



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 10:50 PM UTC

PDB ID : 8GT0 / pdb_00008gt0
Title : Structure of falcipain and human Stefin A complex
Authors : Chakraborty, S.; Biswas, S.
Deposited on : 2022-09-07
Resolution : 3.28 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

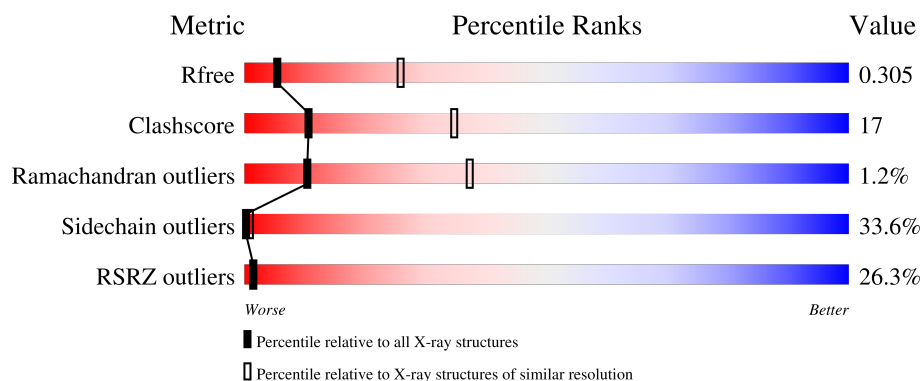
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.28 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1303 (3.30-3.26)
Clashscore	190562	1354 (3.30-3.26)
Ramachandran outliers	187476	1334 (3.30-3.26)
Sidechain outliers	187428	1333 (3.30-3.26)
RSRZ outliers	180081	1303 (3.30-3.26)

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

Mol	Chain	Length	Quality of chain
1	A	241	28% 55% 38% 7%
1	C	241	30% 44% 40% 15%
1	E	241	93%
2	B	98	23% 40% 45% 14%
2	D	98	19% 43% 43% 13%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7032 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

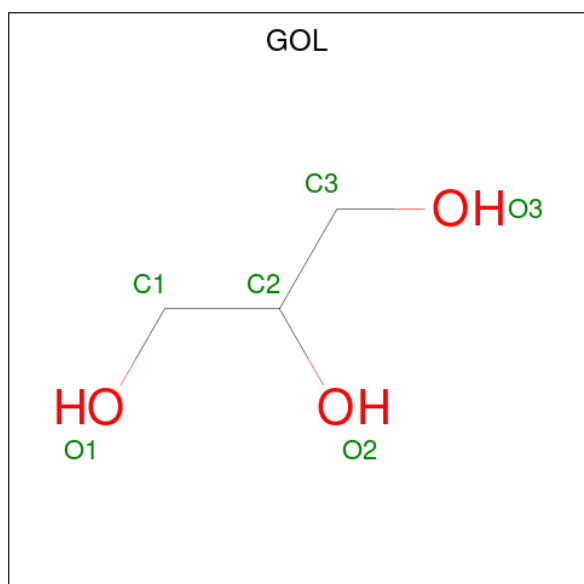
- Molecule 1 is a protein called Cysteine protease falcipain-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	0	0
			1909	1210	314	371	14			
1	C	241	Total	C	N	O	S	0	0	0
			1909	1210	314	371	14			
1	E	18	Total	C	N	O	S	0	0	0
			135	89	22	22	2			

- Molecule 2 is a protein called Cystatin-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	98	Total	C	N	O	S	0	0	0
			775	492	126	155	2			
2	D	98	Total	C	N	O	S	0	0	0
			775	492	126	155	2			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		

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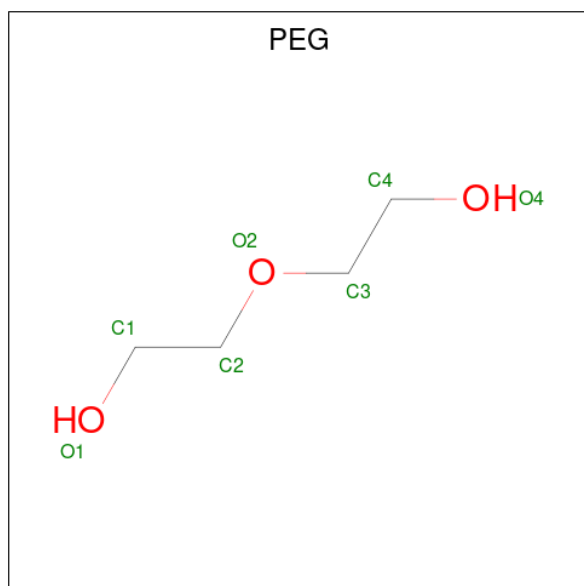
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Na	0	0
			4	4		
4	B	6	Total	Na	0	0
			6	6		
4	C	5	Total	Na	0	0
			5	5		
4	D	8	Total	Na	0	0
			8	8		
4	E	2	Total	Na	0	0
			2	2		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃) (labeled as "Ligand of Interest" by depositor).



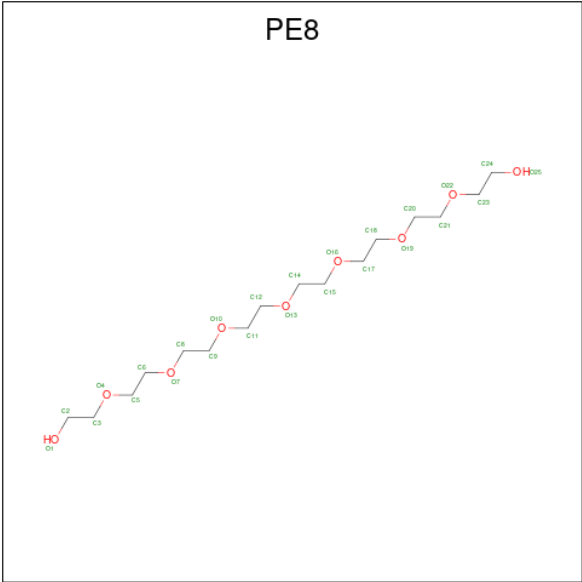
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		

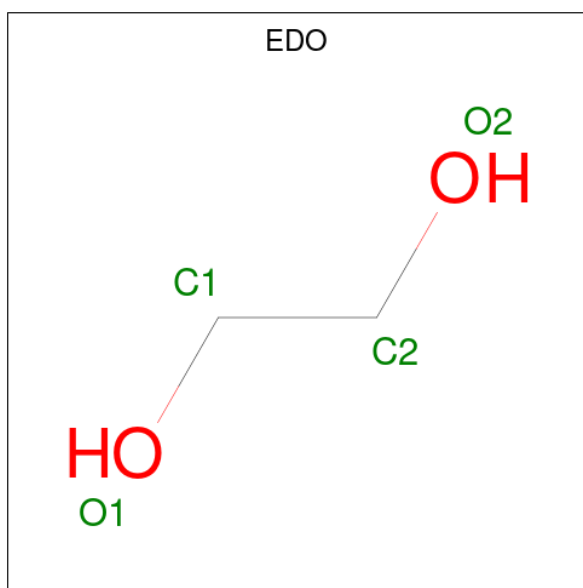
- Molecule 6 is 3,6,9,12,15,18,21-HEPTAOXATRICOSANE-1,23-DIOL (CCD ID: PE8) (formula: C₁₆H₃₄O₉) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			25	16	9		
6	A	1	Total	C	O	0	0
			25	16	9		
6	A	1	Total	C	O	0	0
			25	16	9		
6	B	1	Total	C	O	0	0
			25	16	9		
6	B	1	Total	C	O	0	0
			25	16	9		
6	B	1	Total	C	O	0	0
			25	16	9		
6	B	1	Total	C	O	0	0
			25	16	9		
6	C	1	Total	C	O	0	0
			25	16	9		
6	C	1	Total	C	O	0	0
			25	16	9		
6	E	1	Total	C	O	0	0
			25	16	9		
6	E	1	Total	C	O	0	0
			25	16	9		
6	E	1	Total	C	O	0	0
			25	16	9		

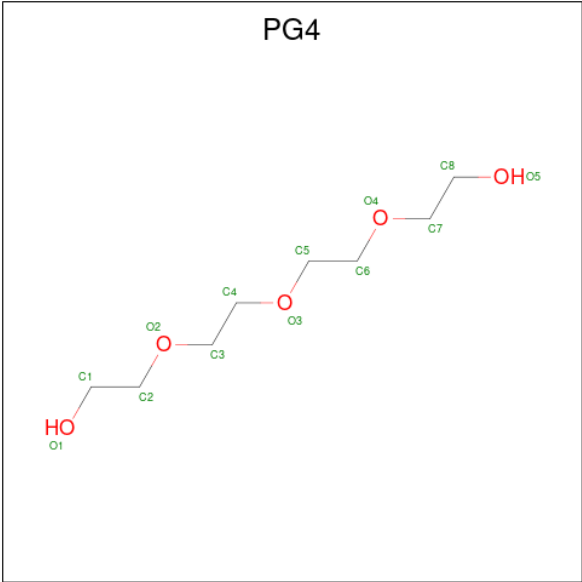
- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂) (labeled as "Ligand

of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅) (labeled as "Ligand of Interest" by depositor).



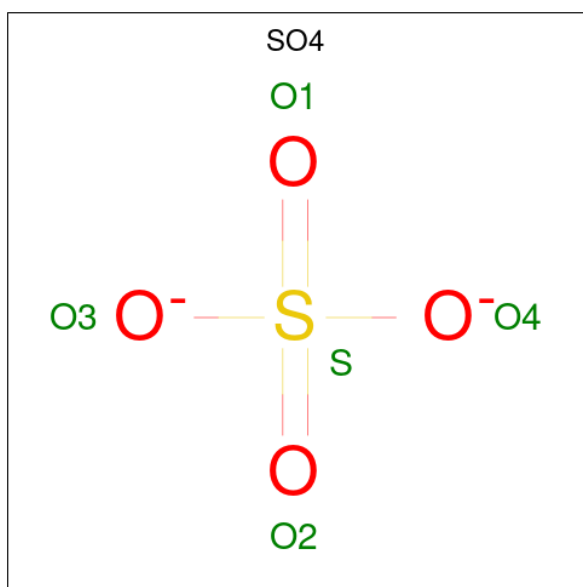
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			13	8	5		
8	A	1	Total	C	O	0	0
			13	8	5		
8	A	1	Total	C	O	0	0
			13	8	5		
8	A	1	Total	C	O	0	0
			13	8	5		
8	A	1	Total	C	O	0	0
			13	8	5		
8	A	1	Total	C	O	0	0
			13	8	5		
8	B	1	Total	C	O	0	0
			13	8	5		
8	B	1	Total	C	O	0	0
			13	8	5		
8	B	1	Total	C	O	0	0
			13	8	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			13	8	5		
8	B	1	Total	C	O	0	0
			13	8	5		
8	C	1	Total	C	O	0	0
			13	8	5		
8	C	1	Total	C	O	0	0
			13	8	5		
8	C	1	Total	C	O	0	0
			13	8	5		
8	C	1	Total	C	O	0	0
			13	8	5		
8	C	1	Total	C	O	0	0
			13	8	5		
8	D	1	Total	C	O	0	0
			13	8	5		
8	D	1	Total	C	O	0	0
			13	8	5		
8	D	1	Total	C	O	0	0
			13	8	5		
8	D	1	Total	C	O	0	0
			13	8	5		
8	D	1	Total	C	O	0	0
			13	8	5		
8	D	1	Total	C	O	0	0
			13	8	5		
8	E	1	Total	C	O	0	0
			13	8	5		

- Molecule 9 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	O	S	0	0
			5	4	1		
9	C	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		
9	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 10 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	1	Total	Cl	0	0
			1	1		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	36	Total	O	0	0
			36	36		

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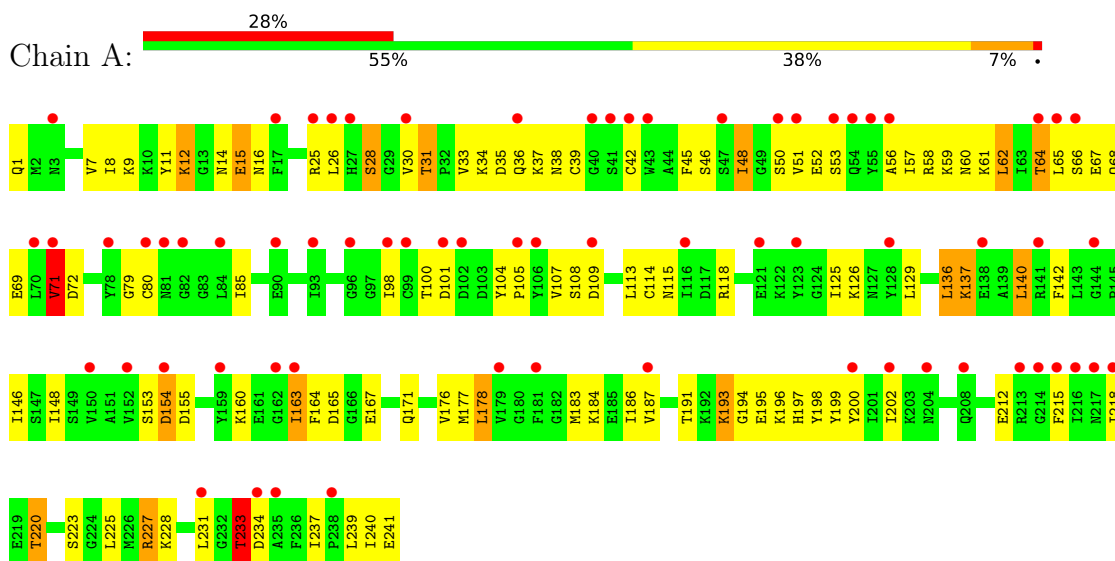
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	36	Total 36	O 36	0	0
11	C	35	Total 35	O 35	0	0
11	D	28	Total 28	O 28	0	0
11	E	9	Total 9	O 9	0	0

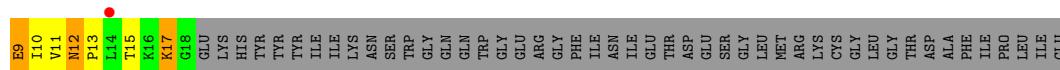
3 Residue-property plots [i](#)

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

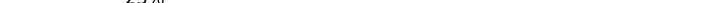
• Molecule 1: Cysteine protease falcipain-2

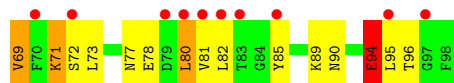


93%

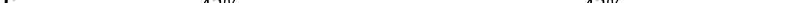


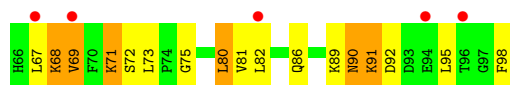
- Molecule 2: Cystatin-A

Chain B:  23% 40% 45% 14%



- Molecule 2: Cystatin-A

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.10Å 118.06Å 119.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.99 – 3.28 43.99 – 3.28	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.99-3.28) 99.8 (43.99-3.28)	Depositor EDS
R_{merge}	0.43	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 3.25Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.278 , 0.299 0.286 , 0.305	Depositor DCC
R_{free} test set	746 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	76.7	Xtriage
Anisotropy	0.676	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 853.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.045 for -h,l,k	Xtriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	7032	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, GOL, SO4, NA, CL, PE8, EDO, PEG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.23	0/1951	0.62	2/2630 (0.1%)
1	C	0.26	0/1951	0.67	0/2630
1	E	0.35	0/136	0.96	0/179
2	B	0.24	0/788	0.69	0/1062
2	D	0.26	0/788	0.64	0/1062
All	All	0.25	0/5614	0.66	2/7563 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	VAL	N-CA-C	-6.60	107.44	113.71
1	A	79	GLY	N-CA-C	5.36	117.82	110.58

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1909	0	1830	50	0
1	C	1909	0	1830	77	0
1	E	135	0	154	8	0
2	B	775	0	780	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	775	0	780	41	0
3	A	102	0	136	2	0
3	B	126	0	168	2	0
3	C	90	0	120	3	0
3	D	48	0	64	3	0
3	E	18	0	24	1	0
4	A	4	0	0	0	0
4	B	6	0	0	0	0
4	C	5	0	0	0	0
4	D	8	0	0	0	0
4	E	2	0	0	0	0
5	A	49	0	70	3	0
5	B	14	0	20	0	0
5	C	63	0	90	0	0
5	D	14	0	20	2	0
5	E	28	0	40	1	0
6	A	75	0	102	5	0
6	B	125	0	170	7	0
6	C	50	0	68	4	0
6	E	75	0	102	5	0
7	A	20	0	30	0	0
7	B	8	0	12	0	0
7	C	16	0	24	0	0
8	A	130	0	180	8	0
8	B	78	0	108	4	0
8	C	78	0	108	8	0
8	D	104	0	144	3	0
8	E	13	0	18	0	0
9	B	5	0	0	0	0
9	C	5	0	0	0	0
9	D	20	0	0	0	0
9	E	5	0	0	0	0
10	D	1	0	0	0	0
11	A	36	0	0	0	0
11	B	36	0	0	0	0
11	C	35	0	0	1	0
11	D	28	0	0	0	0
11	E	9	0	0	0	0
All	All	7032	0	7192	236	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 17.

The worst 5 of 236 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:B:35:TYR:HB3	2:B:38:LEU:HD21	1.59	0.85
8:A:330:PG4:H31	1:C:111:PRO:HG3	1.65	0.78
2:D:19:ILE:HG23	2:D:80:LEU:HD21	1.67	0.77
1:C:45:PHE:HA	1:C:67:GLU:HG2	1.67	0.75
1:C:128:TYR:OH	11:C:401:HOH:O	2.03	0.75

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	239/241 (99%)	201 (84%)	37 (16%)	1 (0%)	30	60
1	C	239/241 (99%)	191 (80%)	47 (20%)	1 (0%)	30	60
1	E	16/241 (7%)	6 (38%)	10 (62%)	0	100	100
2	B	96/98 (98%)	73 (76%)	19 (20%)	4 (4%)	2	14
2	D	96/98 (98%)	77 (80%)	17 (18%)	2 (2%)	5	26
All	All	686/919 (75%)	548 (80%)	130 (19%)	8 (1%)	10	37

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	17	GLN
2	B	77	ASN
2	D	55	ILE
1	A	233	THR
2	B	94	GLU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	207/207 (100%)	147 (71%)	60 (29%)	0	1
1	C	207/207 (100%)	130 (63%)	77 (37%)	0	0
1	E	15/207 (7%)	12 (80%)	3 (20%)	1	6
2	B	85/85 (100%)	48 (56%)	37 (44%)	0	0
2	D	85/85 (100%)	61 (72%)	24 (28%)	0	1
All	All	599/791 (76%)	398 (66%)	201 (34%)	0	1

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	51	VAL
1	C	138	GLU
1	E	12	ASN
1	C	68	GLN
1	C	102	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	27	HIS
1	C	38	ASN
2	D	86	GLN
1	C	68	GLN
1	A	86	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 [i](#)

Of 176 ligands modelled in this entry, 26 are monoatomic - leaving 150 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	D	109	-	5,5,5	0.99	0	5,5,5	1.08	0
8	PG4	B	128	-	12,12,12	0.11	0	11,11,11	0.61	0
3	GOL	A	345	-	5,5,5	0.98	0	5,5,5	1.07	0
8	PG4	D	119	-	12,12,12	0.12	0	11,11,11	0.57	0
7	EDO	B	124	-	3,3,3	0.42	0	2,2,2	0.39	0
3	GOL	B	134	-	5,5,5	1.03	0	5,5,5	1.00	0
3	GOL	B	114	-	5,5,5	0.93	0	5,5,5	1.08	0
7	EDO	A	336	-	3,3,3	0.42	0	2,2,2	0.39	0
8	PG4	E	101	-	12,12,12	0.11	0	11,11,11	0.61	0
5	PEG	D	123	-	6,6,6	0.10	0	5,5,5	0.16	0
3	GOL	D	124	-	5,5,5	0.98	0	5,5,5	0.93	0
8	PG4	C	332	-	12,12,12	0.10	0	11,11,11	0.66	0
5	PEG	C	318	-	6,6,6	0.16	0	5,5,5	0.17	0
5	PEG	C	320	-	6,6,6	0.07	0	5,5,5	0.27	0
9	SO4	E	107	-	4,4,4	0.23	0	6,6,6	0.06	0
8	PG4	A	332	-	12,12,12	0.13	0	11,11,11	0.58	0
9	SO4	D	112	-	4,4,4	0.23	0	6,6,6	0.11	0
8	PG4	C	327	-	12,12,12	0.13	0	11,11,11	0.61	0
3	GOL	C	308	-	5,5,5	0.91	0	5,5,5	1.02	0
7	EDO	C	323	-	3,3,3	0.43	0	2,2,2	0.36	0
7	EDO	A	343	-	3,3,3	0.43	0	2,2,2	0.36	0
3	GOL	B	140	-	5,5,5	1.01	0	5,5,5	1.03	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PEG	E	109	-	6,6,6	0.10	0	5,5,5	0.11	0
8	PG4	D	118	-	12,12,12	0.11	0	11,11,11	0.55	0
6	PE8	A	324	-	24,24,24	0.55	0	23,23,23	0.37	0
3	GOL	C	311	-	5,5,5	0.96	0	5,5,5	0.99	0
3	GOL	D	122	-	5,5,5	0.90	0	5,5,5	1.13	1 (20%)
3	GOL	A	305	-	5,5,5	0.97	0	5,5,5	1.03	0
5	PEG	A	319	-	6,6,6	0.10	0	5,5,5	0.13	0
9	SO4	D	126	-	4,4,4	0.26	0	6,6,6	0.08	0
9	SO4	D	113	-	4,4,4	0.23	0	6,6,6	0.11	0
3	GOL	B	111	-	5,5,5	0.95	0	5,5,5	1.02	0
3	GOL	B	107	-	5,5,5	0.98	0	5,5,5	1.11	0
8	PG4	C	326	-	12,12,12	0.18	0	11,11,11	0.53	0
3	GOL	B	110	-	5,5,5	0.92	0	5,5,5	1.12	0
8	PG4	B	126	-	12,12,12	0.11	0	11,11,11	0.62	0
3	GOL	E	104	-	5,5,5	0.96	0	5,5,5	1.05	0
3	GOL	B	116	-	5,5,5	0.94	0	5,5,5	1.07	0
3	GOL	B	101	-	5,5,5	0.94	0	5,5,5	1.02	0
3	GOL	B	102	-	5,5,5	0.99	0	5,5,5	0.94	0
5	PEG	C	317	-	6,6,6	0.09	0	5,5,5	0.16	0
7	EDO	B	103	-	3,3,3	0.43	0	2,2,2	0.39	0
7	EDO	A	326	-	3,3,3	0.41	0	2,2,2	0.43	0
5	PEG	C	316	-	6,6,6	0.11	0	5,5,5	0.10	0
8	PG4	D	116	-	12,12,12	0.12	0	11,11,11	0.63	0
8	PG4	A	331	-	12,12,12	0.11	0	11,11,11	0.66	0
7	EDO	C	334	-	3,3,3	0.41	0	2,2,2	0.44	0
3	GOL	C	310	-	5,5,5	0.91	0	5,5,5	1.06	0
6	PE8	A	322	-	24,24,24	0.54	0	23,23,23	0.31	0
3	GOL	A	306	-	5,5,5	0.99	0	5,5,5	0.94	0
8	PG4	C	325	-	12,12,12	0.12	0	11,11,11	0.62	0
3	GOL	B	132	-	5,5,5	0.93	0	5,5,5	1.10	0
6	PE8	B	131	-	24,24,24	0.54	0	23,23,23	0.25	0
3	GOL	A	303	-	5,5,5	0.96	0	5,5,5	1.07	0
3	GOL	C	338	-	5,5,5	0.92	0	5,5,5	1.12	0
5	PEG	A	335	-	6,6,6	0.17	0	5,5,5	0.23	0
3	GOL	B	115	-	5,5,5	1.02	0	5,5,5	0.94	0
3	GOL	A	346	-	5,5,5	0.98	0	5,5,5	1.01	0
3	GOL	C	341	-	5,5,5	0.94	0	5,5,5	1.22	1 (20%)
8	PG4	B	127	-	12,12,12	0.12	0	11,11,11	0.62	0
3	GOL	A	302	-	5,5,5	0.97	0	5,5,5	1.00	0
3	GOL	A	309	-	5,5,5	0.94	0	5,5,5	1.08	0
8	PG4	A	337	-	12,12,12	0.12	0	11,11,11	0.75	1 (9%)
5	PEG	A	341	-	6,6,6	0.11	0	5,5,5	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	SO4	B	119	-	4,4,4	0.23	0	6,6,6	0.07	0
3	GOL	C	307	-	5,5,5	1.03	0	5,5,5	0.89	0
3	GOL	C	301	-	5,5,5	0.92	0	5,5,5	1.08	0
5	PEG	C	330	-	6,6,6	0.10	0	5,5,5	0.09	0
9	SO4	C	336	-	4,4,4	0.26	0	6,6,6	0.07	0
3	GOL	B	136	-	5,5,5	0.95	0	5,5,5	1.06	0
3	GOL	C	302	-	5,5,5	0.94	0	5,5,5	1.06	0
6	PE8	A	323	-	24,24,24	0.55	0	23,23,23	0.28	0
8	PG4	A	333	-	12,12,12	0.14	0	11,11,11	0.66	0
3	GOL	B	106	-	5,5,5	0.97	0	5,5,5	0.99	0
3	GOL	B	138	-	5,5,5	1.04	0	5,5,5	1.12	0
3	GOL	B	112	-	5,5,5	0.97	0	5,5,5	1.08	0
9	SO4	D	114	-	4,4,4	0.23	0	6,6,6	0.10	0
3	GOL	D	110	-	5,5,5	1.03	0	5,5,5	0.89	0
3	GOL	A	304	-	5,5,5	0.99	0	5,5,5	0.98	0
3	GOL	E	102	-	5,5,5	0.93	0	5,5,5	1.06	0
5	PEG	C	339	-	6,6,6	0.10	0	5,5,5	0.12	0
3	GOL	D	108	-	5,5,5	0.92	0	5,5,5	1.11	0
3	GOL	D	106	-	5,5,5	0.92	0	5,5,5	1.12	0
6	PE8	C	322	-	24,24,24	0.55	0	23,23,23	0.26	0
3	GOL	B	137	-	5,5,5	0.98	0	5,5,5	0.97	0
3	GOL	C	304	-	5,5,5	0.94	0	5,5,5	1.10	0
3	GOL	C	342	-	5,5,5	0.94	0	5,5,5	1.03	0
3	GOL	C	331	-	5,5,5	0.93	0	5,5,5	1.05	0
5	PEG	A	321	-	6,6,6	0.08	0	5,5,5	0.14	0
3	GOL	B	113	-	5,5,5	1.06	0	5,5,5	0.92	0
8	PG4	D	121	-	12,12,12	0.10	0	11,11,11	0.60	0
3	GOL	A	340	-	5,5,5	0.92	0	5,5,5	1.09	0
5	PEG	A	320	-	6,6,6	0.12	0	5,5,5	0.06	0
6	PE8	C	321	-	24,24,24	0.55	0	23,23,23	0.37	0
3	GOL	B	130	-	5,5,5	1.01	0	5,5,5	0.87	0
8	PG4	A	329	-	12,12,12	0.14	0	11,11,11	0.52	0
8	PG4	D	117	-	12,12,12	0.11	0	11,11,11	0.60	0
6	PE8	B	121	-	24,24,24	0.55	0	23,23,23	0.27	0
5	PEG	B	120	-	6,6,6	0.11	0	5,5,5	0.08	0
5	PEG	E	110	-	6,6,6	0.11	0	5,5,5	0.13	0
5	PEG	C	315	-	6,6,6	0.09	0	5,5,5	0.14	0
8	PG4	A	334	-	12,12,12	0.12	0	11,11,11	0.68	0
8	PG4	A	344	-	12,12,12	0.11	0	11,11,11	0.62	0
3	GOL	A	312	-	5,5,5	0.96	0	5,5,5	1.08	0
8	PG4	B	129	4	12,12,12	0.12	0	11,11,11	0.55	0
3	GOL	A	311	-	5,5,5	0.92	0	5,5,5	1.05	0
8	PG4	D	101	-	12,12,12	0.12	0	11,11,11	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	109	-	5,5,5	0.99	0	5,5,5	1.00	0
3	GOL	D	107	-	5,5,5	0.93	0	5,5,5	1.08	0
3	GOL	A	308	-	5,5,5	0.99	0	5,5,5	0.96	0
3	GOL	A	314	-	5,5,5	1.00	0	5,5,5	0.91	0
5	PEG	D	115	-	6,6,6	0.12	0	5,5,5	0.12	0
7	EDO	C	328	-	3,3,3	0.42	0	2,2,2	0.39	0
3	GOL	E	103	-	5,5,5	0.95	0	5,5,5	1.05	0
6	PE8	B	123	-	24,24,24	0.55	0	23,23,23	0.30	0
5	PEG	B	139	-	6,6,6	0.11	0	5,5,5	0.10	0
3	GOL	B	135	-	5,5,5	0.97	0	5,5,5	1.05	0
5	PEG	A	342	-	6,6,6	0.11	0	5,5,5	0.11	0
8	PG4	B	104	-	12,12,12	0.11	0	11,11,11	0.74	0
5	PEG	C	340	-	6,6,6	0.09	0	5,5,5	0.12	0
8	PG4	A	338	-	12,12,12	0.13	0	11,11,11	0.59	0
3	GOL	C	306	-	5,5,5	0.92	0	5,5,5	1.08	0
8	PG4	A	330	-	12,12,12	0.11	0	11,11,11	0.60	0
5	PEG	A	318	-	6,6,6	0.12	0	5,5,5	0.07	0
6	PE8	E	112	-	24,24,24	0.54	0	23,23,23	0.30	0
8	PG4	D	127	-	12,12,12	0.10	0	11,11,11	0.65	0
3	GOL	C	303	-	5,5,5	0.95	0	5,5,5	1.06	0
3	GOL	A	310	-	5,5,5	1.00	0	5,5,5	0.98	0
3	GOL	C	305	-	5,5,5	0.92	0	5,5,5	1.12	0
8	PG4	B	125	-	12,12,12	0.09	0	11,11,11	0.69	0
3	GOL	A	313	-	5,5,5	0.89	0	5,5,5	1.13	0
5	PEG	C	319	-	6,6,6	0.14	0	5,5,5	0.05	0
6	PE8	E	114	-	24,24,24	0.54	0	23,23,23	0.31	0
8	PG4	D	105	-	12,12,12	0.13	0	11,11,11	0.77	0
6	PE8	B	105	-	24,24,24	0.54	0	23,23,23	0.35	0
6	PE8	E	113	-	24,24,24	0.54	0	23,23,23	0.26	0
5	PEG	E	111	-	6,6,6	0.11	0	5,5,5	0.07	0
8	PG4	C	324	-	12,12,12	0.15	0	11,11,11	0.41	0
3	GOL	B	108	-	5,5,5	0.93	0	5,5,5	1.04	0
6	PE8	B	122	-	24,24,24	0.54	0	23,23,23	0.27	0
7	EDO	A	325	-	3,3,3	0.43	0	2,2,2	0.37	0
8	PG4	A	328	-	12,12,12	0.14	0	11,11,11	0.50	0
3	GOL	C	309	-	5,5,5	0.94	0	5,5,5	1.08	0
3	GOL	A	301	-	5,5,5	0.93	0	5,5,5	1.09	0
5	PEG	E	108	-	6,6,6	0.10	0	5,5,5	0.11	0
7	EDO	A	327	-	3,3,3	0.42	0	2,2,2	0.40	0
3	GOL	D	103	-	5,5,5	0.97	0	5,5,5	1.00	0
8	PG4	C	337	-	12,12,12	0.12	0	11,11,11	0.57	0
3	GOL	A	307	-	5,5,5	1.01	0	5,5,5	0.95	0
7	EDO	C	329	-	3,3,3	0.42	0	2,2,2	0.40	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	D	109	-	-	4/4/4/4	-
8	PG4	B	128	-	-	6/10/10/10	-
3	GOL	A	345	-	-	4/4/4/4	-
8	PG4	D	119	-	-	6/10/10/10	-
7	EDO	B	124	-	-	0/1/1/1	-
3	GOL	B	134	-	-	4/4/4/4	-
3	GOL	B	114	-	-	2/4/4/4	-
7	EDO	A	336	-	-	1/1/1/1	-
8	PG4	E	101	-	-	8/10/10/10	-
5	PEG	D	123	-	-	2/4/4/4	-
3	GOL	D	124	-	-	2/4/4/4	-
8	PG4	C	332	-	-	3/10/10/10	-
5	PEG	C	318	-	-	3/4/4/4	-
5	PEG	C	320	-	-	2/4/4/4	-
8	PG4	A	332	-	-	6/10/10/10	-
8	PG4	C	327	-	-	6/10/10/10	-
3	GOL	C	308	-	-	3/4/4/4	-
7	EDO	C	323	-	-	1/1/1/1	-
7	EDO	A	343	-	-	1/1/1/1	-
3	GOL	B	140	-	-	2/4/4/4	-
5	PEG	E	109	-	-	2/4/4/4	-
8	PG4	D	118	-	-	4/10/10/10	-
6	PE8	A	324	-	-	16/22/22/22	-
3	GOL	C	311	-	-	2/4/4/4	-
3	GOL	D	122	-	-	2/4/4/4	-
3	GOL	A	305	-	-	4/4/4/4	-
5	PEG	A	319	-	-	3/4/4/4	-
3	GOL	B	111	-	-	3/4/4/4	-
3	GOL	B	107	-	-	3/4/4/4	-
8	PG4	C	326	-	-	7/10/10/10	-
3	GOL	B	110	-	-	2/4/4/4	-
8	PG4	B	126	-	-	7/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	E	104	-	-	2/4/4/4	-
3	GOL	B	116	-	-	1/4/4/4	-
3	GOL	B	101	-	-	2/4/4/4	-
3	GOL	B	102	-	-	2/4/4/4	-
5	PEG	C	317	-	-	4/4/4/4	-
7	EDO	B	103	-	-	1/1/1/1	-
7	EDO	A	326	-	-	1/1/1/1	-
5	PEG	C	316	-	-	2/4/4/4	-
8	PG4	D	116	-	-	5/10/10/10	-
8	PG4	A	331	-	-	8/10/10/10	-
7	EDO	C	334	-	-	1/1/1/1	-
3	GOL	C	310	-	-	2/4/4/4	-
6	PE8	A	322	-	-	13/22/22/22	-
3	GOL	A	306	-	-	4/4/4/4	-
8	PG4	C	325	-	-	8/10/10/10	-
3	GOL	B	132	-	-	4/4/4/4	-
6	PE8	B	131	-	-	13/22/22/22	-
3	GOL	A	303	-	-	2/4/4/4	-
3	GOL	C	338	-	-	2/4/4/4	-
5	PEG	A	335	-	-	3/4/4/4	-
3	GOL	B	115	-	-	4/4/4/4	-
3	GOL	A	346	-	-	0/4/4/4	-
3	GOL	C	341	-	-	4/4/4/4	-
8	PG4	B	127	-	-	5/10/10/10	-
3	GOL	A	302	-	-	0/4/4/4	-
3	GOL	A	309	-	-	0/4/4/4	-
8	PG4	A	337	-	-	7/10/10/10	-
5	PEG	A	341	-	-	3/4/4/4	-
3	GOL	C	307	-	-	4/4/4/4	-
3	GOL	C	301	-	-	2/4/4/4	-
5	PEG	C	330	-	-	1/4/4/4	-
3	GOL	B	136	-	-	2/4/4/4	-
3	GOL	C	302	-	-	4/4/4/4	-
6	PE8	A	323	-	-	11/22/22/22	-
8	PG4	A	333	-	-	5/10/10/10	-
3	GOL	B	106	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	138	-	-	4/4/4/4	-
3	GOL	B	112	-	-	4/4/4/4	-
3	GOL	D	110	-	-	2/4/4/4	-
3	GOL	A	304	-	-	1/4/4/4	-
3	GOL	E	102	-	-	2/4/4/4	-
5	PEG	C	339	-	-	2/4/4/4	-
3	GOL	D	108	-	-	2/4/4/4	-
3	GOL	D	106	-	-	2/4/4/4	-
6	PE8	C	322	-	-	13/22/22/22	-
3	GOL	B	137	-	-	2/4/4/4	-
3	GOL	C	304	-	-	1/4/4/4	-
3	GOL	C	342	-	-	2/4/4/4	-
3	GOL	C	331	-	-	1/4/4/4	-
5	PEG	A	321	-	-	1/4/4/4	-
3	GOL	B	113	-	-	0/4/4/4	-
8	PG4	D	121	-	-	6/10/10/10	-
3	GOL	A	340	-	-	2/4/4/4	-
5	PEG	A	320	-	-	2/4/4/4	-
6	PE8	C	321	-	-	10/22/22/22	-
3	GOL	B	130	-	-	4/4/4/4	-
8	PG4	A	329	-	-	4/10/10/10	-
8	PG4	D	117	-	-	5/10/10/10	-
6	PE8	B	121	-	-	13/22/22/22	-
5	PEG	B	120	-	-	1/4/4/4	-
5	PEG	E	110	-	-	3/4/4/4	-
5	PEG	C	315	-	-	2/4/4/4	-
8	PG4	A	334	-	-	6/10/10/10	-
8	PG4	A	344	-	-	5/10/10/10	-
3	GOL	A	312	-	-	4/4/4/4	-
8	PG4	B	129	4	-	7/10/10/10	-
3	GOL	A	311	-	-	0/4/4/4	-
8	PG4	D	101	-	-	4/10/10/10	-
3	GOL	B	109	-	-	2/4/4/4	-
3	GOL	D	107	-	-	2/4/4/4	-
3	GOL	A	308	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	314	-	-	4/4/4/4	-
5	PEG	D	115	-	-	2/4/4/4	-
7	EDO	C	328	-	-	1/1/1/1	-
3	GOL	E	103	-	-	0/4/4/4	-
6	PE8	B	123	-	-	16/22/22/22	-
5	PEG	B	139	-	-	0/4/4/4	-
3	GOL	B	135	-	-	4/4/4/4	-
5	PEG	A	342	-	-	3/4/4/4	-
8	PG4	B	104	-	-	3/10/10/10	-
5	PEG	C	340	-	-	4/4/4/4	-
8	PG4	A	338	-	-	6/10/10/10	-
3	GOL	C	306	-	-	4/4/4/4	-
8	PG4	A	330	-	-	6/10/10/10	-
5	PEG	A	318	-	-	3/4/4/4	-
6	PE8	E	112	-	-	14/22/22/22	-
8	PG4	D	127	-	-	8/10/10/10	-
3	GOL	C	303	-	-	3/4/4/4	-
3	GOL	A	310	-	-	2/4/4/4	-
3	GOL	C	305	-	-	4/4/4/4	-
8	PG4	B	125	-	-	5/10/10/10	-
3	GOL	A	313	-	-	0/4/4/4	-
5	PEG	C	319	-	-	4/4/4/4	-
6	PE8	E	114	-	-	15/22/22/22	-
8	PG4	D	105	-	-	3/10/10/10	-
6	PE8	B	105	-	-	15/22/22/22	-
6	PE8	E	113	-	-	16/22/22/22	-
5	PEG	E	111	-	-	3/4/4/4	-
8	PG4	C	324	-	-	7/10/10/10	-
3	GOL	B	108	-	-	2/4/4/4	-
6	PE8	B	122	-	-	13/22/22/22	-
7	EDO	A	325	-	-	1/1/1/1	-
8	PG4	A	328	-	-	6/10/10/10	-
3	GOL	C	309	-	-	2/4/4/4	-
3	GOL	A	301	-	-	2/4/4/4	-
5	PEG	E	108	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	A	327	-	-	1/1/1/1	-
3	GOL	D	103	-	-	2/4/4/4	-
8	PG4	C	337	-	-	3/10/10/10	-
3	GOL	A	307	-	-	2/4/4/4	-
7	EDO	C	329	-	-	1/1/1/1	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	341	GOL	C3-C2-C1	-2.07	104.19	111.80
8	A	337	PG4	C5-O3-C4	-2.04	104.35	113.26
3	D	122	GOL	C3-C2-C1	-2.00	104.45	111.80

There are no chirality outliers.

5 of 571 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	GOL	C1-C2-C3-O3
3	A	303	GOL	O1-C1-C2-O2
3	A	303	GOL	O1-C1-C2-C3
3	A	305	GOL	C1-C2-C3-O3
3	A	306	GOL	O1-C1-C2-C3

There are no ring outliers.

40 monomers are involved in 50 short contacts:

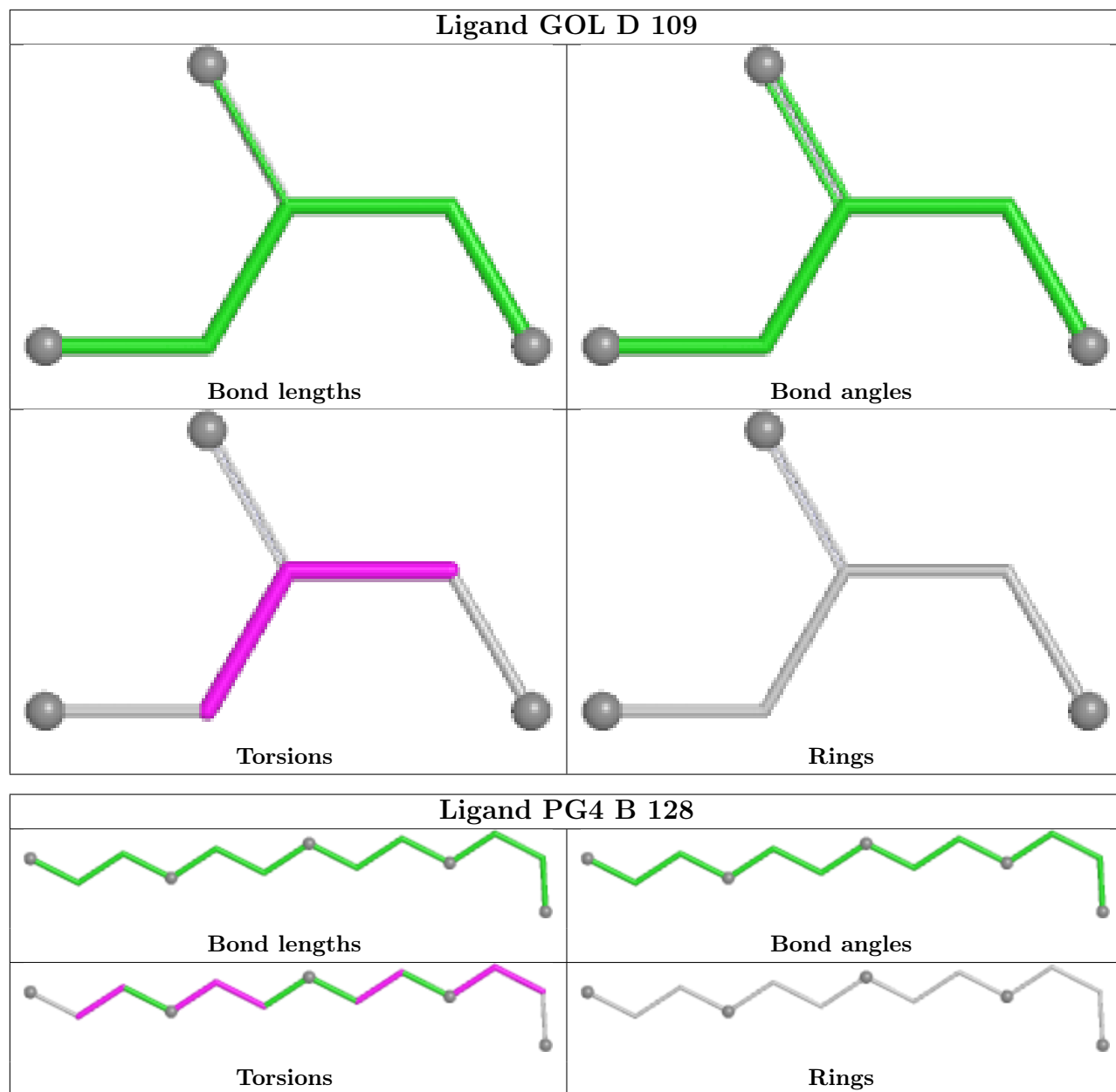
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	345	GOL	1	0
5	D	123	PEG	1	0
3	D	124	GOL	1	0
8	C	332	PG4	1	0
5	E	109	PEG	1	0
8	D	118	PG4	1	0
6	A	324	PE8	1	0
8	C	326	PG4	1	0
8	B	126	PG4	1	0
3	E	104	GOL	1	0
3	B	116	GOL	1	0
8	D	116	PG4	1	0

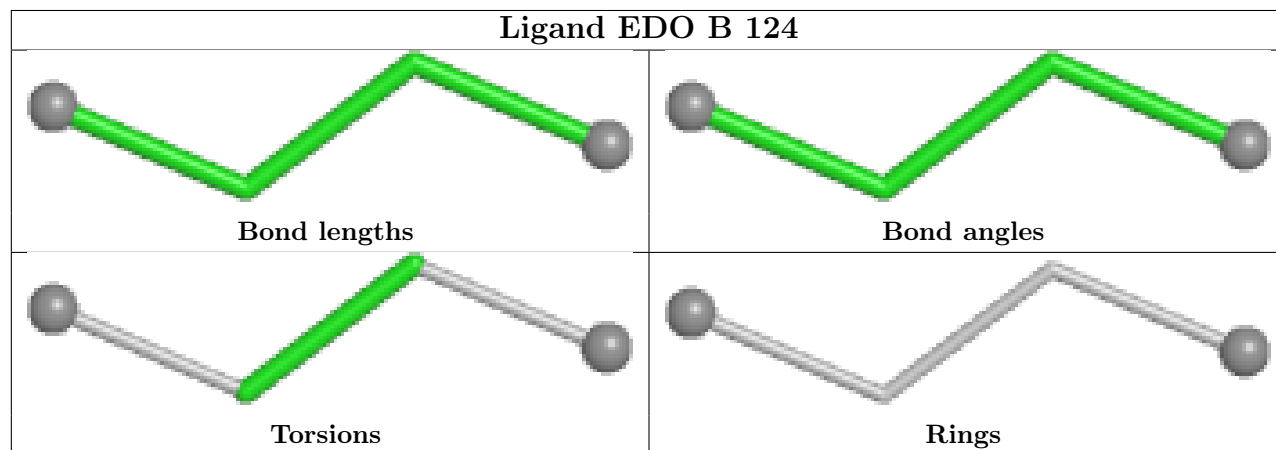
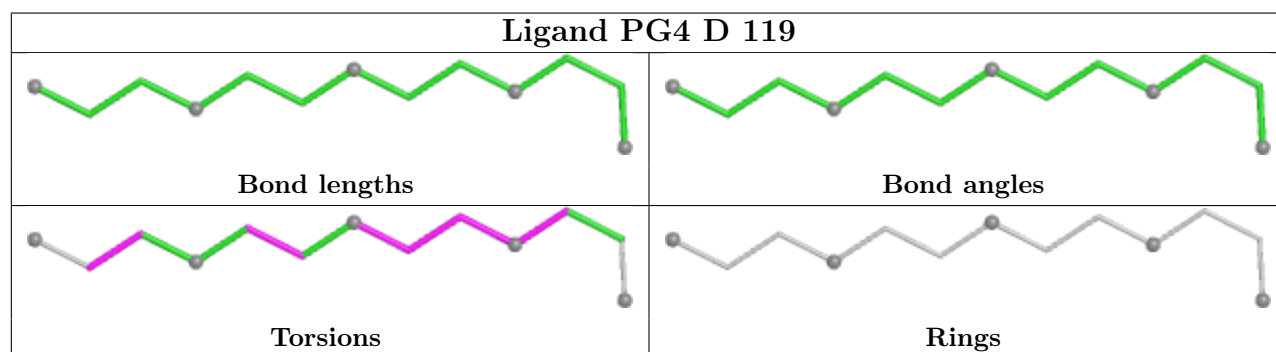
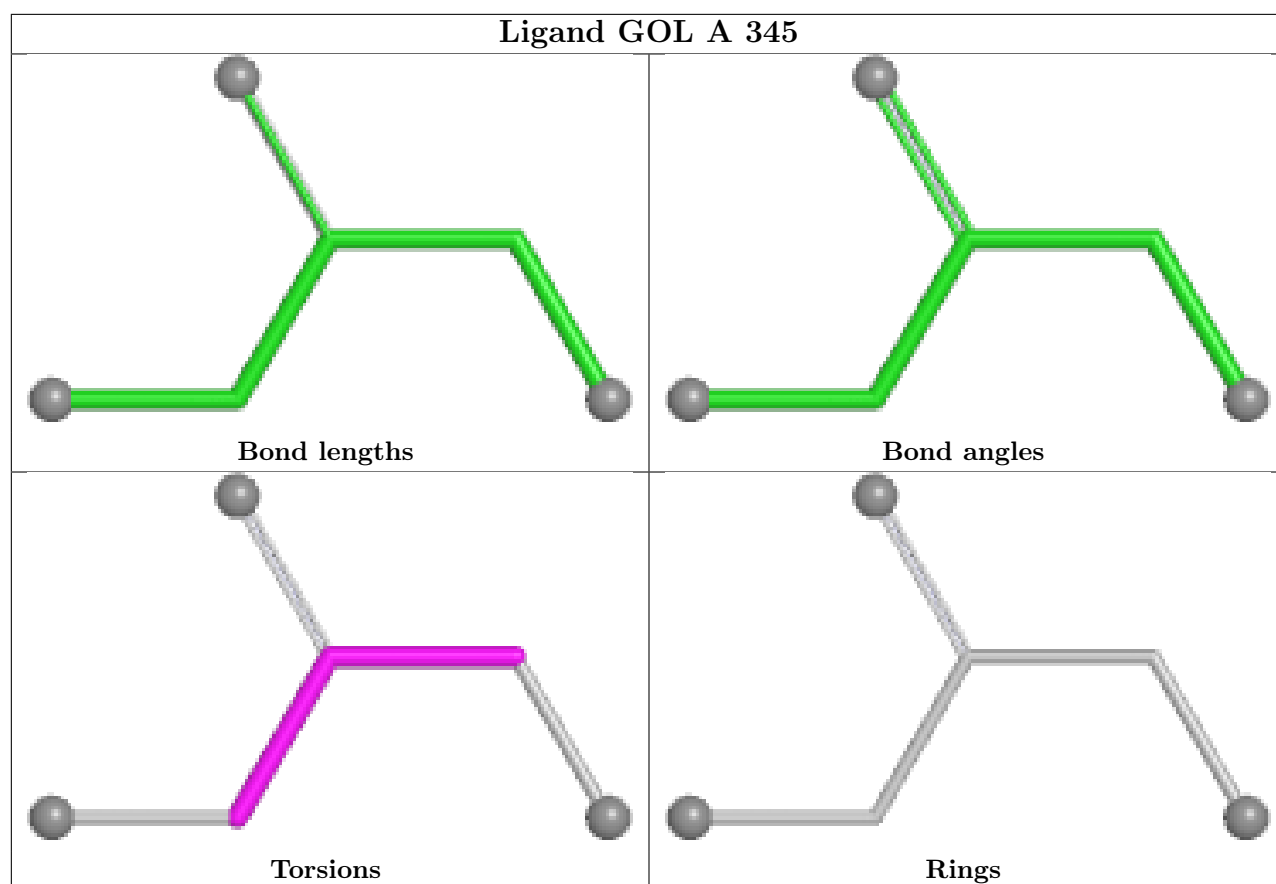
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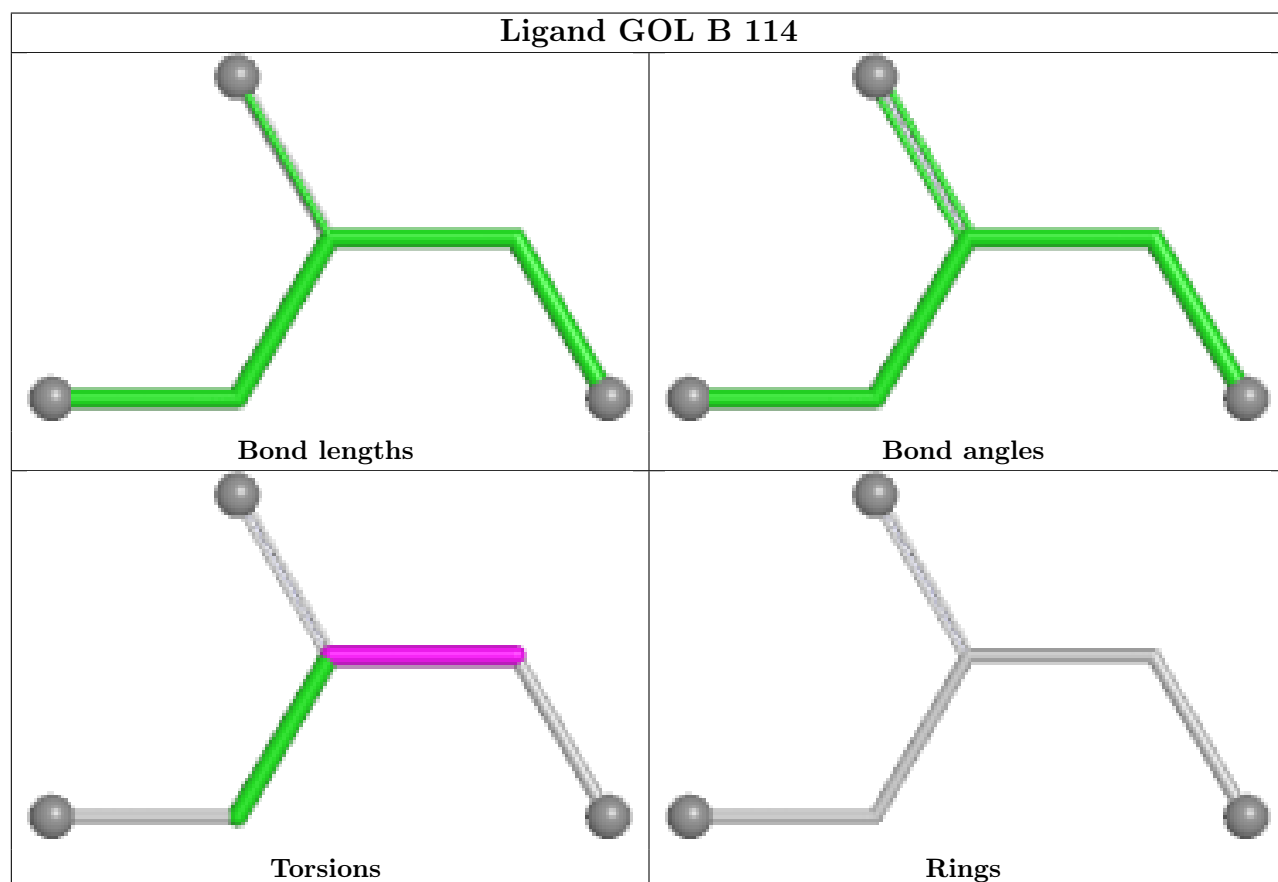
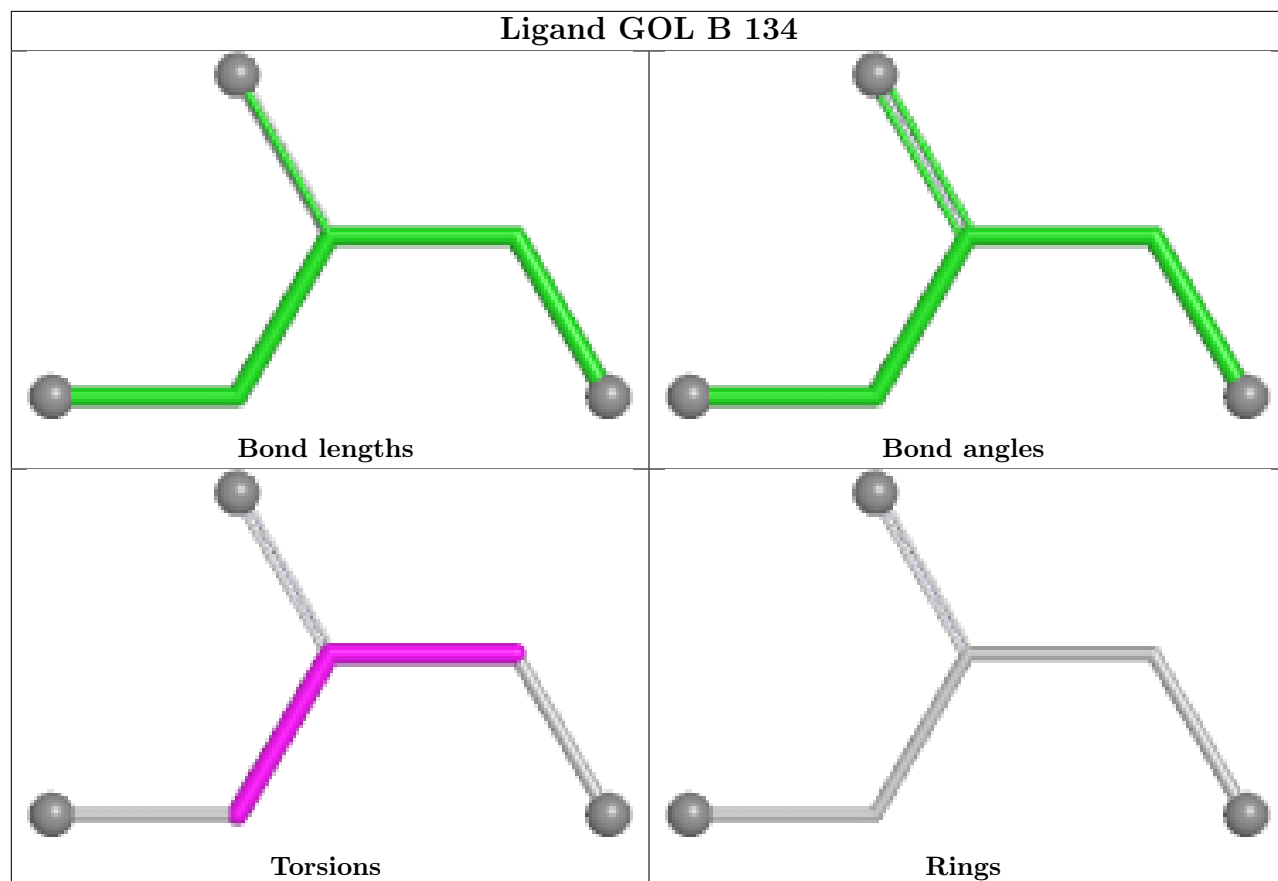
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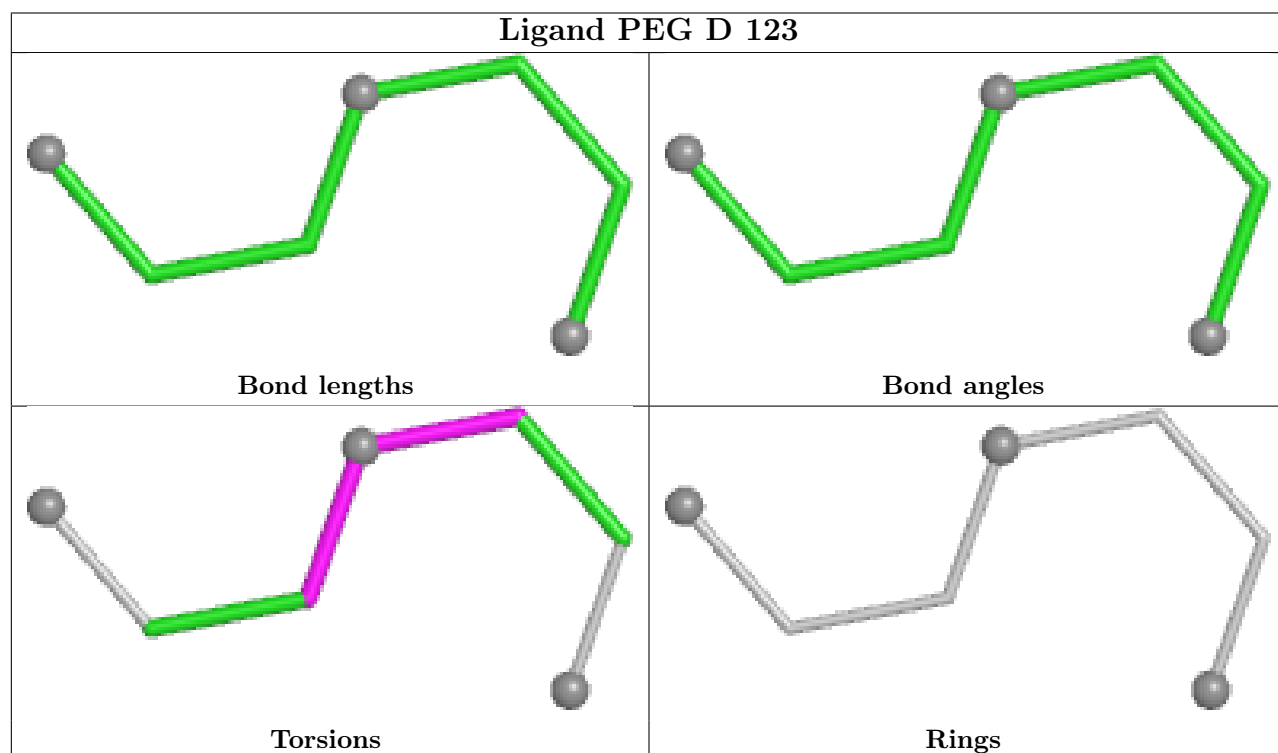
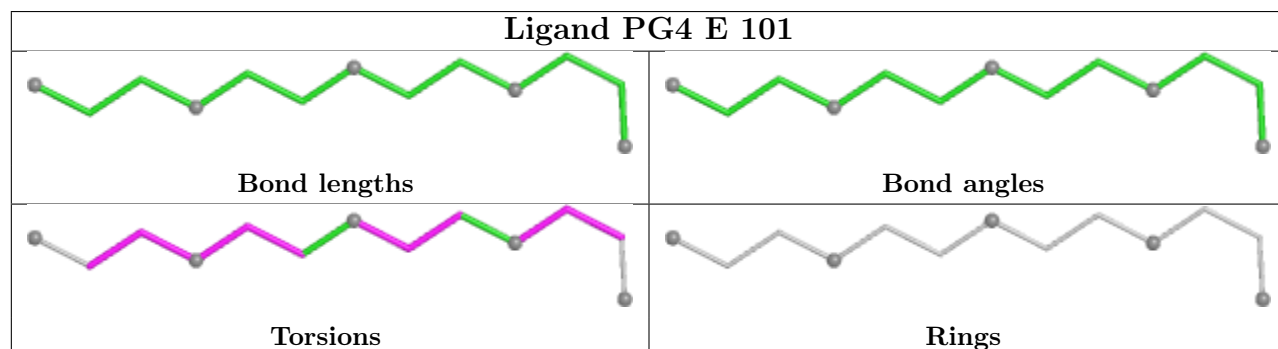
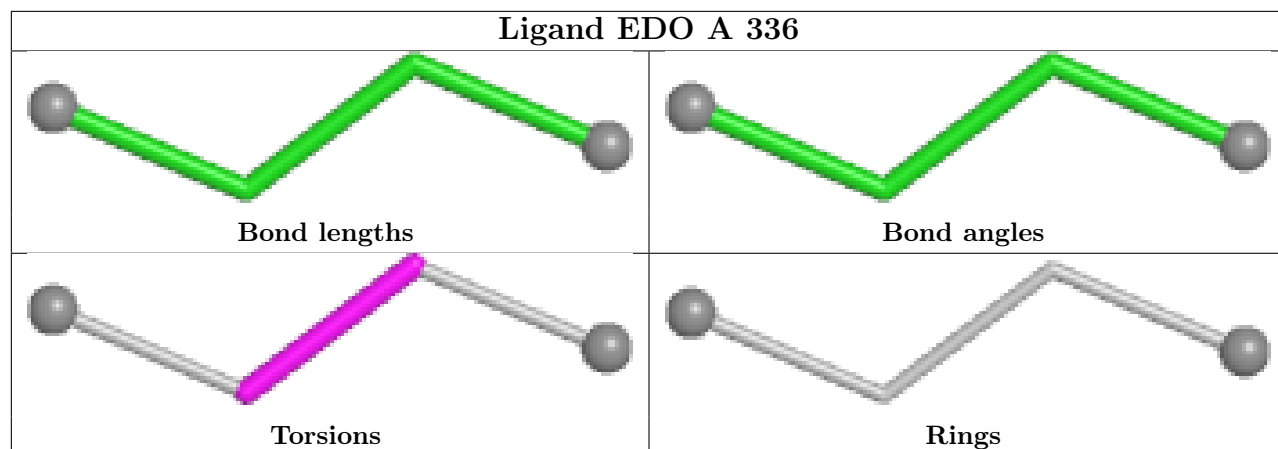
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	331	PG4	1	0
6	A	322	PE8	4	0
6	B	131	PE8	2	0
5	A	335	PEG	2	0
3	A	346	GOL	1	0
8	A	337	PG4	1	0
3	D	110	GOL	1	0
3	C	342	GOL	2	0
5	A	320	PEG	1	0
6	C	321	PE8	4	0
8	A	329	PG4	1	0
8	A	334	PG4	1	0
8	A	344	PG4	1	0
8	B	129	PG4	1	0
3	B	109	GOL	1	0
5	D	115	PEG	1	0
6	B	123	PE8	2	0
8	A	330	PG4	4	0
3	C	303	GOL	1	0
8	B	125	PG4	2	0
6	E	114	PE8	2	0
8	D	105	PG4	2	0
6	B	105	PE8	3	0
6	E	113	PE8	3	0
8	C	324	PG4	3	0
8	A	328	PG4	1	0
3	D	103	GOL	1	0
8	C	337	PG4	3	0

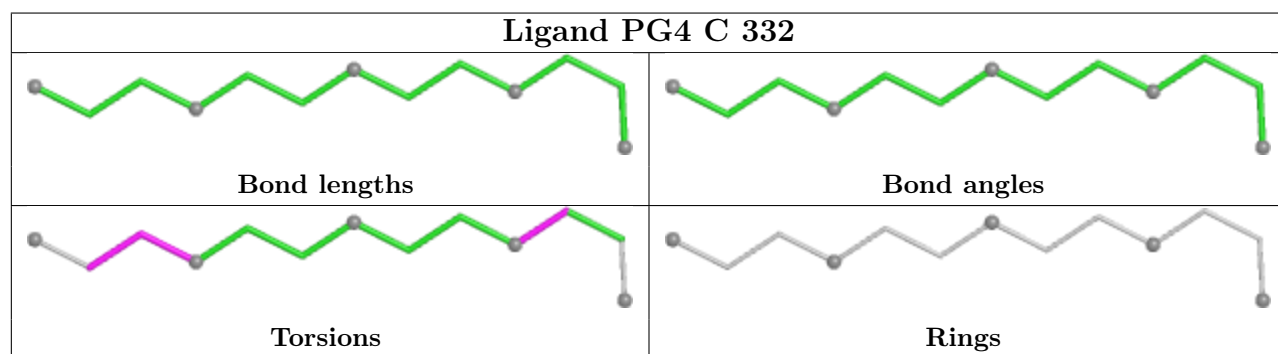
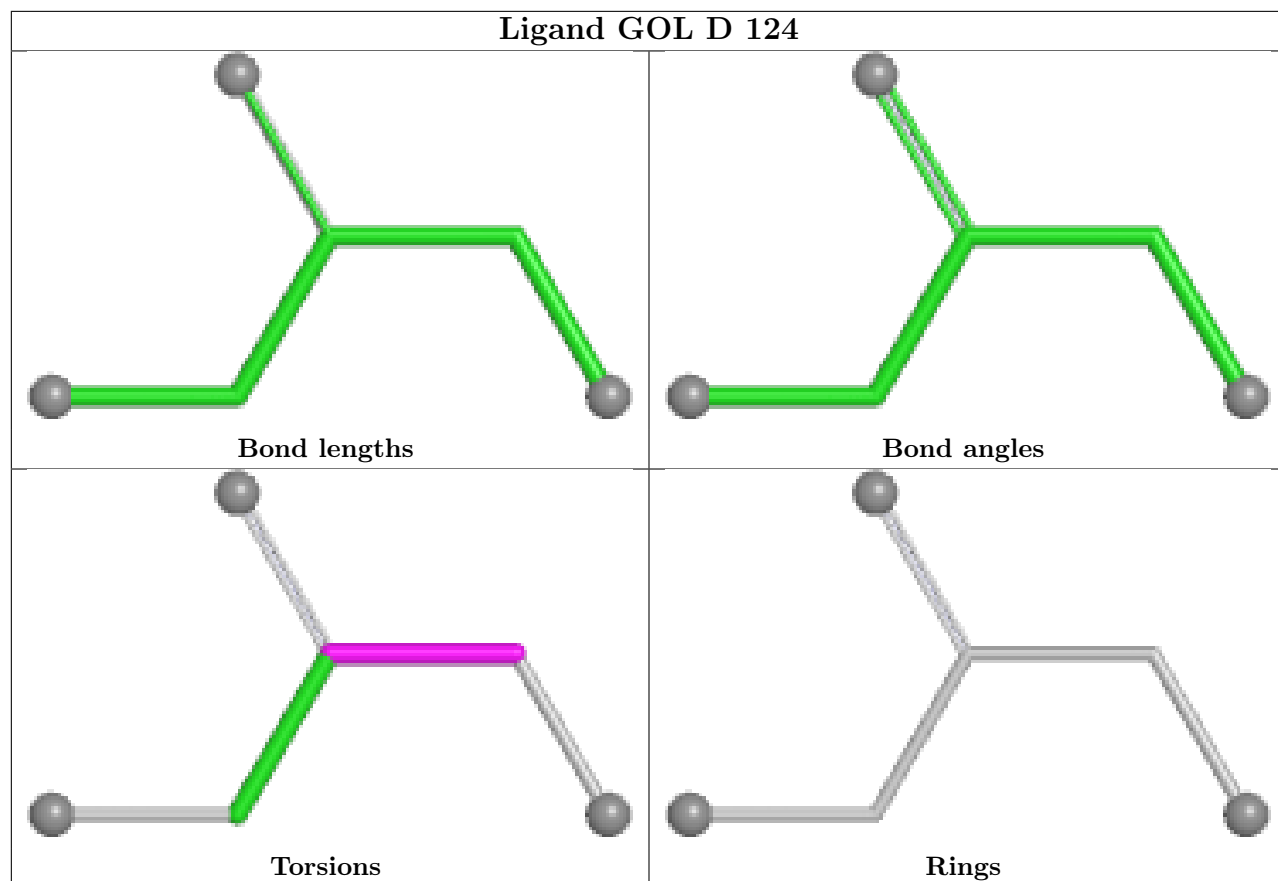
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

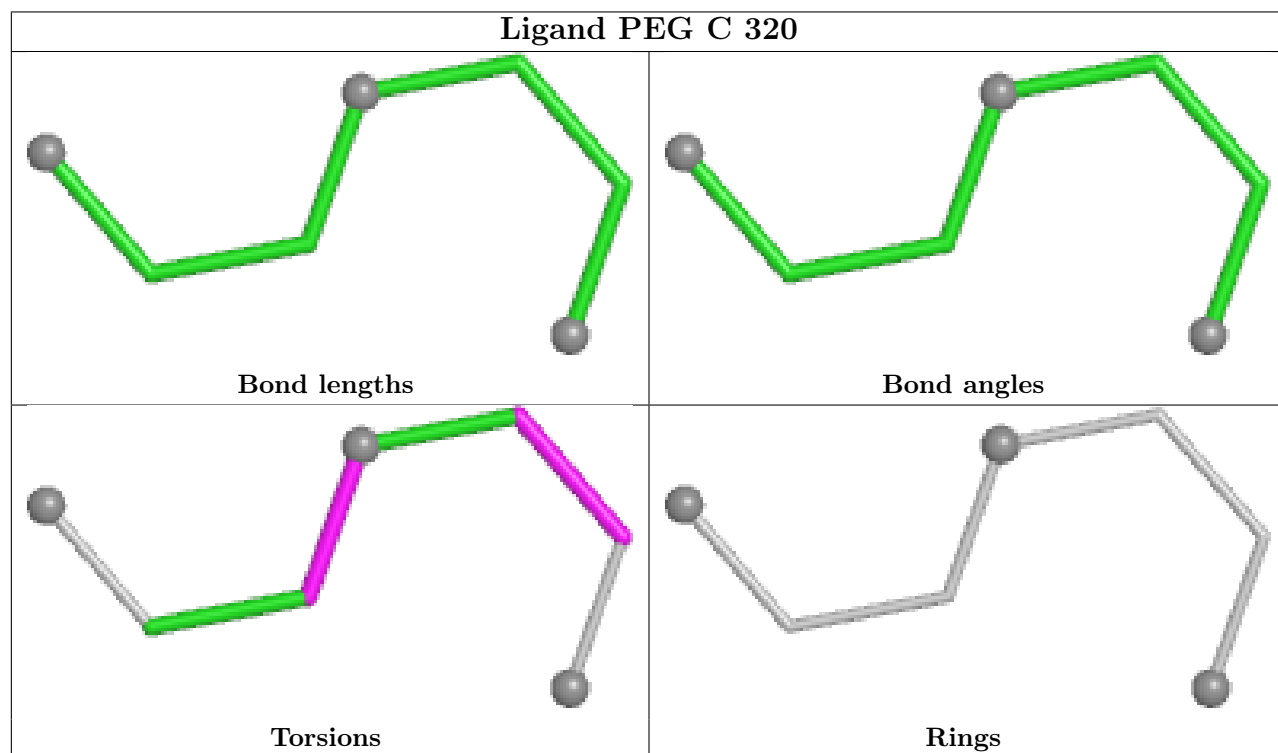
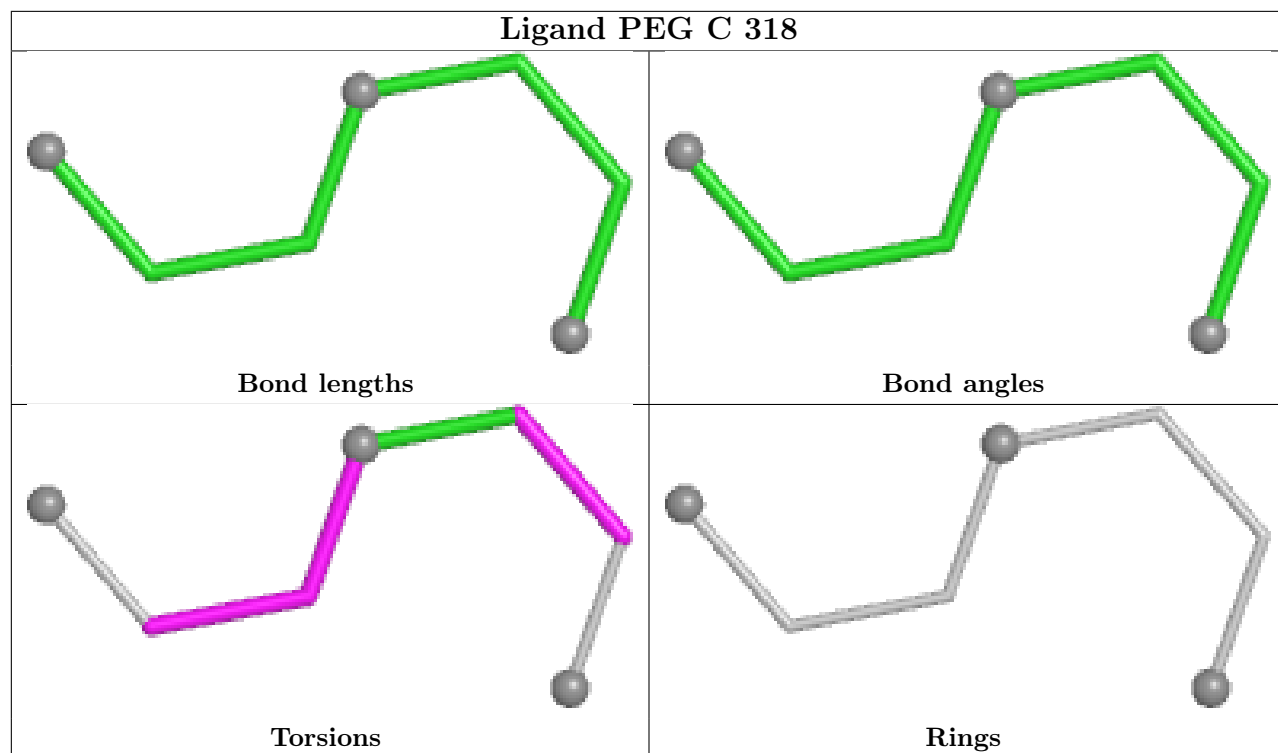


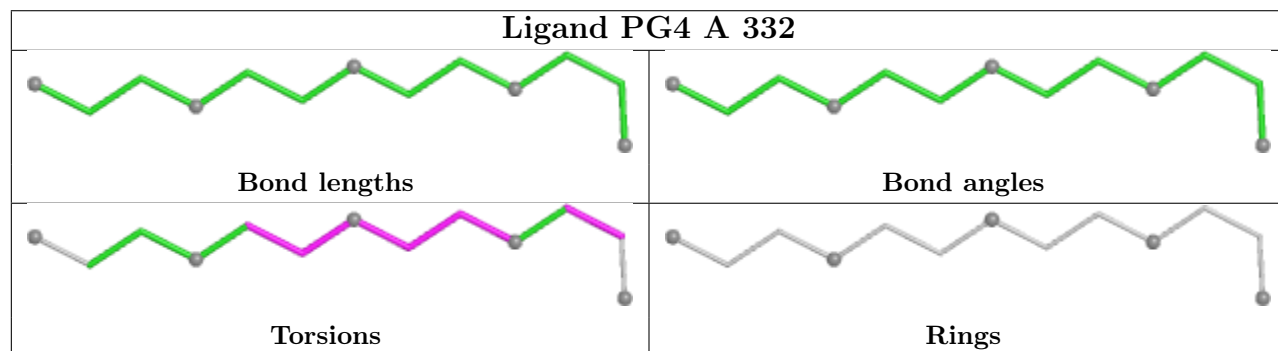
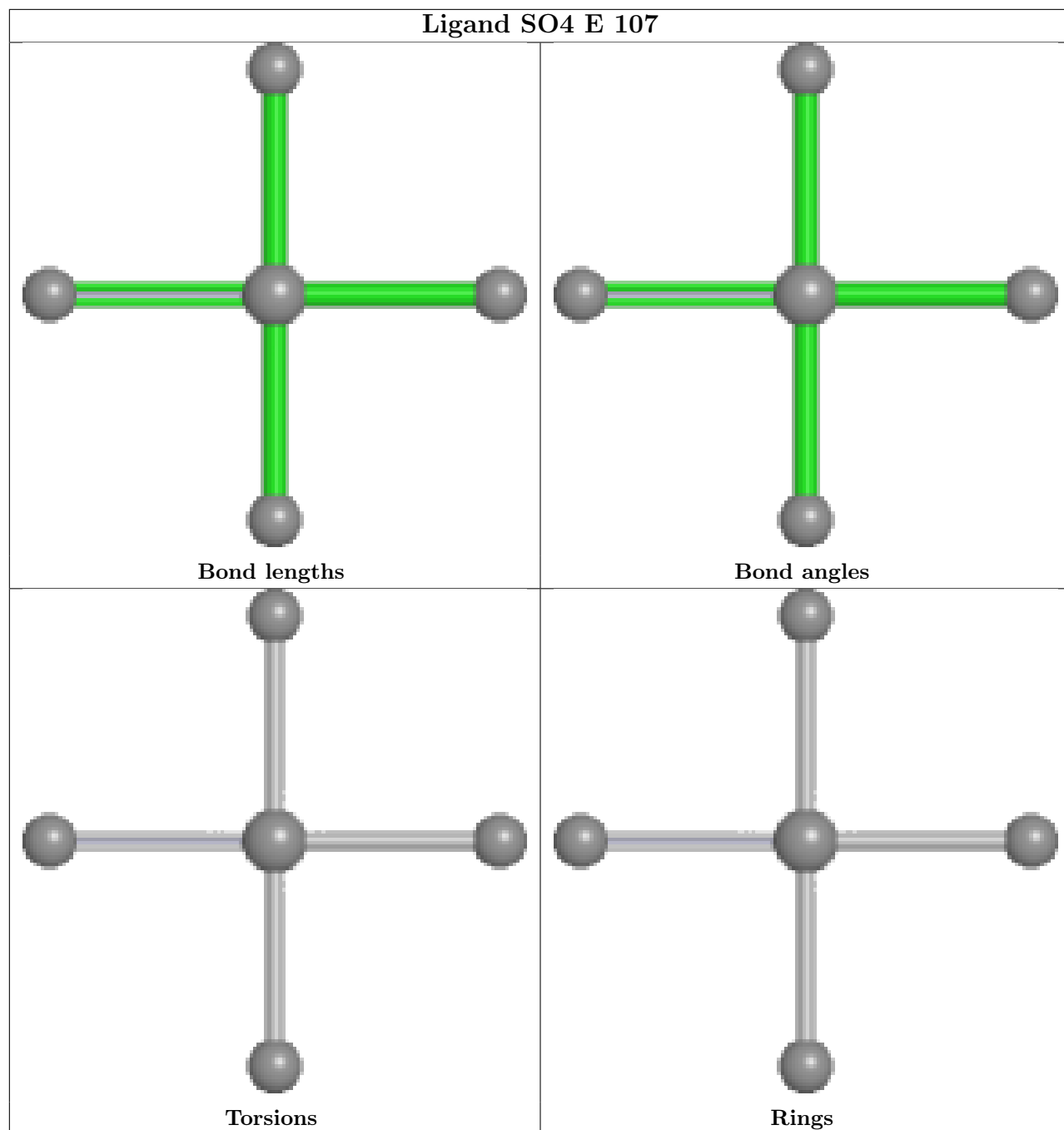


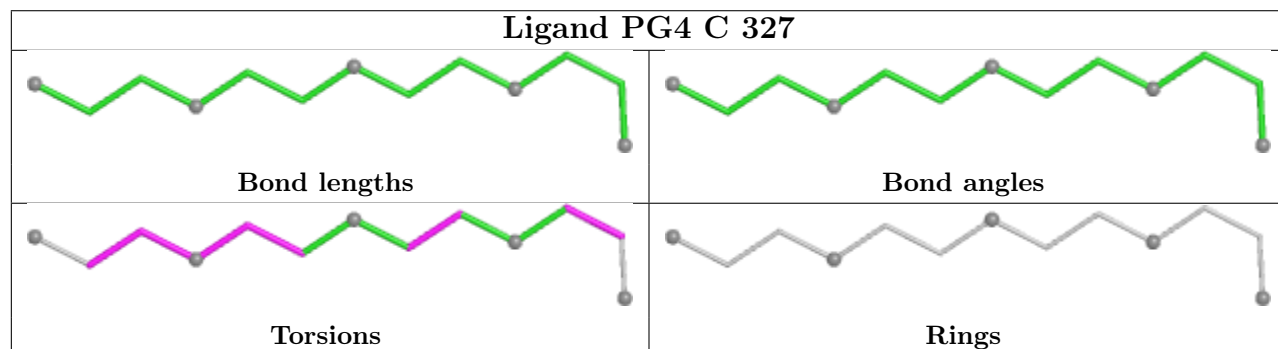
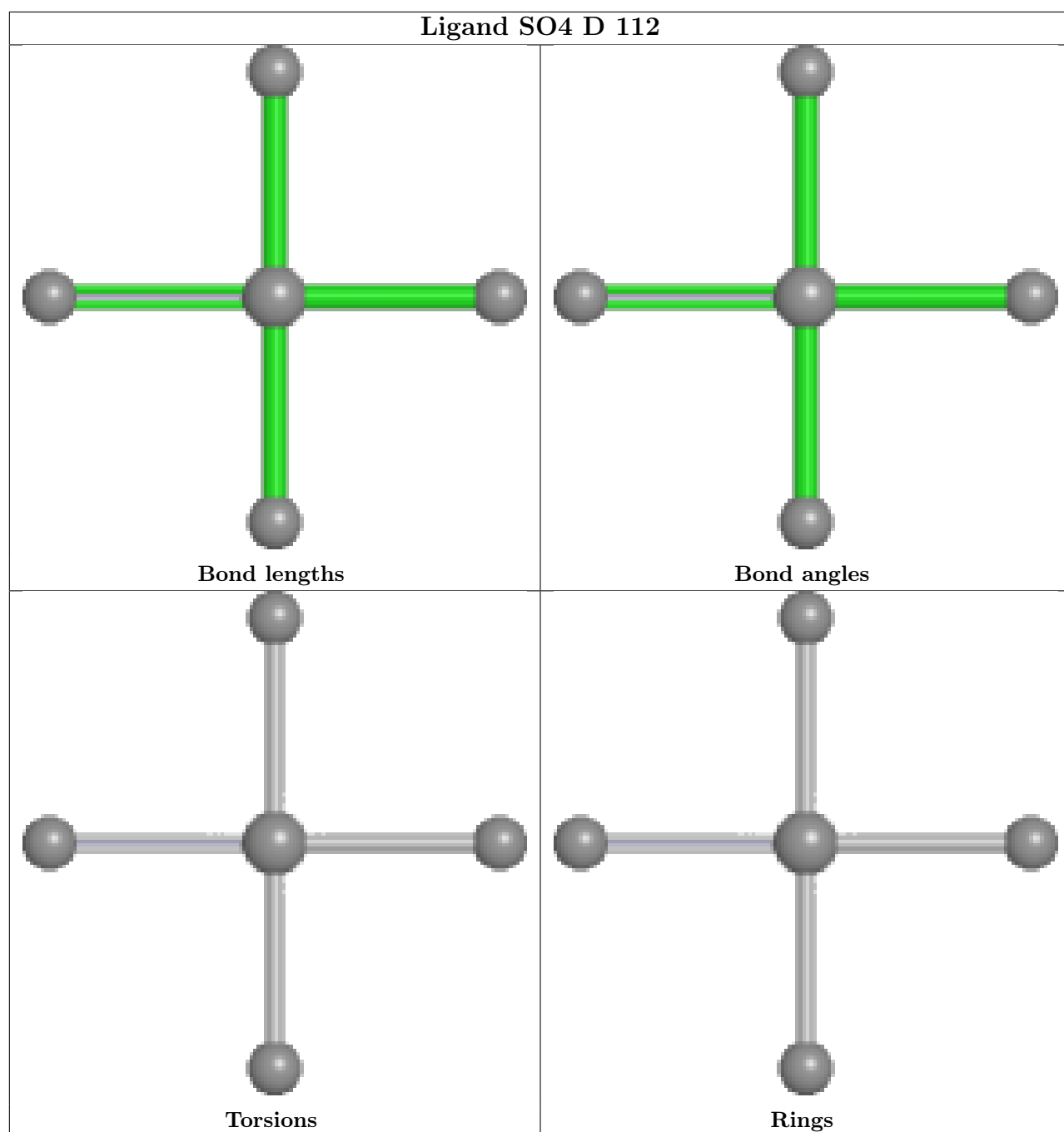


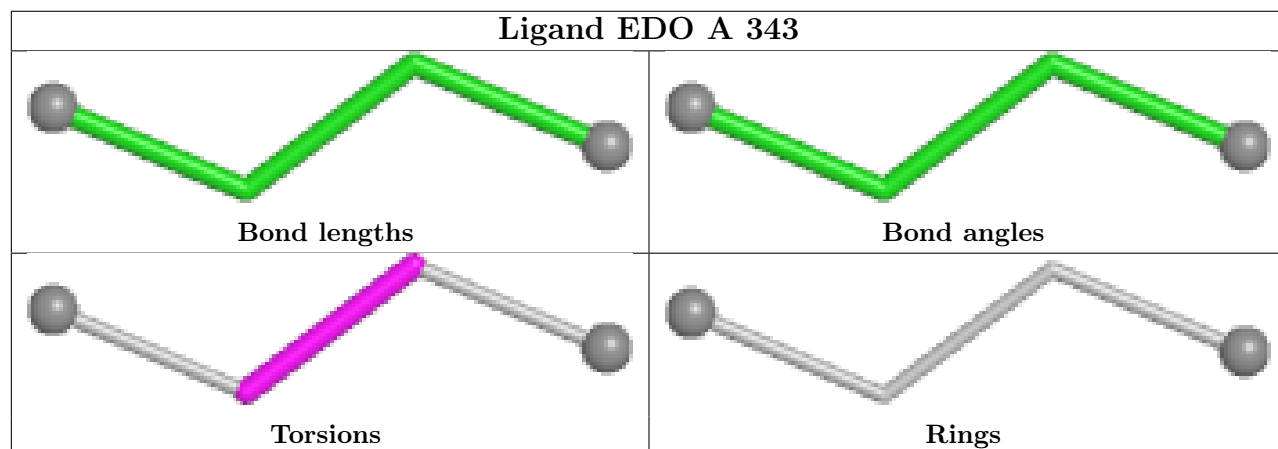
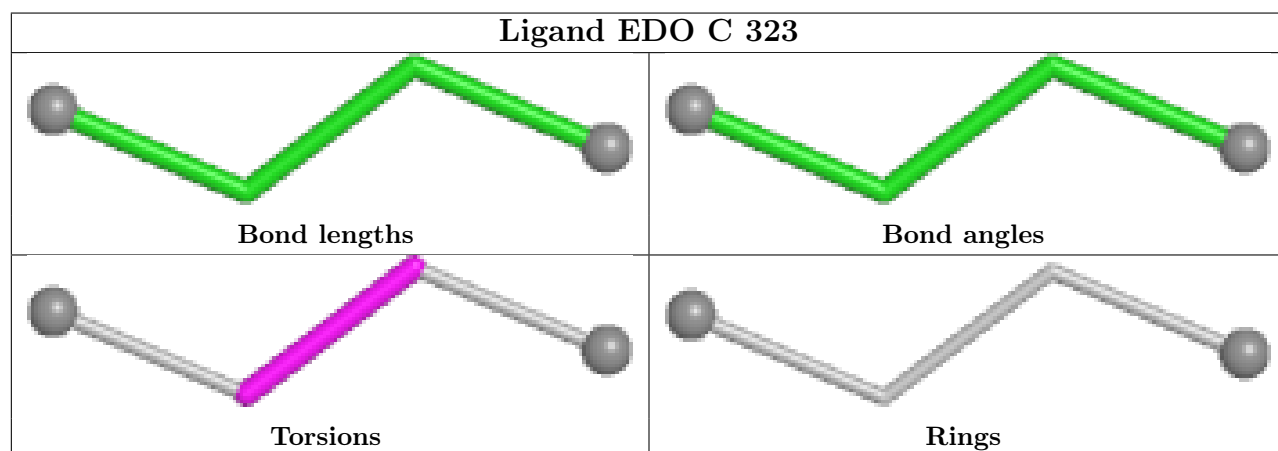
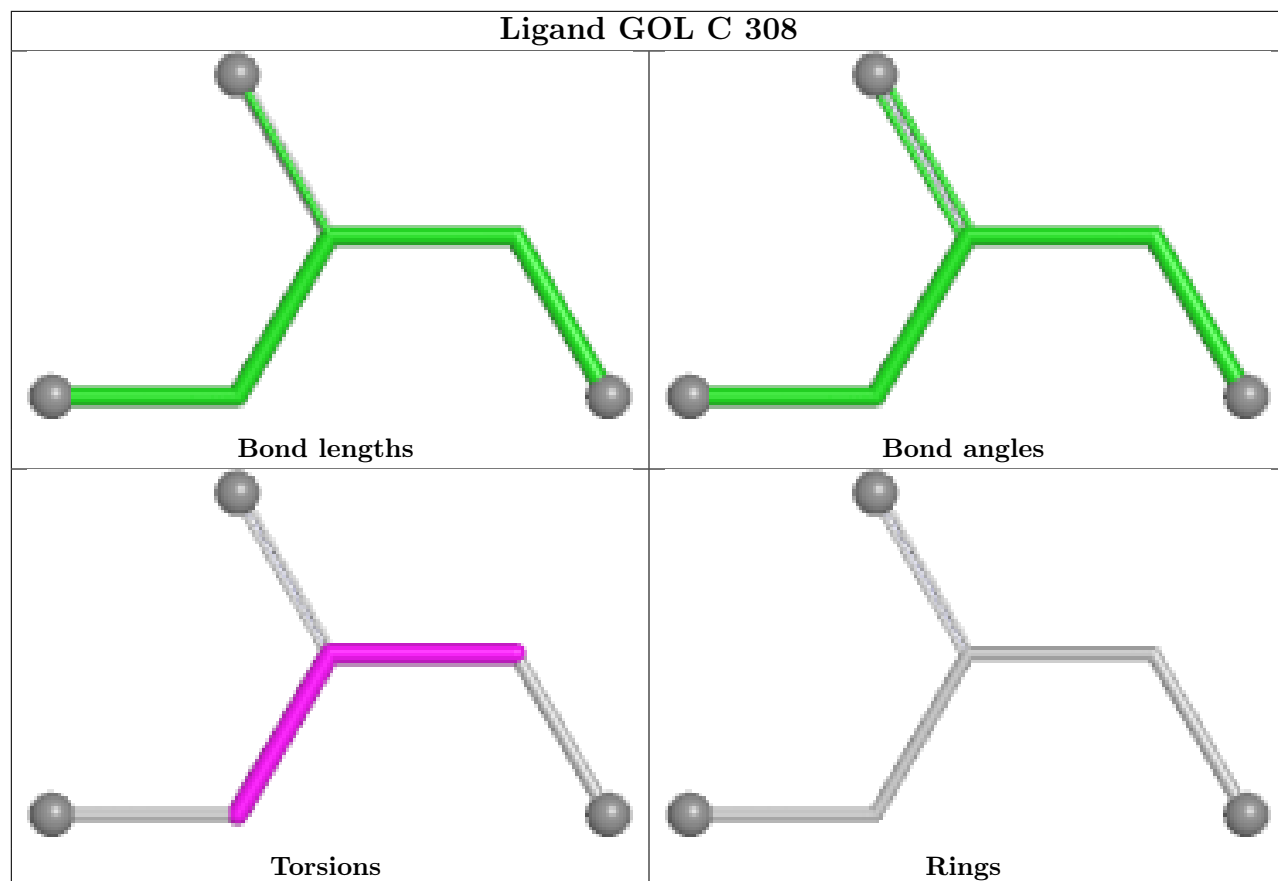


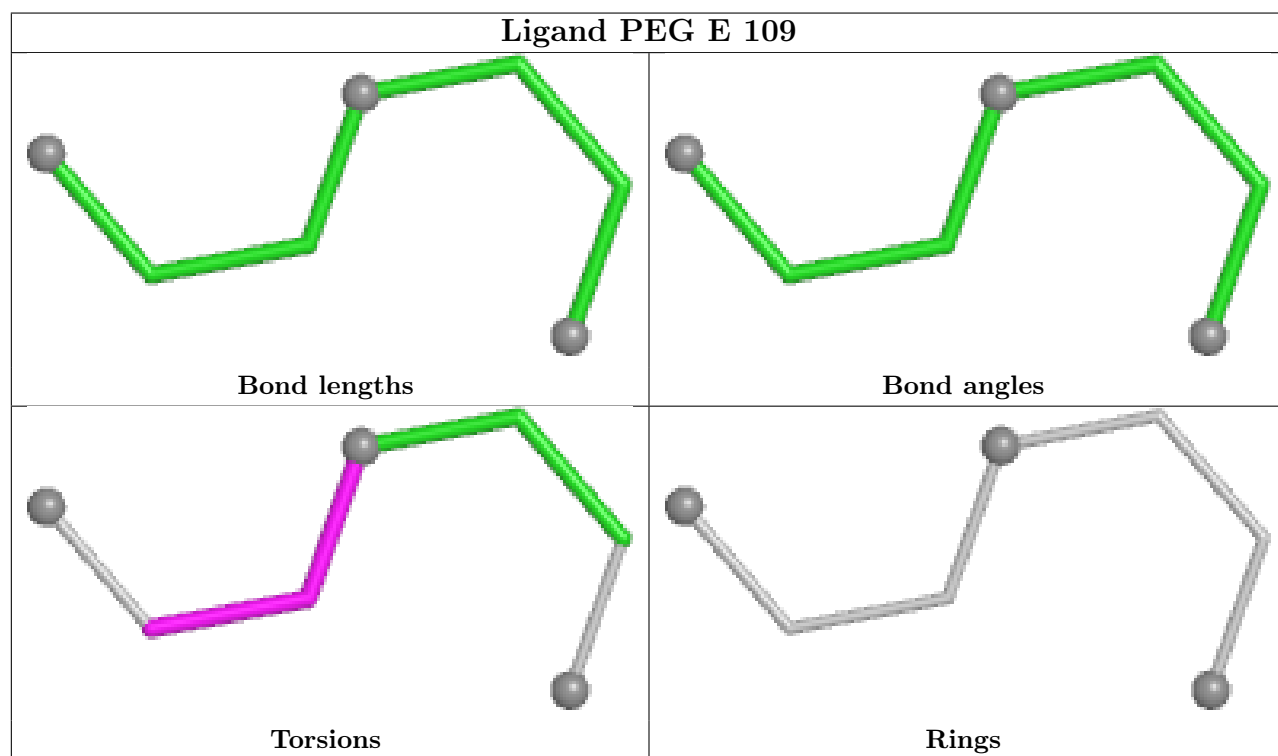
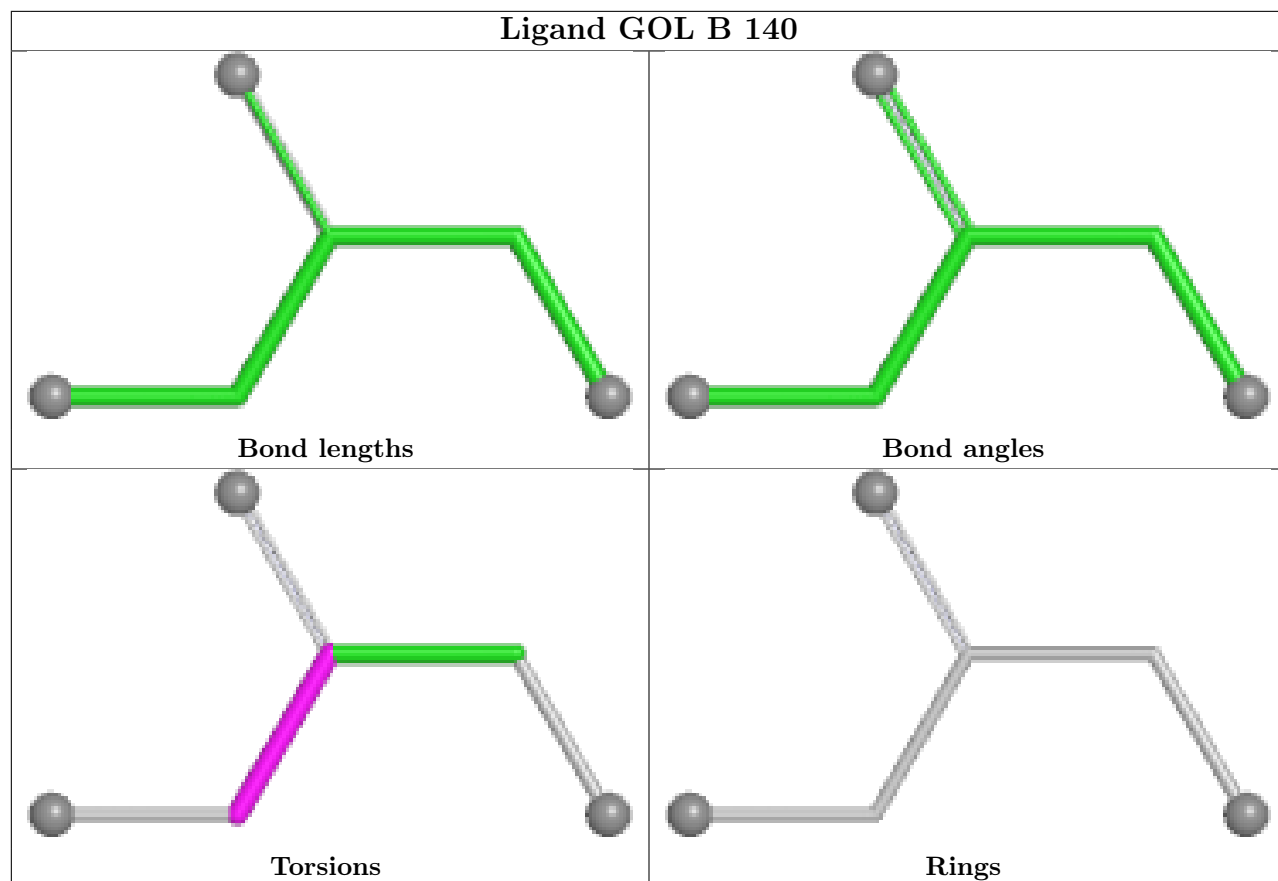


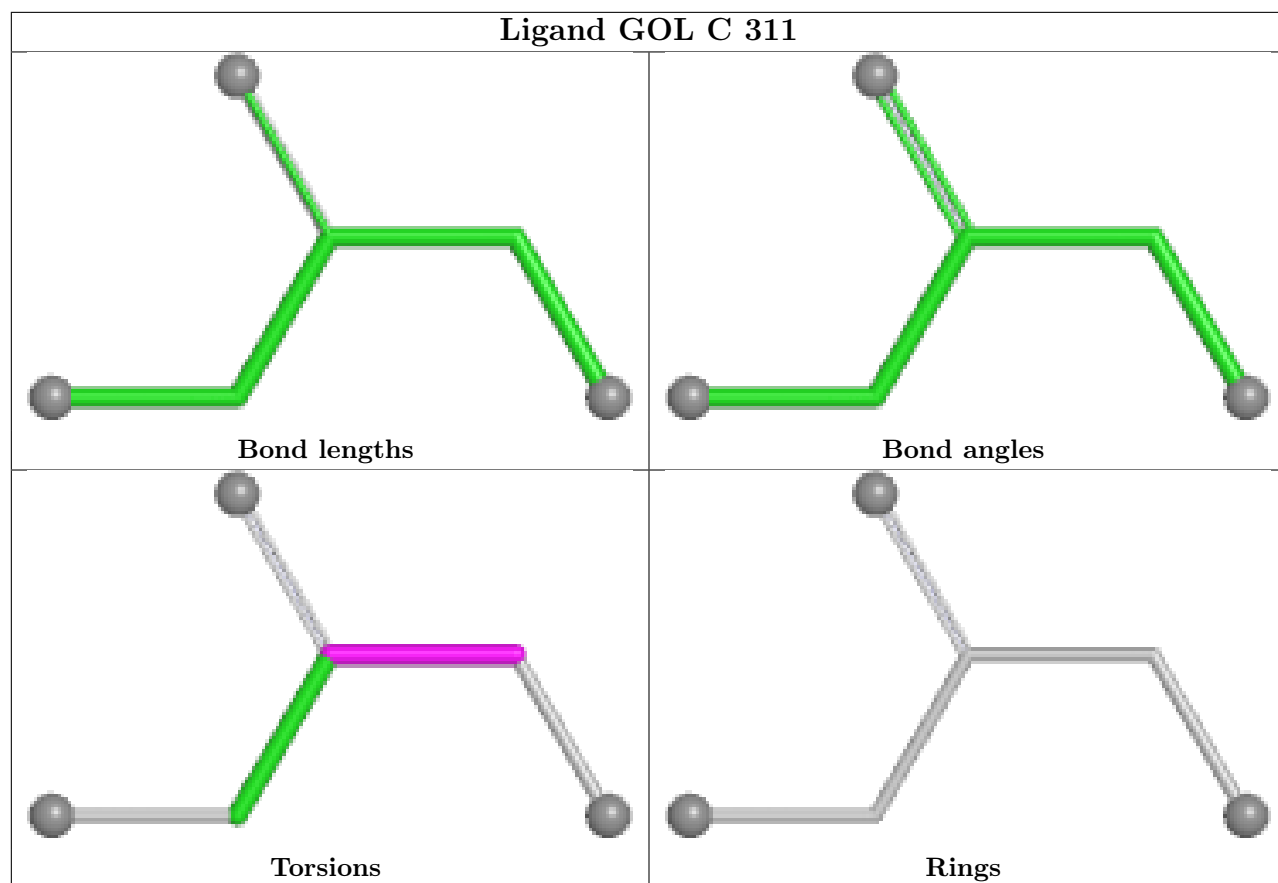
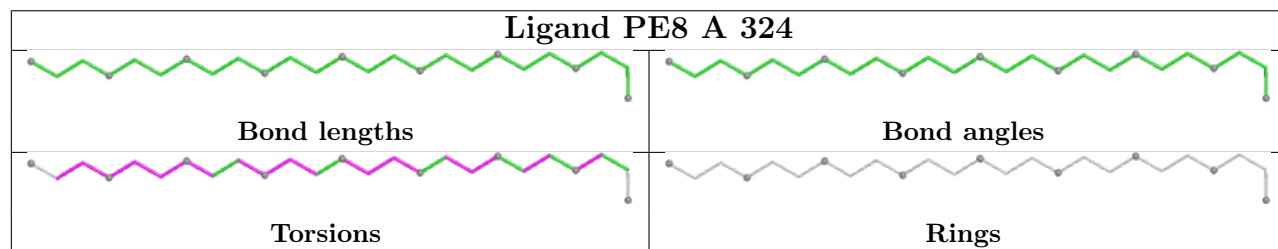
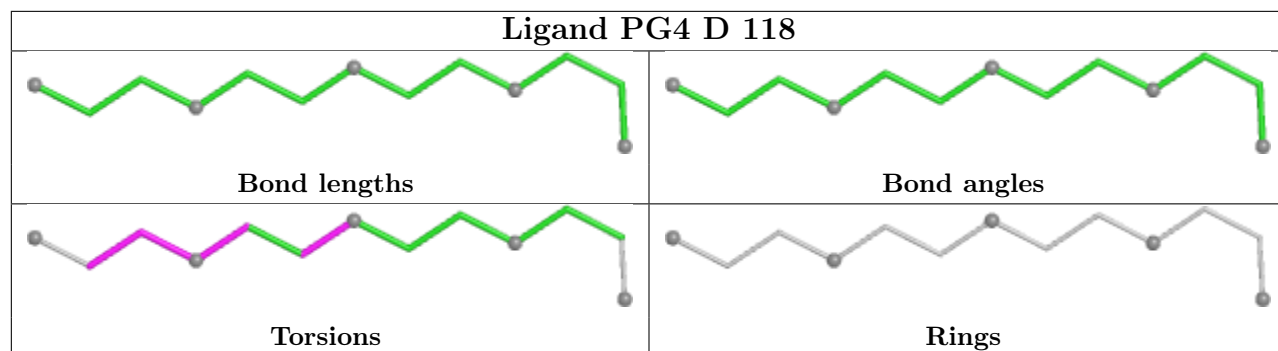


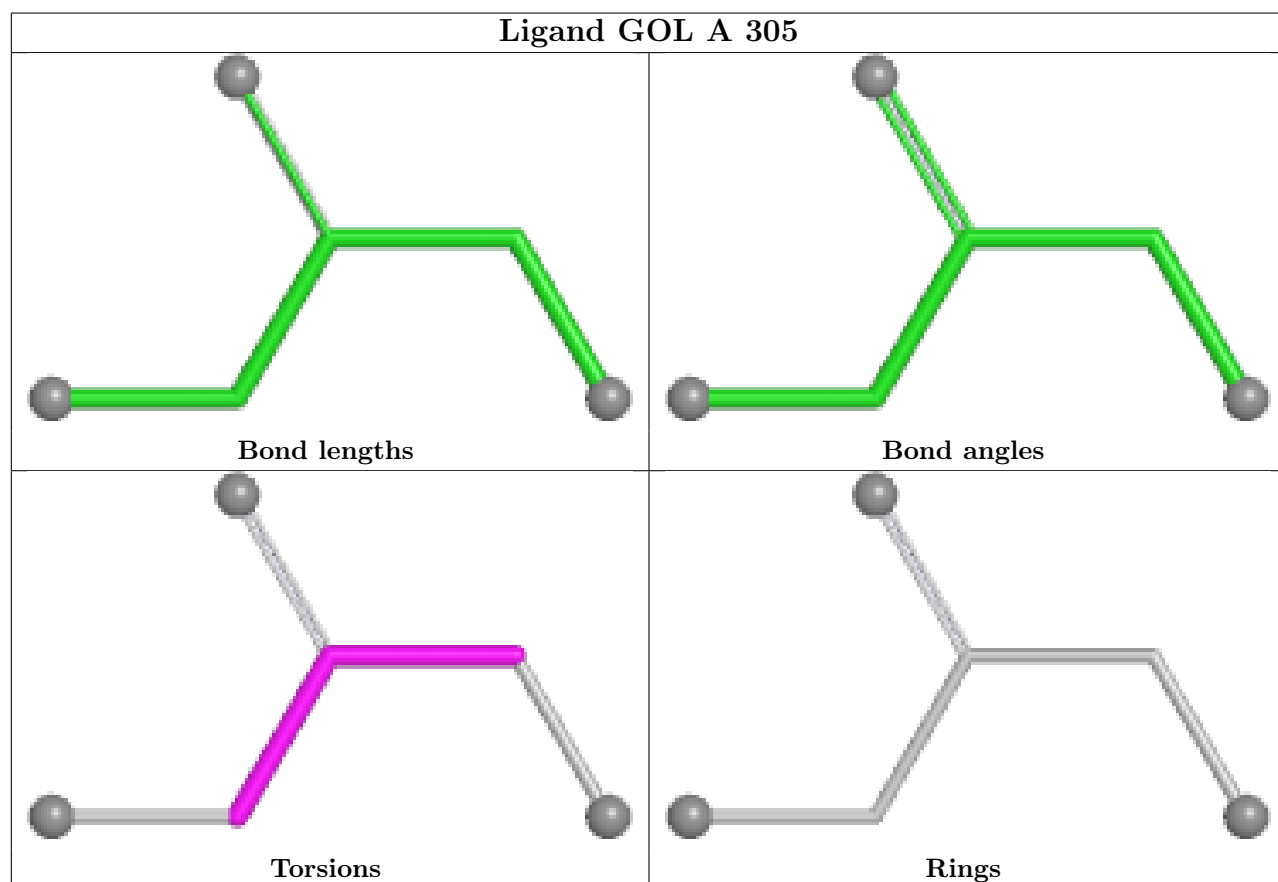
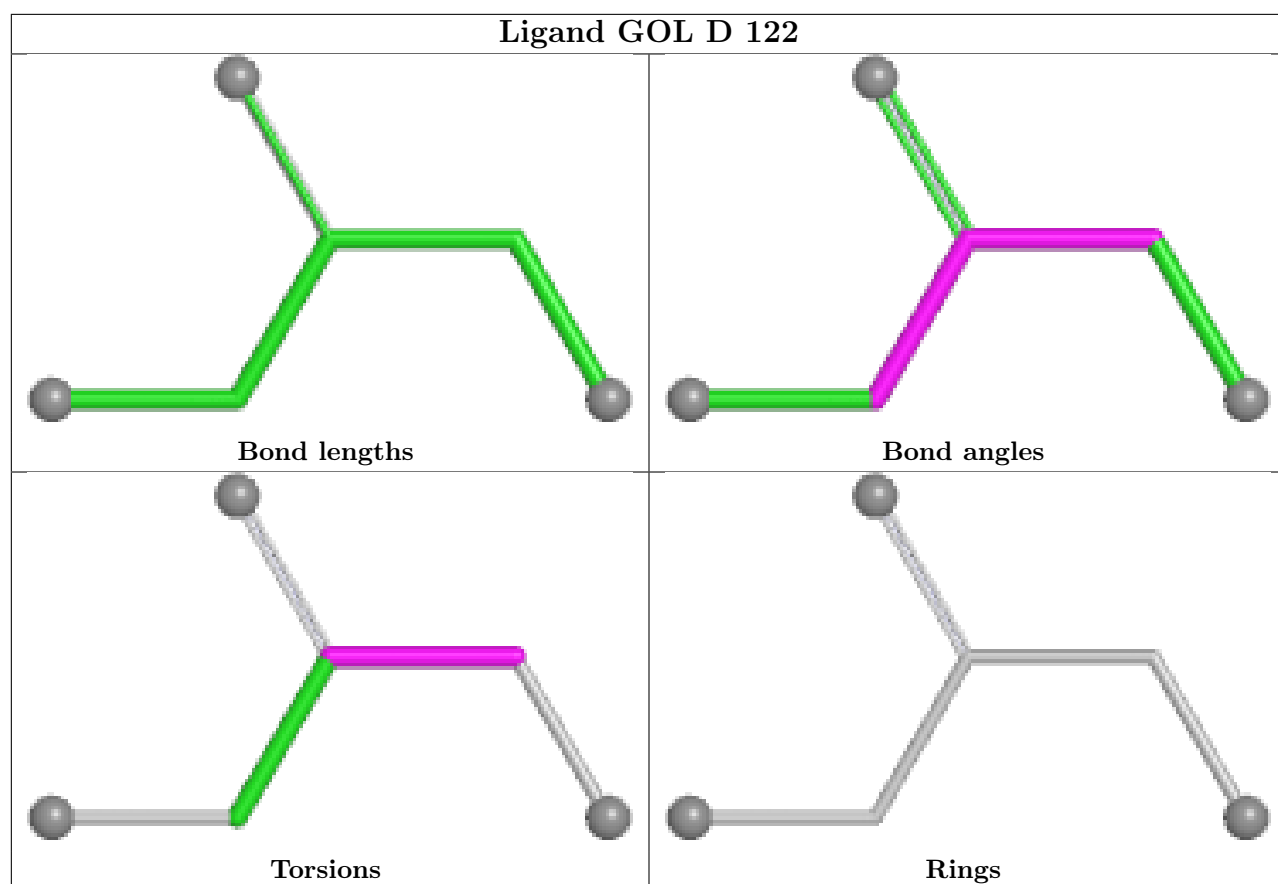


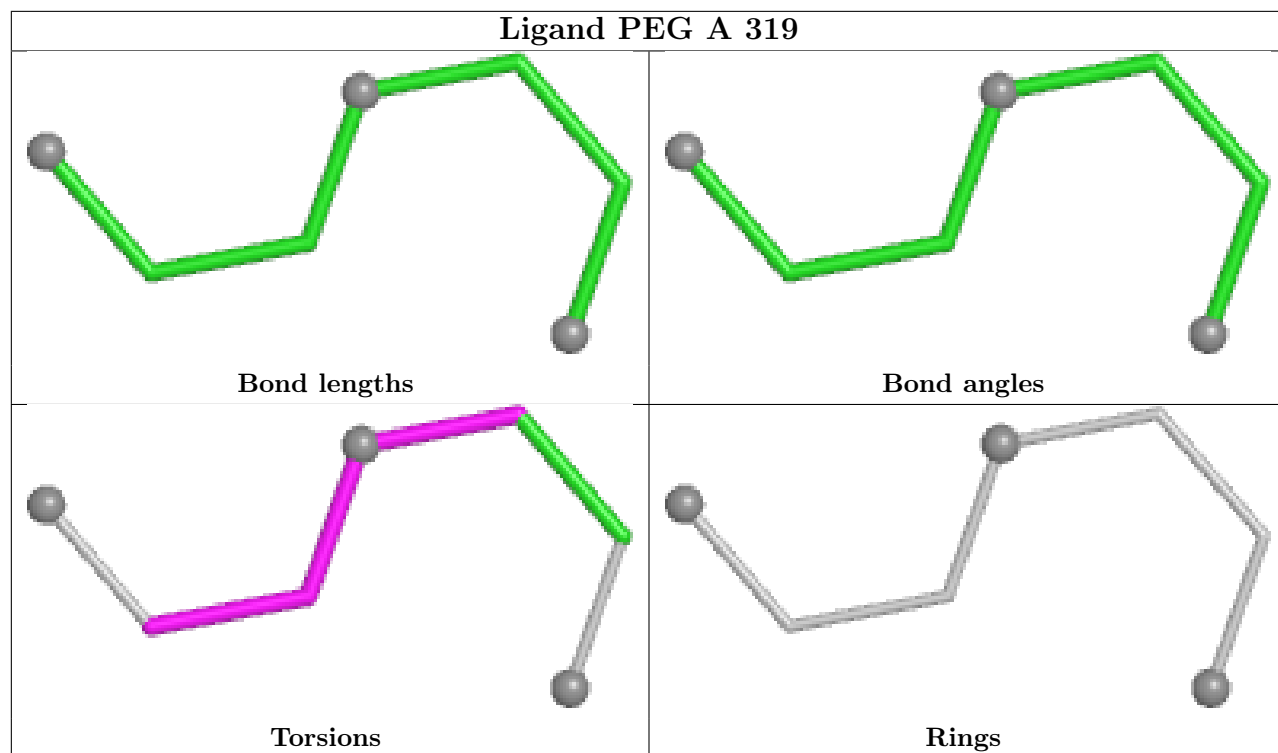


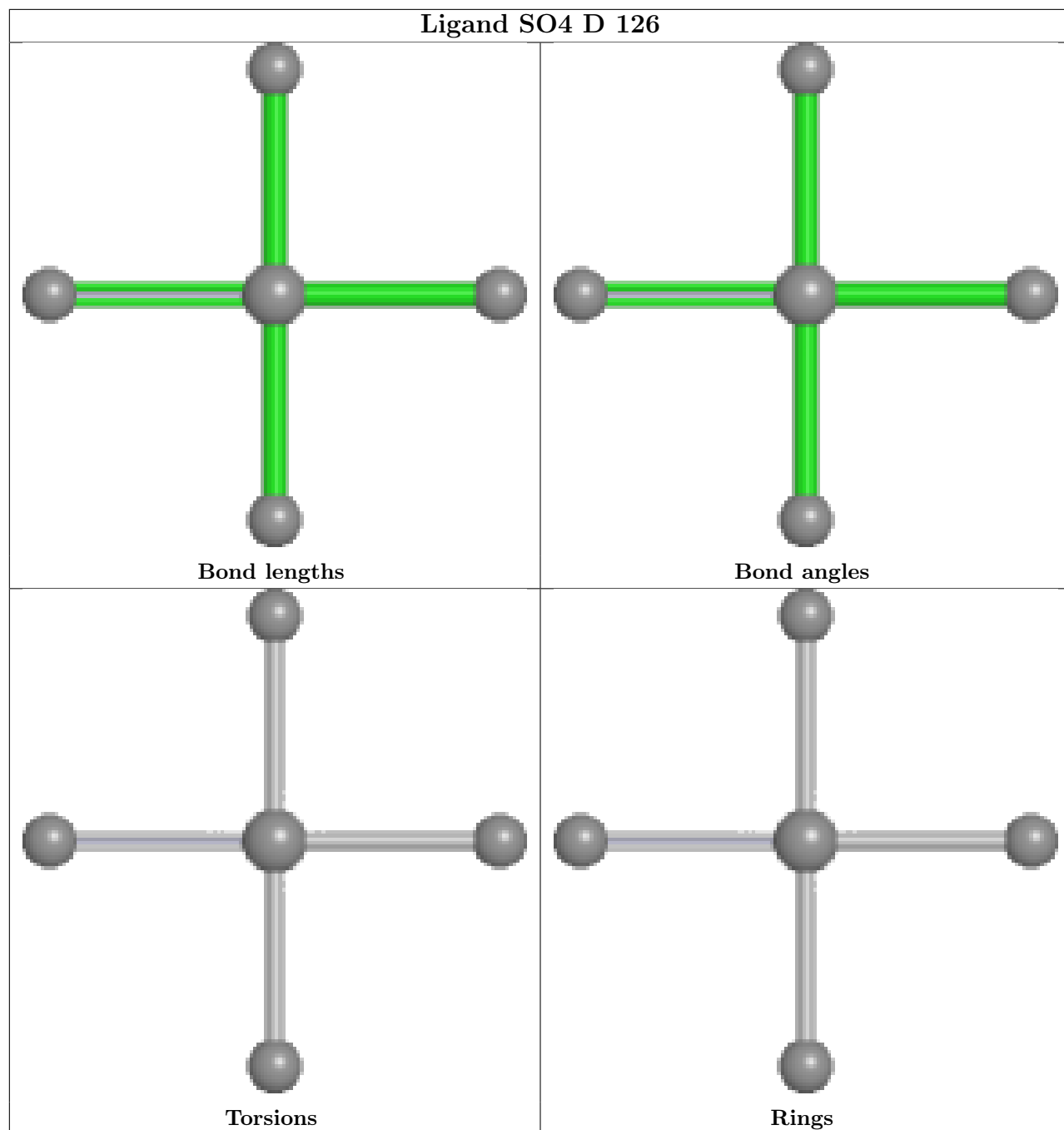


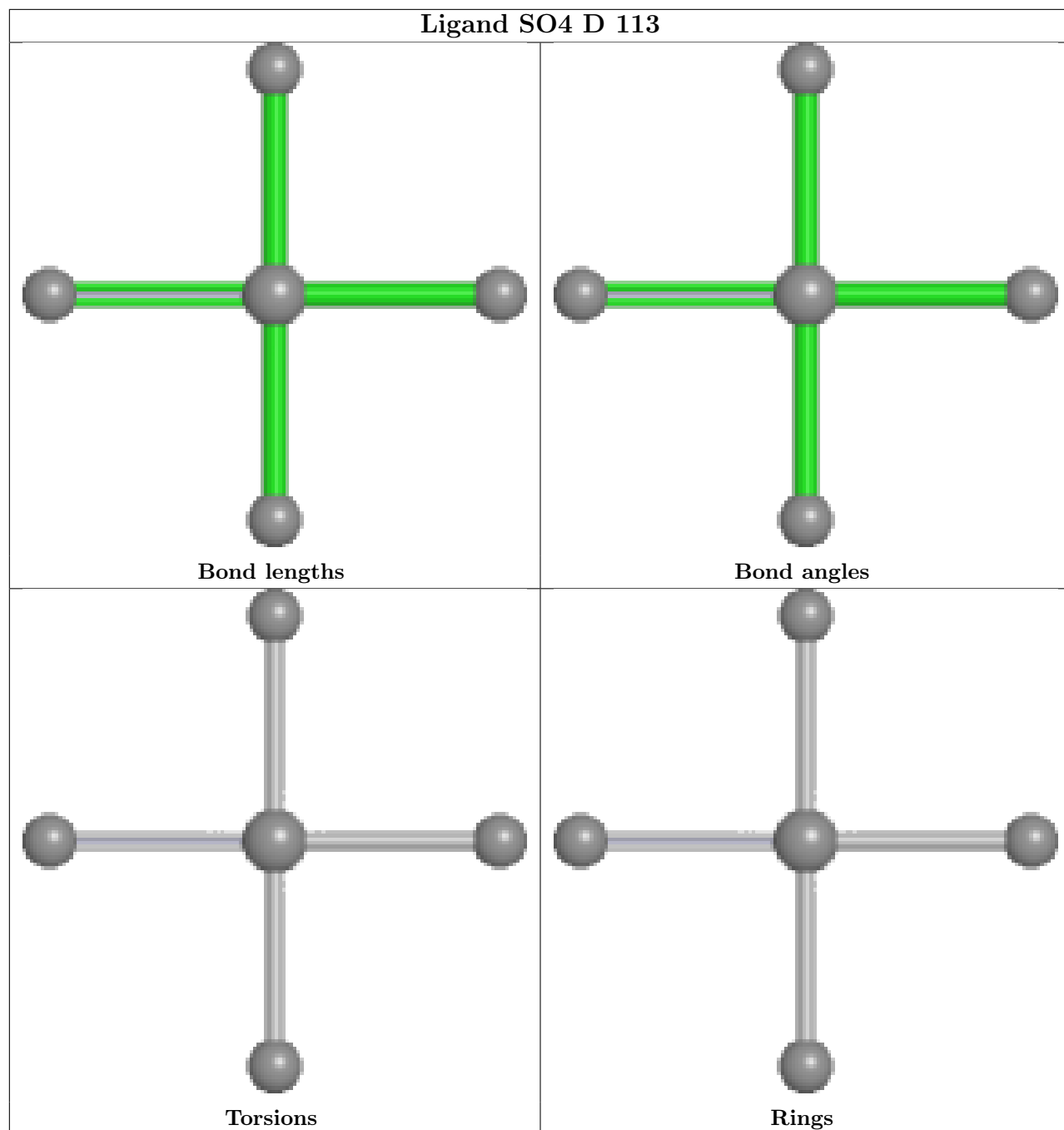


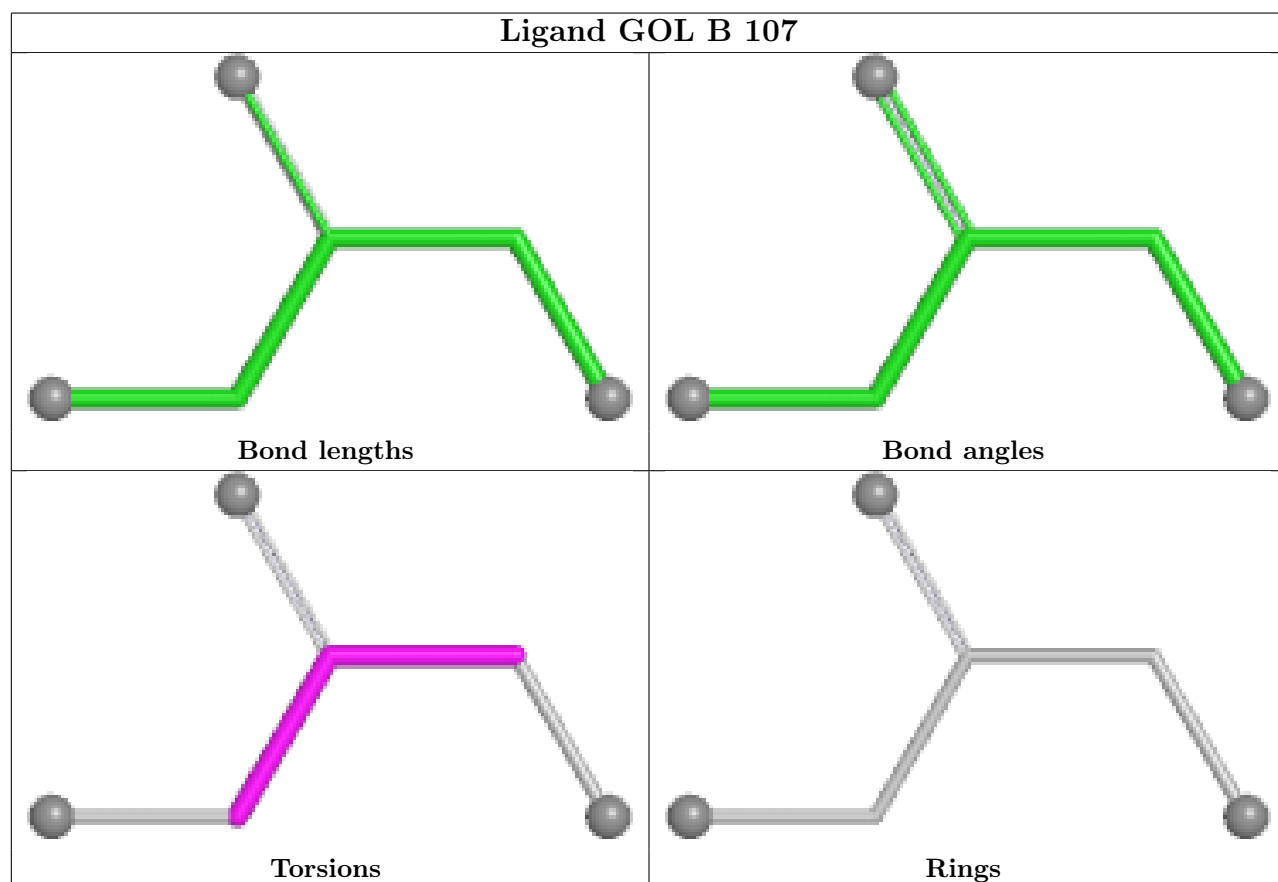
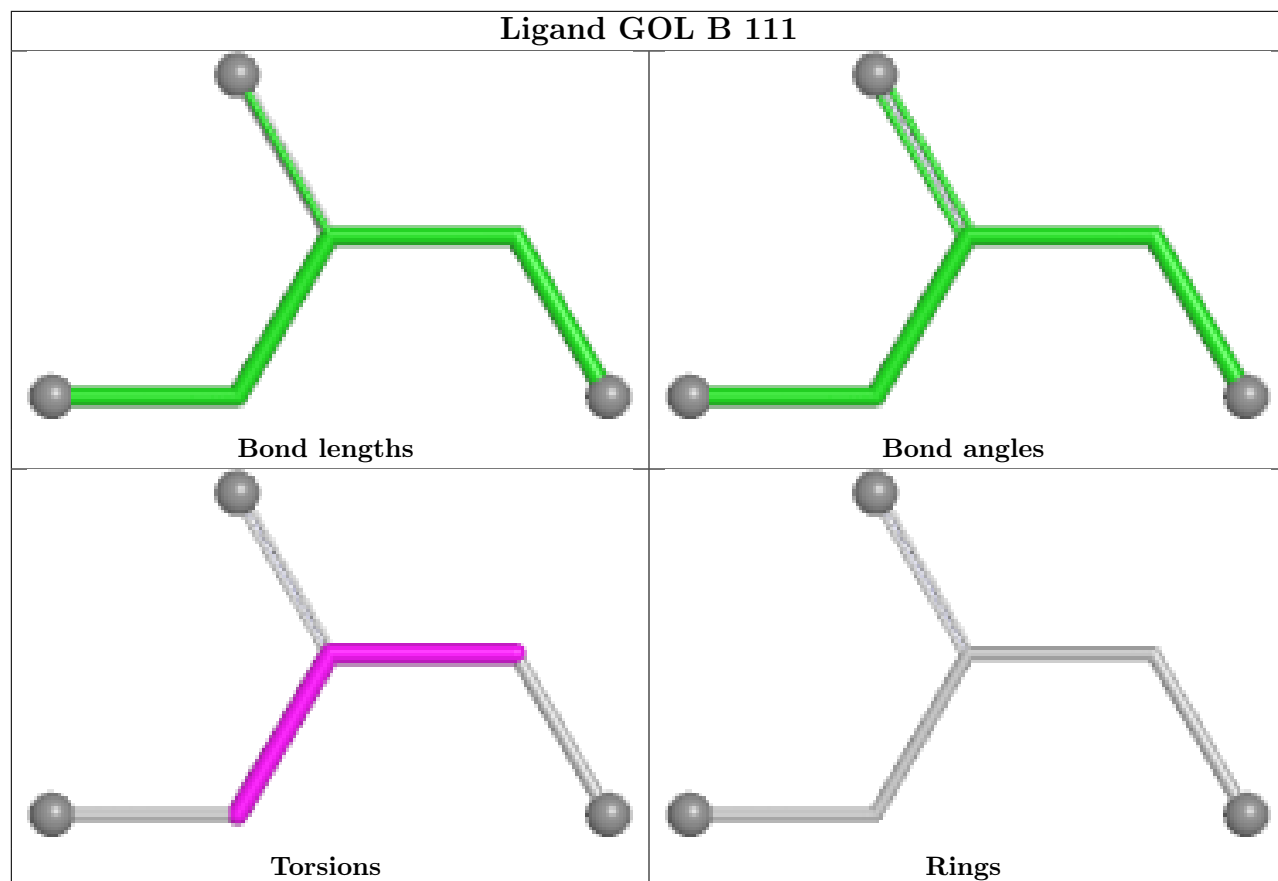


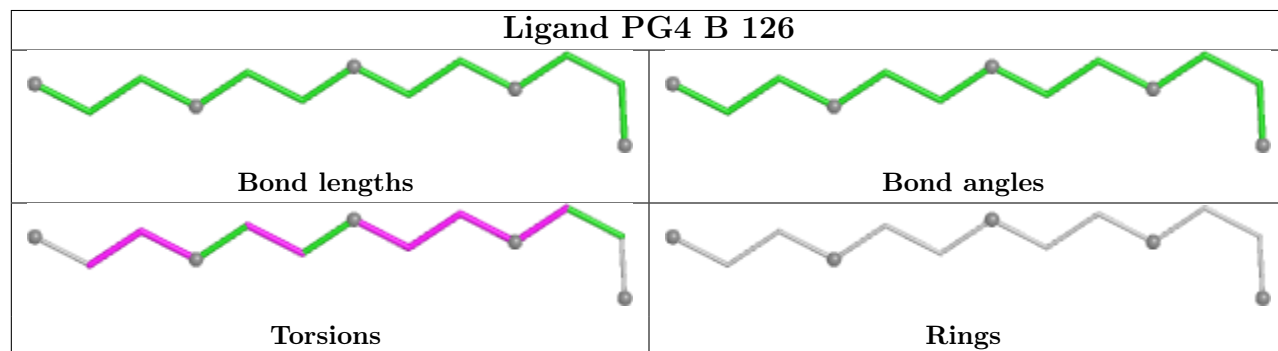
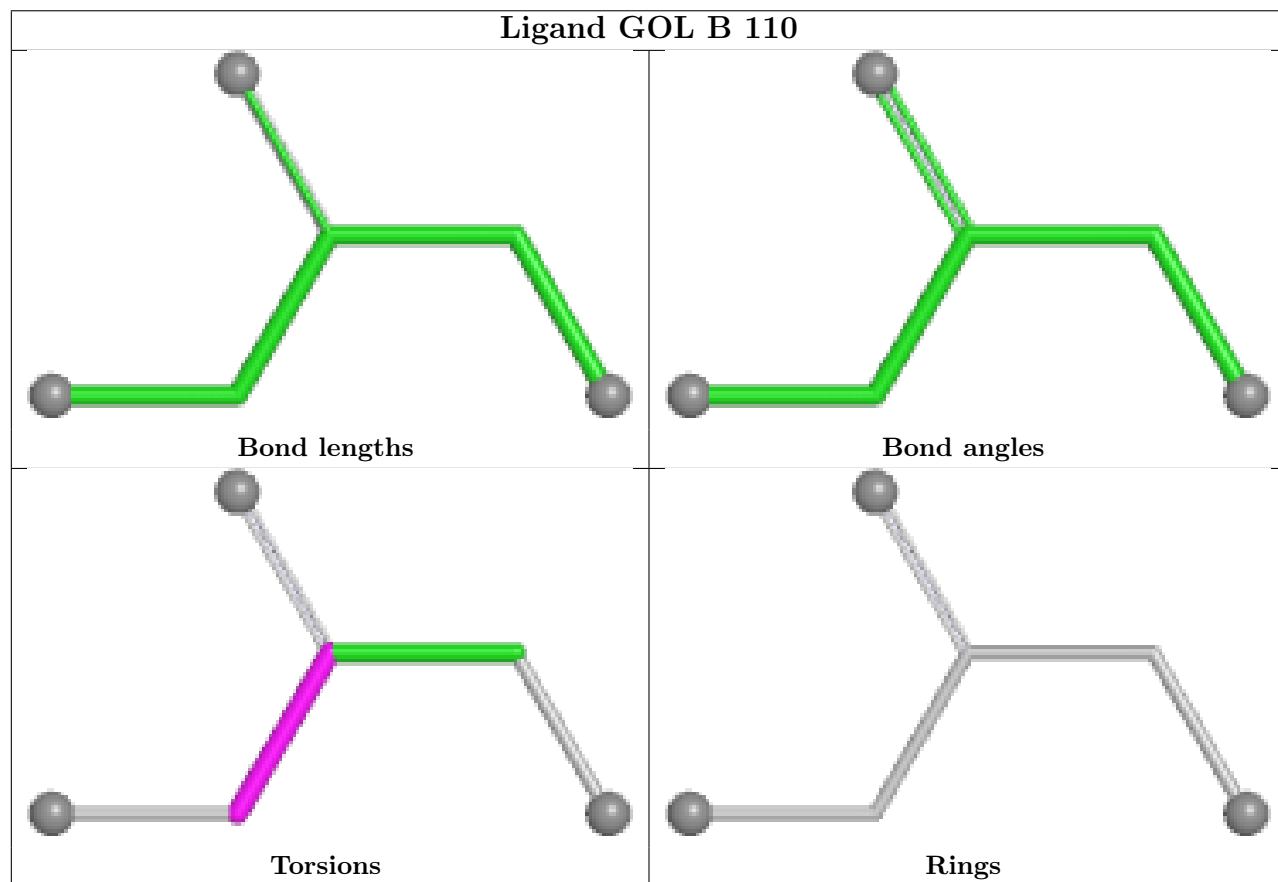
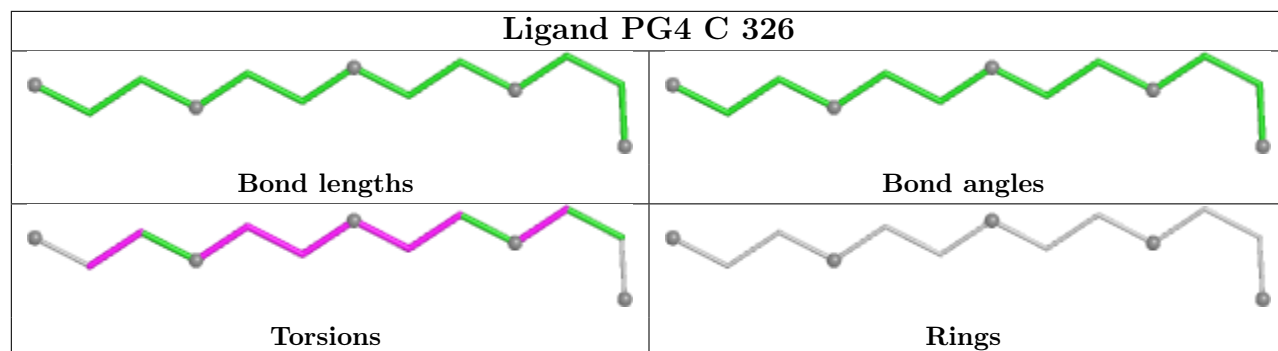


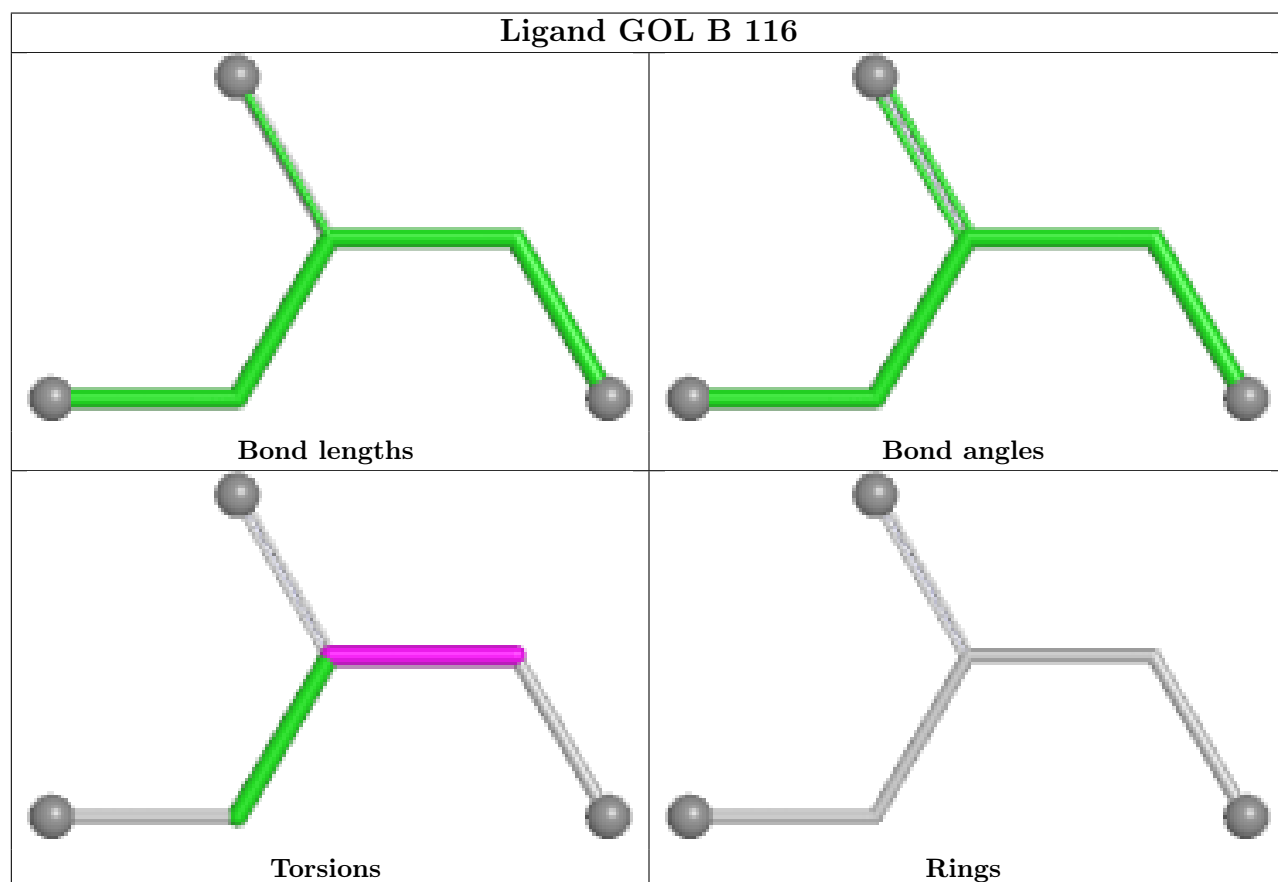
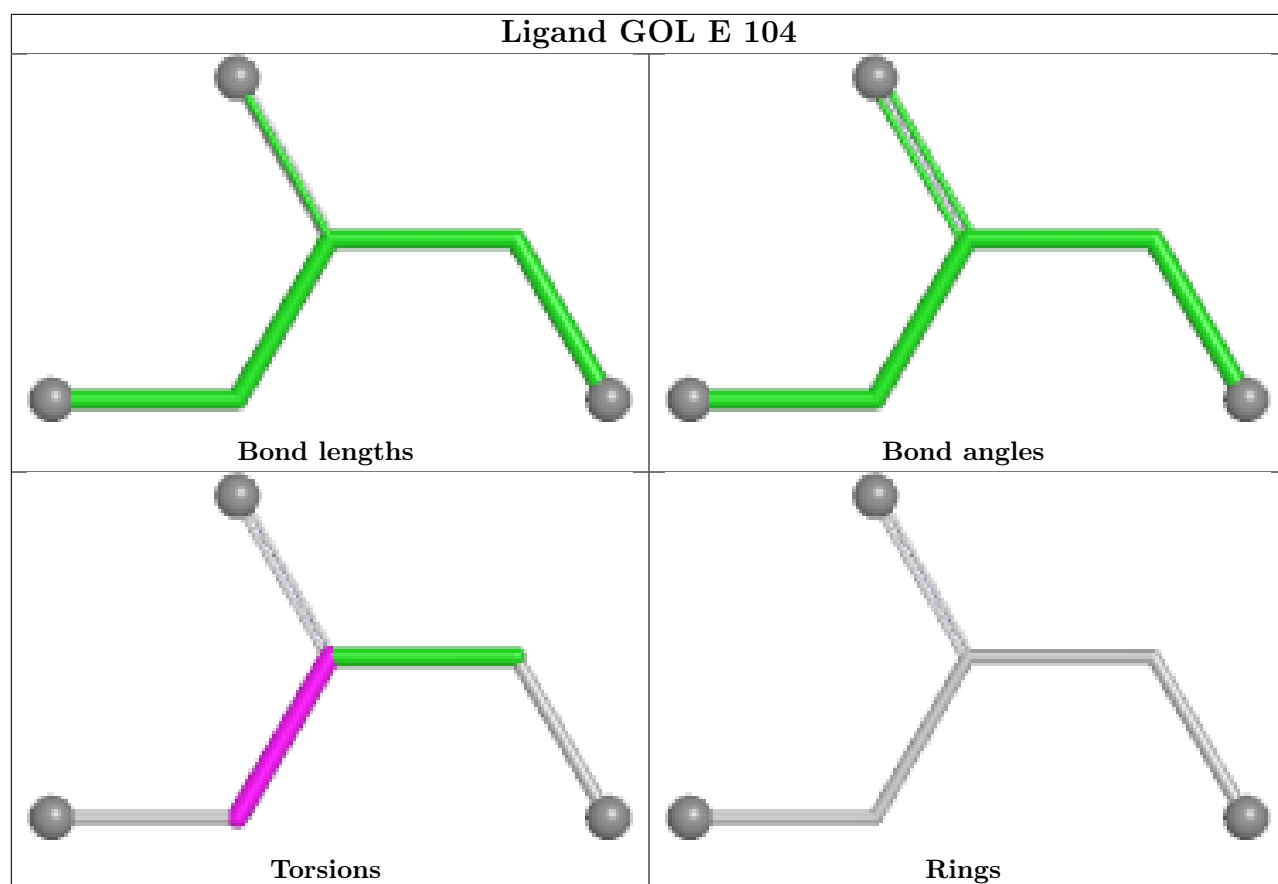


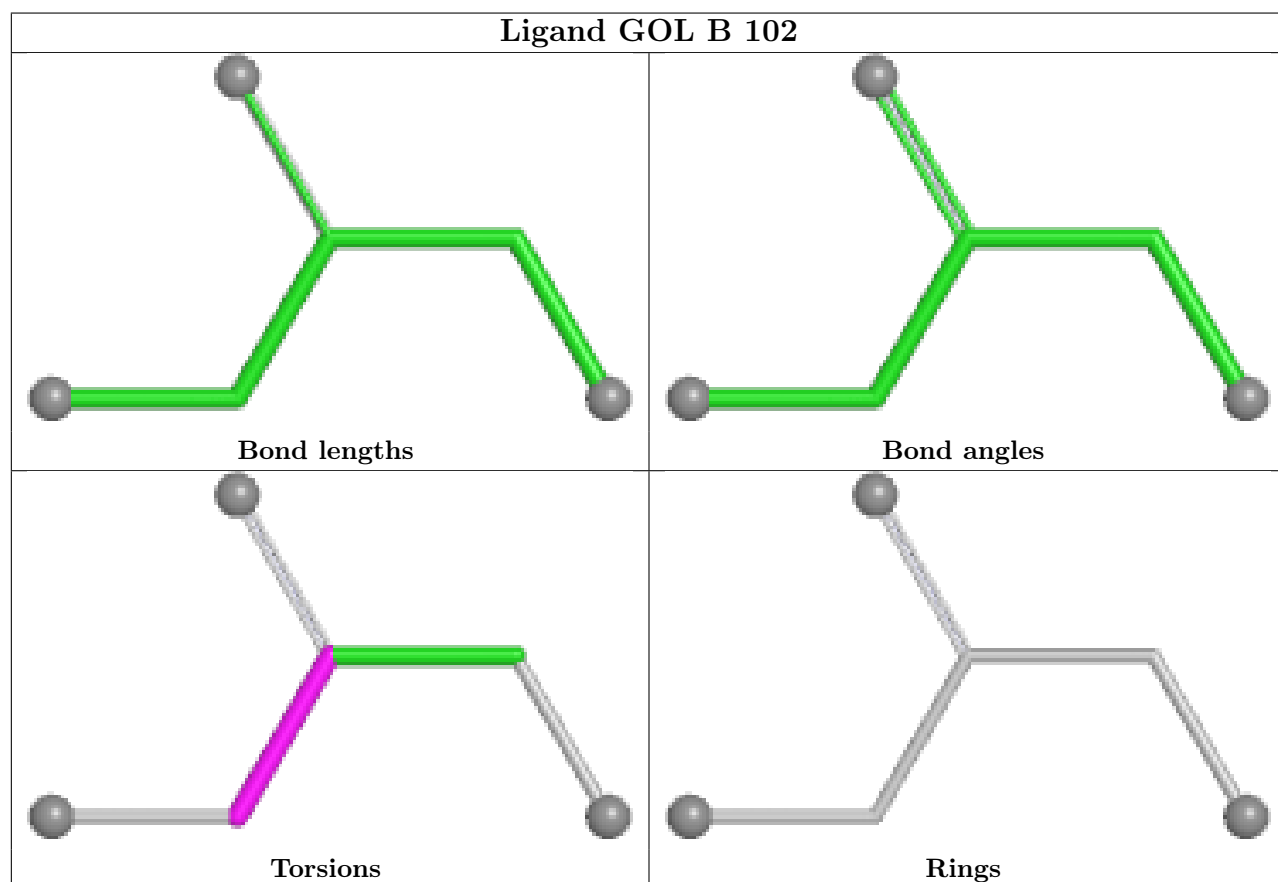
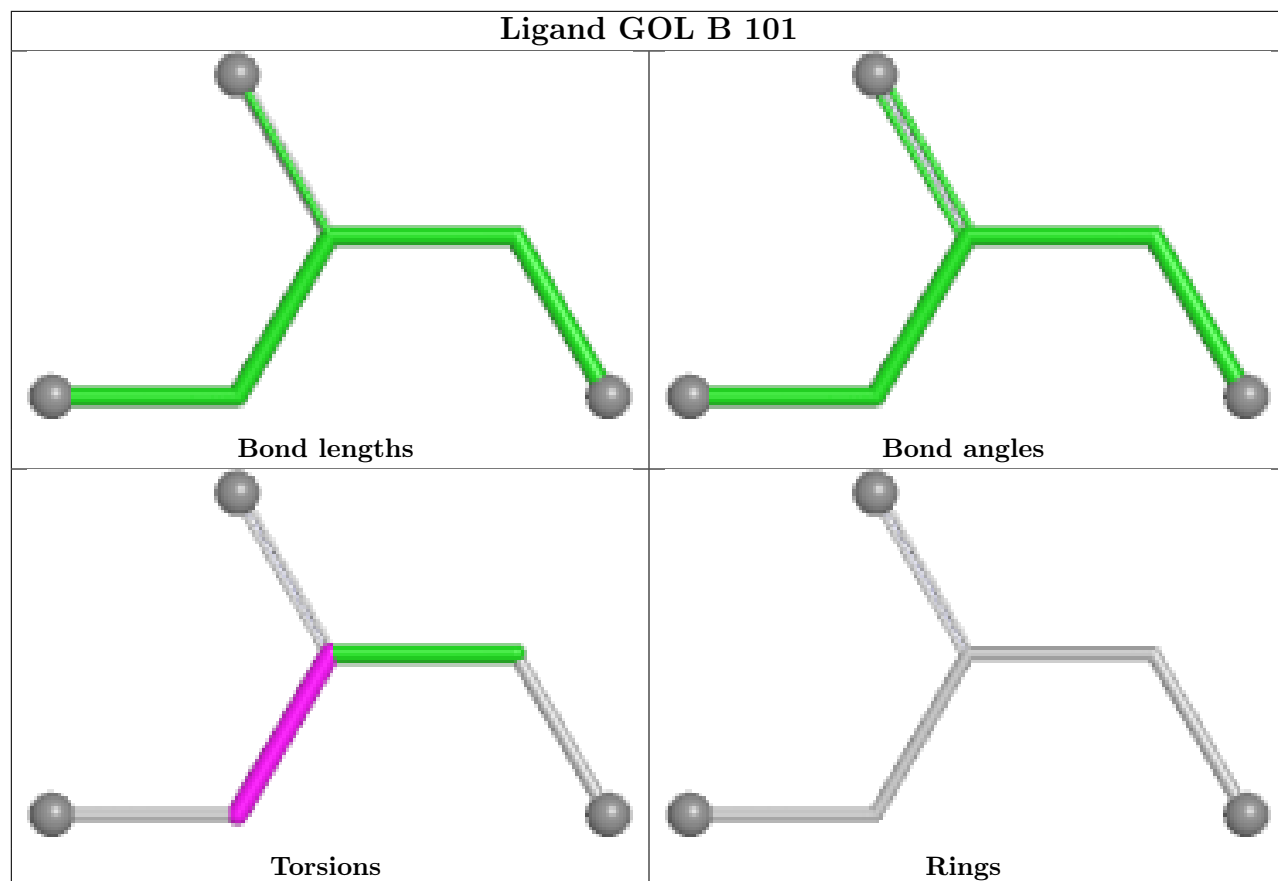


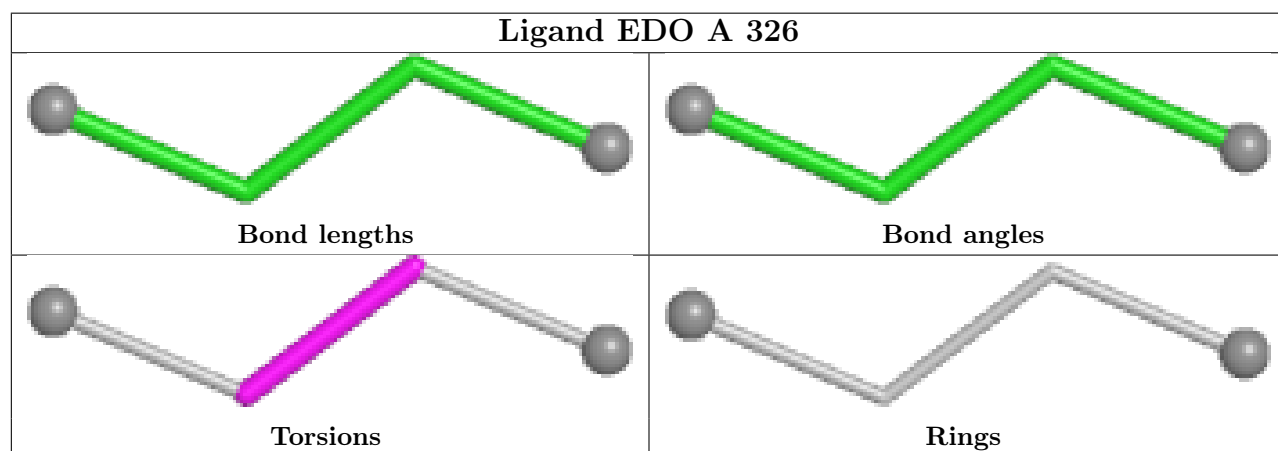
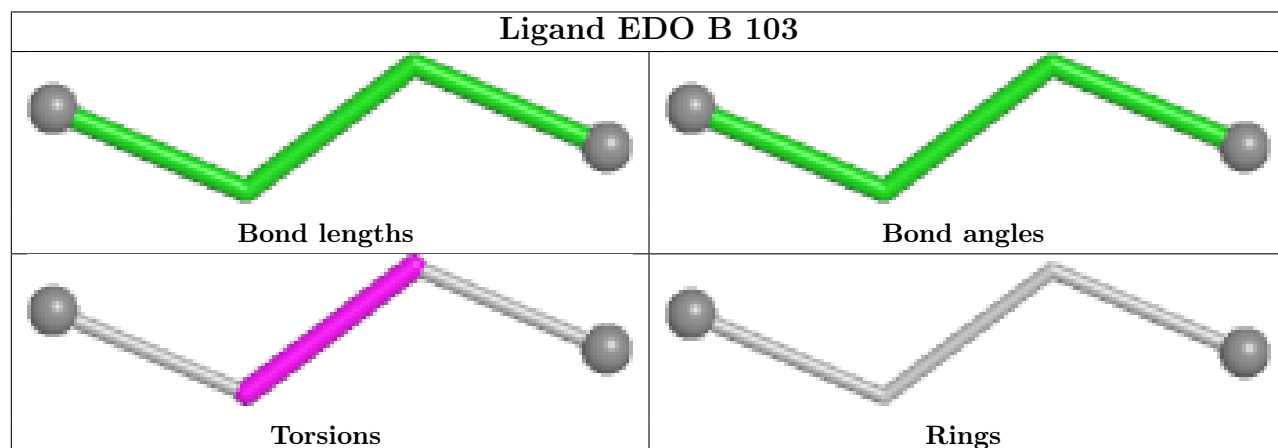
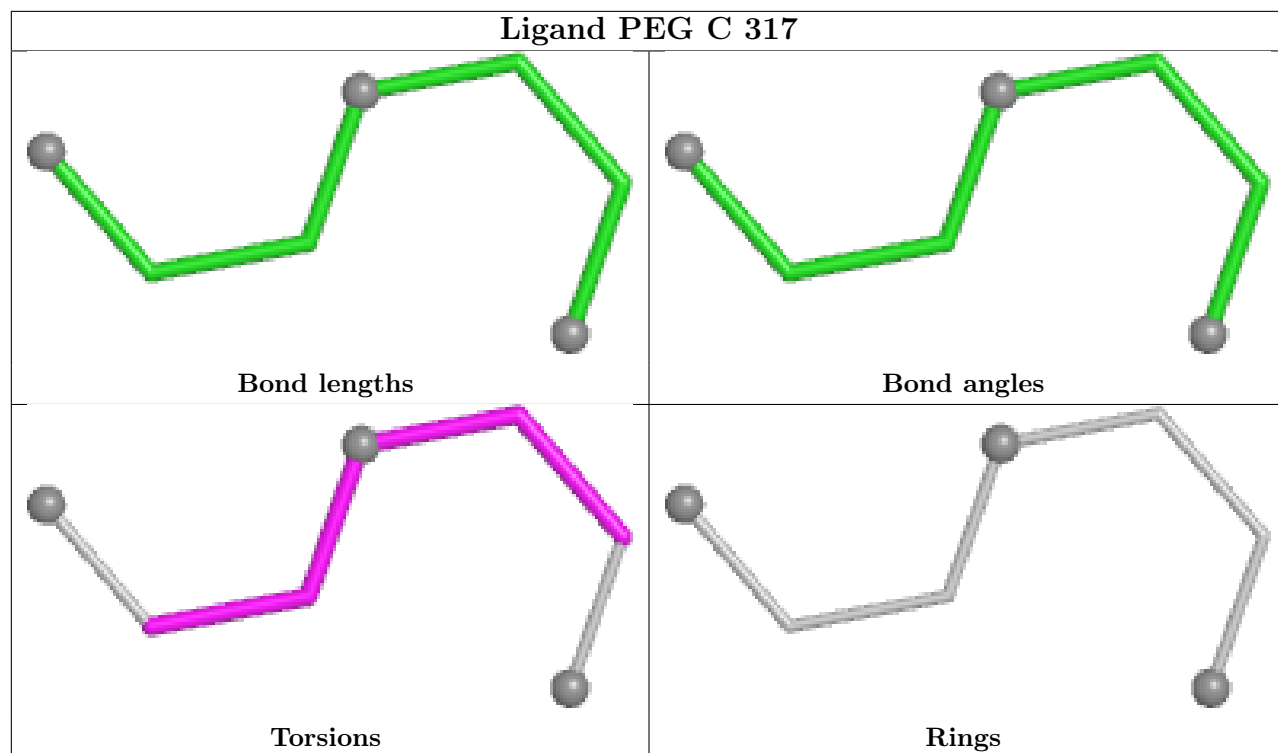


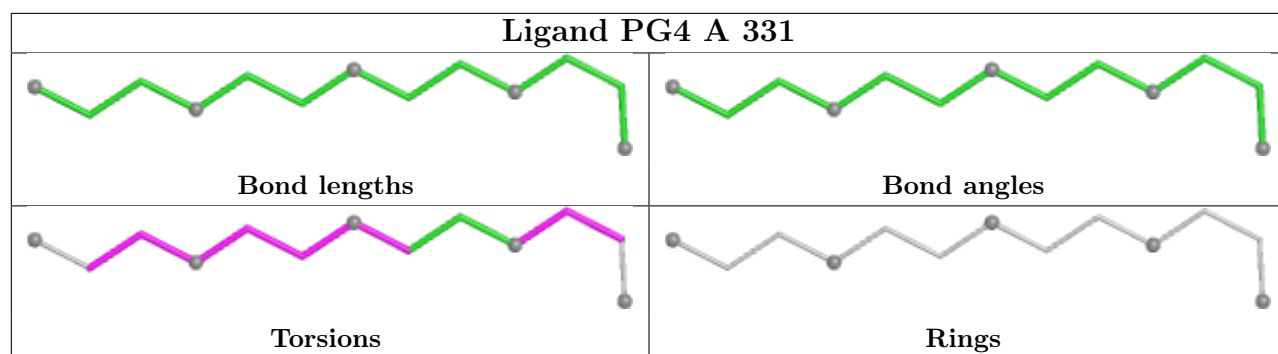
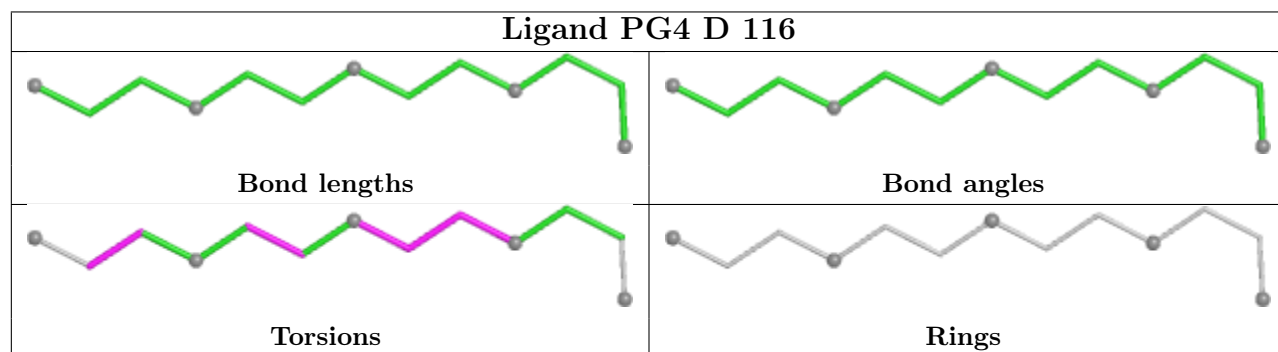
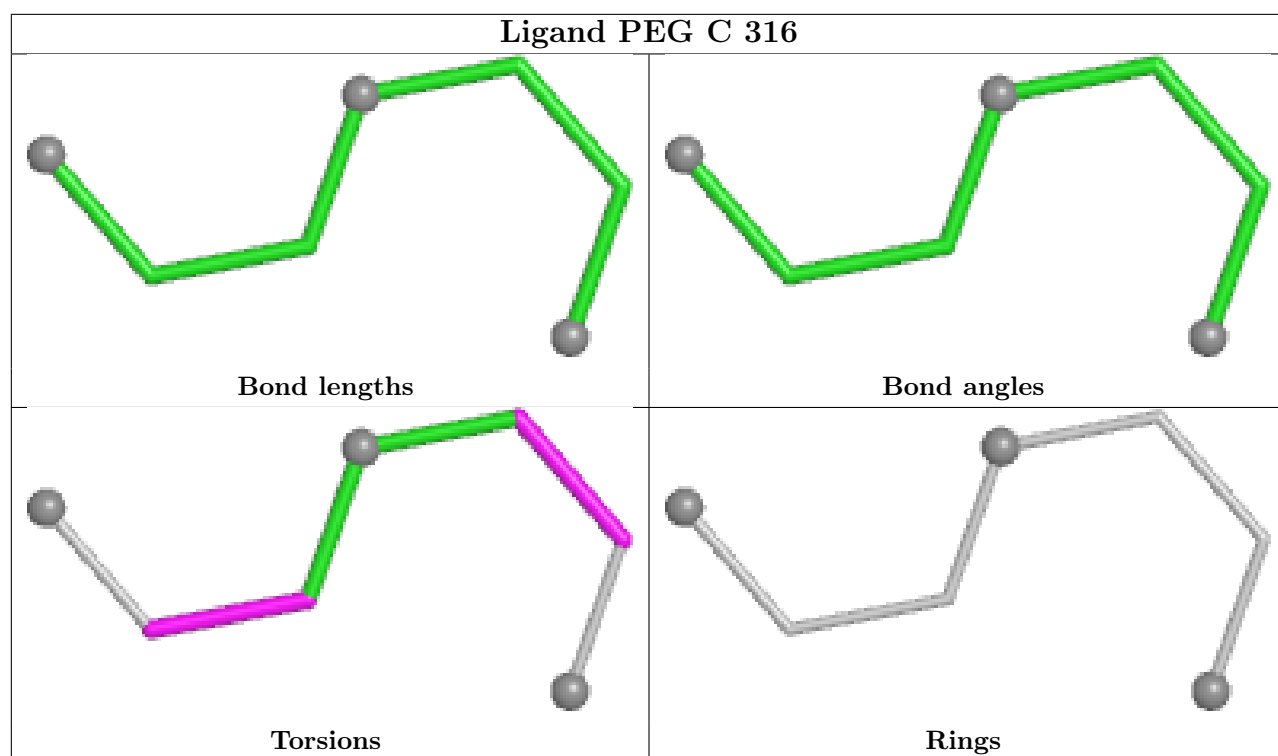


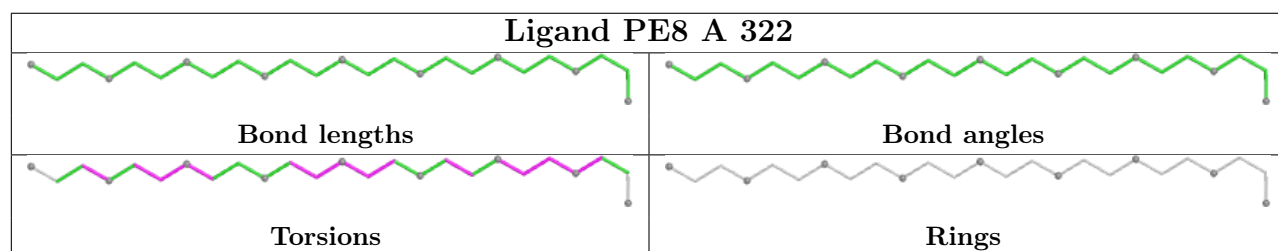
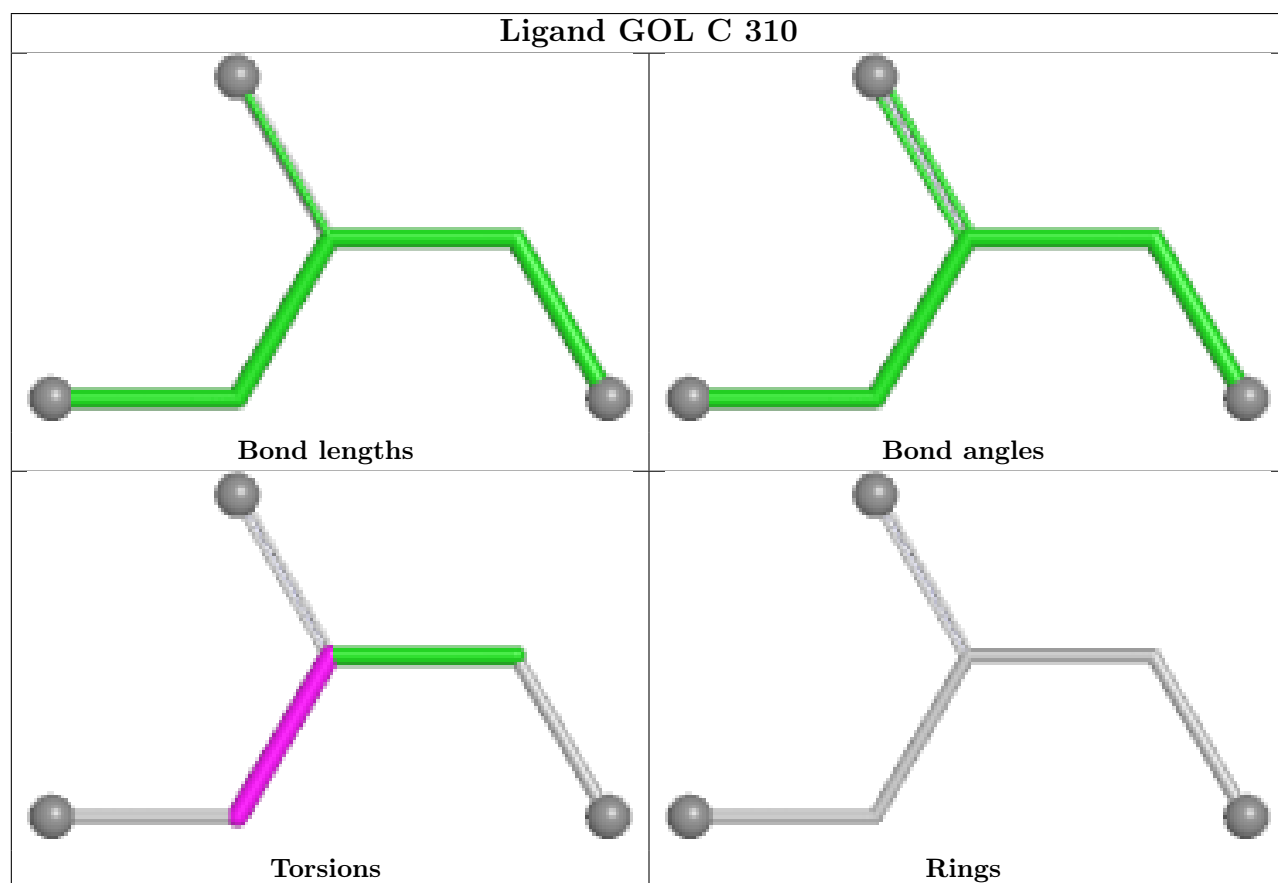
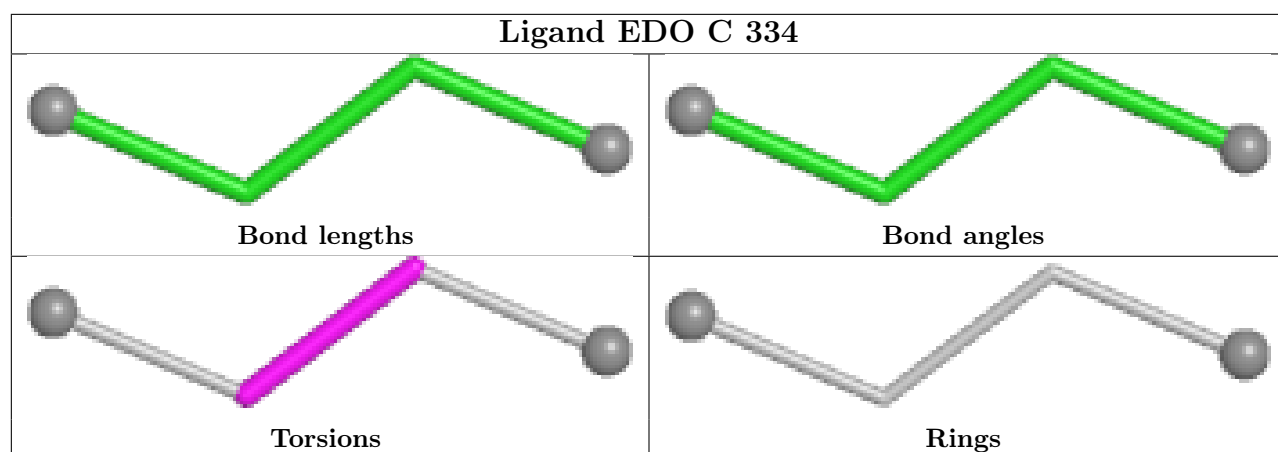


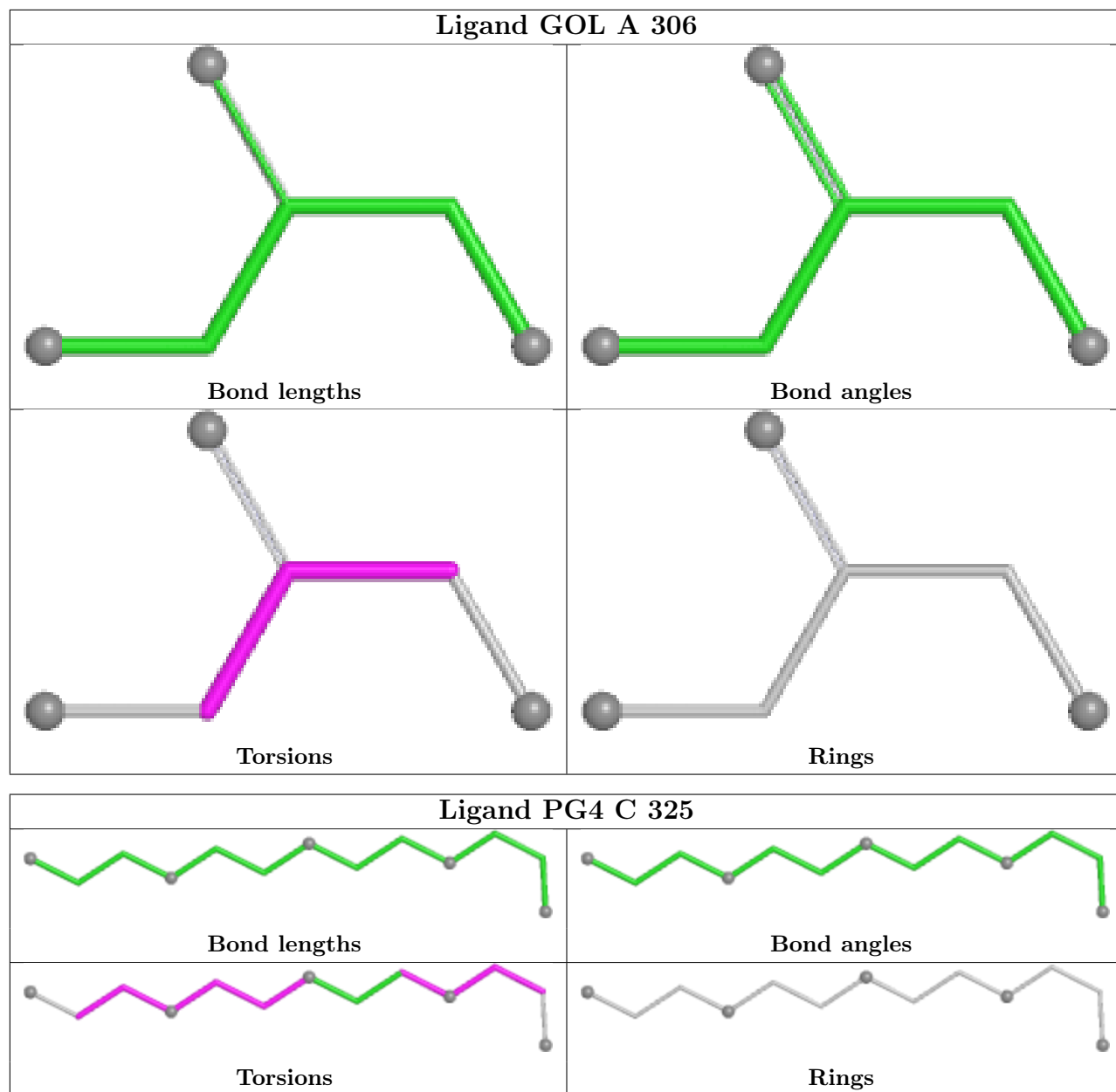


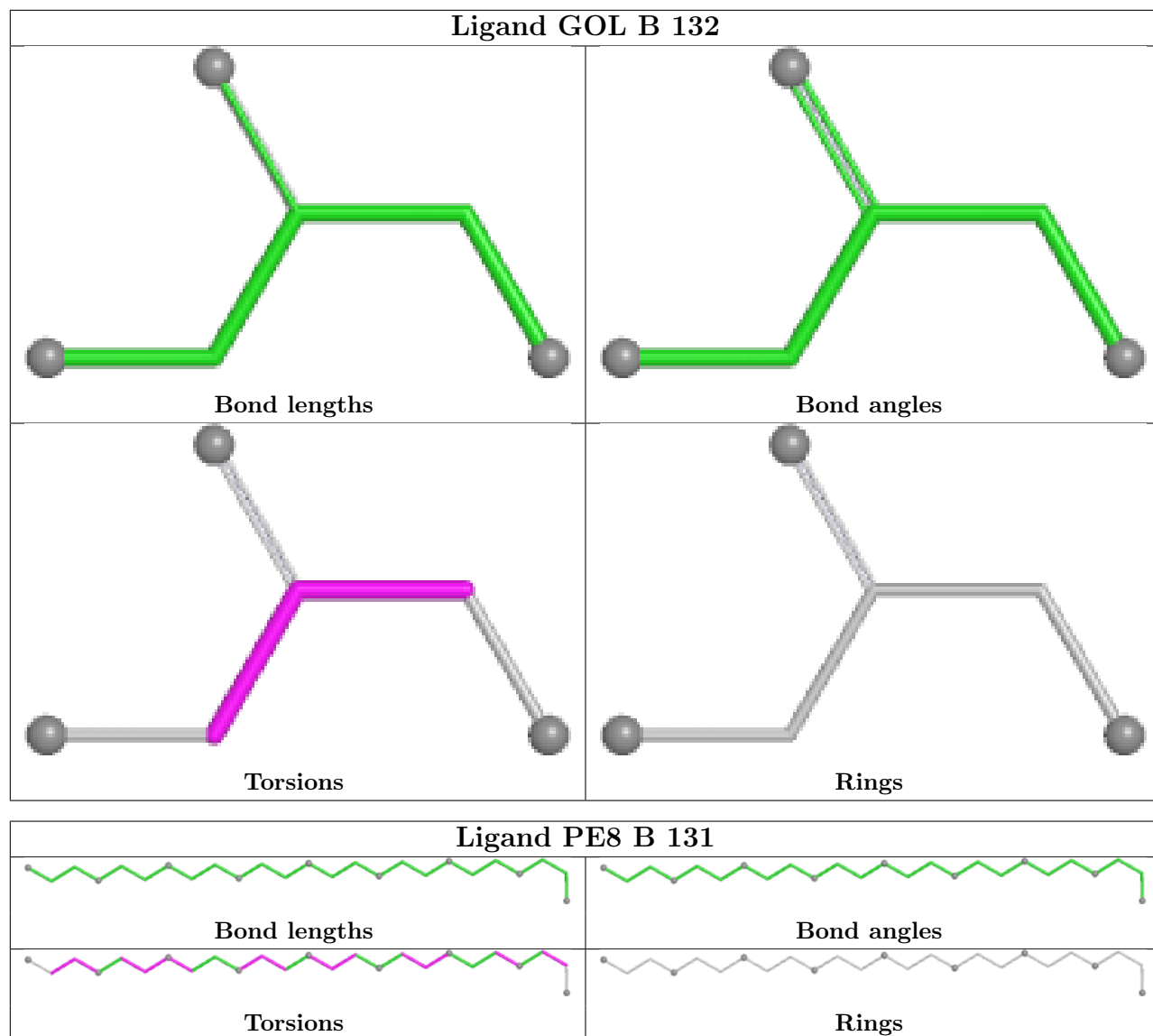


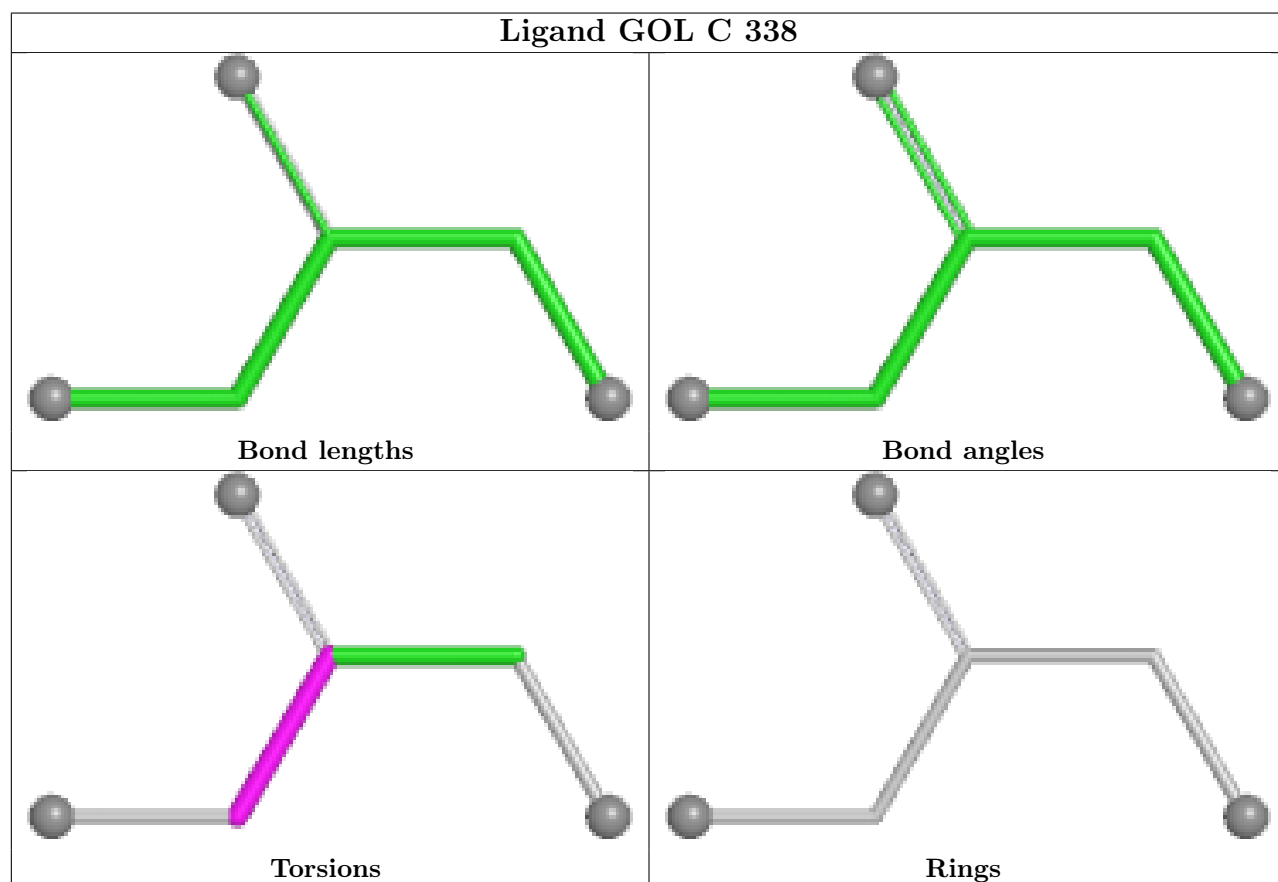
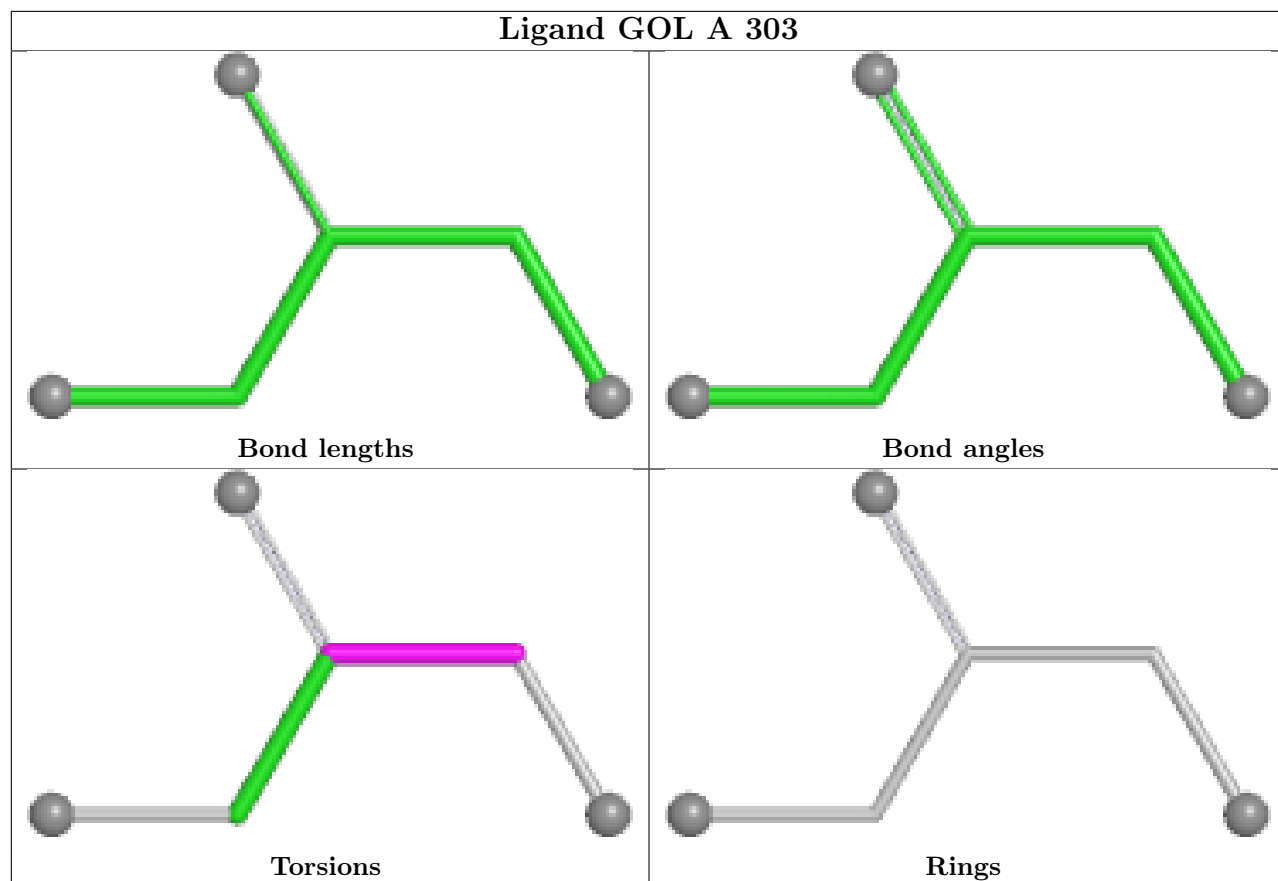


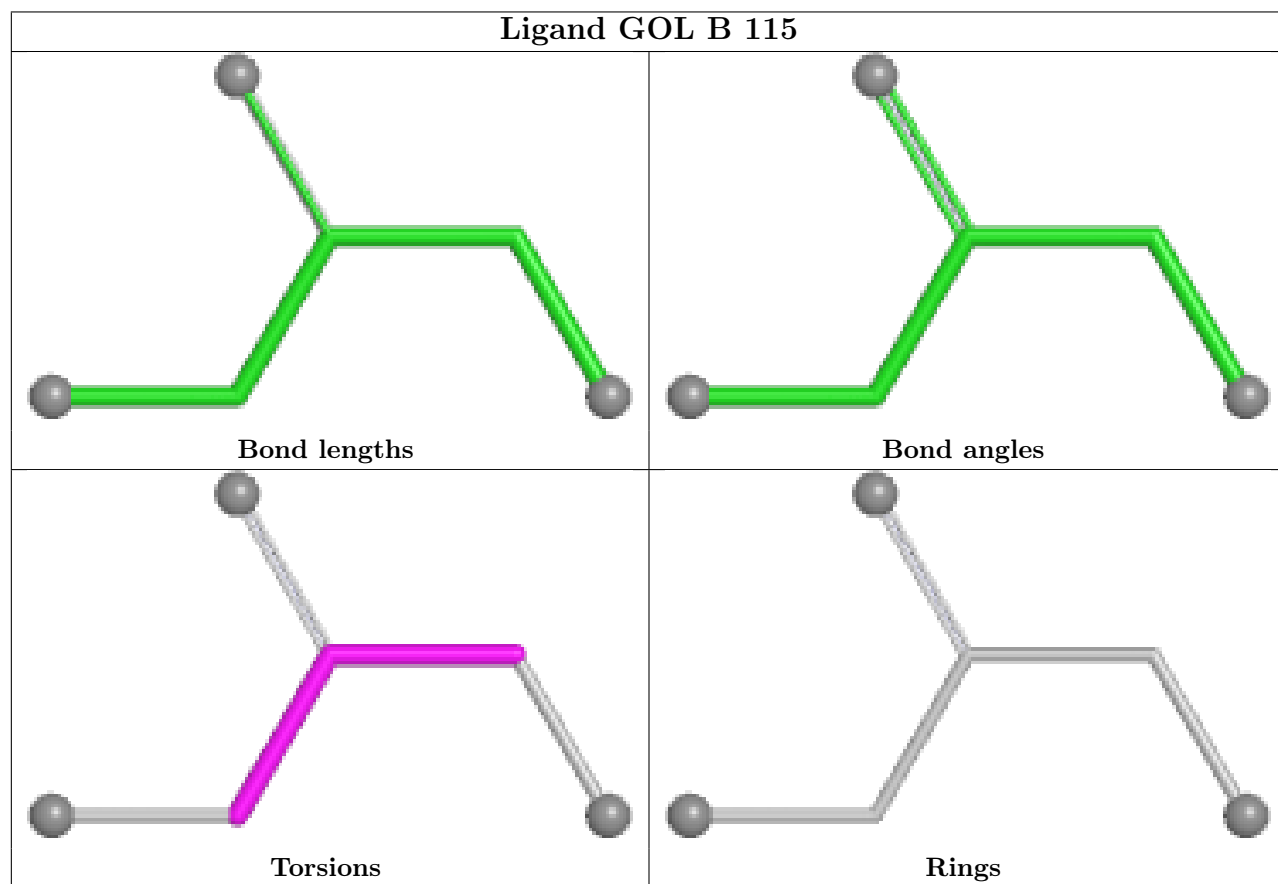
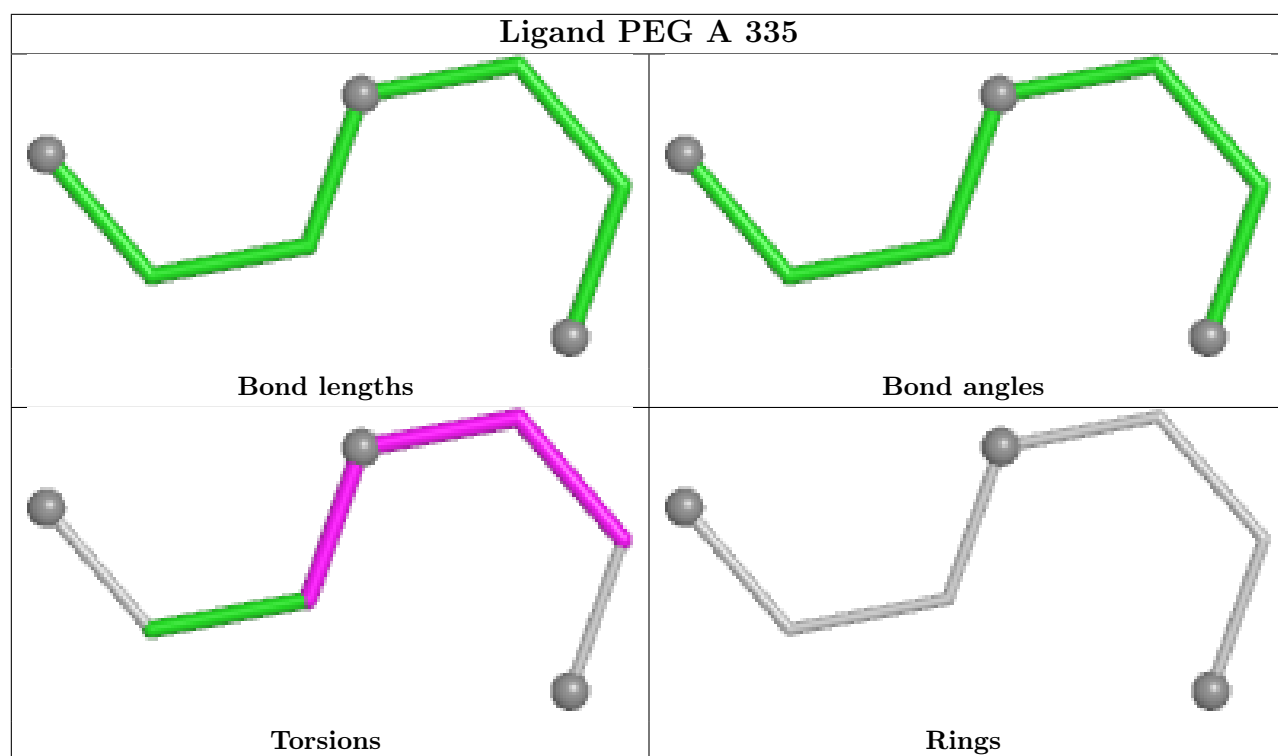


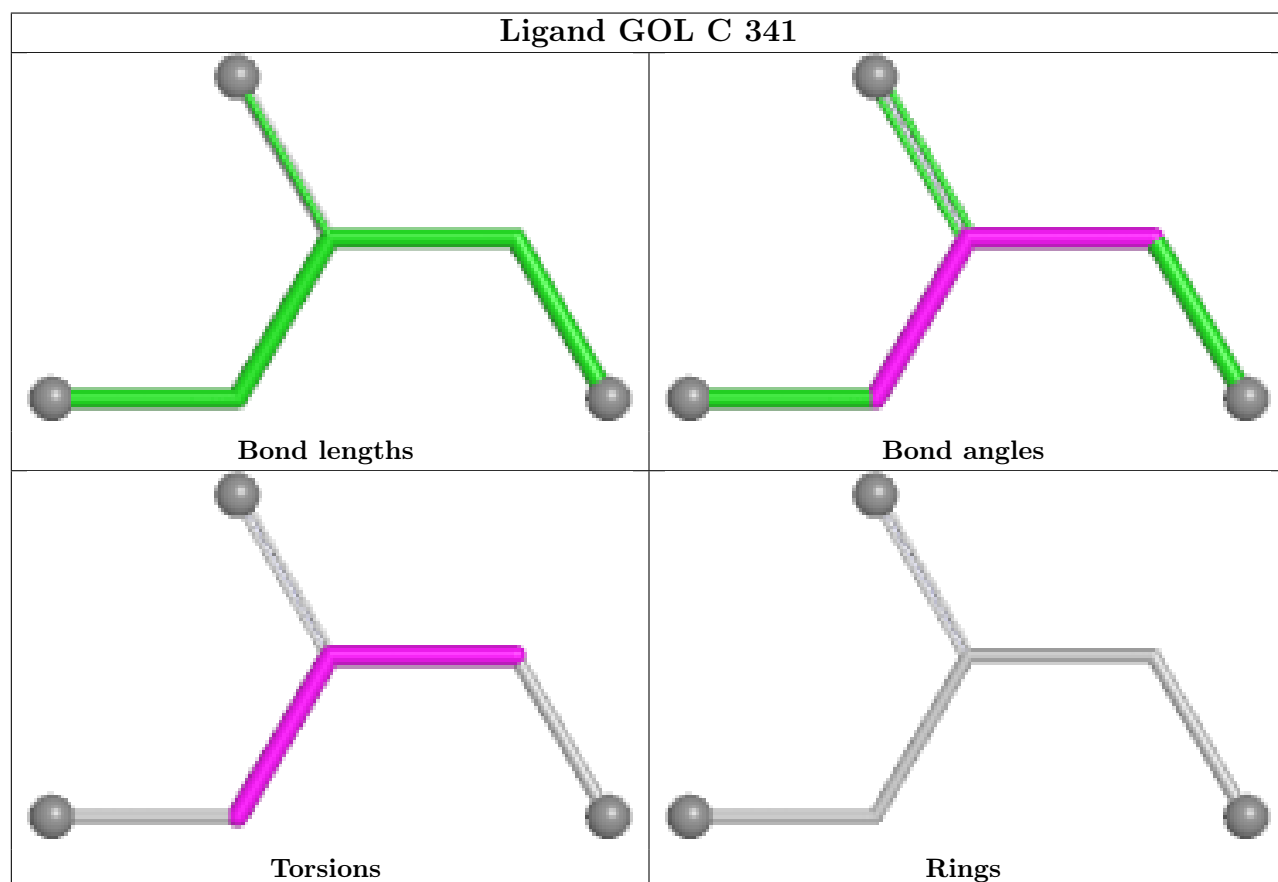
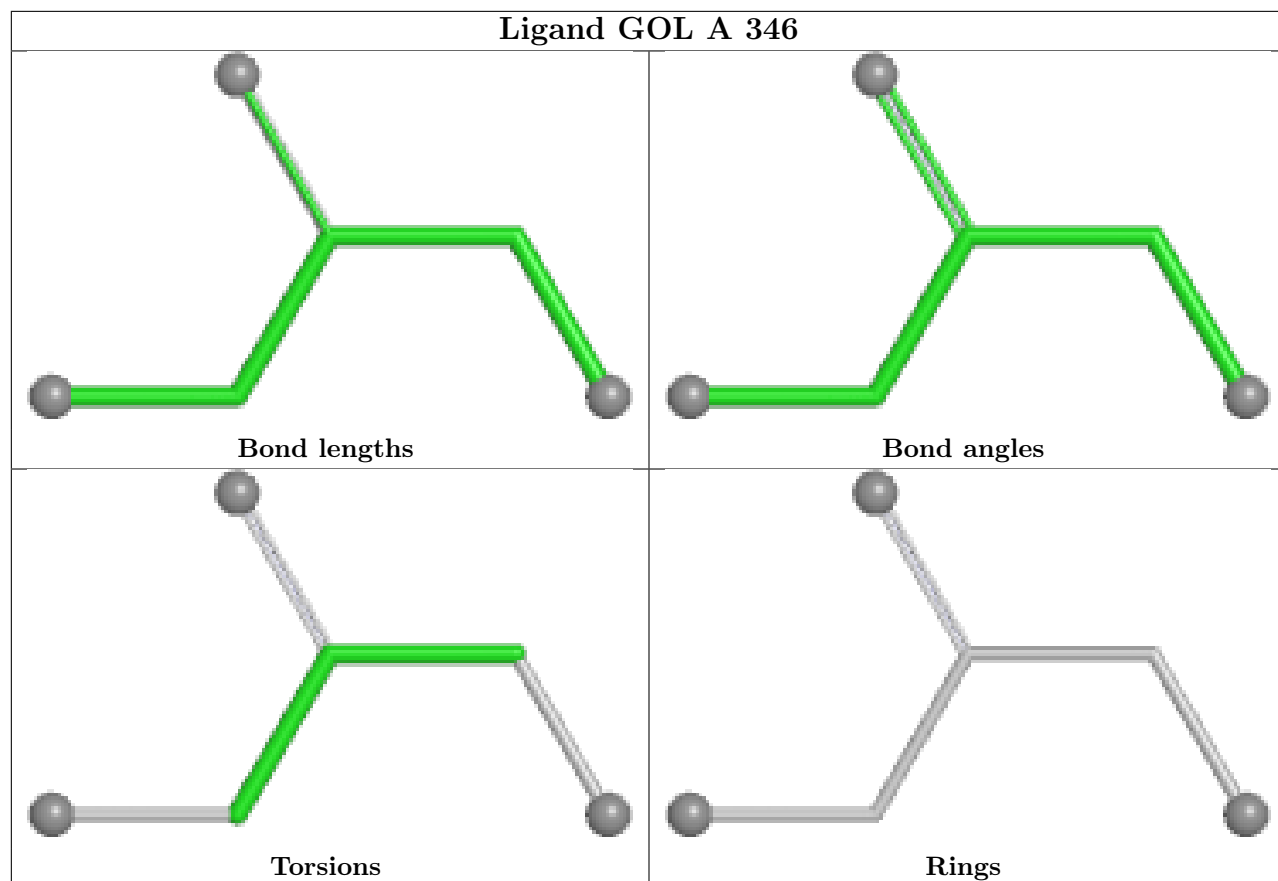


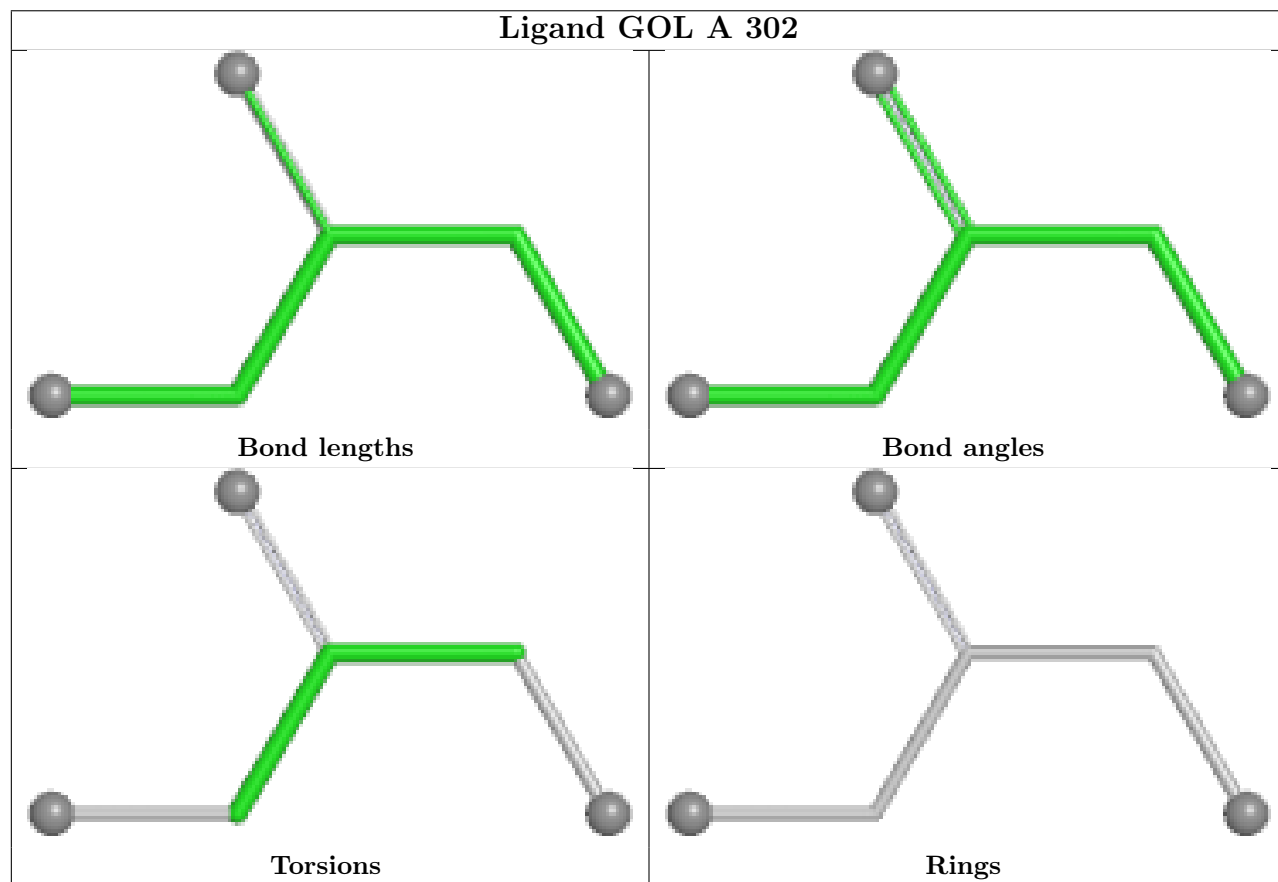
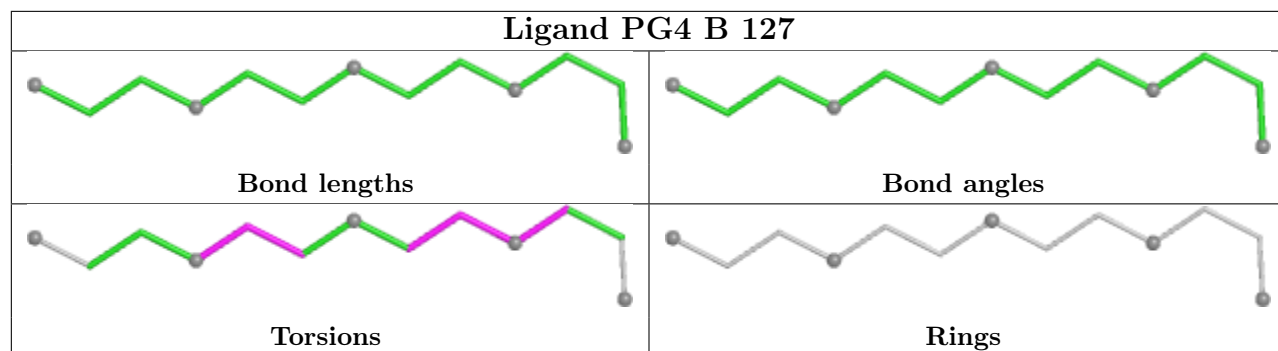


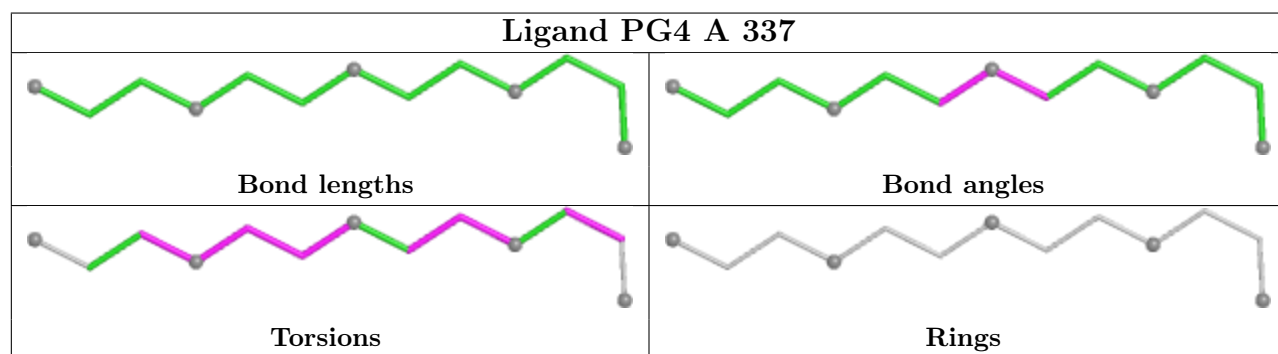
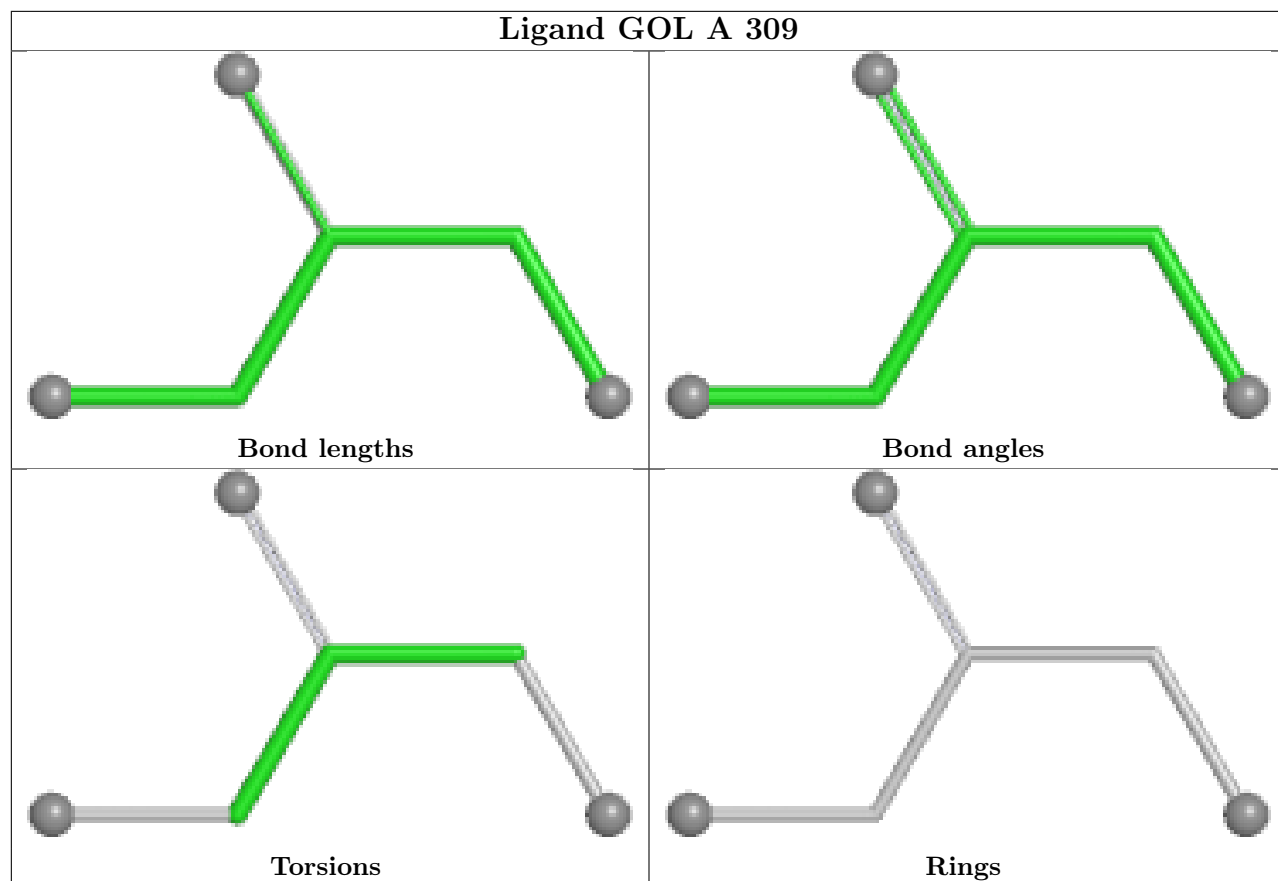


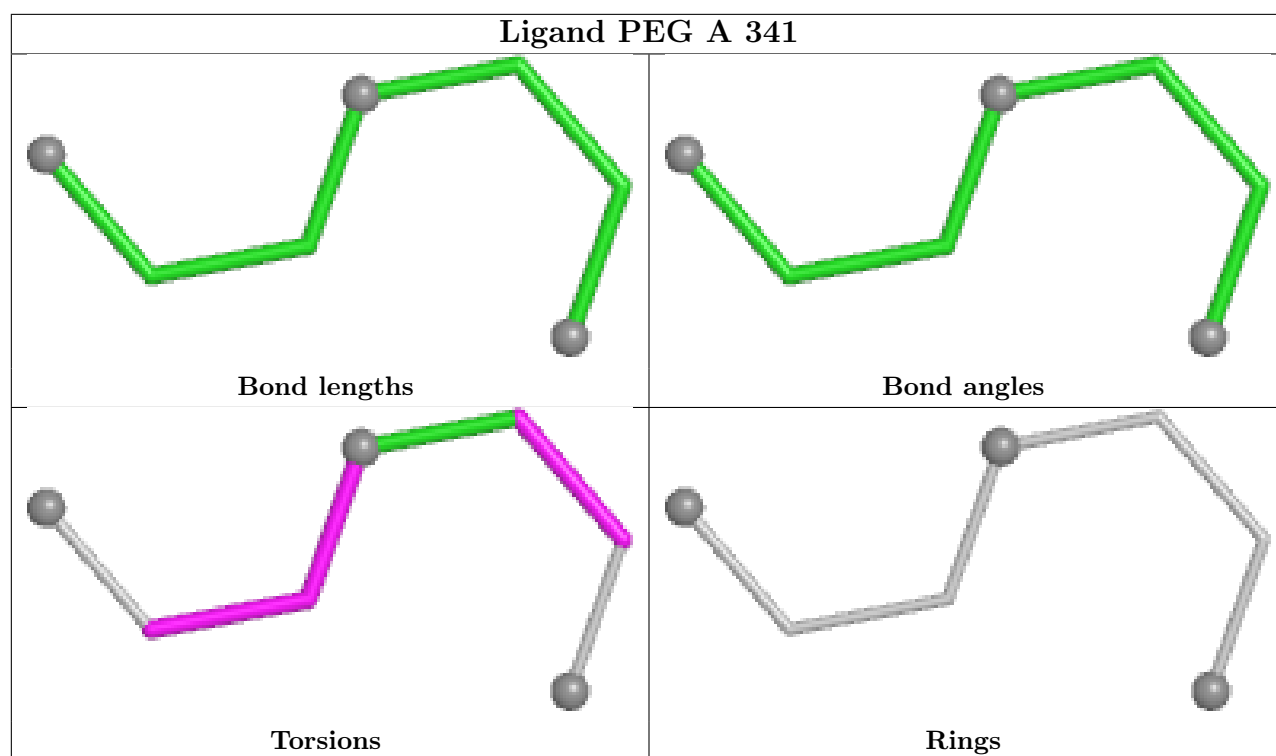


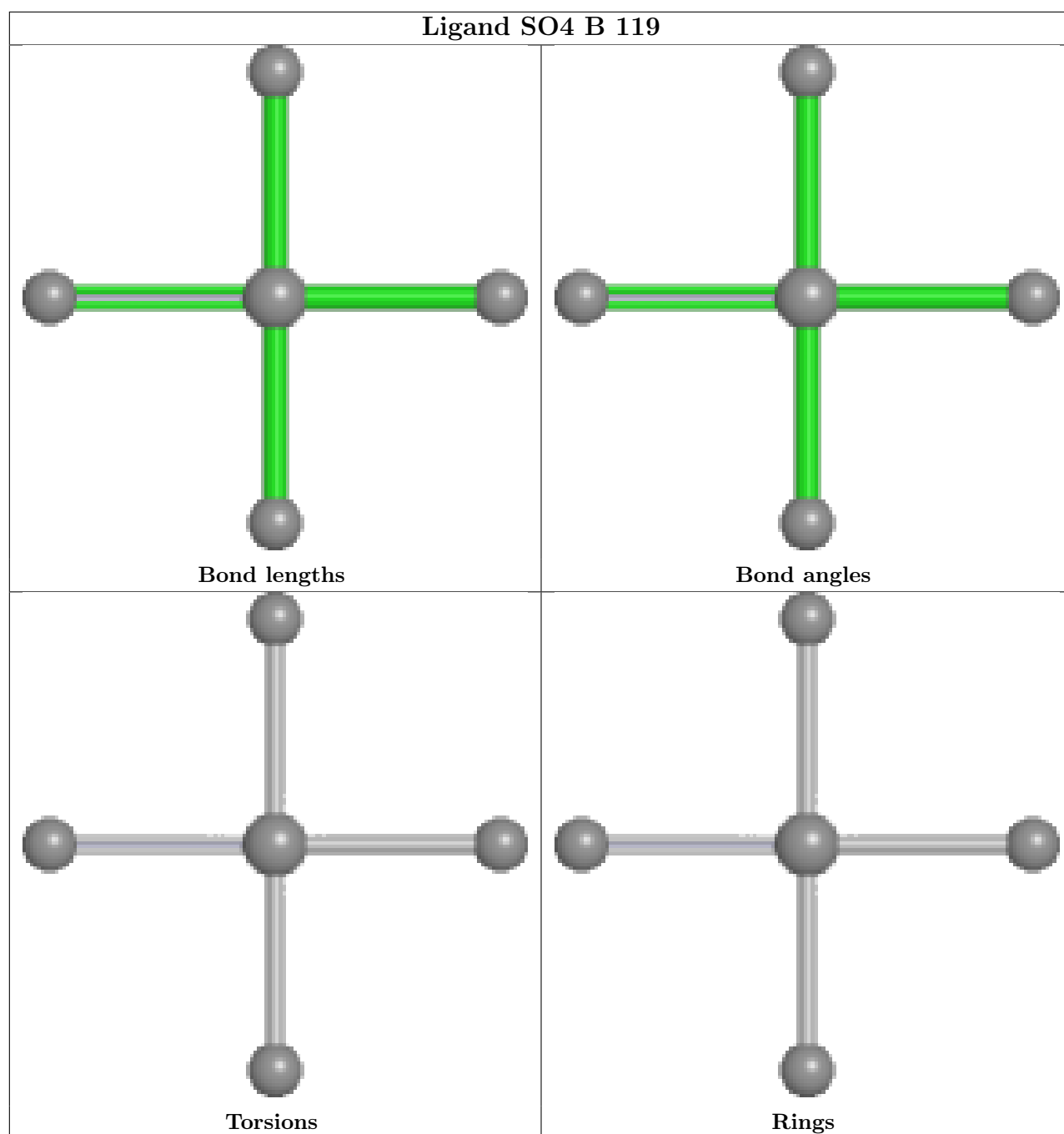


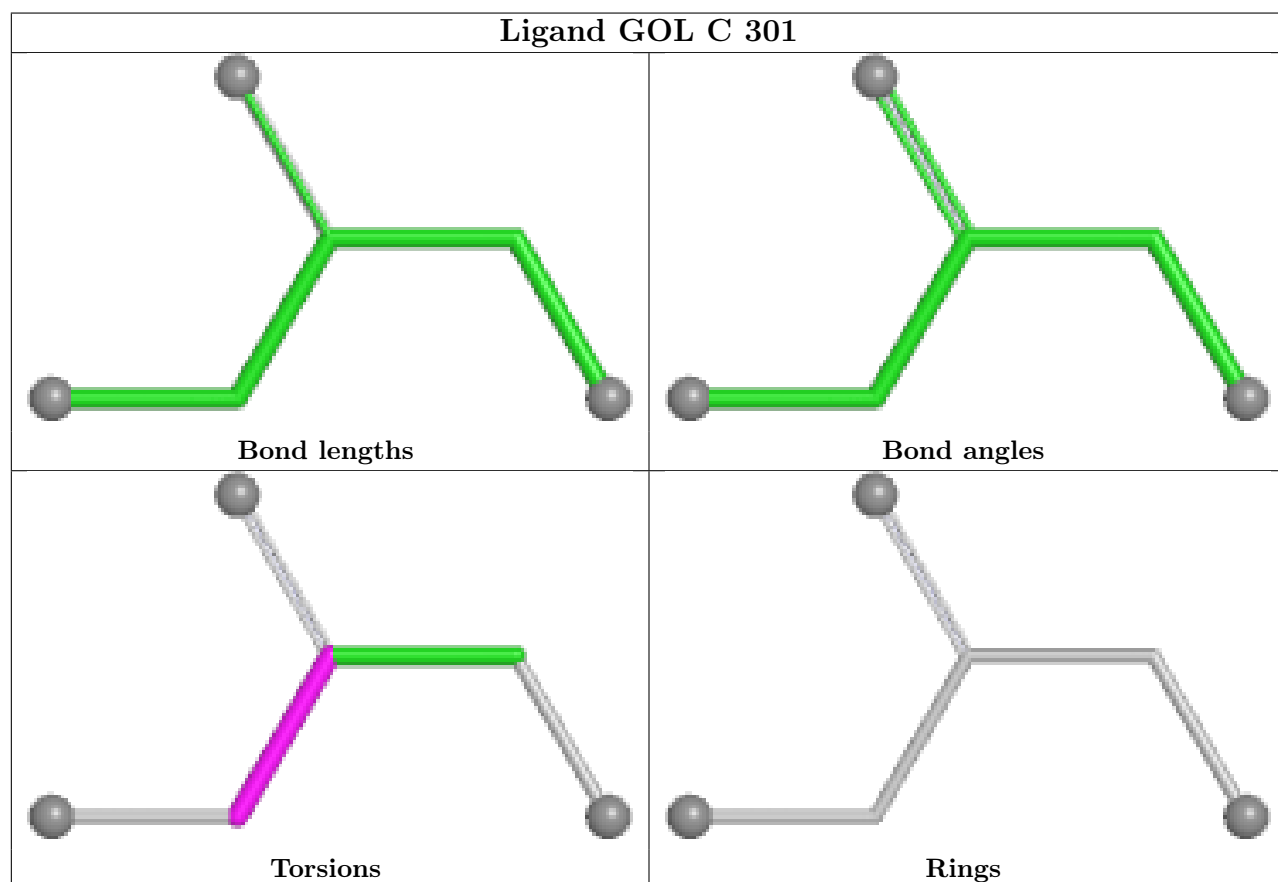
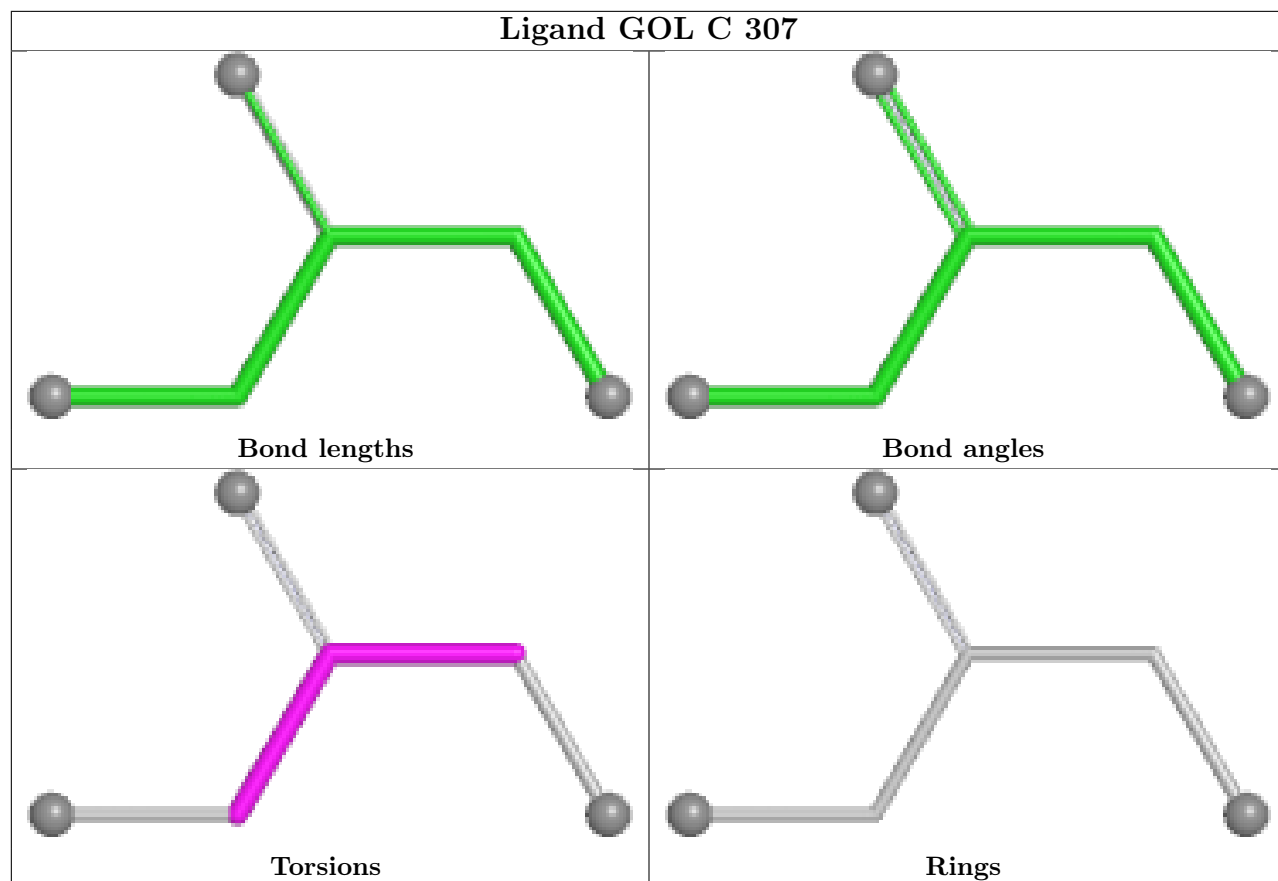


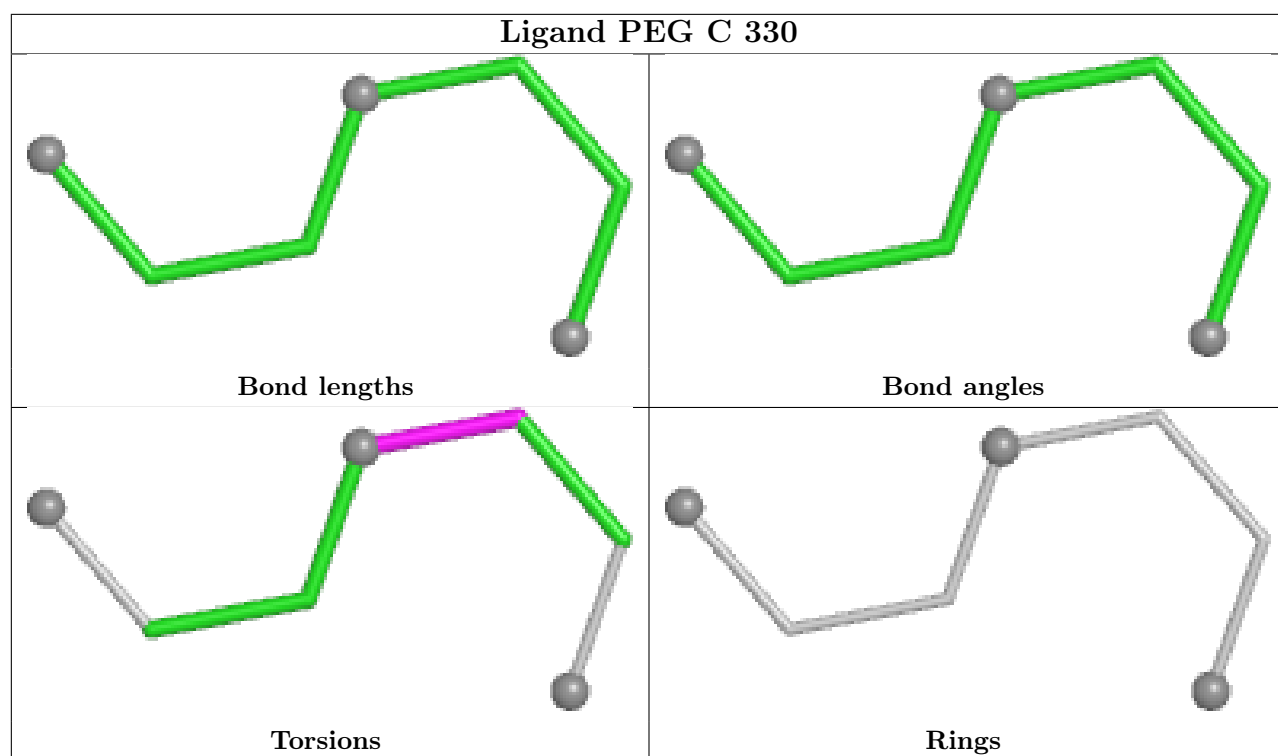


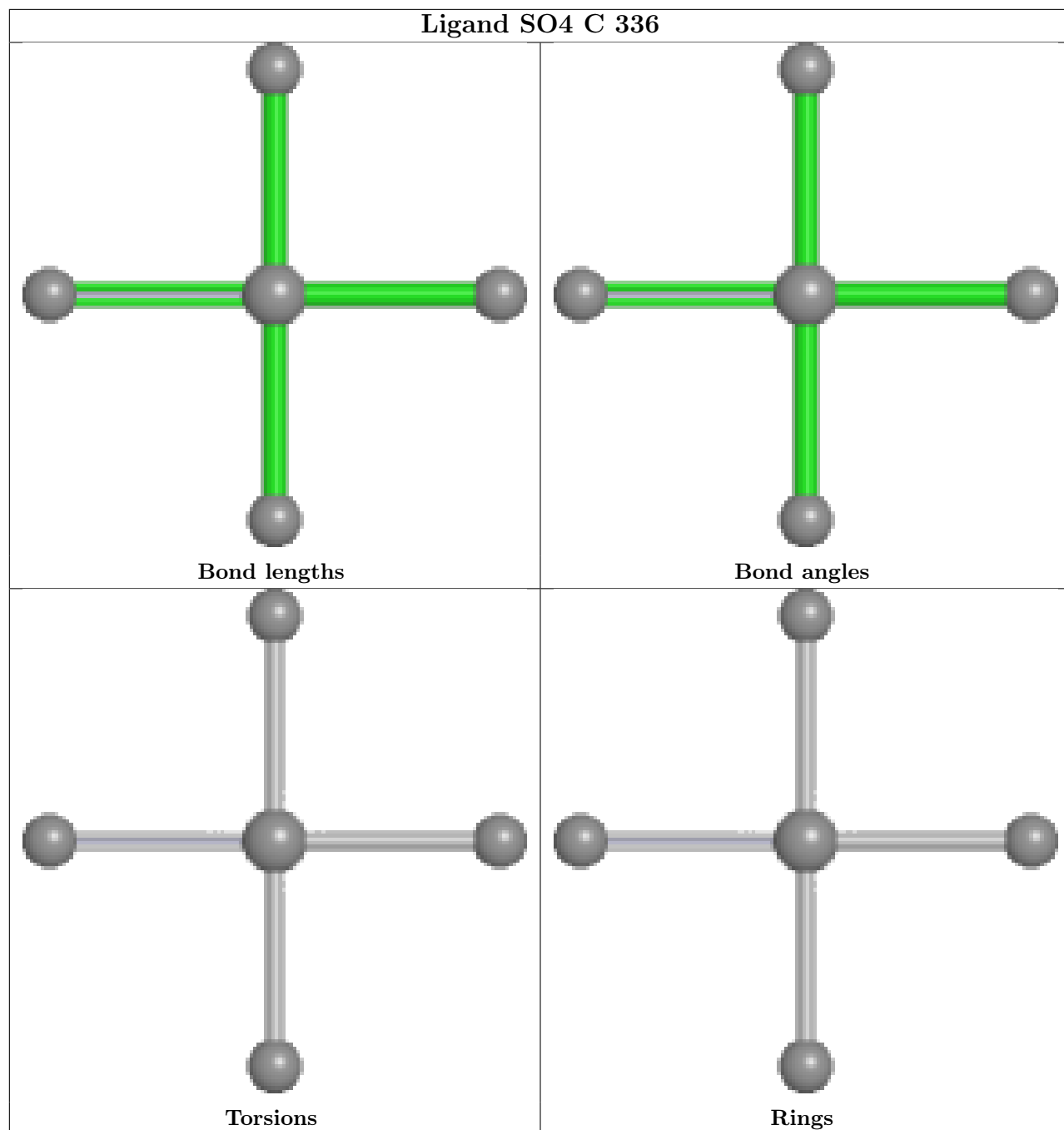




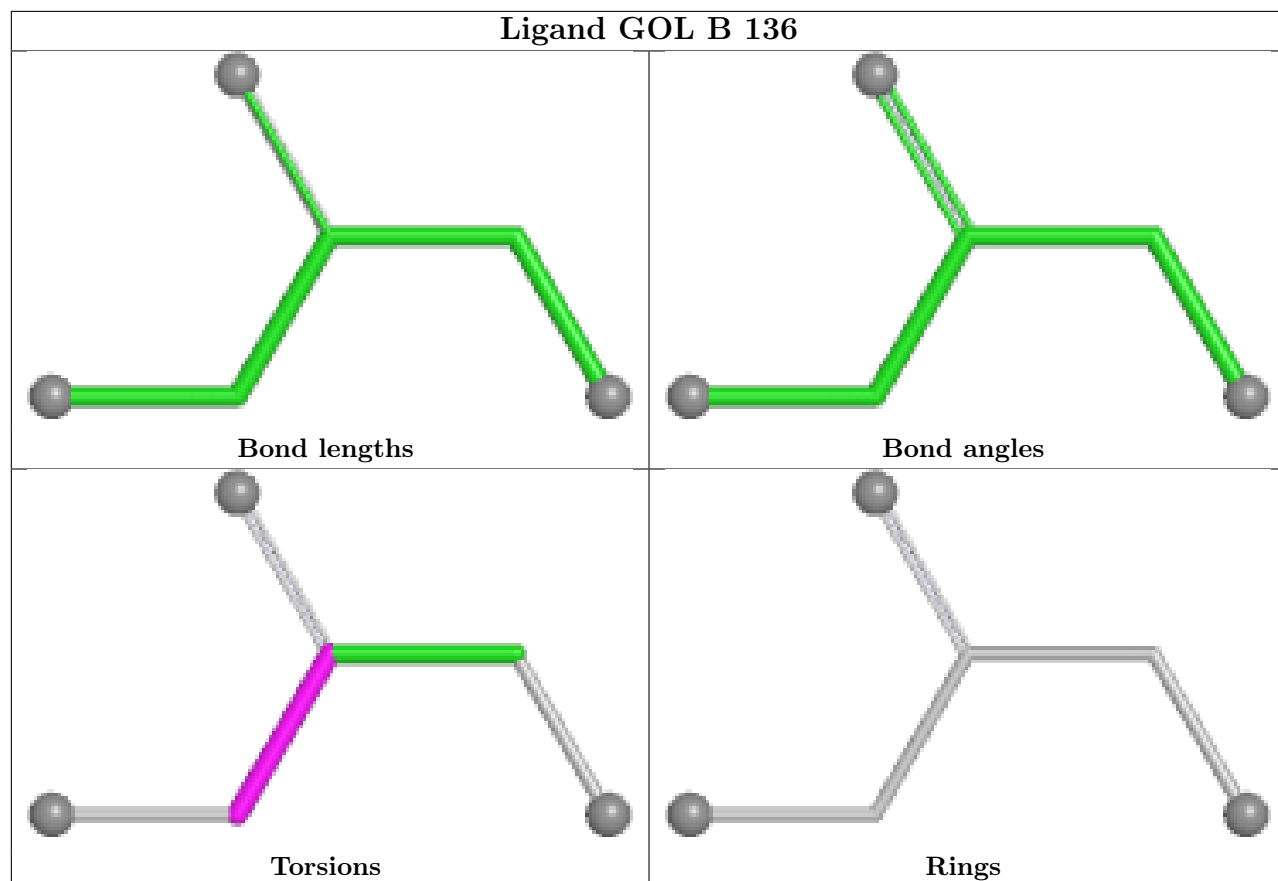




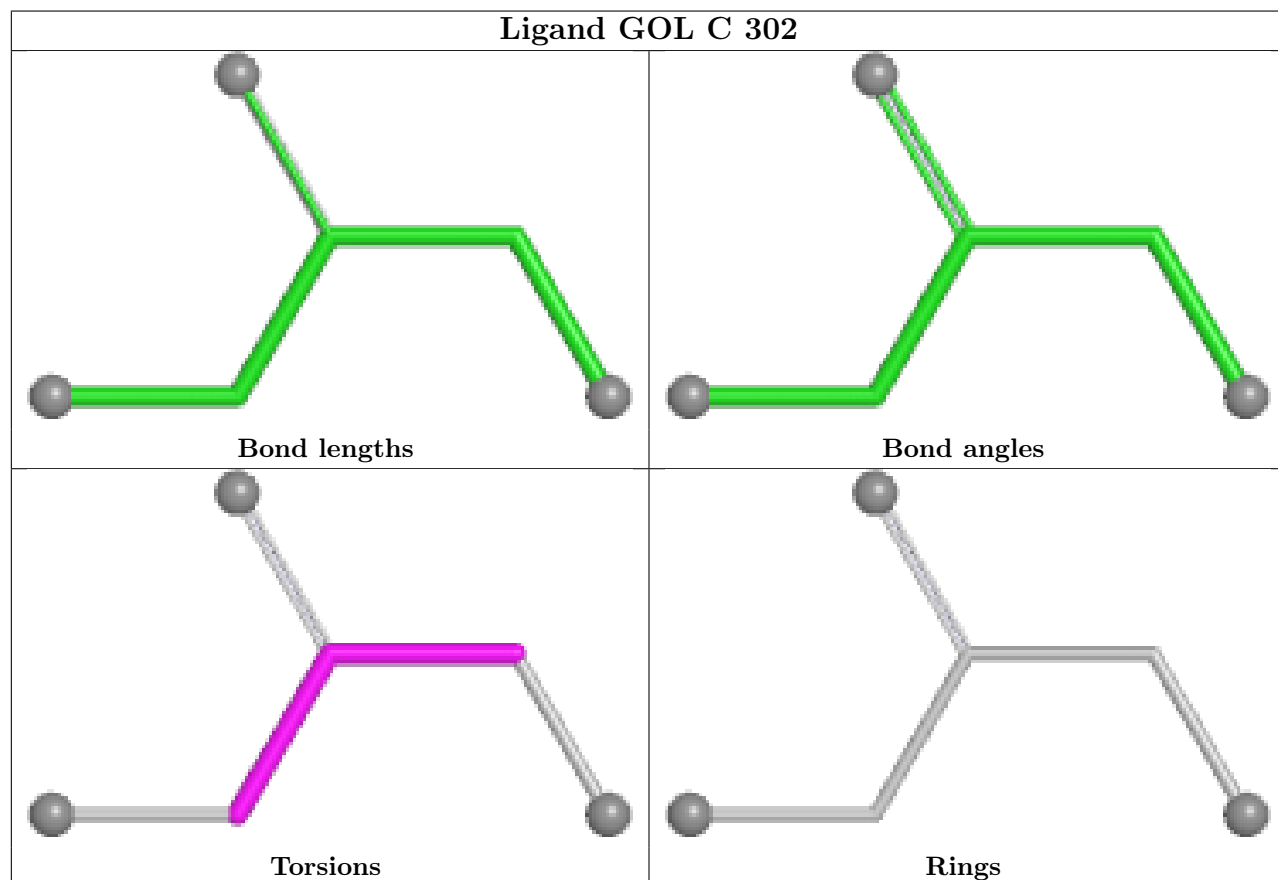


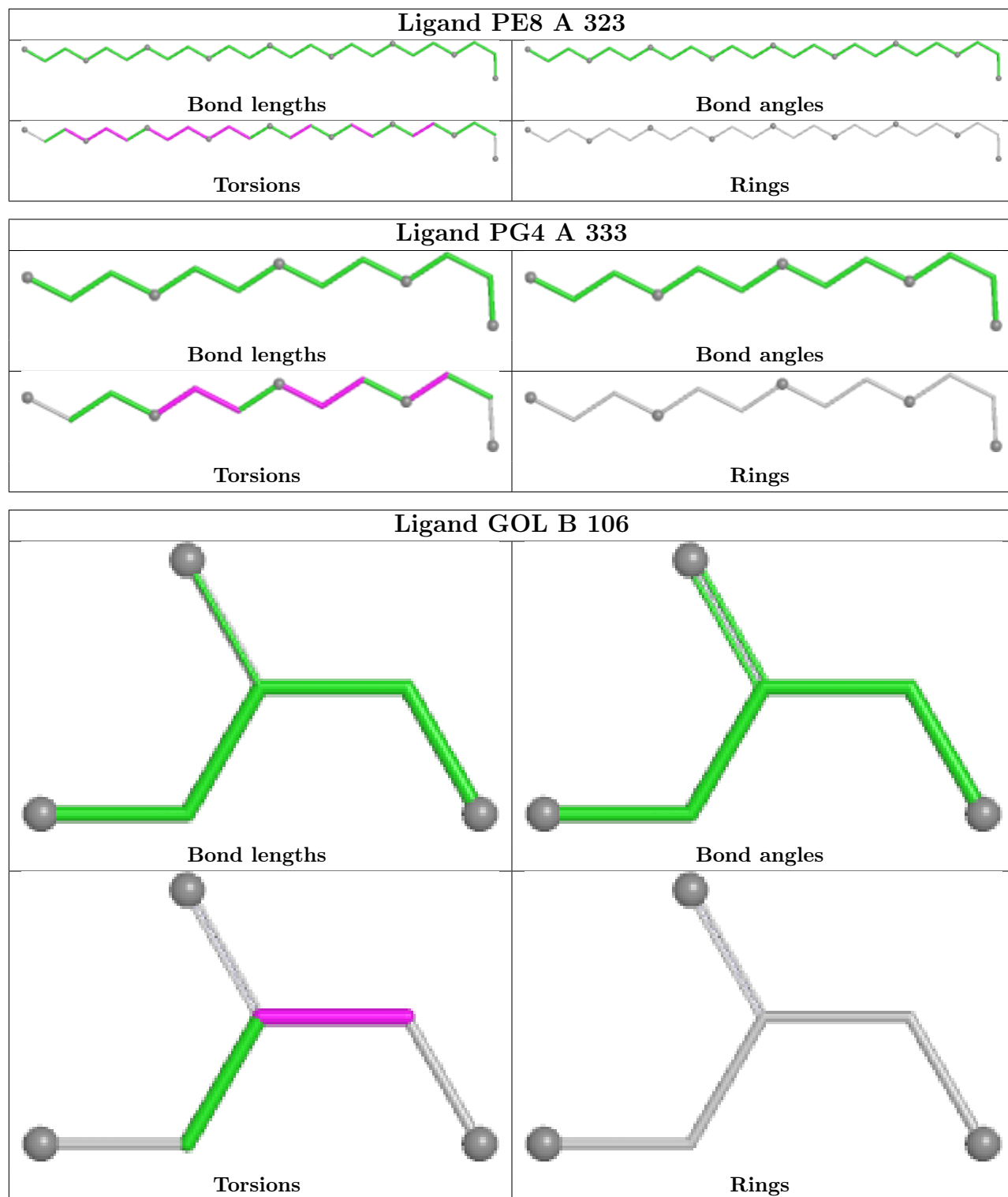


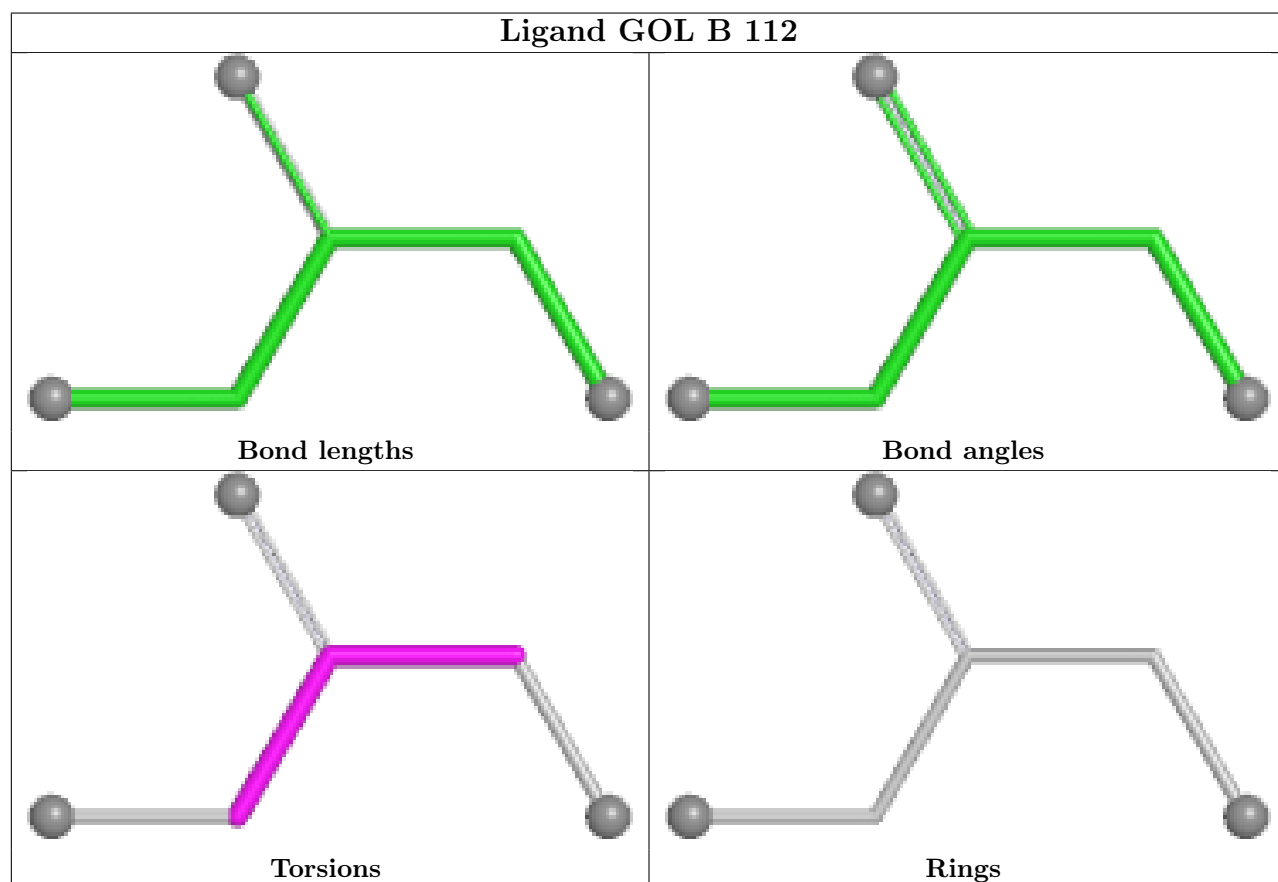
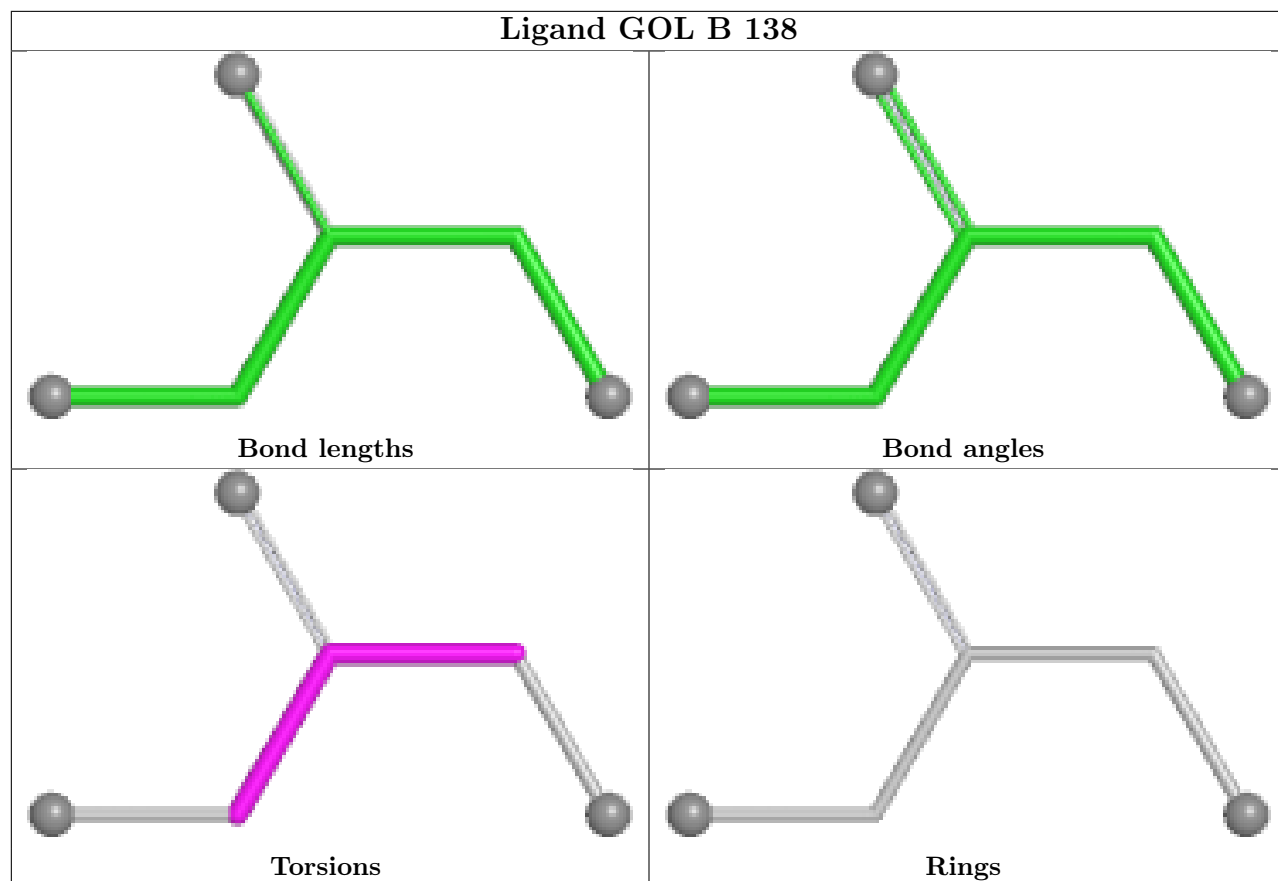
Ligand GOL B 136

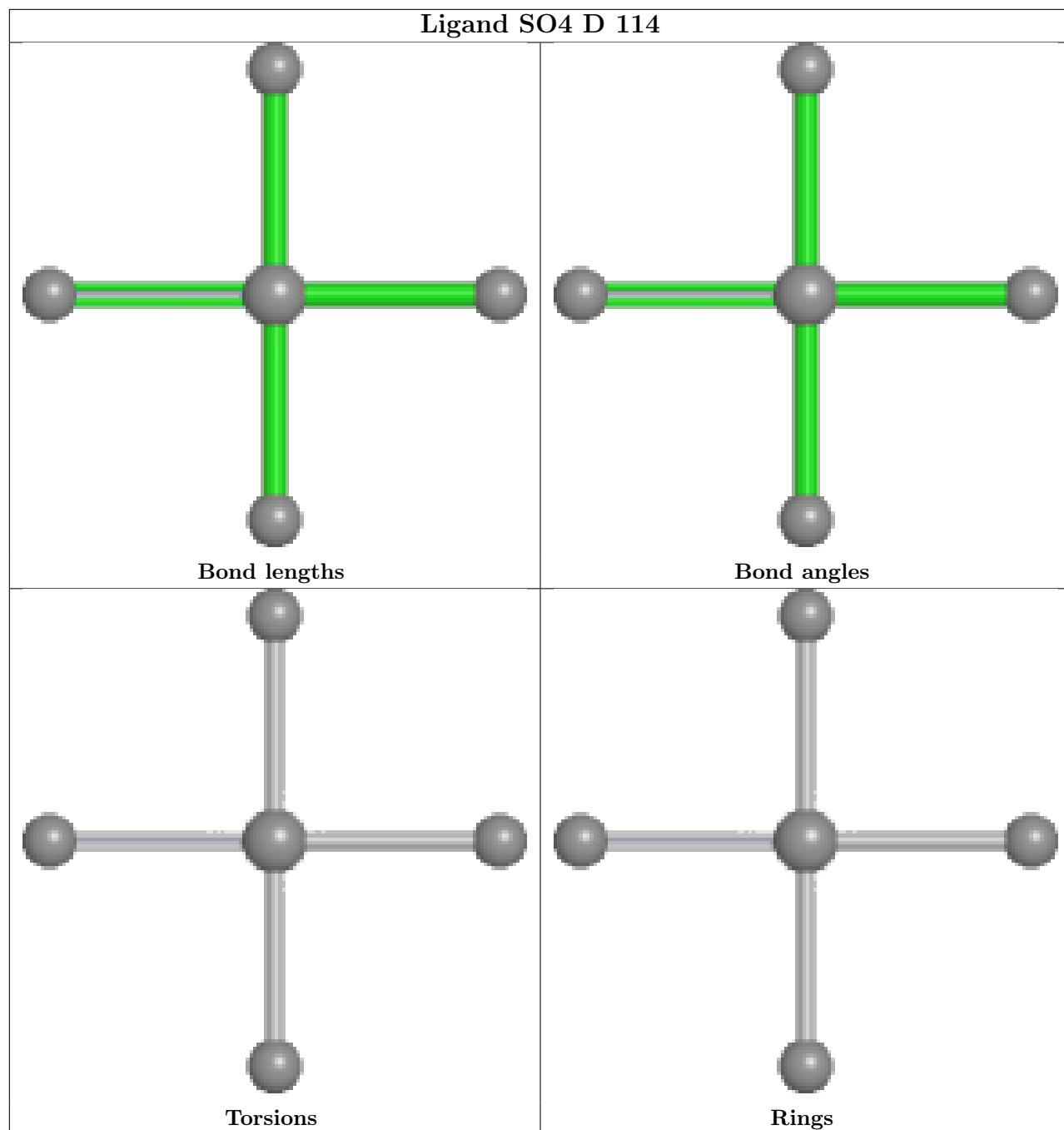


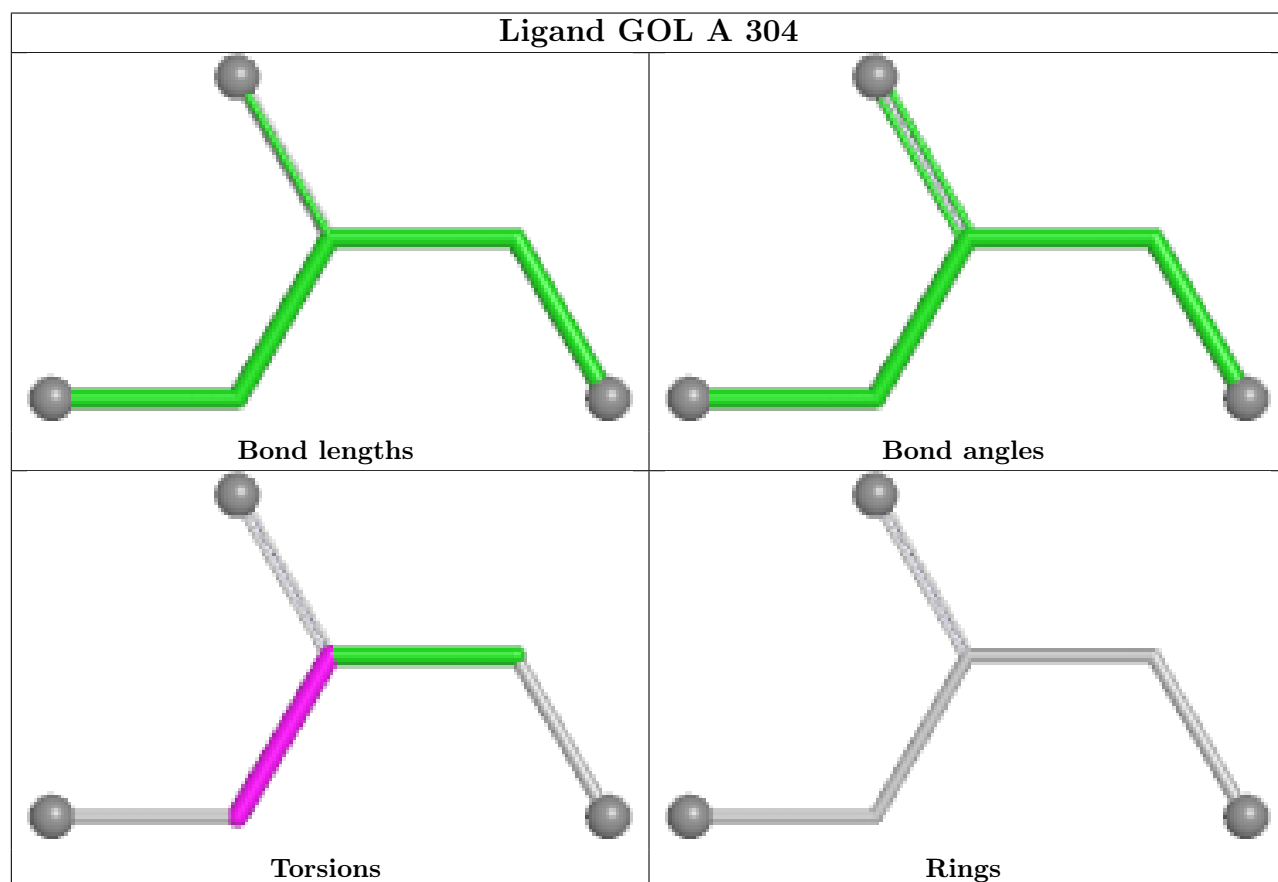
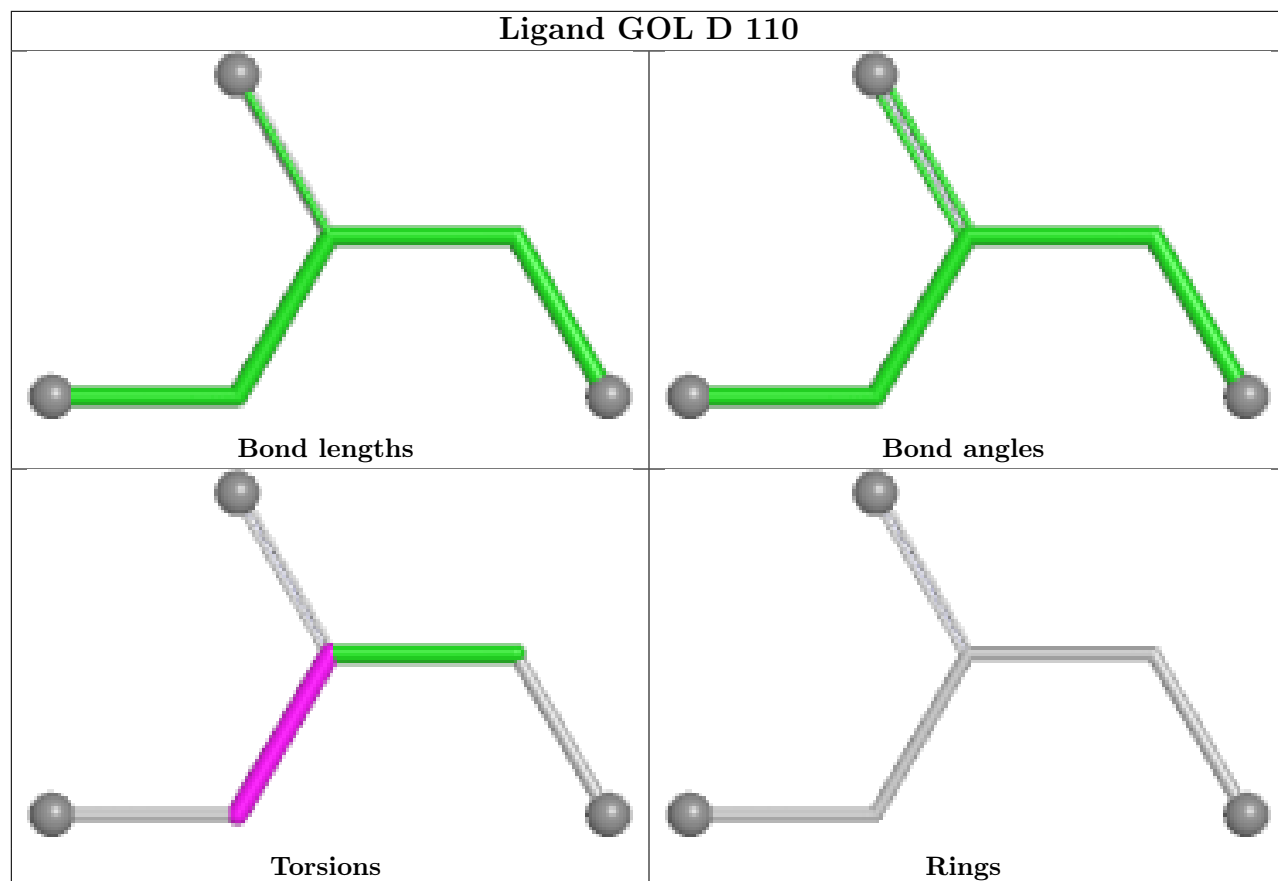
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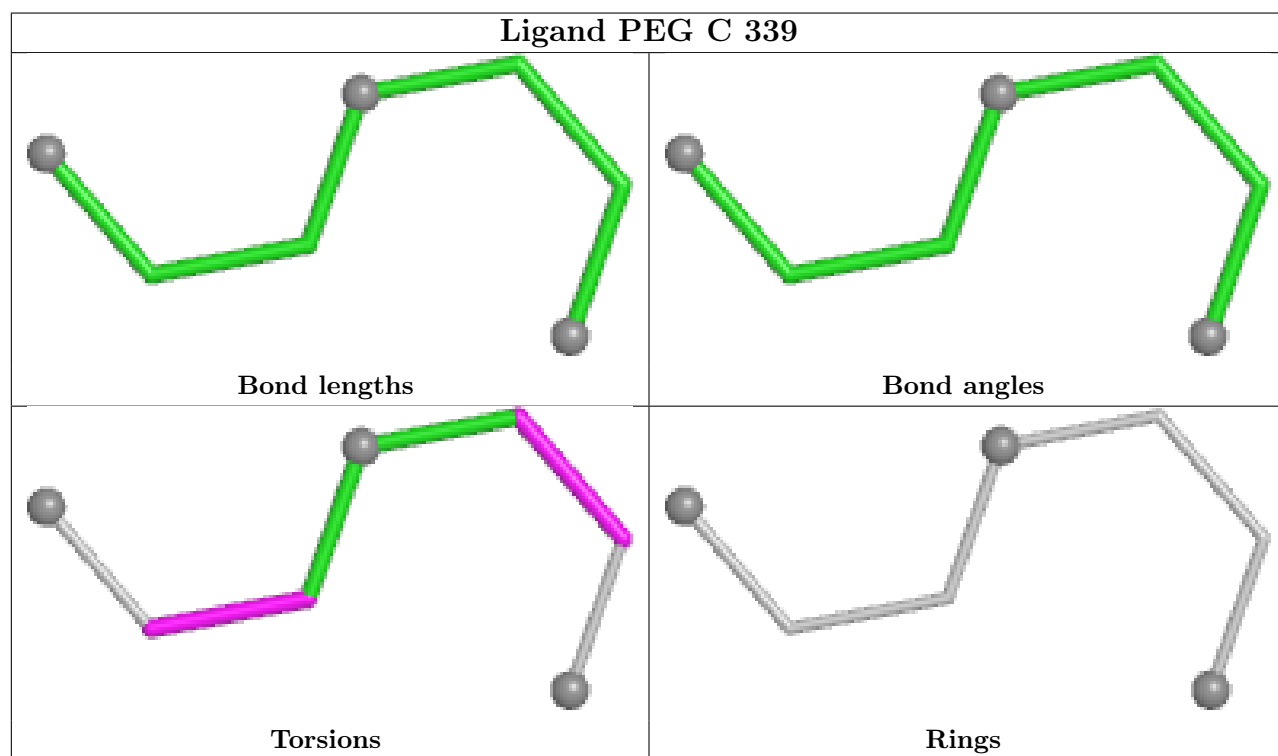
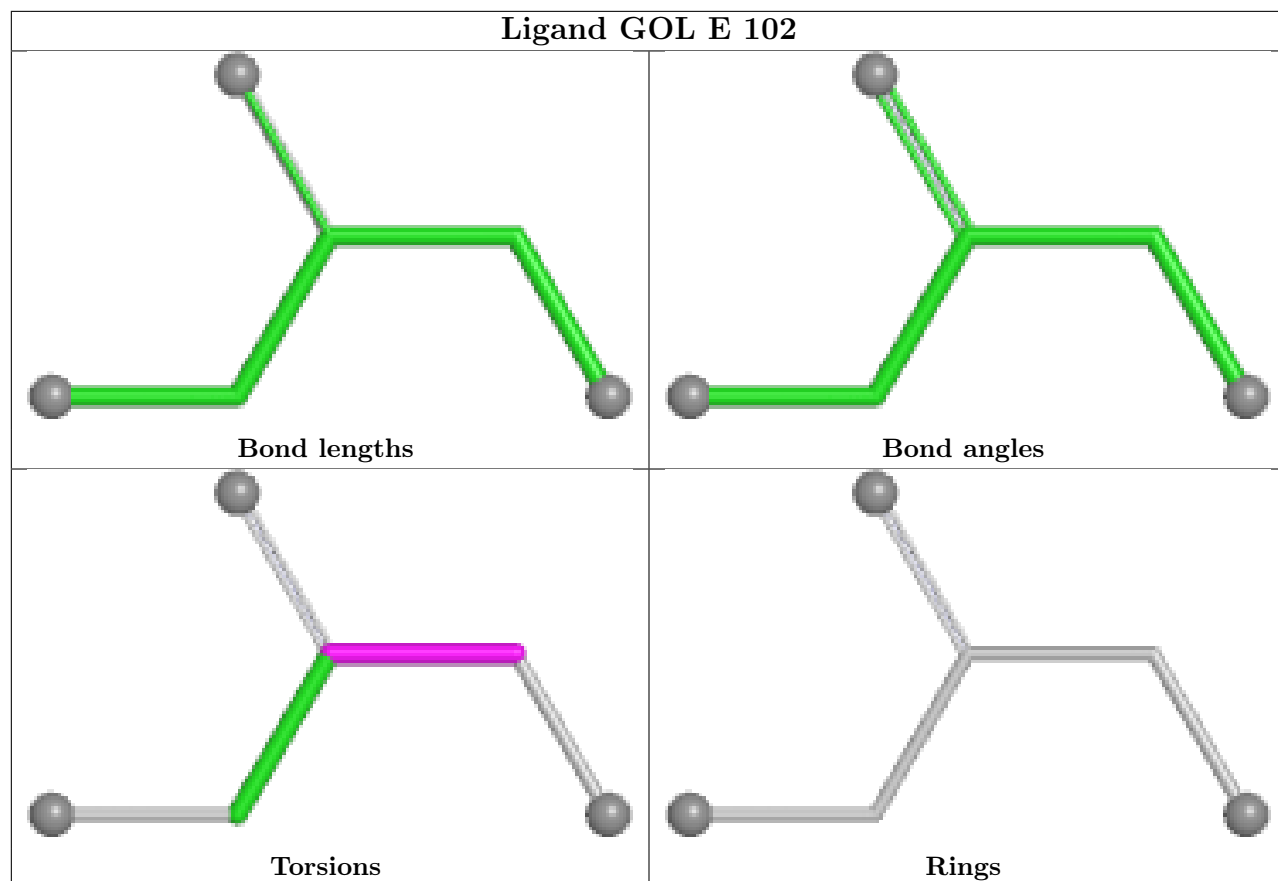


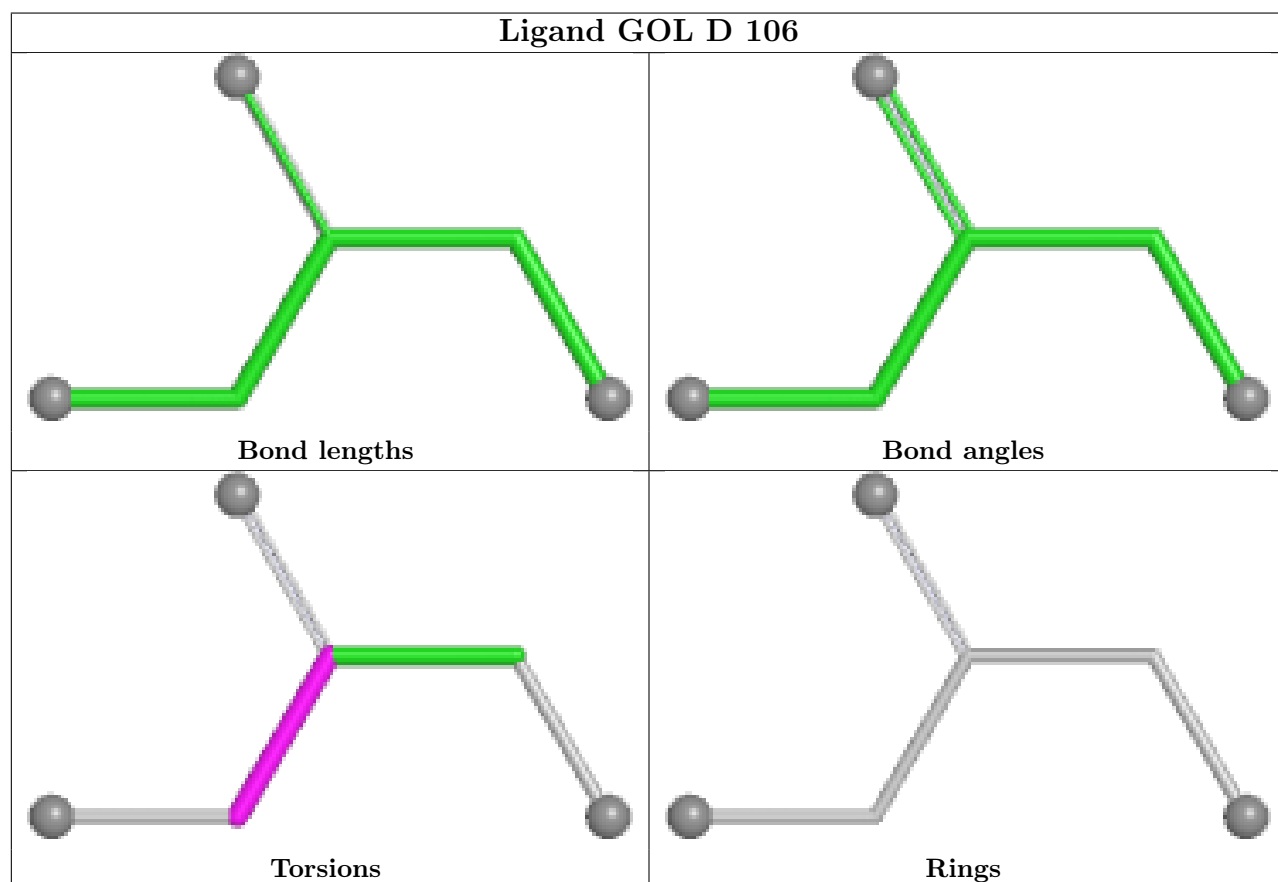
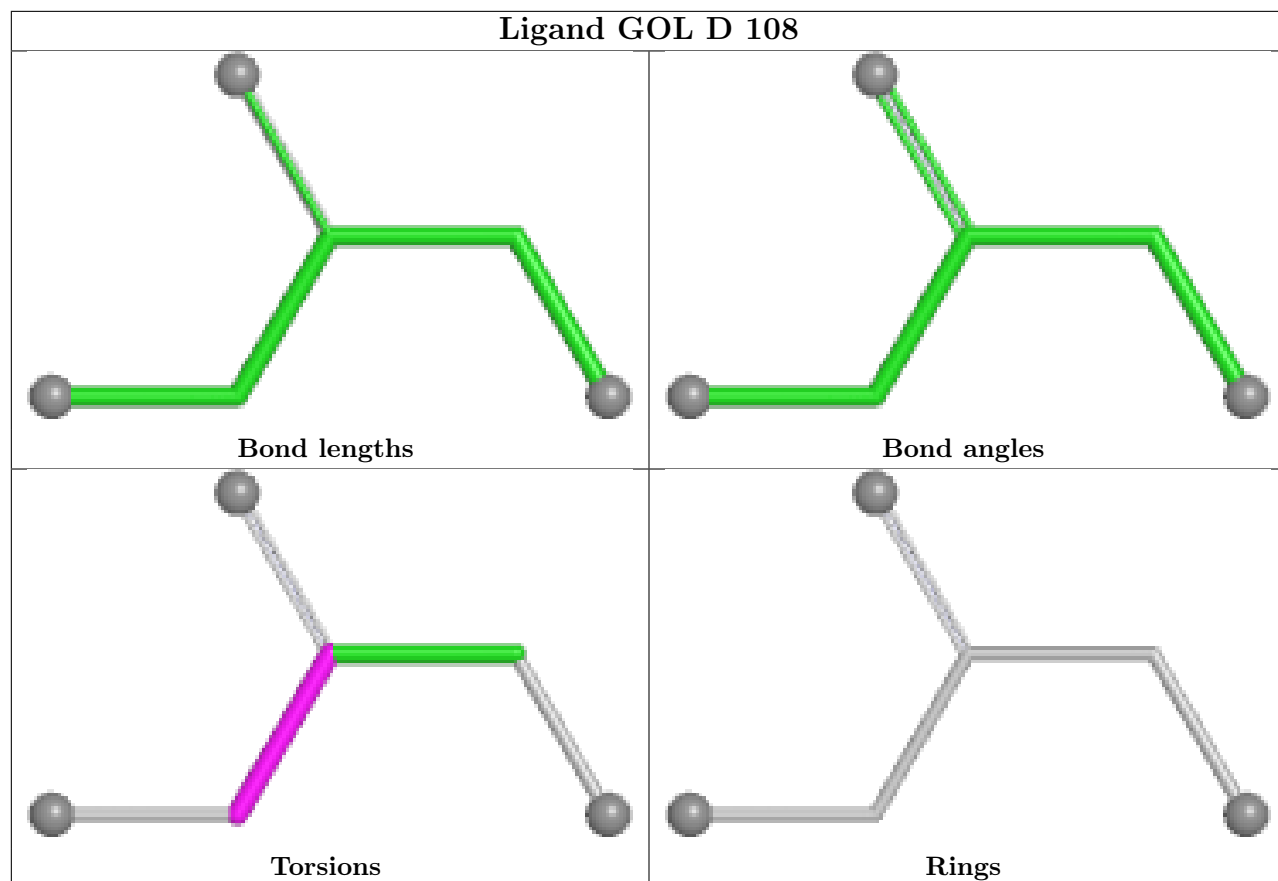


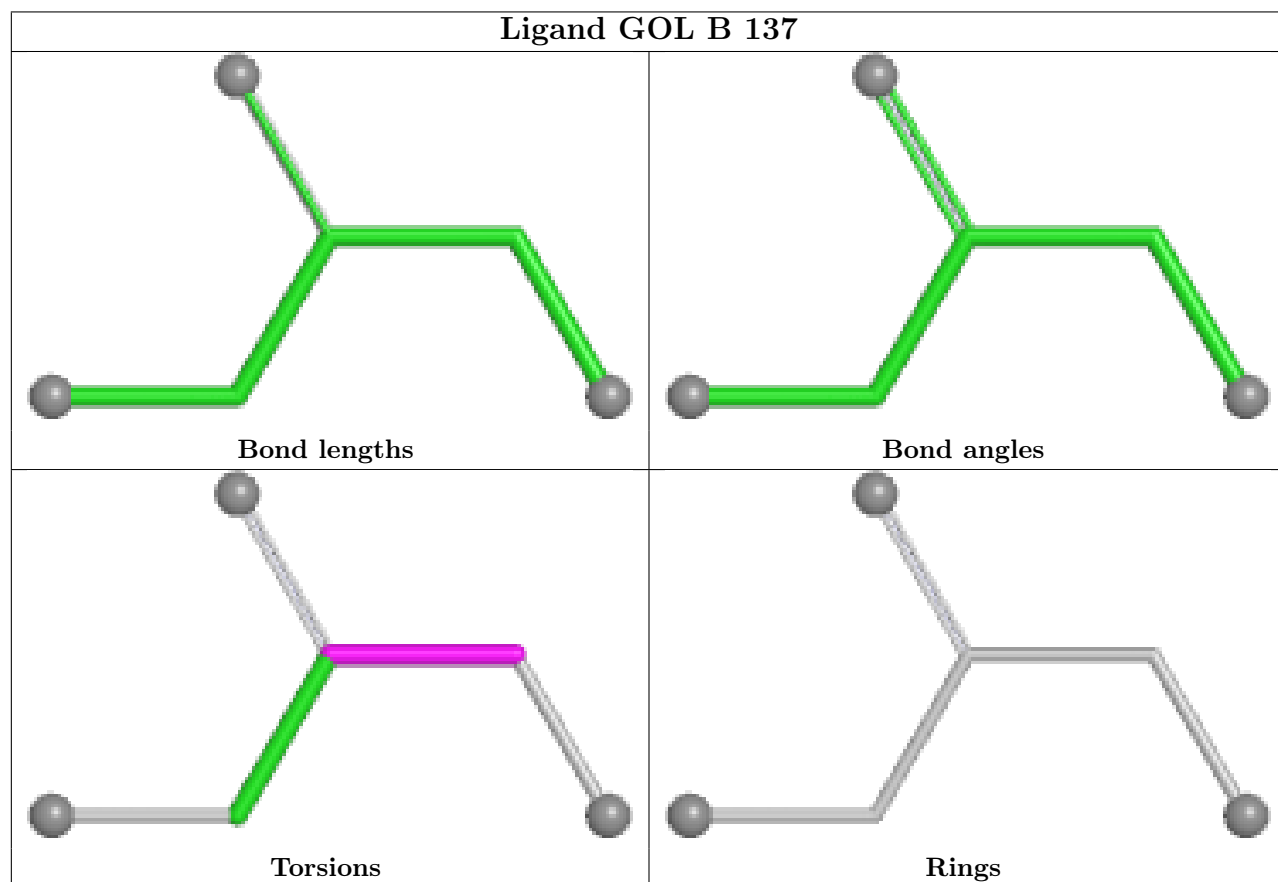
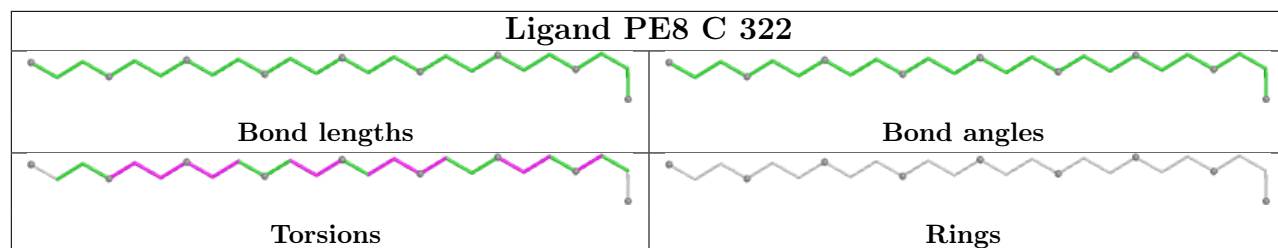


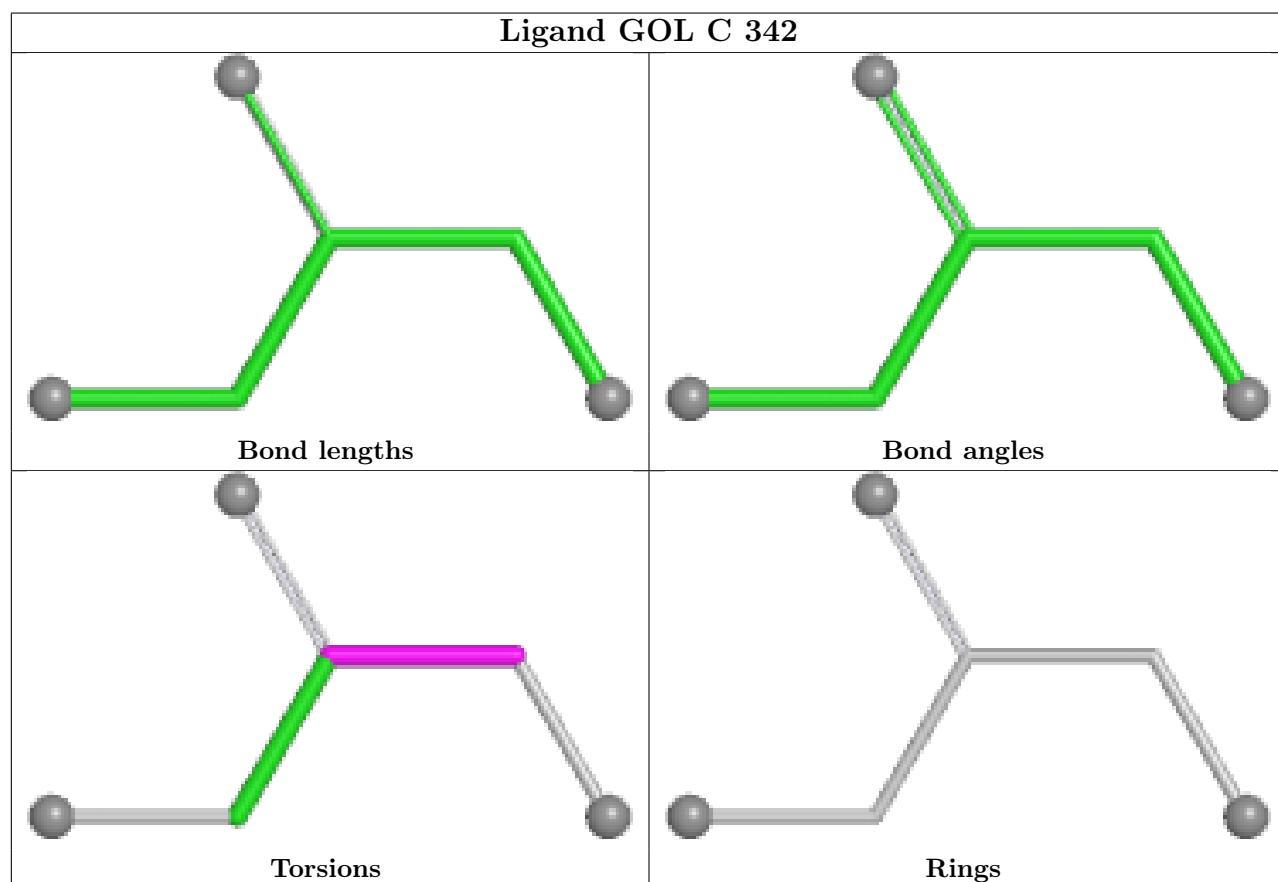
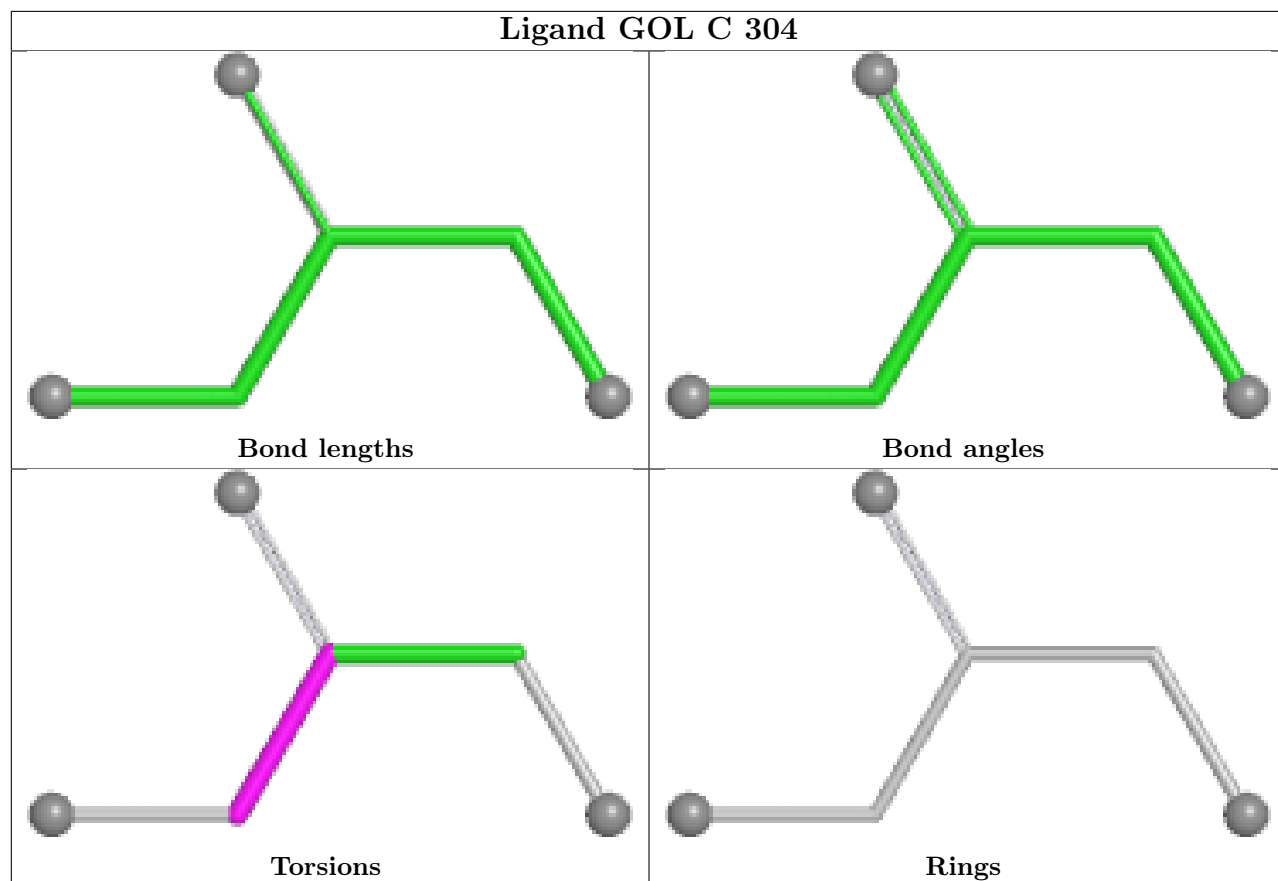


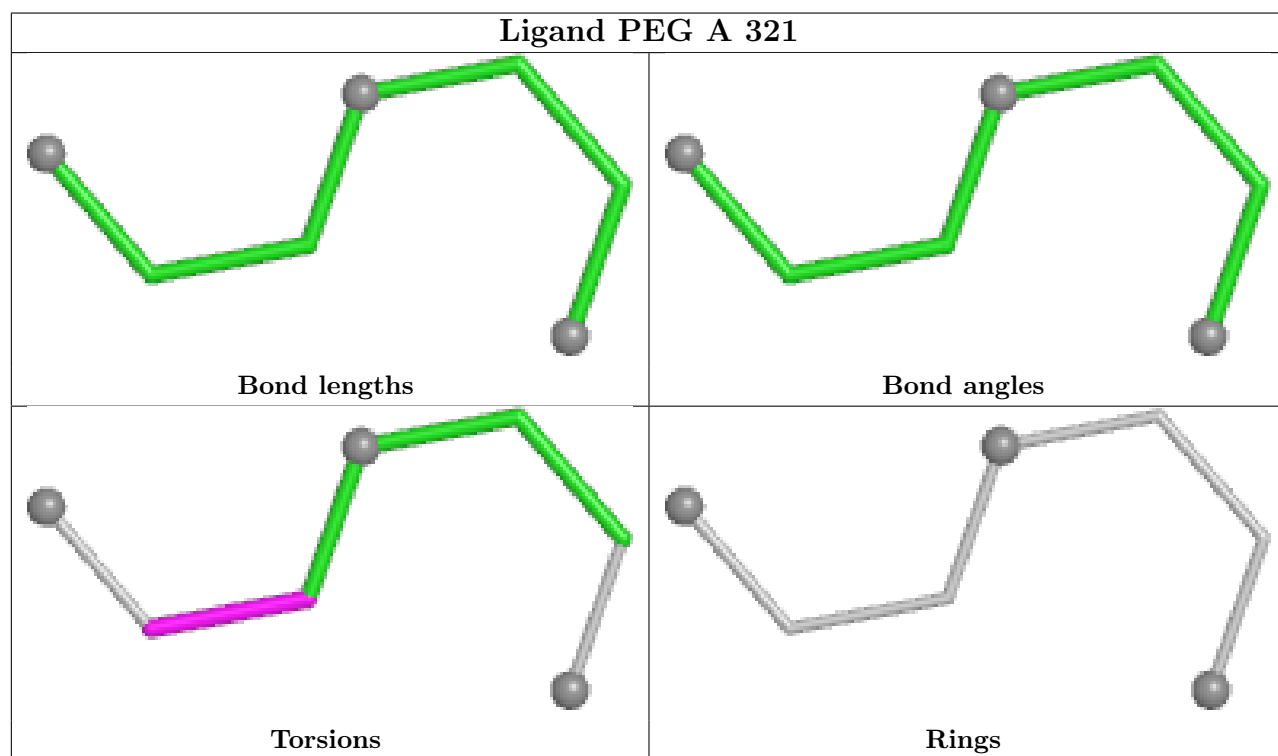
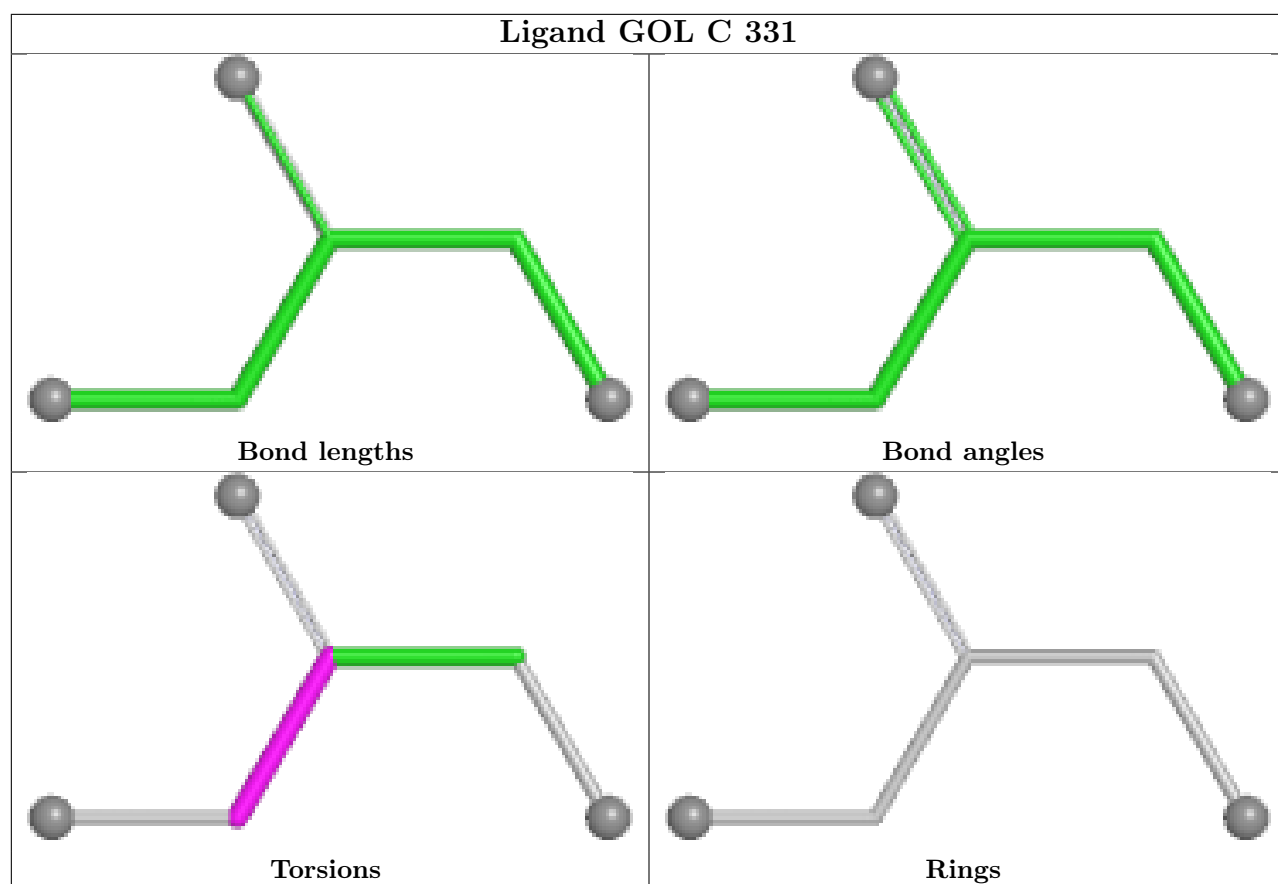


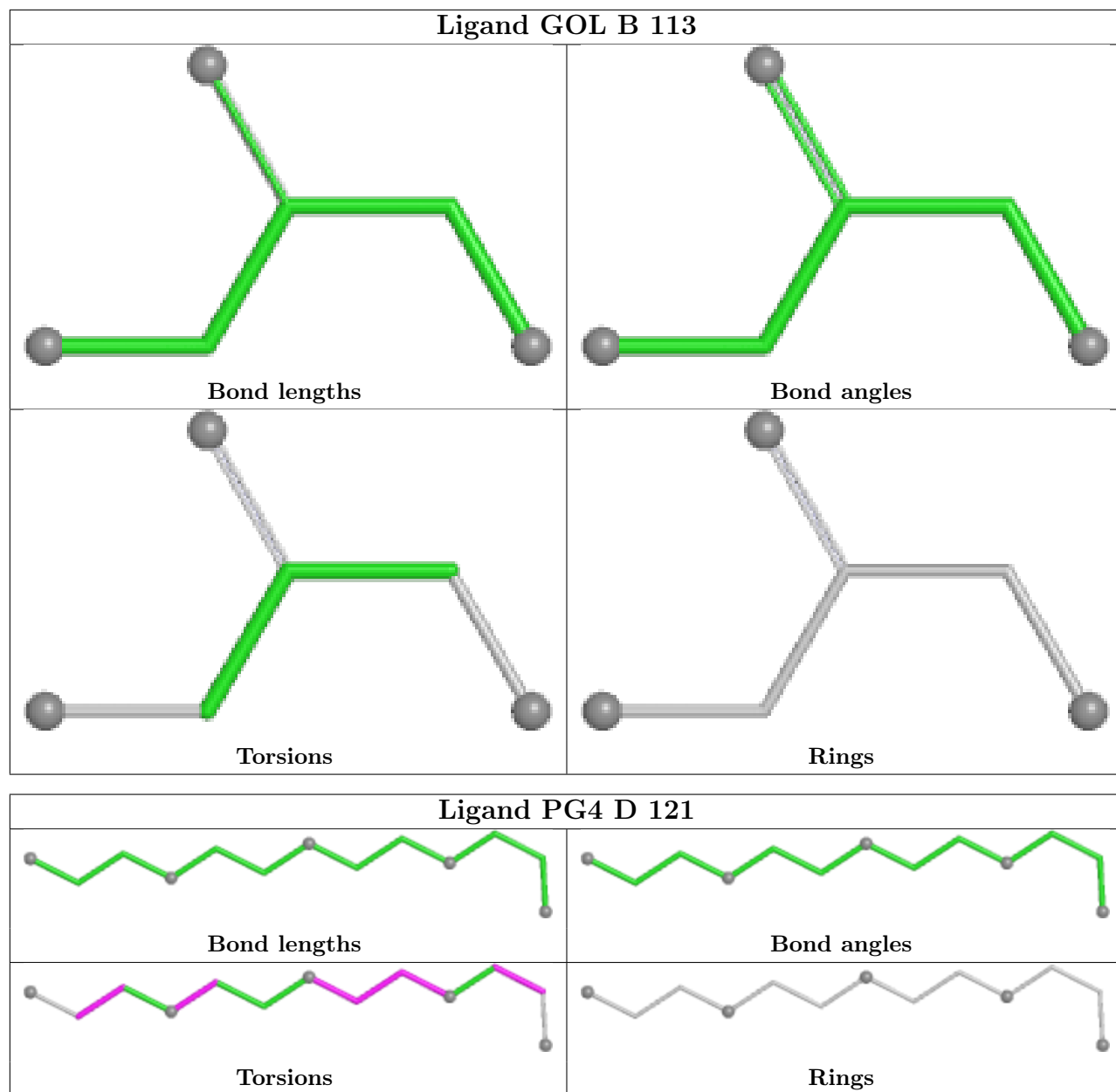


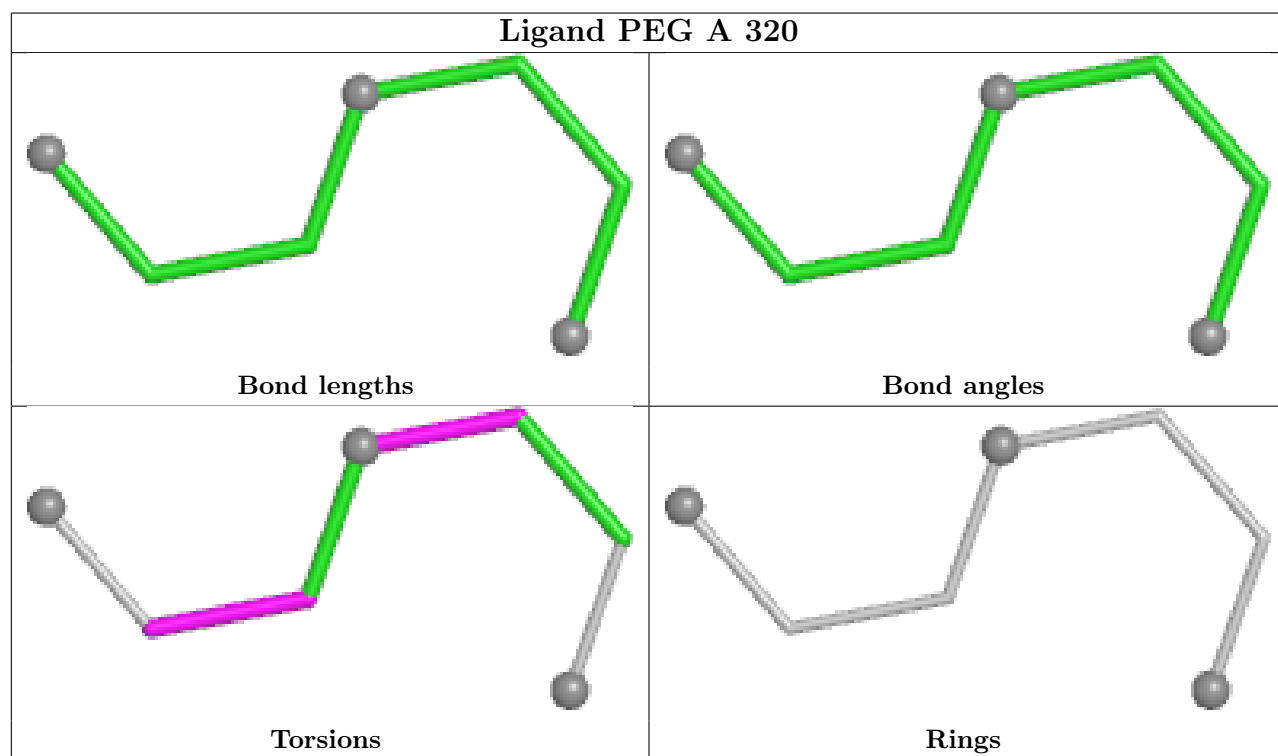
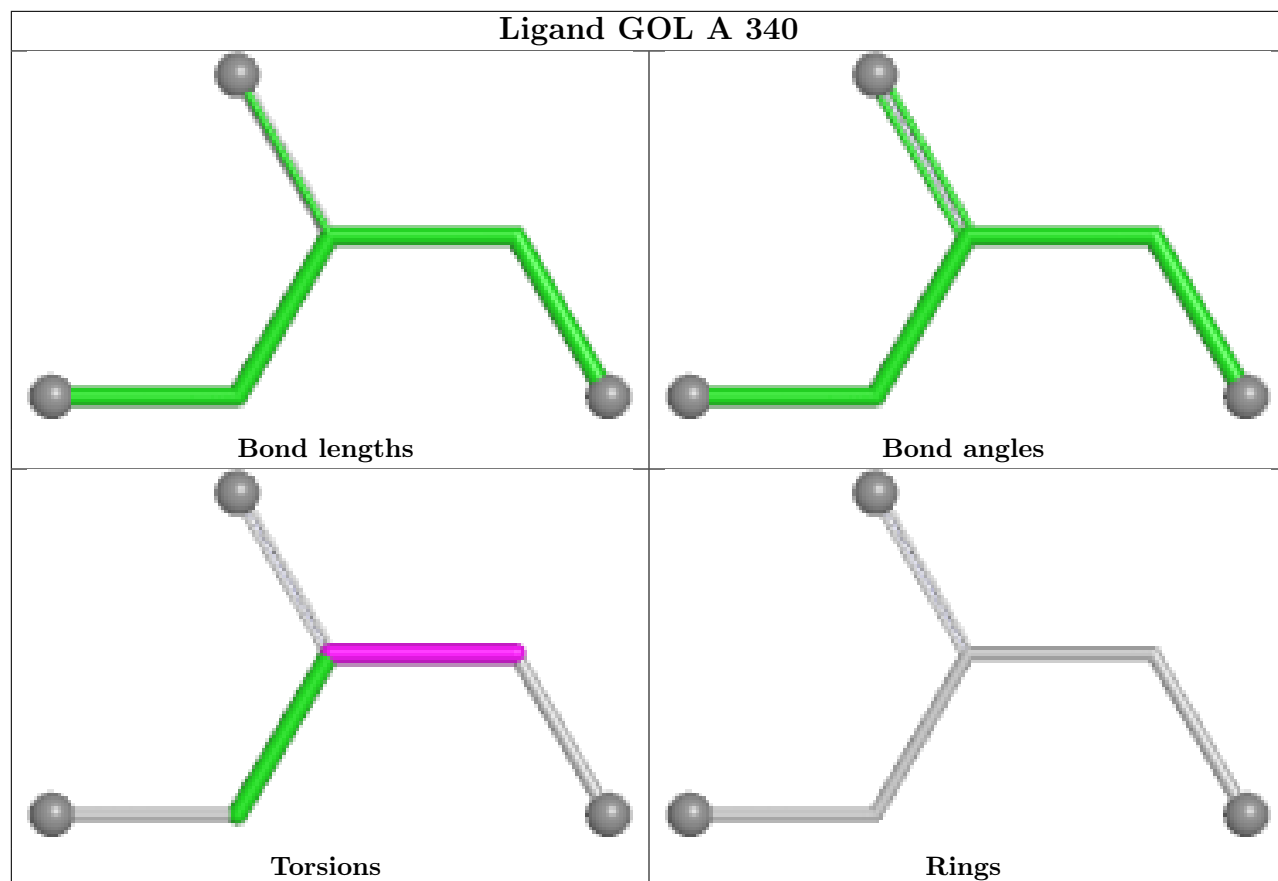


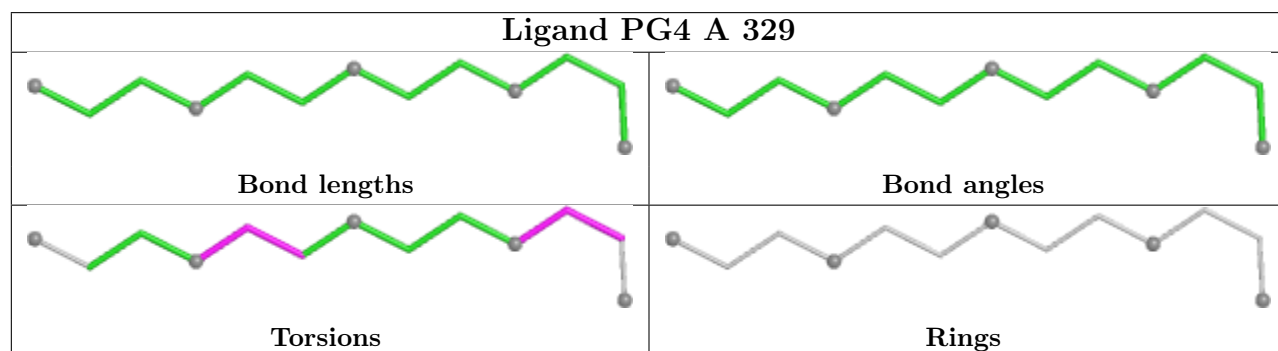
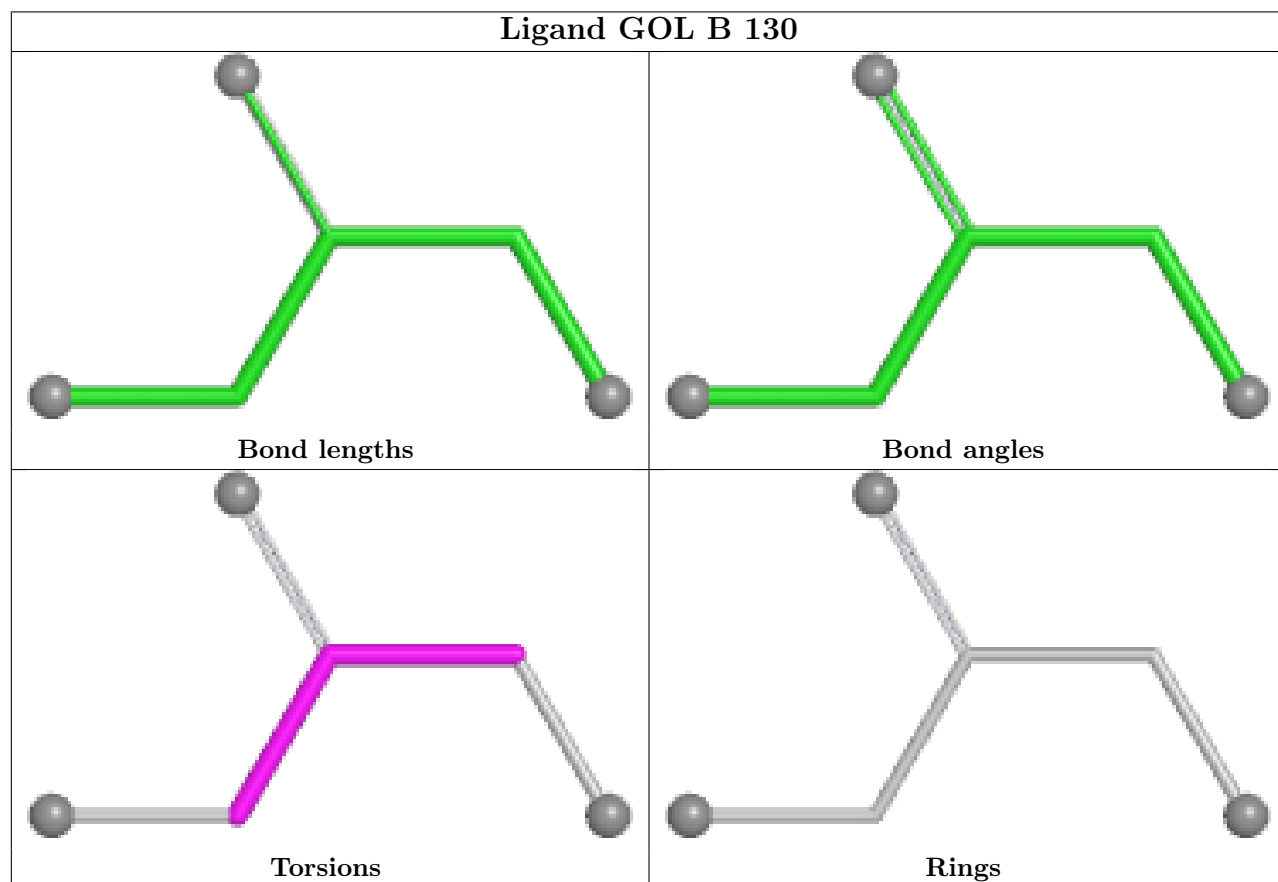
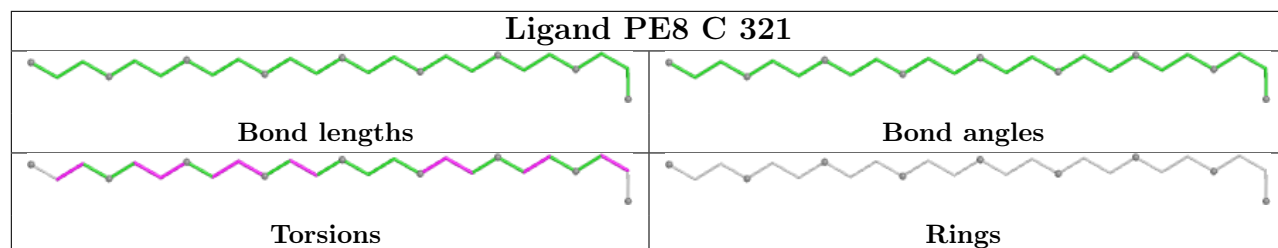


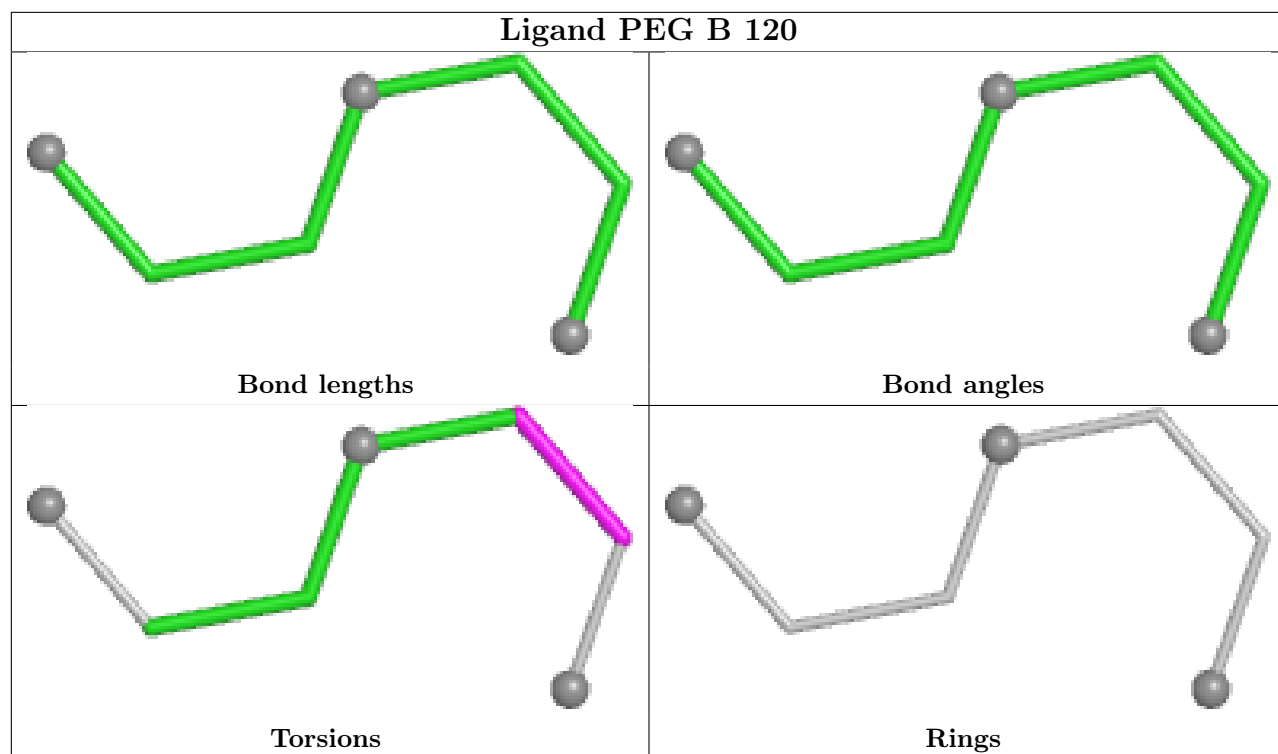
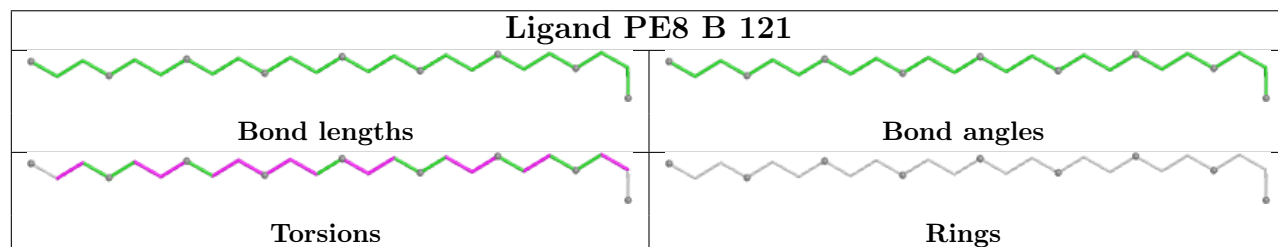
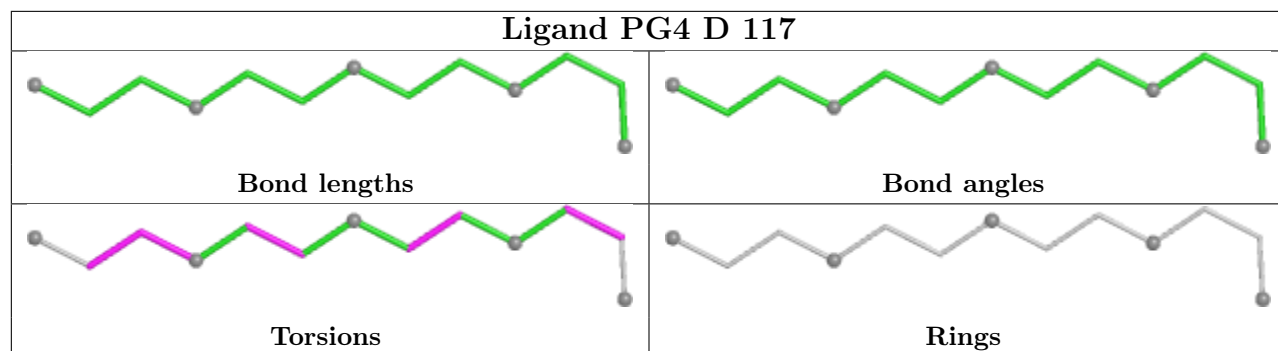


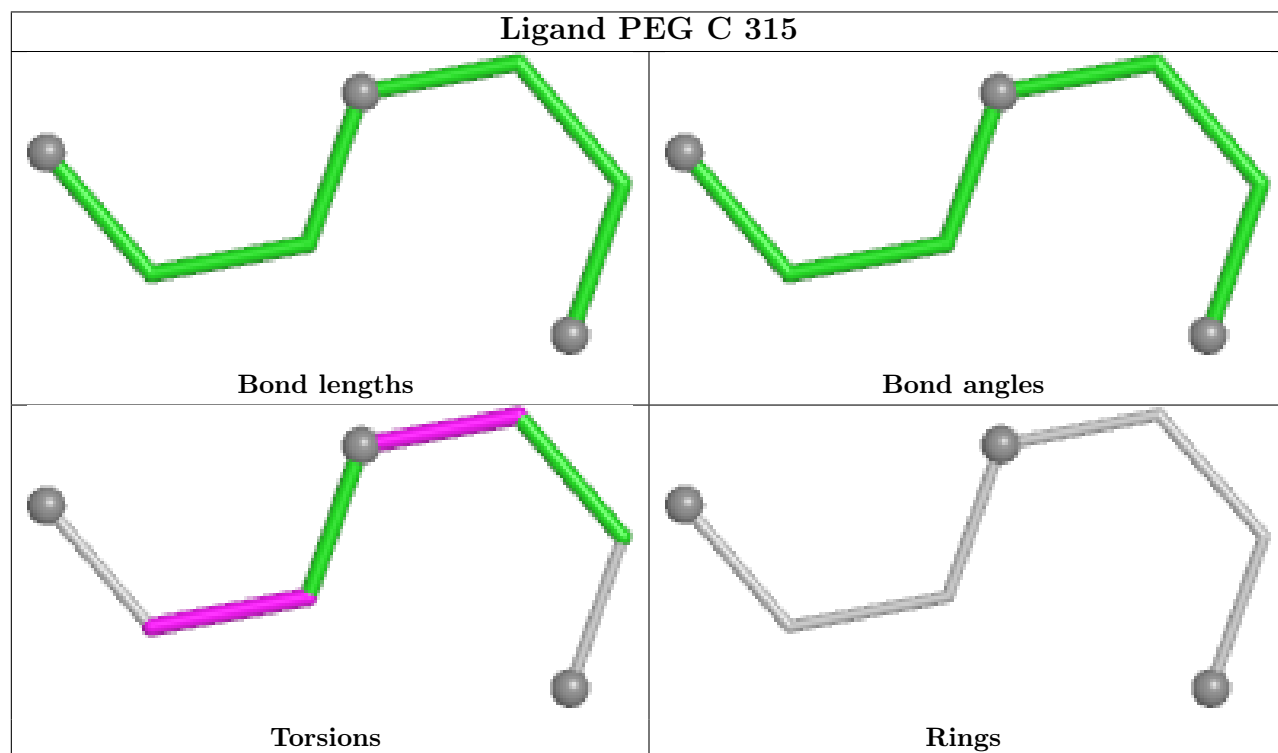
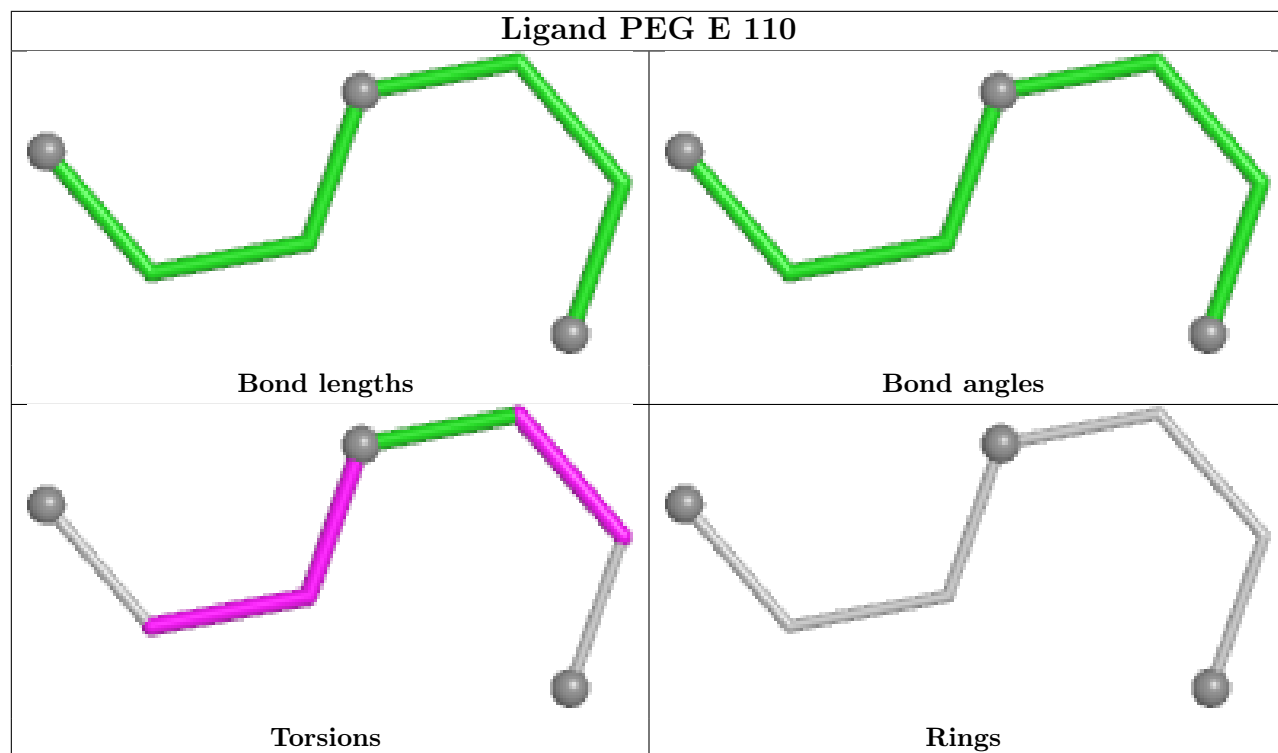


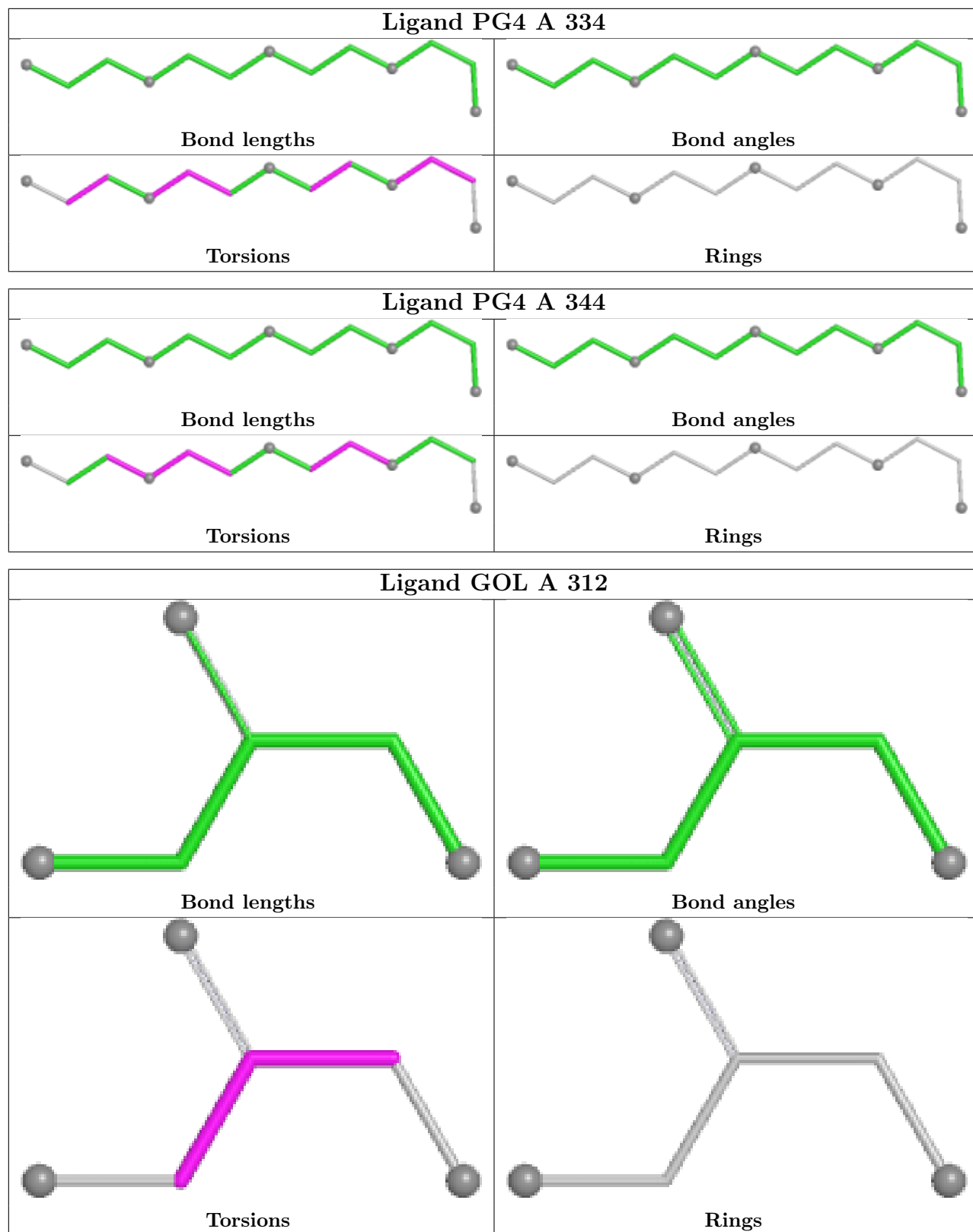


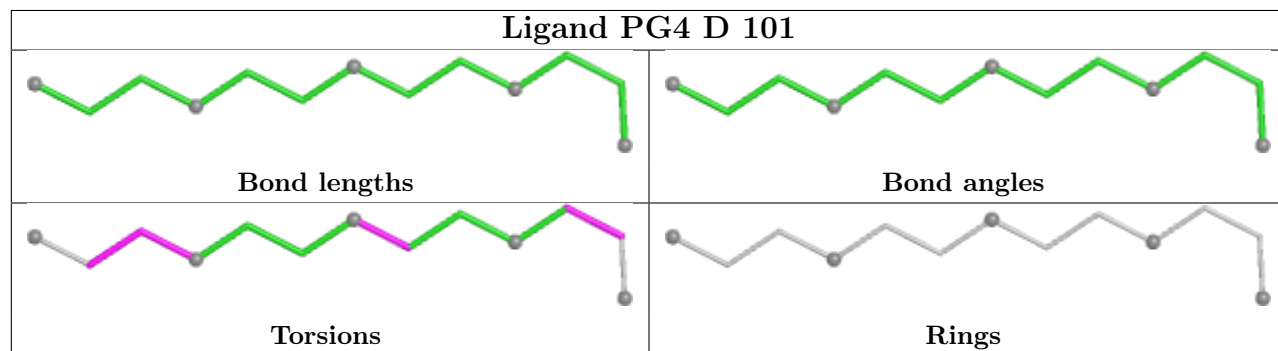
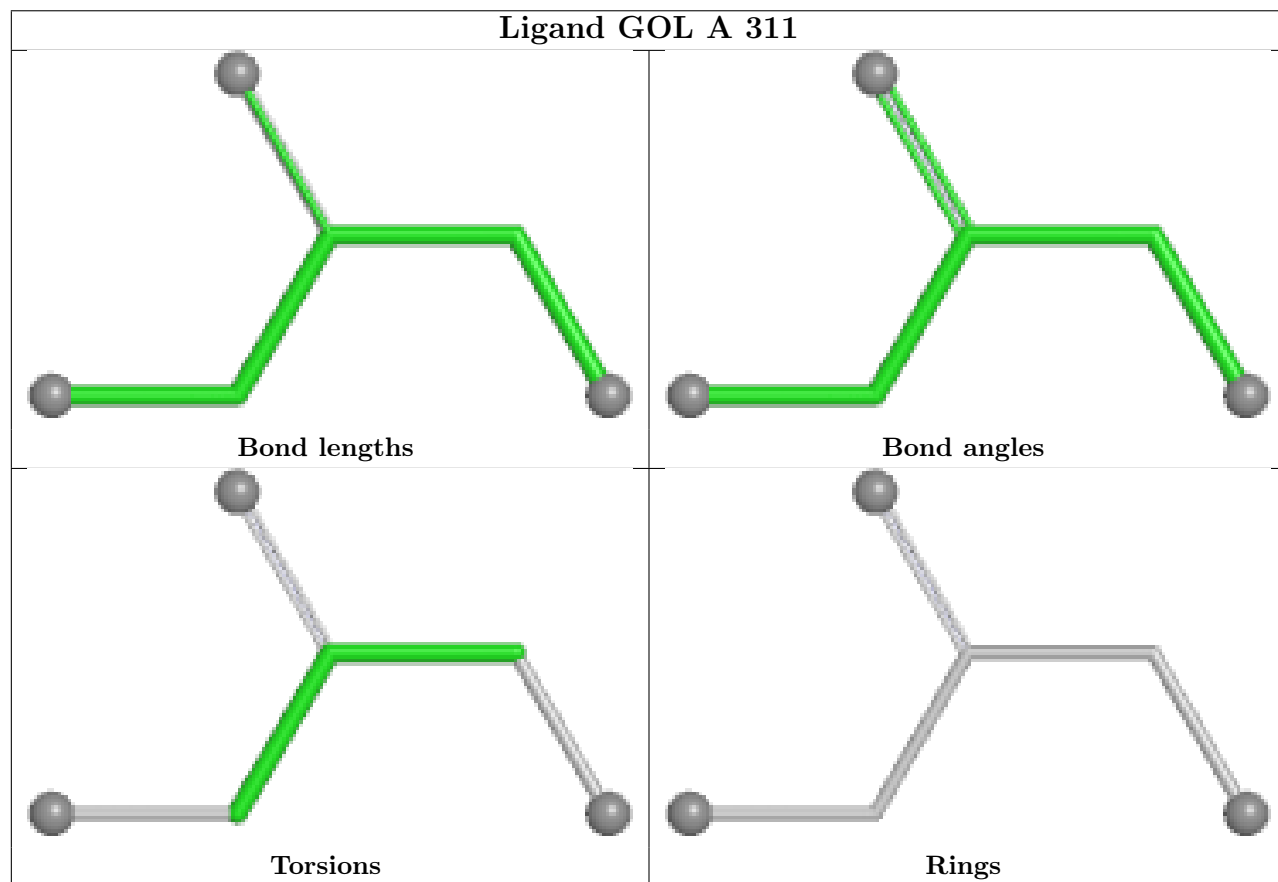
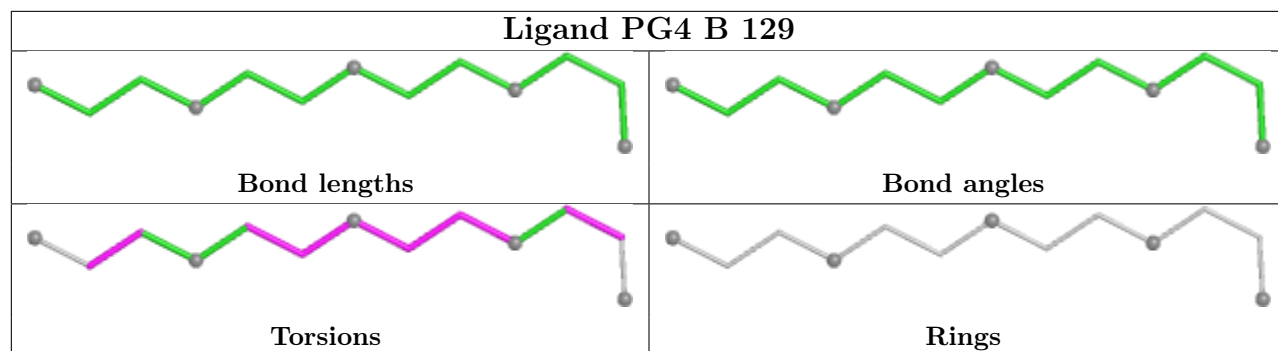


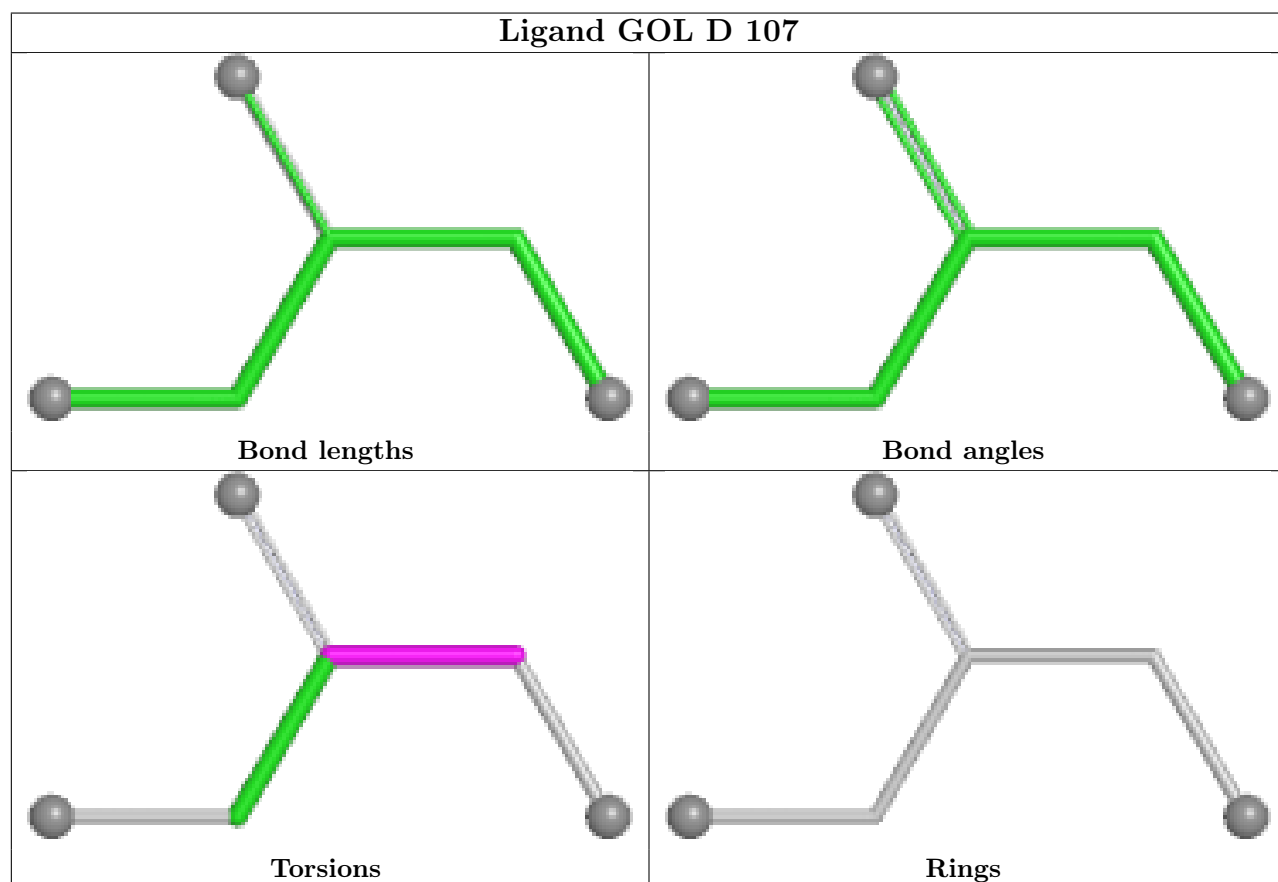
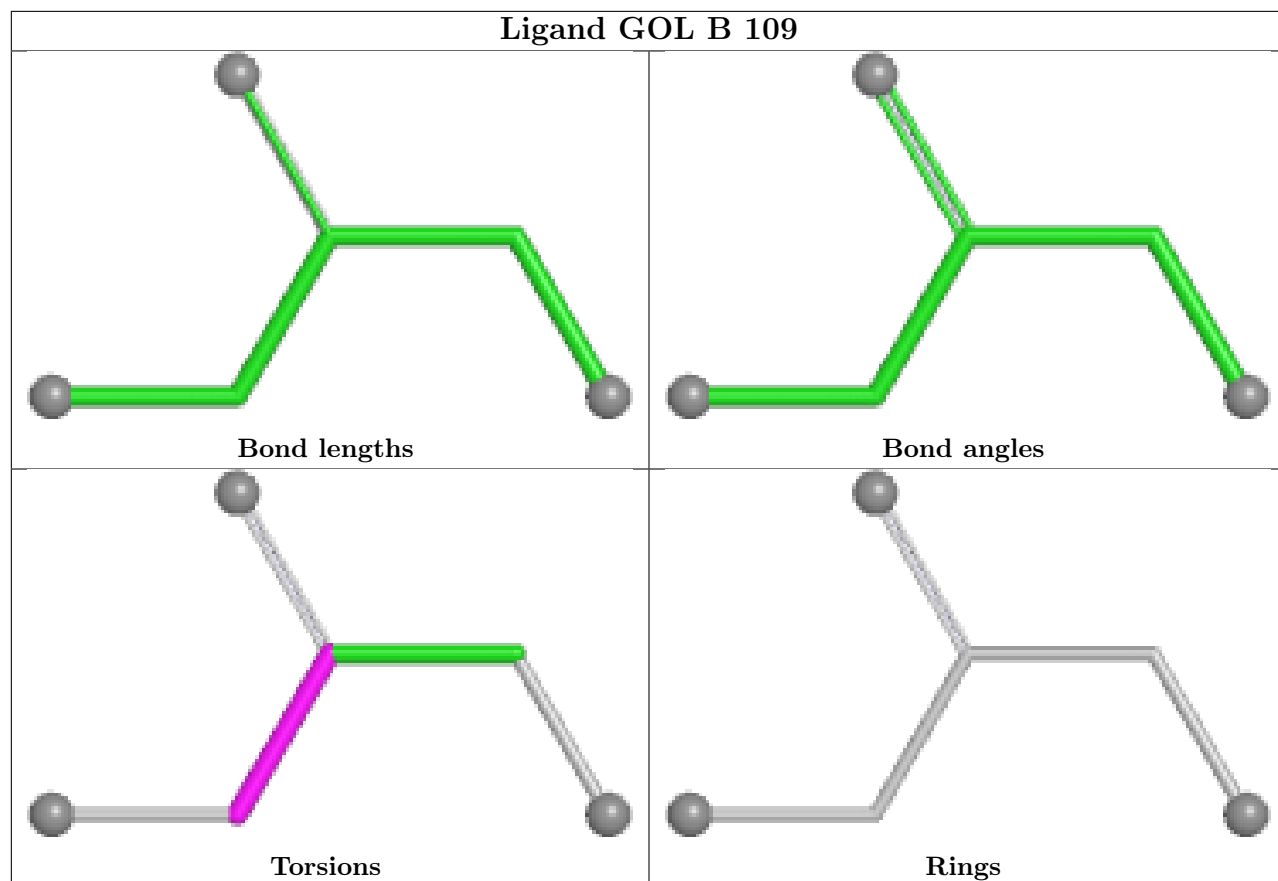


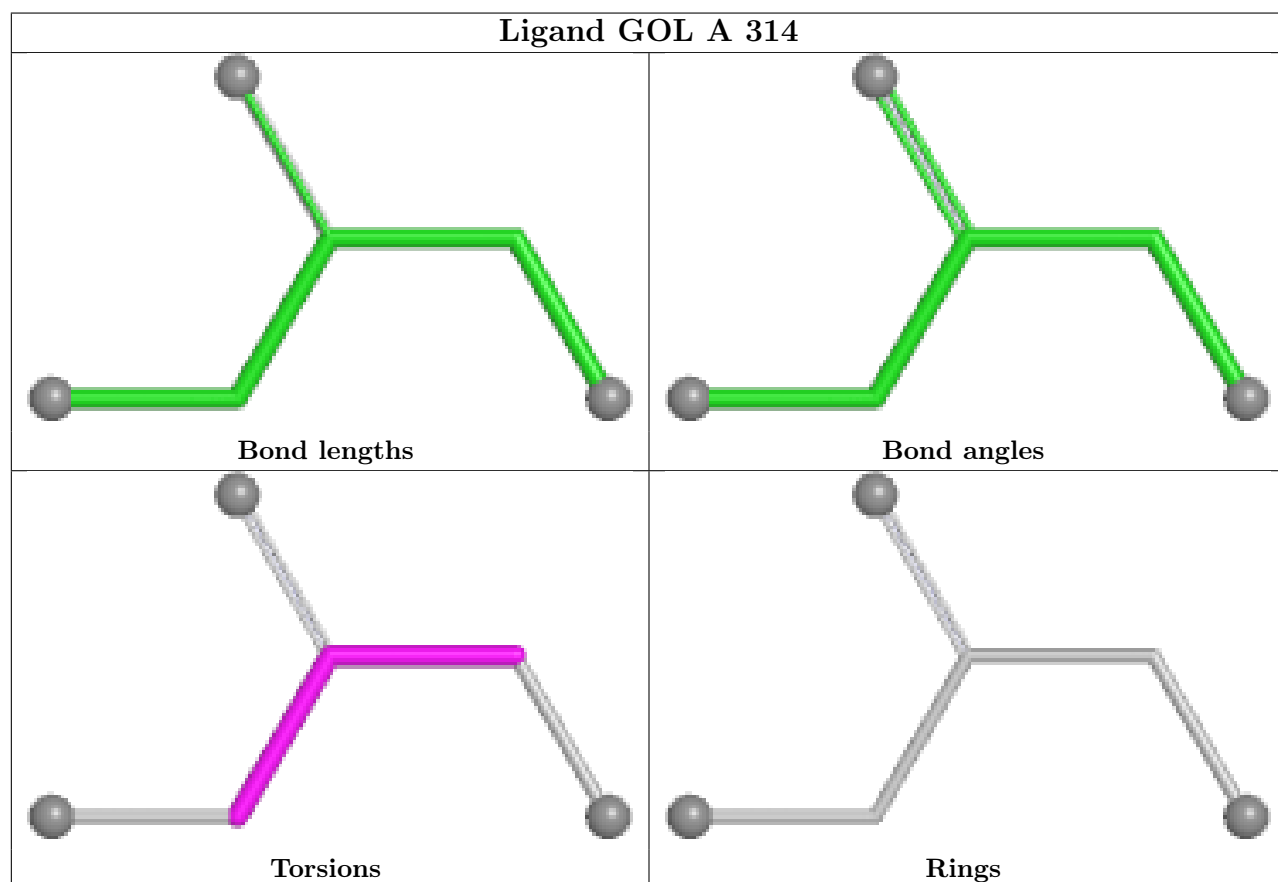
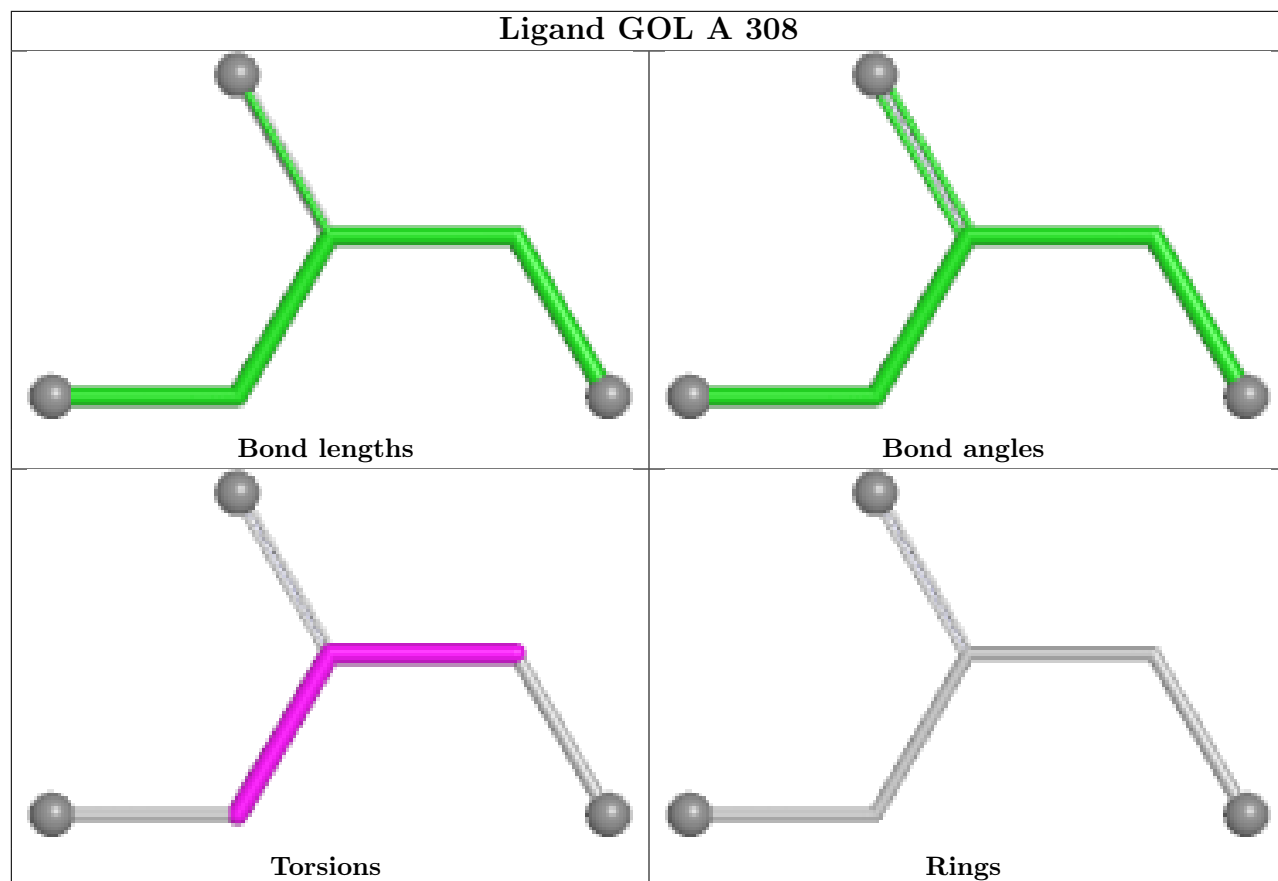


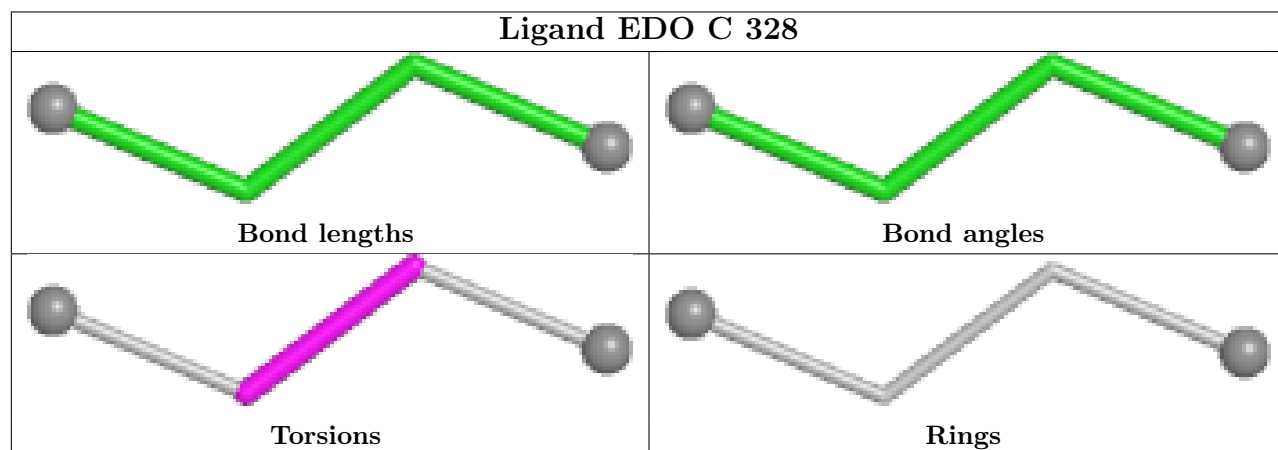
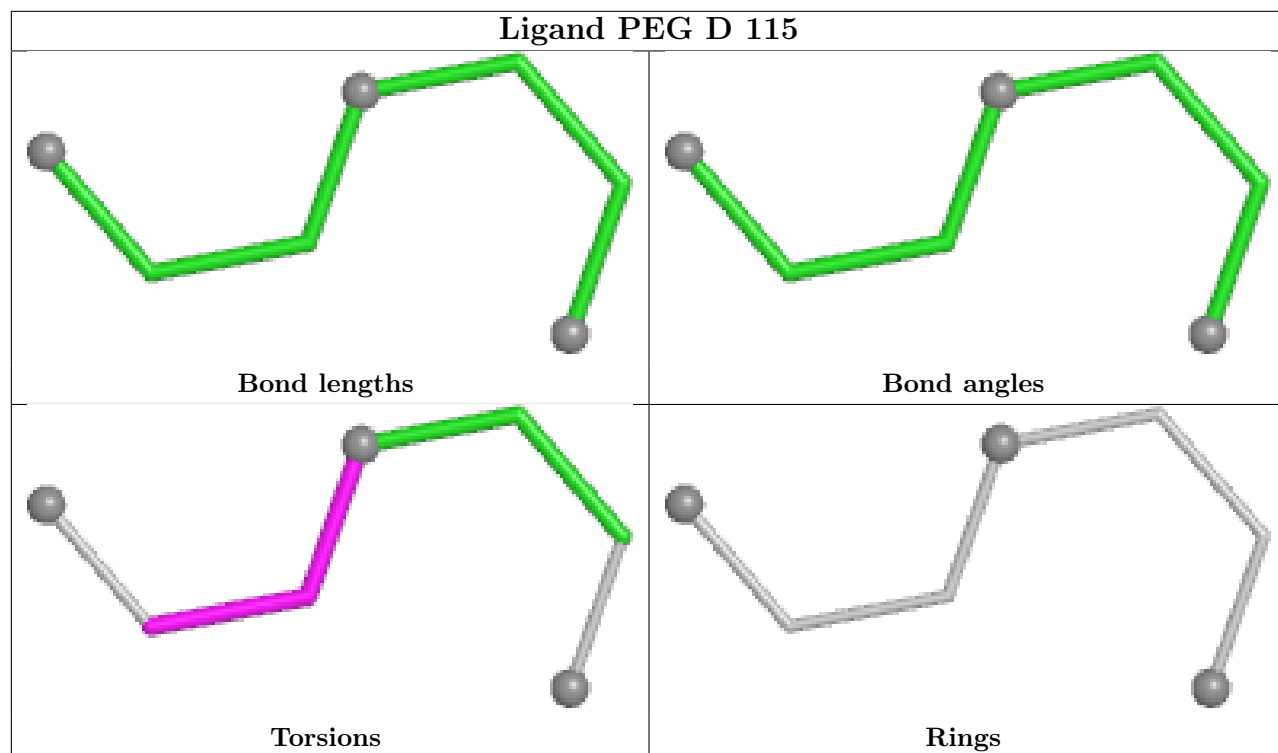


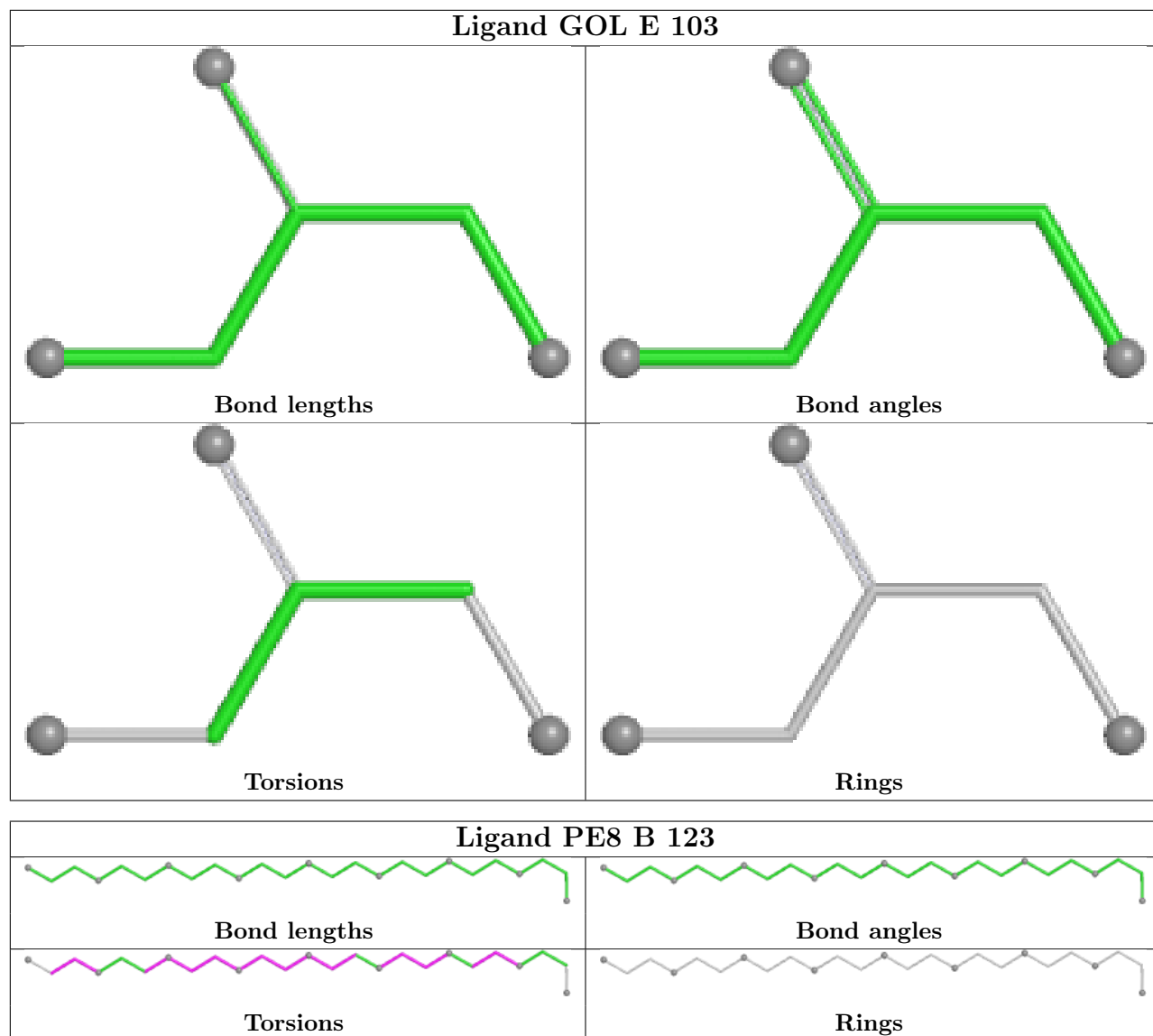


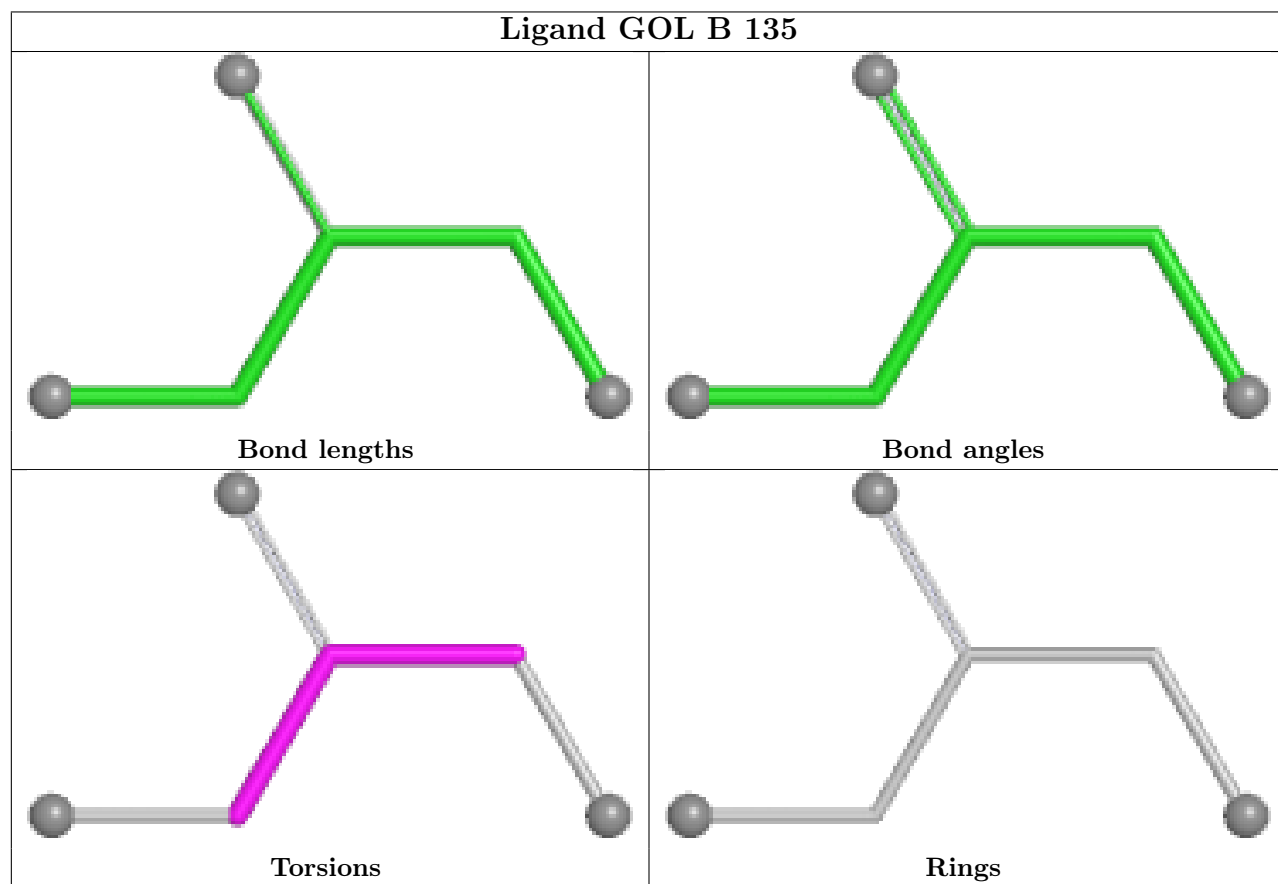
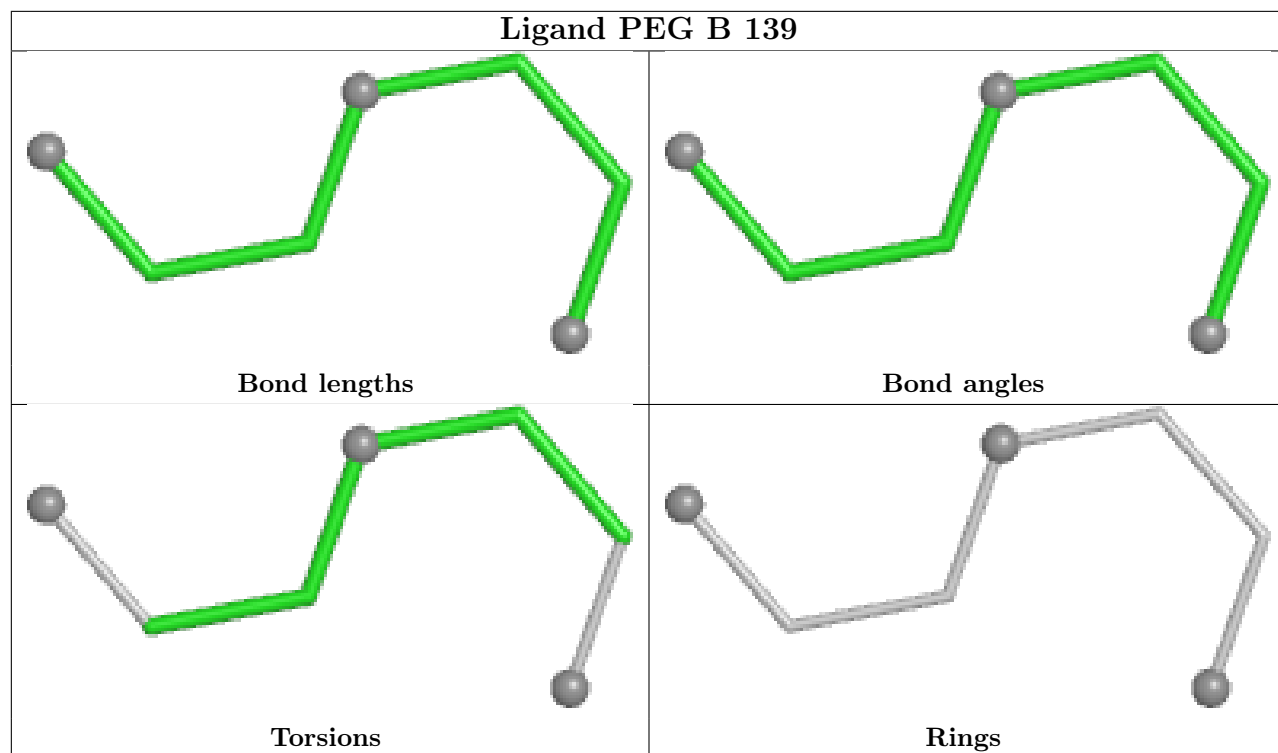


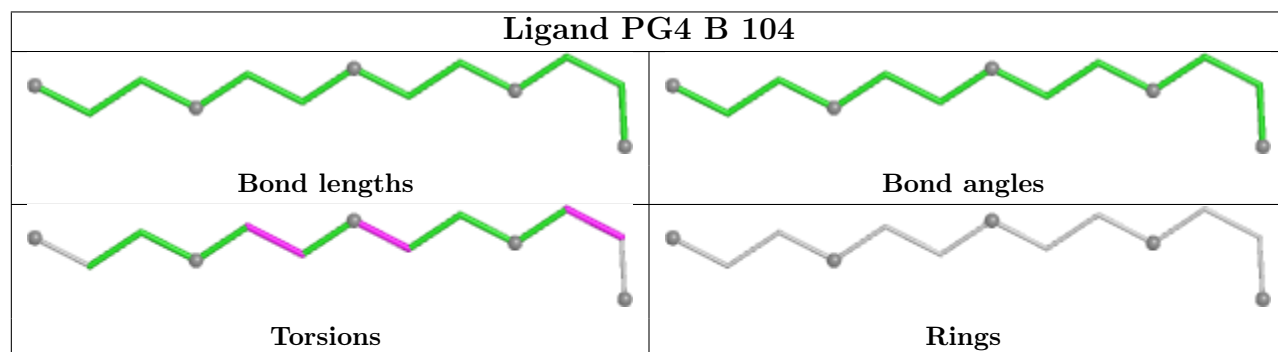
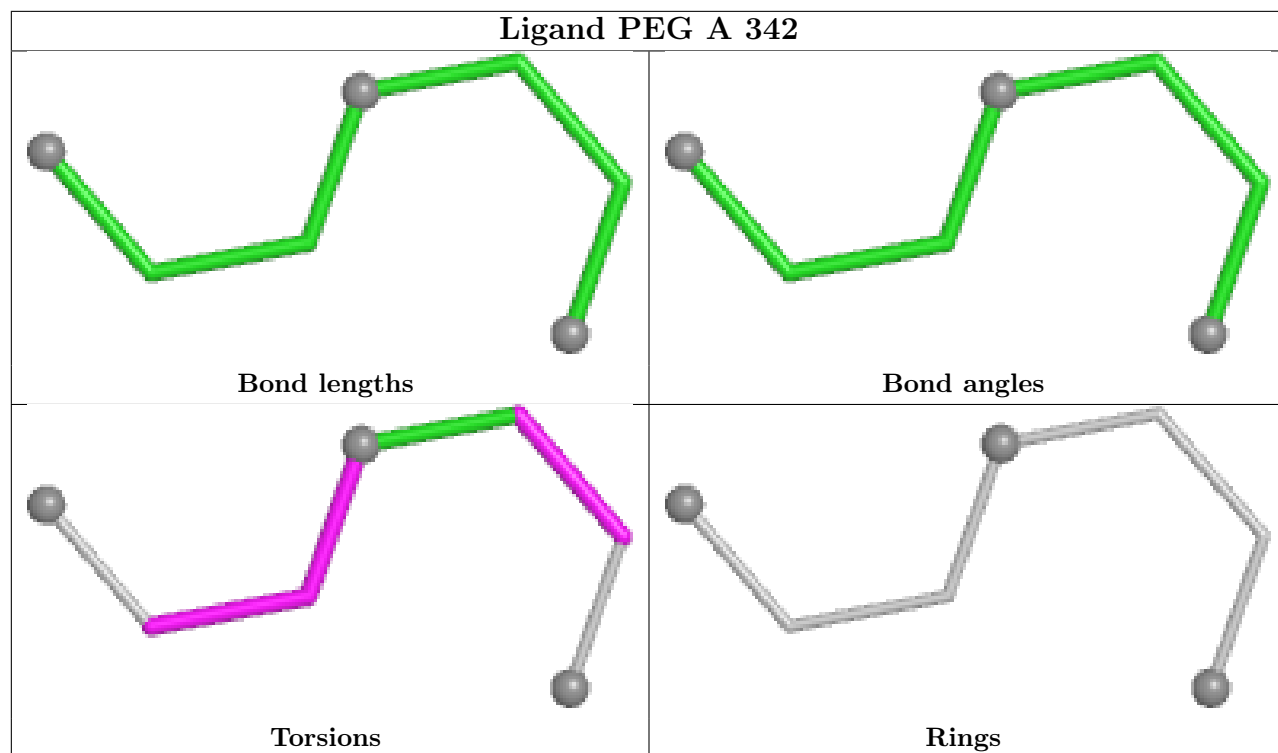


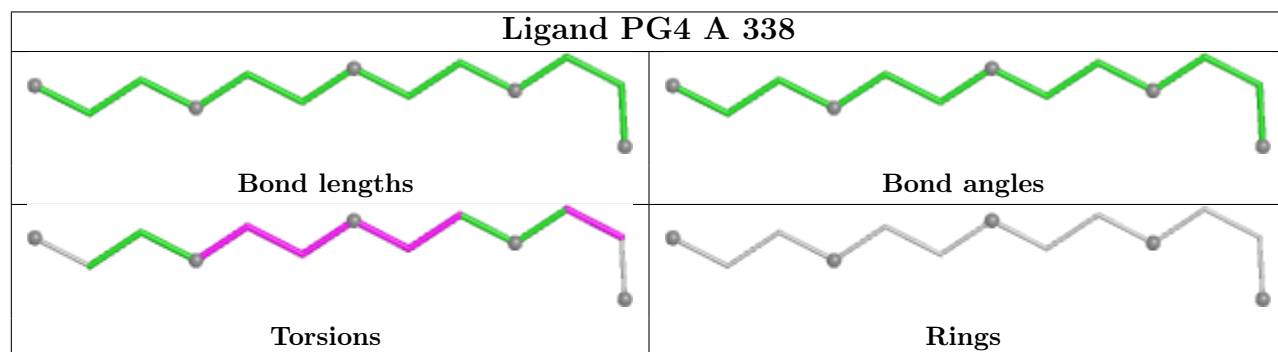
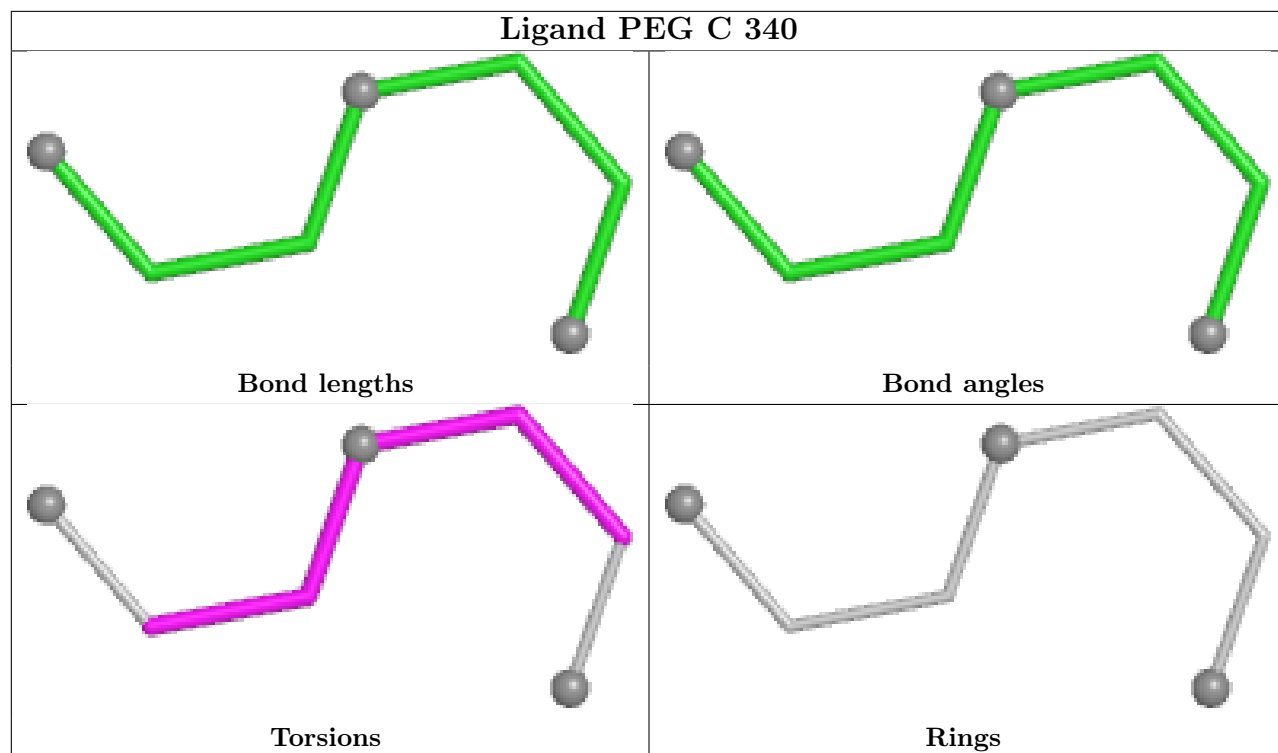


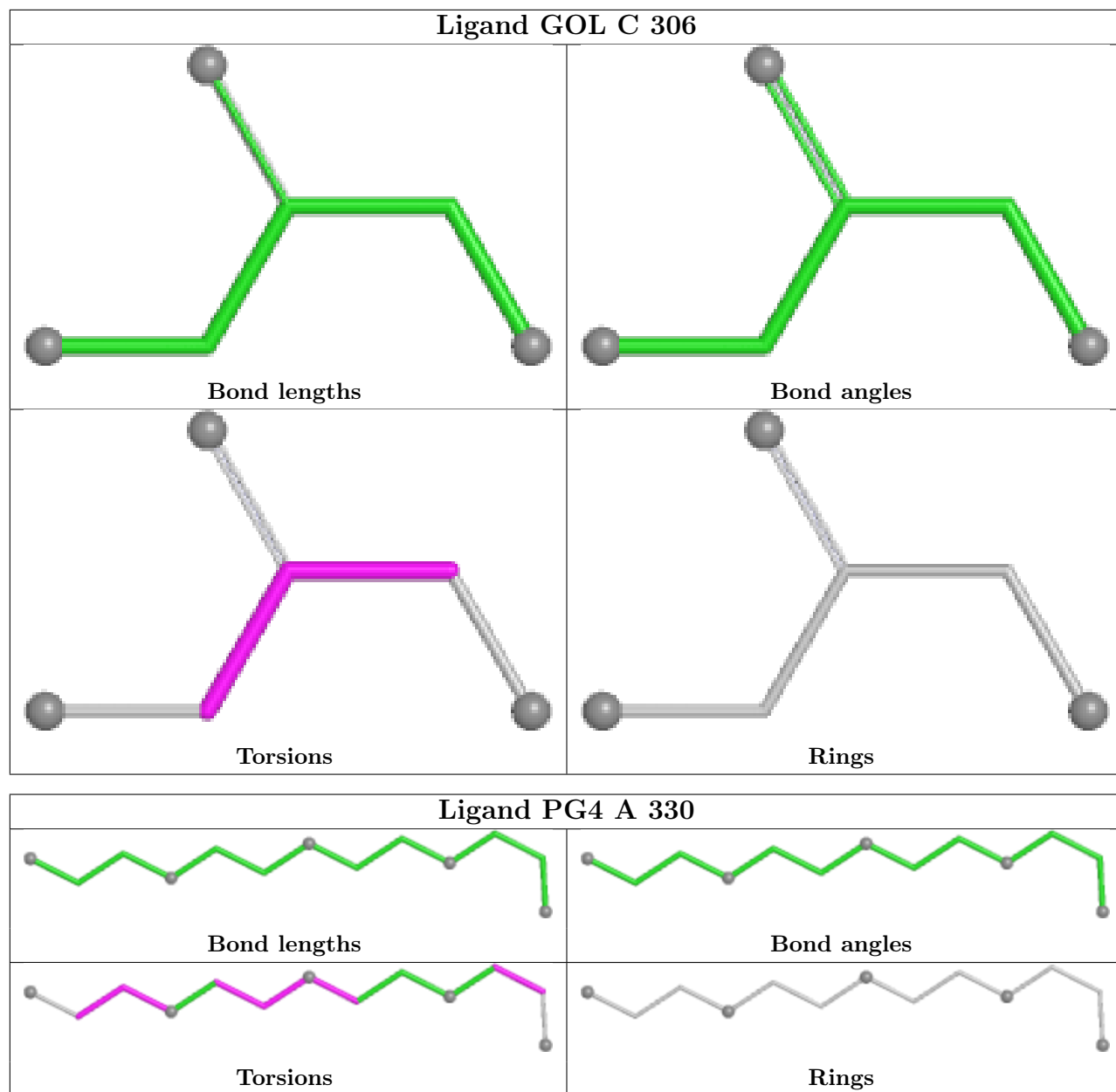


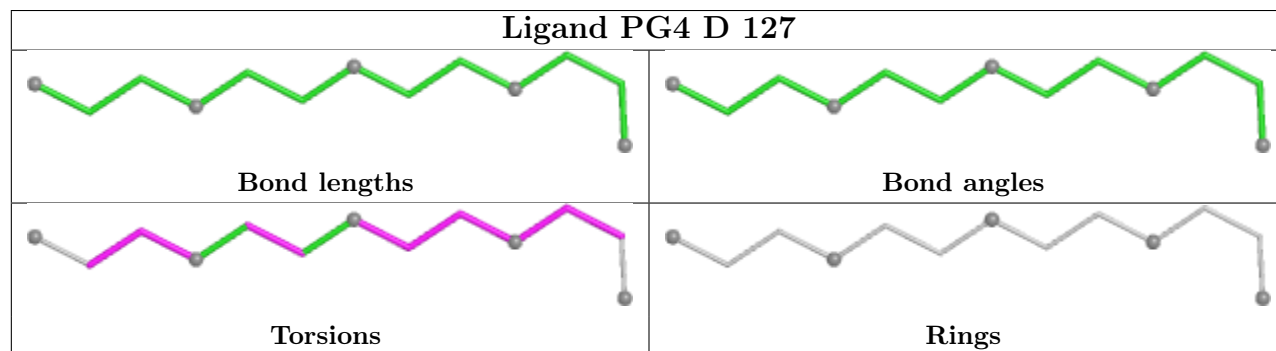
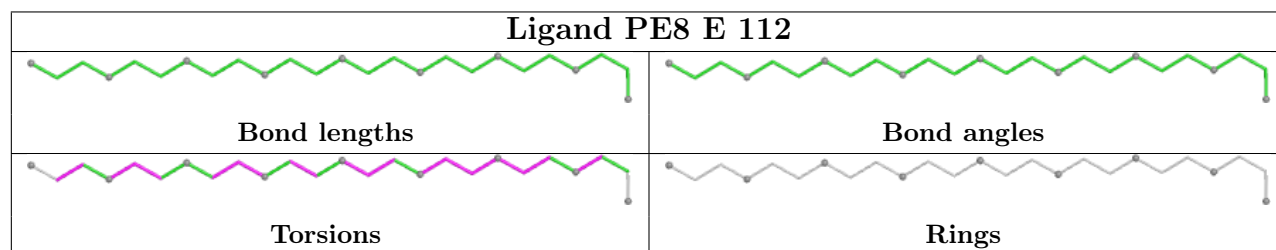
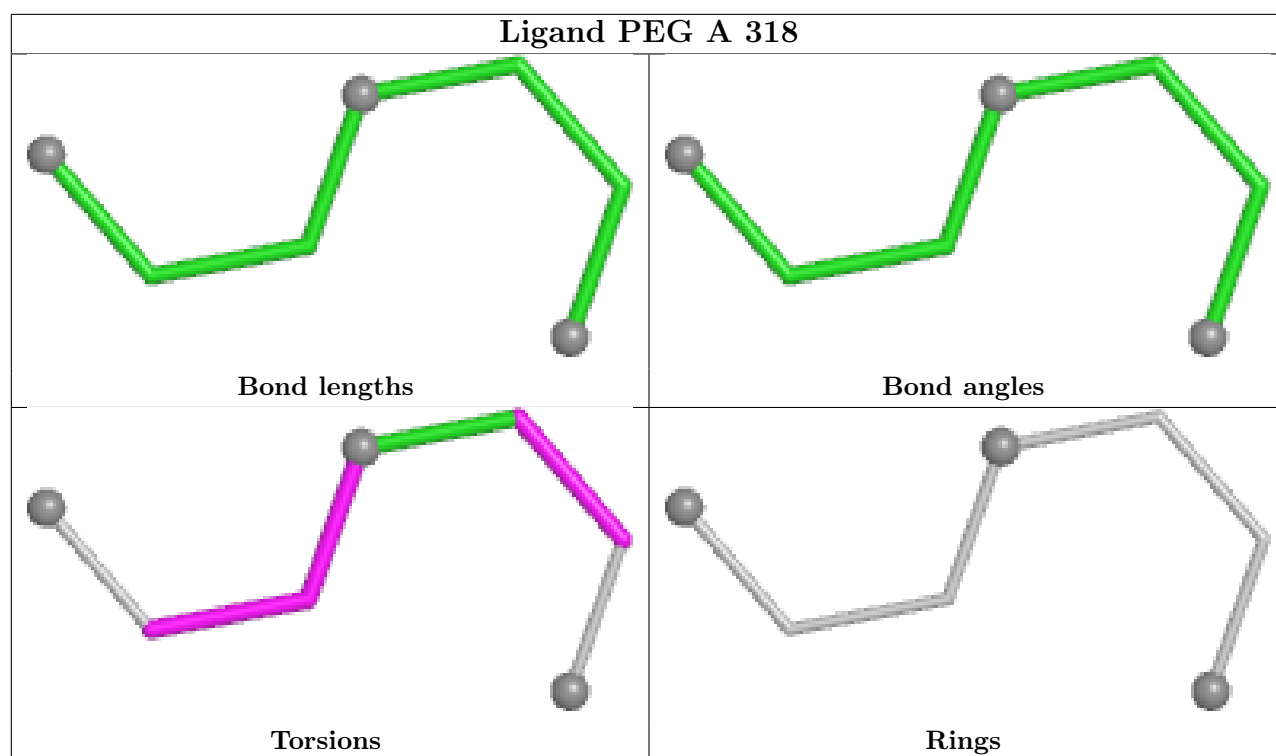


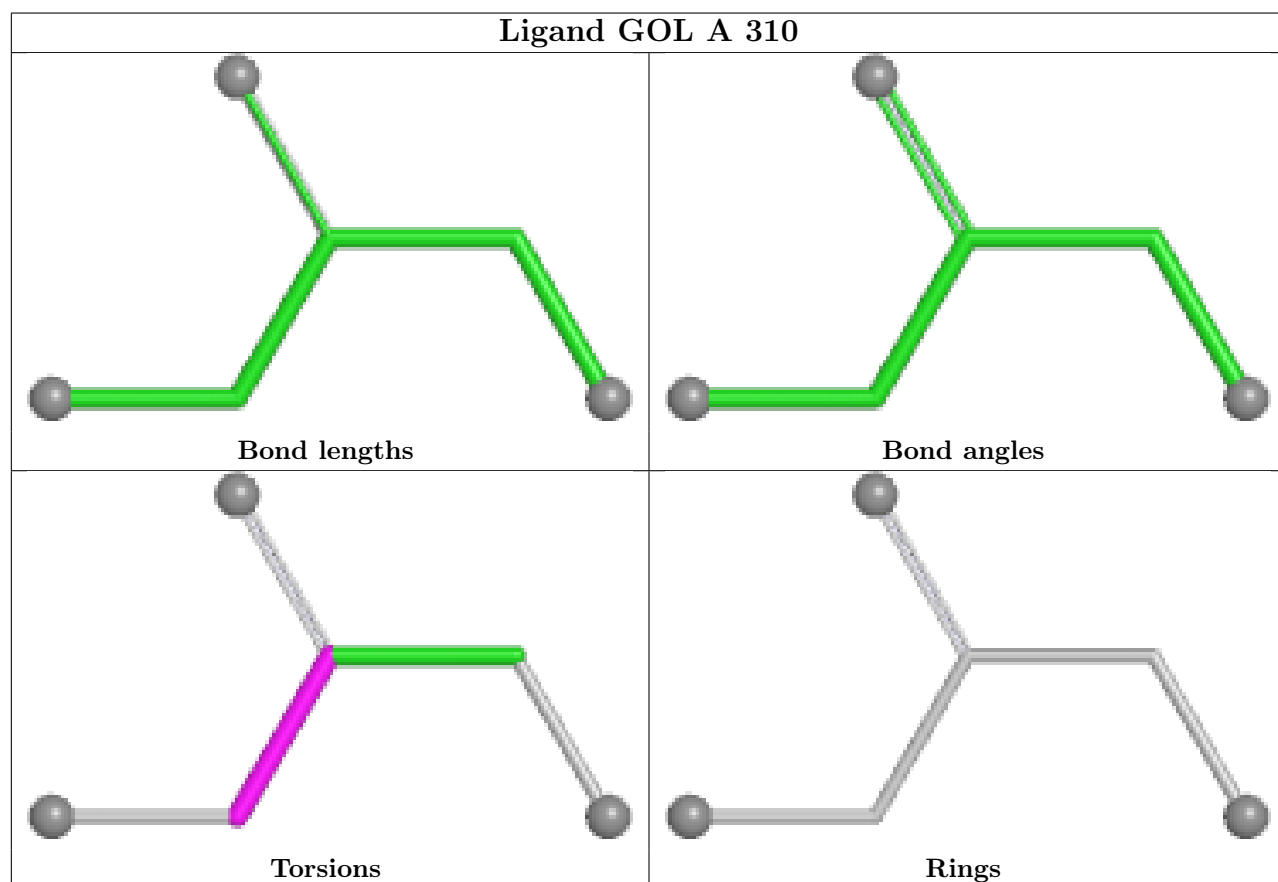
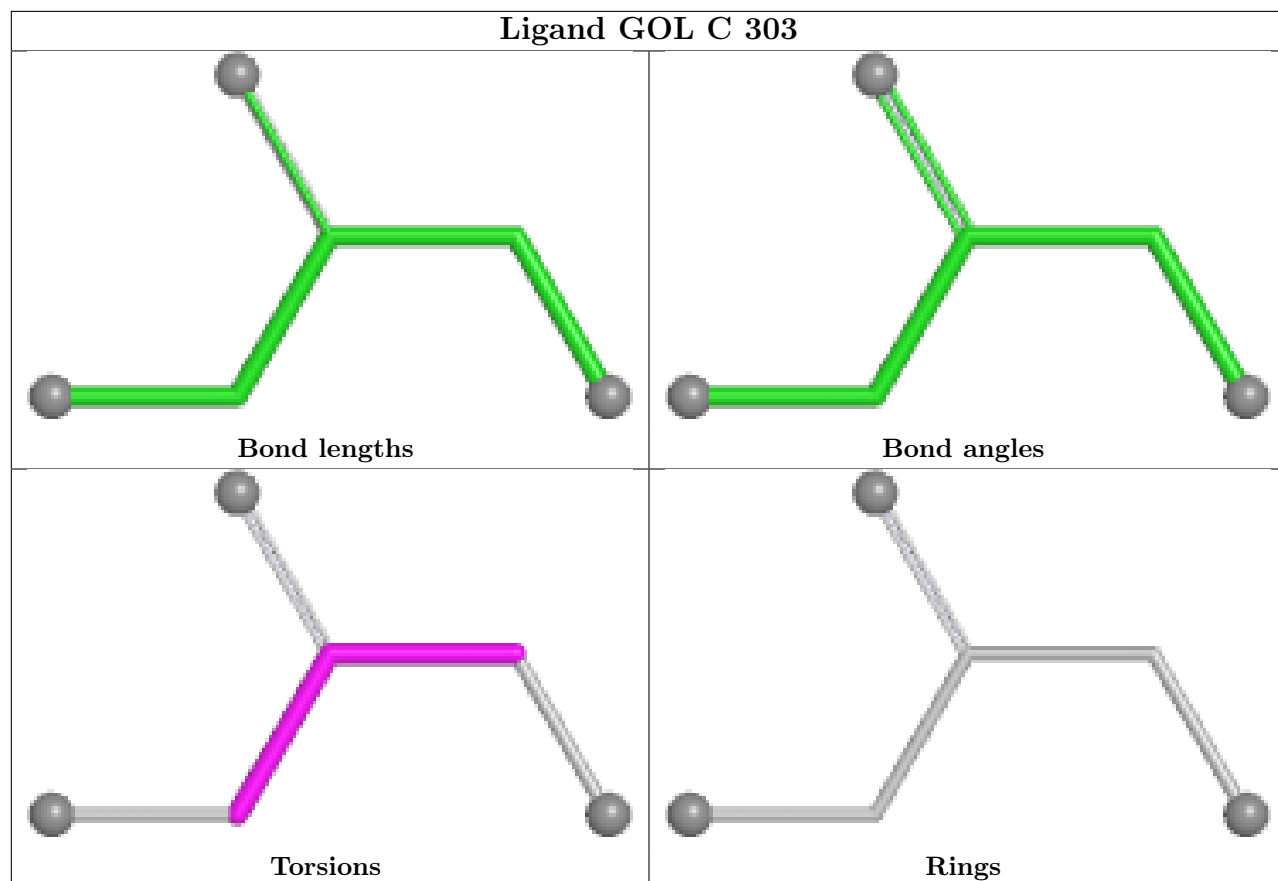


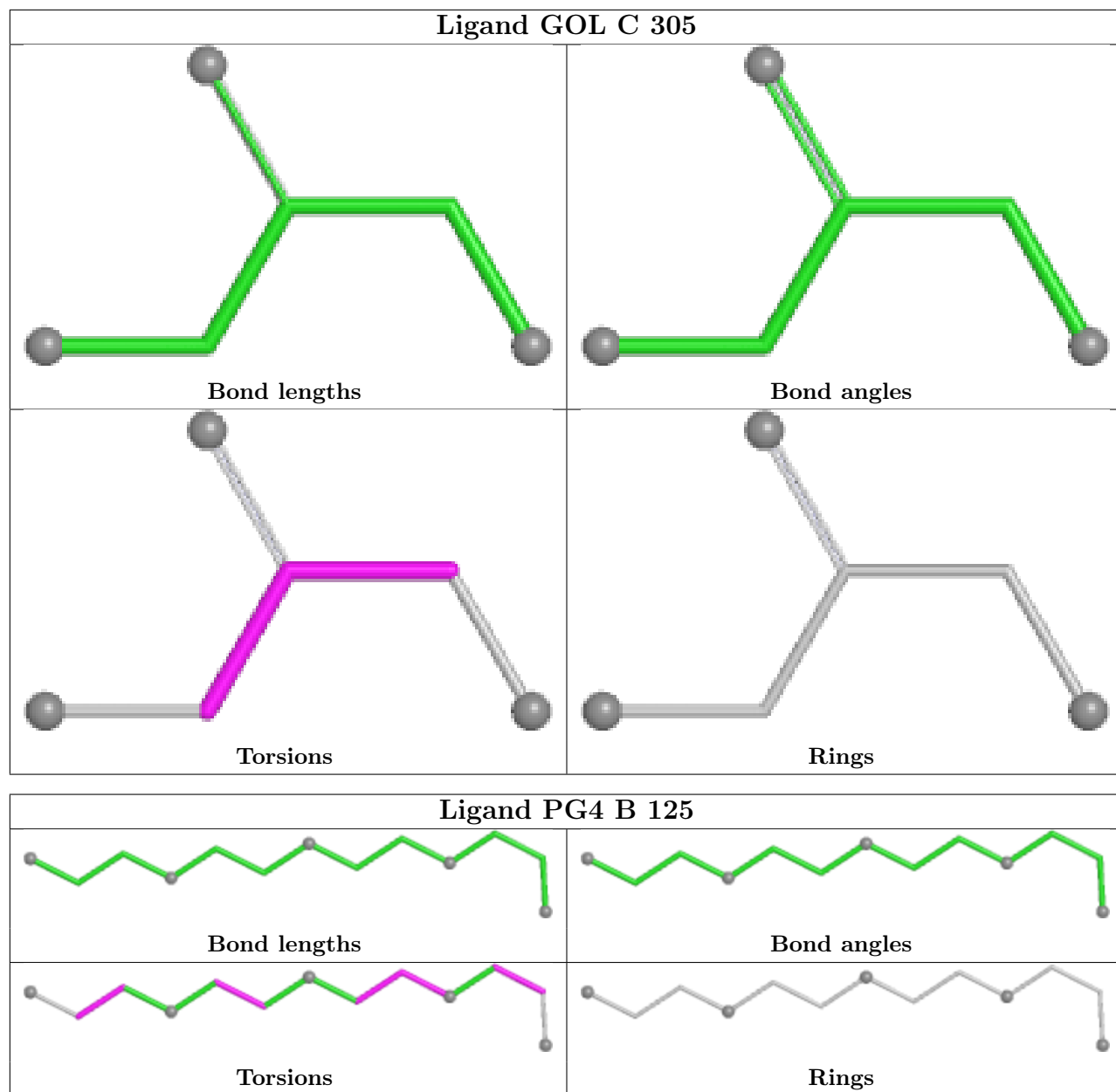


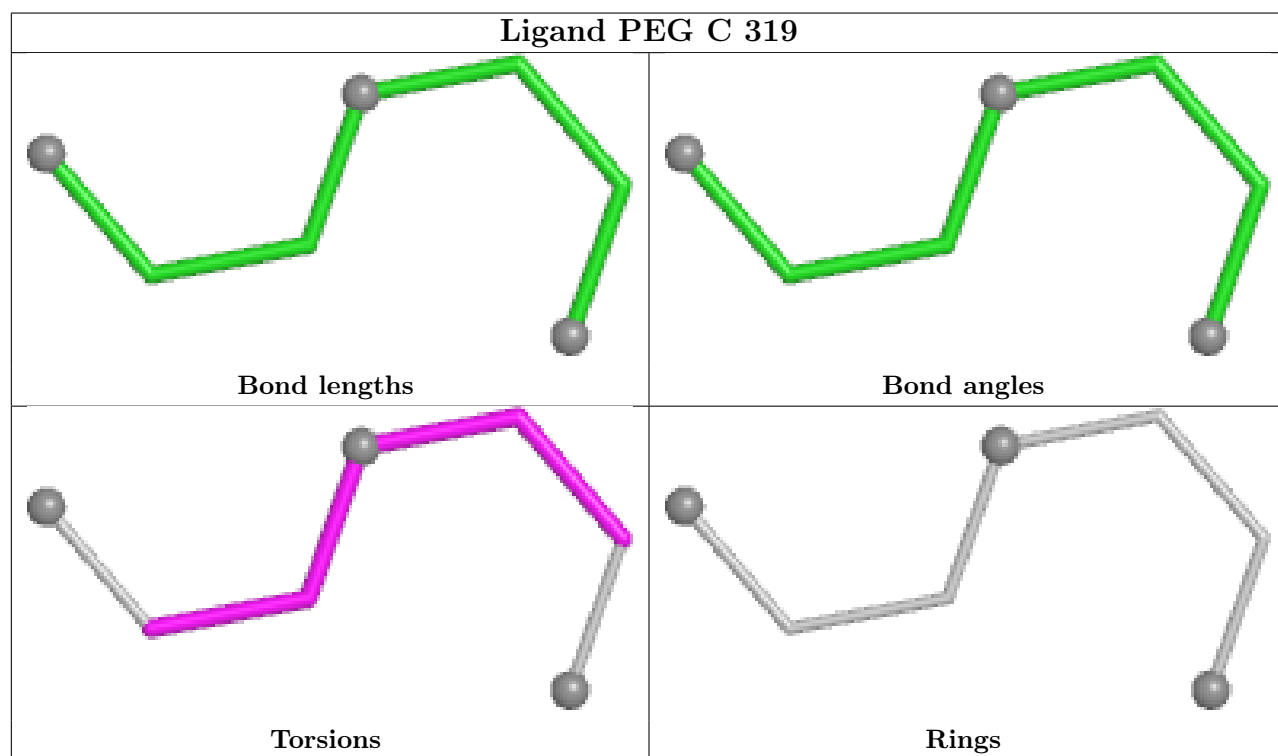
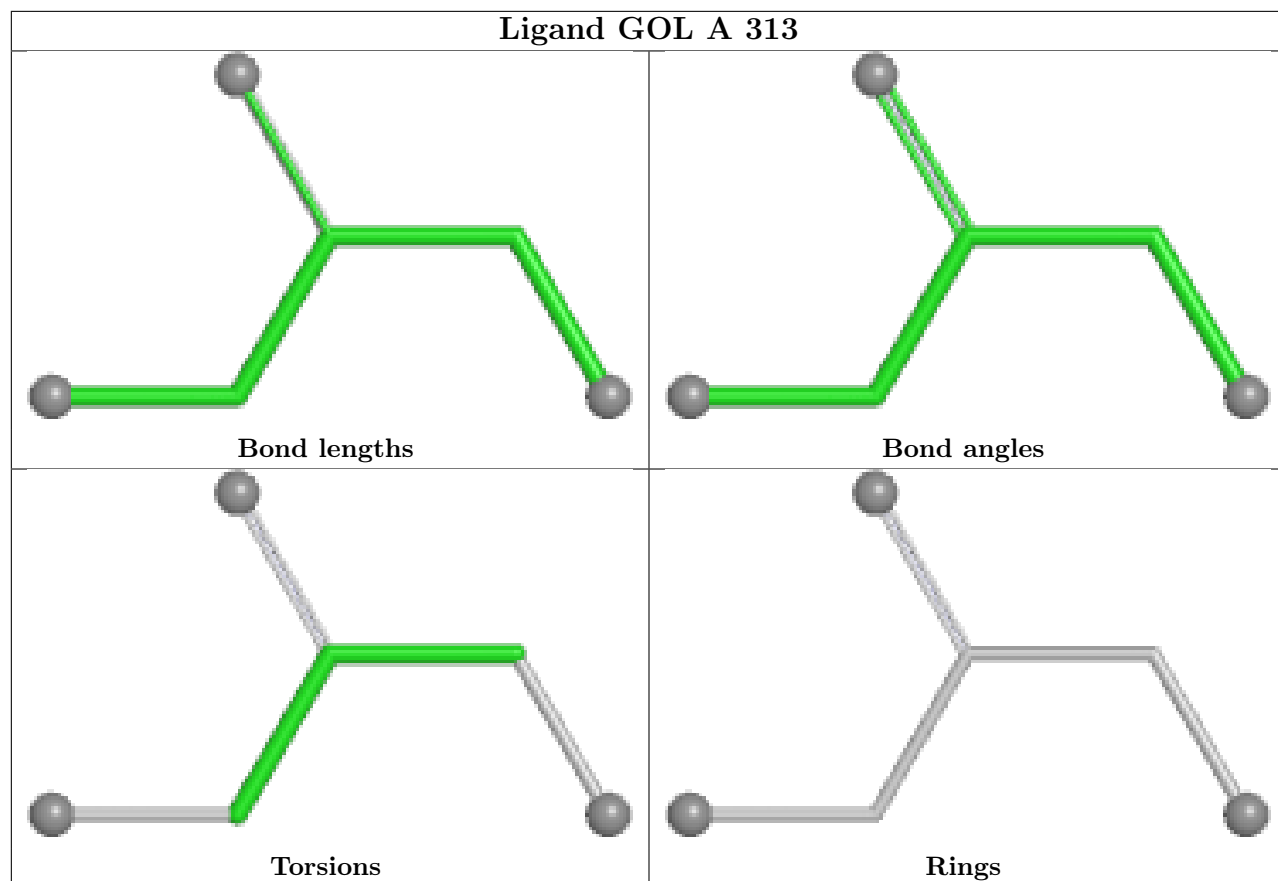


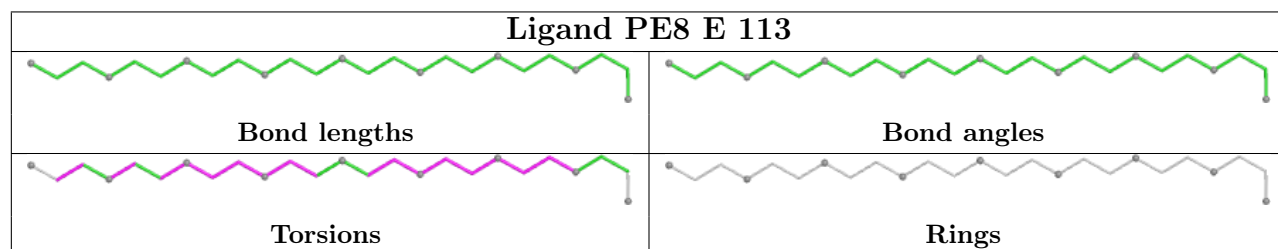
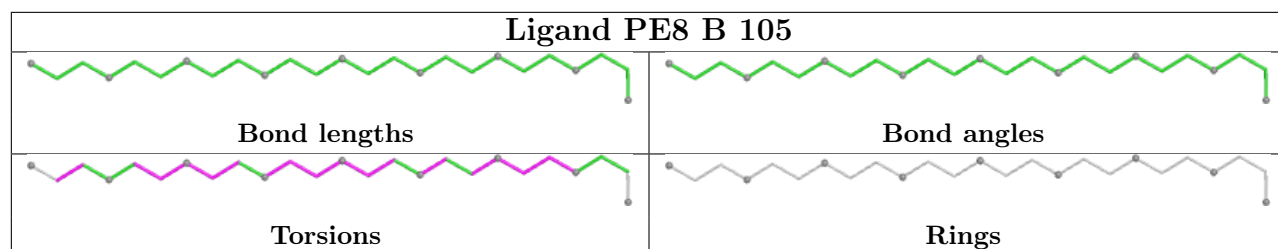
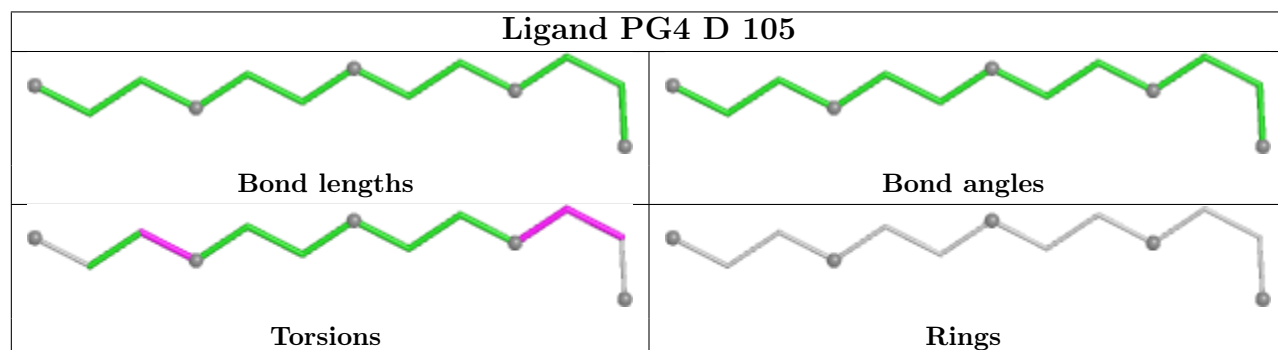
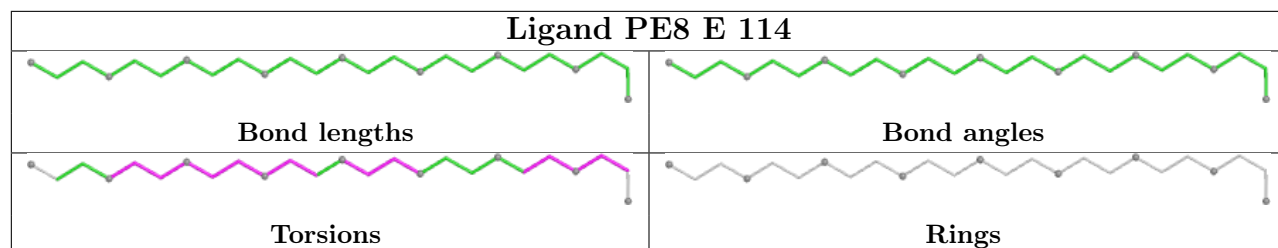


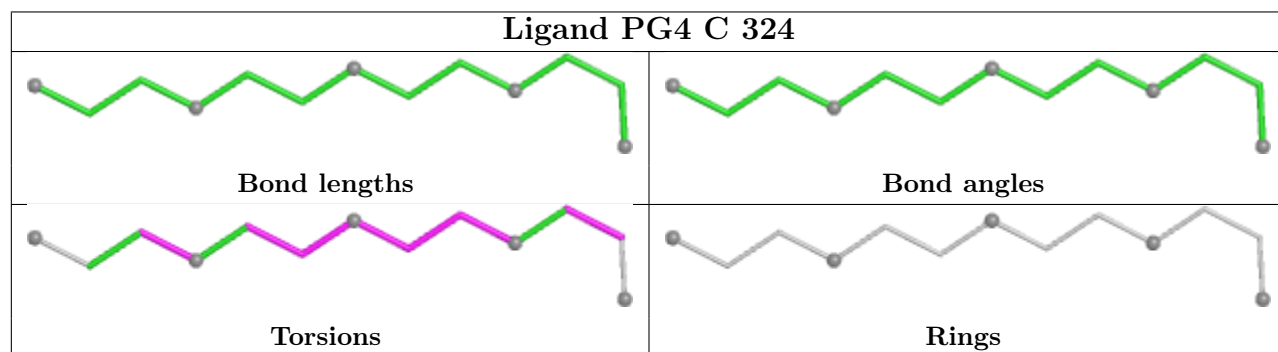
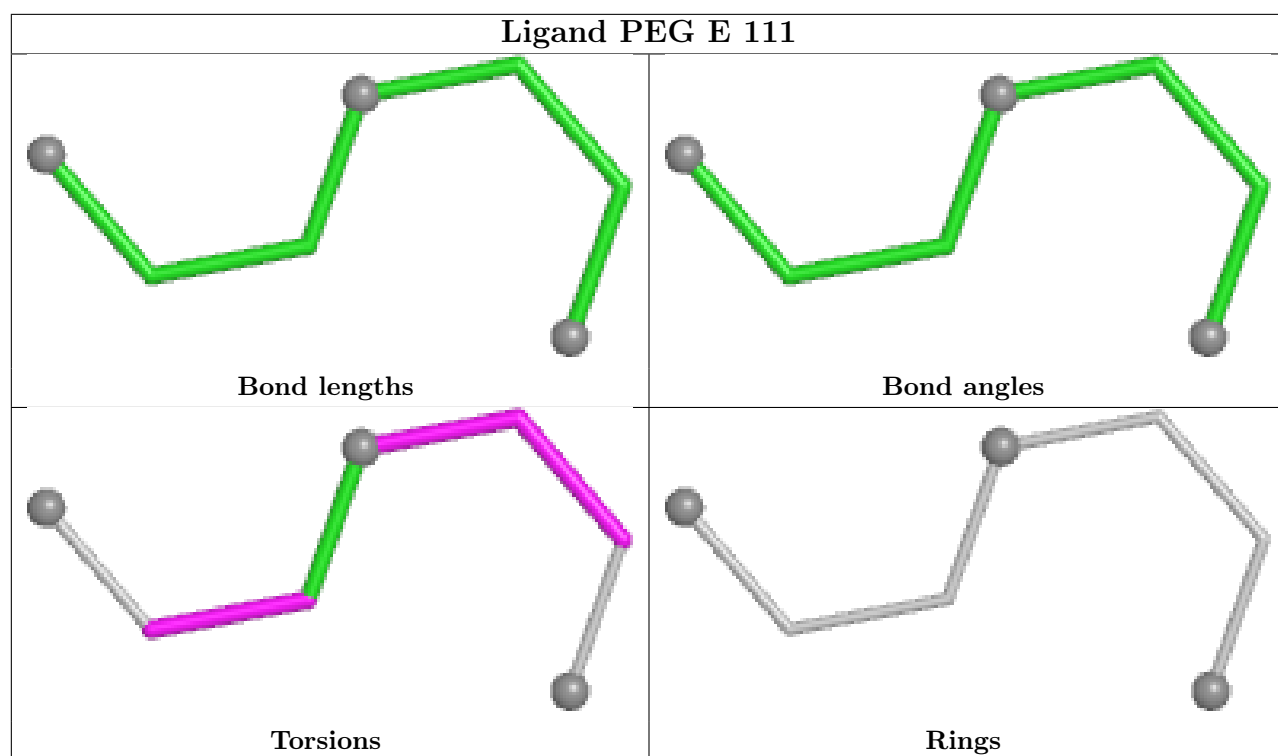


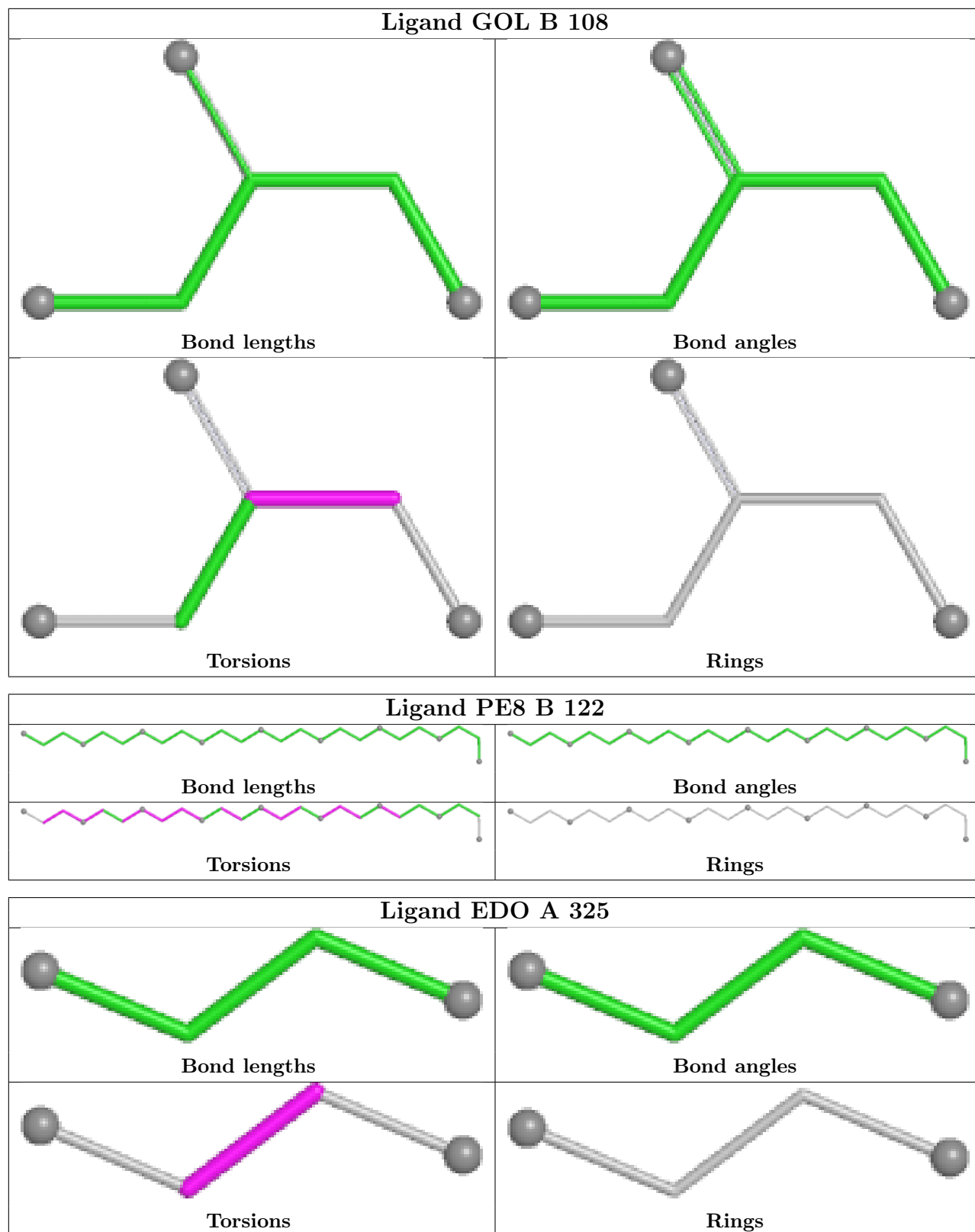


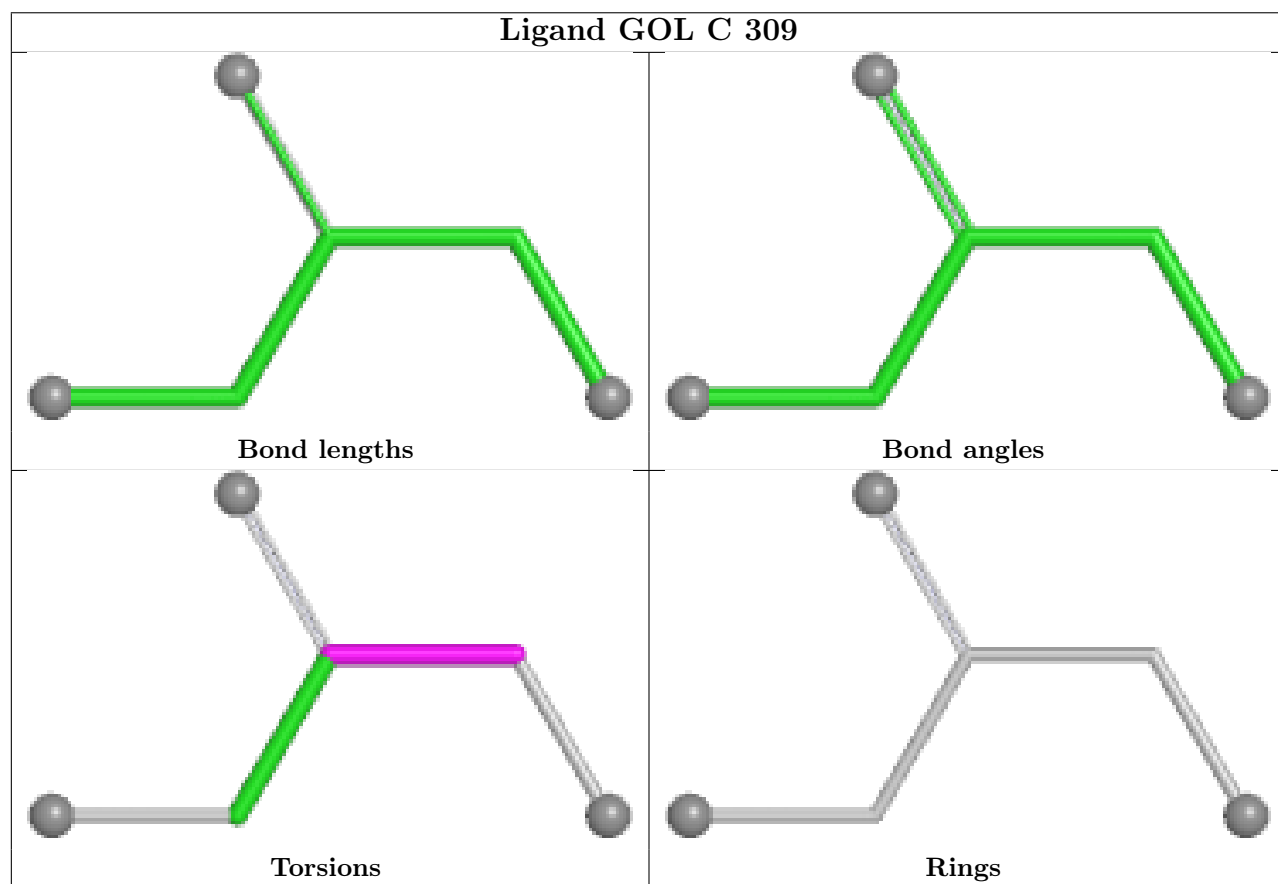
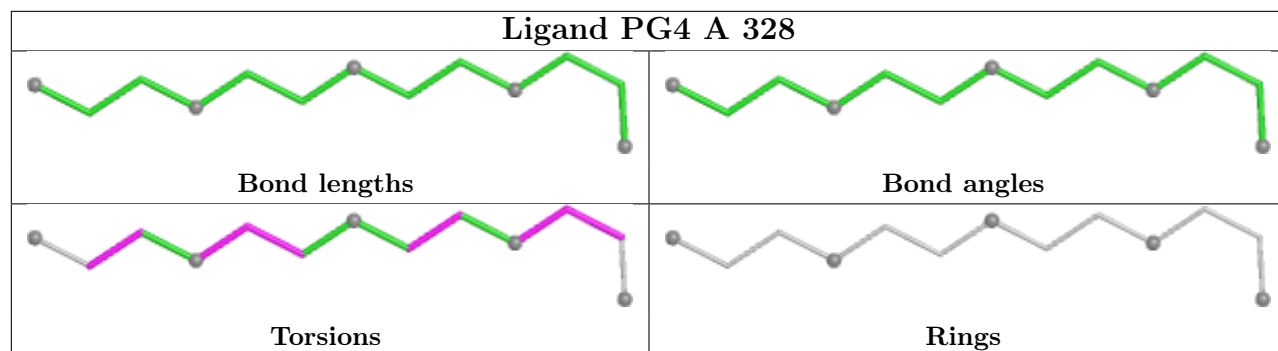


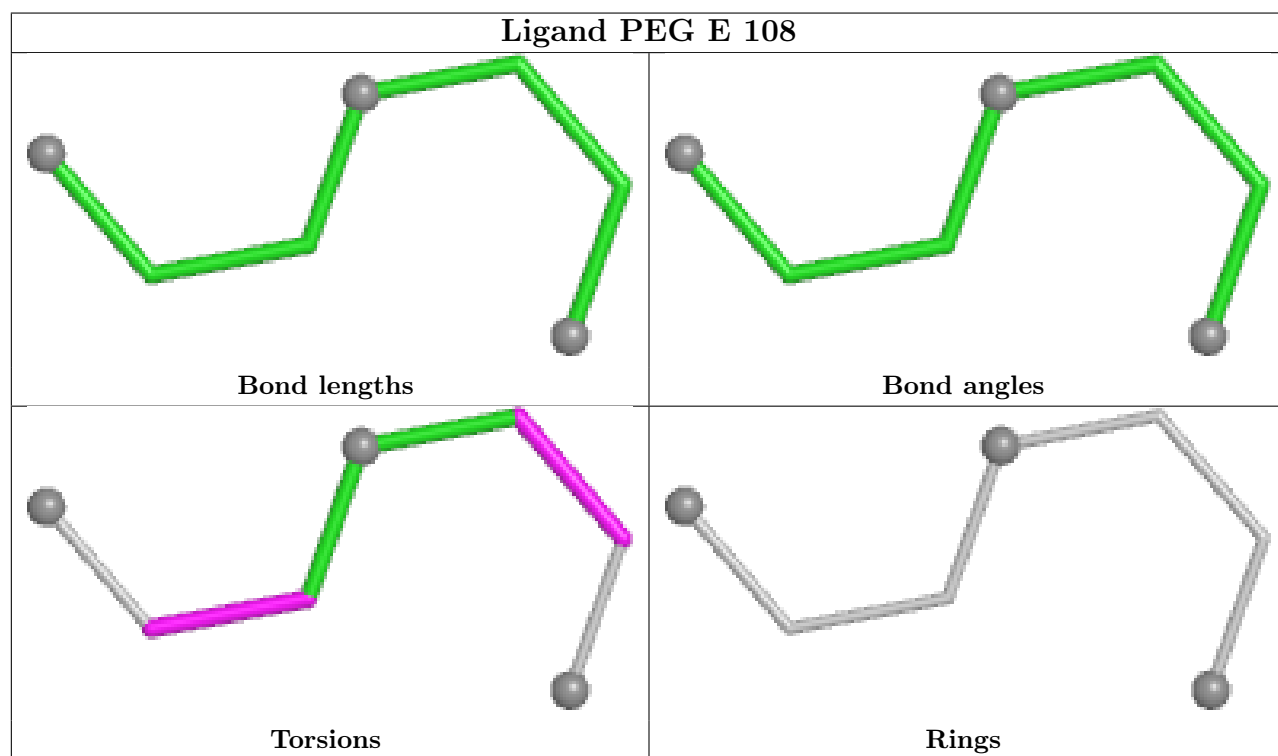
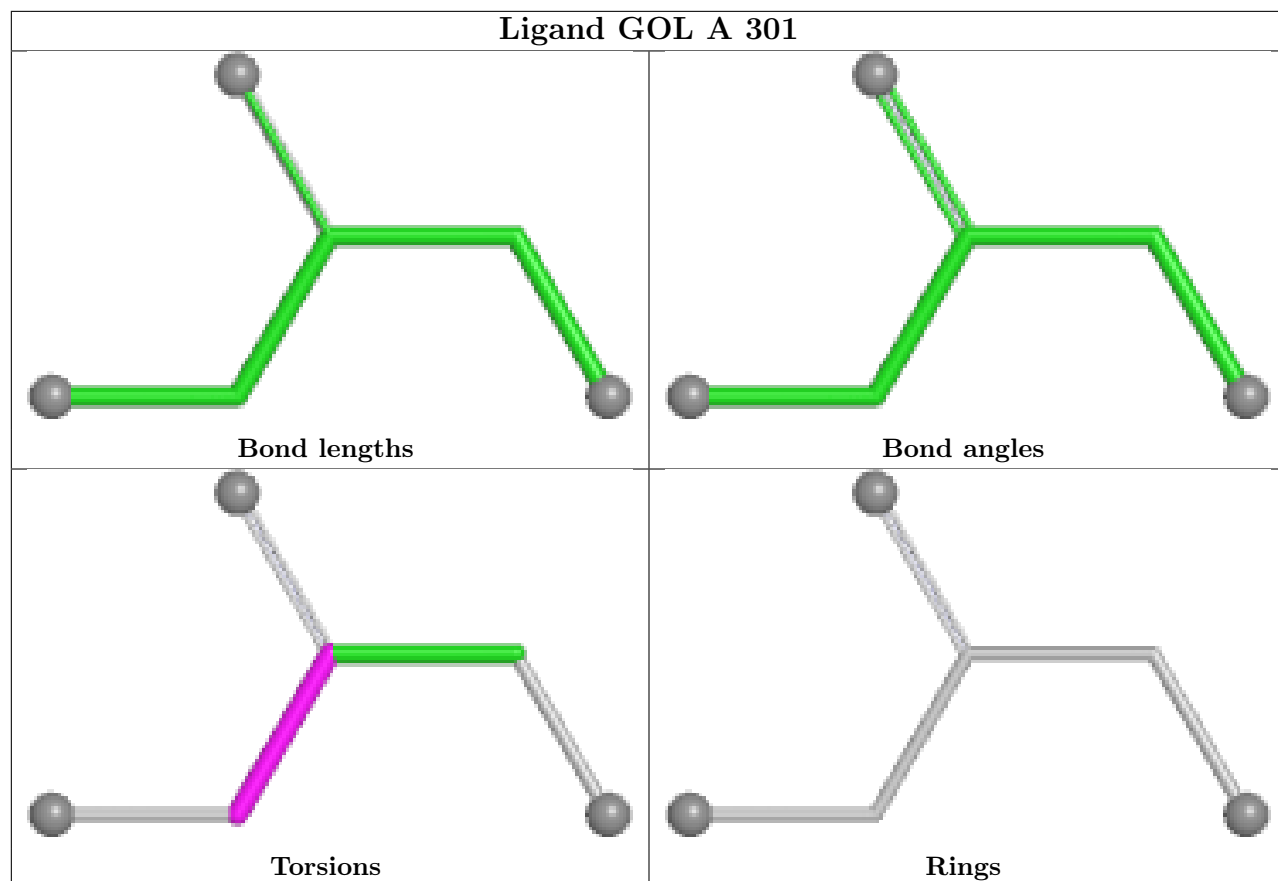


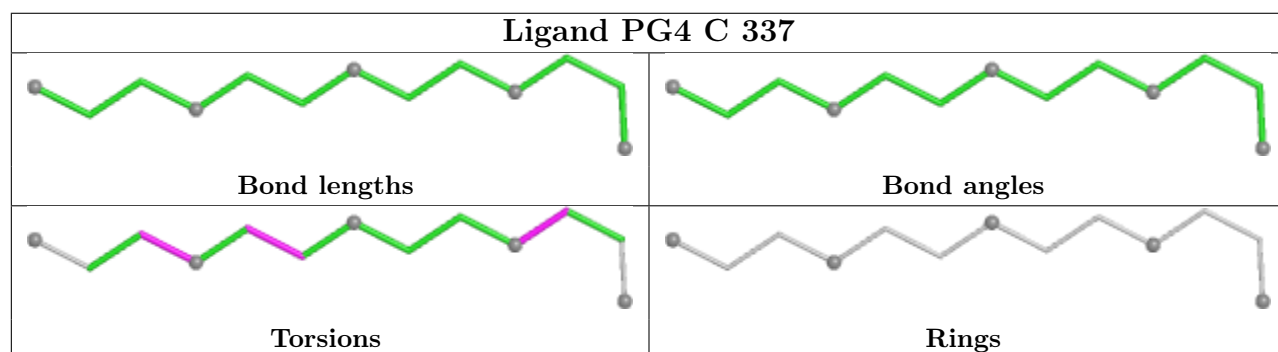
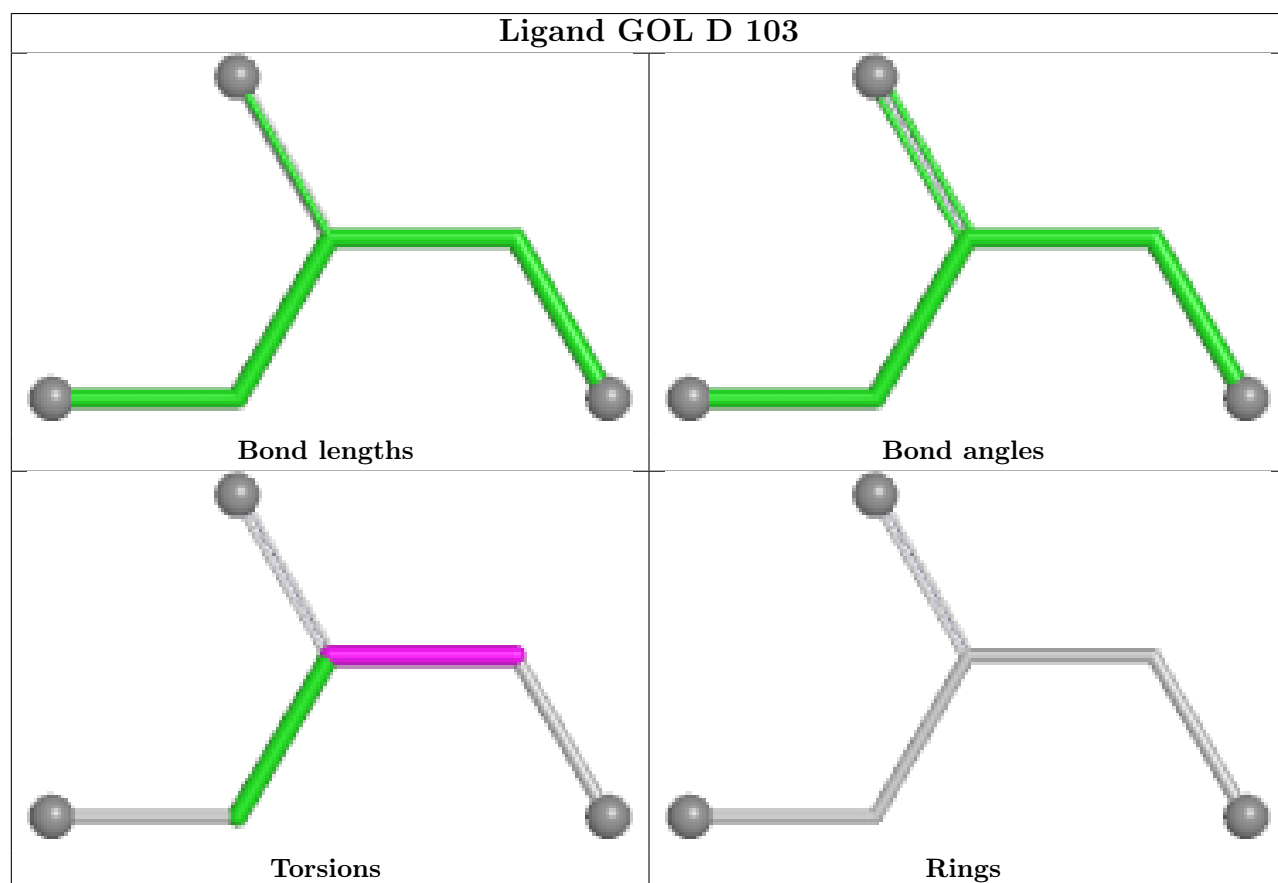
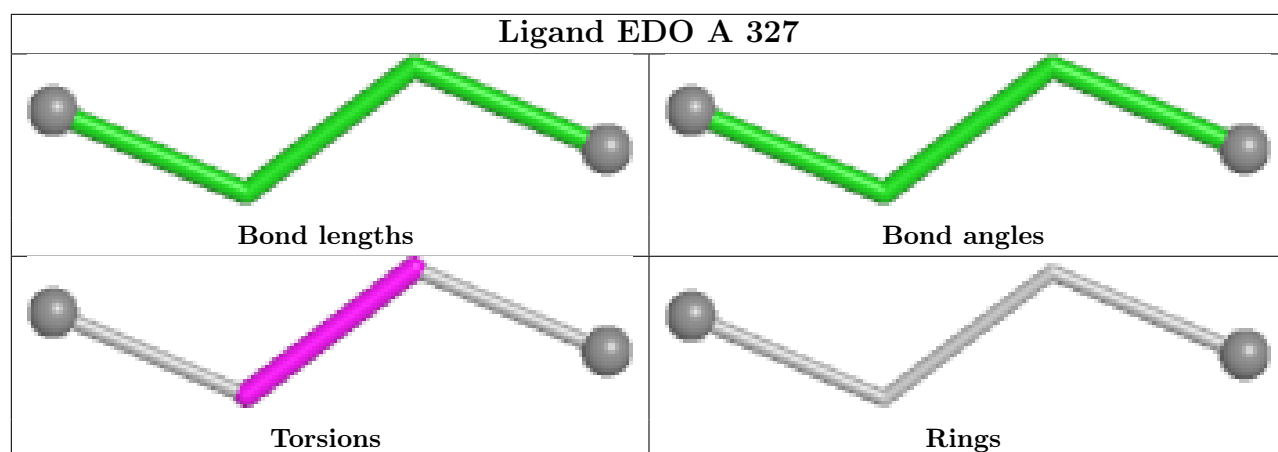


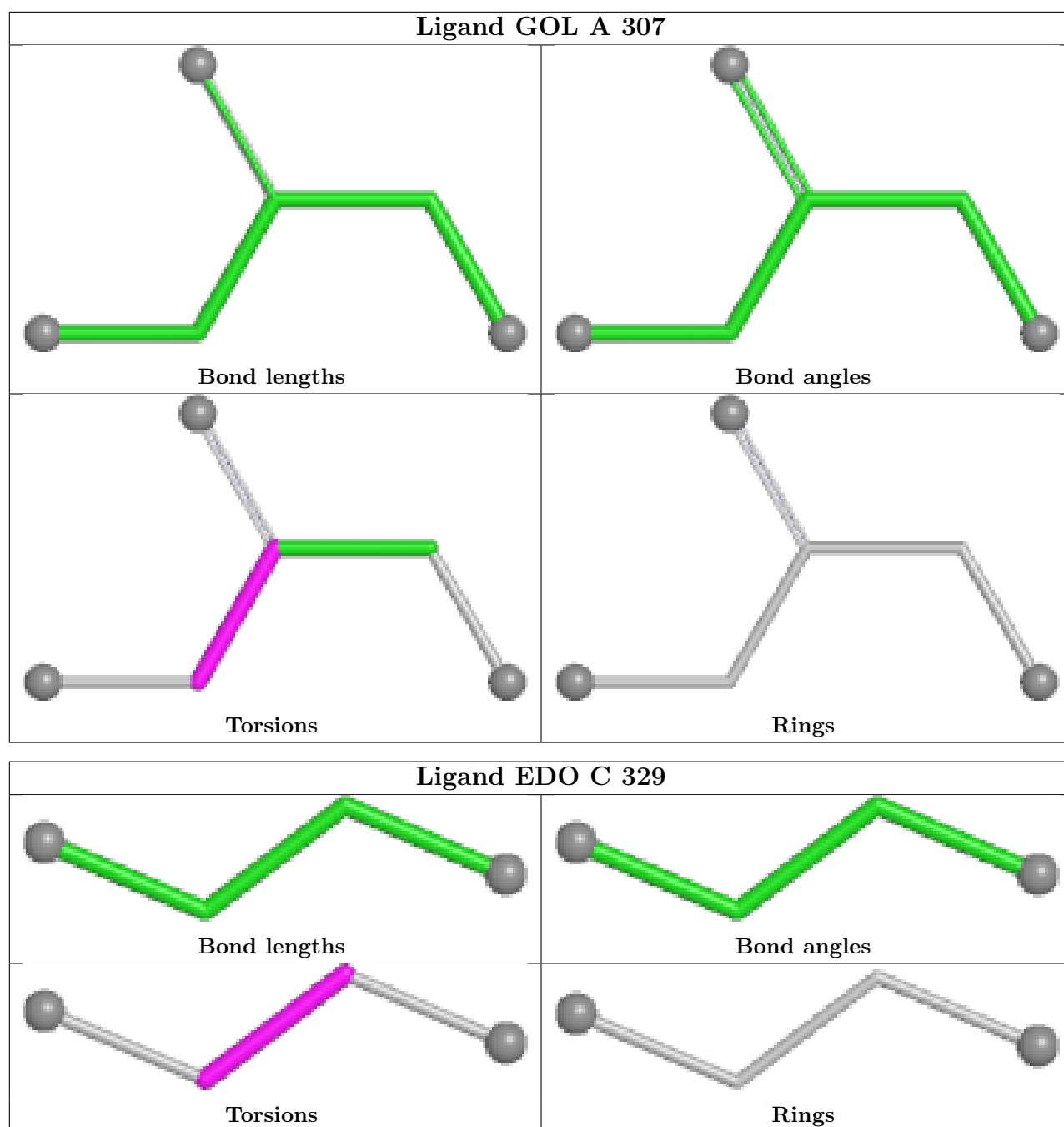












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	241/241 (100%)	1.49	68 (28%) 1 1	31, 50, 63, 71	0
1	C	241/241 (100%)	1.60	72 (29%) 1 1	36, 54, 64, 76	0
1	E	18/241 (7%)	0.71	1 (5%) 30 20	37, 56, 69, 72	0
2	B	98/98 (100%)	1.44	23 (23%) 2 2	42, 64, 78, 85	0
2	D	98/98 (100%)	1.37	19 (19%) 3 3	36, 54, 66, 69	0
All	All	696/919 (75%)	1.48	183 (26%) 1 1	31, 53, 70, 85	0

The worst 5 of 183 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	149	SER	7.0
1	C	116	ILE	6.6
1	C	28	SER	6.4
1	A	51	VAL	6.2
2	D	54	TYR	6.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NA	B	143	1/1	0.45	0.15	29,29,29,29	0
4	NA	D	104	1/1	0.58	0.18	41,41,41,41	0
3	GOL	B	114	6/6	0.64	0.13	33,37,42,48	0
7	EDO	C	328	4/4	0.64	0.24	44,45,47,48	0
3	GOL	A	303	6/6	0.67	0.17	46,53,58,60	0
3	GOL	C	303	6/6	0.68	0.16	50,67,68,72	0
3	GOL	A	310	6/6	0.68	0.21	39,46,54,61	0
5	PEG	C	316	7/7	0.69	0.15	37,47,51,57	0
3	GOL	C	307	6/6	0.69	0.12	45,51,53,56	0
5	PEG	A	320	7/7	0.71	0.16	38,49,57,61	0
8	PG4	C	327	13/13	0.71	0.14	45,53,57,59	0
9	SO4	B	119	5/5	0.72	0.12	78,80,90,96	0
3	GOL	B	137	6/6	0.73	0.12	28,41,44,55	0
5	PEG	E	108	7/7	0.73	0.15	45,53,58,62	0
6	PE8	C	321	25/25	0.73	0.12	36,44,50,51	0
4	NA	D	129	1/1	0.74	0.08	34,34,34,34	0
8	PG4	C	332	13/13	0.74	0.15	38,46,57,57	0
5	PEG	A	342	7/7	0.74	0.16	34,36,45,46	0
3	GOL	C	302	6/6	0.75	0.14	43,53,58,59	0
3	GOL	A	314	6/6	0.75	0.16	32,33,40,42	0
7	EDO	A	336	4/4	0.75	0.26	48,51,52,53	0
5	PEG	A	319	7/7	0.75	0.15	29,36,40,43	0
3	GOL	B	116	6/6	0.75	0.13	46,48,51,52	0
3	GOL	C	331	6/6	0.75	0.16	22,26,34,35	0
3	GOL	B	101	6/6	0.75	0.13	30,38,42,54	0
8	PG4	C	324	13/13	0.76	0.12	46,53,62,62	0
7	EDO	A	327	4/4	0.76	0.09	54,57,63,63	0
3	GOL	B	115	6/6	0.76	0.15	31,40,57,67	0
3	GOL	C	308	6/6	0.76	0.16	30,42,48,54	0
3	GOL	B	110	6/6	0.77	0.11	38,41,45,46	0
5	PEG	C	320	7/7	0.77	0.17	18,25,32,36	0
5	PEG	D	123	7/7	0.77	0.11	39,41,51,53	0
4	NA	B	117	1/1	0.78	0.10	30,30,30,30	0
3	GOL	C	306	6/6	0.78	0.13	42,47,52,52	0
6	PE8	E	112	25/25	0.78	0.13	16,39,48,52	0
3	GOL	A	308	6/6	0.78	0.17	41,44,45,47	0
5	PEG	A	335	7/7	0.78	0.19	30,31,38,40	0
4	NA	D	111	1/1	0.79	0.15	35,35,35,35	0
3	GOL	B	102	6/6	0.79	0.13	44,53,61,63	0
5	PEG	E	109	7/7	0.79	0.15	32,43,52,56	0
8	PG4	A	330	13/13	0.79	0.15	28,36,50,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	PE8	B	105	25/25	0.79	0.12	36,45,54,55	0
3	GOL	D	108	6/6	0.79	0.15	12,16,21,24	0
3	GOL	D	124	6/6	0.79	0.12	35,45,50,53	0
6	PE8	E	114	25/25	0.79	0.11	34,42,47,49	0
3	GOL	D	122	6/6	0.80	0.14	2,11,18,21	0
3	GOL	D	107	6/6	0.80	0.13	16,23,30,34	0
3	GOL	C	304	6/6	0.80	0.14	35,41,48,52	0
8	PG4	D	101	13/13	0.80	0.18	33,55,67,69	0
8	PG4	D	117	13/13	0.80	0.13	43,51,59,60	0
8	PG4	A	337	13/13	0.80	0.13	27,30,52,52	0
5	PEG	D	115	7/7	0.81	0.13	27,38,42,47	0
3	GOL	E	103	6/6	0.81	0.12	29,38,39,45	0
3	GOL	C	310	6/6	0.81	0.12	33,44,46,48	0
6	PE8	E	113	25/25	0.81	0.13	18,31,39,44	0
3	GOL	C	309	6/6	0.81	0.16	41,46,49,55	0
8	PG4	B	127	13/13	0.81	0.12	32,40,54,57	0
8	PG4	A	331	13/13	0.82	0.11	34,49,60,63	0
3	GOL	D	110	6/6	0.82	0.12	40,45,51,51	0
3	GOL	D	106	6/6	0.82	0.13	22,26,30,32	0
3	GOL	B	138	6/6	0.82	0.15	20,29,36,39	0
5	PEG	C	330	7/7	0.82	0.12	38,41,47,50	0
6	PE8	B	122	25/25	0.82	0.11	20,32,41,44	0
6	PE8	B	123	25/25	0.82	0.13	22,43,56,64	0
8	PG4	A	328	13/13	0.82	0.14	30,39,47,48	0
8	PG4	D	118	13/13	0.82	0.13	24,43,50,51	0
3	GOL	B	109	6/6	0.82	0.18	37,40,47,48	0
8	PG4	C	325	13/13	0.83	0.13	36,45,53,54	0
3	GOL	A	307	6/6	0.83	0.14	38,42,44,45	0
5	PEG	C	318	7/7	0.83	0.16	32,33,50,50	0
8	PG4	B	104	13/13	0.83	0.10	20,30,35,35	0
8	PG4	D	116	13/13	0.83	0.14	24,36,40,41	0
8	PG4	B	125	13/13	0.83	0.12	37,44,50,50	0
5	PEG	C	319	7/7	0.83	0.13	50,54,60,61	0
6	PE8	A	324	25/25	0.83	0.10	22,33,51,54	0
3	GOL	A	309	6/6	0.84	0.09	33,40,50,50	0
3	GOL	C	311	6/6	0.84	0.08	37,48,49,53	0
5	PEG	A	341	7/7	0.84	0.10	14,24,29,34	0
8	PG4	A	338	13/13	0.84	0.11	24,40,57,59	0
8	PG4	D	105	13/13	0.84	0.14	29,36,47,61	0
3	GOL	B	111	6/6	0.84	0.11	43,46,53,55	0
7	EDO	C	329	4/4	0.84	0.11	38,43,43,45	0
7	EDO	C	334	4/4	0.84	0.12	31,33,38,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	113	6/6	0.84	0.14	29,38,44,48	0
9	SO4	D	113	5/5	0.84	0.10	52,62,65,67	0
3	GOL	C	342	6/6	0.85	0.12	28,34,36,37	0
8	PG4	A	332	13/13	0.85	0.17	24,34,46,53	0
3	GOL	A	311	6/6	0.85	0.09	23,27,30,31	0
5	PEG	C	317	7/7	0.85	0.14	37,41,44,50	0
6	PE8	B	131	25/25	0.85	0.12	20,33,46,53	0
4	NA	C	333	1/1	0.85	0.12	31,31,31,31	0
6	PE8	C	322	25/25	0.85	0.10	15,31,41,44	0
8	PG4	D	119	13/13	0.85	0.11	15,24,28,30	0
8	PG4	D	127	13/13	0.85	0.10	19,26,32,34	0
3	GOL	B	130	6/6	0.85	0.13	37,44,50,52	0
9	SO4	C	336	5/5	0.85	0.11	44,51,56,62	0
3	GOL	B	136	6/6	0.85	0.13	23,31,35,35	0
5	PEG	C	339	7/7	0.86	0.10	24,26,31,33	0
3	GOL	A	346	6/6	0.86	0.13	32,34,37,43	0
8	PG4	B	128	13/13	0.86	0.12	27,33,41,46	0
8	PG4	B	129	13/13	0.86	0.12	25,27,32,33	0
4	NA	A	316	1/1	0.86	0.16	15,15,15,15	0
3	GOL	B	140	6/6	0.86	0.21	25,28,31,32	0
3	GOL	D	109	6/6	0.86	0.10	22,24,25,26	0
6	PE8	A	322	25/25	0.86	0.10	20,31,42,48	0
4	NA	B	144	1/1	0.86	0.07	26,26,26,26	0
5	PEG	B	120	7/7	0.87	0.08	24,27,28,28	0
8	PG4	D	121	13/13	0.87	0.09	9,23,29,30	0
5	PEG	C	315	7/7	0.87	0.08	17,34,38,39	0
8	PG4	B	126	13/13	0.87	0.12	26,33,45,48	0
7	EDO	A	343	4/4	0.87	0.14	34,37,39,43	0
9	SO4	D	112	5/5	0.87	0.10	47,57,65,75	0
3	GOL	B	135	6/6	0.87	0.09	20,30,35,35	0
6	PE8	A	323	25/25	0.88	0.10	9,18,28,29	0
3	GOL	B	112	6/6	0.88	0.10	34,36,40,41	0
4	NA	A	339	1/1	0.88	0.18	53,53,53,53	0
3	GOL	B	107	6/6	0.88	0.10	8,22,36,42	0
7	EDO	A	326	4/4	0.88	0.10	22,24,26,28	0
3	GOL	A	345	6/6	0.88	0.11	28,29,35,47	0
5	PEG	E	111	7/7	0.88	0.11	28,38,47,49	0
8	PG4	E	101	13/13	0.88	0.10	16,25,34,34	0
8	PG4	A	334	13/13	0.88	0.10	29,40,45,51	0
4	NA	D	128	1/1	0.88	0.11	44,44,44,44	0
7	EDO	C	323	4/4	0.88	0.16	32,37,48,50	0
8	PG4	A	344	13/13	0.88	0.07	33,37,47,51	0

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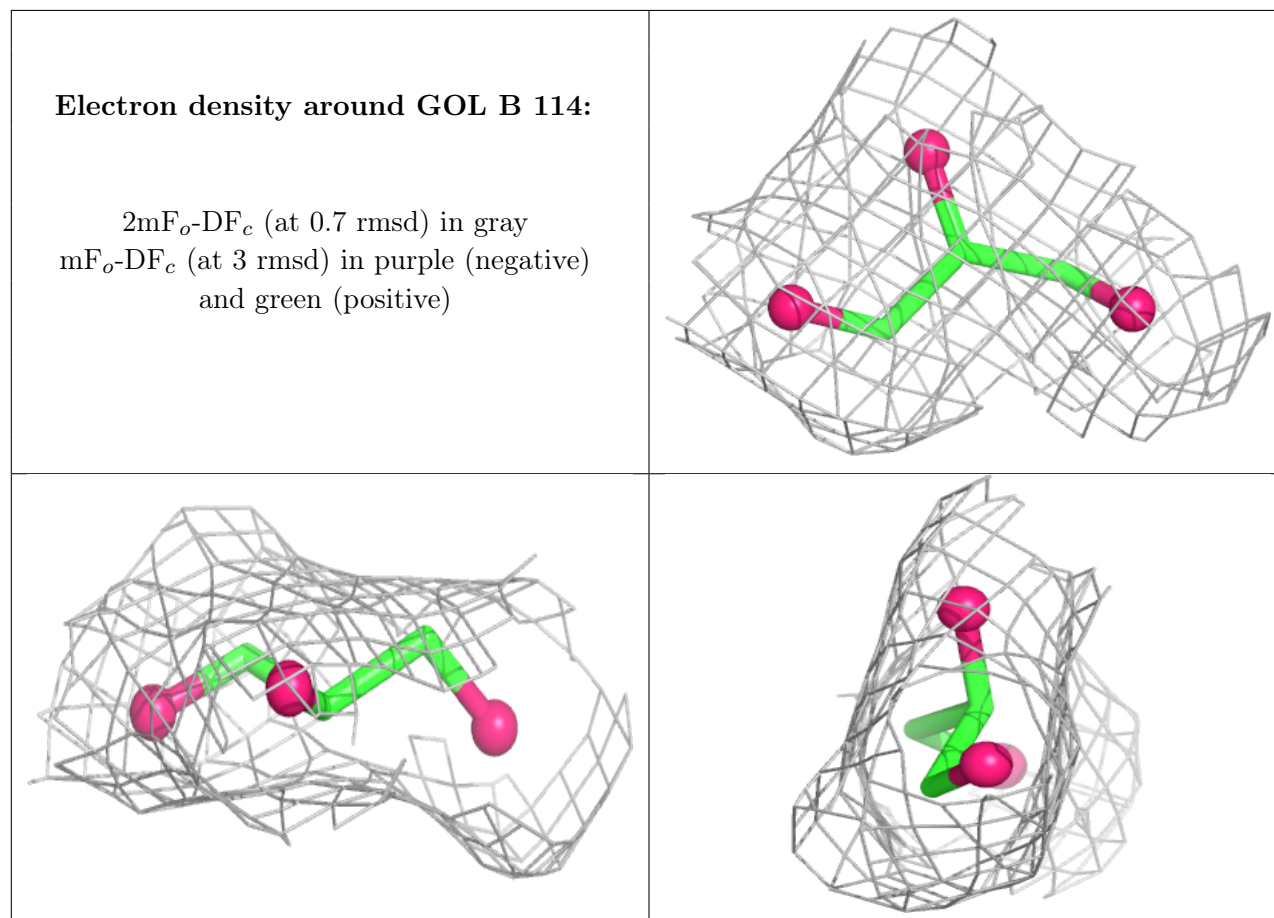
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NA	D	102	1/1	0.89	0.12	37,37,37,37	0
7	EDO	B	124	4/4	0.89	0.09	32,38,45,46	0
3	GOL	C	301	6/6	0.89	0.08	34,35,40,40	0
3	GOL	A	304	6/6	0.89	0.14	21,26,27,27	0
3	GOL	A	312	6/6	0.89	0.08	26,38,45,50	0
3	GOL	B	108	6/6	0.89	0.11	27,36,41,50	0
5	PEG	E	110	7/7	0.89	0.11	18,22,25,29	0
5	PEG	A	318	7/7	0.89	0.11	15,19,33,33	0
3	GOL	A	305	6/6	0.89	0.10	35,40,44,47	0
3	GOL	B	132	6/6	0.89	0.07	28,34,44,46	0
5	PEG	A	321	7/7	0.89	0.10	19,35,41,43	0
3	GOL	D	103	6/6	0.89	0.10	37,45,54,56	0
8	PG4	C	337	13/13	0.89	0.10	11,27,35,35	0
4	NA	B	142	1/1	0.90	0.09	8,8,8,8	0
3	GOL	A	313	6/6	0.90	0.08	7,19,27,28	0
5	PEG	B	139	7/7	0.90	0.07	23,28,38,41	0
3	GOL	E	102	6/6	0.90	0.08	32,37,40,41	0
4	NA	C	314	1/1	0.90	0.12	13,13,13,13	0
7	EDO	B	103	4/4	0.90	0.08	20,20,20,21	0
3	GOL	A	340	6/6	0.90	0.07	22,29,33,33	0
8	PG4	A	333	13/13	0.90	0.09	14,20,24,24	0
4	NA	E	105	1/1	0.90	0.15	35,35,35,35	0
9	SO4	D	114	5/5	0.90	0.16	40,46,47,48	0
8	PG4	C	326	13/13	0.91	0.07	23,36,39,39	0
3	GOL	E	104	6/6	0.91	0.07	29,32,34,35	0
4	NA	B	118	1/1	0.91	0.11	59,59,59,59	0
3	GOL	C	338	6/6	0.91	0.09	14,23,33,34	0
3	GOL	A	306	6/6	0.91	0.17	22,34,39,39	0
6	PE8	B	121	25/25	0.91	0.09	20,27,33,37	0
5	PEG	C	340	7/7	0.92	0.07	19,26,36,39	0
3	GOL	A	301	6/6	0.92	0.11	25,28,30,36	0
3	GOL	B	134	6/6	0.92	0.08	18,21,35,42	0
3	GOL	A	302	6/6	0.92	0.08	12,16,22,24	0
7	EDO	A	325	4/4	0.92	0.10	24,27,30,31	0
9	SO4	D	126	5/5	0.92	0.12	39,48,58,66	0
8	PG4	A	329	13/13	0.93	0.06	18,33,51,54	0
4	NA	B	133	1/1	0.93	0.17	26,26,26,26	0
3	GOL	C	341	6/6	0.93	0.08	11,27,37,45	0
4	NA	C	312	1/1	0.93	0.15	30,30,30,30	0
9	SO4	E	107	5/5	0.93	0.09	49,50,57,61	0
3	GOL	B	106	6/6	0.94	0.12	26,31,32,36	0
4	NA	C	335	1/1	0.94	0.08	19,19,19,19	0

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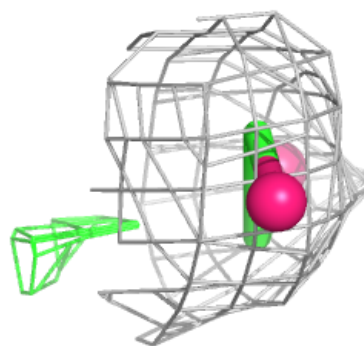
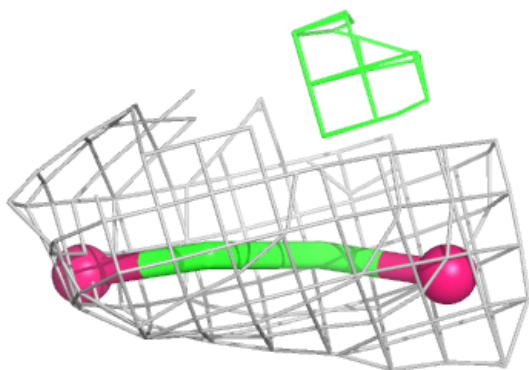
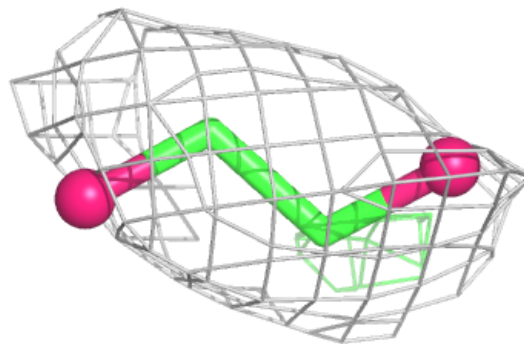
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	CL	D	120	1/1	0.94	0.04	41,41,41,41	0
4	NA	C	313	1/1	0.95	0.03	34,34,34,34	0
4	NA	D	125	1/1	0.95	0.10	35,35,35,35	0
4	NA	A	315	1/1	0.95	0.12	14,14,14,14	0
4	NA	A	317	1/1	0.95	0.07	21,21,21,21	0
3	GOL	C	305	6/6	0.96	0.06	5,14,21,24	0
4	NA	D	130	1/1	0.96	0.06	10,10,10,10	0
4	NA	E	106	1/1	0.97	0.10	16,16,16,16	0
4	NA	D	131	1/1	0.98	0.06	10,10,10,10	0

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



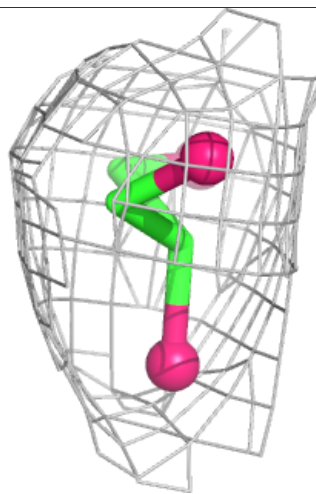
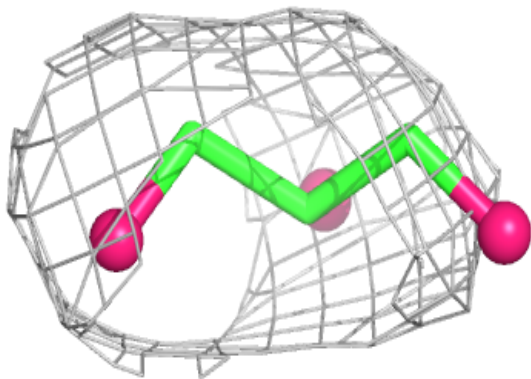
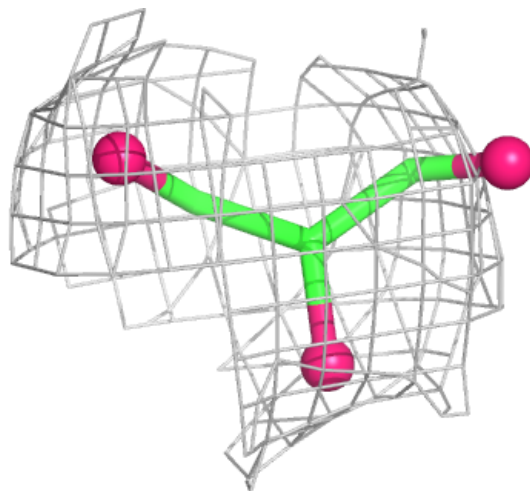
Electron density around EDO C 328:

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



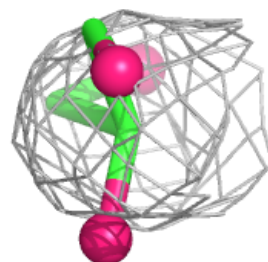
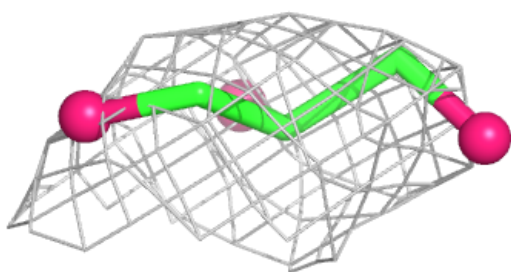
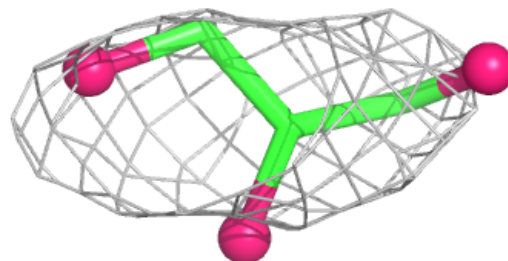
Electron density around GOL A 303:

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

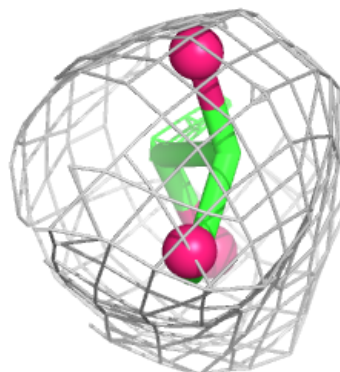
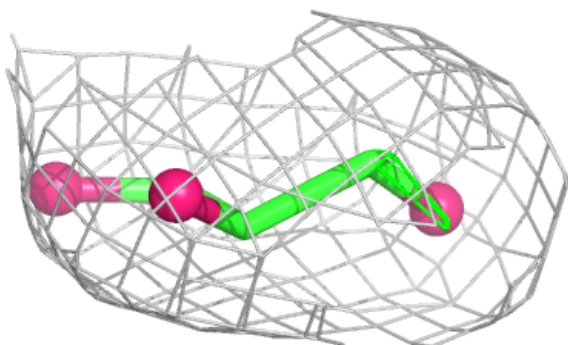
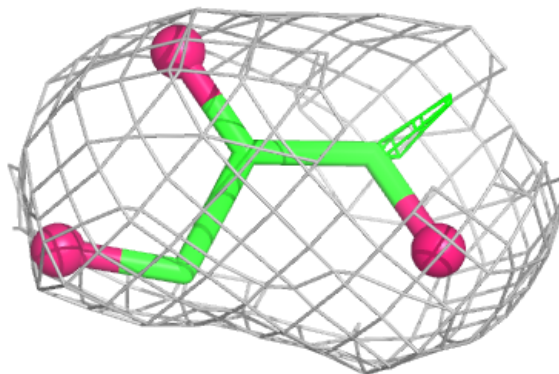


Electron density around GOL C 303:

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

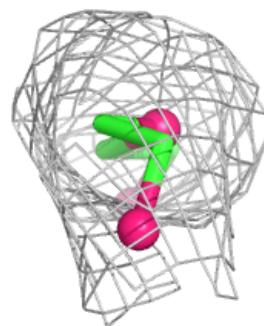
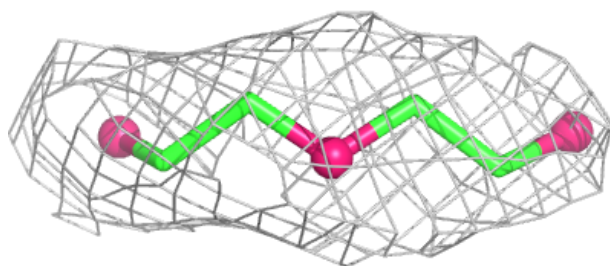
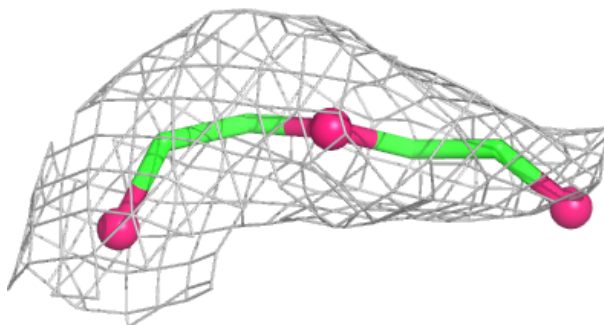
**Electron density around GOL A 310:**

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



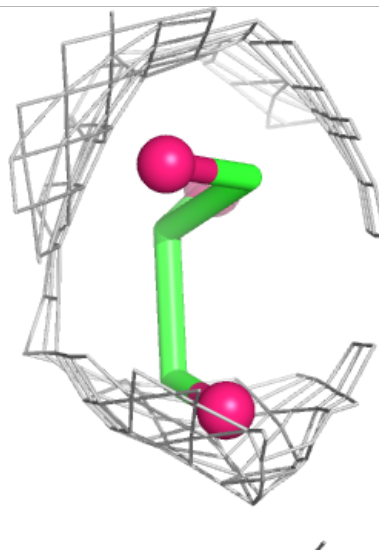
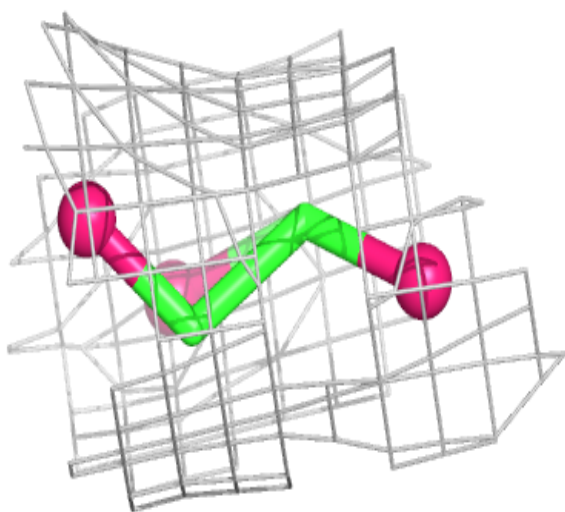
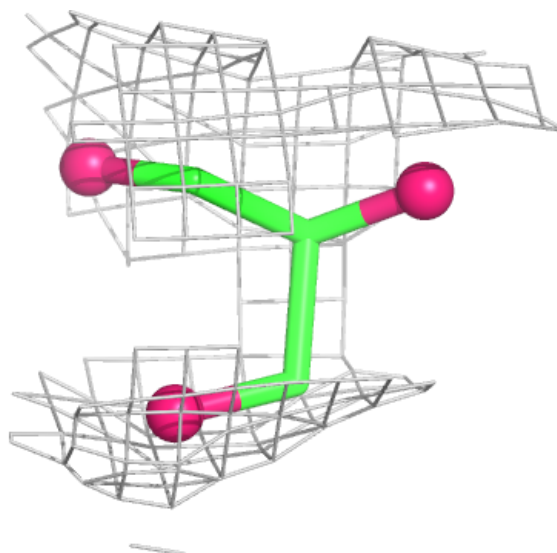
Electron density around PEG C 316:

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



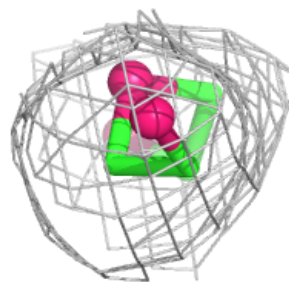
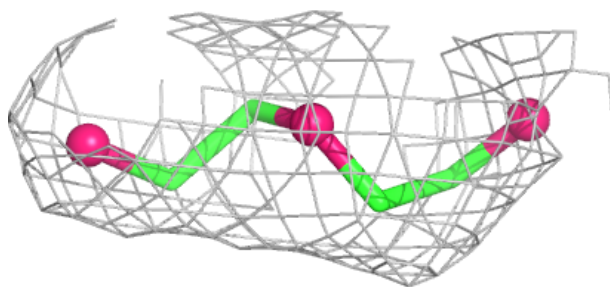
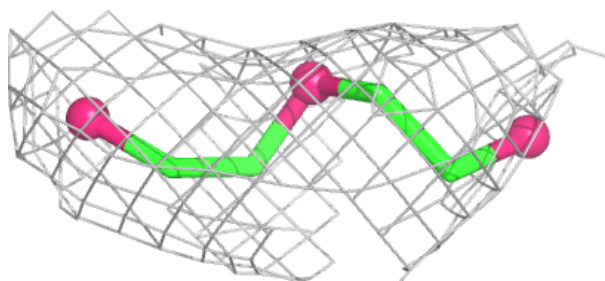
Electron density around GOL C 307:

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

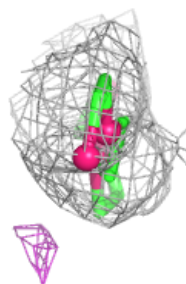
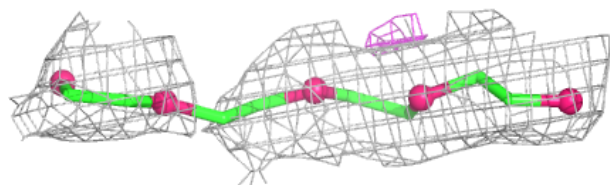
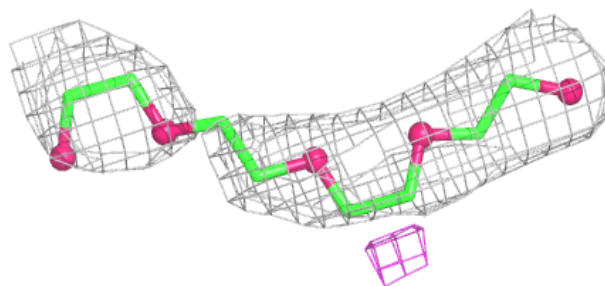


Electron density around PEG A 320:

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

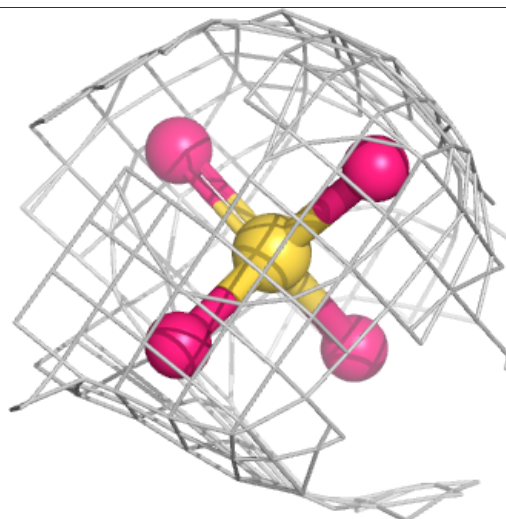
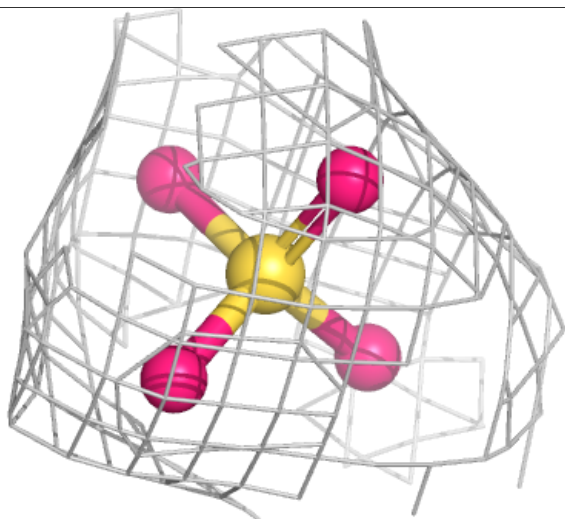
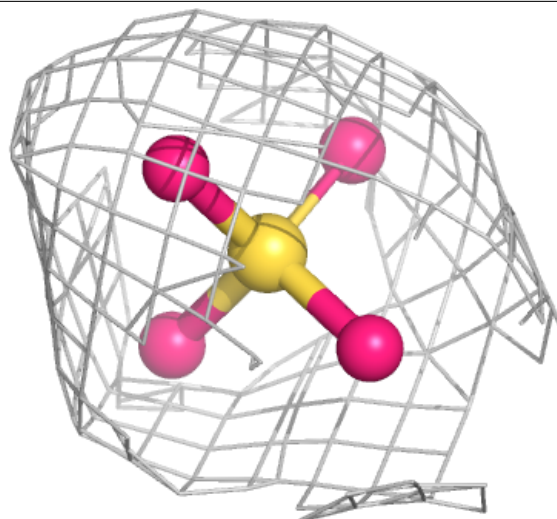
**Electron density around PG4 C 327:**

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



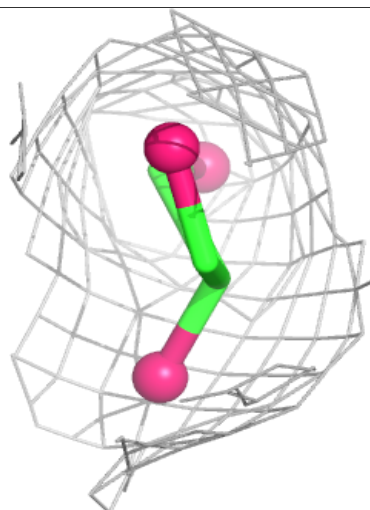
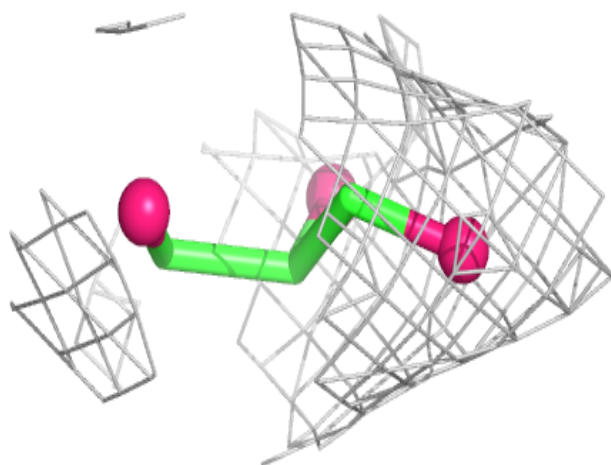
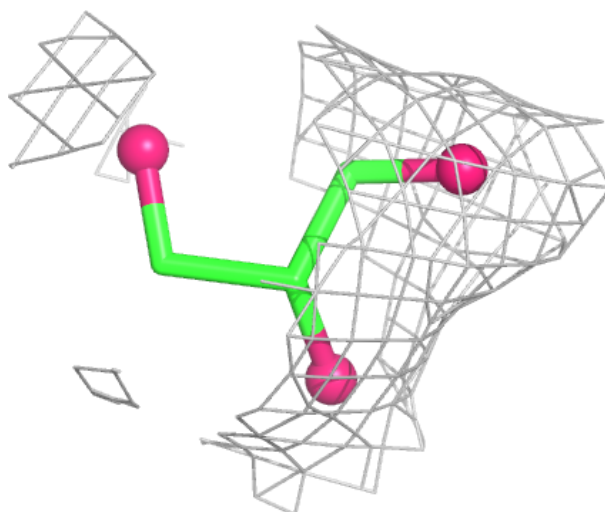
Electron density around SO4 B 119:

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



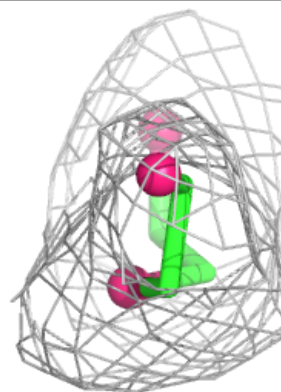
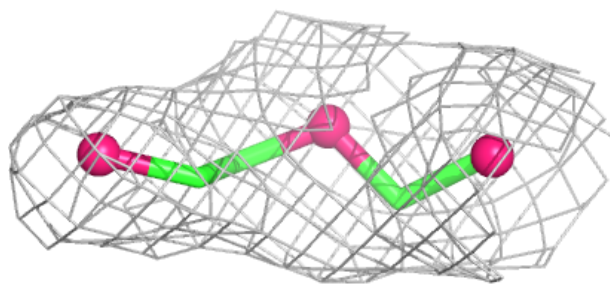
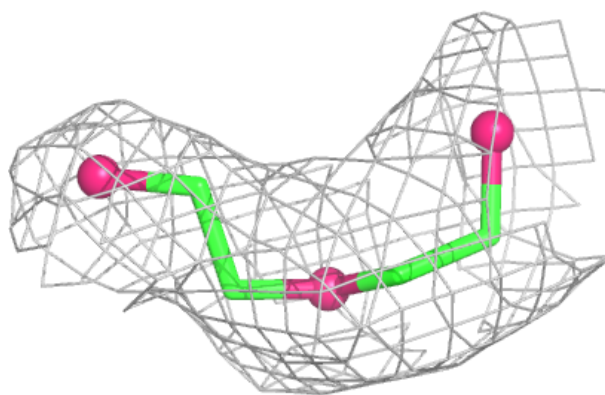
Electron density around GOL B 137:

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

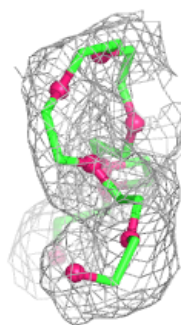
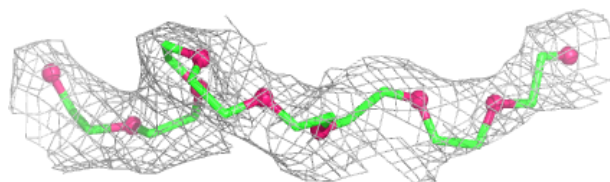
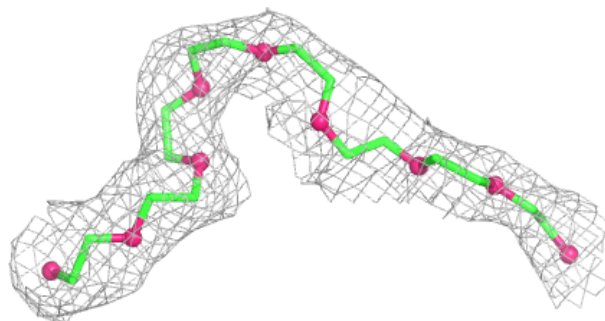


Electron density around PEG E 108:

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

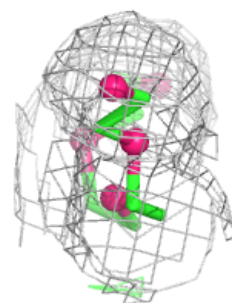
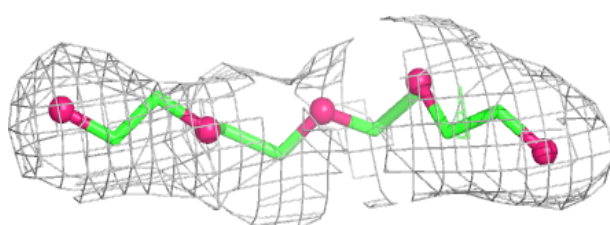
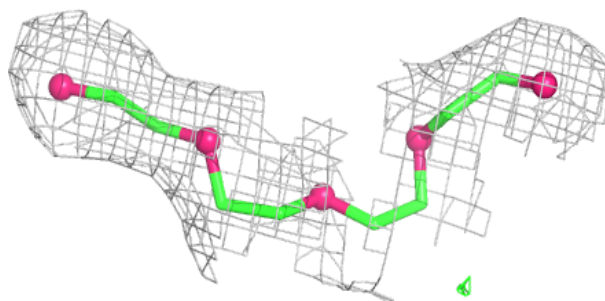
**Electron density around PE8 C 321:**

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

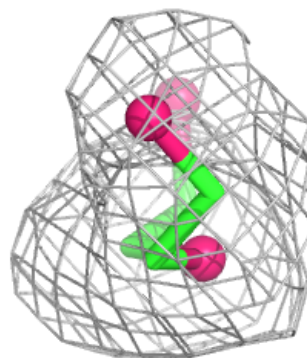
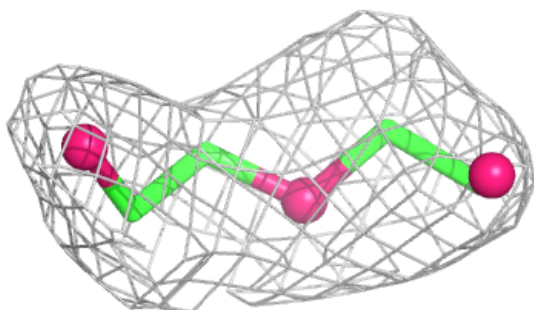
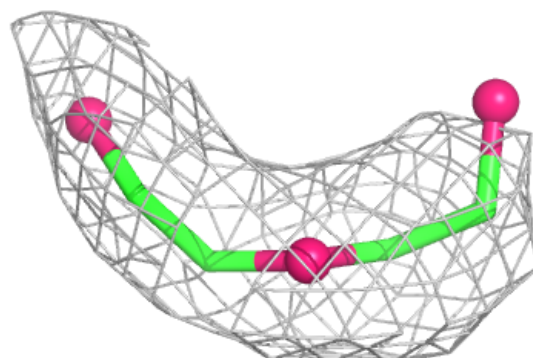


Electron density around PG4 C 332:

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

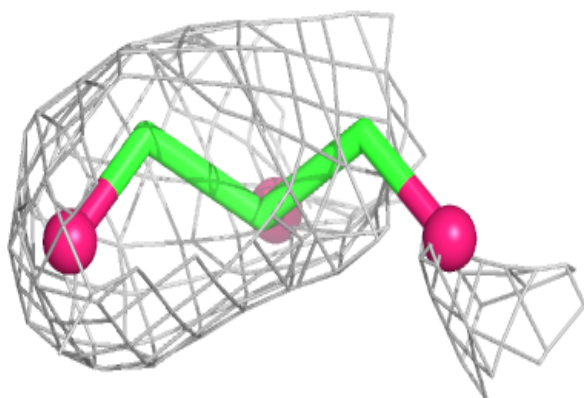
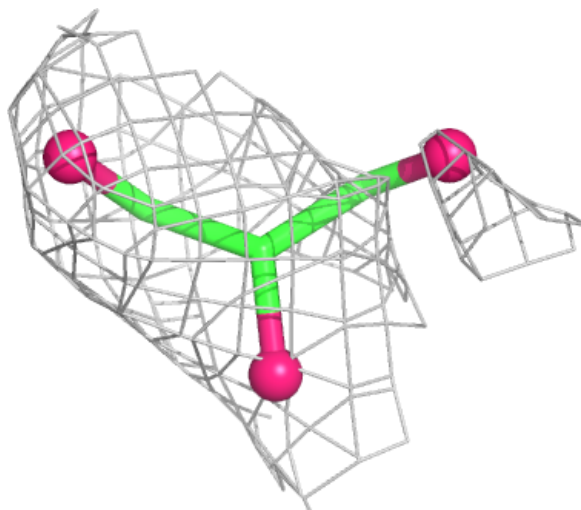
**Electron density around PEG A 342:**

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



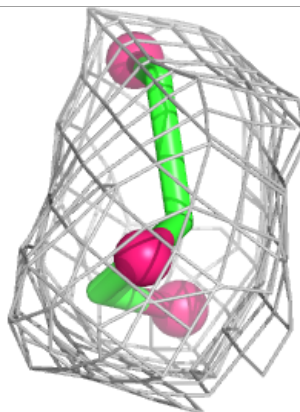
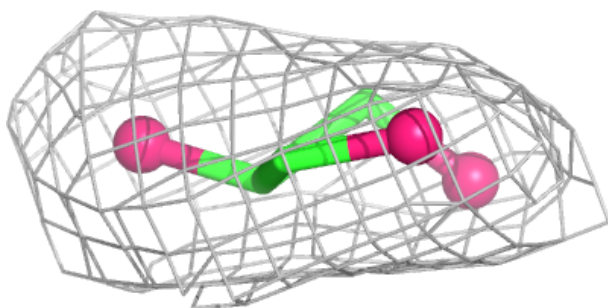
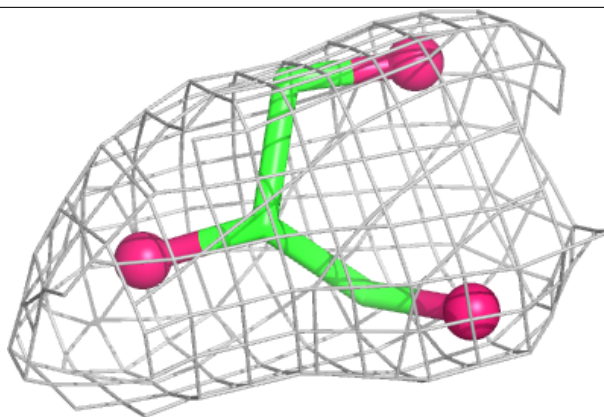
Electron density around GOL C 302:

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

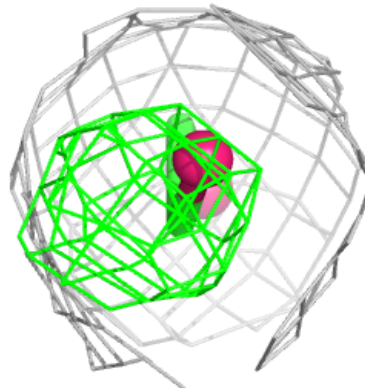
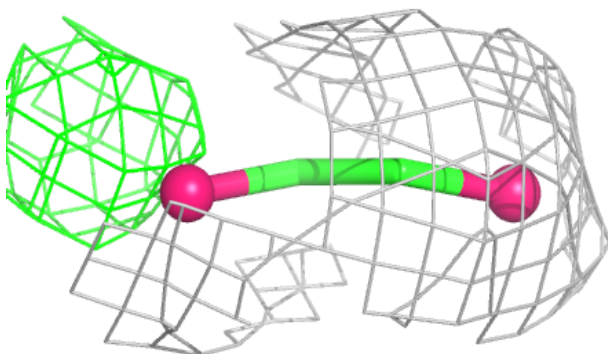
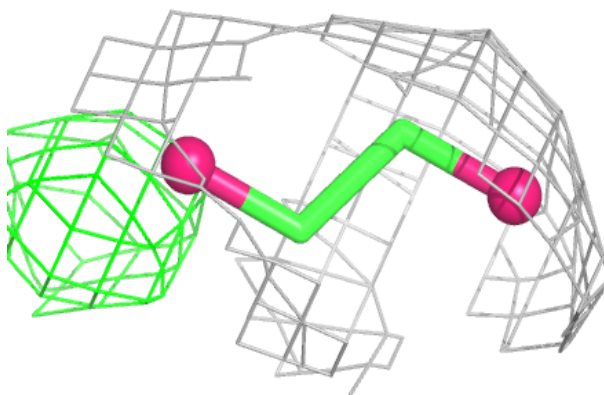


Electron density around GOL A 314:

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

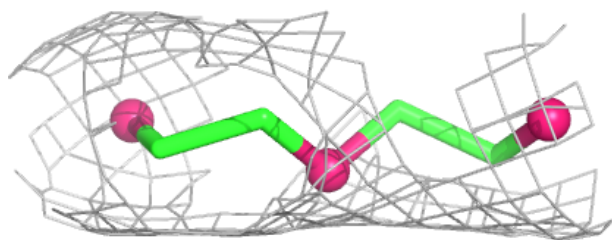
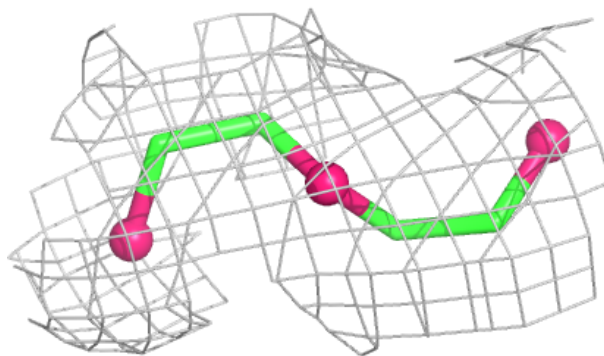
**Electron density around EDO A 336:**

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

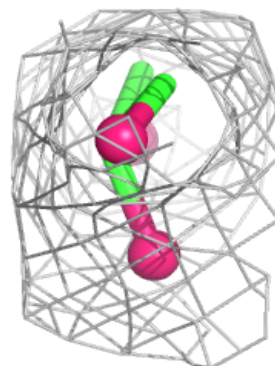
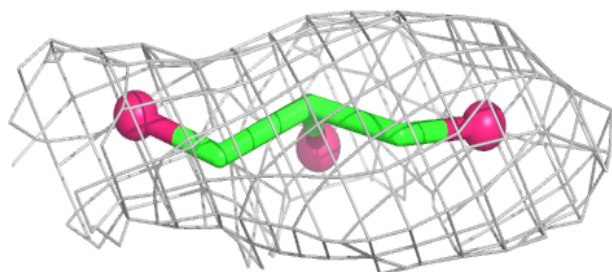
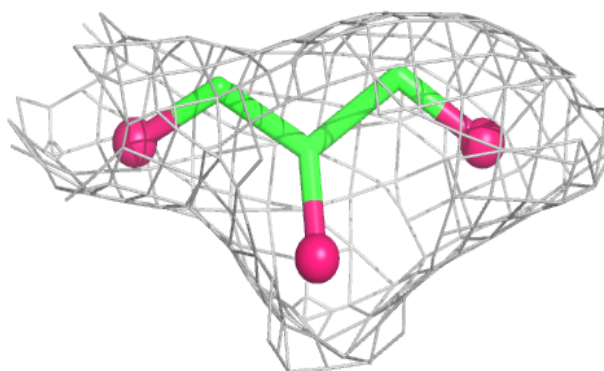


Electron density around PEG A 319:

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

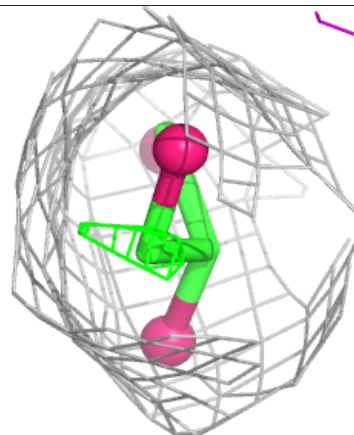
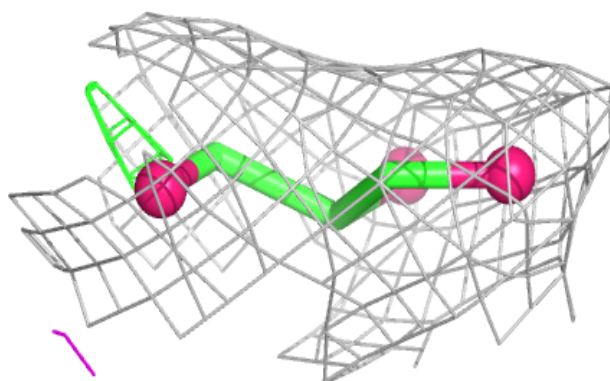
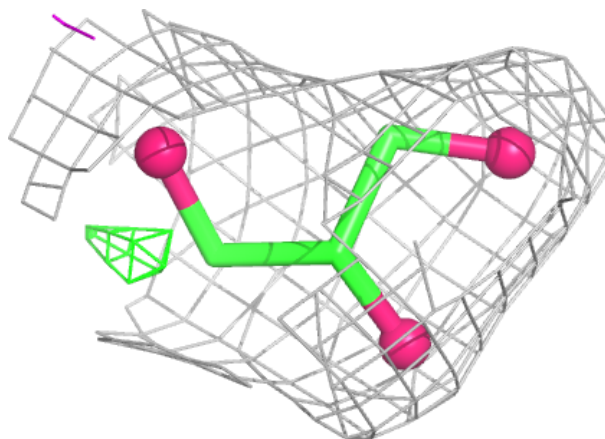
**Electron density around GOL B 116:**

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

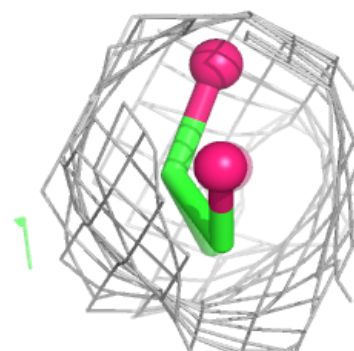
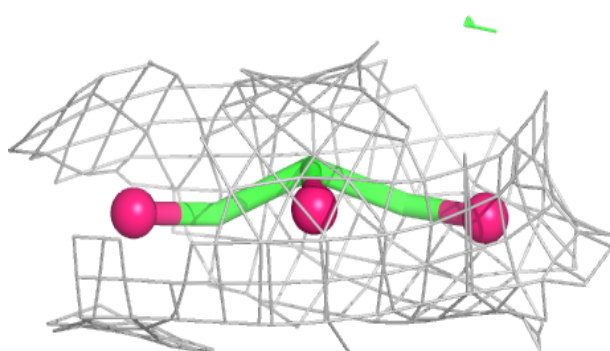
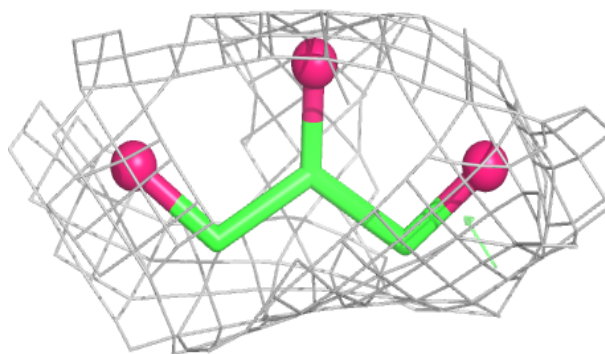


Electron density around GOL C 331:

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

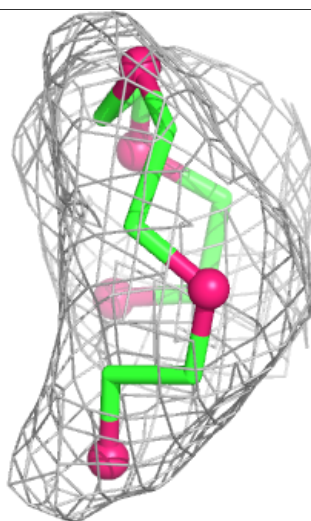
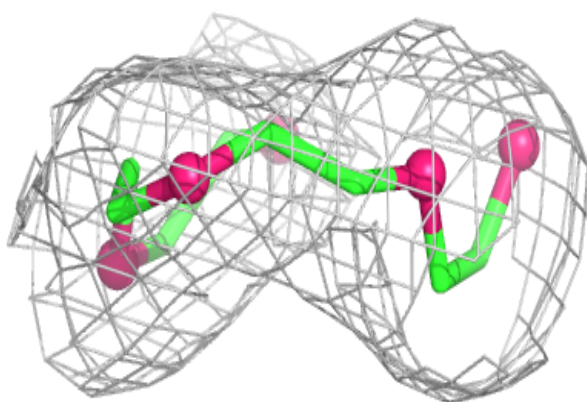
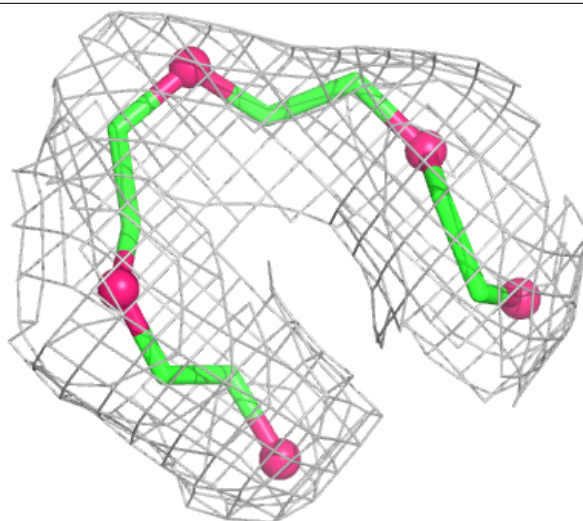
**Electron density around GOL B 101:**

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



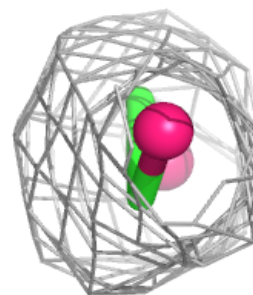
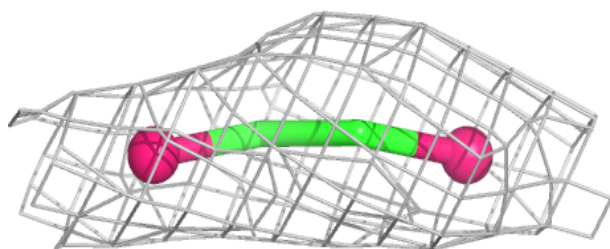
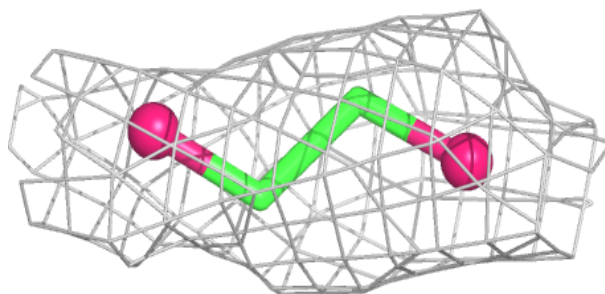
Electron density around PG4 C 324:

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



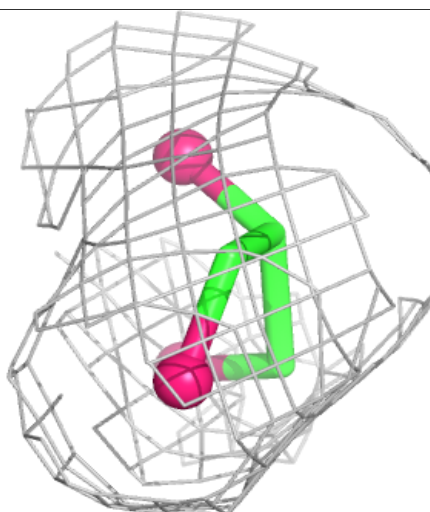
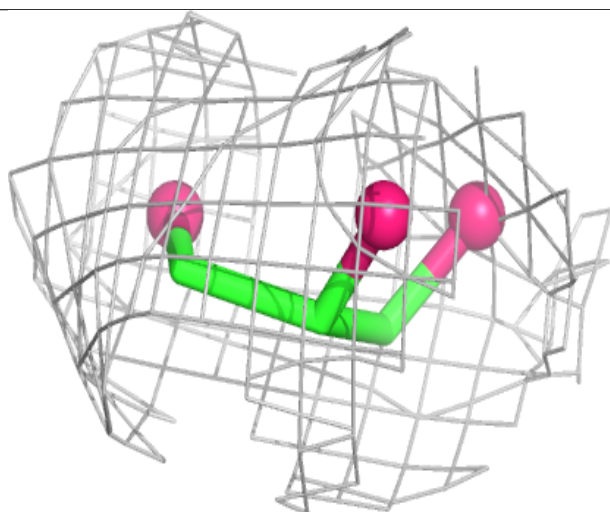
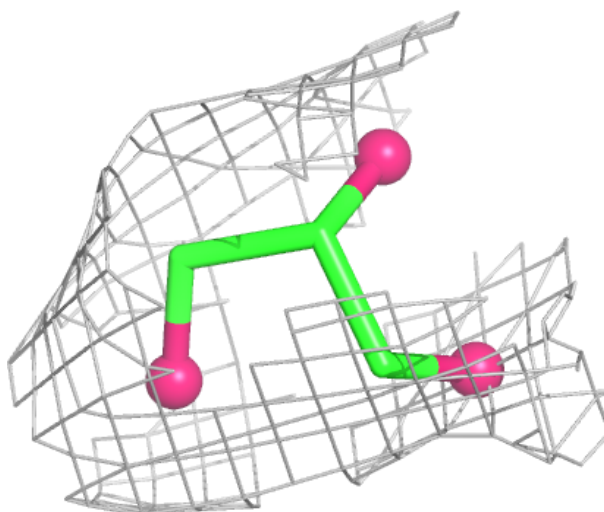
Electron density around EDO A 327:

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



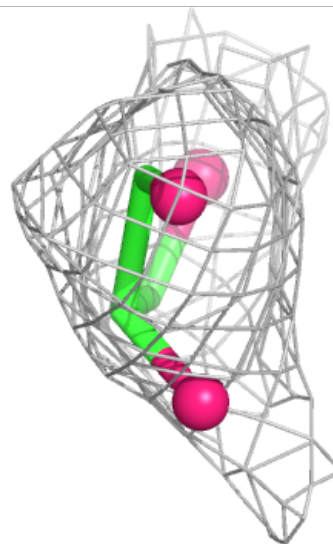
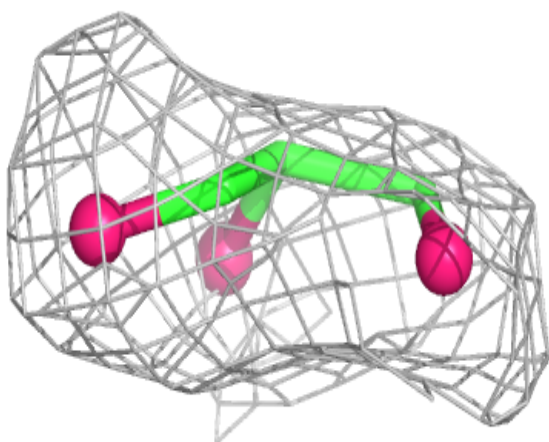
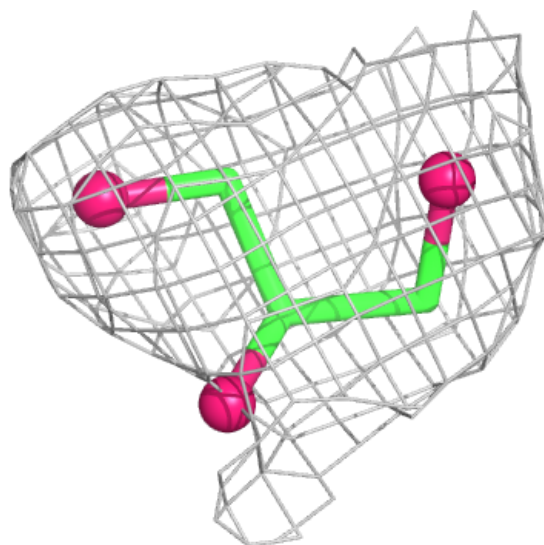
Electron density around GOL B 115:

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



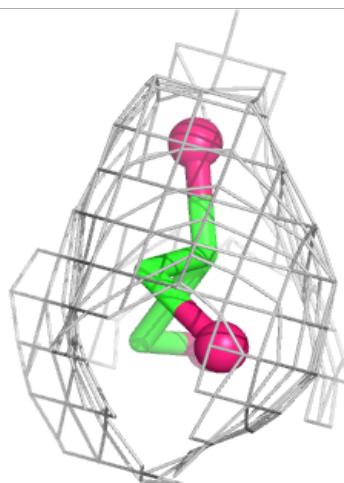
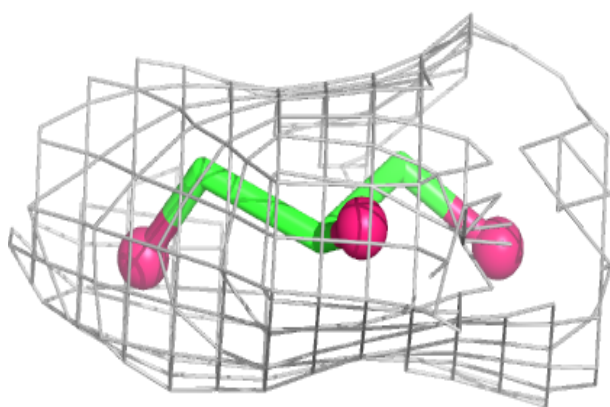
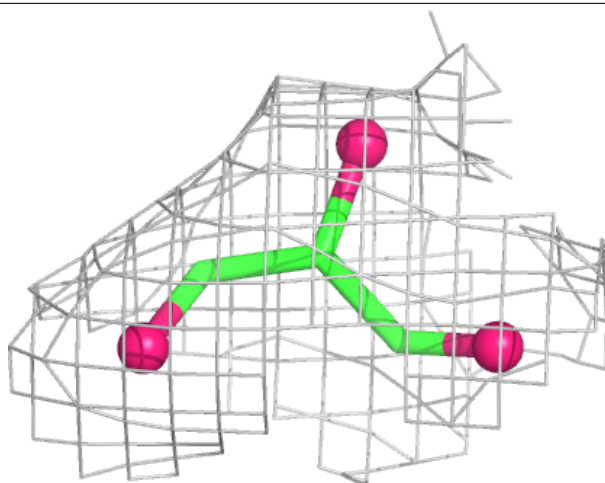
Electron density around GOL C 308:

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



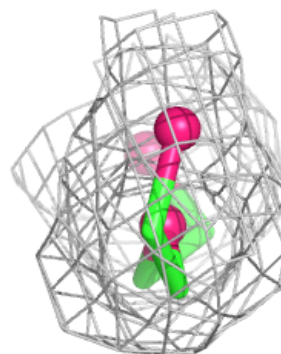
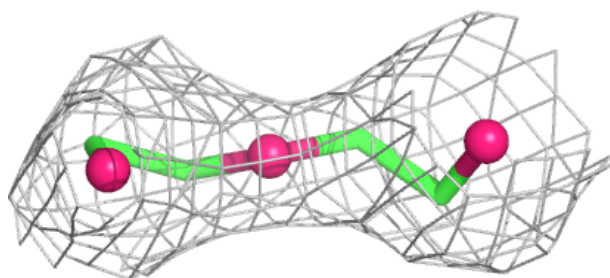
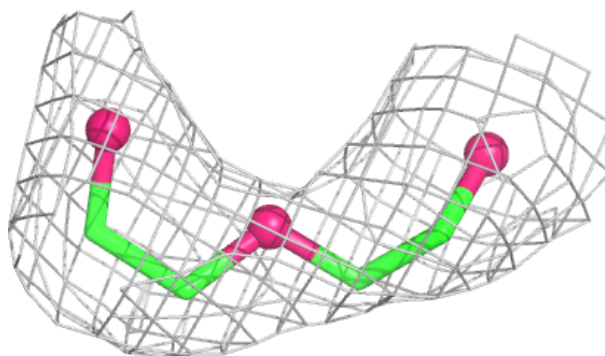
Electron density around GOL B 110:

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

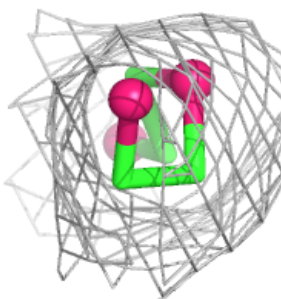
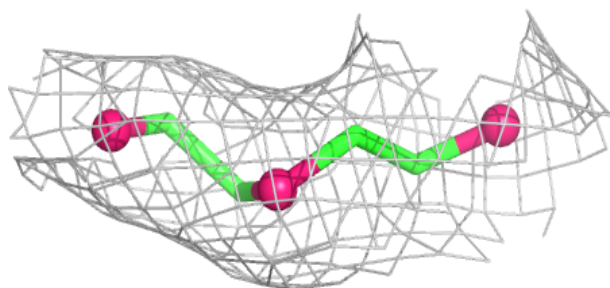
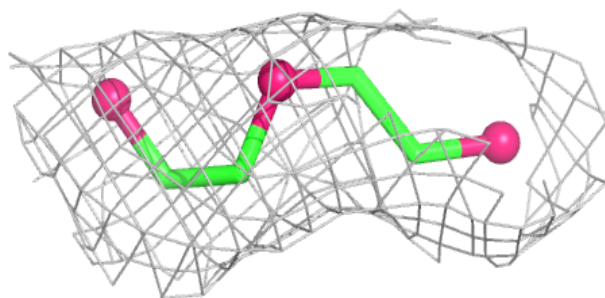


Electron density around PEG C 320:

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

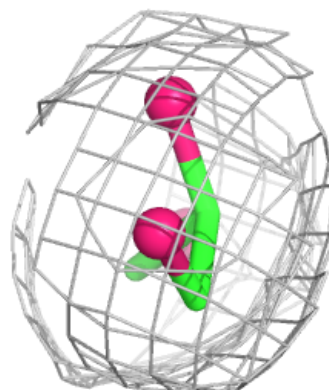
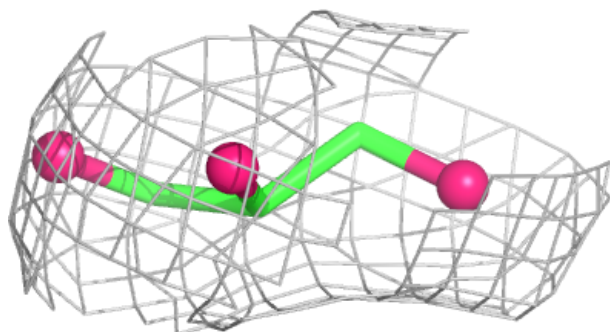
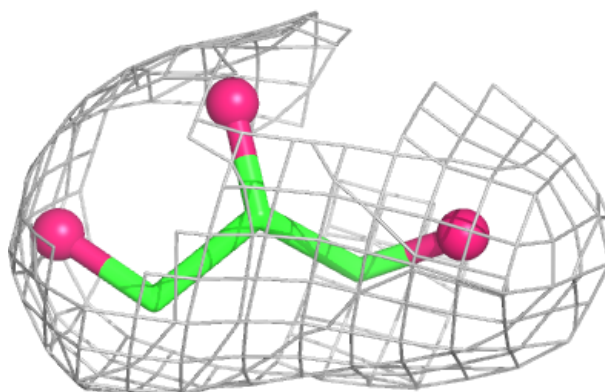
**Electron density around PEG D 123:**

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

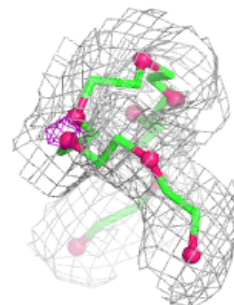
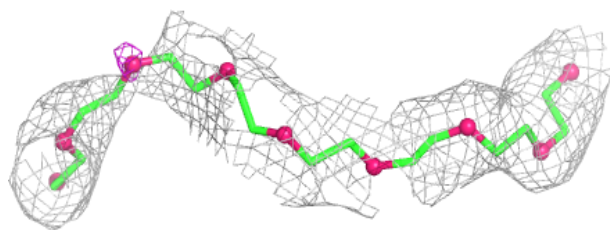
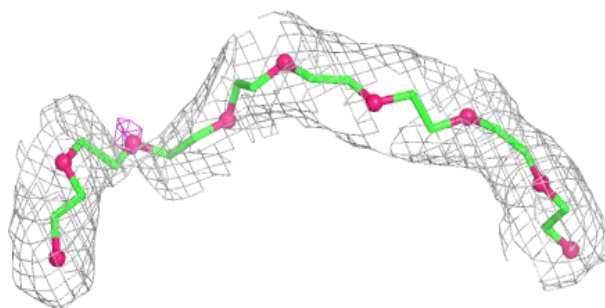


Electron density around GOL C 306:

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

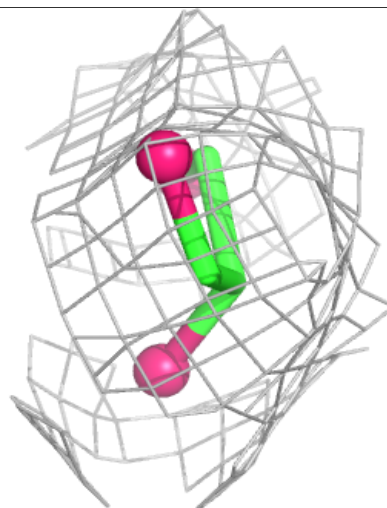
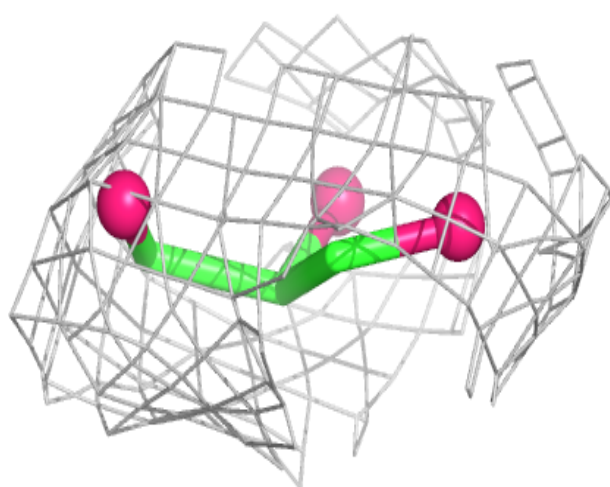
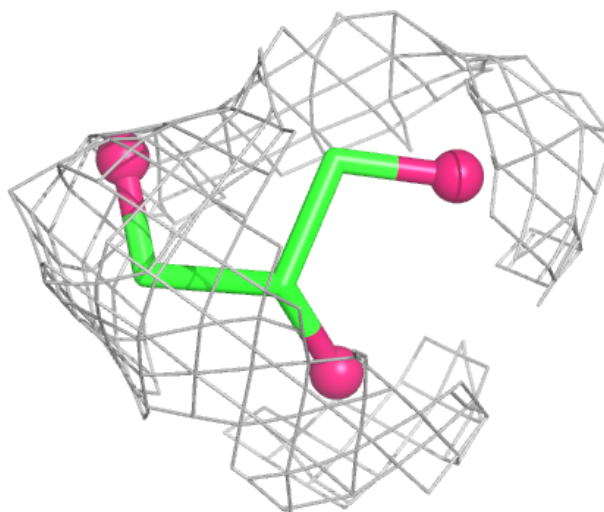
**Electron density around PE8 E 112:**

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



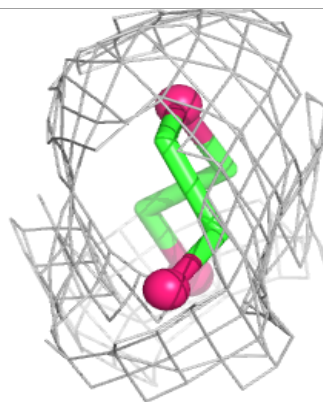
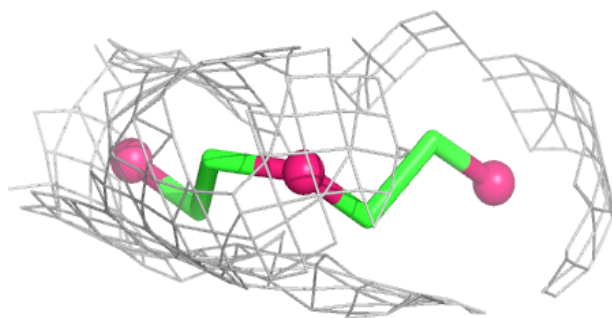
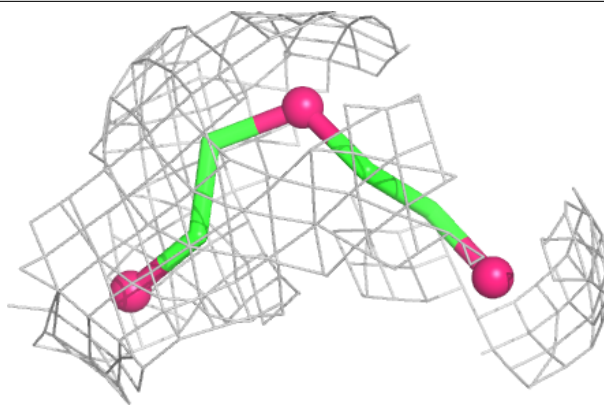
Electron density around GOL A 308:

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



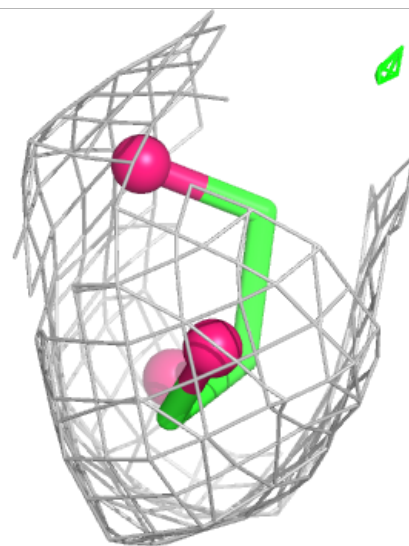
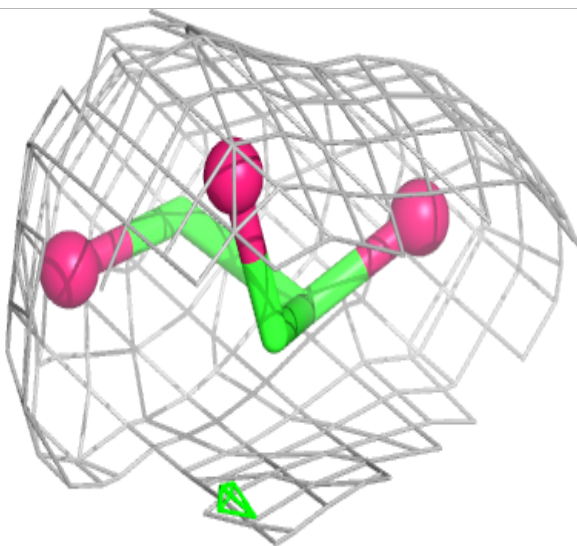
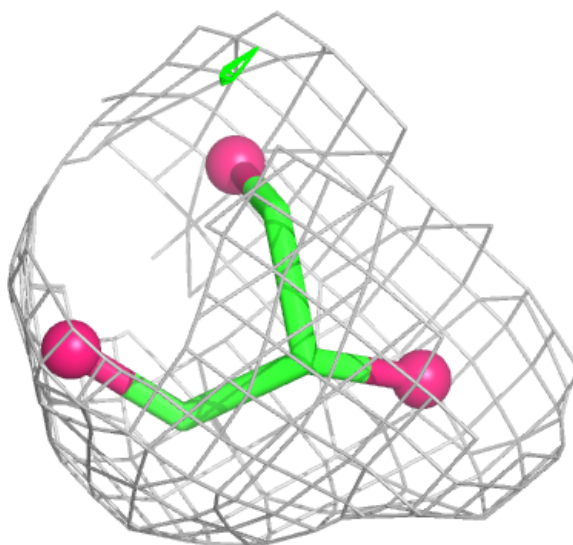
Electron density around PEG A 335:

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



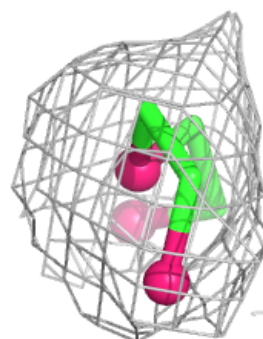
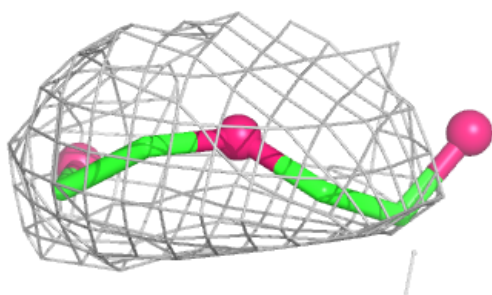
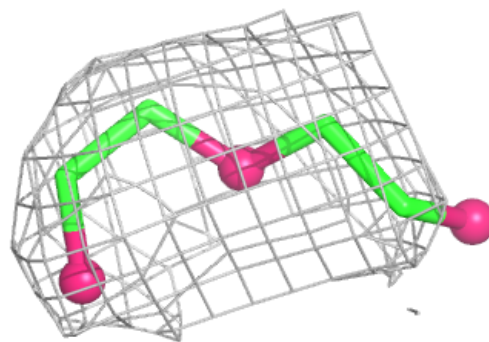
Electron density around GOL B 102:

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

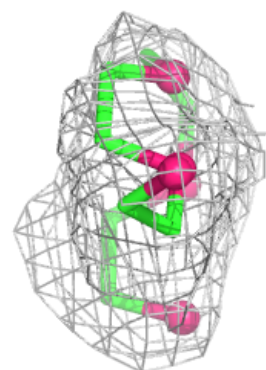
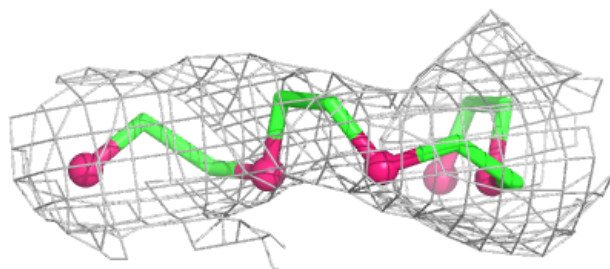


Electron density around PEG E 109:

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

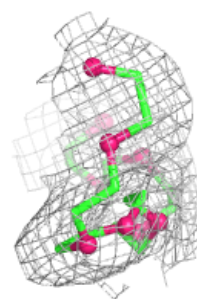
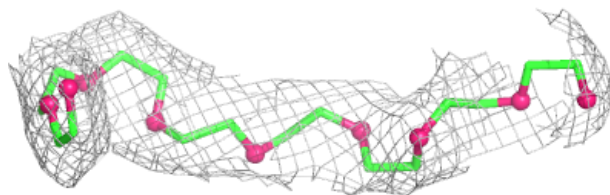
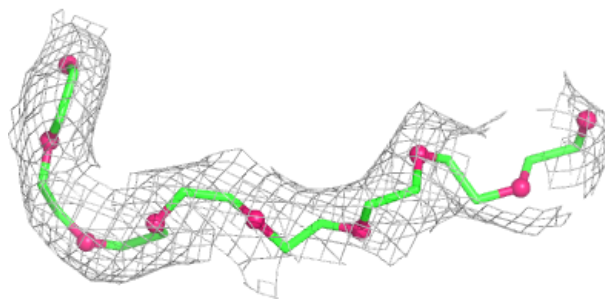
**Electron density around PG4 A 330:**

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

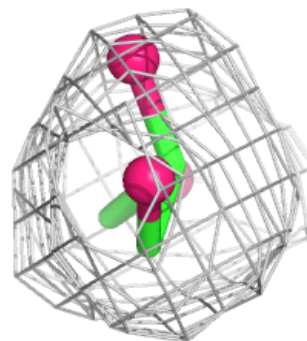
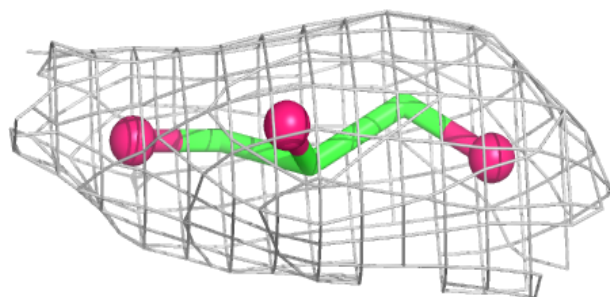
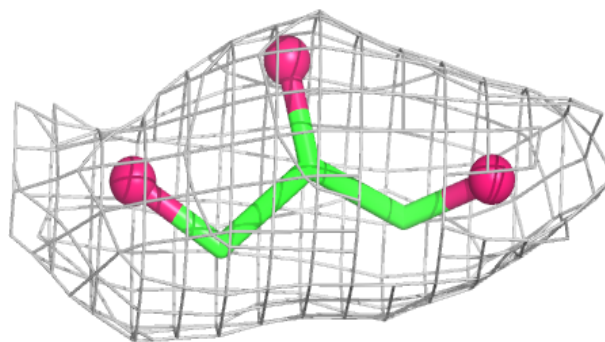


Electron density around PE8 B 105:

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

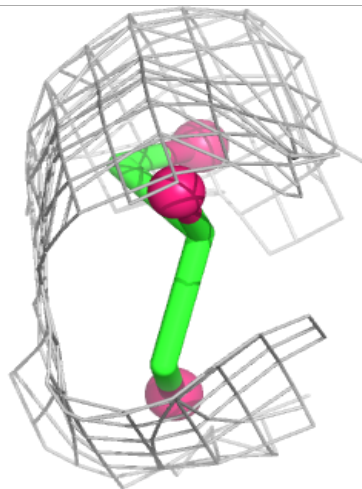
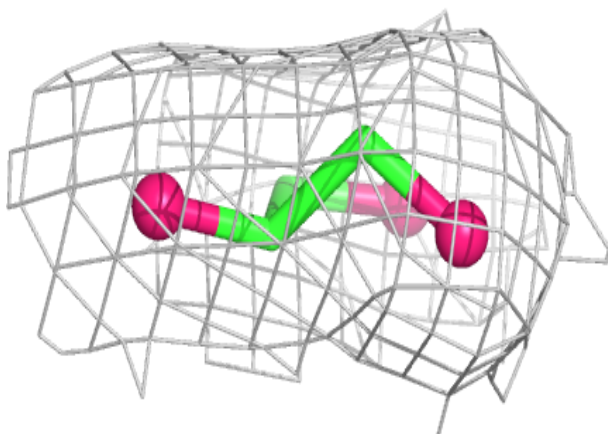
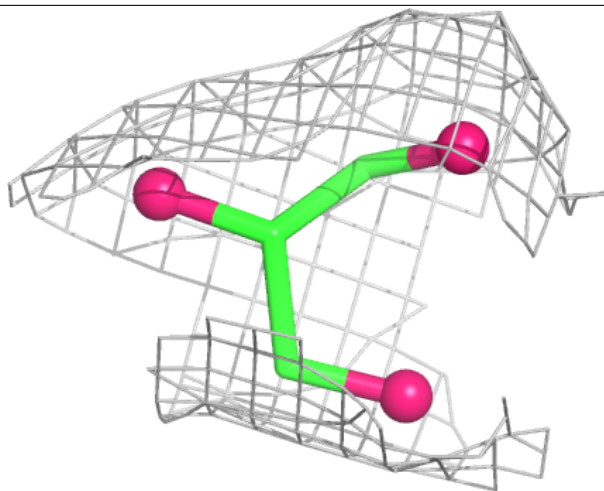
**Electron density around GOL D 108:**

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



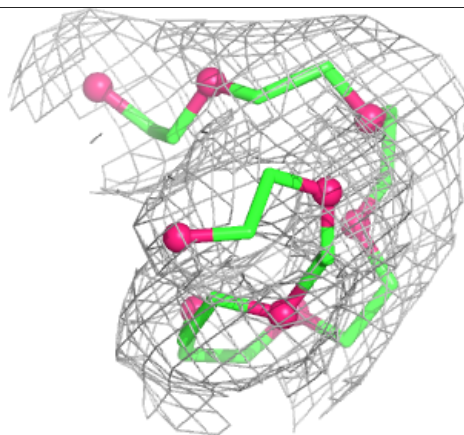
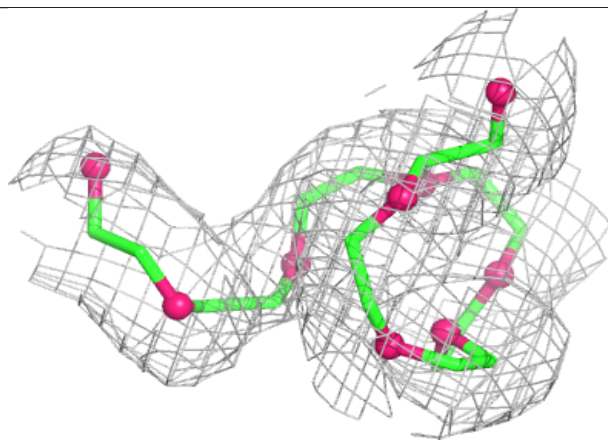
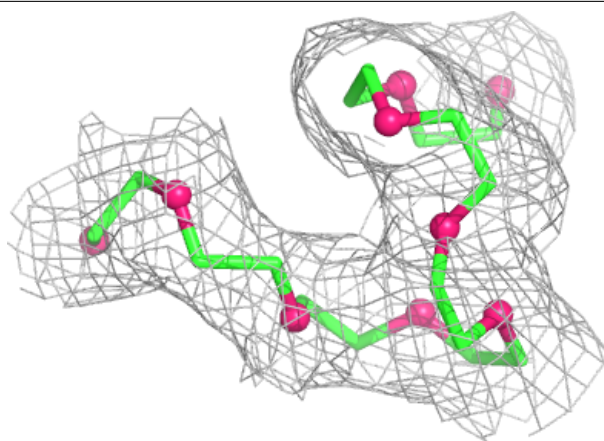
Electron density around GOL D 124:

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

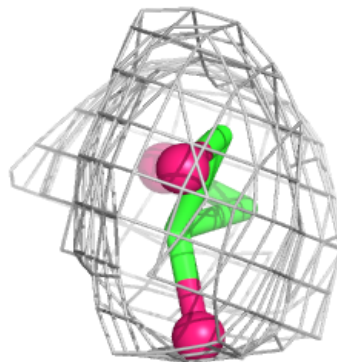
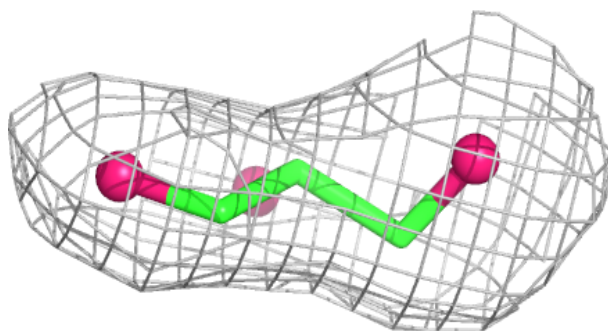
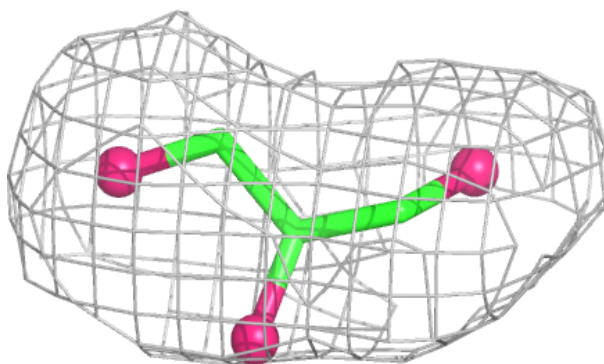


Electron density around PE8 E 114:

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

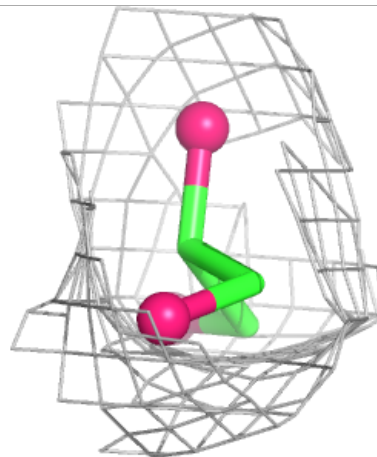
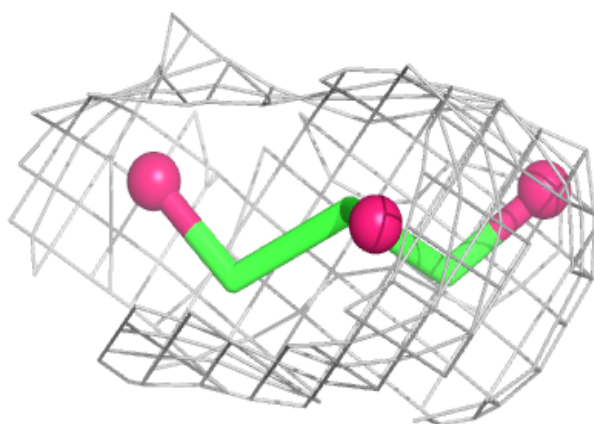
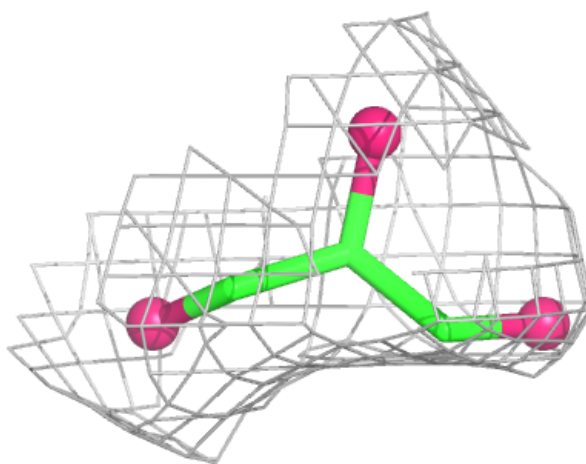
**Electron density around GOL D 122:**

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



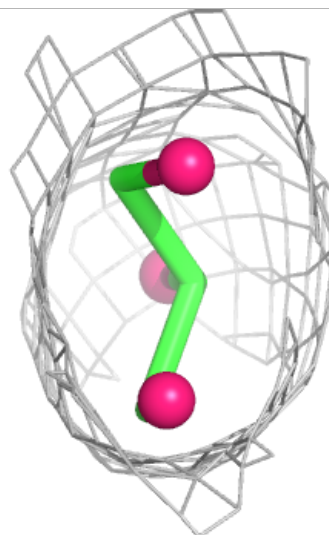
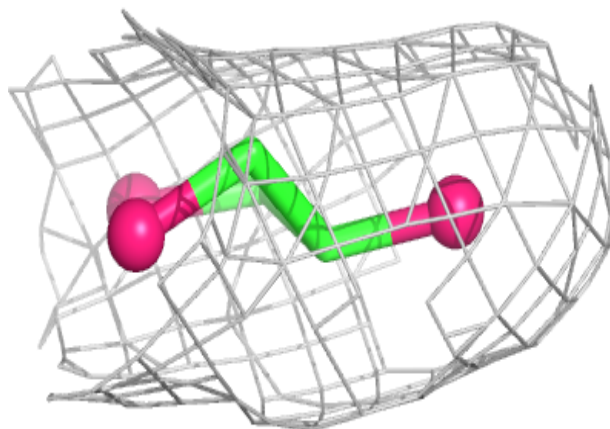
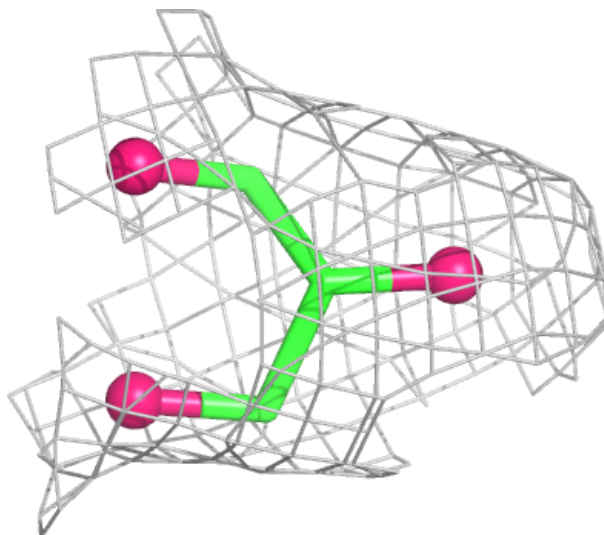
Electron density around GOL D 107:

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



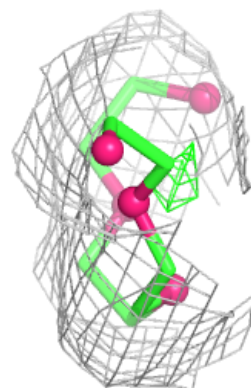
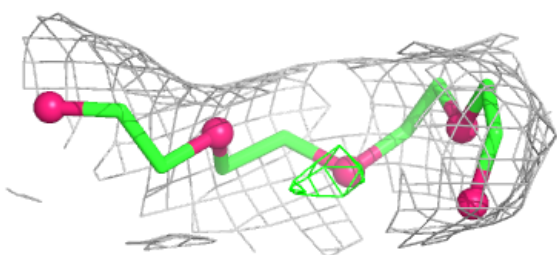
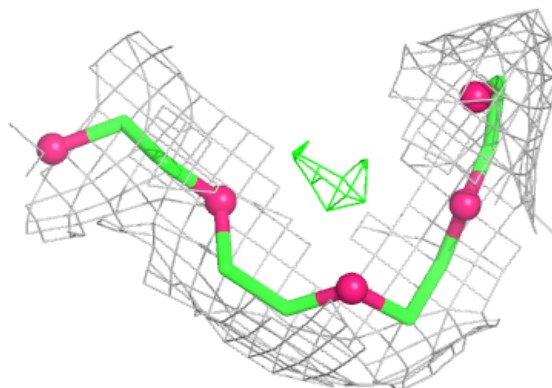
Electron density around GOL C 304:

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

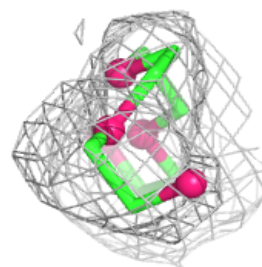
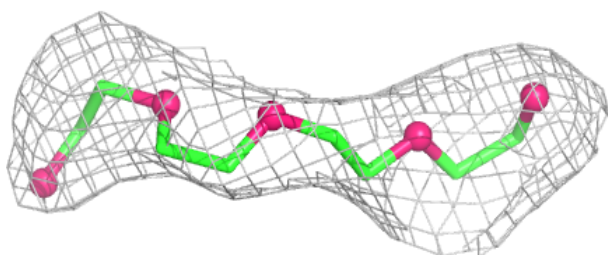
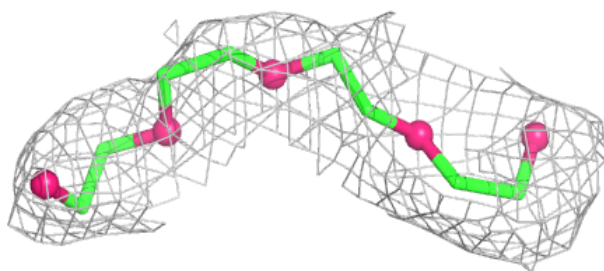


Electron density around PG4 D 101:

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

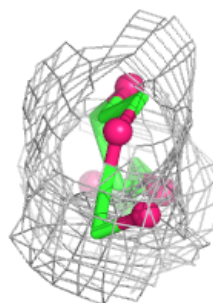
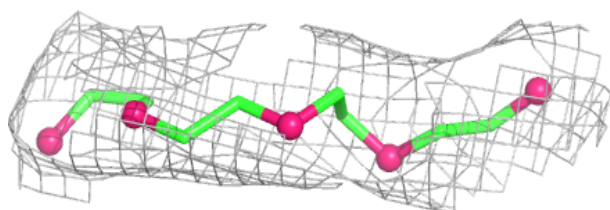
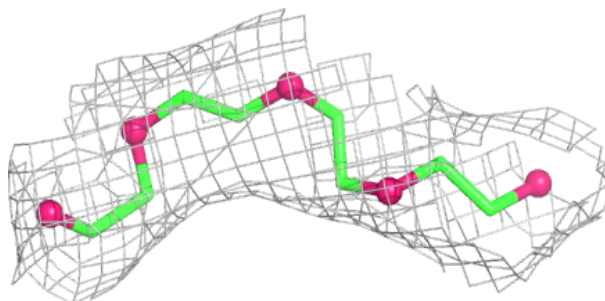
**Electron density around PG4 D 117:**

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

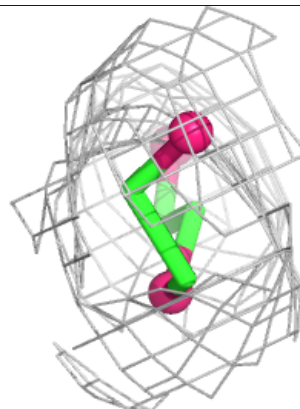
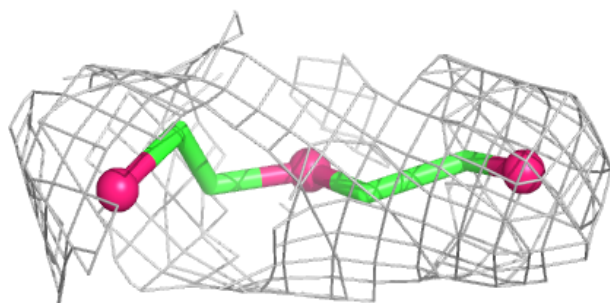
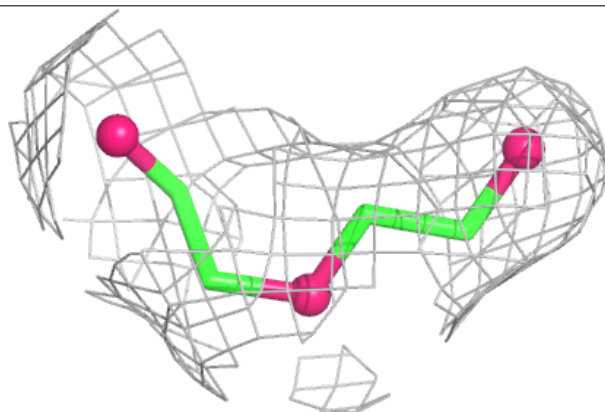


Electron density around PG4 A 337:

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

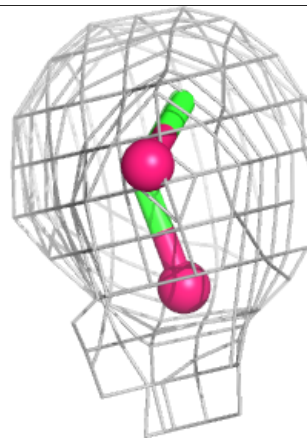
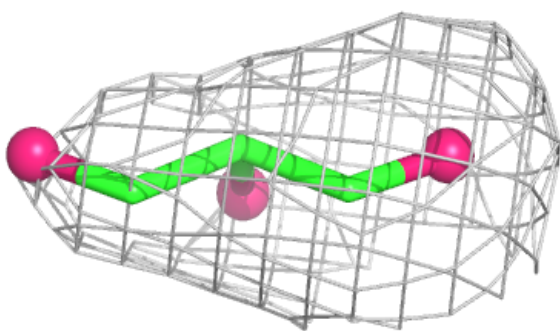
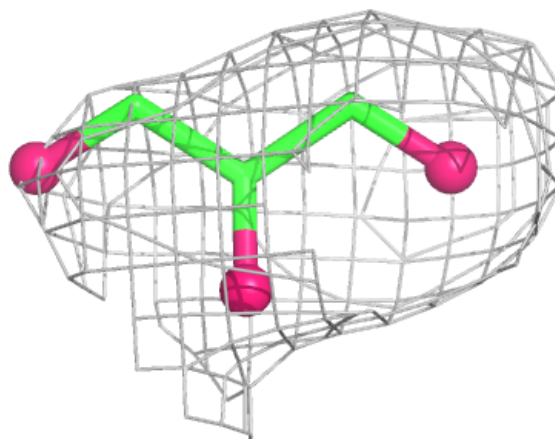
**Electron density around PEG D 115:**

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



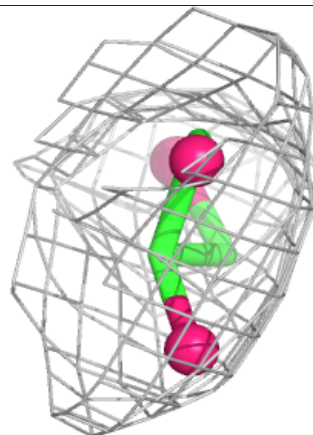
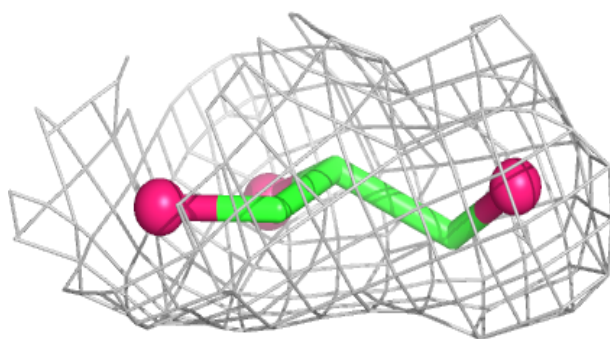
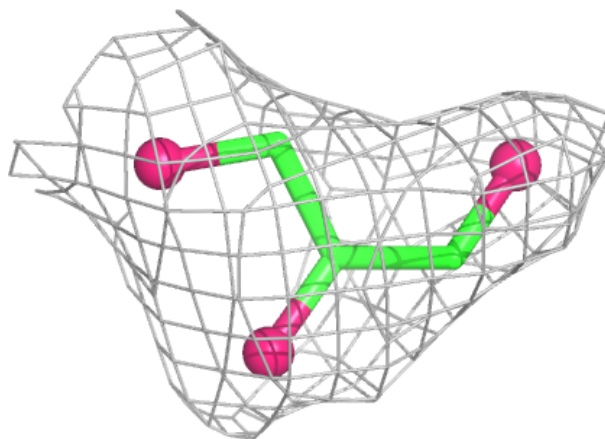
Electron density around GOL E 103:

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

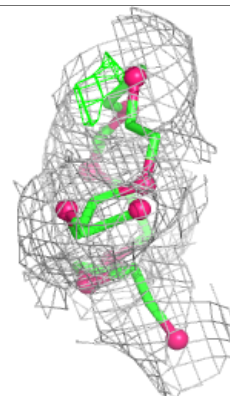
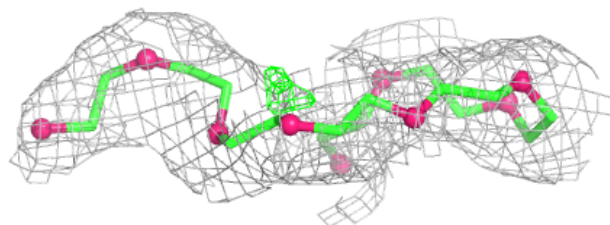
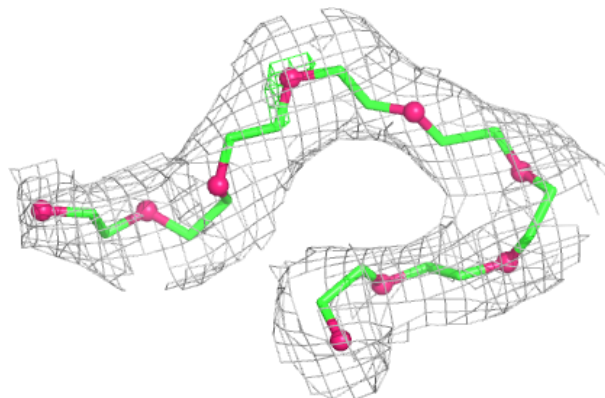


Electron density around GOL C 310:

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

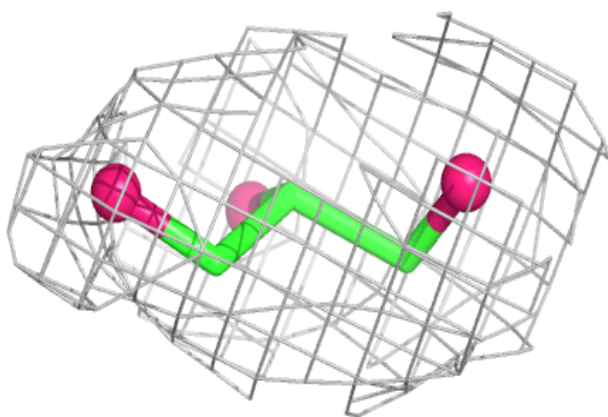
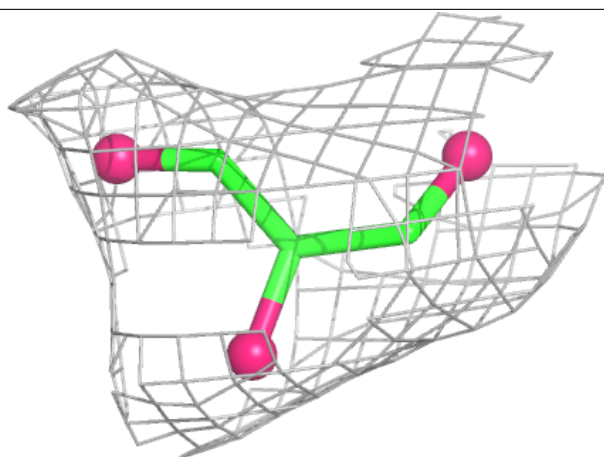
**Electron density around PE8 E 113:**

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



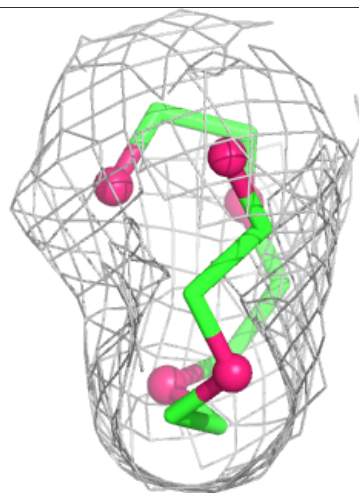
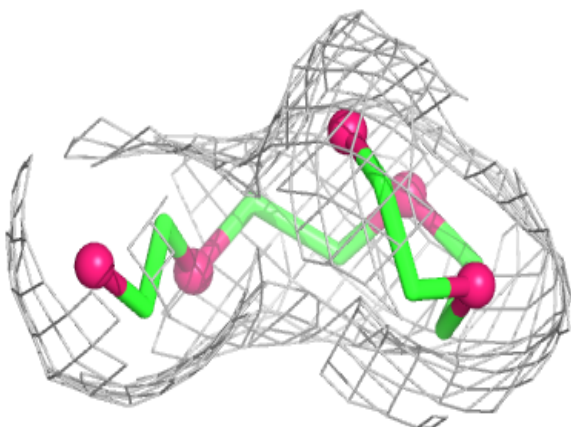
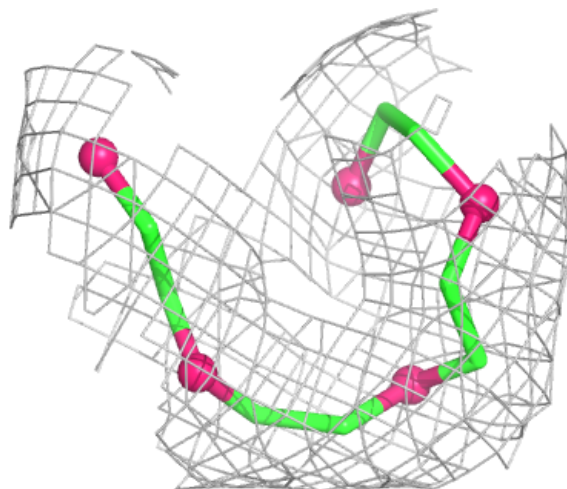
Electron density around GOL C 309:

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



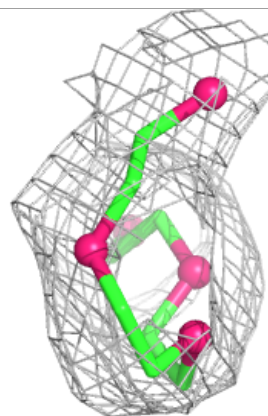
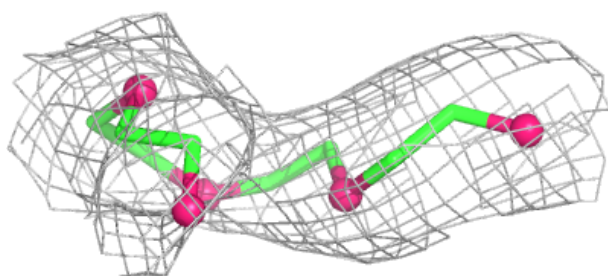
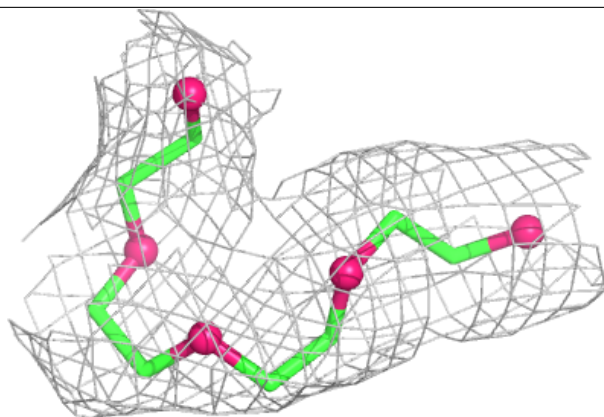
Electron density around PG4 B 127:

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

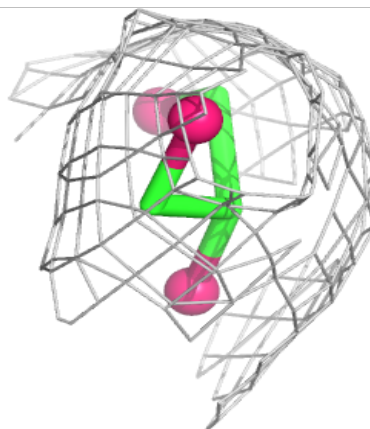
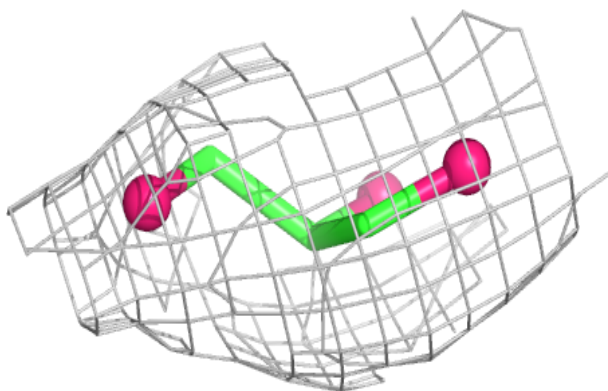
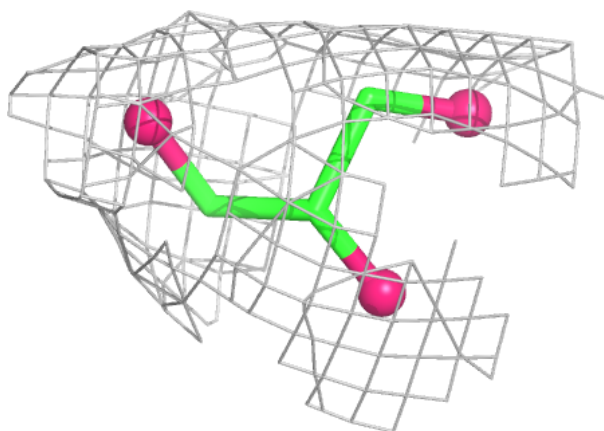


Electron density around PG4 A 331:

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

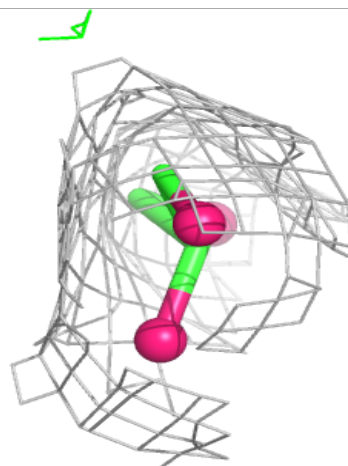
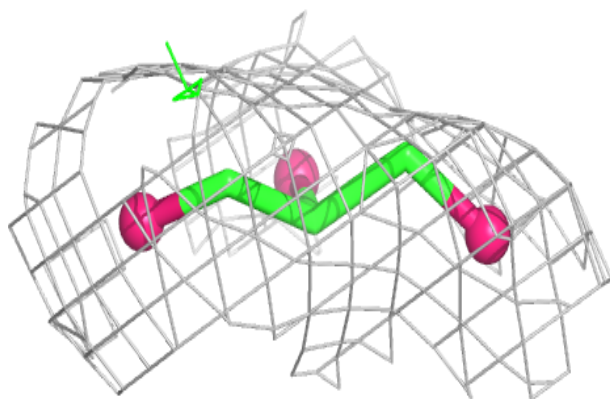
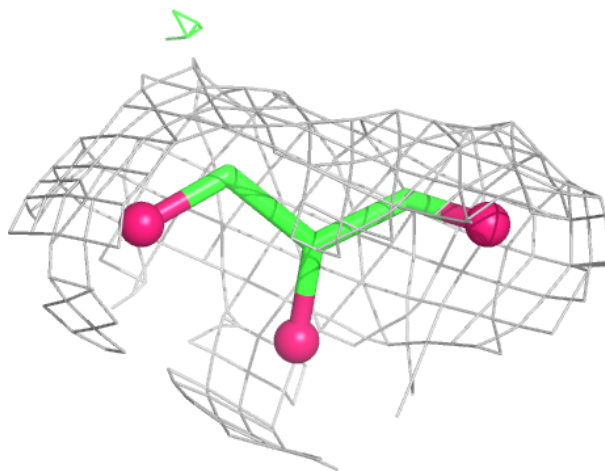
**Electron density around GOL D 110:**

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



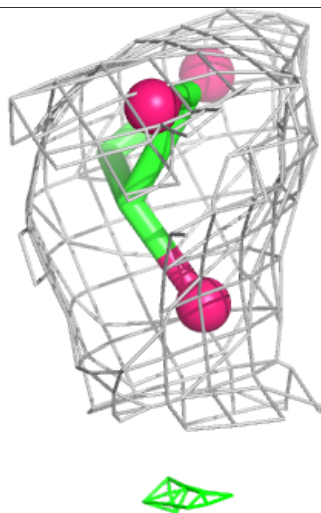
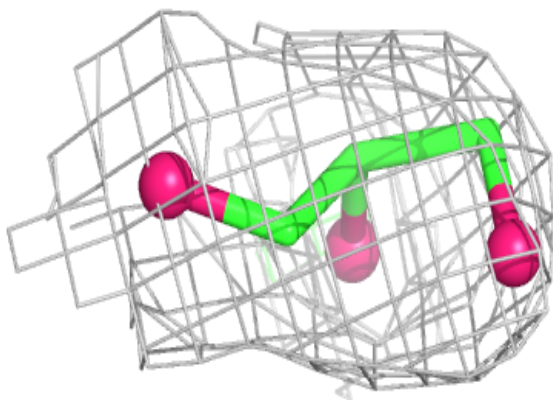
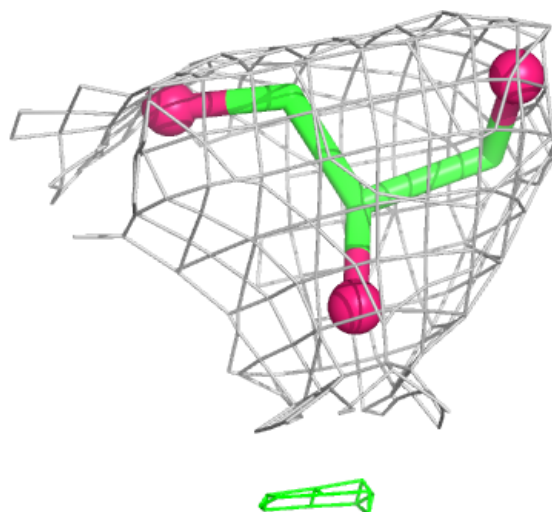
Electron density around GOL D 106:

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



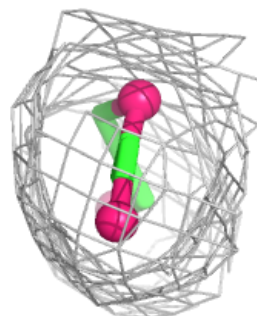
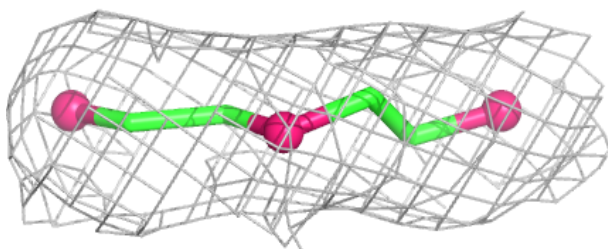
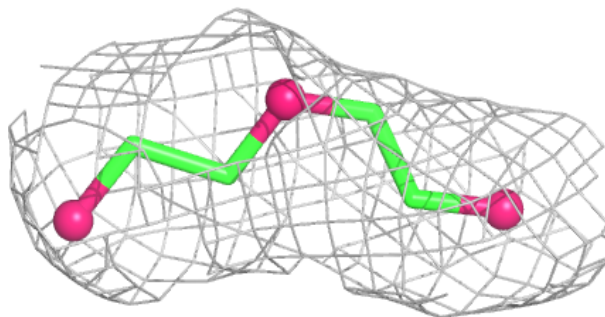
Electron density around GOL B 138:

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

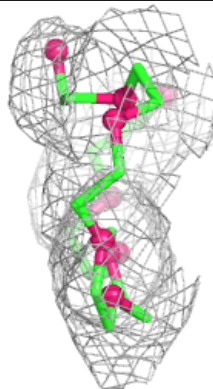
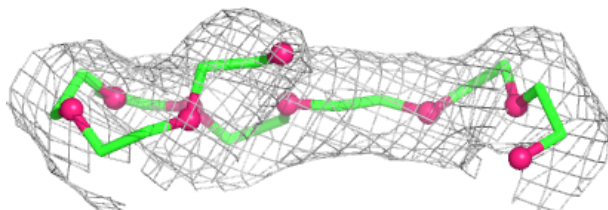
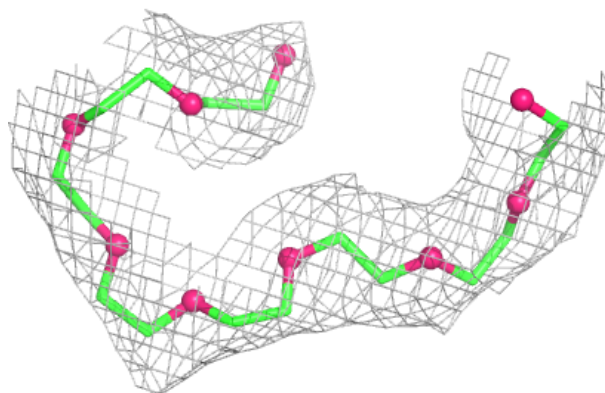


Electron density around PEG C 330:

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

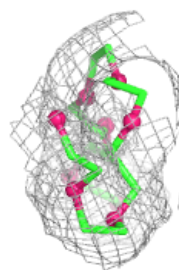
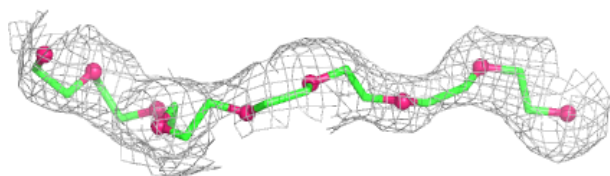
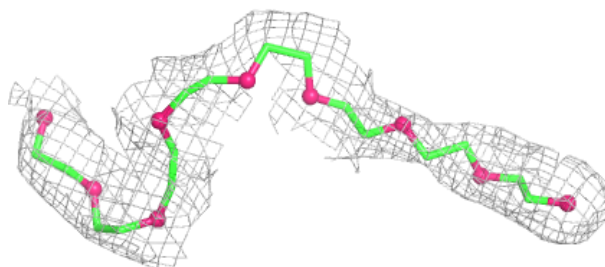
**Electron density around PE8 B 122:**

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

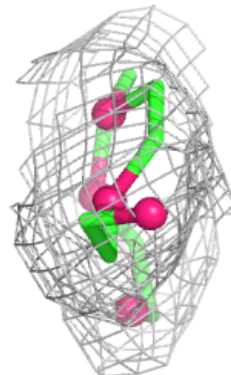
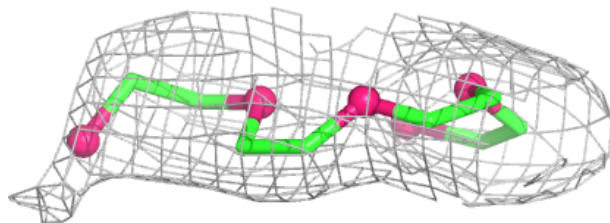
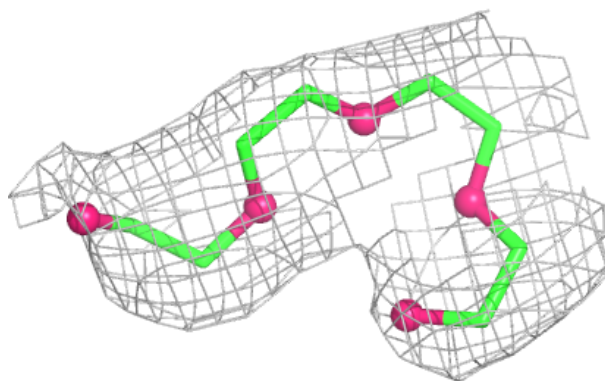


Electron density around PE8 B 123:

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

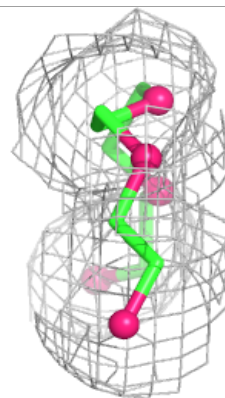
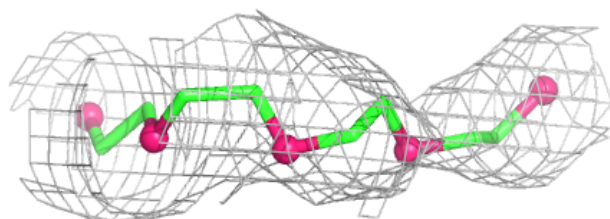
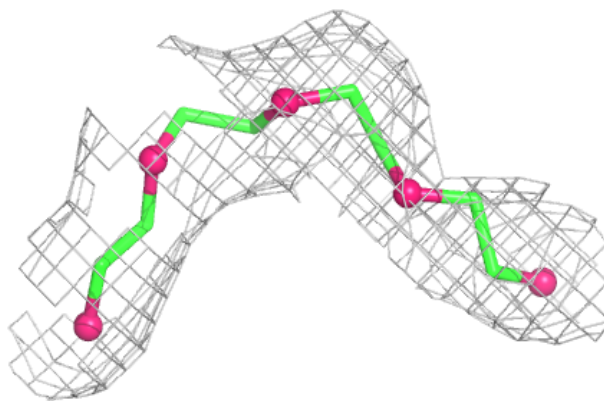
**Electron density around PG4 A 328:**

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

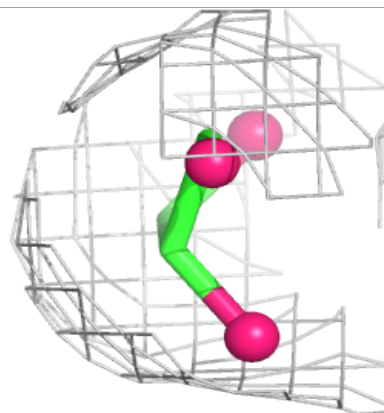
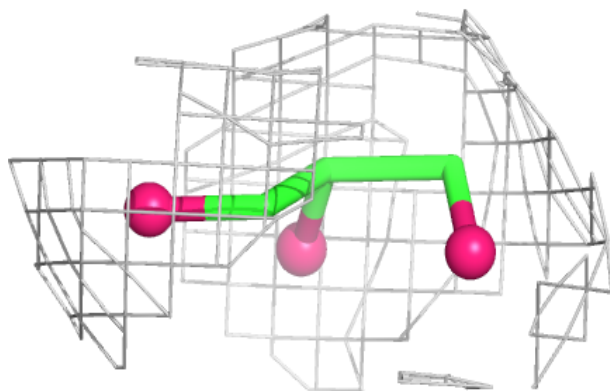
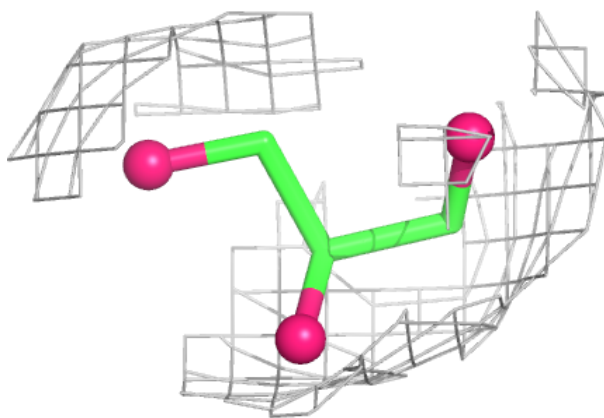


Electron density around PG4 D 118:

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

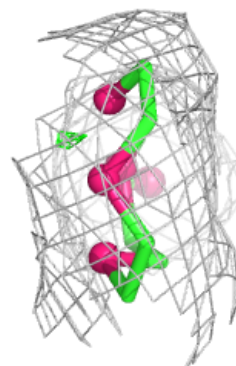
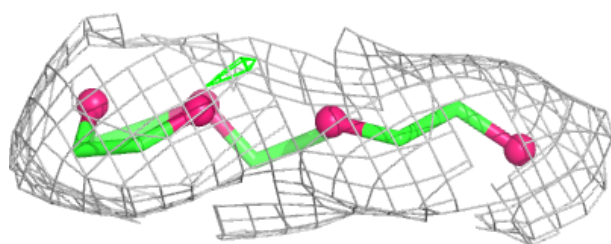
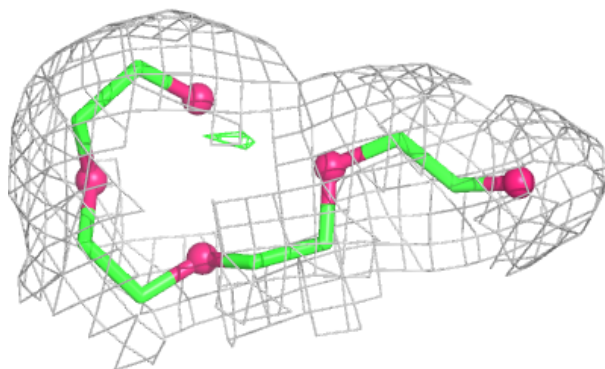
**Electron density around GOL B 109:**

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

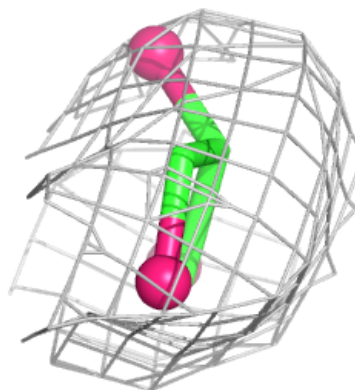
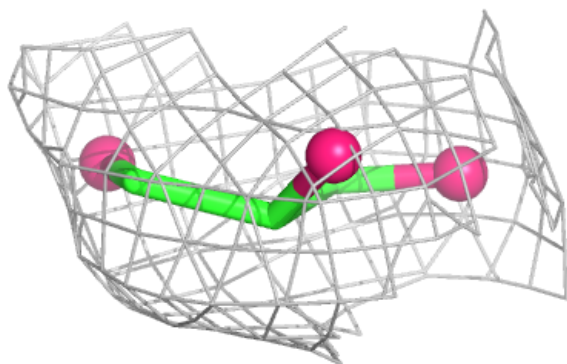
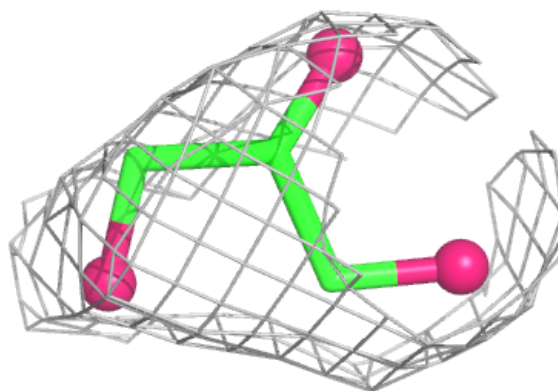


Electron density around PG4 C 325:

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

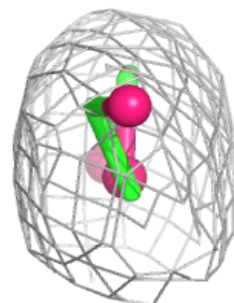
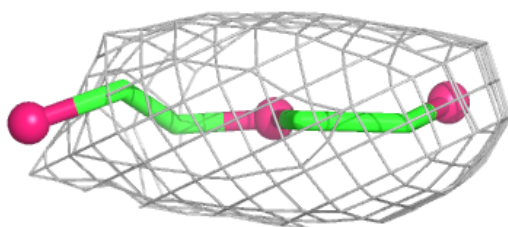
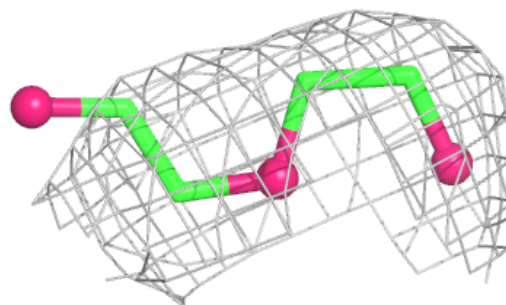
**Electron density around GOL A 307:**

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

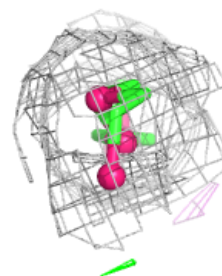
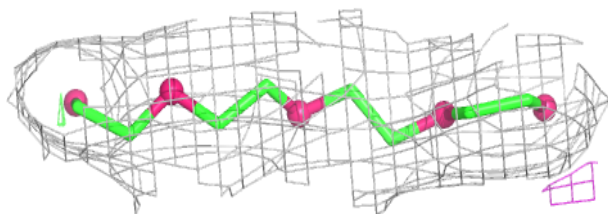
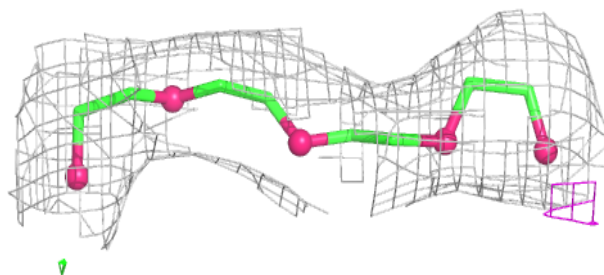


Electron density around PEG C 318:

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

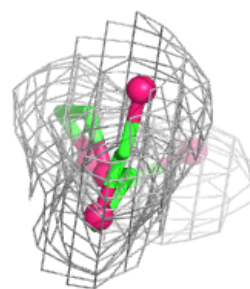
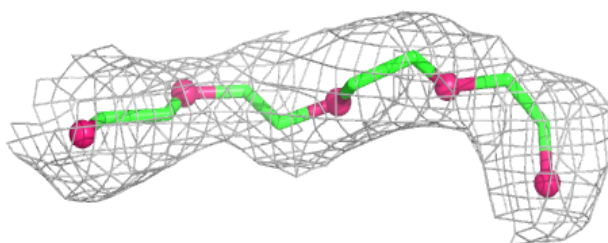
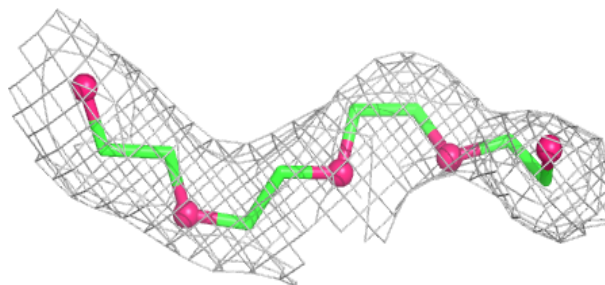
**Electron density around PG4 B 104:**

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

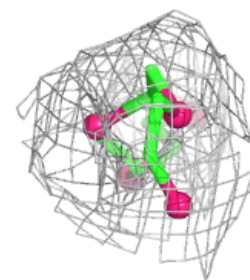
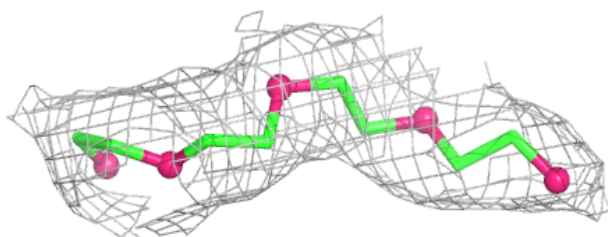
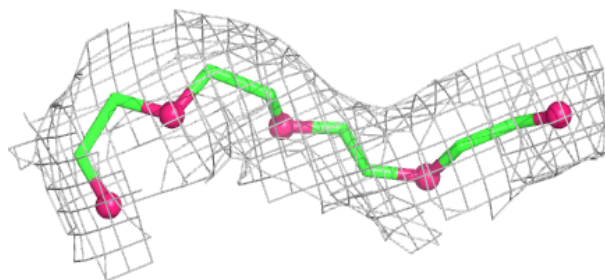


Electron density around PG4 D 116:

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

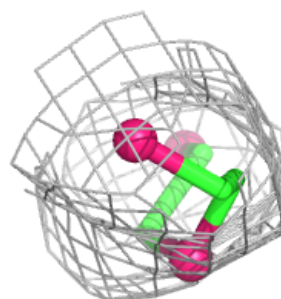
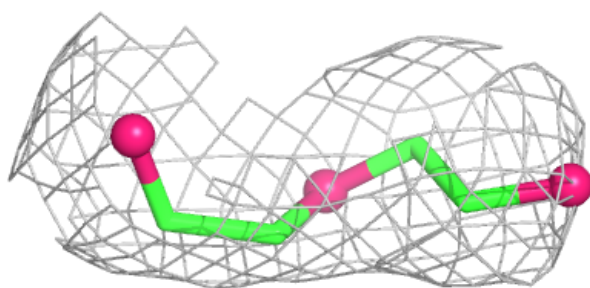
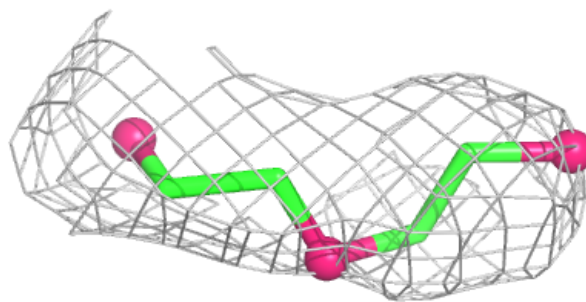
**Electron density around PG4 B 125:**

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

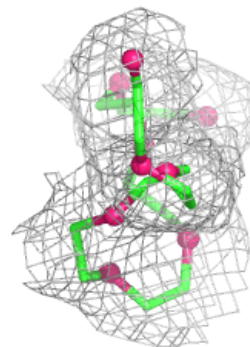
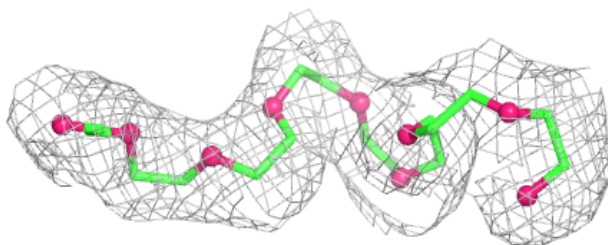
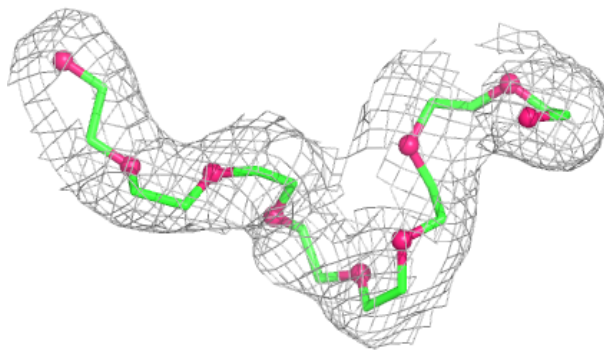


Electron density around PEG C 319:

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

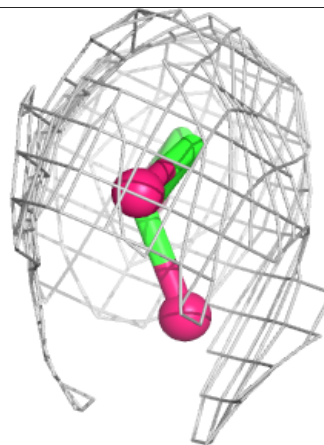
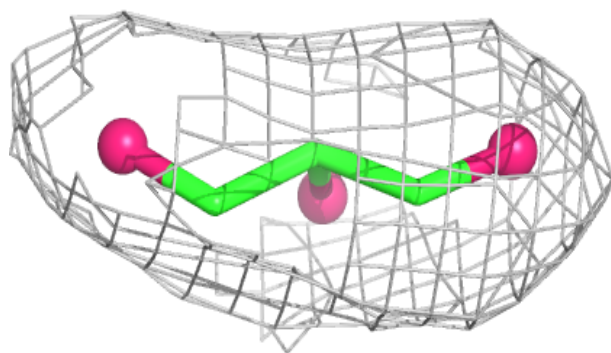
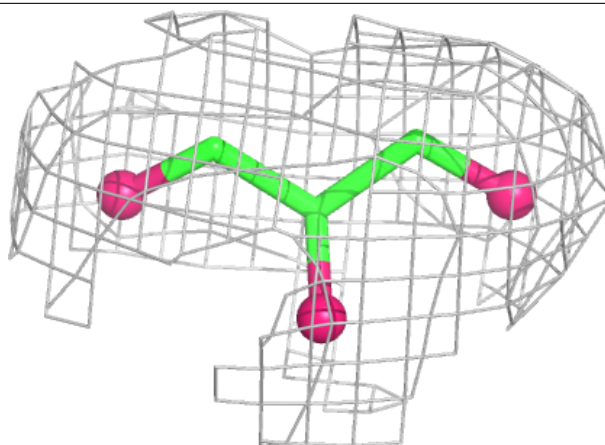
**Electron density around PE8 A 324:**

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



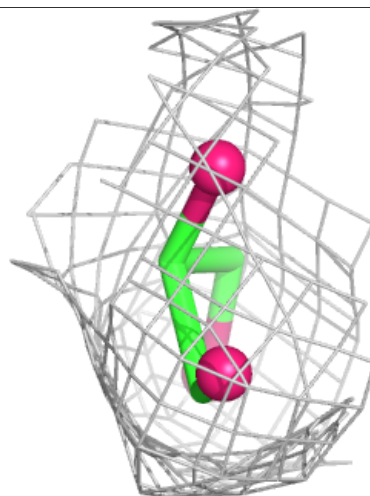
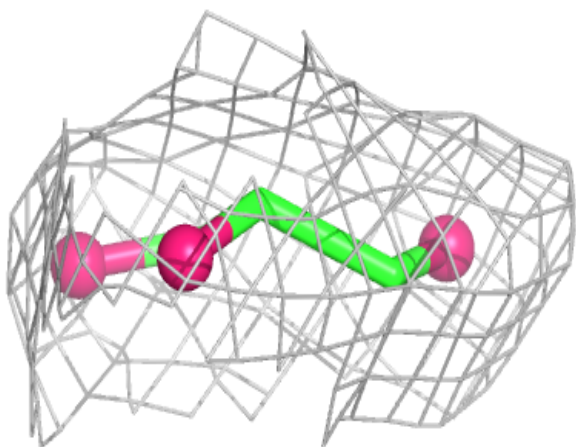
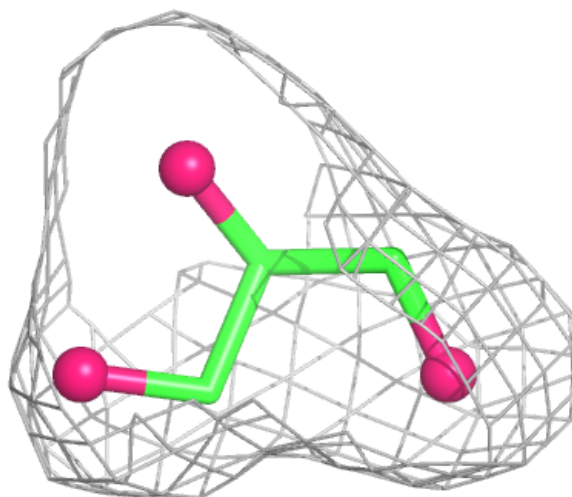
Electron density around GOL A 309:

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



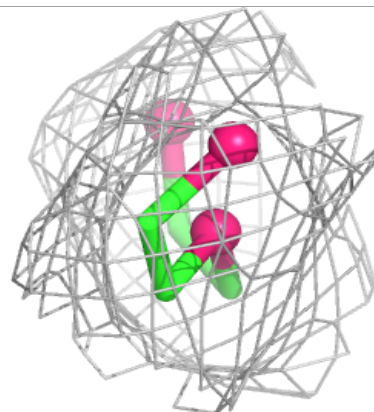
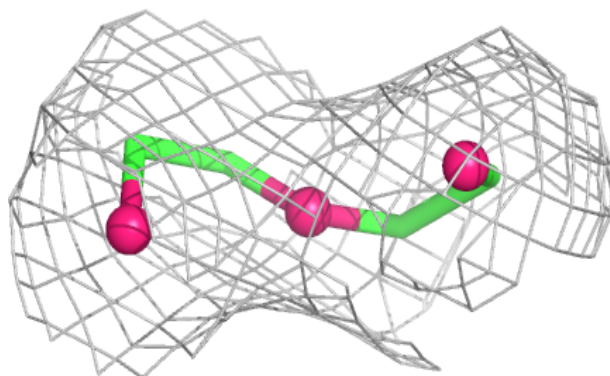
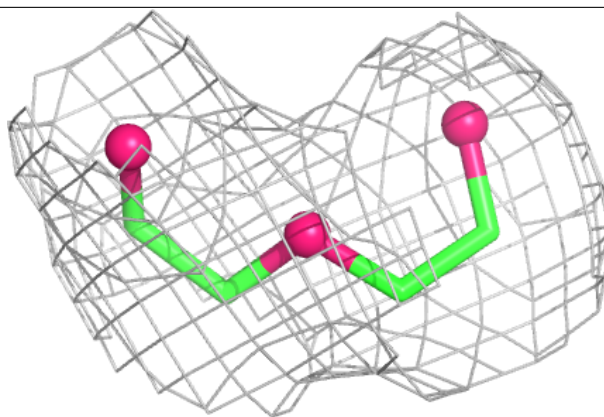
Electron density around GOL C 311:

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

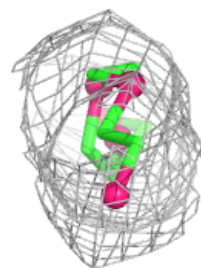
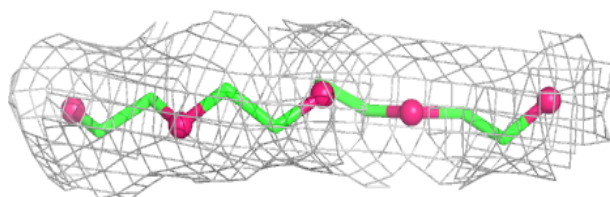
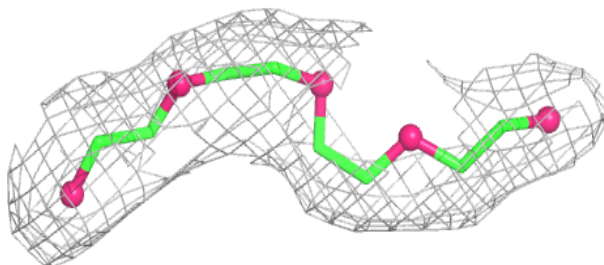


Electron density around PEG A 341:

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

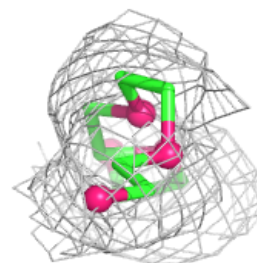
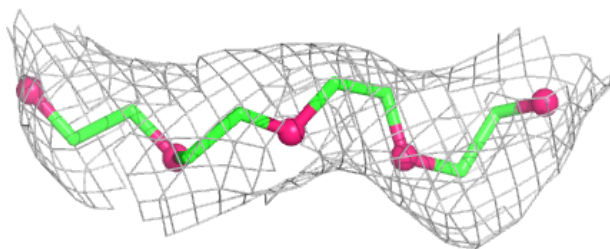
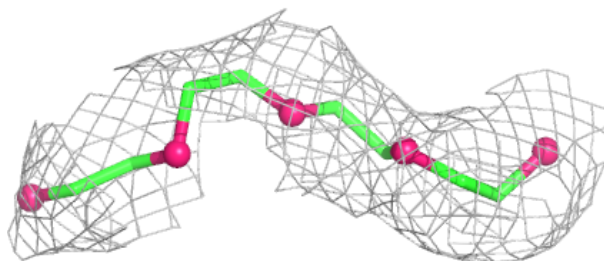
**Electron density around PG4 A 338:**

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



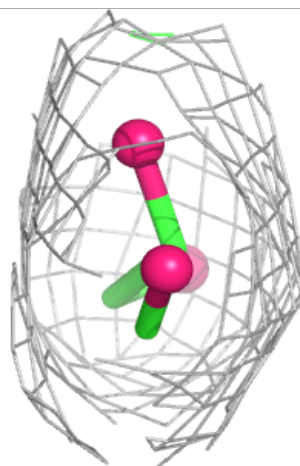
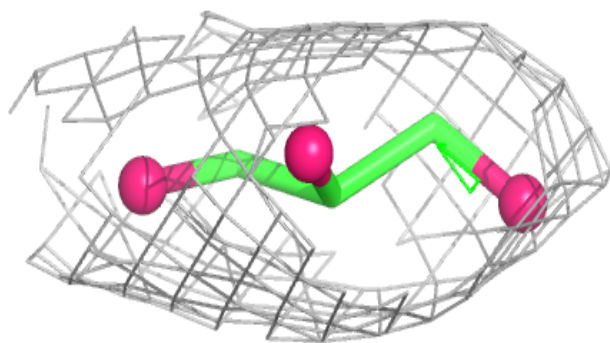
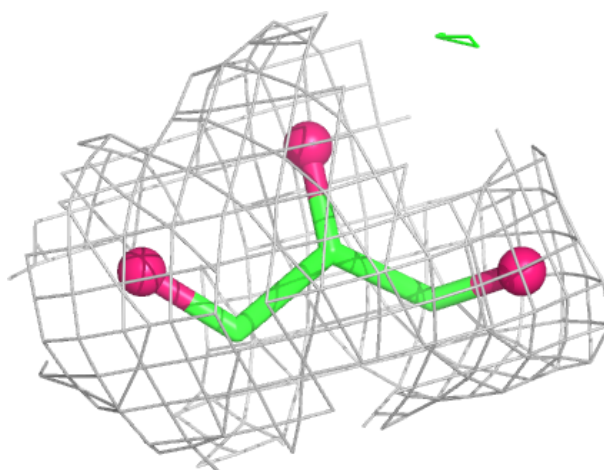
Electron density around PG4 D 105:

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



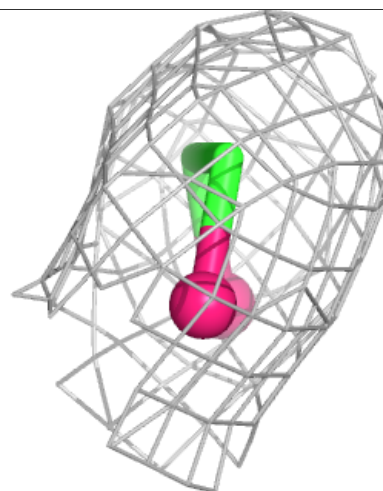
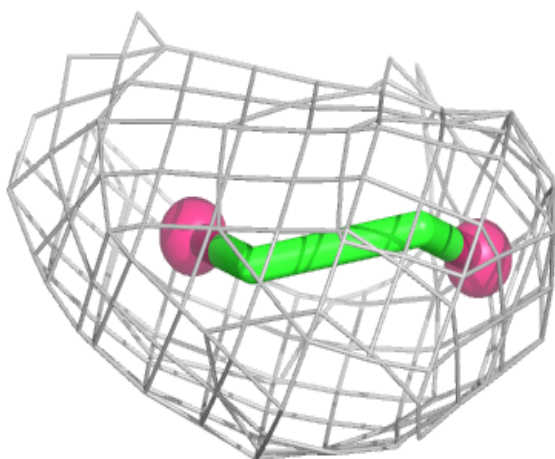
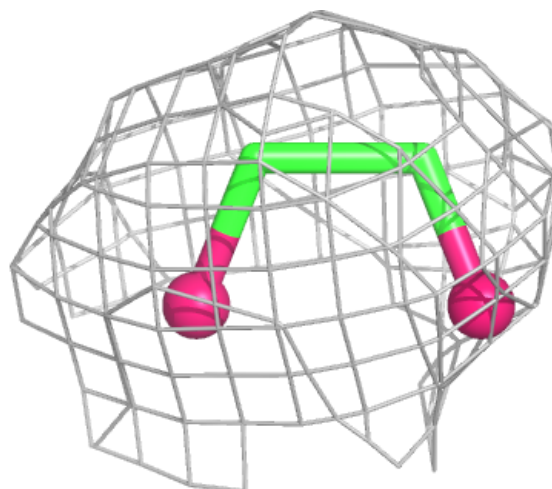
Electron density around GOL B 111:

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



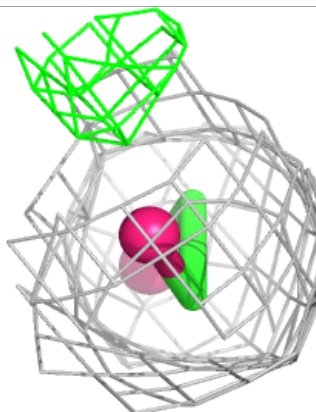
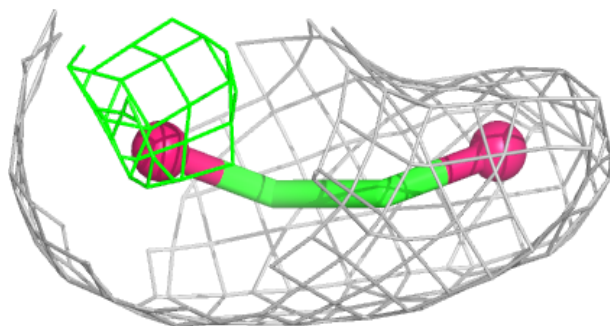
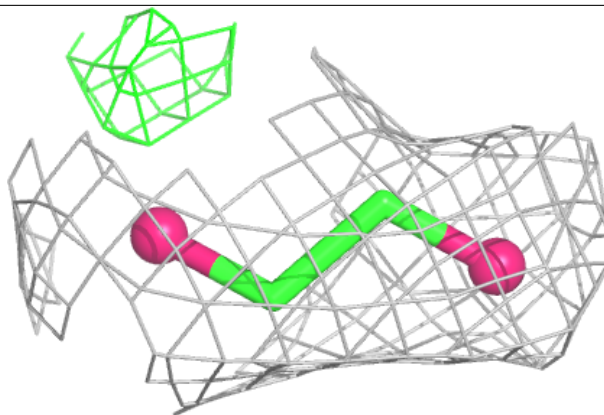
Electron density around EDO C 329:

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

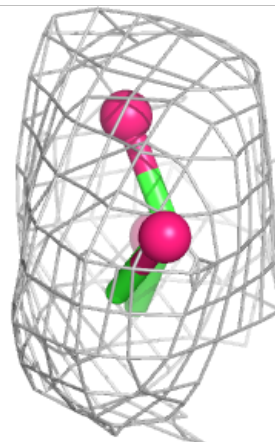
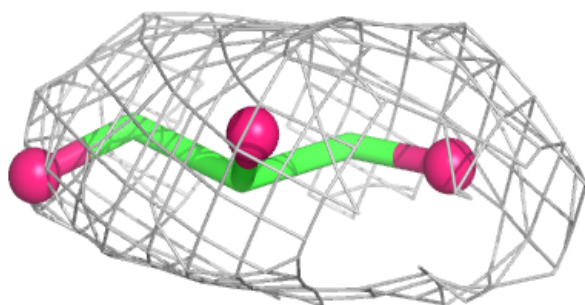
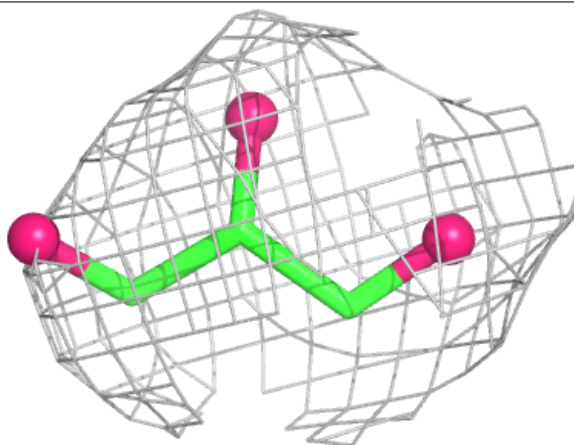


Electron density around EDO C 334:

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

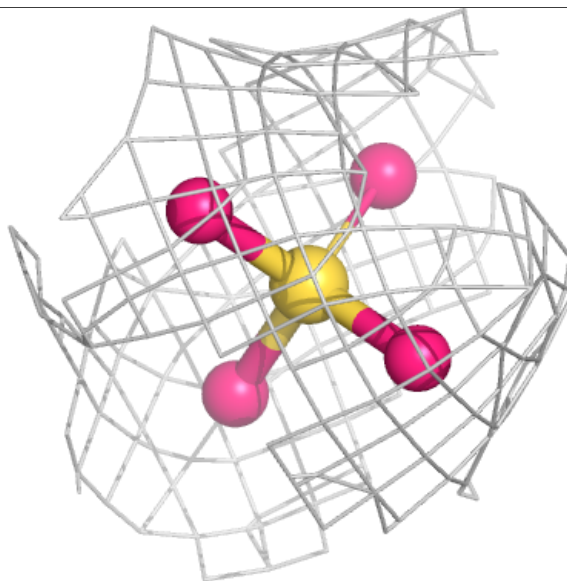
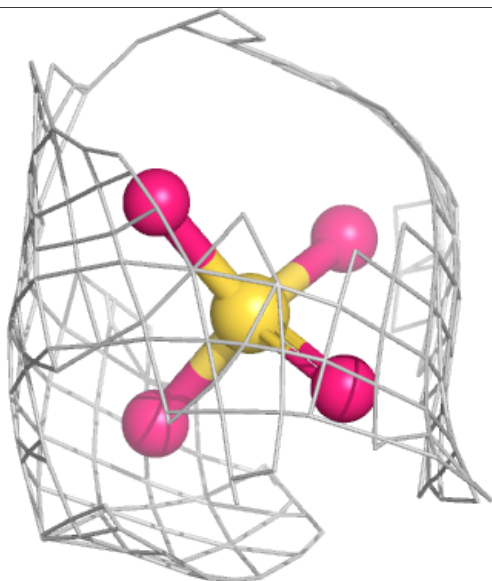
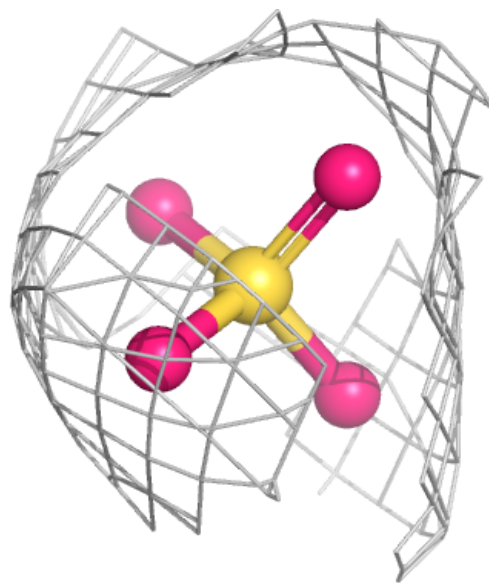
**Electron density around GOL B 113:**

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



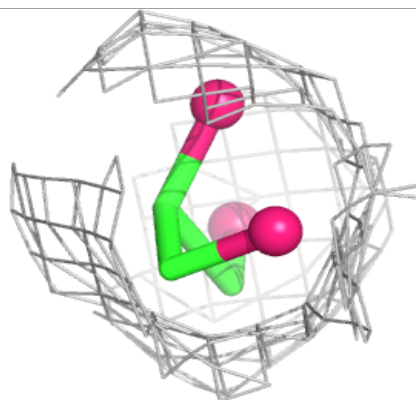
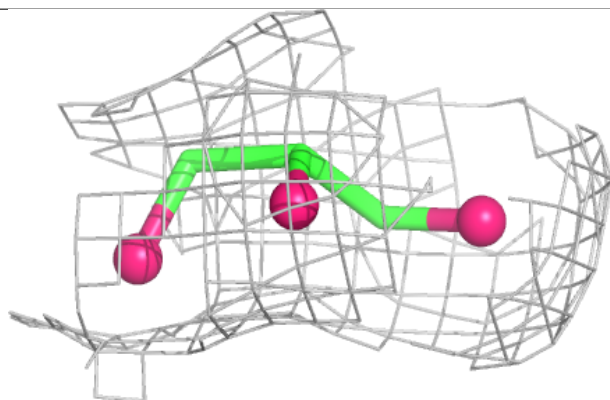
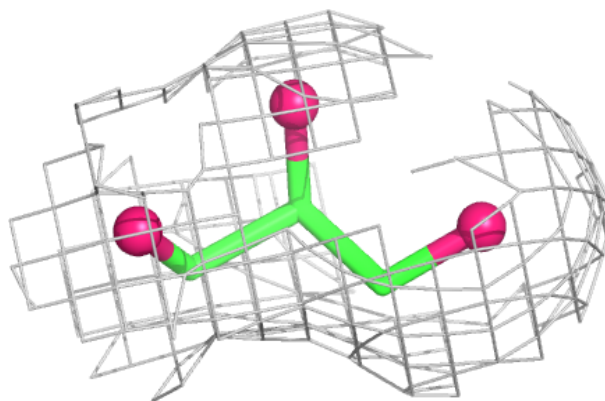
Electron density around SO4 D 113:

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

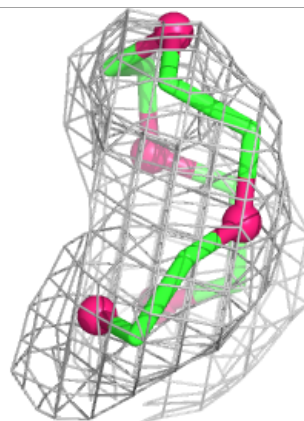
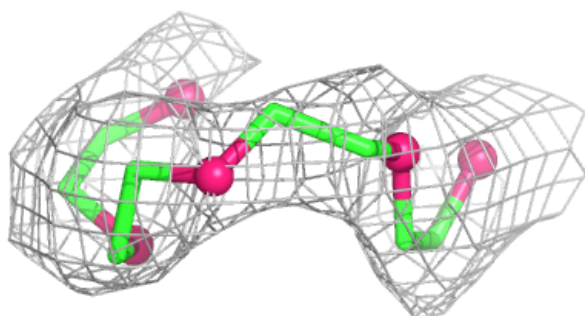
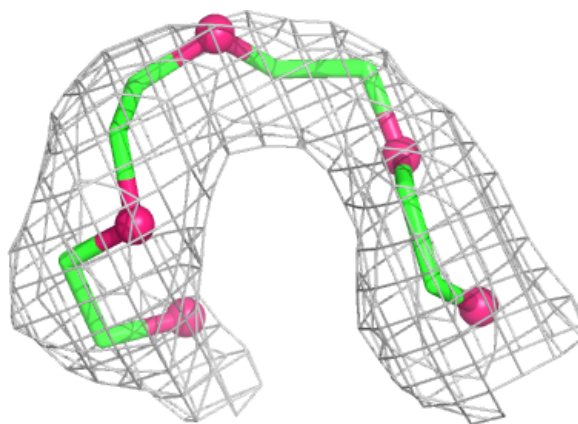


Electron density around GOL C 342:

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

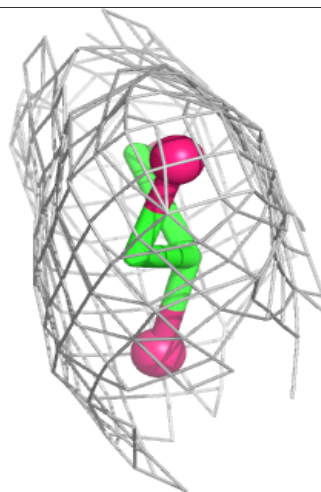
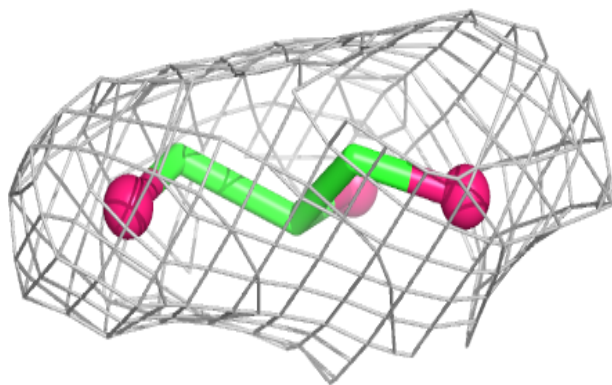
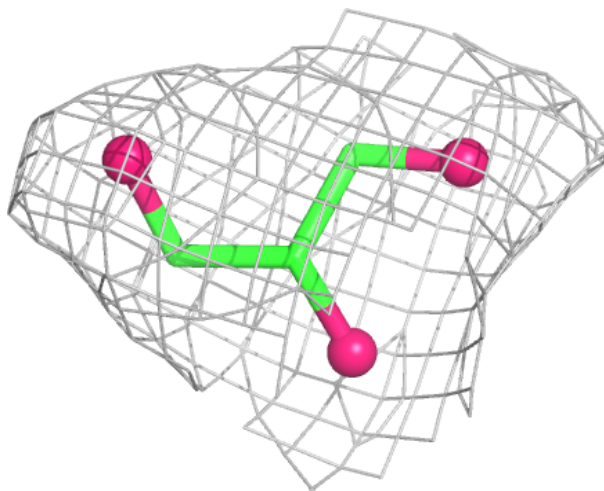
**Electron density around PG4 A 332:**

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



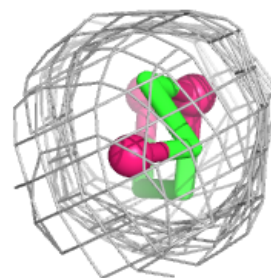
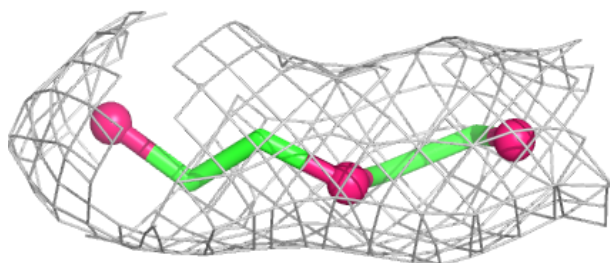
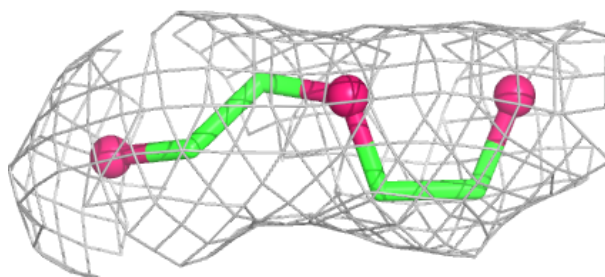
Electron density around GOL A 311:

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



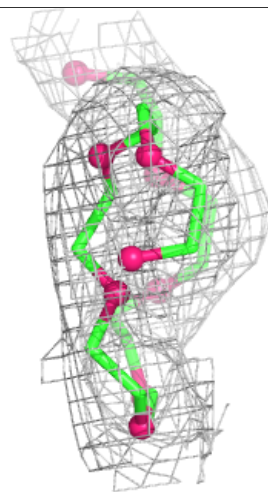
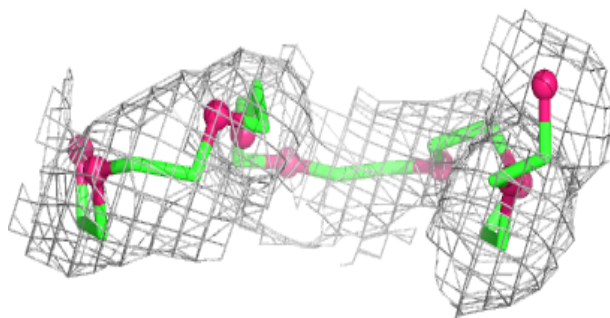
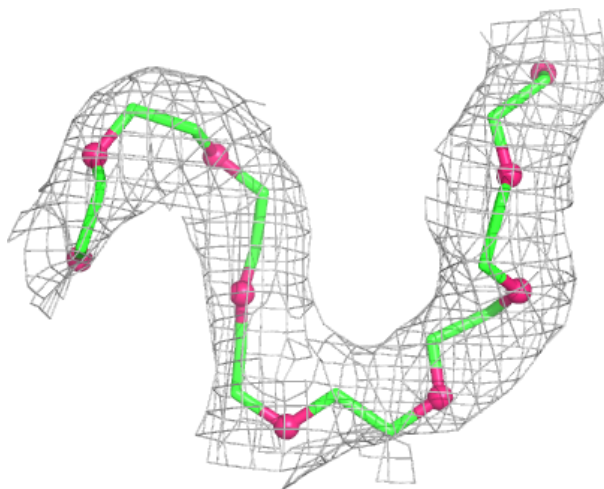
Electron density around PEG C 317:

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



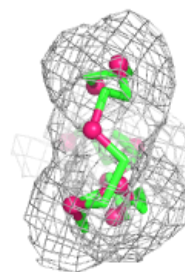
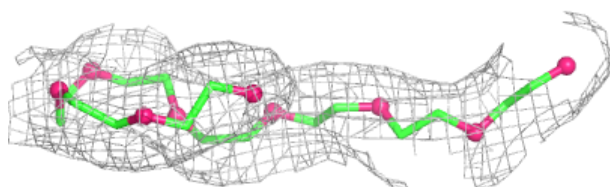
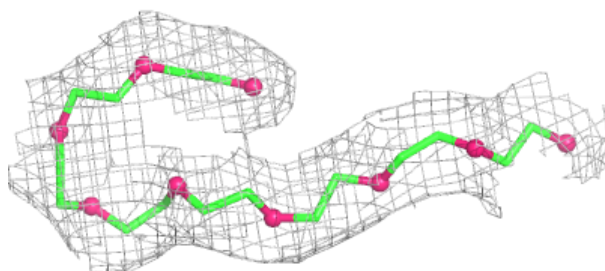
Electron density around PE8 B 131:

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

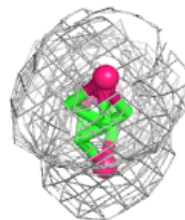
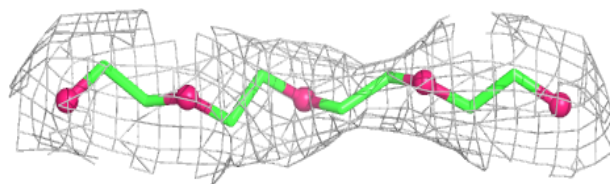
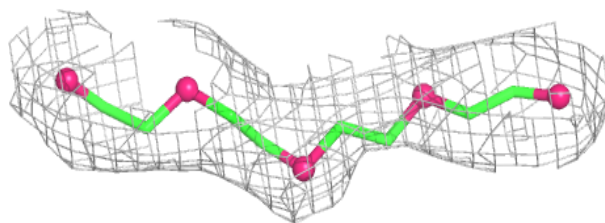


Electron density around PE8 C 322:

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

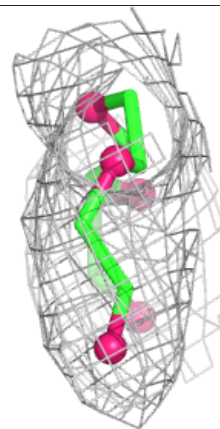
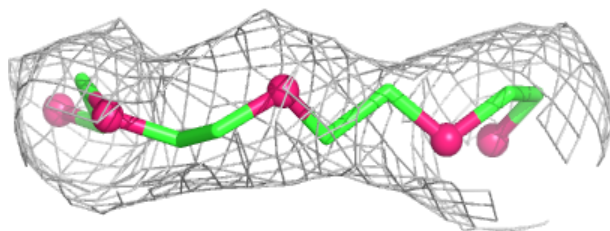
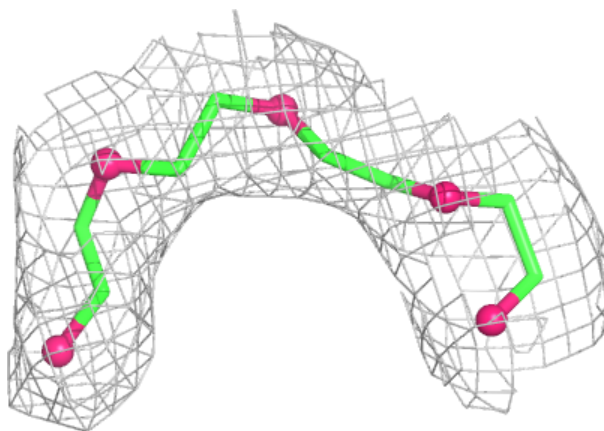
**Electron density around PG4 D 119:**

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



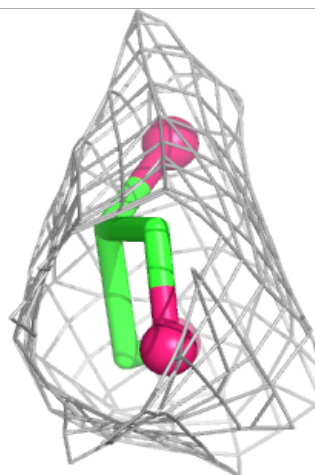
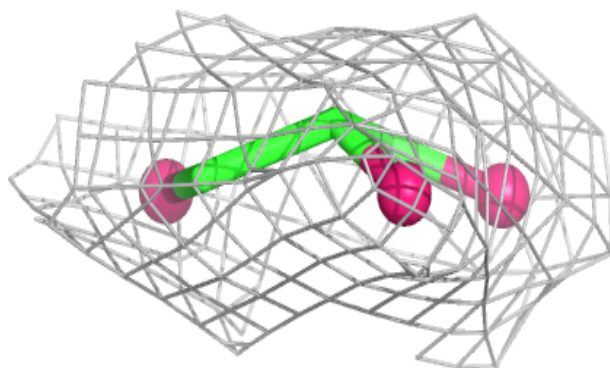
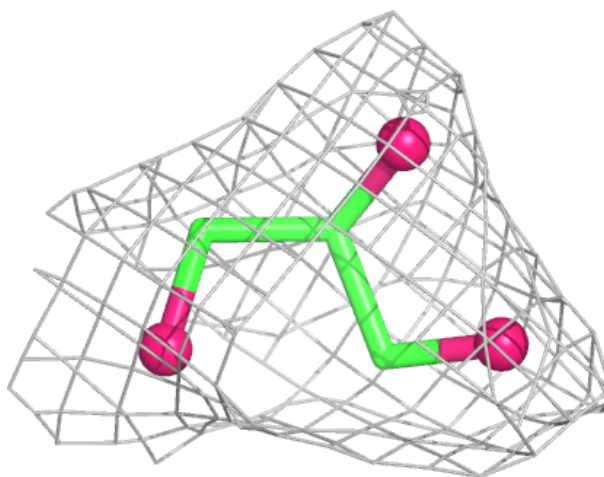
Electron density around PG4 D 127:

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



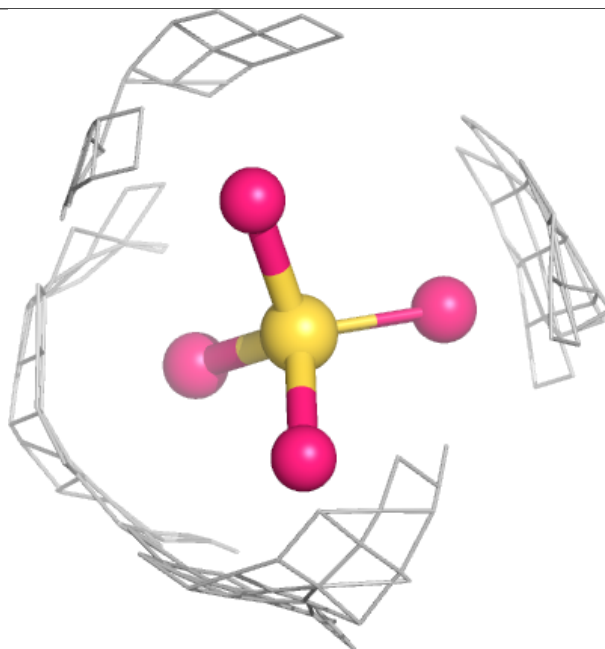
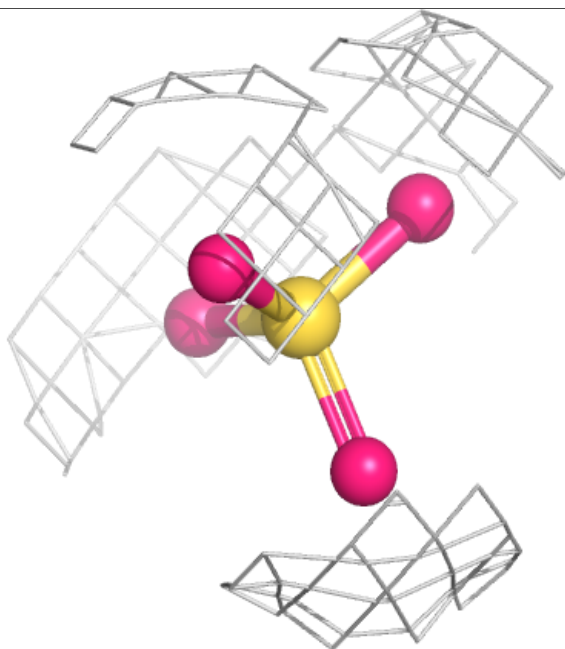
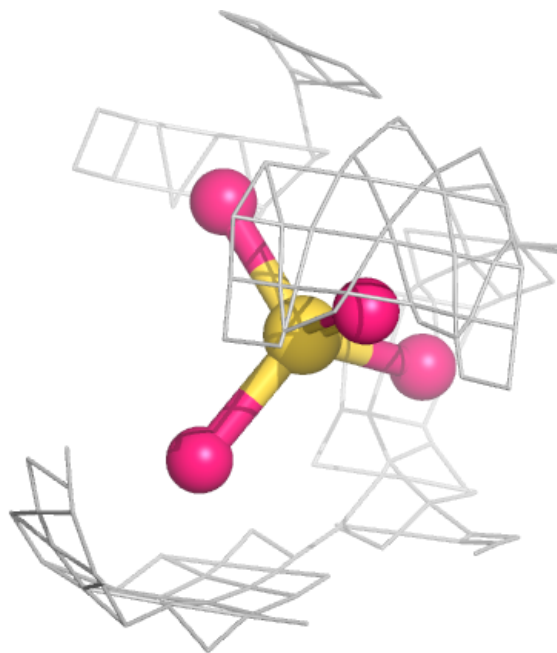
Electron density around GOL B 130:

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



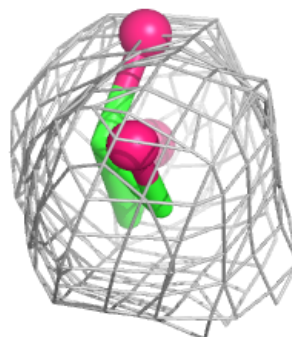
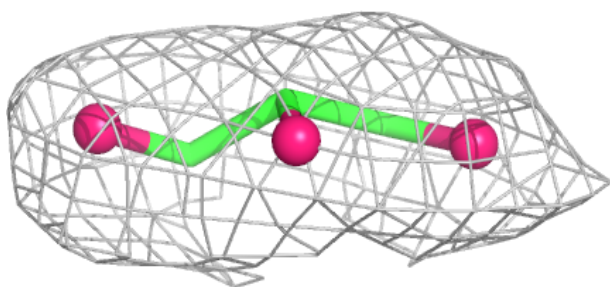
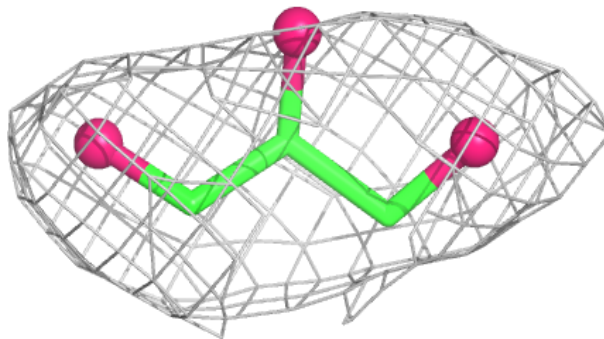
Electron density around SO4 C 336:

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

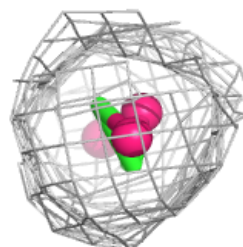
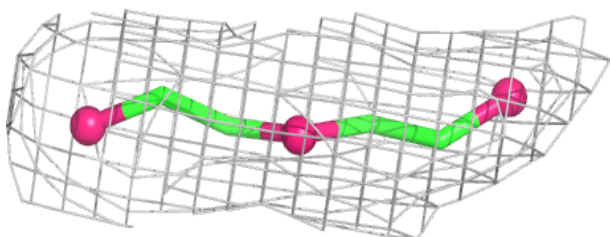
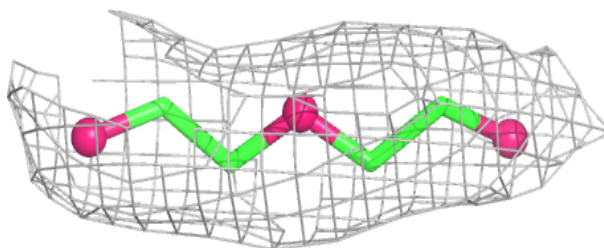


Electron density around GOL B 136:

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

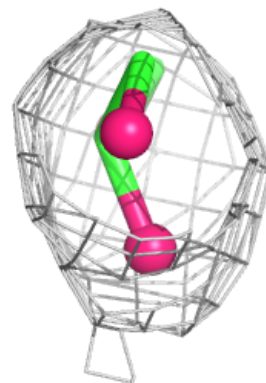
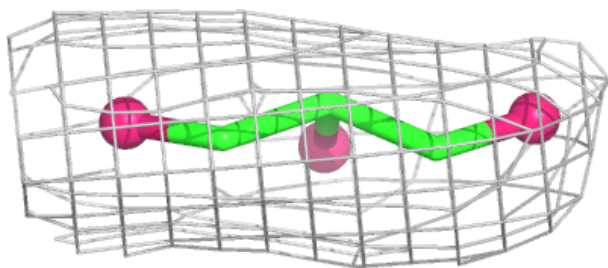
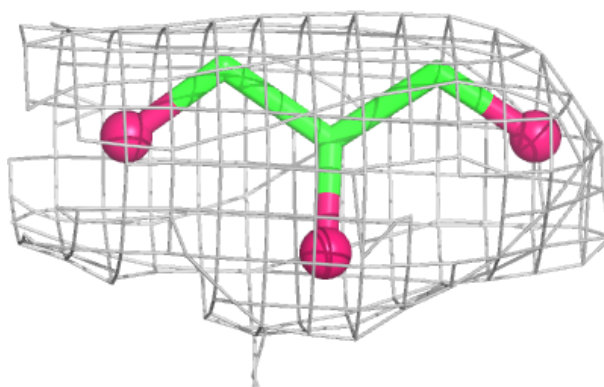
**Electron density around PEG C 339:**

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

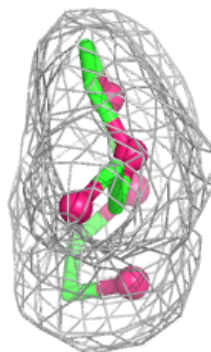
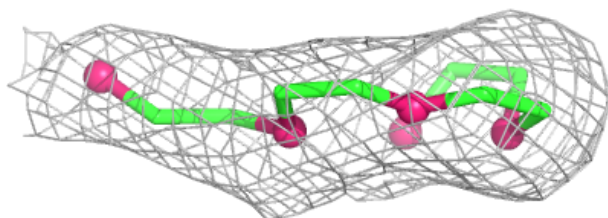
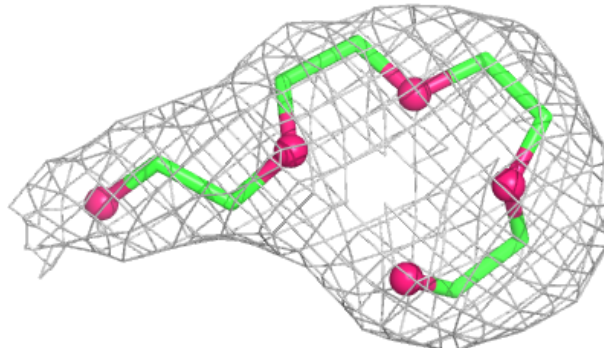


Electron density around GOL A 346:

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

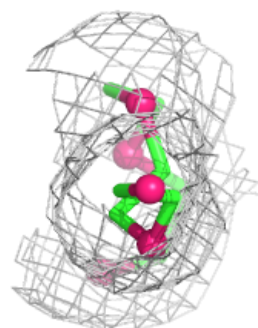
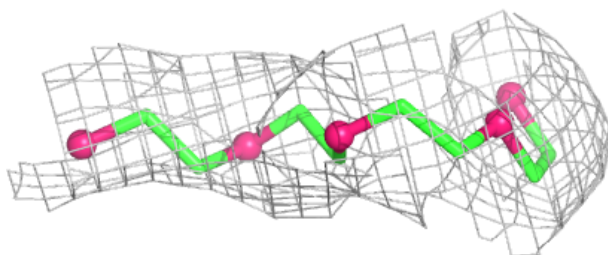
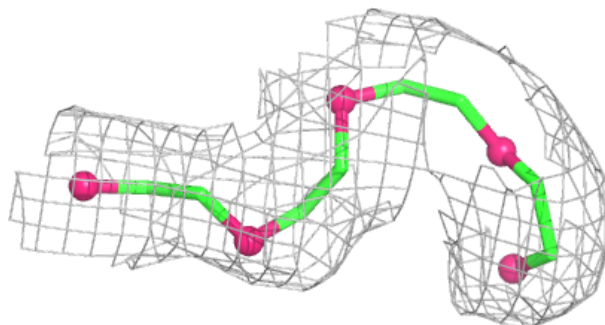
**Electron density around PG4 B 128:**

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

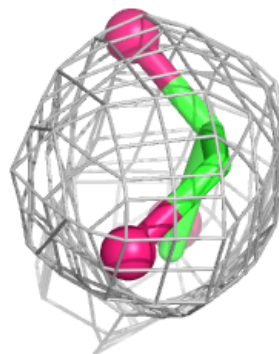
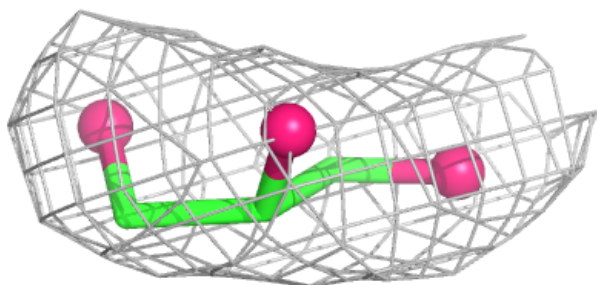
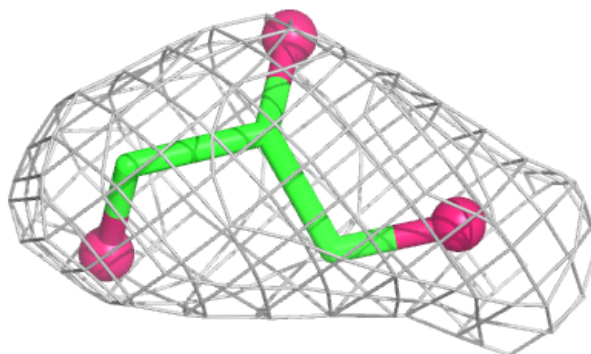


Electron density around PG4 B 129:

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

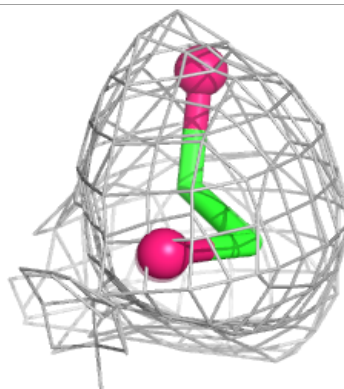
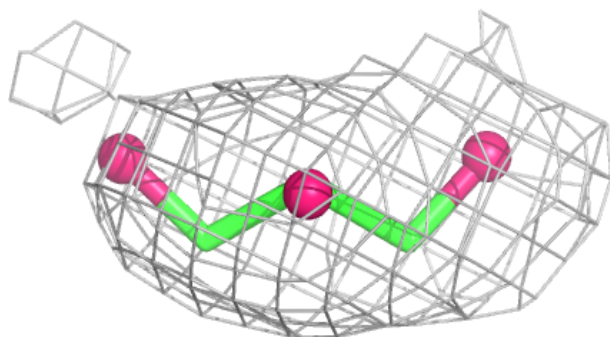
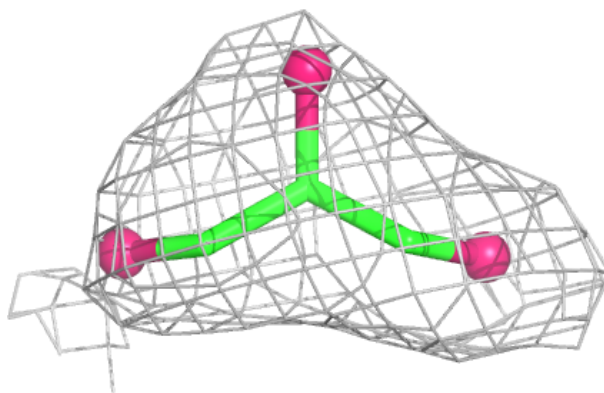
**Electron density around GOL B 140:**

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

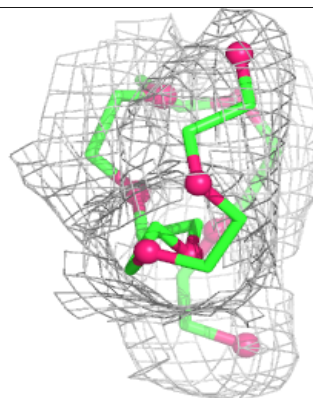
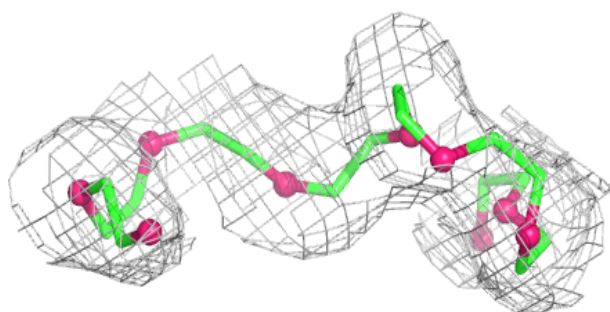
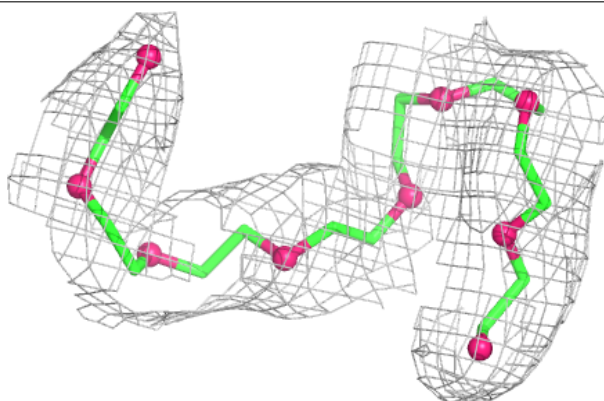


Electron density around GOL D 109:

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

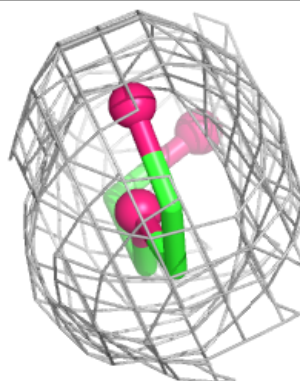
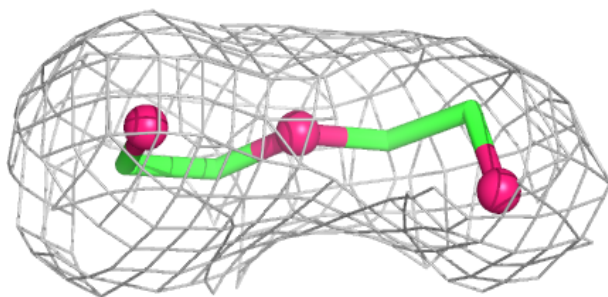
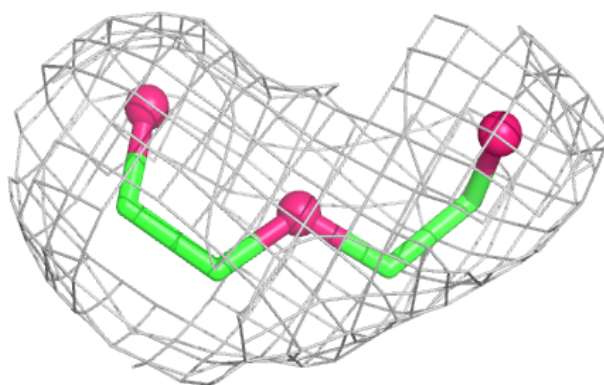
**Electron density around PE8 A 322:**

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

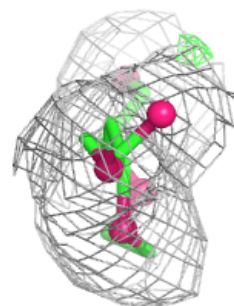
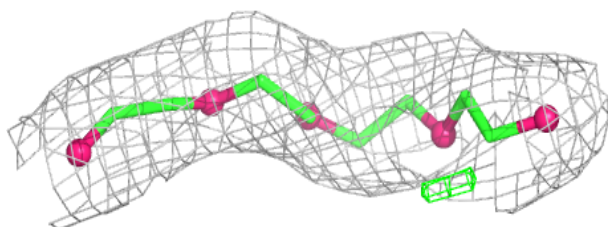
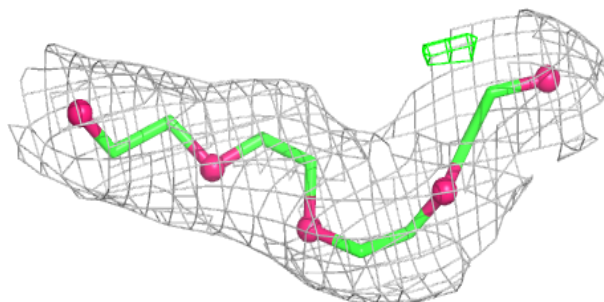


Electron density around PEG B 120:

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

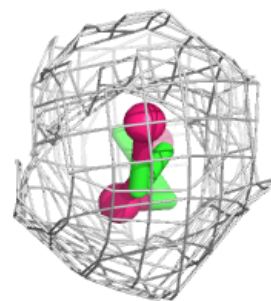
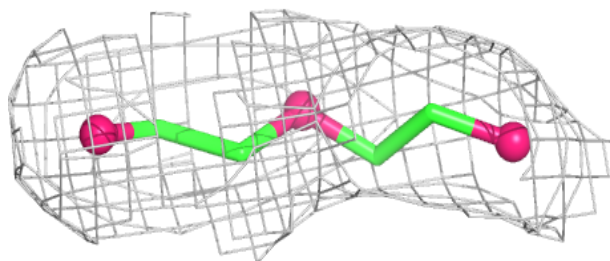
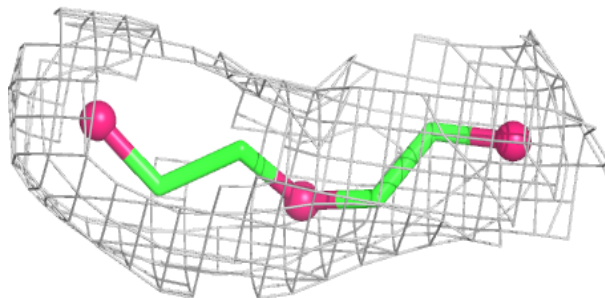
**Electron density around PG4 D 121:**

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

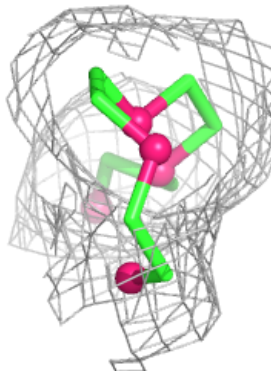
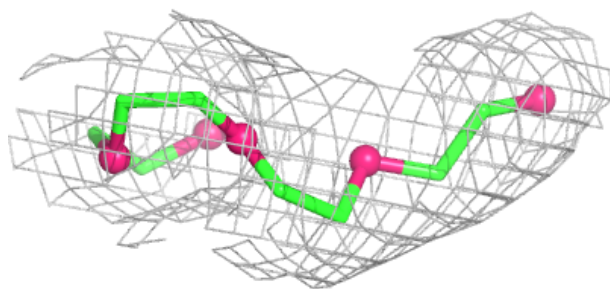
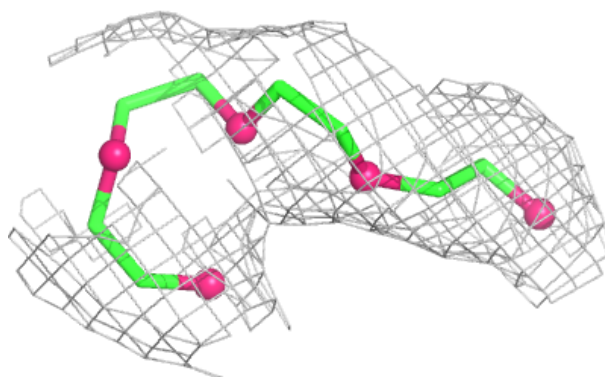


Electron density around PEG C 315:

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

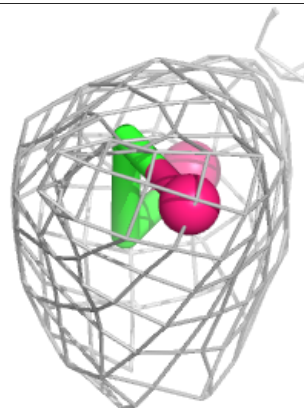
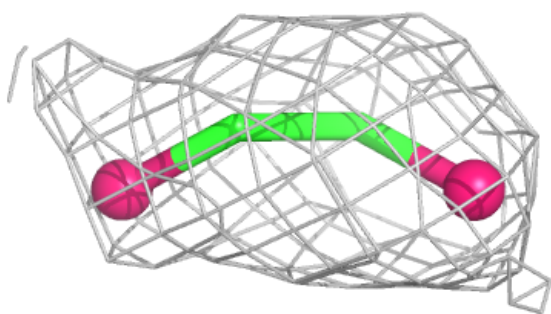
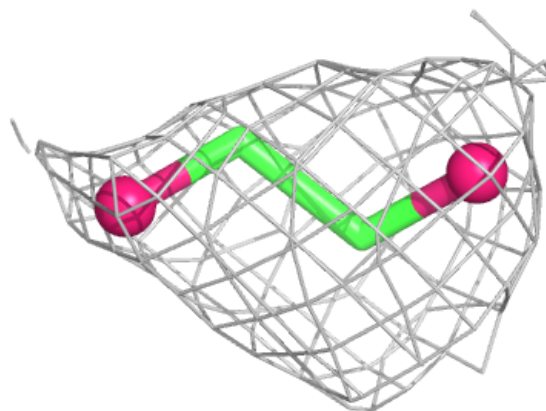
**Electron density around PG4 B 126:**

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



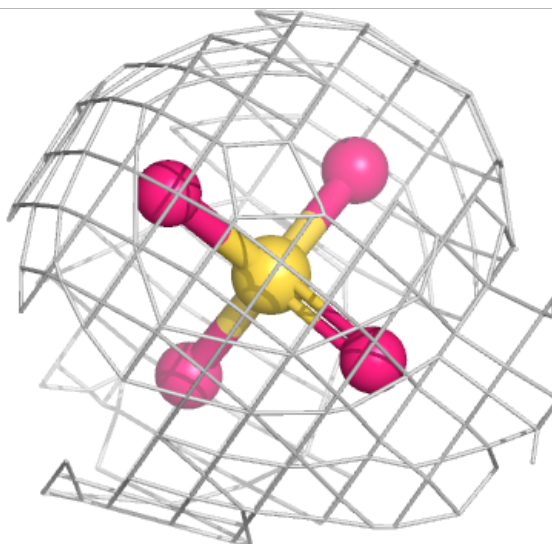
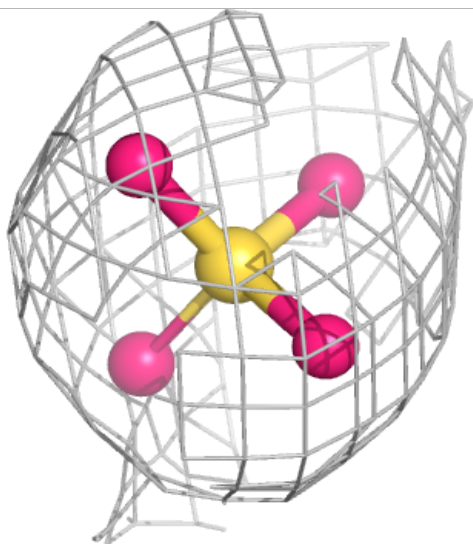
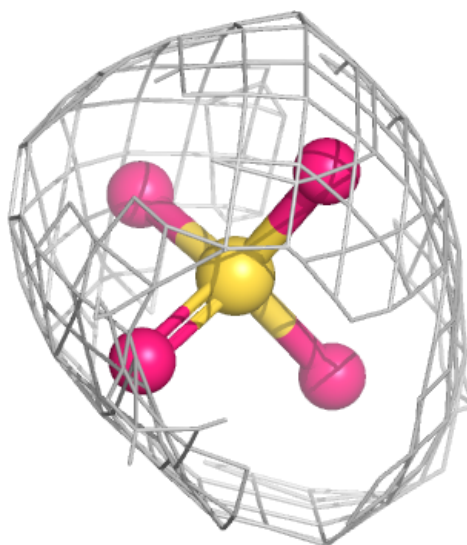
Electron density around EDO A 343:

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



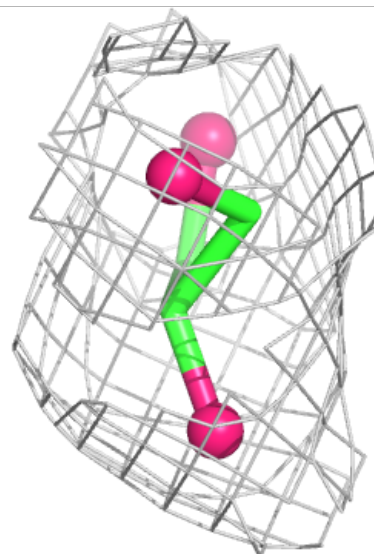
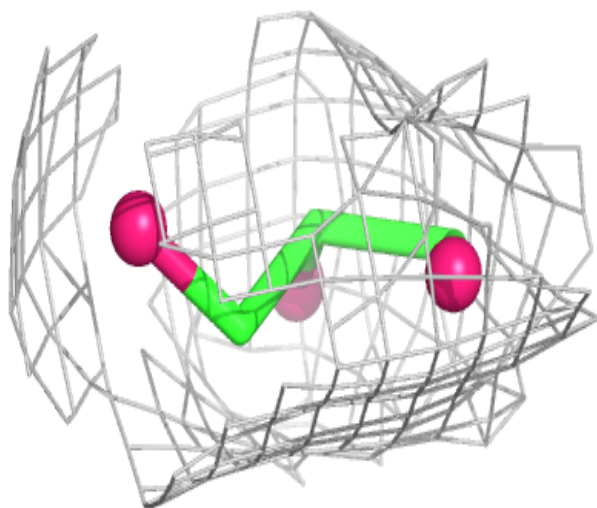
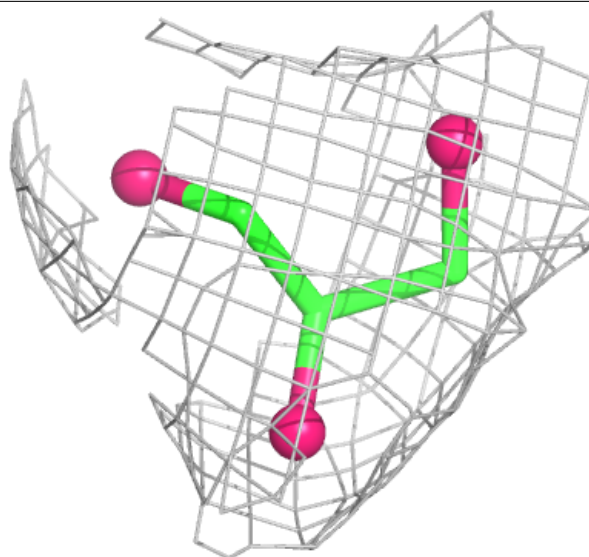
Electron density around SO4 D 112:

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



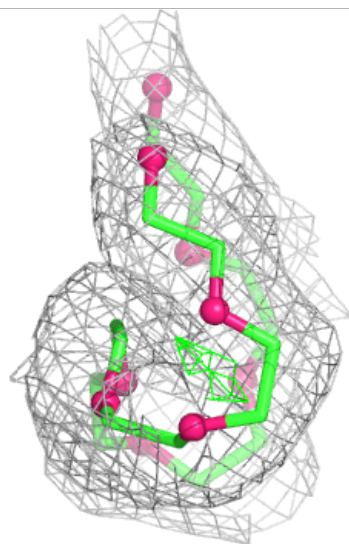
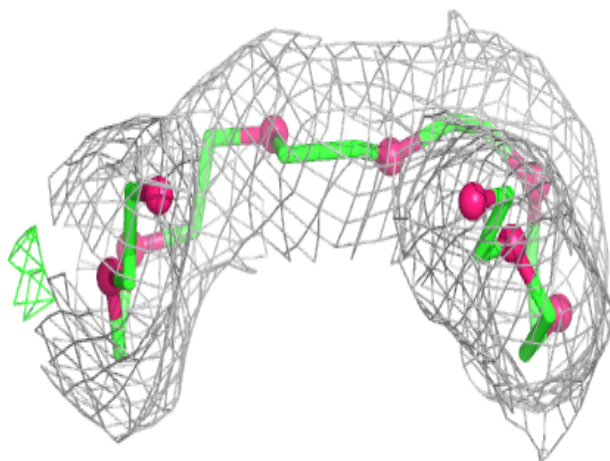
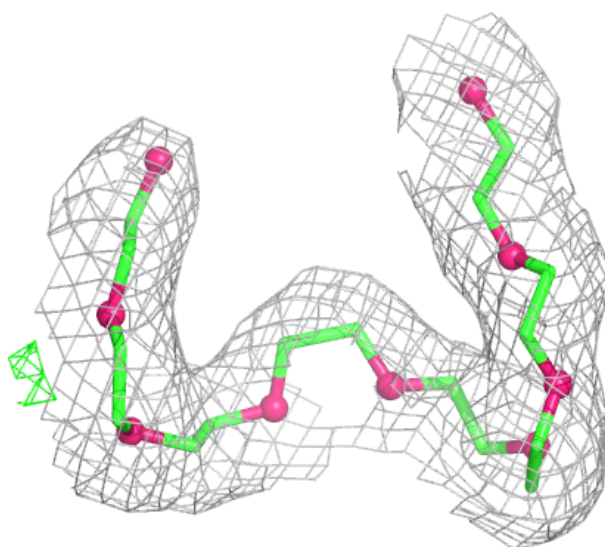
Electron density around GOL B 135:

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



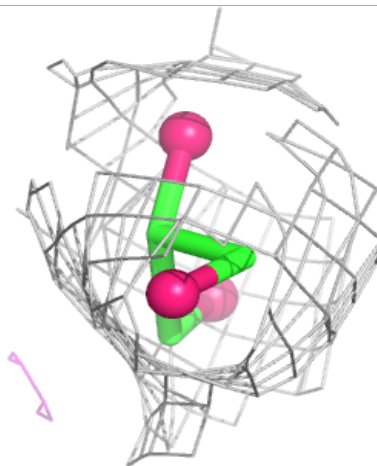
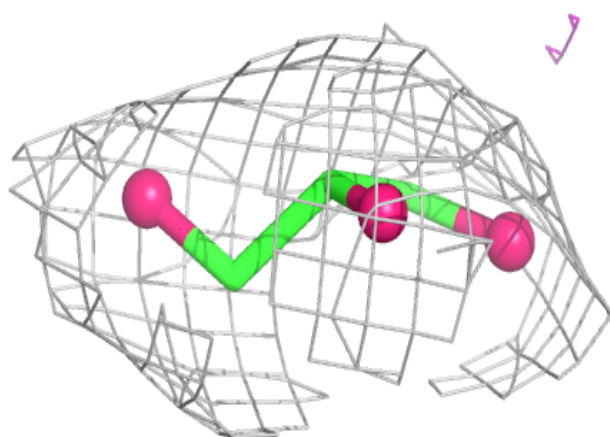
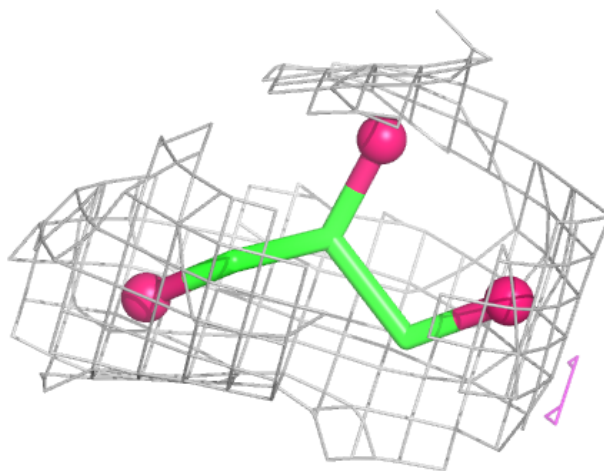
Electron density around PE8 A 323:

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



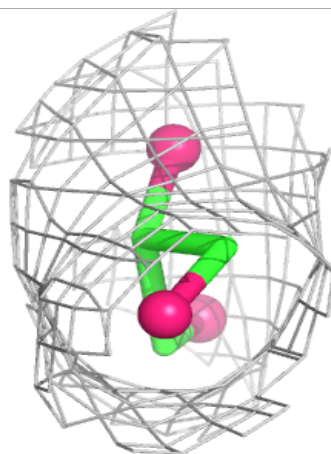
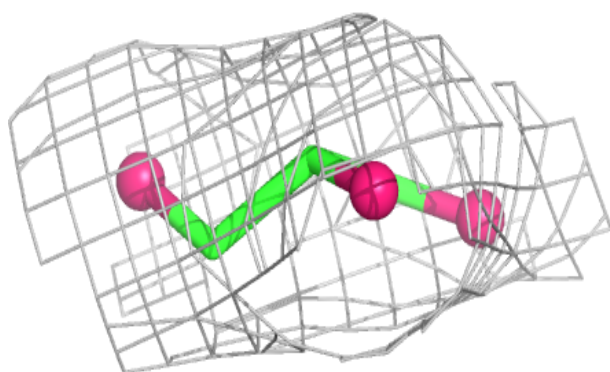
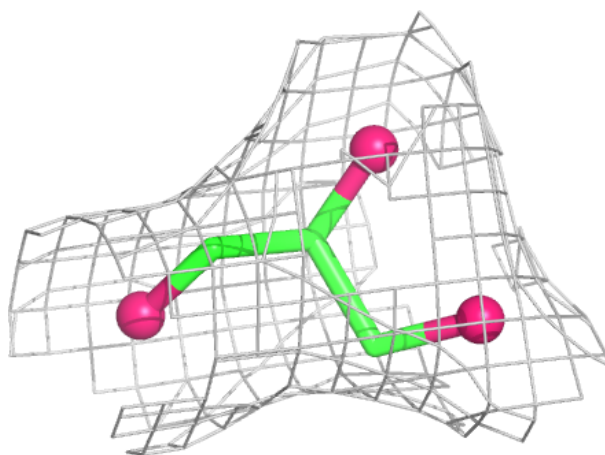
Electron density around GOL B 112:

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



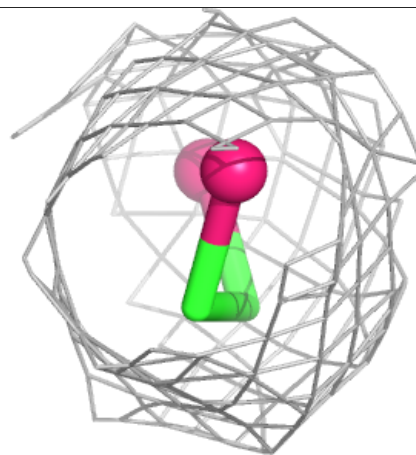
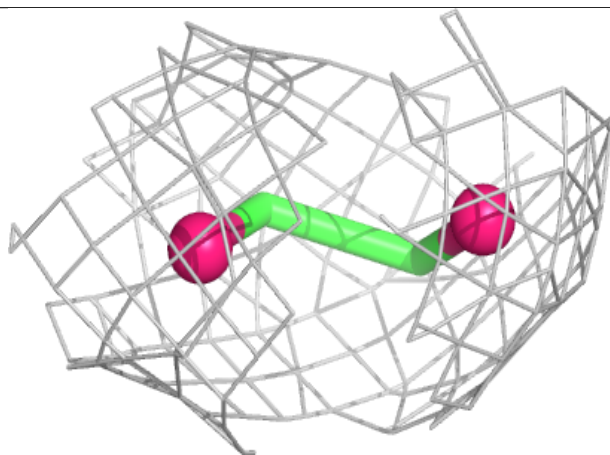
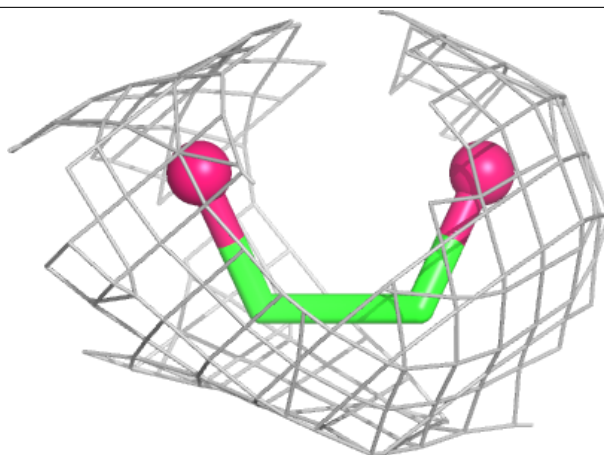
Electron density around GOL B 107:

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

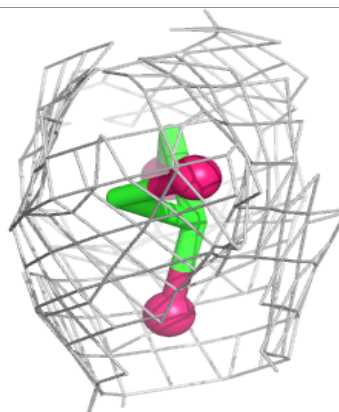
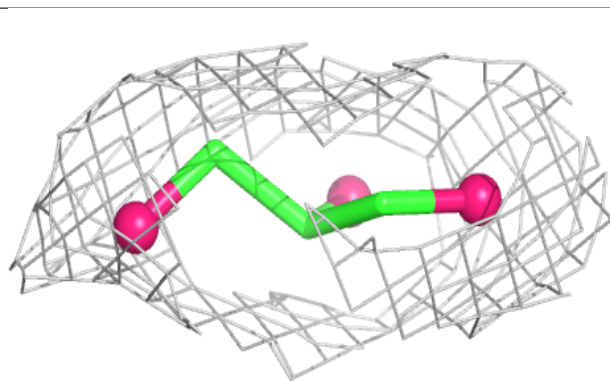
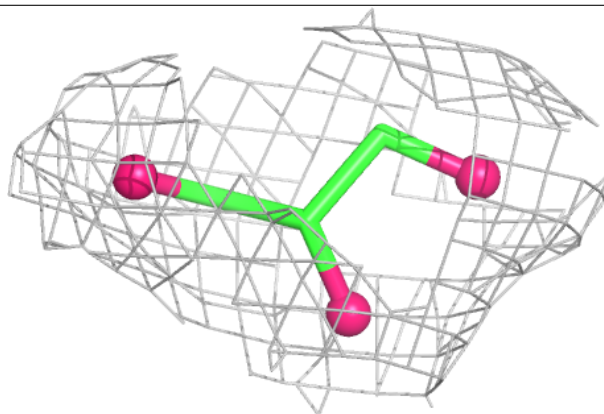


Electron density around EDO A 326:

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

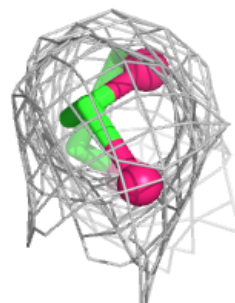
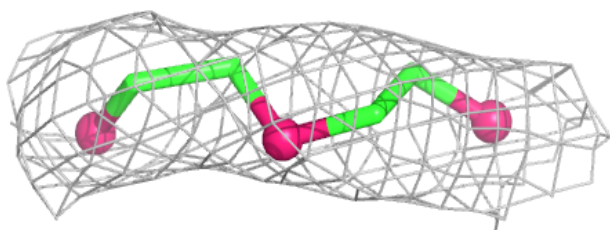
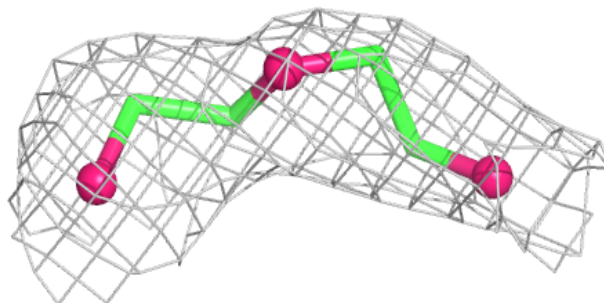
**Electron density around GOL A 345:**

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

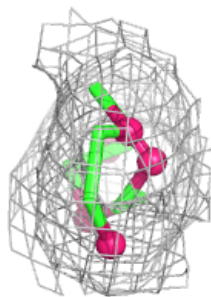
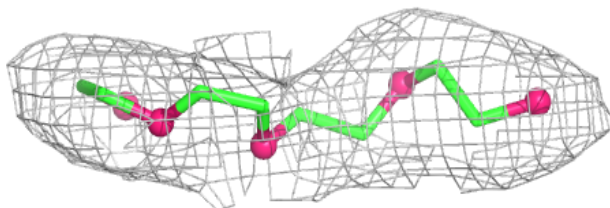


Electron density around PEG E 111:

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

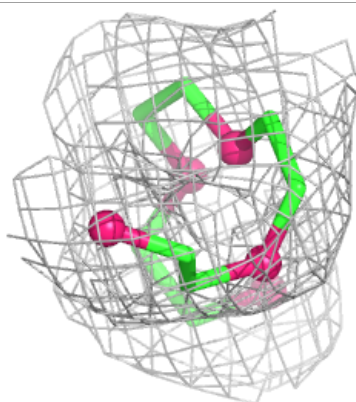
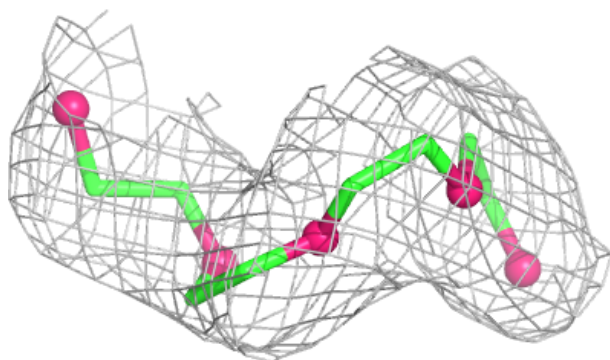
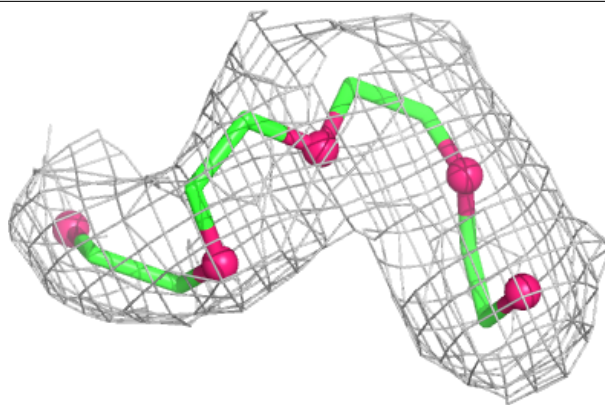
**Electron density around PG4 E 101:**

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

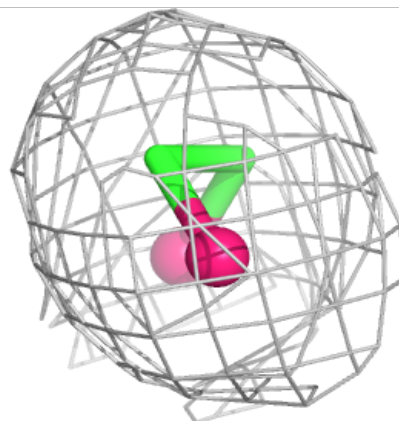
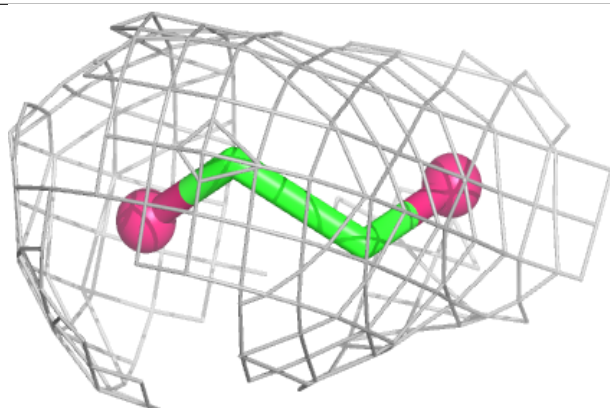
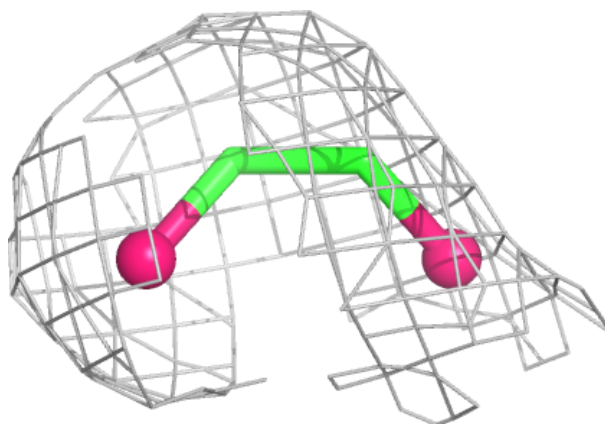


Electron density around PG4 A 334:

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

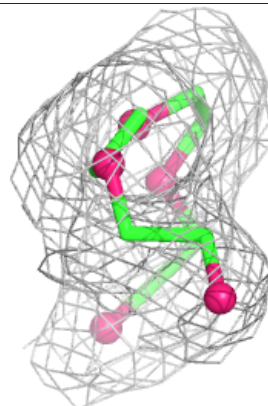
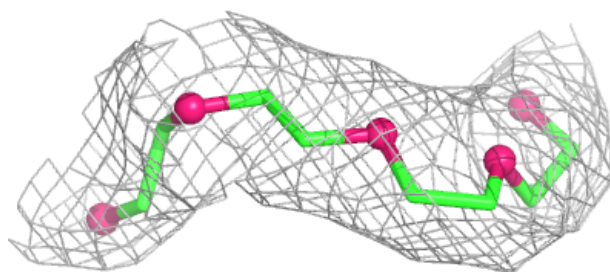
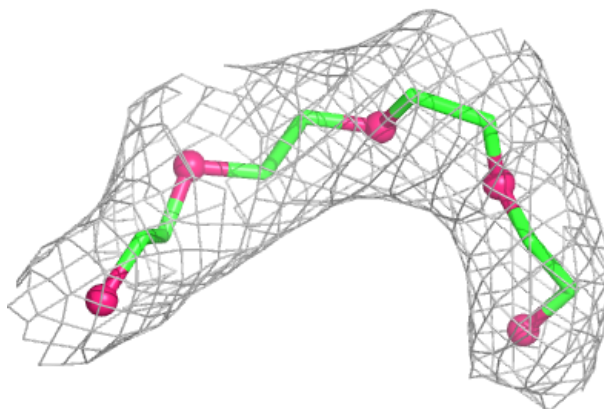
**Electron density around EDO C 323:**

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

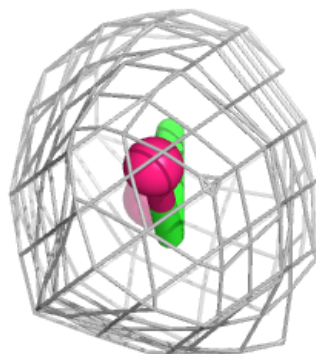
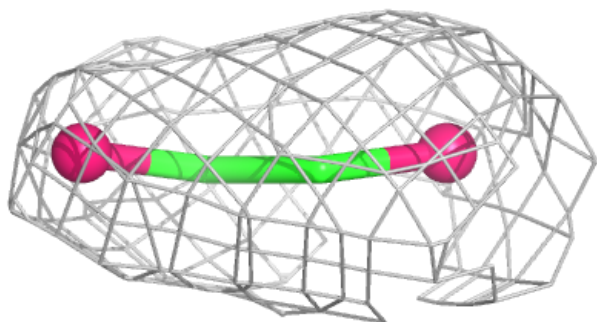
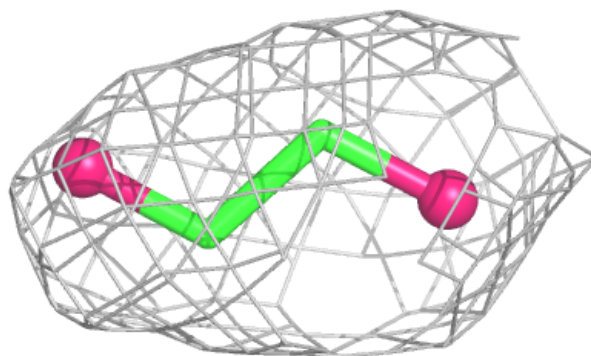


Electron density around PG4 A 344:

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

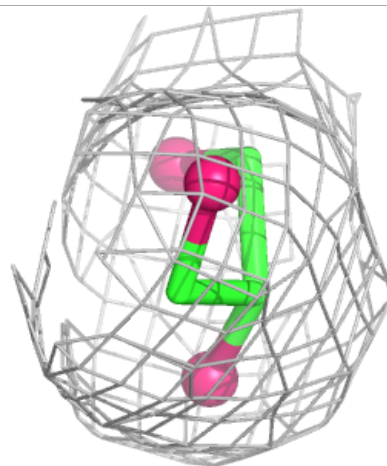
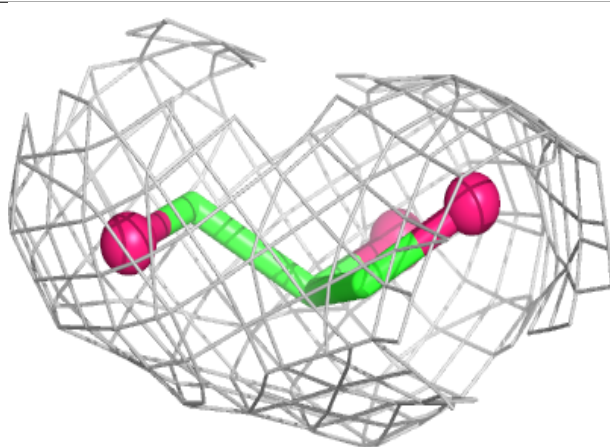
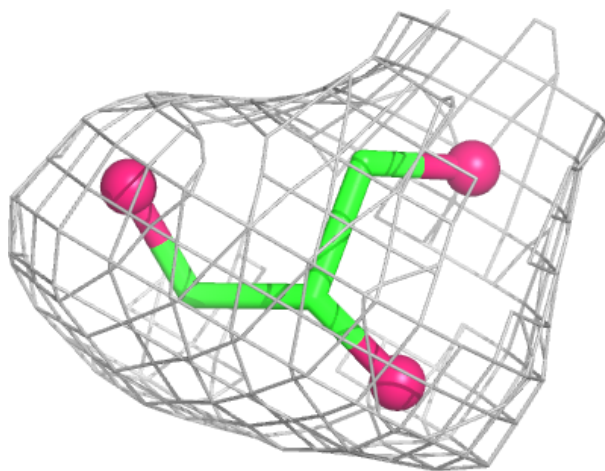
**Electron density around EDO B 124:**

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



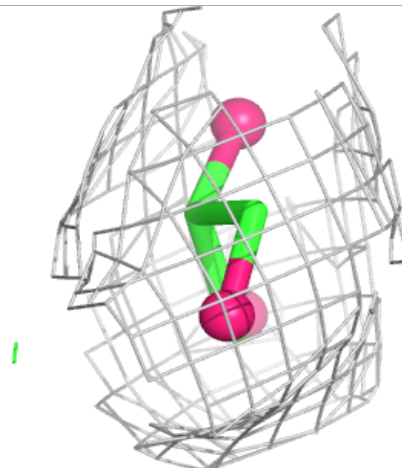
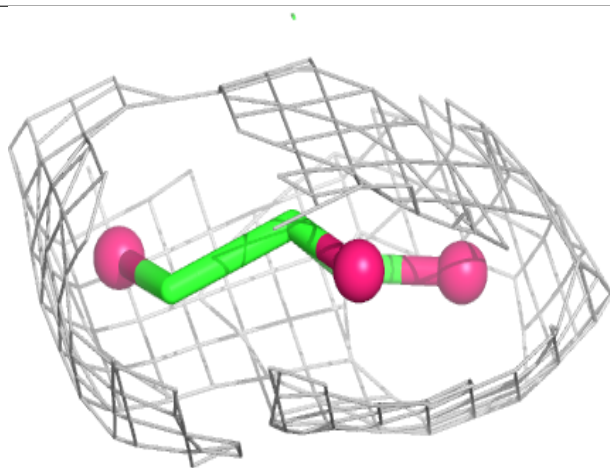
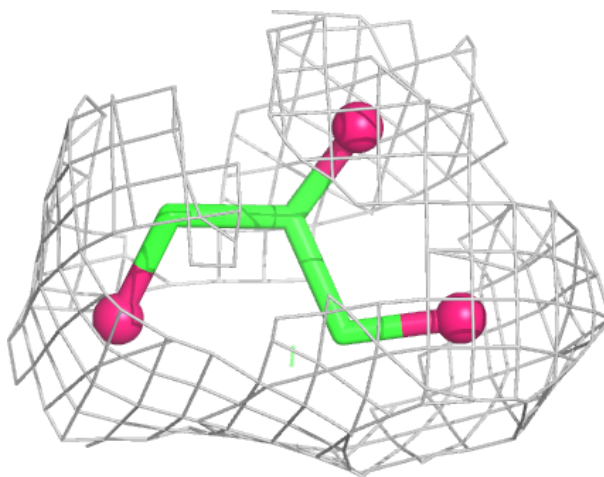
Electron density around GOL C 301:

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



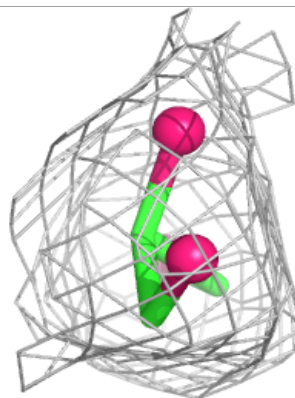
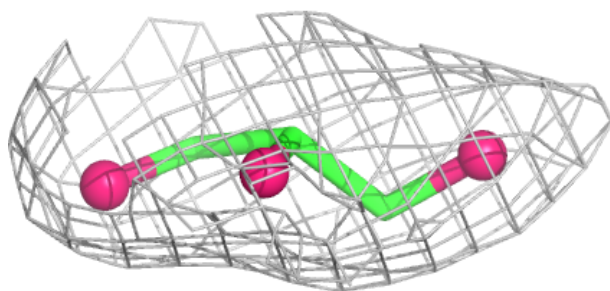
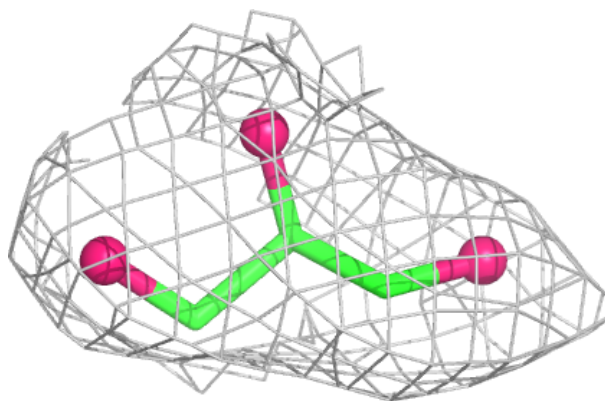
Electron density around GOL A 304:

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



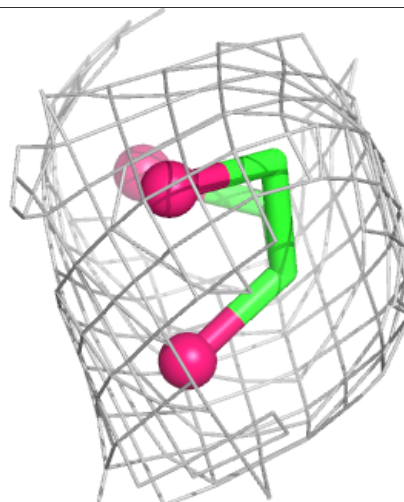
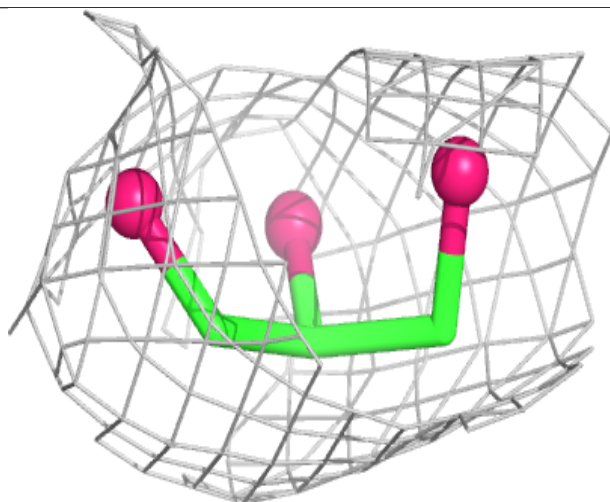
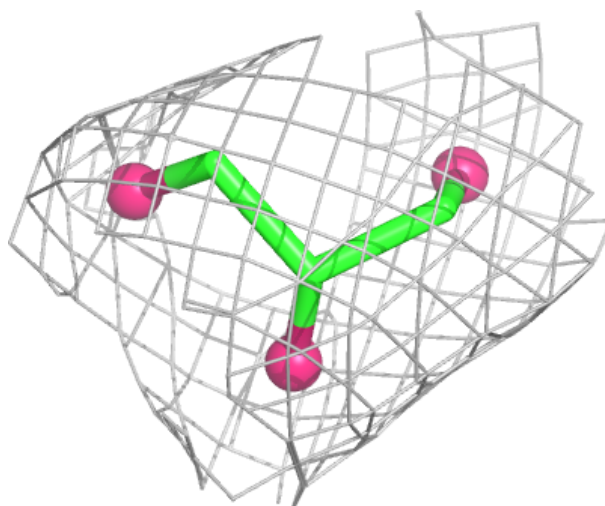
Electron density around GOL A 312:

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



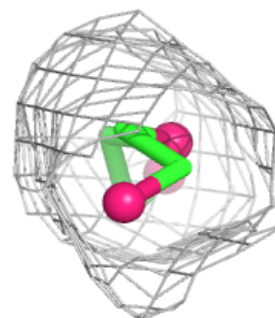
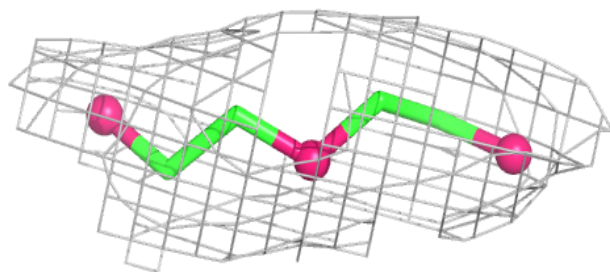
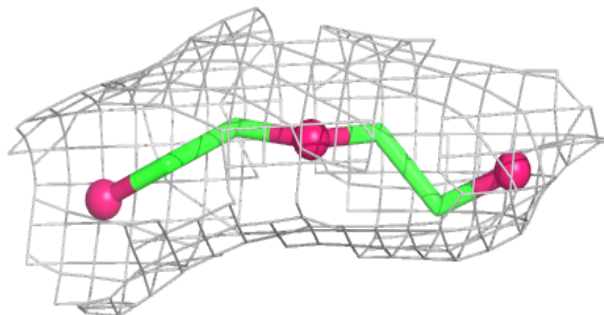
Electron density around GOL B 108:

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

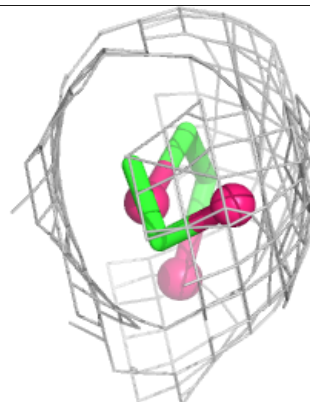
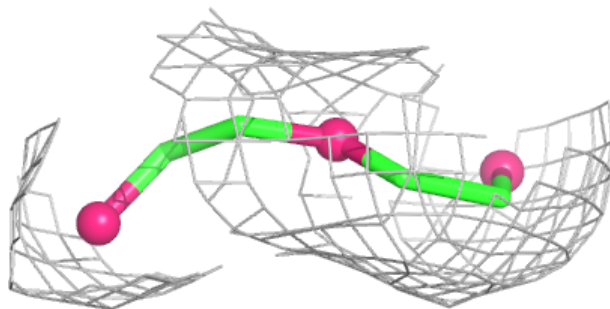
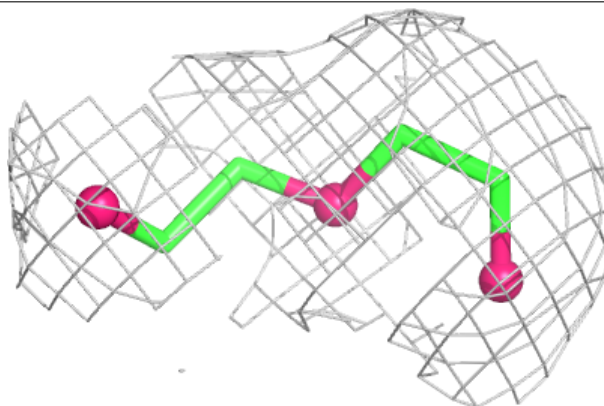


Electron density around PEG E 110:

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

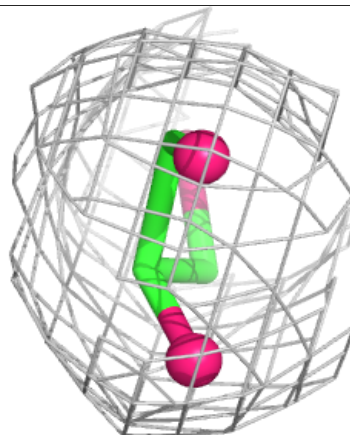
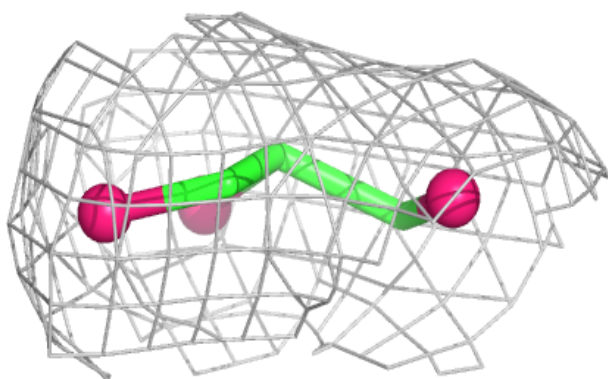
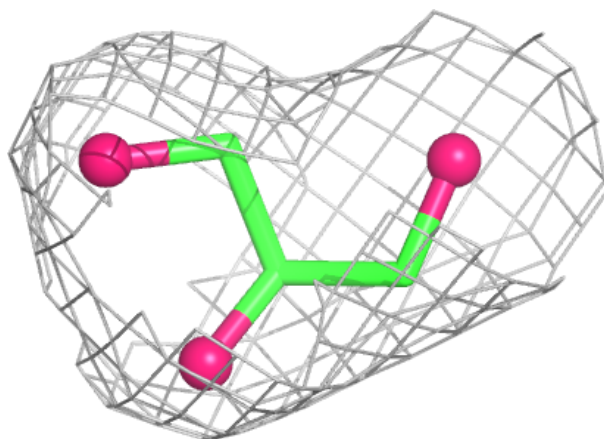
**Electron density around PEG A 318:**

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

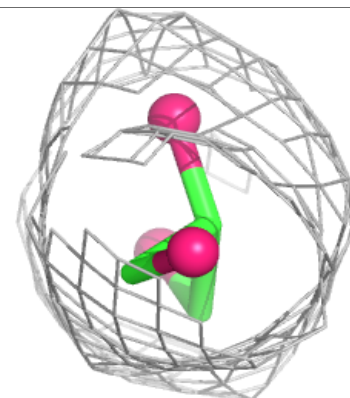
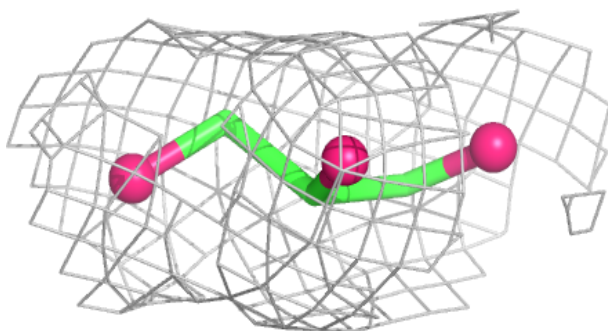
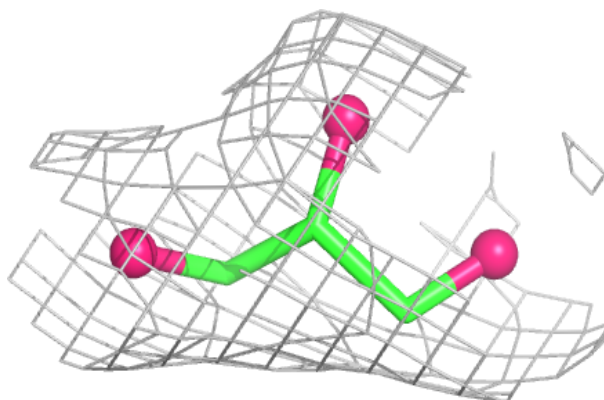


Electron density around GOL A 305:

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

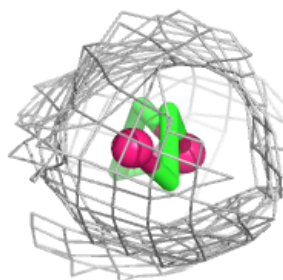
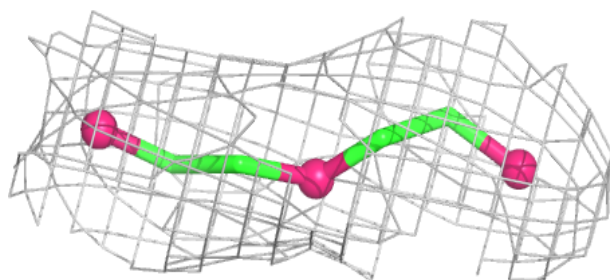
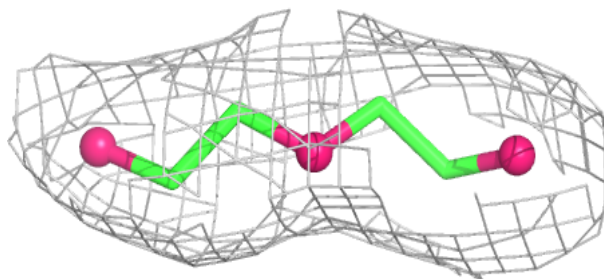
**Electron density around GOL B 132:**

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

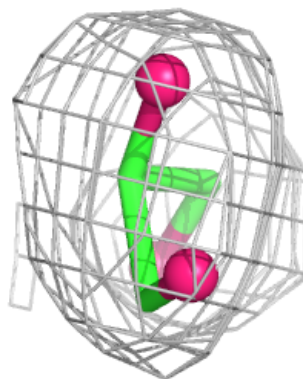
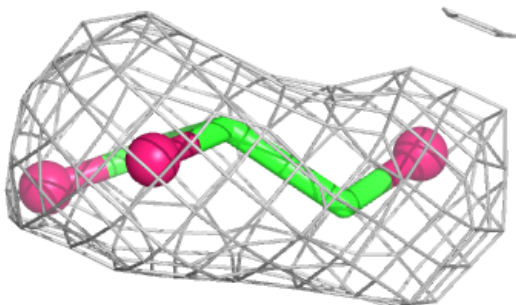
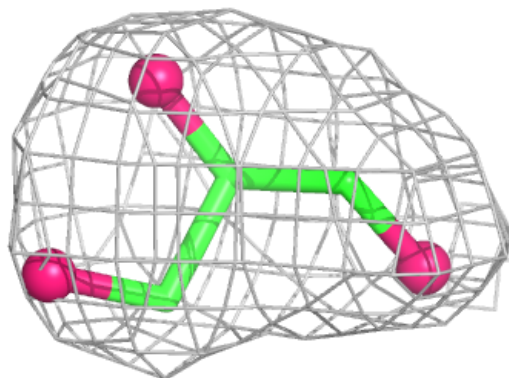


Electron density around PEG A 321:

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

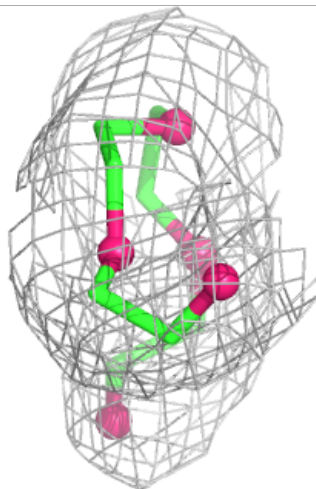
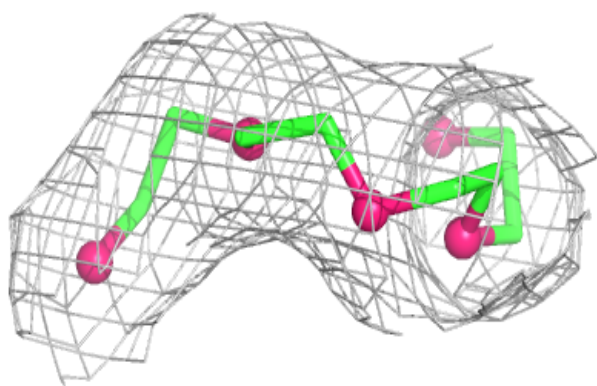
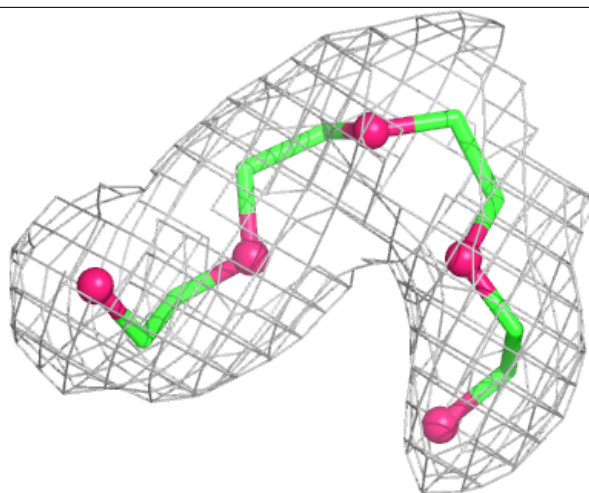
**Electron density around GOL D 103:**

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



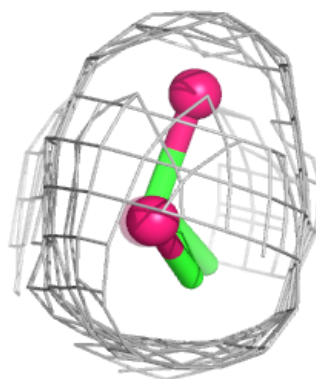
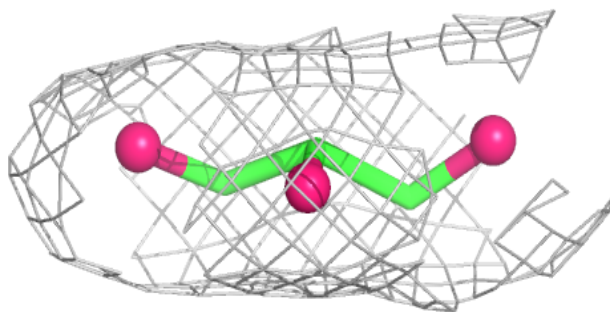
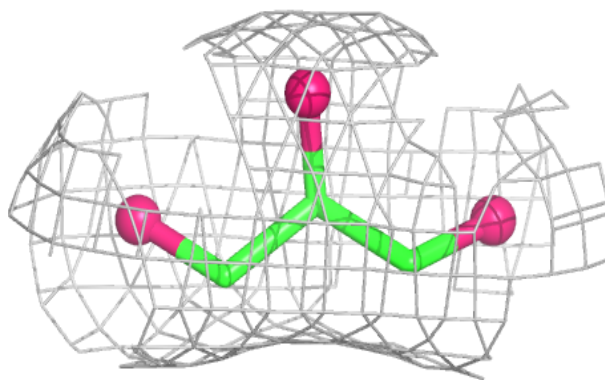
Electron density around PG4 C 337:

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

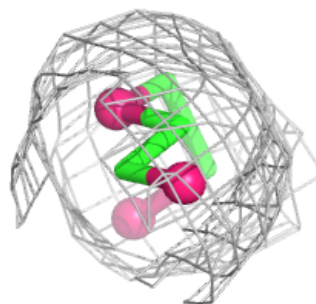
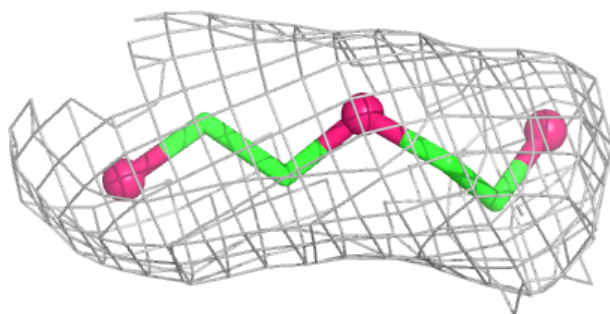
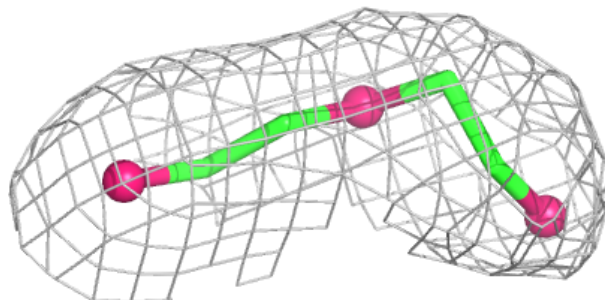


Electron density around GOL A 313:

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

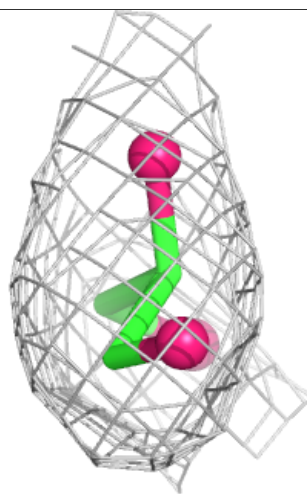
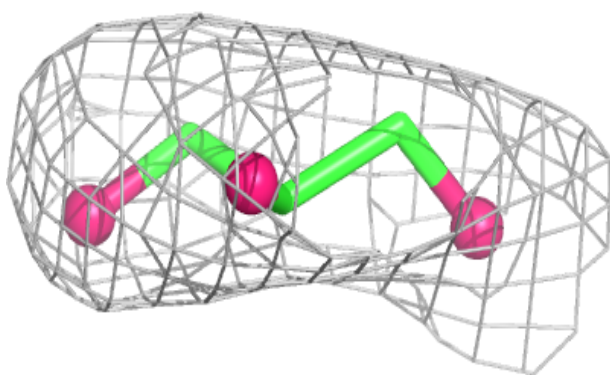
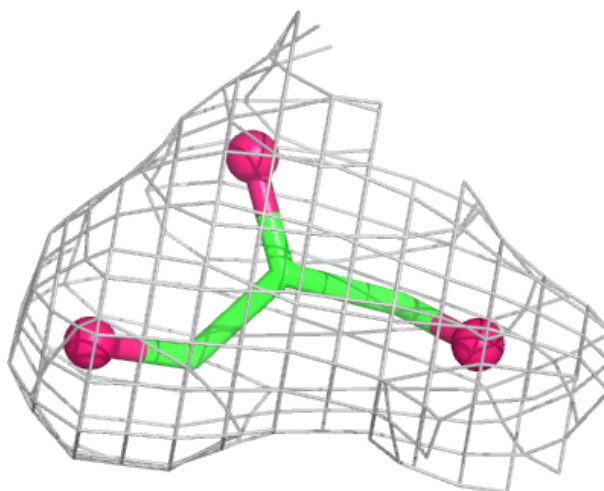
**Electron density around PEG B 139:**

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



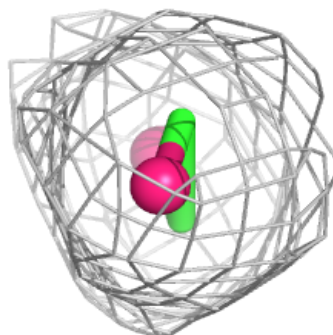
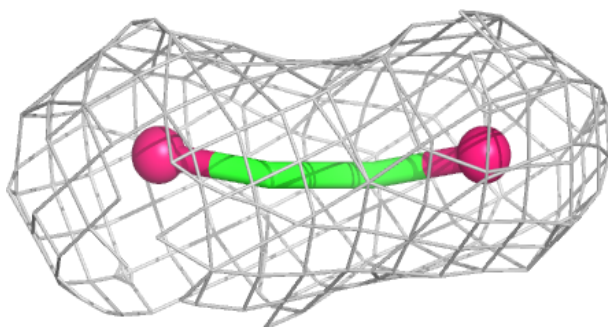
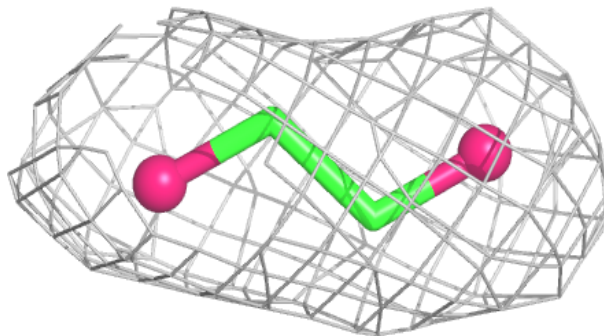
Electron density around GOL E 102:

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

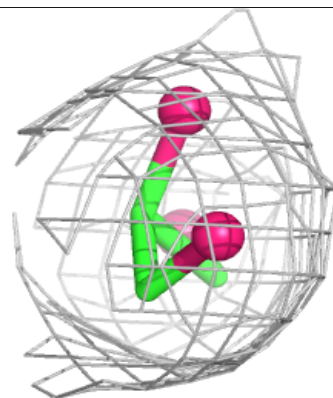
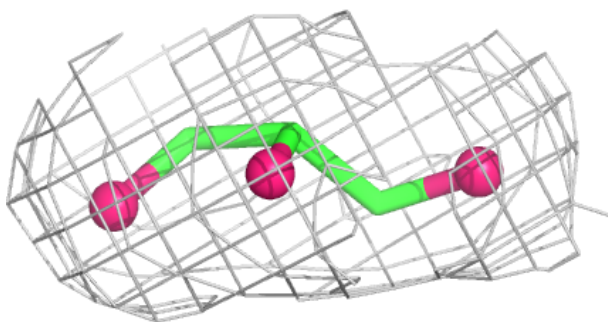
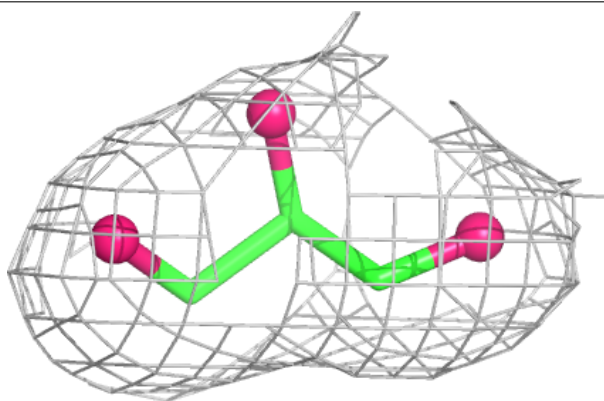


Electron density around EDO B 103:

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

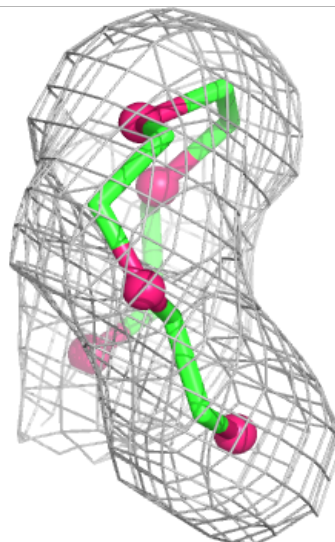
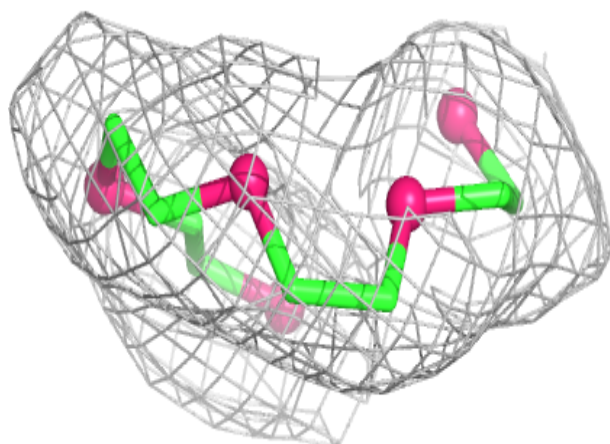
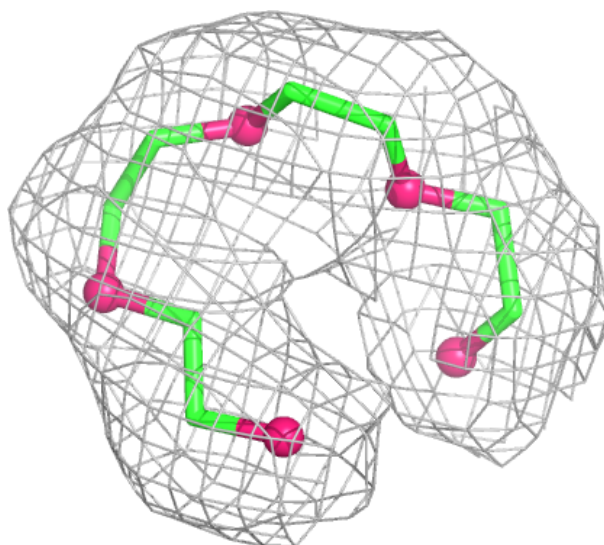
**Electron density around GOL A 340:**

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



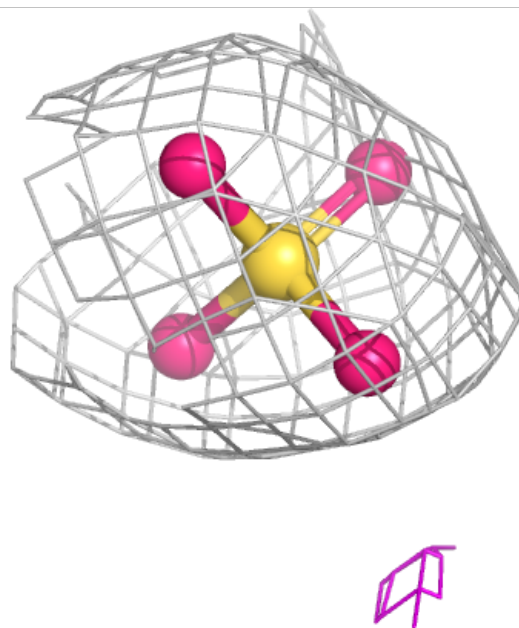
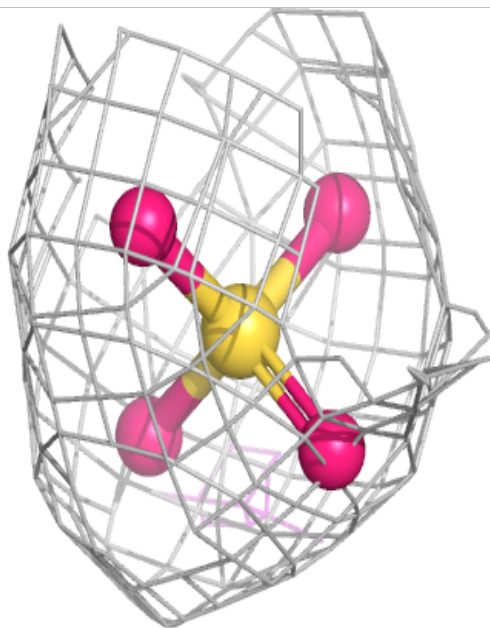
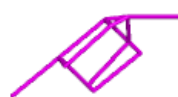
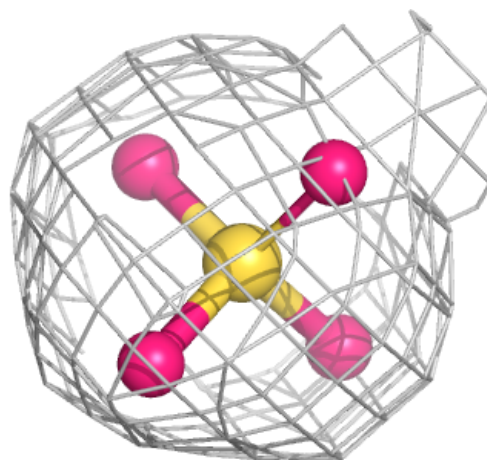
Electron density around PG4 A 333:

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



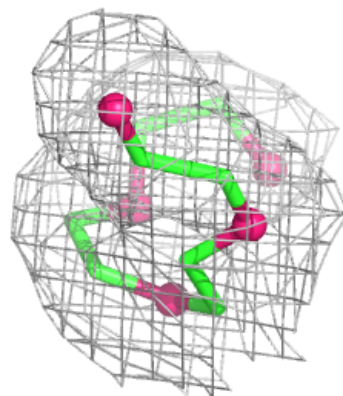
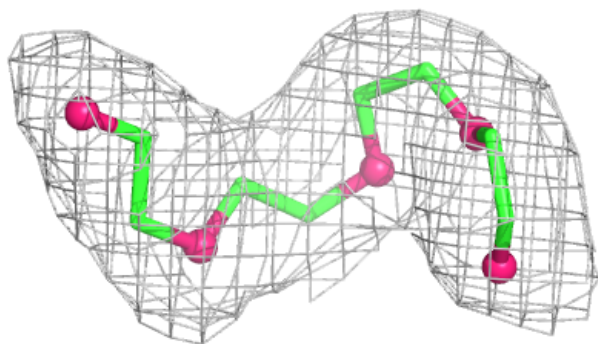
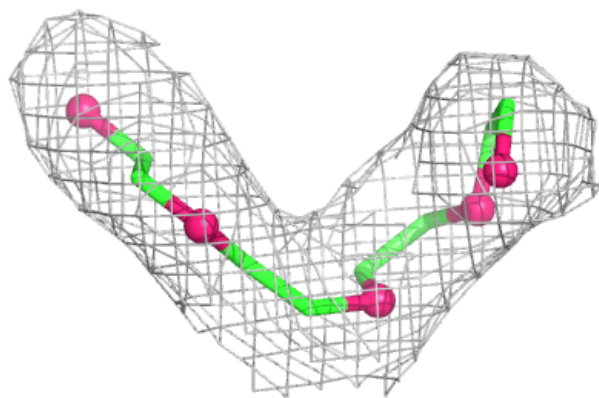
Electron density around SO4 D 114:

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



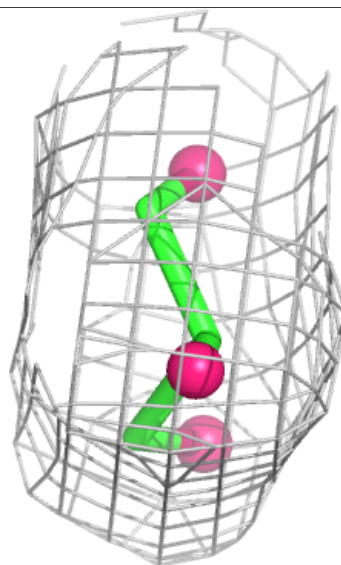
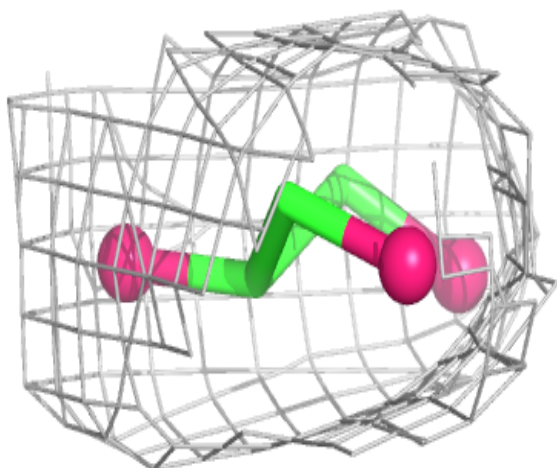
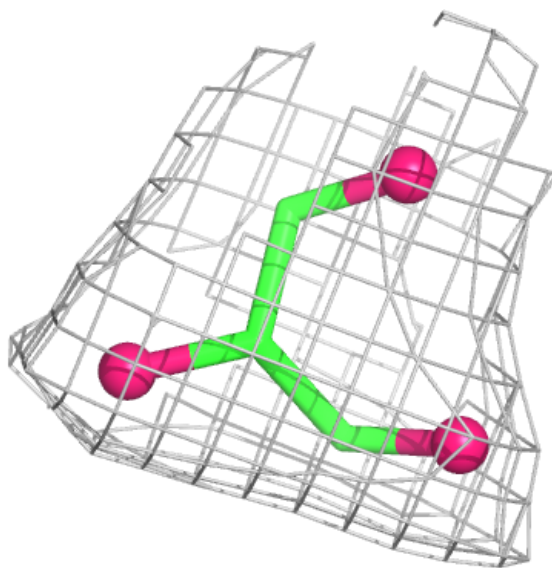
Electron density around PG4 C 326:

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



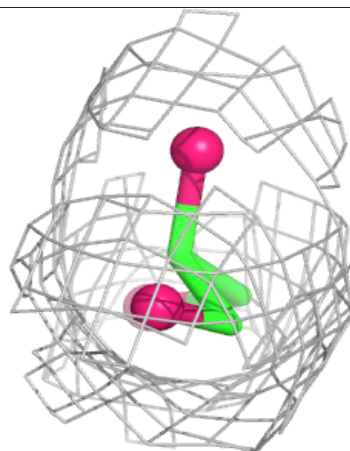
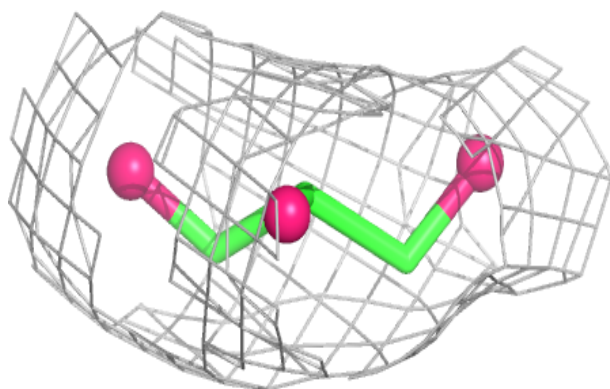
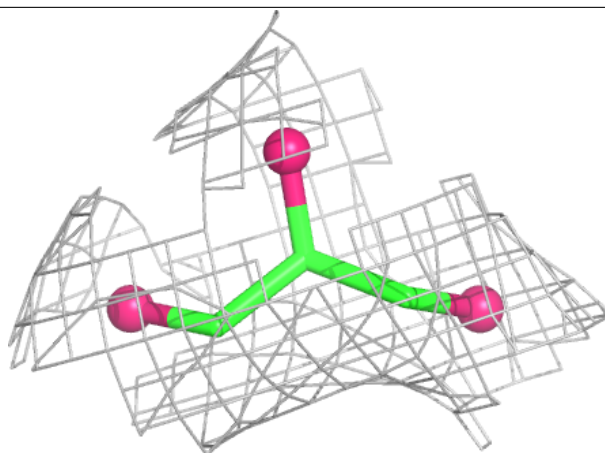
Electron density around GOL E 104:

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



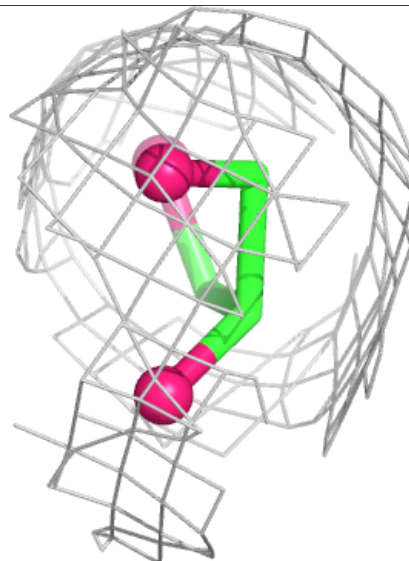
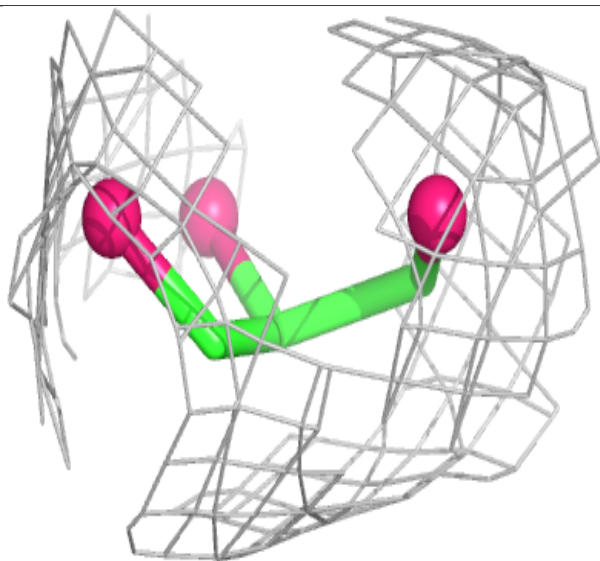
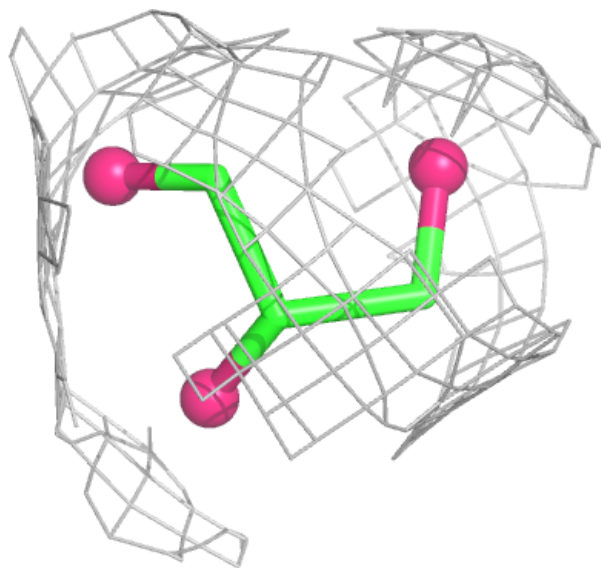
Electron density around GOL C 338:

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



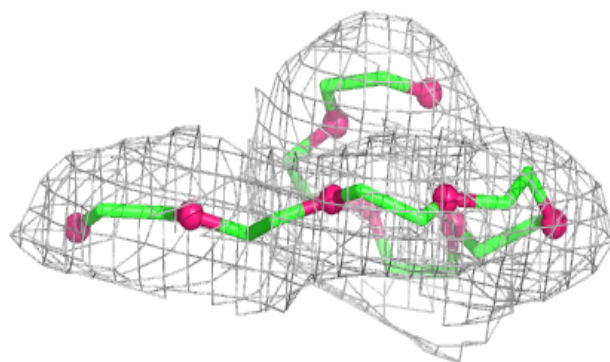
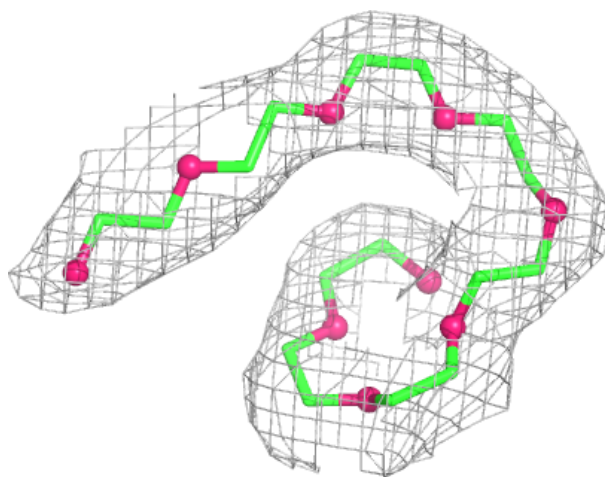
Electron density around GOL A 306:

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



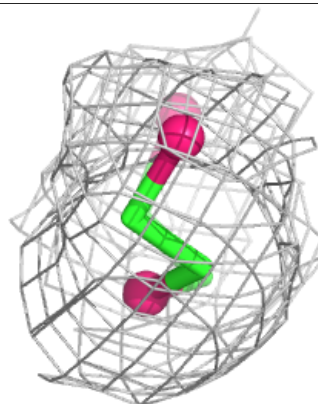
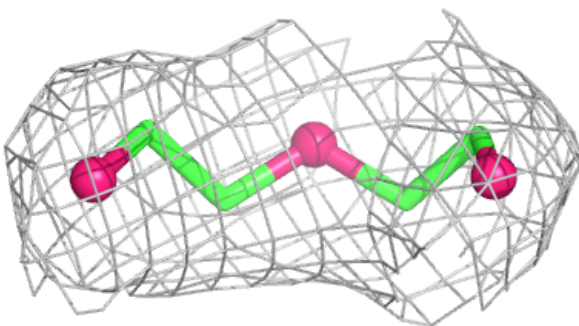
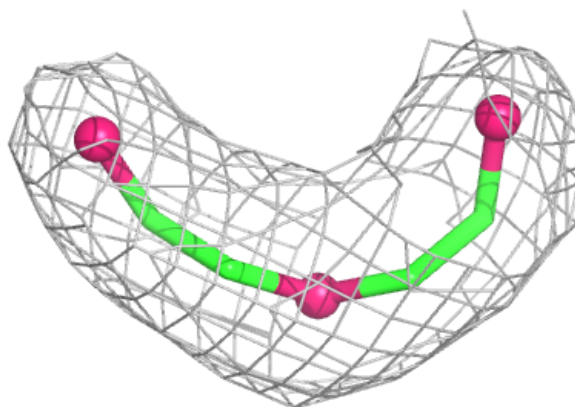
Electron density around PE8 B 121:

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



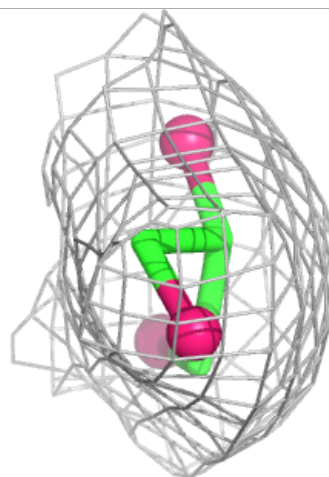
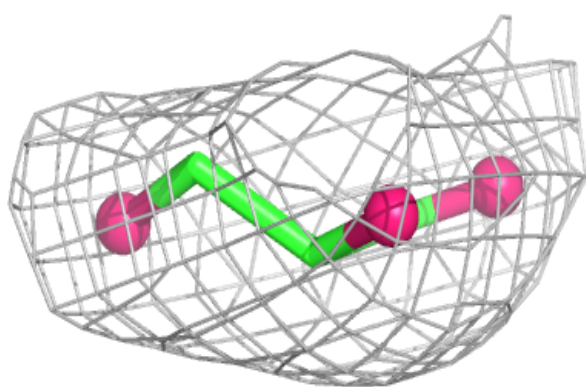
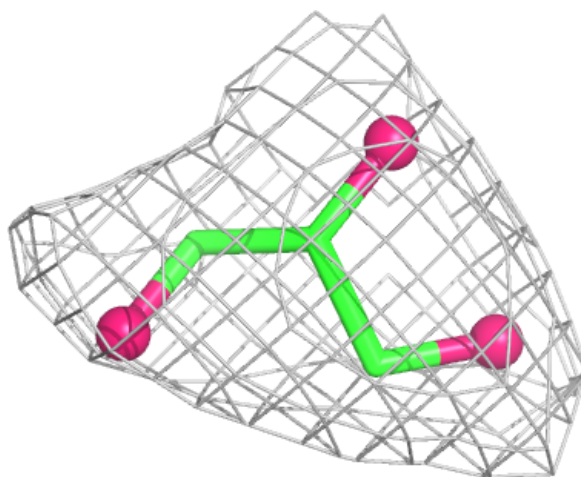
Electron density around PEG C 340:

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



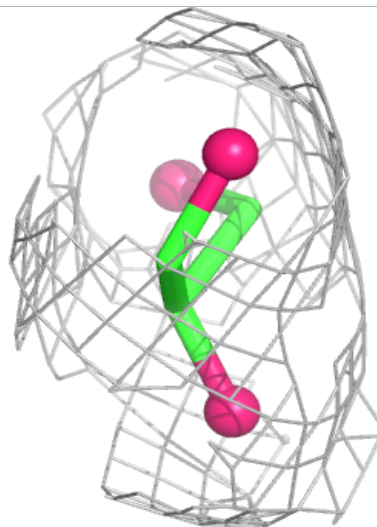
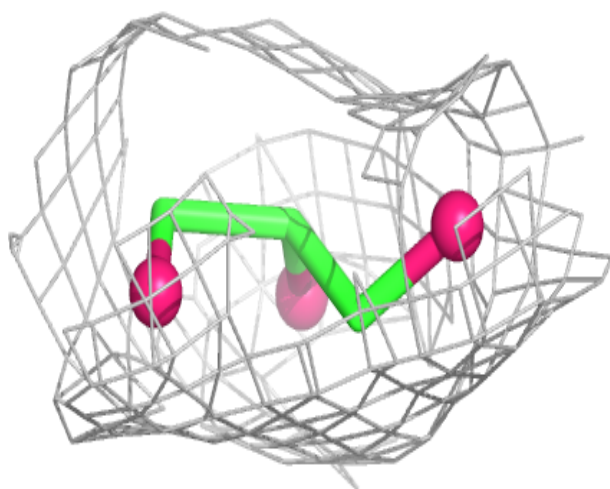
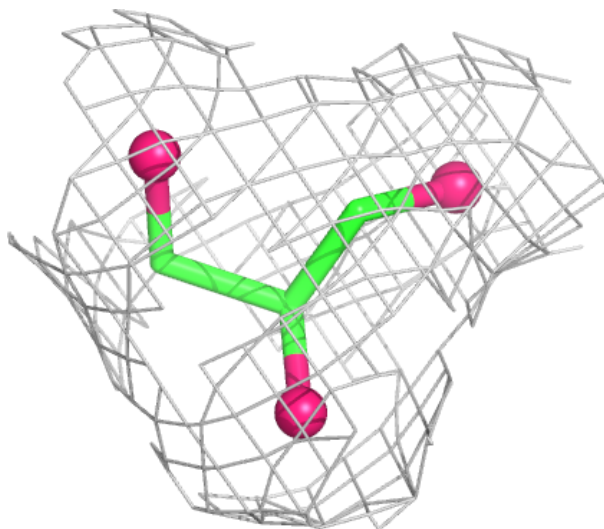
Electron density around GOL A 301:

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



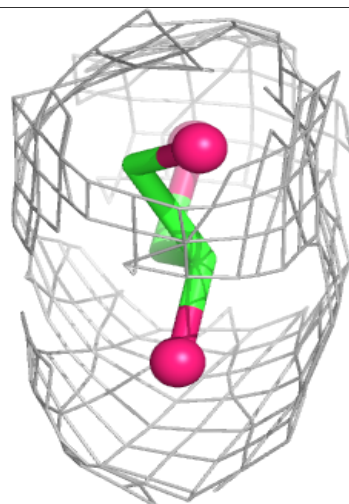
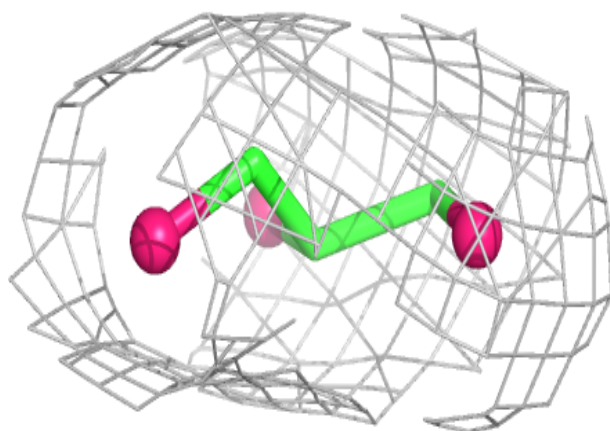
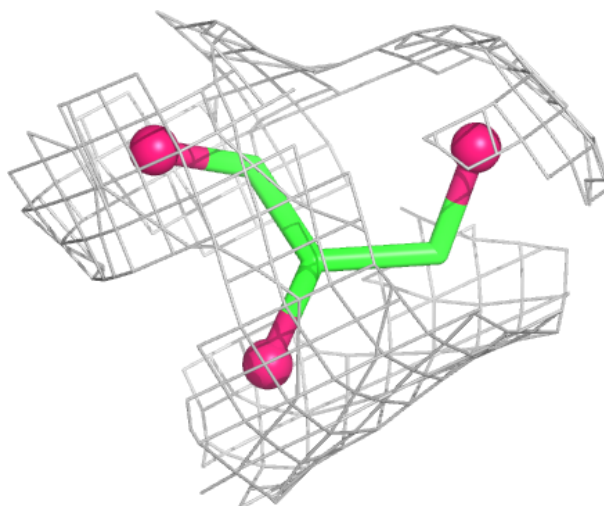
Electron density around GOL B 134:

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



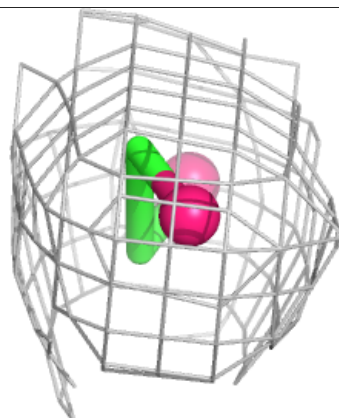
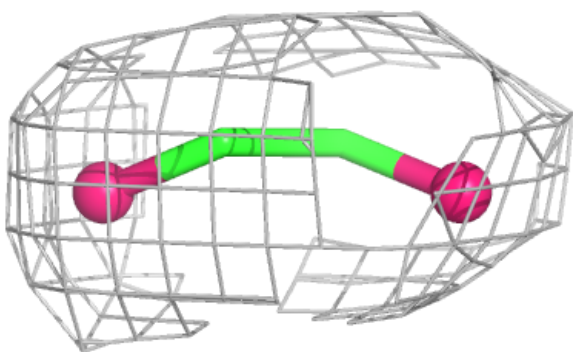
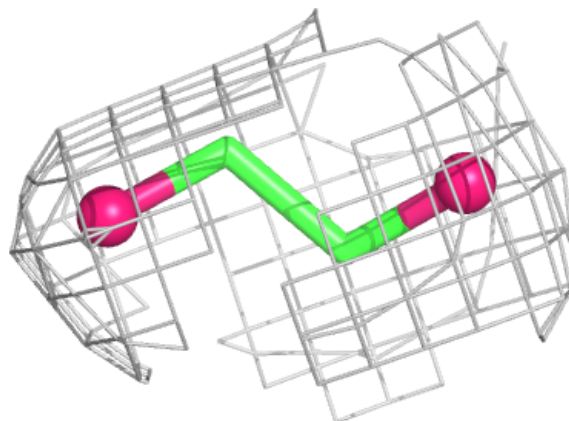
Electron density around GOL A 302:

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



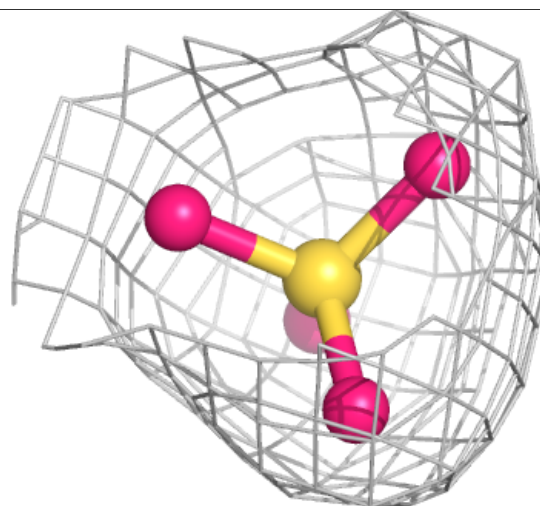
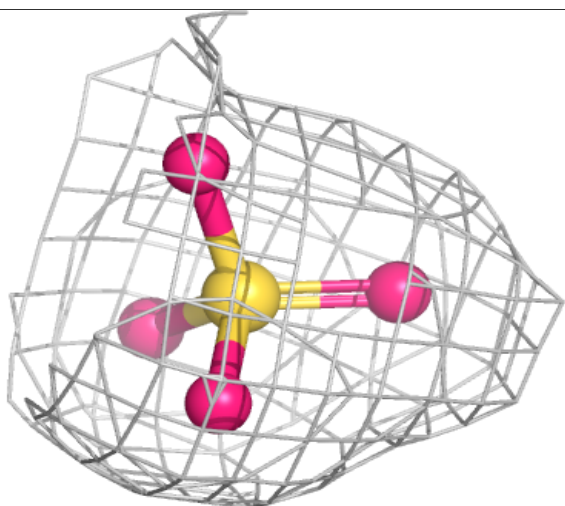
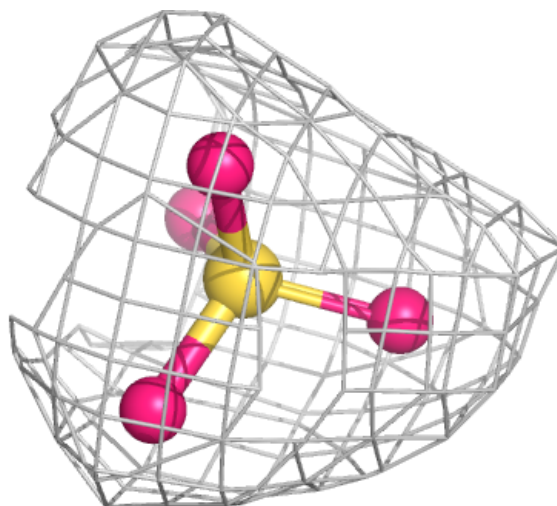
Electron density around EDO A 325:

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



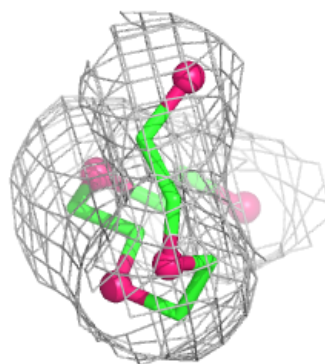
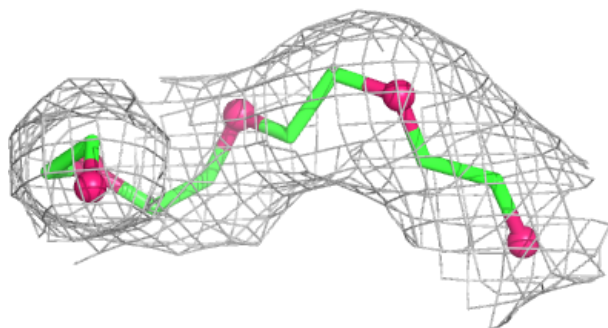
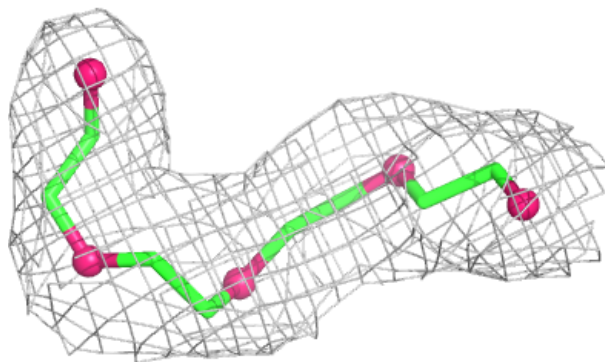
Electron density around SO4 D 126:

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

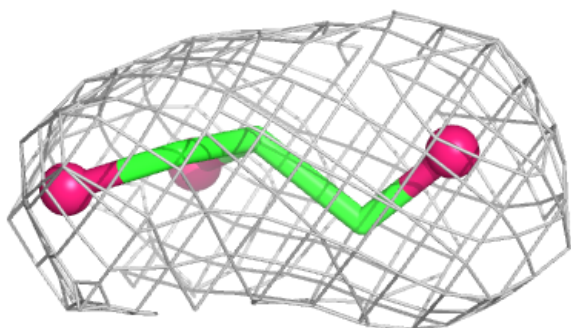
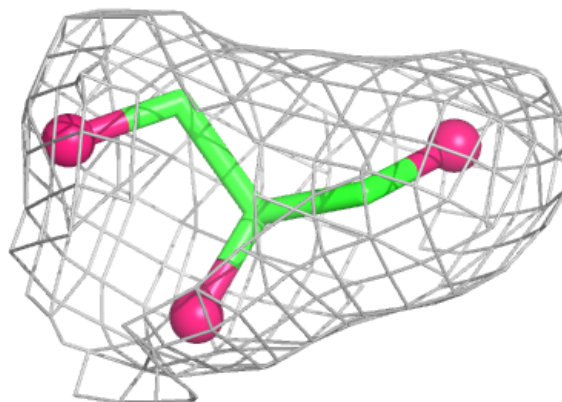


Electron density around PG4 A 329:

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

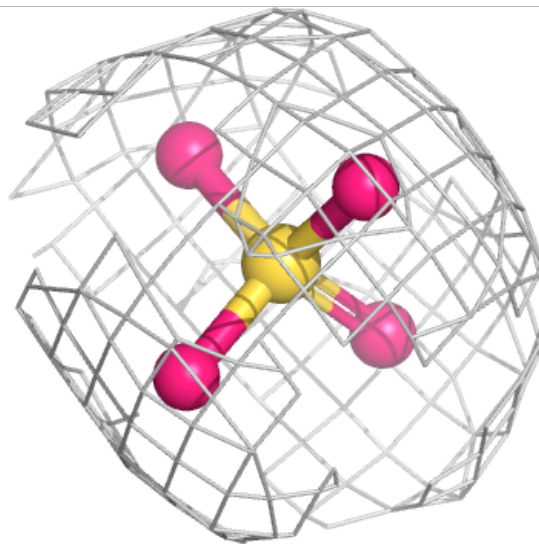
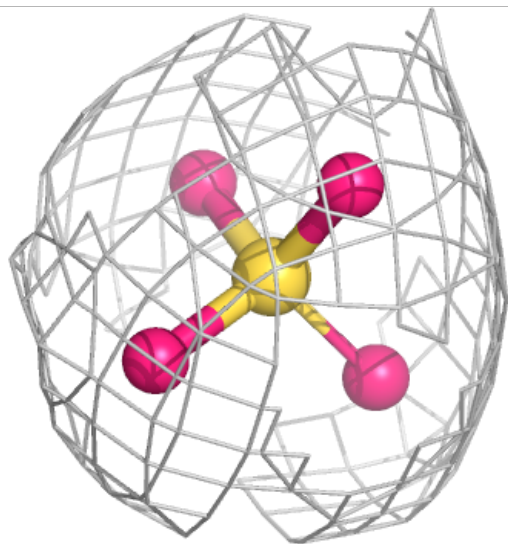
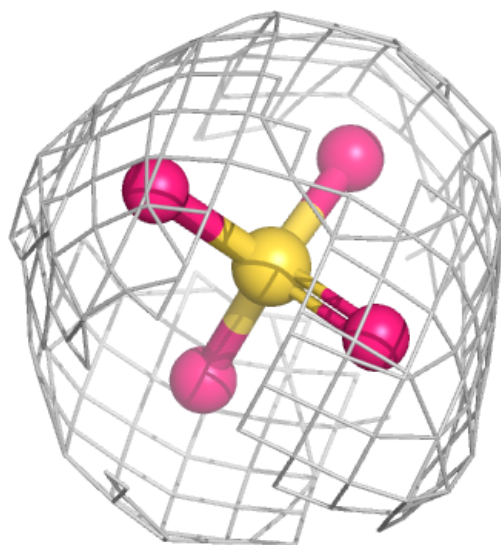
**Electron density around GOL C 341:**

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



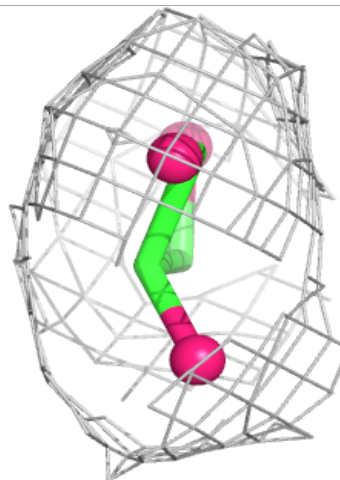
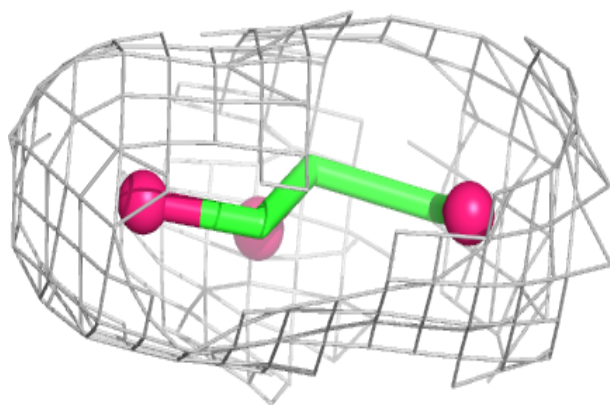
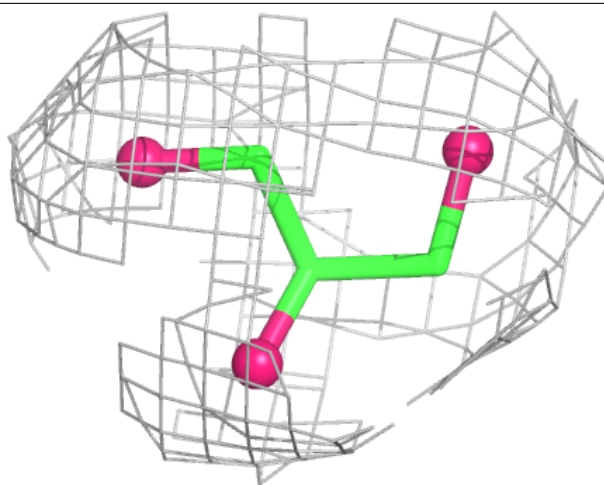
Electron density around SO4 E 107:

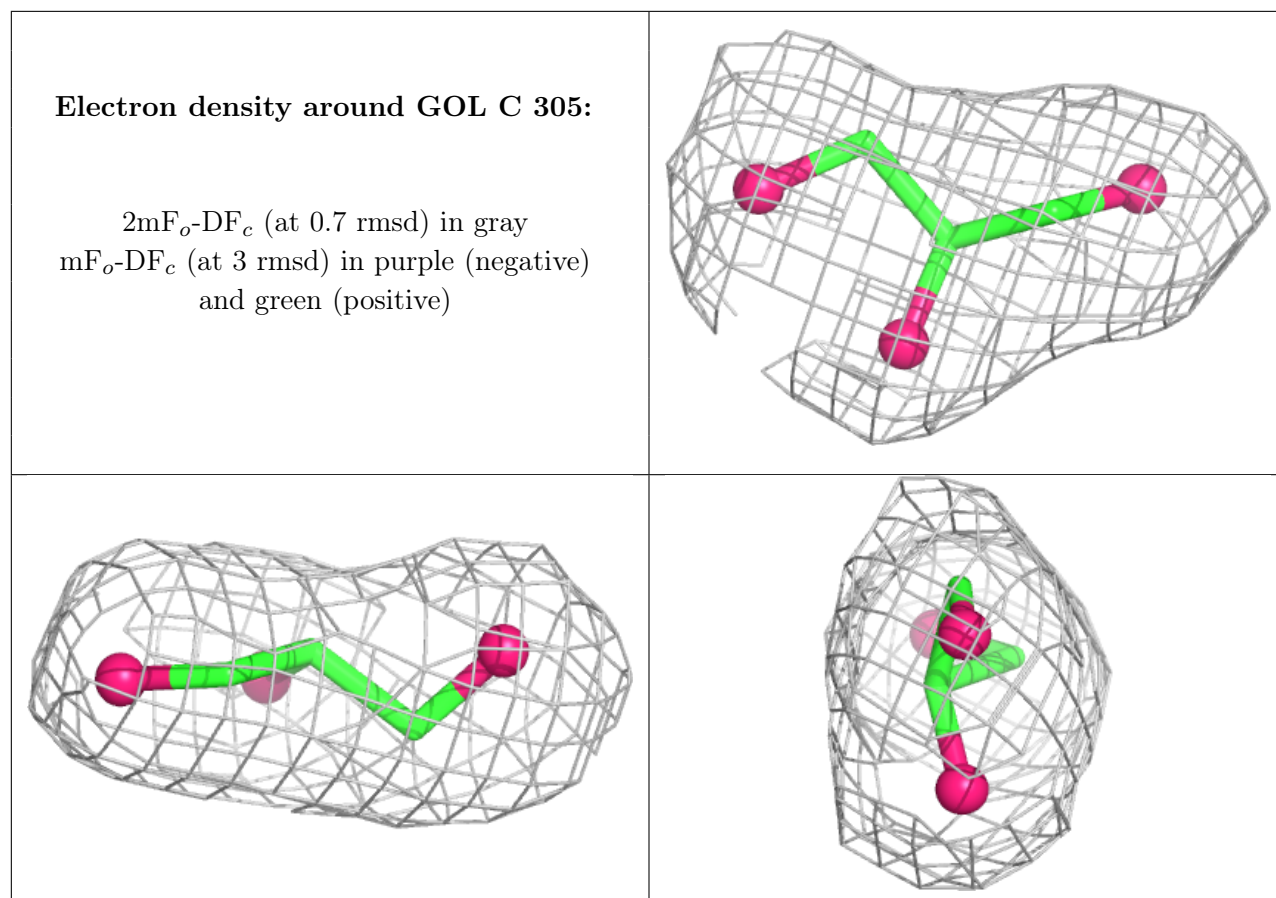
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GOL B 106:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.