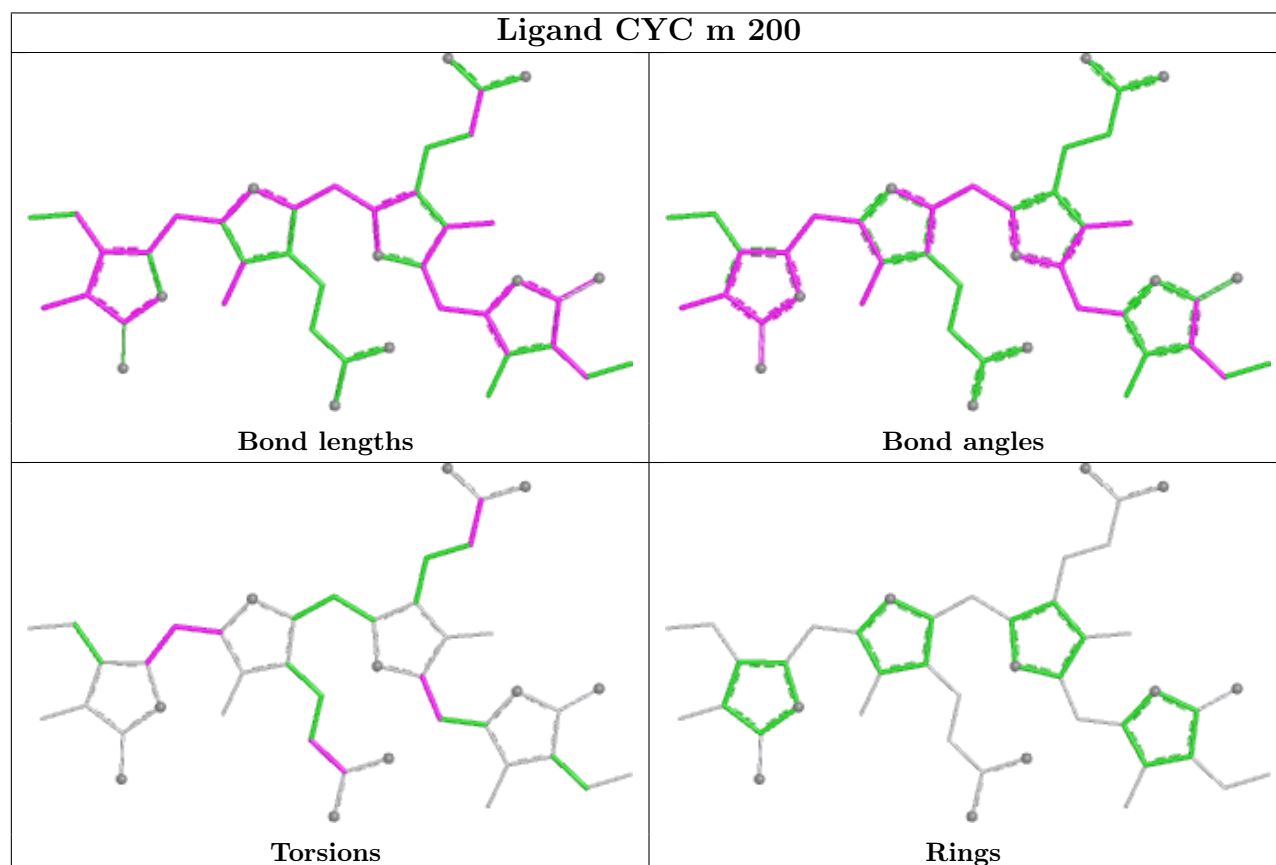
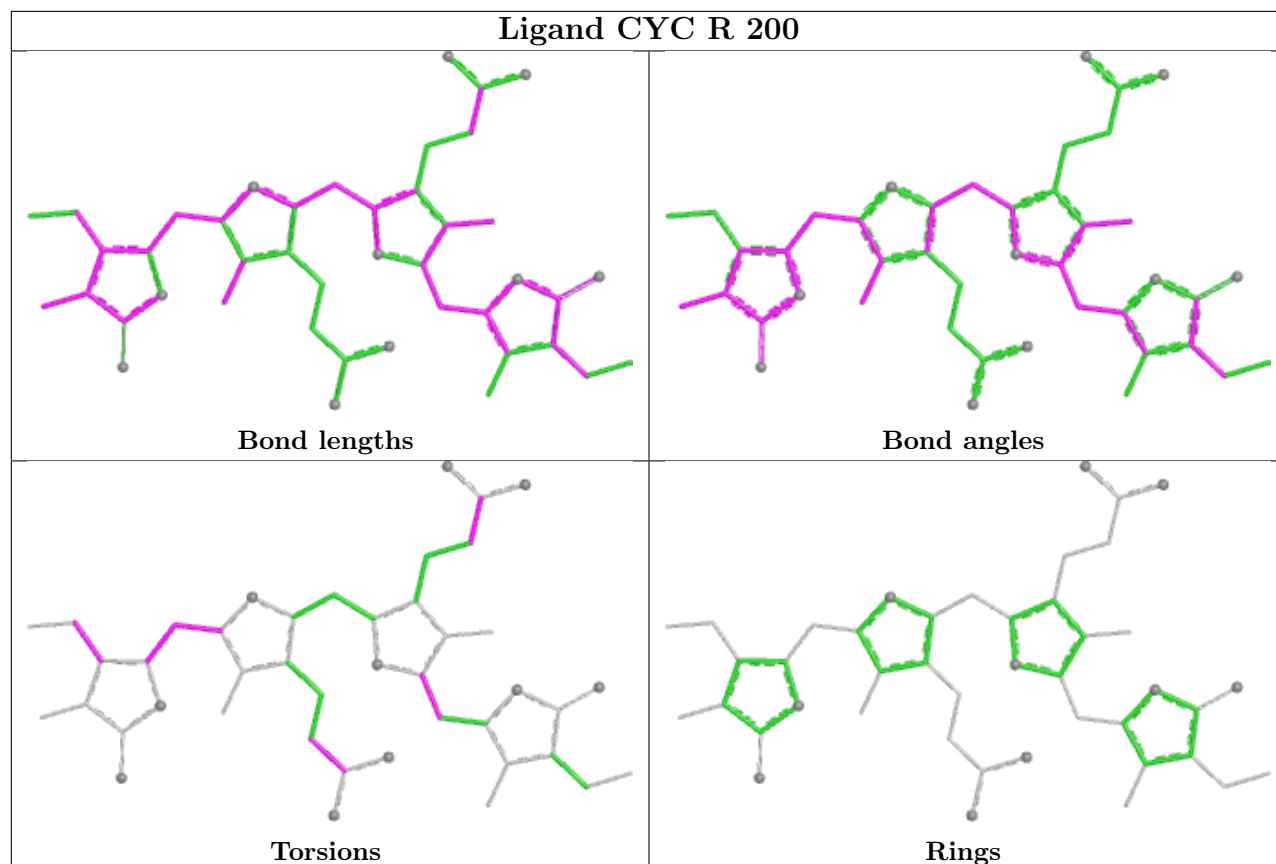


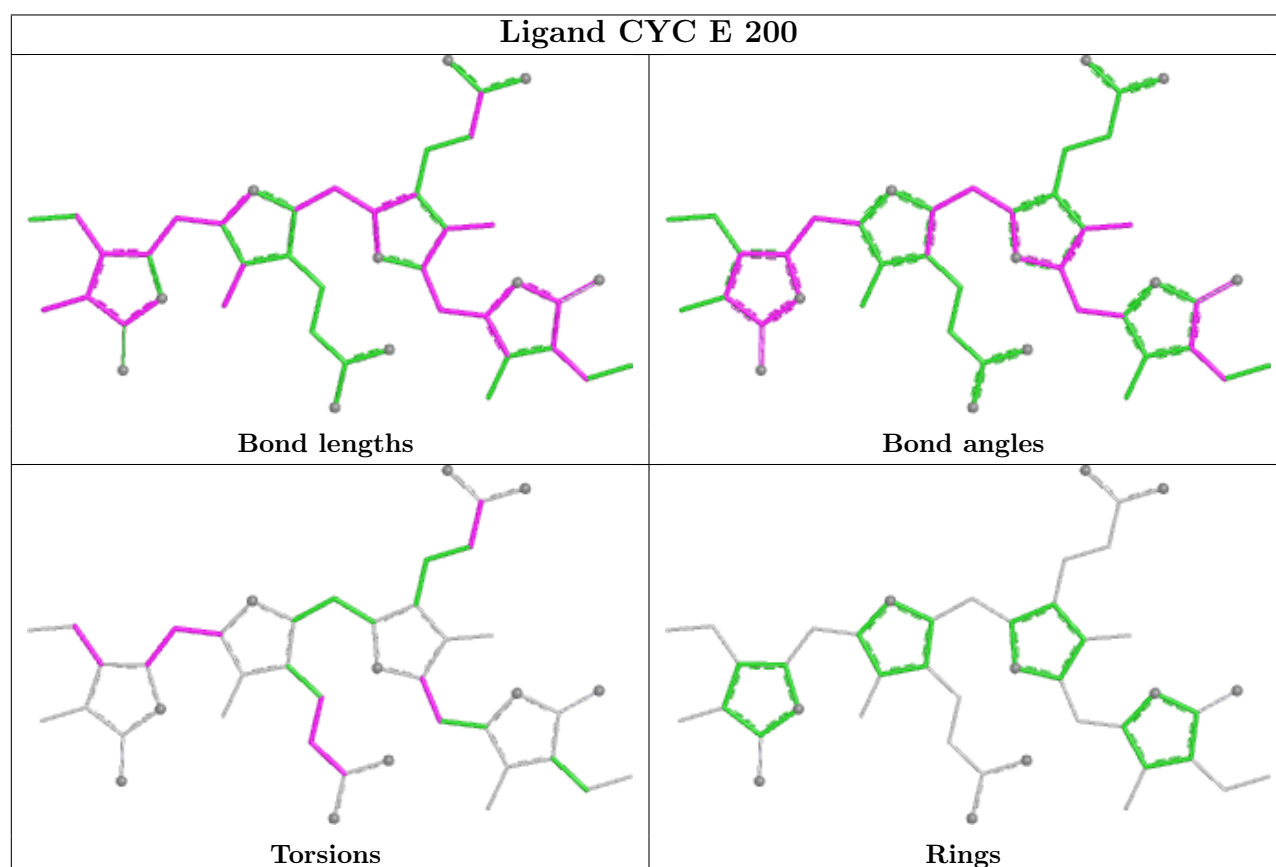
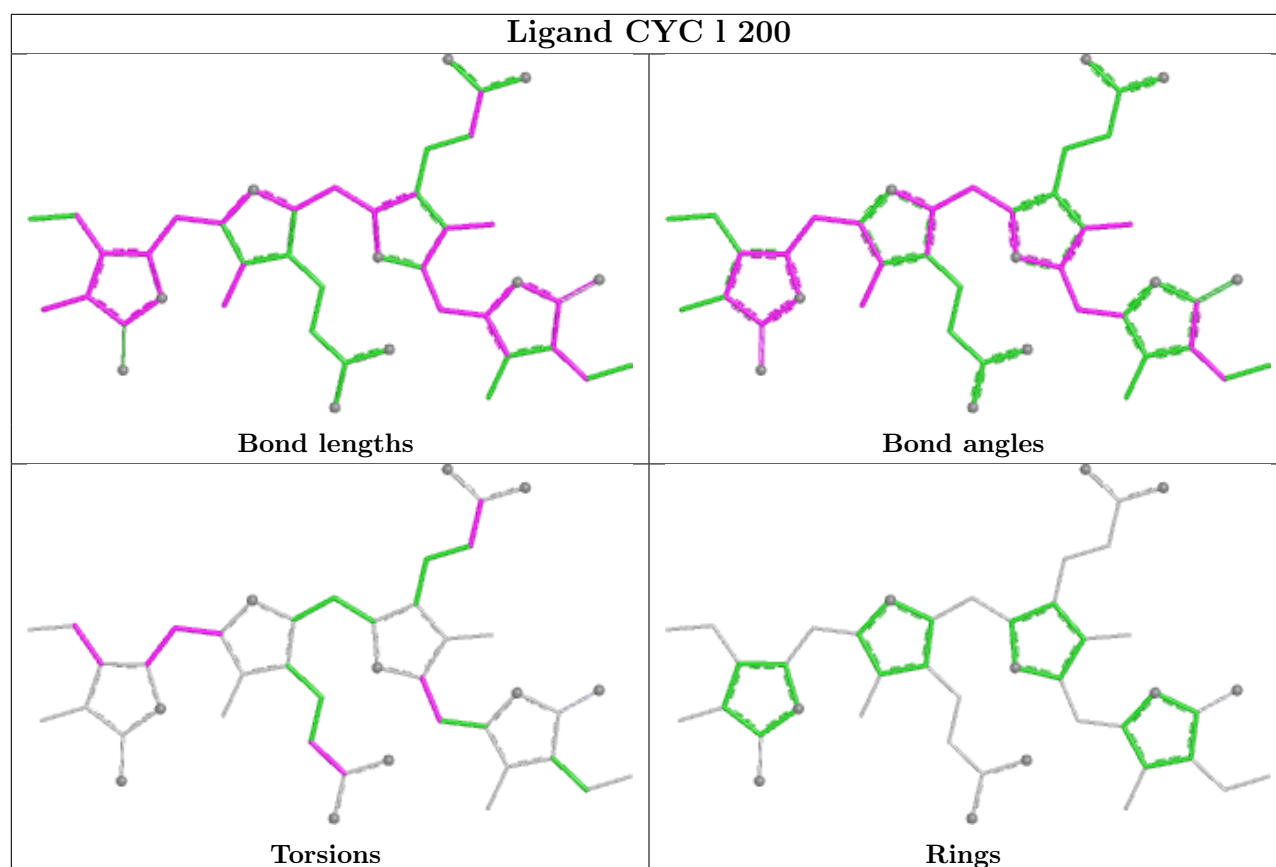


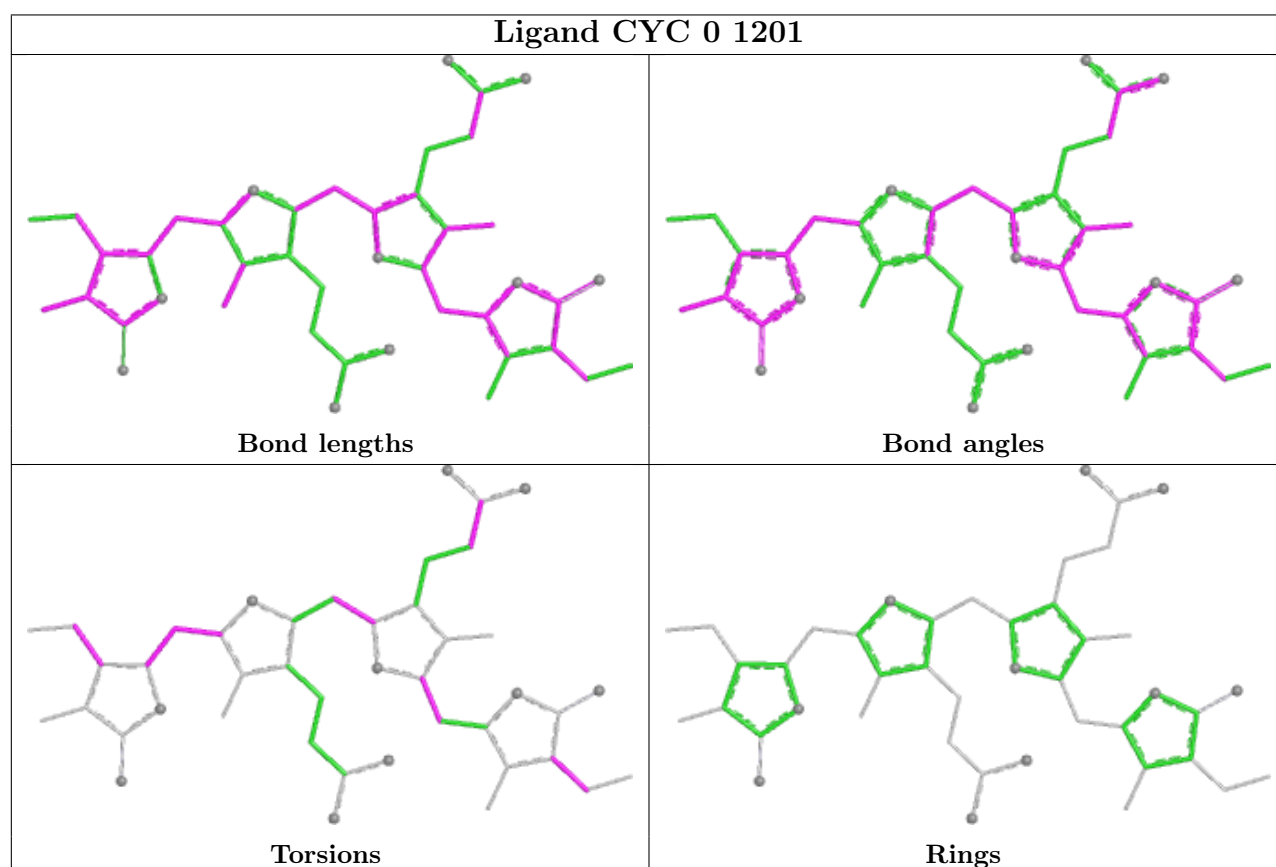
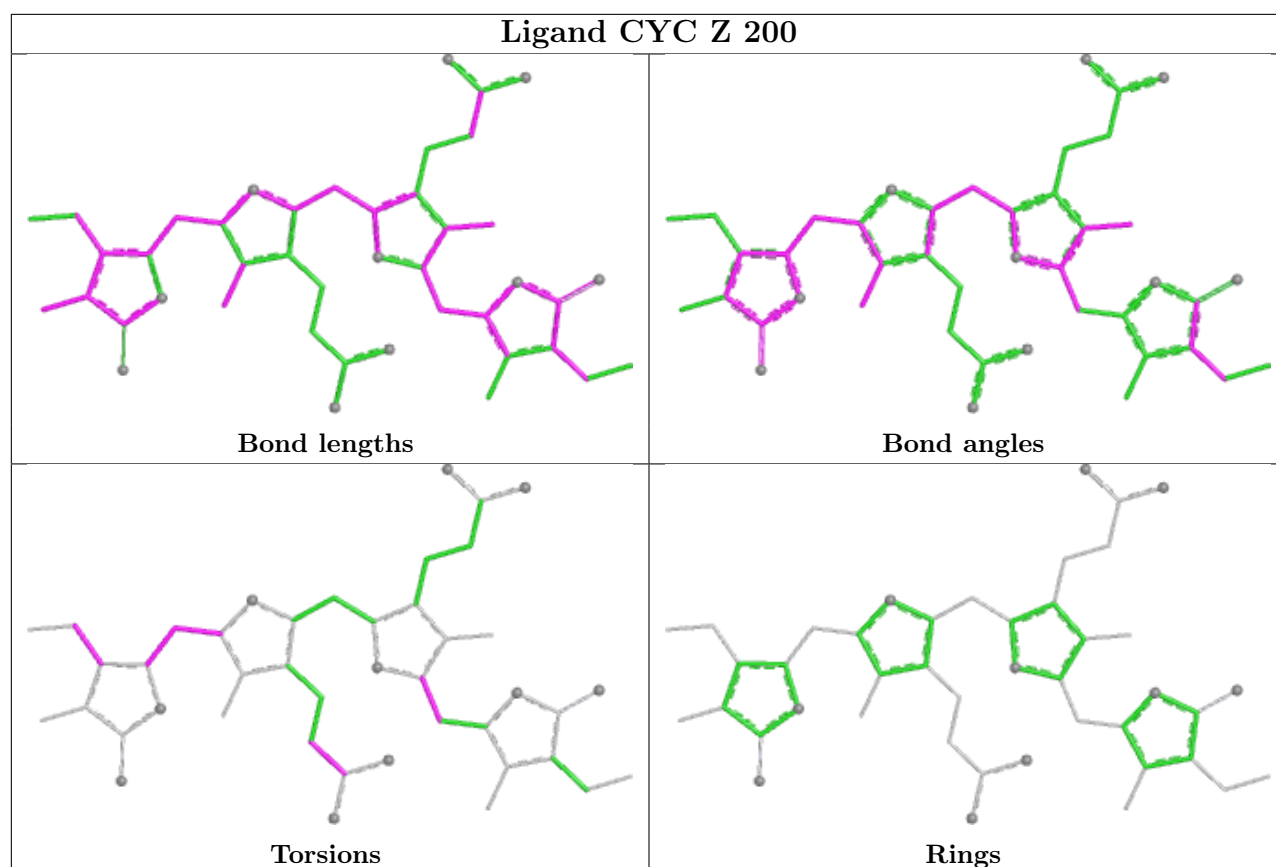


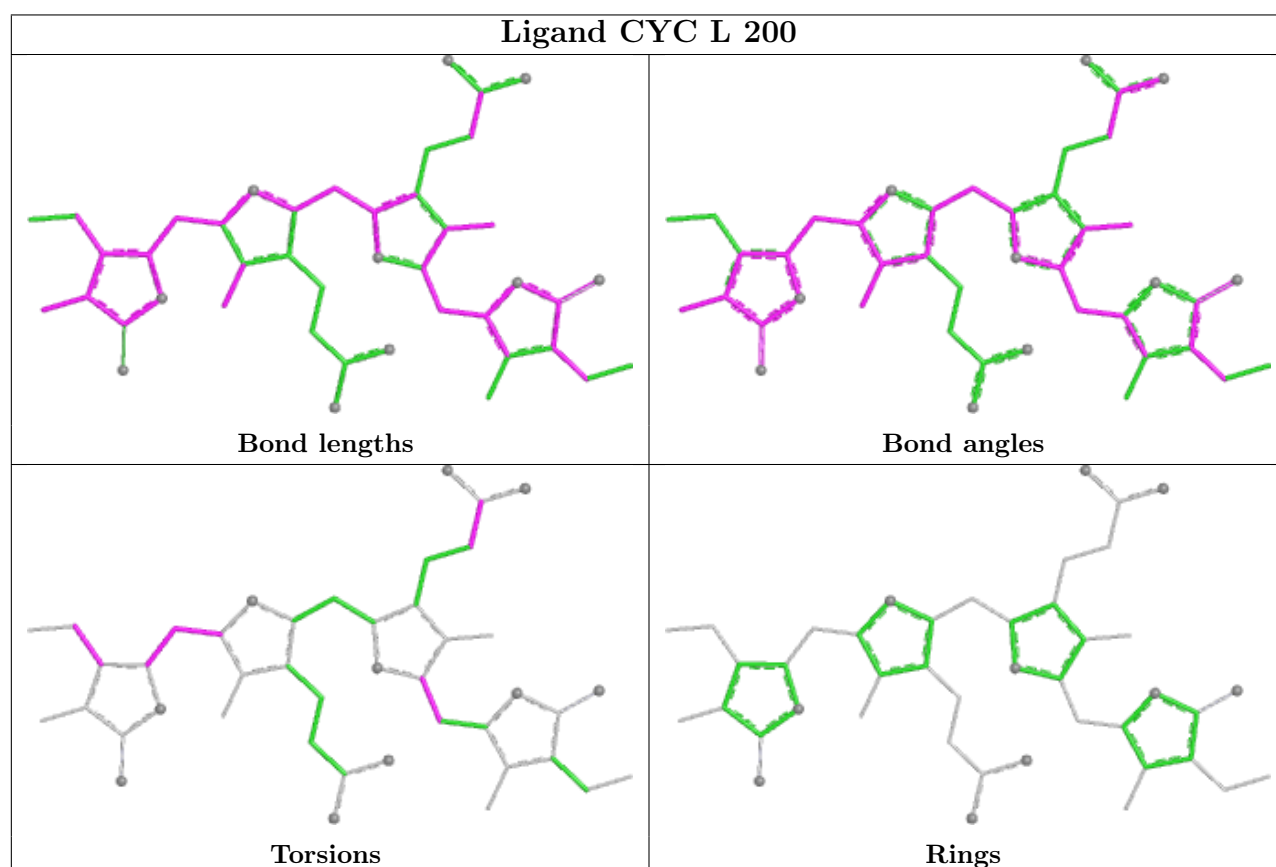
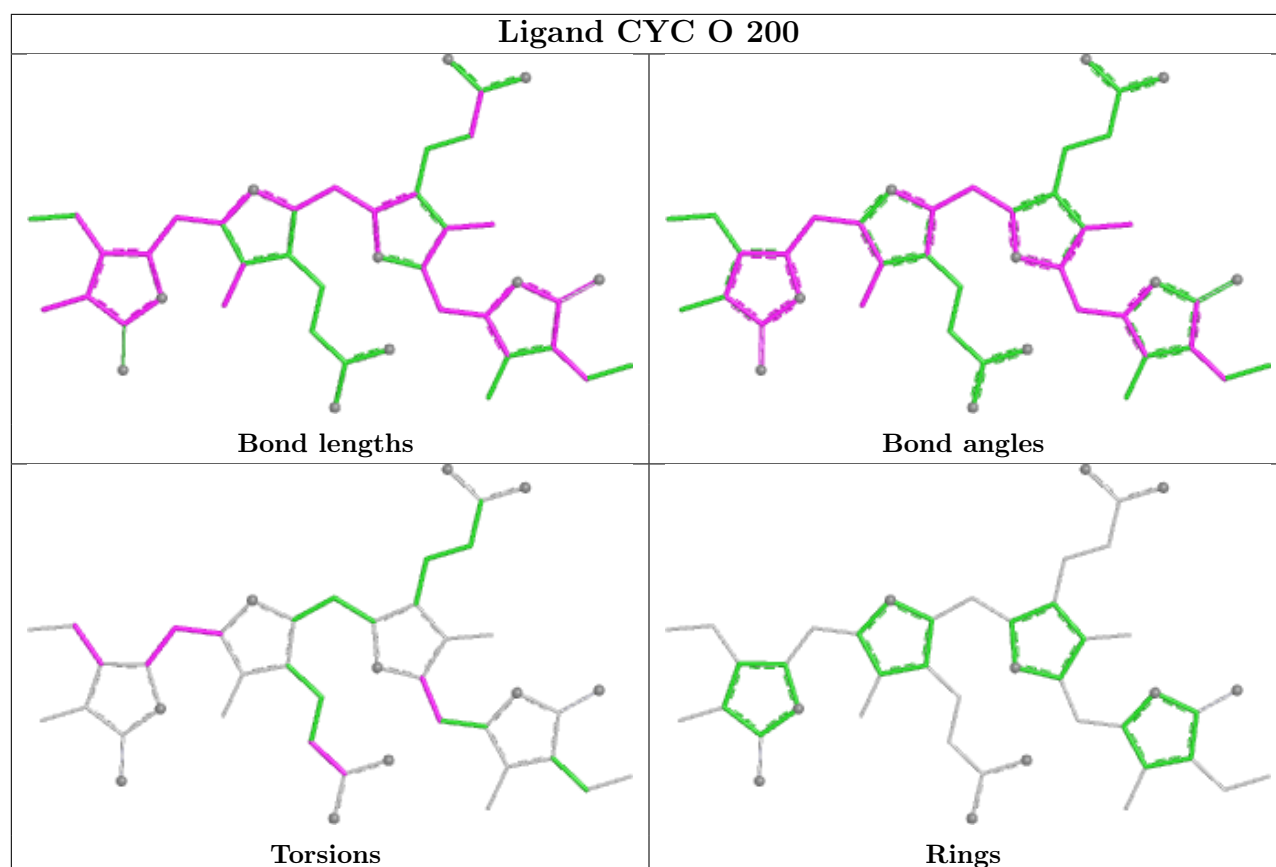


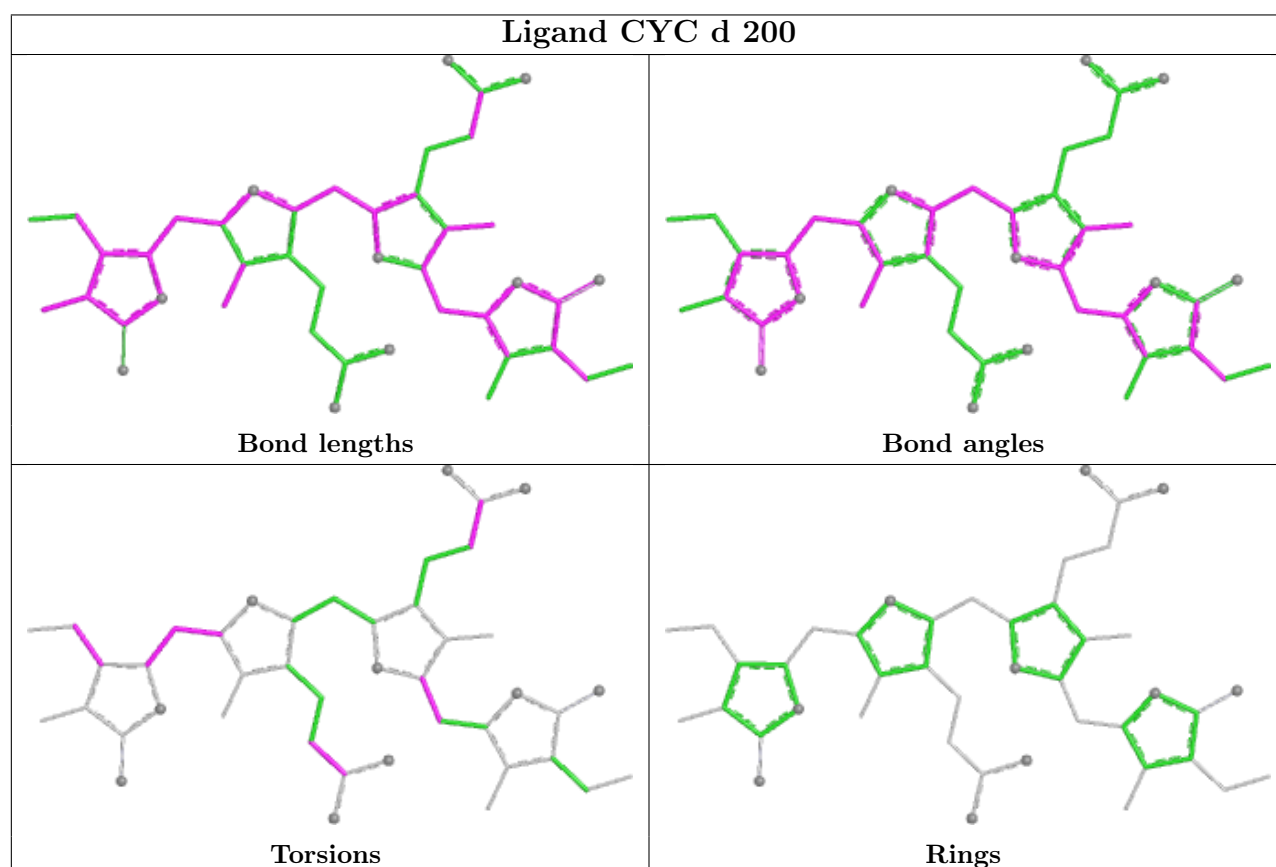
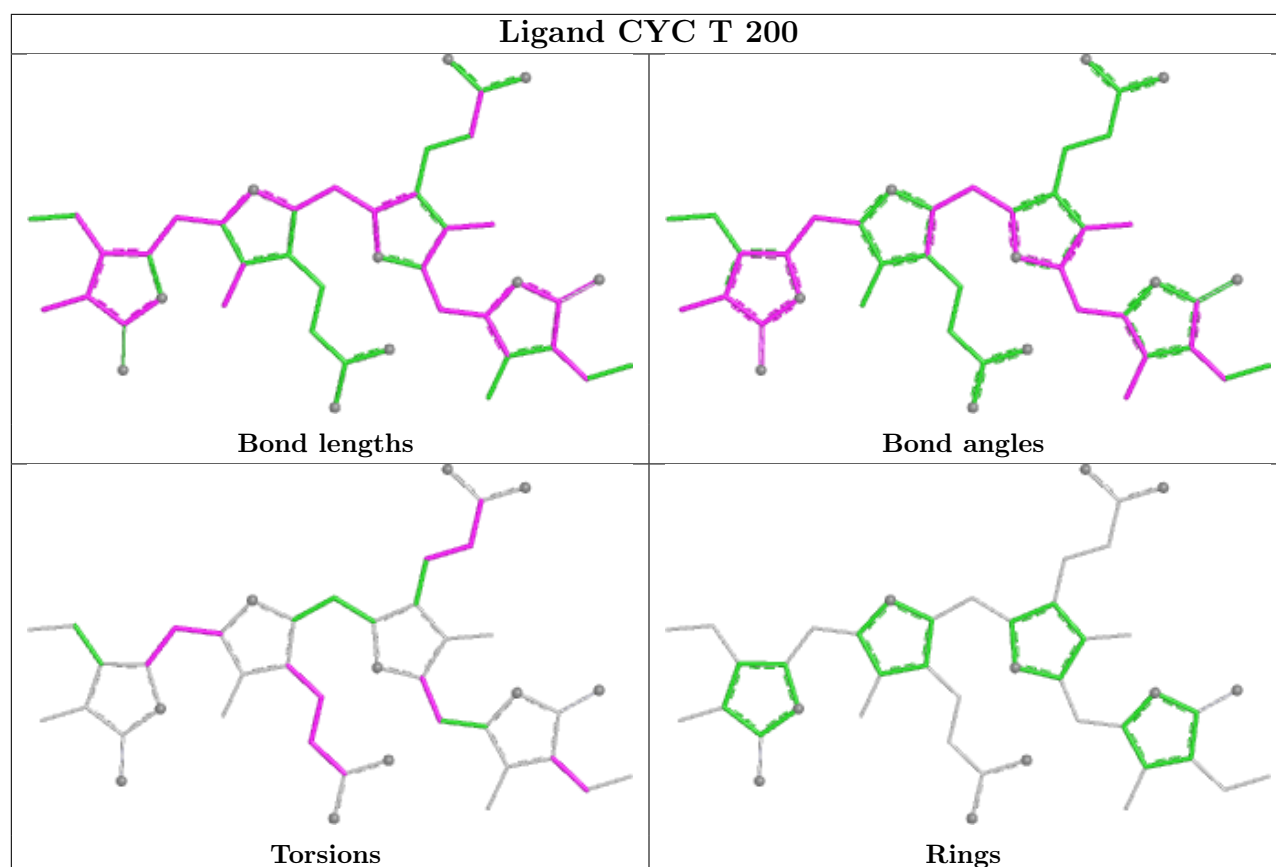












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

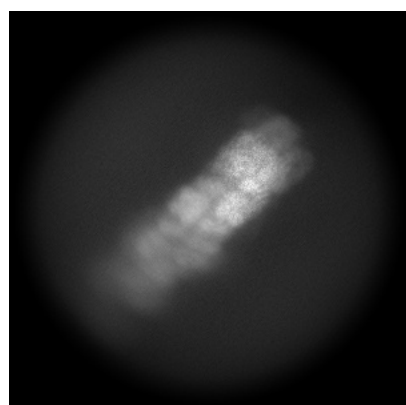
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35565. These allow visual inspection of the internal detail of the map and identification of artifacts.

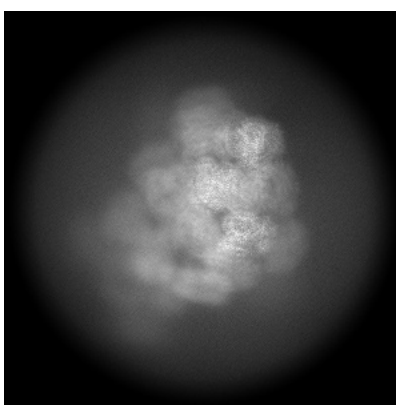
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

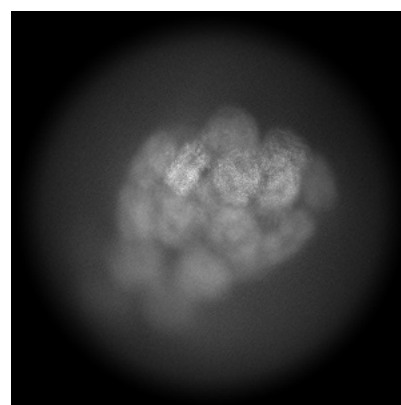
6.1.1 Primary map



X



Y

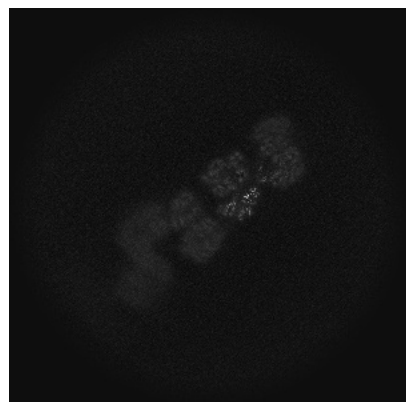


Z

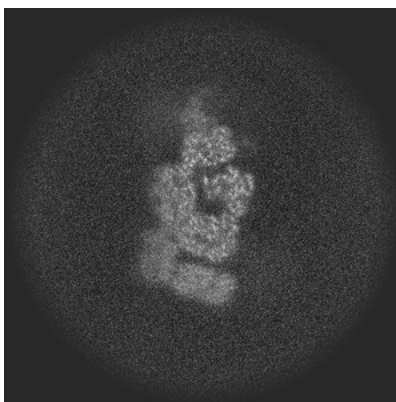
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

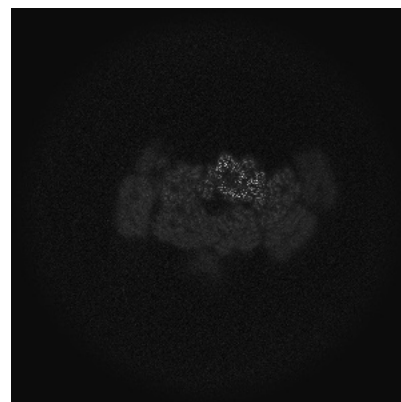
6.2.1 Primary map



X Index: 340



Y Index: 340

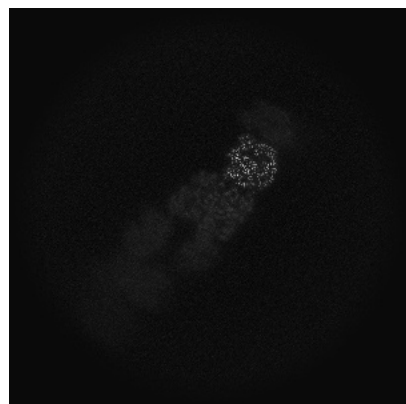


Z Index: 340

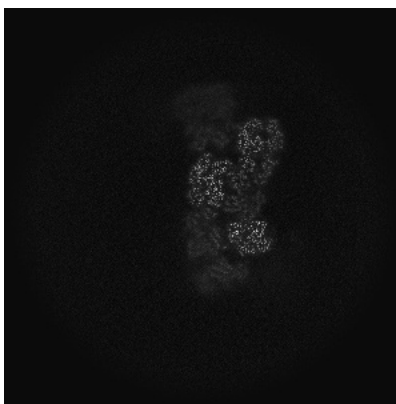
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

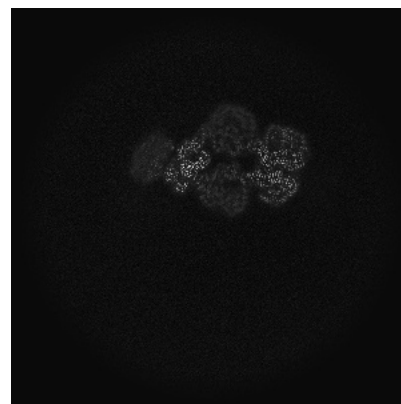
6.3.1 Primary map



X Index: 300



Y Index: 388

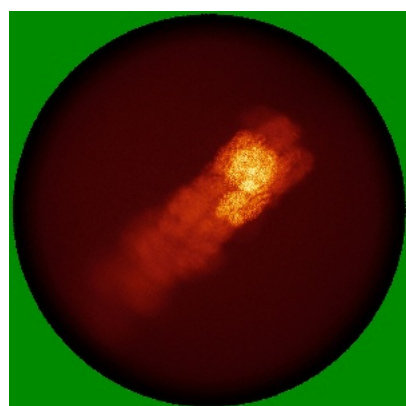


Z Index: 411

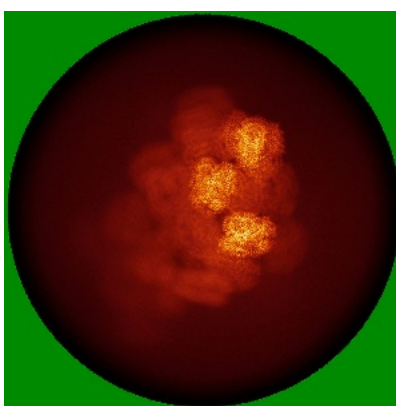
The images above show the largest variance slices of the map in three orthogonal directions.

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

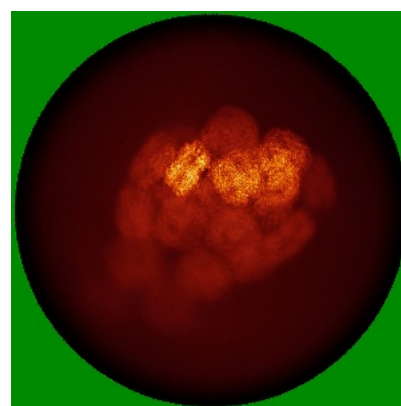
6.4.1 Primary map



X



Y

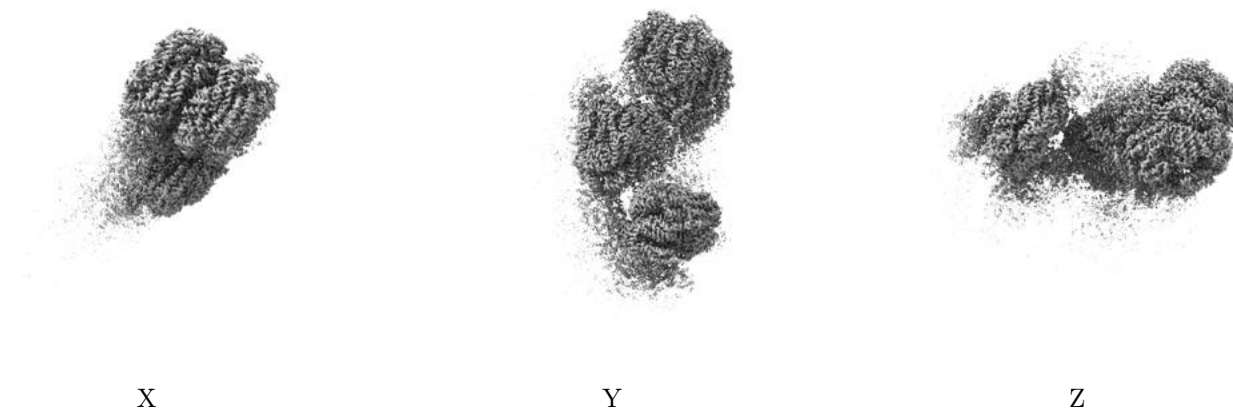


Z

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 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

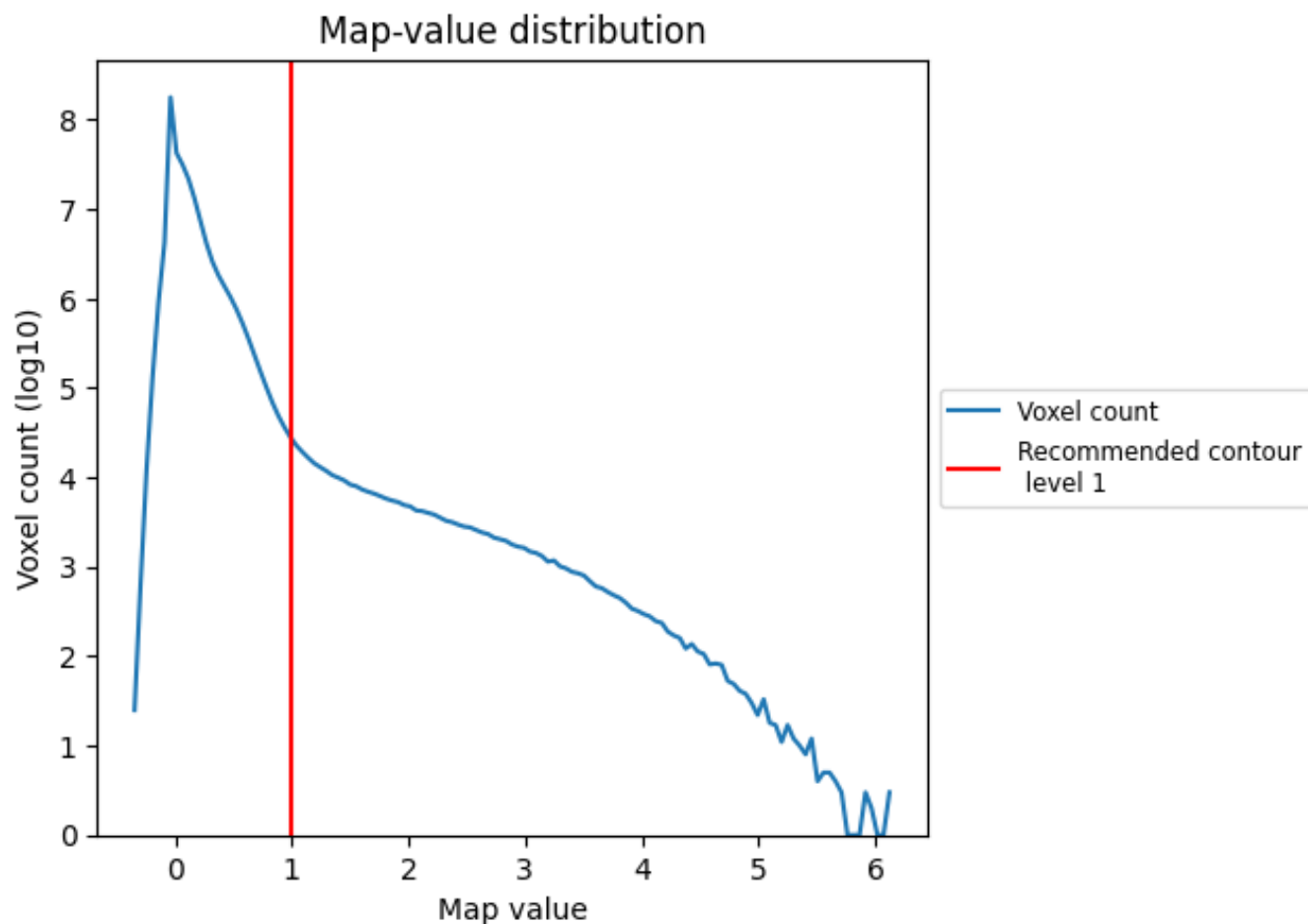
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

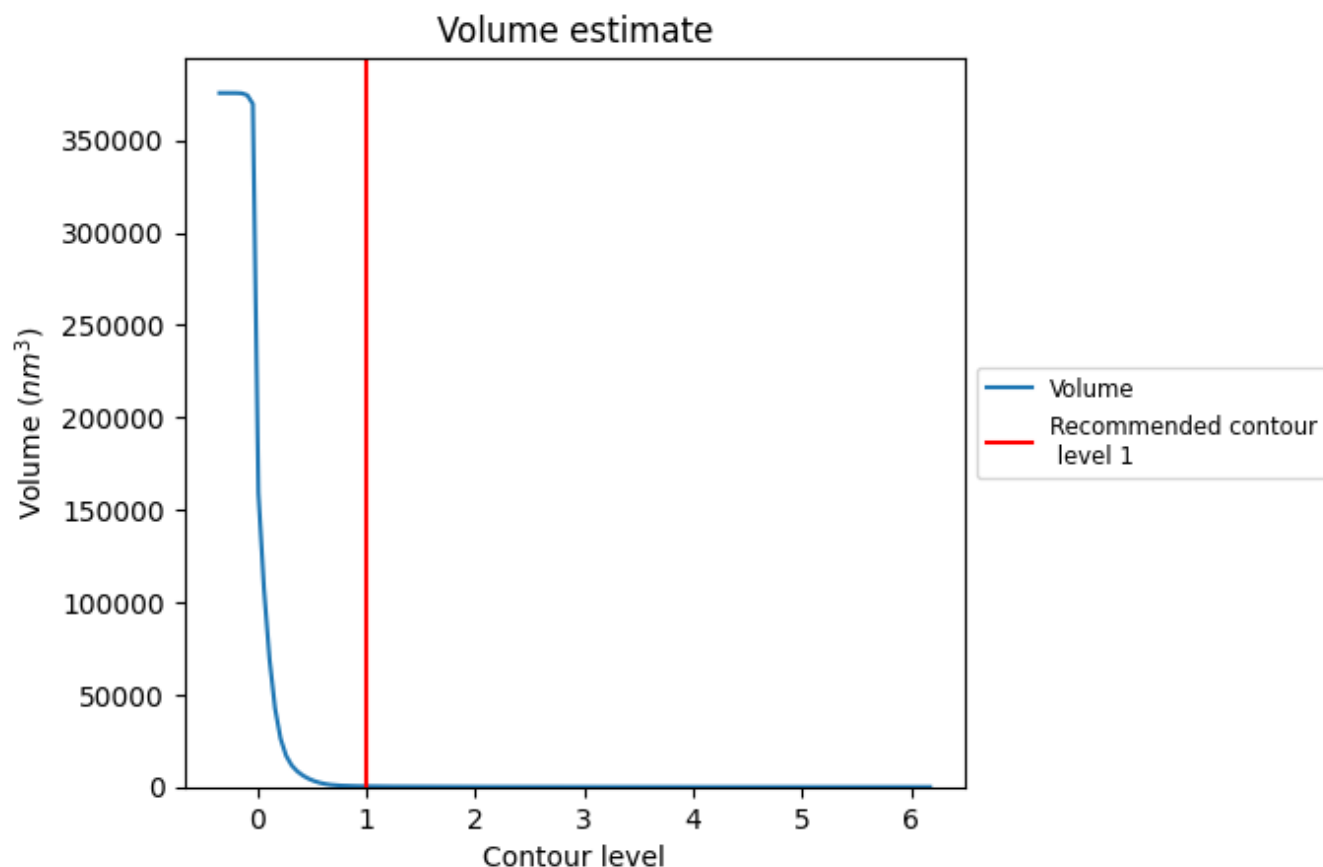
This section contains the results of statistical analysis of the map.

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.

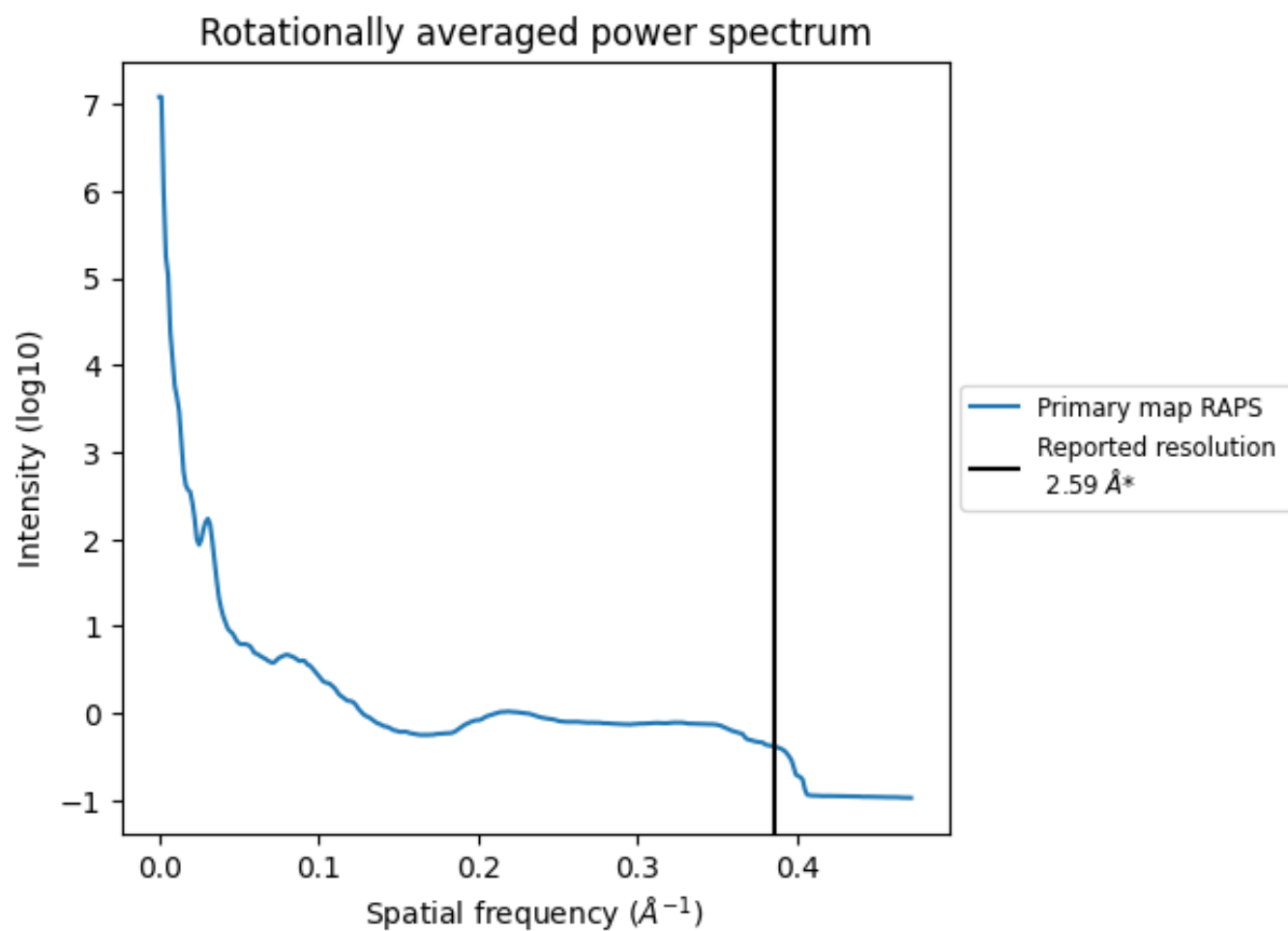
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 347 nm^3 ; this corresponds to an approximate mass of 314 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.386 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

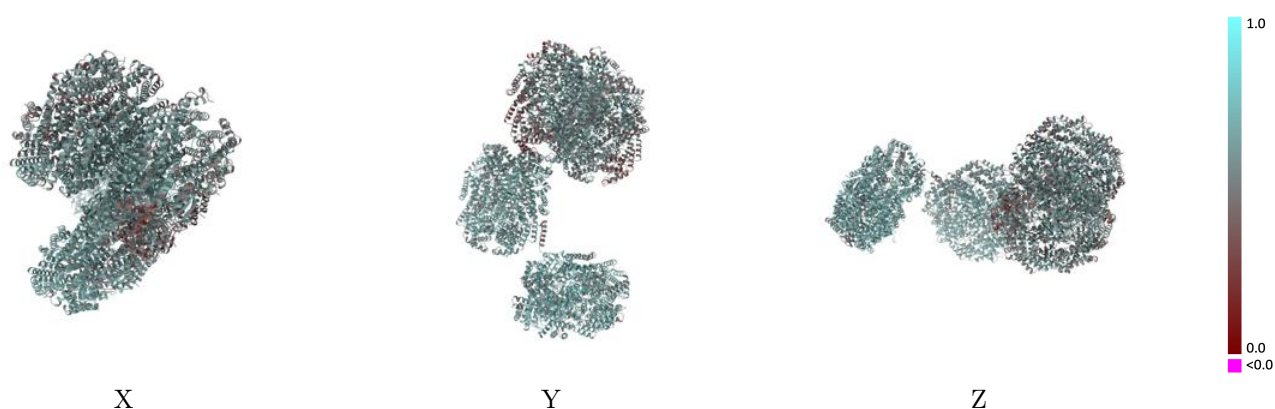
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-35565 and PDB model 8IMI. 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](#)

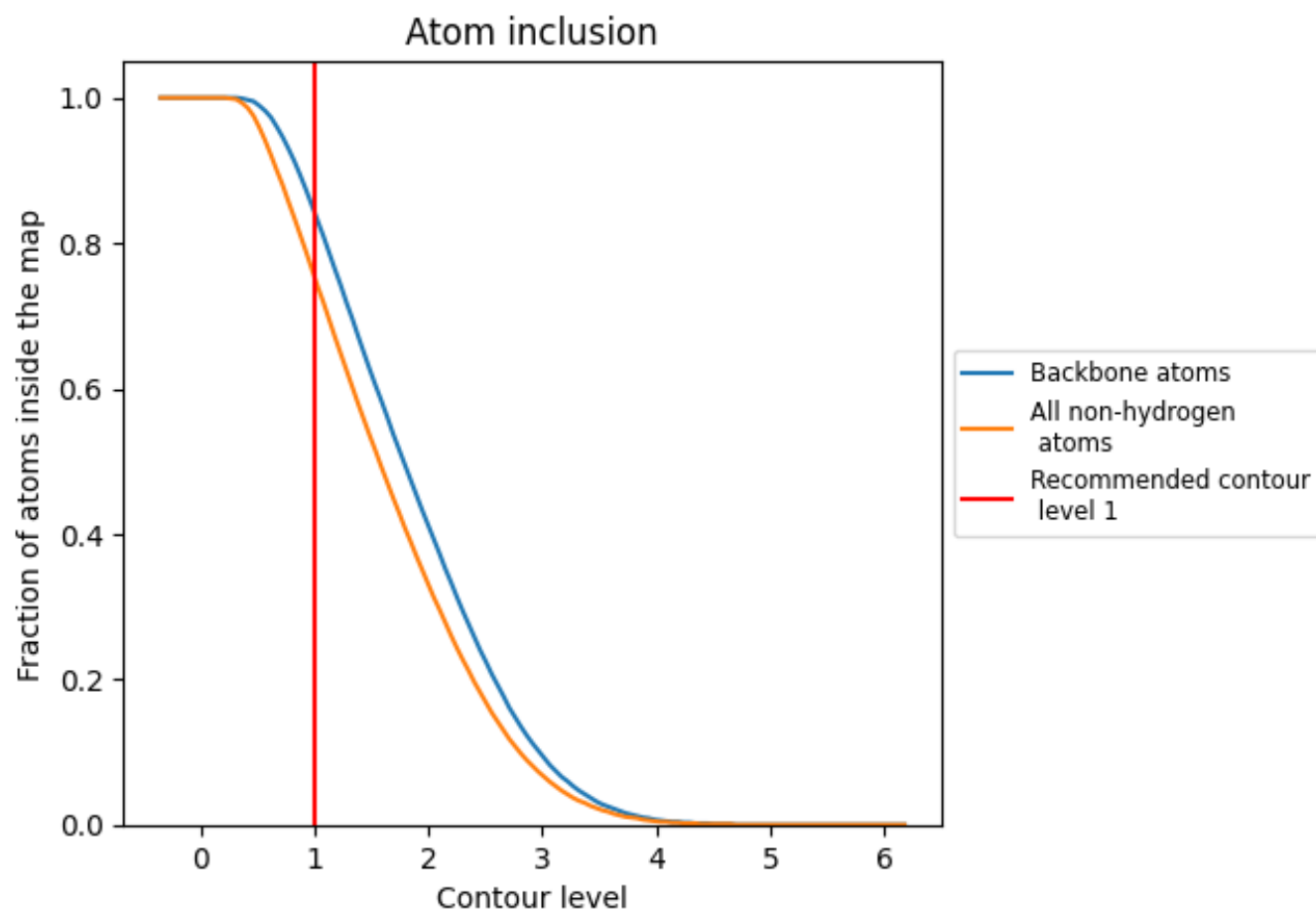


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% of all backbone atoms, 75% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7540	 0.5990
0	 0.8190	 0.6310
A	 0.4340	 0.5300
B	 0.8060	 0.5950
C	 0.1270	 0.3990
D	 0.7410	 0.5880
E	 0.3990	 0.4960
G	 0.4950	 0.5460
H	 0.3920	 0.4980
I	 0.3330	 0.4460
J	 0.8170	 0.6140
K	 0.8740	 0.6350
L	 0.8080	 0.6170
M	 0.5650	 0.5660
N	 0.3960	 0.4210
O	 0.6680	 0.5510
P	 0.5700	 0.5260
Q	 0.7810	 0.5800
R	 0.6980	 0.5680
S	 0.7830	 0.5830
T	 0.6120	 0.5220
U	 0.5980	 0.5270
V	 0.5600	 0.5250
W	 0.8220	 0.5960
X	 0.8270	 0.6060
Y	 0.8450	 0.6100
Z	 0.4910	 0.5160
a	 0.7810	 0.6080
b	 0.8860	 0.6400
c	 0.7910	 0.6050
d	 0.8830	 0.6470
e	 0.8240	 0.6200
f	 0.8800	 0.6460
g	 0.7600	 0.6040
h	 0.8550	 0.6370



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.8770	 0.6460
j	 0.9190	 0.6690
k	 0.9150	 0.6710
l	 0.9170	 0.6710
m	 0.5750	 0.5540
n	 0.8460	 0.6230
o	 0.8450	 0.6300
p	 0.8270	 0.6250
q	 0.8770	 0.6360
r	 0.8690	 0.6250
s	 0.8940	 0.6410
t	 0.8980	 0.6510
u	 0.8710	 0.6520
v	 0.9150	 0.6600
w	 0.8950	 0.6610
x	 0.9230	 0.6750
y	 0.9230	 0.6660
z	 0.7720	 0.6000