



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 07:32 PM EDT

PDB ID : 2EIK / pdb_00002eik
Title : Cadmium ion binding structure of bovine heart cytochrome C oxidase in the fully reduced state
Authors : Muramoto, K.; Hirata, K.; Shinzawa-Itoh, K.; Yoko-O, S.; Yamashita, E.; Aoyama, H.; Tsukihara, T.; Yoshikawa, S.
Deposited on : 2007-03-13
Resolution : 2.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

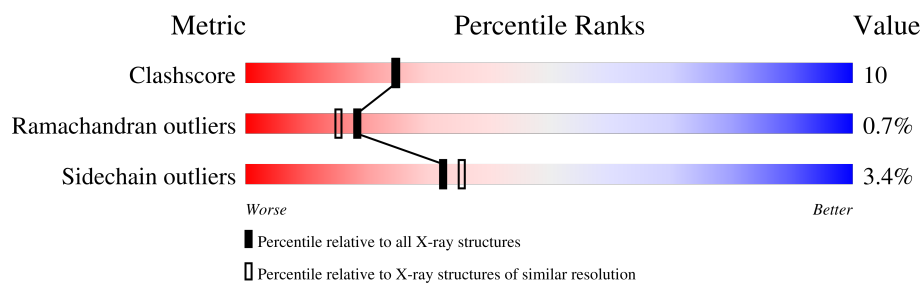
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	514	81% 18% .
1	N	514	77% 21% .
2	B	227	78% 19% ..
2	O	227	71% 26% .
3	C	261	82% 17% .
3	P	261	81% 17% ..
4	D	147	83% 15% .
4	Q	147	71% 26% ..

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Mol	Chain	Length	Quality of chain
5	E	109	
5	R	109	
6	F	98	
6	S	98	
7	G	85	
7	T	85	
8	H	85	
8	U	85	
9	I	73	
9	V	73	
10	J	59	
10	W	59	
11	K	56	
11	X	56	
12	L	47	
12	Y	47	
13	M	46	
13	Z	46	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
19	TGL	L	522	-	-	X	-
23	CHD	C	271	X	-	-	-
23	CHD	J	60	X	-	-	-
23	CHD	P	1271	X	-	-	-
23	CHD	W	1060	X	-	-	-
24	DMU	C	272	X	-	-	-
24	DMU	M	526	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	DMU	P	1272	X	-	-	-
24	DMU	Z	1526	X	-	-	-
26	CDL	G	269	-	-	X	-

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 32450 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 Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			
1	N	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			

- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	227	Total	C	N	O	S	0	0	0
			1824	1185	281	340	18			
2	O	227	Total	C	N	O	S	0	0	0
			1824	1185	281	340	18			

- Molecule 3 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	259	Total	C	N	O	S	0	0	0
			2110	1412	336	350	12			
3	P	259	Total	C	N	O	S	0	0	0
			2110	1412	336	350	12			

- Molecule 4 is a protein called Cytochrome c oxidase subunit 4 isoform 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			
4	Q	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			

- Molecule 5 is a protein called Cytochrome c oxidase polypeptide Va.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			
5	R	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			

- Molecule 6 is a protein called Cytochrome c oxidase polypeptide Vb.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			
6	S	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			

- Molecule 7 is a protein called Cytochrome c oxidase polypeptide VIa-heart.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
7	G	84	Total 675	C 431	N 129	O 113	P 1	S 1	0	0	0
7	T	84	Total 675	C 431	N 129	O 113	P 1	S 1	0	0	0

- Molecule 8 is a protein called Cytochrome c oxidase subunit VIb isoform 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			
8	U	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			

- Molecule 9 is a protein called Cytochrome c oxidase polypeptide VIc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			
9	V	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			

- Molecule 10 is a protein called Cytochrome c oxidase polypeptide VIIa-heart.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

- Molecule 11 is a protein called Cytochrome c oxidase polypeptide VIIb.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	49	Total	C	N	O	S	0	0	0
			384	250	65	67	2			
11	X	49	Total	C	N	O	S	0	0	0
			384	250	65	67	2			

- Molecule 12 is a protein called Cytochrome c oxidase polypeptide VIIc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	46	Total	C	N	O	S	0	0	0
			380	254	64	60	2			
12	Y	46	Total	C	N	O	S	0	0	0
			380	254	64	60	2			

- Molecule 13 is a protein called Cytochrome c oxidase polypeptide VIII-heart.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	43	Total	C	N	O	0	0	0
			335	223	53	59			
13	Z	43	Total	C	N	O	0	0	0
			335	223	53	59			

- Molecule 14 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	1	Total	Cu	0	0
			1	1		
14	N	1	Total	Cu	0	0
			1	1		

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total	Mg	0	0
			1	1		
15	N	1	Total	Mg	0	0
			1	1		

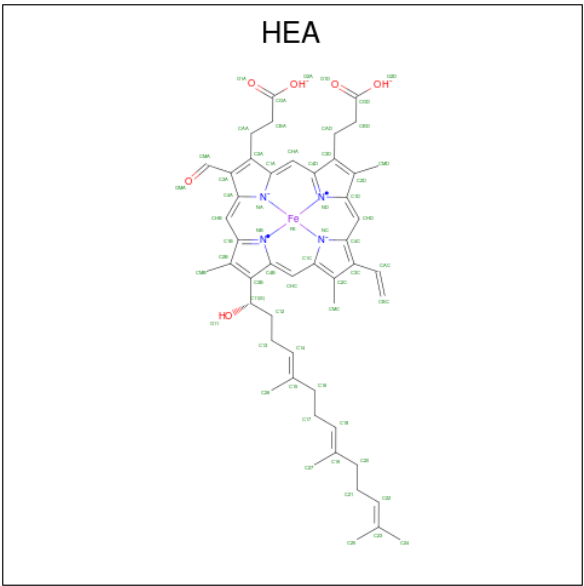
- Molecule 16 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	1	Total	Na	0	0
			1	1		
16	N	1	Total	Na	0	0
			1	1		

- Molecule 17 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Cd	0	0
			1	1		
17	C	1	Total	Cd	0	0
			1	1		
17	E	1	Total	Cd	0	0
			1	1		
17	N	1	Total	Cd	0	0
			1	1		
17	P	2	Total	Cd	0	0
			2	2		

- Molecule 18 is HEME-A (CCD ID: HEA) (formula: C₄₉H₅₆FeN₄O₆).



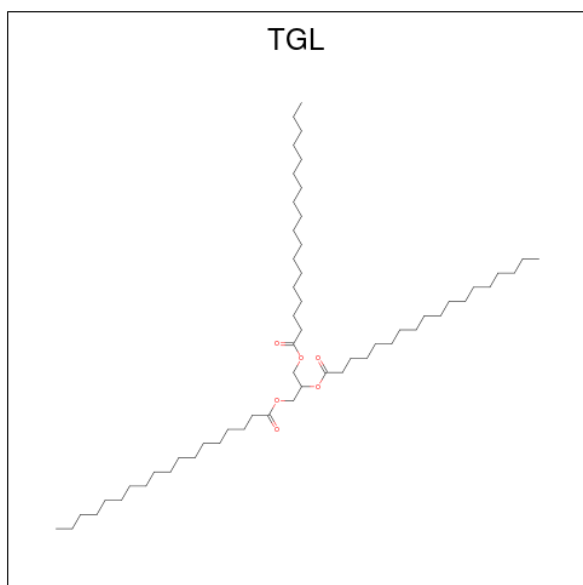
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
18	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0

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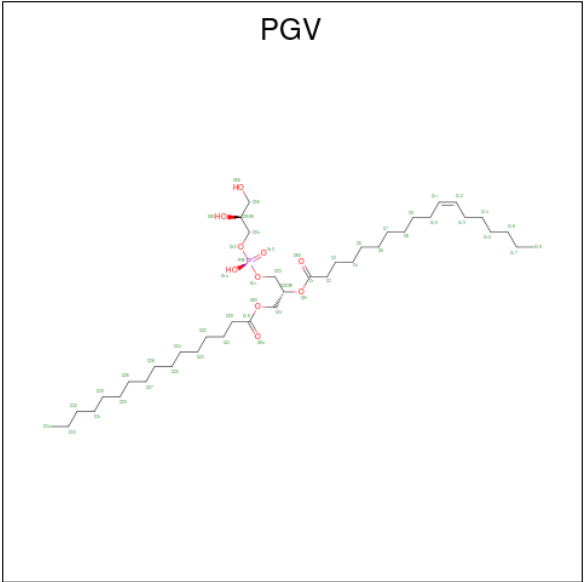
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
18	N	1	Total	C	Fe	N	O	
			60	49	1	4	6	
18	N	1	Total	C	Fe	N	O	
			60	49	1	4	6	

- Molecule 19 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: $C_{57}H_{110}O_6$).



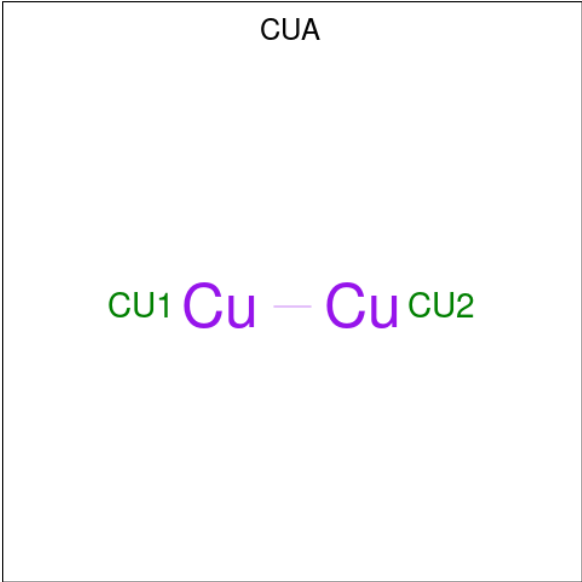
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	A	1	Total	C	O		
			63	57	6		
19	A	1	Total	C	O		
			63	57	6		
19	L	1	Total	C	O		
			63	57	6		
19	N	1	Total	C	O		
			63	57	6		
19	Q	1	Total	C	O		
			63	57	6		
19	Y	1	Total	C	O		
			63	57	6		

- Molecule 20 is (1R)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: $C_{40}H_{77}O_{10}P$).



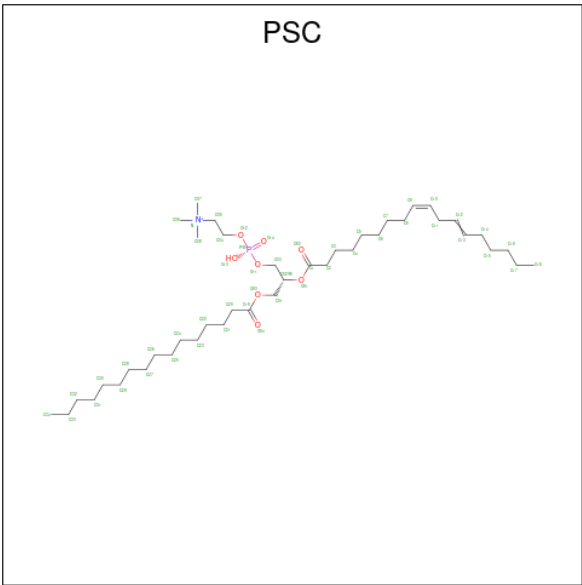
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
20	A	1	Total	C	O	P	0	0
			51	40	10	1		
20	A	1	Total	C	O	P	0	0
			51	40	10	1		
20	C	1	Total	C	O	P	0	0
			51	40	10	1		
20	C	1	Total	C	O	P	0	0
			51	40	10	1		
20	N	1	Total	C	O	P	0	0
			51	40	10	1		
20	N	1	Total	C	O	P	0	0
			51	40	10	1		
20	P	1	Total	C	O	P	0	0
			51	40	10	1		
20	P	1	Total	C	O	P	0	0
			51	40	10	1		

- Molecule 21 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	B	1	Total	Cu	0	0
			2	2		
21	O	1	Total	Cu	0	0
			2	2		

- Molecule 22 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITO YLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (CCD ID: PSC) (formula: C₄₂H₈₁NO₈P).



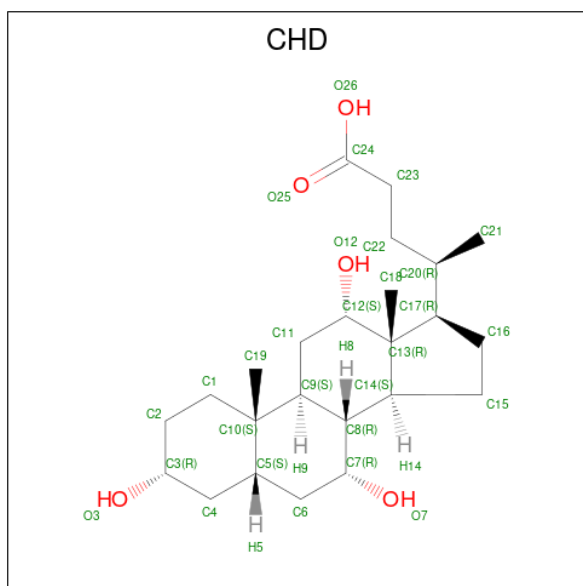
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
22	B	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

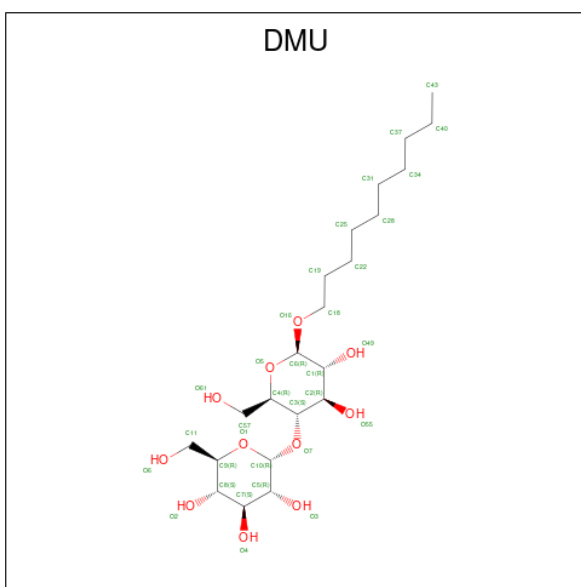
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
22	O	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

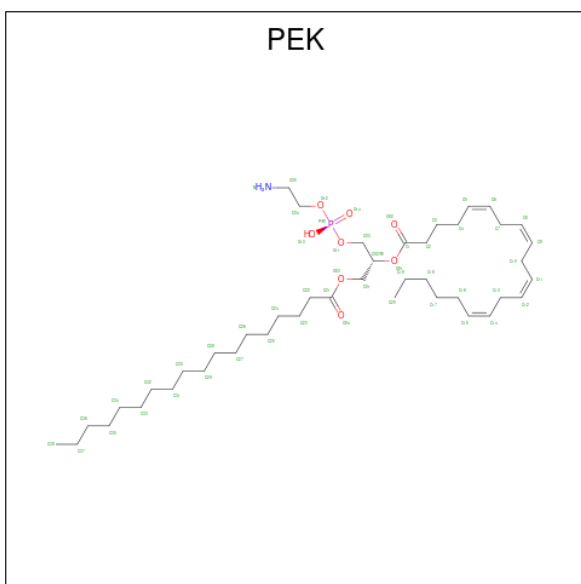
- Molecule 23 is CHOLIC ACID (CCD ID: CHD) (formula: $C_{24}H_{40}O_5$).





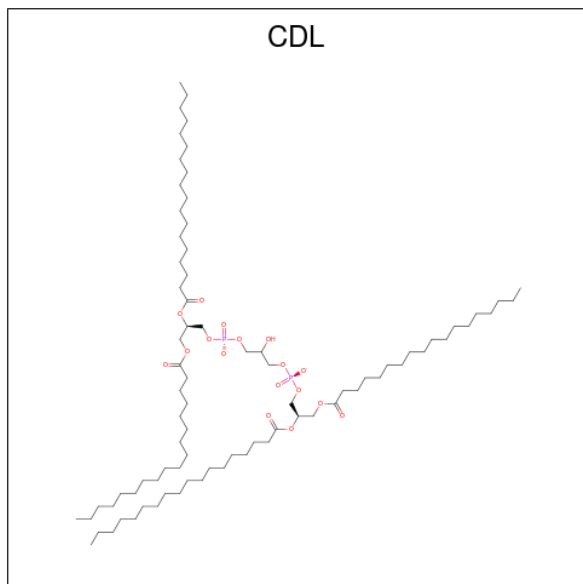
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	C	1	Total 33	C 22	O 11	0	0
24	M	1	Total 33	C 22	O 11	0	0
24	P	1	Total 33	C 22	O 11	0	0
24	Z	1	Total 33	C 22	O 11	0	0

- Molecule 25 is (1S)-2-[[[2-AMINOETHOXY](HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (CCD ID: PEK) (formula: $C_{43}H_{78}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	P	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	P	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		

- Molecule 26 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
26	C	1	Total	C	O	P	0	0
			100	81	17	2		
26	G	1	Total	C	O	P	0	0
			100	81	17	2		
26	P	1	Total	C	O	P	0	0
			100	81	17	2		
26	T	1	Total	C	O	P	0	0
			100	81	17	2		

- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	F	1	Total 1	Zn 1	0	0
27	S	1	Total 1	Zn 1	0	0

- Molecule 28 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	A	223	Total 223	O 223	0	0
28	B	146	Total 146	O 146	0	0
28	C	102	Total 102	O 102	0	0
28	D	98	Total 98	O 98	0	0
28	E	60	Total 60	O 60	0	0
28	F	85	Total 85	O 85	0	0
28	G	41	Total 41	O 41	0	0
28	H	49	Total 49	O 49	0	0
28	I	44	Total 44	O 44	0	0
28	J	26	Total 26	O 26	0	0
28	K	25	Total 25	O 25	0	0
28	L	23	Total 23	O 23	0	0
28	M	22	Total 22	O 22	0	0
28	N	213	Total 213	O 213	0	0
28	O	116	Total 116	O 116	0	0
28	P	103	Total 103	O 103	0	0
28	Q	52	Total 52	O 52	0	0
28	R	41	Total 41	O 41	0	0

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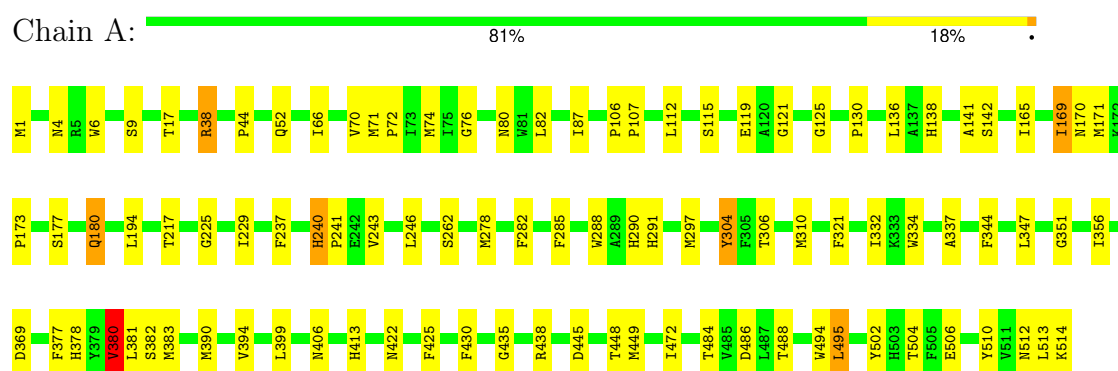
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	S	69	Total 69	O 69	0	0
28	T	47	Total 47	O 47	0	0
28	U	43	Total 43	O 43	0	0
28	V	25	Total 25	O 25	0	0
28	W	15	Total 15	O 15	0	0
28	X	17	Total 17	O 17	0	0
28	Y	15	Total 15	O 15	0	0
28	Z	14	Total 14	O 14	0	0

3 Residue-property plots

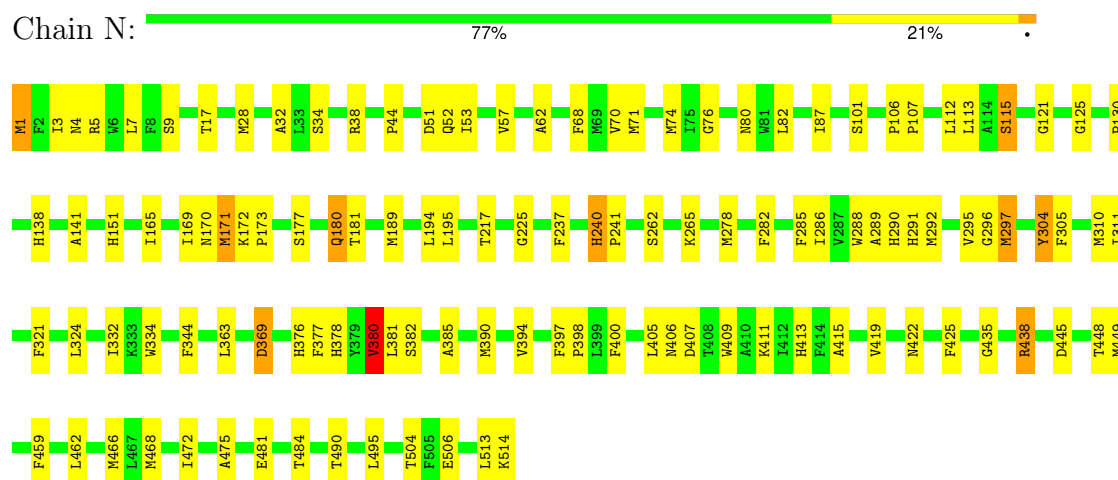
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

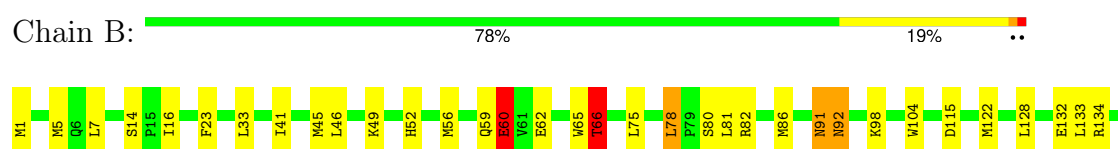
• Molecule 1: Cytochrome c oxidase subunit 1



• Molecule 1: Cytochrome c oxidase subunit 1

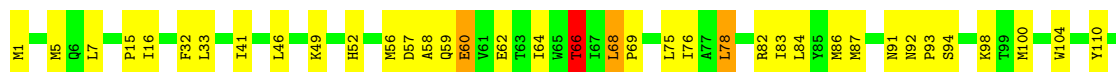


• Molecule 2: Cytochrome c oxidase subunit 2

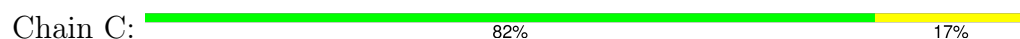




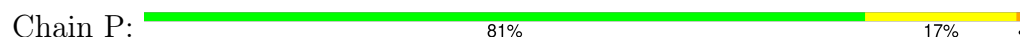
• Molecule 2: Cytochrome c oxidase subunit 2



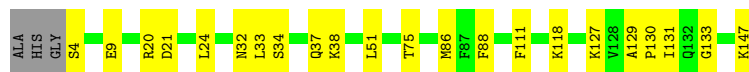
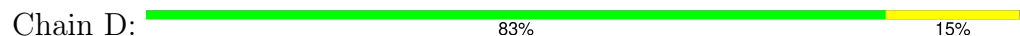
• Molecule 3: Cytochrome c oxidase subunit 3



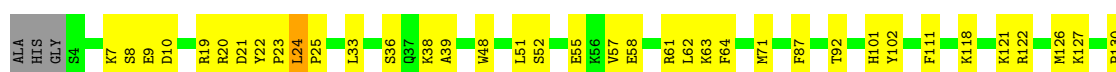
• Molecule 3: Cytochrome c oxidase subunit 3



• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1



• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1



- Molecule 5: Cytochrome c oxidase polypeptide Va

Chain E:  84% 12% .



- Molecule 5: Cytochrome c oxidase polypeptide Va

Chain R:  64% 31% . .



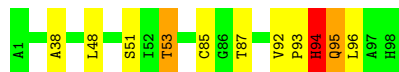
- Molecule 6: Cytochrome c oxidase polypeptide Vb

Chain F:  83% 15% . .



- Molecule 6: Cytochrome c oxidase polypeptide Vb

Chain S:  89% 8% . .



- Molecule 7: Cytochrome c oxidase polypeptide VIa-heart

Chain G:  74% 19% 6% .



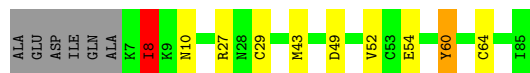
- Molecule 7: Cytochrome c oxidase polypeptide VIa-heart

Chain T:  72% 21% 6% .



- Molecule 8: Cytochrome c oxidase subunit VIb isoform 1

Chain H:  81% 9% . . 7%



- Molecule 8: Cytochrome c oxidase subunit VIb isoform 1

Chain U:  75% 14% 7%



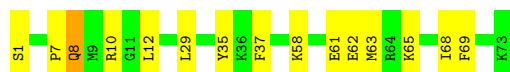
- Molecule 9: Cytochrome c oxidase polypeptide VIc

Chain I:  85% 14%



- Molecule 9: Cytochrome c oxidase polypeptide VIc

Chain V:  79% 19%



- Molecule 10: Cytochrome c oxidase polypeptide VIIa-heart

Chain J:  85% 12%



- Molecule 10: Cytochrome c oxidase polypeptide VIIa-heart

Chain W:  85% 12%



- Molecule 11: Cytochrome c oxidase polypeptide VIIb

Chain K:  70% 18% 12%



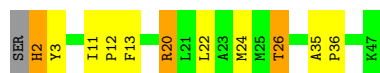
- Molecule 11: Cytochrome c oxidase polypeptide VIIb

Chain X:  73% 12% 12%



- Molecule 12: Cytochrome c oxidase polypeptide VIIc

Chain L:  74% 17% 6% •



- Molecule 12: Cytochrome c oxidase polypeptide VIIc

Chain Y:  74% 21% • •



- Molecule 13: Cytochrome c oxidase polypeptide VIII-heart

Chain M:  72% 20% • 7%



- Molecule 13: Cytochrome c oxidase polypeptide VIII-heart

Chain Z:  72% 22% 7%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	183.32Å 206.53Å 178.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (40.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.199 , 0.228	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	32450	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HEA, DMU, TGL, FME, PEK, CHD, TPO, CUA, NA, CDL, CD, ZN, SAC, PGV, PSC, CU, MG

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	0.68	1/4156 (0.0%)	1.08	28/5678 (0.5%)
1	N	0.61	0/4156	1.06	23/5678 (0.4%)
2	B	0.64	0/1860	1.04	5/2534 (0.2%)
2	O	0.63	0/1860	1.07	6/2534 (0.2%)
3	C	0.59	0/2197	0.95	6/3005 (0.2%)
3	P	0.56	0/2197	0.98	7/3005 (0.2%)
4	D	0.58	0/1229	1.00	5/1658 (0.3%)
4	Q	0.63	0/1229	1.03	4/1658 (0.2%)
5	E	0.64	0/871	1.04	2/1182 (0.2%)
5	R	0.64	0/871	1.11	5/1182 (0.4%)
6	F	0.62	0/765	1.15	3/1038 (0.3%)
6	S	0.64	0/765	1.13	4/1038 (0.4%)
7	G	0.60	0/690	1.02	1/937 (0.1%)
7	T	0.62	0/690	1.02	2/937 (0.2%)
8	H	0.60	0/682	1.04	4/921 (0.4%)
8	U	0.57	0/682	1.03	3/921 (0.3%)
9	I	0.55	0/605	0.92	2/802 (0.2%)
9	V	0.54	0/605	0.91	1/802 (0.1%)
10	J	0.57	0/471	0.93	1/636 (0.2%)
10	W	0.54	0/471	0.97	1/636 (0.2%)
11	K	0.66	0/398	1.15	3/546 (0.5%)
11	X	0.58	0/398	1.11	3/546 (0.5%)
12	L	0.66	0/393	0.96	1/526 (0.2%)
12	Y	0.61	0/393	1.00	1/526 (0.2%)
13	M	0.58	0/345	0.98	1/470 (0.2%)
13	Z	0.53	0/345	0.98	1/470 (0.2%)
All	All	0.61	1/29324 (0.0%)	1.04	123/39866 (0.3%)

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

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	N	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	106	PRO	CA-C	6.05	1.57	1.52

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	133	GLY	N-CA-C	11.68	127.72	112.77
4	Q	133	GLY	N-CA-C	10.96	126.80	112.77
6	F	93	PRO	N-CA-C	10.49	126.33	111.33
6	S	93	PRO	N-CA-C	9.05	125.36	111.34
5	R	42	VAL	N-CA-C	-8.85	97.61	108.05

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	HIS	Sidechain
1	A	304	TYR	Sidechain
1	N	240	HIS	Sidechain
1	N	304	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4027	0	4001	66	0
1	N	4027	0	4001	82	0
2	B	1824	0	1833	33	0
2	O	1824	0	1833	46	0
3	C	2110	0	2027	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	P	2110	0	2027	46	0
4	D	1195	0	1183	17	0
4	Q	1195	0	1183	22	0
5	E	852	0	845	4	0
5	R	852	0	845	22	0
6	F	748	0	728	9	0
6	S	748	0	728	9	0
7	G	675	0	644	24	0
7	T	675	0	644	25	0
8	H	662	0	623	7	0
8	U	662	0	623	13	0
9	I	601	0	613	9	0
9	V	601	0	613	12	0
10	J	460	0	459	7	0
10	W	460	0	459	7	0
11	K	384	0	366	5	0
11	X	384	0	366	4	0
12	L	380	0	380	19	0
12	Y	380	0	380	11	0
13	M	335	0	352	8	0
13	Z	335	0	352	5	0
14	A	1	0	0	0	0
14	N	1	0	0	0	0
15	A	1	0	0	0	0
15	N	1	0	0	0	0
16	A	1	0	0	0	0
16	N	1	0	0	0	0
17	A	1	0	0	0	0
17	C	1	0	0	0	0
17	E	1	0	0	0	0
17	N	1	0	0	0	0
17	P	2	0	0	0	0
18	A	120	0	108	3	0
18	N	120	0	108	3	0
19	A	126	0	220	16	0
19	L	63	0	110	23	0
19	N	63	0	110	8	0
19	Q	63	0	110	7	0
19	Y	63	0	110	18	0
20	A	102	0	152	9	0
20	C	102	0	152	8	0
20	N	102	0	152	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	P	102	0	152	7	0
21	B	2	0	0	0	0
21	O	2	0	0	0	0
22	B	52	0	80	14	0
22	O	52	0	80	15	0
23	B	29	0	39	1	0
23	C	58	0	78	7	0
23	J	29	0	39	3	0
23	O	29	0	39	1	0
23	P	58	0	78	1	0
23	W	29	0	39	5	0
24	C	33	0	36	2	0
24	M	33	0	38	0	0
24	P	33	0	36	8	0
24	Z	33	0	38	0	0
25	C	106	0	154	11	0
25	G	53	0	77	10	0
25	P	106	0	154	12	0
25	T	53	0	77	9	0
26	C	100	0	156	17	0
26	G	100	0	156	21	0
26	P	100	0	156	18	0
26	T	100	0	156	19	0
27	F	1	0	0	0	0
27	S	1	0	0	0	0
28	A	223	0	0	2	0
28	B	146	0	0	4	0
28	C	102	0	0	2	0
28	D	98	0	0	4	0
28	E	60	0	0	1	0
28	F	85	0	0	1	0
28	G	41	0	0	1	0
28	H	49	0	0	2	0
28	I	44	0	0	4	0
28	J	26	0	0	2	0
28	K	25	0	0	1	0
28	L	23	0	0	0	0
28	M	22	0	0	1	0
28	N	213	0	0	3	0
28	O	116	0	0	1	0
28	P	103	0	0	2	0
28	Q	52	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	R	41	0	0	0	0
28	S	69	0	0	3	0
28	T	47	0	0	4	0
28	U	43	0	0	1	0
28	V	25	0	0	1	0
28	W	15	0	0	2	0
28	X	17	0	0	0	0
28	Y	15	0	0	1	0
28	Z	14	0	0	1	0
All	All	32450	0	31298	605	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 10.

The worst 5 of 605 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)
10:W:33:ARG:HG2	23:W:1060:CHD:H152	1.31	1.11
22:O:1230:PSC:H142	22:O:1230:PSC:H343	1.39	1.02
7:T:5:LYS:HB2	25:T:263:PEK:H362	1.42	1.00
10:J:33:ARG:HG2	23:J:60:CHD:H152	1.40	0.99
22:B:230:PSC:H343	22:B:230:PSC:H142	1.40	0.99

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	512/514 (100%)	499 (98%)	13 (2%)	0	100	100
1	N	512/514 (100%)	500 (98%)	12 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	225/227 (99%)	212 (94%)	11 (5%)	2 (1%)	14	10
2	O	225/227 (99%)	211 (94%)	13 (6%)	1 (0%)	30	28
3	C	257/261 (98%)	251 (98%)	6 (2%)	0	100	100
3	P	257/261 (98%)	251 (98%)	6 (2%)	0	100	100
4	D	142/147 (97%)	139 (98%)	3 (2%)	0	100	100
4	Q	142/147 (97%)	138 (97%)	4 (3%)	0	100	100
5	E	103/109 (94%)	100 (97%)	3 (3%)	0	100	100
5	R	103/109 (94%)	101 (98%)	2 (2%)	0	100	100
6	F	96/98 (98%)	88 (92%)	5 (5%)	3 (3%)	3	1
6	S	96/98 (98%)	89 (93%)	4 (4%)	3 (3%)	3	1
7	G	81/85 (95%)	65 (80%)	9 (11%)	7 (9%)	0	0
7	T	81/85 (95%)	66 (82%)	8 (10%)	7 (9%)	0	0
8	H	77/85 (91%)	70 (91%)	6 (8%)	1 (1%)	9	6
8	U	77/85 (91%)	70 (91%)	6 (8%)	1 (1%)	9	6
9	I	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
9	V	71/73 (97%)	67 (94%)	4 (6%)	0	100	100
10	J	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
10	W	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
11	K	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
11	X	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
12	L	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
12	Y	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
13	M	41/46 (89%)	41 (100%)	0	0	100	100
13	Z	41/46 (89%)	41 (100%)	0	0	100	100
All	All	3504/3614 (97%)	3354 (96%)	125 (4%)	25 (1%)	18	15

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	95	GLN
7	G	4	ALA
7	G	7	ASP
7	G	8	HIS
7	G	39	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	426/426 (100%)	415 (97%)	11 (3%)	40	46
1	N	426/426 (100%)	415 (97%)	11 (3%)	40	46
2	B	210/210 (100%)	201 (96%)	9 (4%)	26	27
2	O	210/210 (100%)	197 (94%)	13 (6%)	16	14
3	C	224/226 (99%)	218 (97%)	6 (3%)	39	45
3	P	224/226 (99%)	219 (98%)	5 (2%)	45	53
4	D	128/129 (99%)	126 (98%)	2 (2%)	55	64
4	Q	128/129 (99%)	124 (97%)	4 (3%)	35	39
5	E	92/95 (97%)	89 (97%)	3 (3%)	33	37
5	R	92/95 (97%)	89 (97%)	3 (3%)	33	37
6	F	81/81 (100%)	79 (98%)	2 (2%)	42	48
6	S	81/81 (100%)	78 (96%)	3 (4%)	30	33
7	G	67/68 (98%)	63 (94%)	4 (6%)	17	15
7	T	67/68 (98%)	65 (97%)	2 (3%)	36	41
8	H	71/75 (95%)	68 (96%)	3 (4%)	26	28
8	U	71/75 (95%)	70 (99%)	1 (1%)	59	67
9	I	57/57 (100%)	56 (98%)	1 (2%)	51	60
9	V	57/57 (100%)	54 (95%)	3 (5%)	20	19
10	J	49/50 (98%)	48 (98%)	1 (2%)	48	56
10	W	49/50 (98%)	48 (98%)	1 (2%)	48	56
11	K	39/46 (85%)	38 (97%)	1 (3%)	40	46
11	X	39/46 (85%)	37 (95%)	2 (5%)	21	21
12	L	39/40 (98%)	37 (95%)	2 (5%)	21	21
12	Y	39/40 (98%)	38 (97%)	1 (3%)	40	46
13	M	37/38 (97%)	33 (89%)	4 (11%)	6	4
13	Z	37/38 (97%)	33 (89%)	4 (11%)	6	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3040/3082 (99%)	2938 (97%)	102 (3%)	32	35

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	484	THR
2	O	205	SER
13	Z	34	LEU
1	N	513	LEU
2	O	78	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	406	ASN
3	P	68	GLN
1	N	512	ASN
2	O	181	GLN
3	P	207	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FME	O	1	2	8,9,10	0.69	0	8,9,11	2.33	2 (25%)
7	TPO	G	11	7	8,10,11	1.64	1 (12%)	10,14,16	1.11	1 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	FME	N	1	1	8,9,10	0.78	0	8,9,11	1.51	1 (12%)
9	SAC	V	1	9	7,8,9	2.84	2 (28%)	7,9,11	1.95	3 (42%)
2	FME	B	1	2	8,9,10	0.65	0	8,9,11	1.73	2 (25%)
7	TPO	T	11	7	8,10,11	1.49	2 (25%)	10,14,16	1.02	1 (10%)
1	FME	A	1	1	8,9,10	0.65	0	8,9,11	0.99	0
9	SAC	I	1	9	7,8,9	2.89	2 (28%)	7,9,11	1.59	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FME	O	1	2	-	2/7/9/11	-
7	TPO	G	11	7	-	5/9/11/13	-
1	FME	N	1	1	-	4/7/9/11	-
9	SAC	V	1	9	-	3/7/8/10	-
2	FME	B	1	2	-	1/7/9/11	-
7	TPO	T	11	7	-	4/9/11/13	-
1	FME	A	1	1	-	3/7/9/11	-
9	SAC	I	1	9	-	3/7/8/10	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	1	SAC	OAC-C1A	5.66	1.35	1.23
9	V	1	SAC	CA-N	5.20	1.54	1.46
9	I	1	SAC	CA-N	4.96	1.53	1.46
9	V	1	SAC	OAC-C1A	4.95	1.34	1.23
7	G	11	TPO	CB-CA	3.25	1.60	1.53

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	1	FME	C-CA-N	5.07	119.29	109.50
2	O	1	FME	CA-N-CN	-3.98	116.71	122.82
2	B	1	FME	C-CA-N	3.74	116.72	109.50
1	N	1	FME	CA-N-CN	-3.51	117.42	122.82
9	V	1	SAC	C2A-C1A-N	3.30	121.59	116.12

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	O1-CN-N-CA
1	A	1	FME	N-CA-CB-CG
2	B	1	FME	O1-CN-N-CA
7	G	11	TPO	N-CA-CB-CG2
7	G	11	TPO	N-CA-CB-OG1

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	11	TPO	1	0
1	N	1	FME	1	0
7	T	11	TPO	1	0
1	A	1	FME	5	0
9	I	1	SAC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 58 ligands modelled in this entry, 14 are monoatomic - leaving 44 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	$\# Z > 2$
25	PEK	C	264	-	52,52,52	1.41	4 (7%)	55,57,57	1.22	5 (9%)
25	PEK	C	265	-	52,52,52	1.63	10 (19%)	55,57,57	1.14	6 (10%)
24	DMU	C	272	-	34,34,34	2.83	12 (35%)	45,45,45	4.20	19 (42%)
25	PEK	G	1263	-	52,52,52	1.79	10 (19%)	55,57,57	1.16	5 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	HEA	A	516	1	67,67,67	1.32	7 (10%)	81,103,103	1.28	10 (12%)
25	PEK	P	1264	-	52,52,52	1.49	5 (9%)	55,57,57	1.17	6 (10%)
18	HEA	N	515	1	67,67,67	1.05	3 (4%)	81,103,103	1.14	5 (6%)
23	CHD	B	1086	-	32,32,32	0.75	0	51,51,51	1.77	11 (21%)
26	CDL	P	1270	-	99,99,99	0.91	5 (5%)	105,111,111	1.02	7 (6%)
24	DMU	Z	1526	-	34,34,34	3.25	9 (26%)	45,45,45	3.97	20 (44%)
23	CHD	C	525	-	32,32,32	0.92	1 (3%)	51,51,51	1.87	14 (27%)
25	PEK	T	263	-	52,52,52	1.82	10 (19%)	55,57,57	1.17	5 (9%)
20	PGV	A	604	-	50,50,50	0.87	1 (2%)	53,56,56	0.75	1 (1%)
19	TGL	N	1521	-	62,62,62	0.74	1 (1%)	65,65,65	1.44	9 (13%)
19	TGL	A	523	-	62,62,62	0.78	1 (1%)	65,65,65	1.29	11 (16%)
18	HEA	A	515	1	67,67,67	1.07	6 (8%)	81,103,103	1.14	4 (4%)
23	CHD	C	271	-	32,32,32	1.00	1 (3%)	51,51,51	3.69	25 (49%)
23	CHD	J	60	-	32,32,32	1.36	3 (9%)	51,51,51	3.52	29 (56%)
24	DMU	P	1272	-	34,34,34	2.87	12 (35%)	45,45,45	4.06	19 (42%)
23	CHD	O	229	-	32,32,32	0.72	0	51,51,51	1.74	12 (23%)
20	PGV	C	267	-	50,50,50	0.84	1 (2%)	53,56,56	0.97	3 (5%)
20	PGV	C	268	-	50,50,50	1.19	3 (6%)	53,56,56	0.82	0
19	TGL	A	521	-	62,62,62	0.74	1 (1%)	65,65,65	1.45	9 (13%)
19	TGL	Y	1522	-	62,62,62	1.17	5 (8%)	65,65,65	1.71	14 (21%)
23	CHD	P	1271	-	32,32,32	0.94	1 (3%)	51,51,51	3.61	26 (50%)
23	CHD	W	1060	-	32,32,32	1.41	3 (9%)	51,51,51	3.55	26 (50%)
21	CUA	O	228	2	0,1,1	-	-	-	-	-
24	DMU	M	526	-	34,34,34	3.34	8 (23%)	45,45,45	4.04	20 (44%)
21	CUA	B	228	2	0,1,1	-	-	-	-	-
26	CDL	G	269	-	99,99,99	1.00	7 (7%)	105,111,111	0.97	6 (5%)
20	PGV	P	1268	-	50,50,50	1.16	2 (4%)	53,56,56	0.86	0
22	PSC	O	1230	-	51,51,51	1.24	3 (5%)	57,59,59	0.92	1 (1%)
19	TGL	Q	1523	-	62,62,62	0.82	1 (1%)	65,65,65	1.26	6 (9%)
26	CDL	T	1269	-	99,99,99	0.98	7 (7%)	105,111,111	0.98	7 (6%)
22	PSC	B	230	-	51,51,51	1.23	3 (5%)	57,59,59	0.91	1 (1%)
20	PGV	A	524	-	50,50,50	1.07	3 (6%)	53,56,56	0.96	3 (5%)
20	PGV	P	1267	-	50,50,50	0.82	1 (2%)	53,56,56	0.87	1 (1%)
25	PEK	P	1265	-	52,52,52	1.64	10 (19%)	55,57,57	1.14	6 (10%)
20	PGV	N	1266	-	50,50,50	0.90	2 (4%)	53,56,56	0.83	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	TGL	L	522	-	62,62,62	1.14	6 (9%)	65,65,65	1.73	14 (21%)
20	PGV	N	1524	-	50,50,50	1.06	4 (8%)	53,56,56	0.94	3 (5%)
23	CHD	P	1525	-	32,32,32	0.91	1 (3%)	51,51,51	1.80	12 (23%)
26	CDL	C	270	-	99,99,99	0.86	4 (4%)	105,111,111	1.02	6 (5%)
18	HEA	N	516	1	67,67,67	1.21	5 (7%)	81,103,103	1.29	6 (7%)

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
25	PEK	C	264	-	-	26/56/56/56	-
25	PEK	C	265	-	-	17/56/56/56	-
24	DMU	C	272	-	6/6/10/10	8/19/59/59	0/2/2/2
25	PEK	G	1263	-	-	29/56/56/56	-
18	HEA	A	516	1	-	7/36/76/76	-
25	PEK	P	1264	-	-	24/56/56/56	-
18	HEA	N	515	1	-	3/36/76/76	-
23	CHD	B	1086	-	-	2/9/74/74	0/4/4/4
26	CDL	P	1270	-	-	68/110/110/110	-
24	DMU	Z	1526	-	5/5/10/10	10/19/59/59	0/2/2/2
23	CHD	C	525	-	-	0/9/74/74	0/4/4/4
25	PEK	T	263	-	-	29/56/56/56	-
18	HEA	A	515	1	-	3/36/76/76	-
19	TGL	N	1521	-	-	14/65/65/65	-
19	TGL	A	523	-	-	13/65/65/65	-
23	CHD	C	271	-	5/5/12/12	8/9/74/74	0/4/4/4
20	PGV	A	604	-	-	13/55/55/55	-
23	CHD	J	60	-	5/5/12/12	8/9/74/74	0/4/4/4
24	DMU	P	1272	-	6/6/10/10	9/19/59/59	0/2/2/2
23	CHD	O	229	-	-	2/9/74/74	0/4/4/4
20	PGV	C	267	-	-	17/55/55/55	-
20	PGV	C	268	-	-	35/55/55/55	-
19	TGL	A	521	-	-	14/65/65/65	-
19	TGL	Y	1522	-	-	16/65/65/65	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CHD	P	1271	-	5/5/12/12	8/9/74/74	0/4/4/4
23	CHD	W	1060	-	5/5/12/12	8/9/74/74	0/4/4/4
26	CDL	G	269	-	-	60/110/110/110	-
24	DMU	M	526	-	5/5/10/10	10/19/59/59	0/2/2/2
20	PGV	P	1268	-	-	35/55/55/55	-
22	PSC	O	1230	-	-	39/55/55/55	-
19	TGL	Q	1523	-	-	14/65/65/65	-
26	CDL	T	1269	-	-	60/110/110/110	-
22	PSC	B	230	-	-	39/55/55/55	-
20	PGV	A	524	-	-	33/55/55/55	-
20	PGV	P	1267	-	-	16/55/55/55	-
25	PEK	P	1265	-	-	17/56/56/56	-
20	PGV	N	1266	-	-	13/55/55/55	-
19	TGL	L	522	-	-	16/65/65/65	-
20	PGV	N	1524	-	-	33/55/55/55	-
23	CHD	P	1525	-	-	0/9/74/74	0/4/4/4
26	CDL	C	270	-	-	67/110/110/110	-
18	HEA	N	516	1	-	7/36/76/76	-

The worst 5 of 182 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	M	526	DMU	O7-C3	-8.53	1.22	1.43
24	Z	1526	DMU	O7-C3	-8.08	1.23	1.43
24	M	526	DMU	O16-C6	-7.91	1.27	1.40
24	Z	1526	DMU	O16-C6	-7.74	1.27	1.40
24	M	526	DMU	O5-C4	-6.81	1.27	1.44

The worst 5 of 396 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	C	272	DMU	O16-C6-C1	11.70	126.04	108.27
24	M	526	DMU	C10-C5-C7	10.24	131.56	110.01
24	Z	1526	DMU	C10-C5-C7	10.10	131.26	110.01
23	C	271	CHD	C17-C13-C14	9.86	110.00	100.11
23	W	1060	CHD	C17-C13-C14	9.84	109.98	100.11

5 of 42 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	C	271	CHD	C8
23	C	271	CHD	C12
23	C	271	CHD	C9
23	C	271	CHD	C14
23	C	271	CHD	C3

5 of 850 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
20	A	524	PGV	C04-O12-P-O11
20	A	524	PGV	C04-O12-P-O13
20	A	524	PGV	C04-O12-P-O14
20	A	524	PGV	C02-C03-O11-P
20	A	524	PGV	C05-C04-O12-P

There are no ring outliers.

38 monomers are involved in 274 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	C	264	PEK	4	0
25	C	265	PEK	7	0
24	C	272	DMU	2	0
25	G	1263	PEK	10	0
18	A	516	HEA	1	0
25	P	1264	PEK	5	0
18	N	515	HEA	2	0
23	B	1086	CHD	1	0
26	P	1270	CDL	18	0
25	T	263	PEK	9	0
20	A	604	PGV	1	0
19	N	1521	TGL	8	0
19	A	523	TGL	6	0
18	A	515	HEA	2	0
23	C	271	CHD	7	0
23	J	60	CHD	3	0
24	P	1272	DMU	8	0
23	O	229	CHD	1	0
20	C	267	PGV	6	0
20	C	268	PGV	2	0
19	A	521	TGL	10	0
19	Y	1522	TGL	18	0
23	P	1271	CHD	1	0
23	W	1060	CHD	5	0

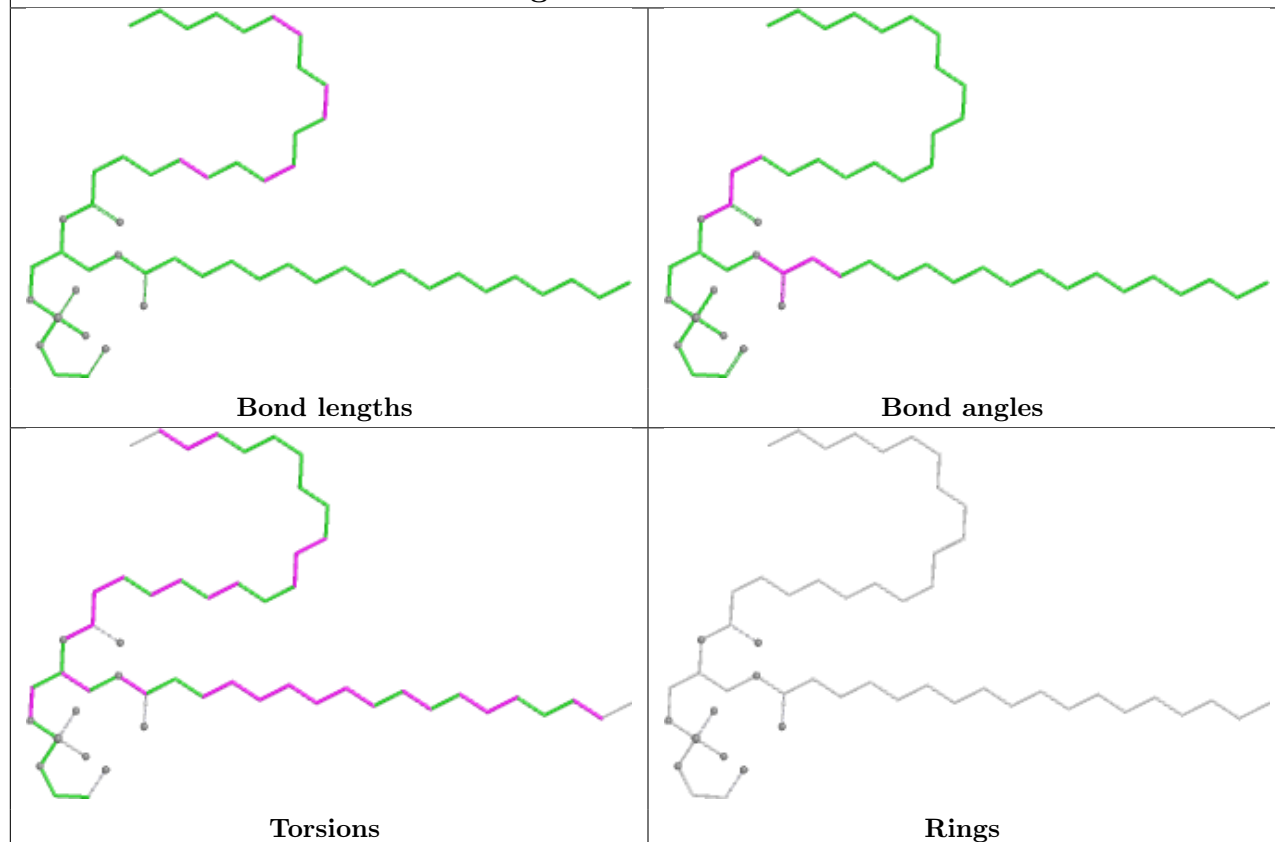
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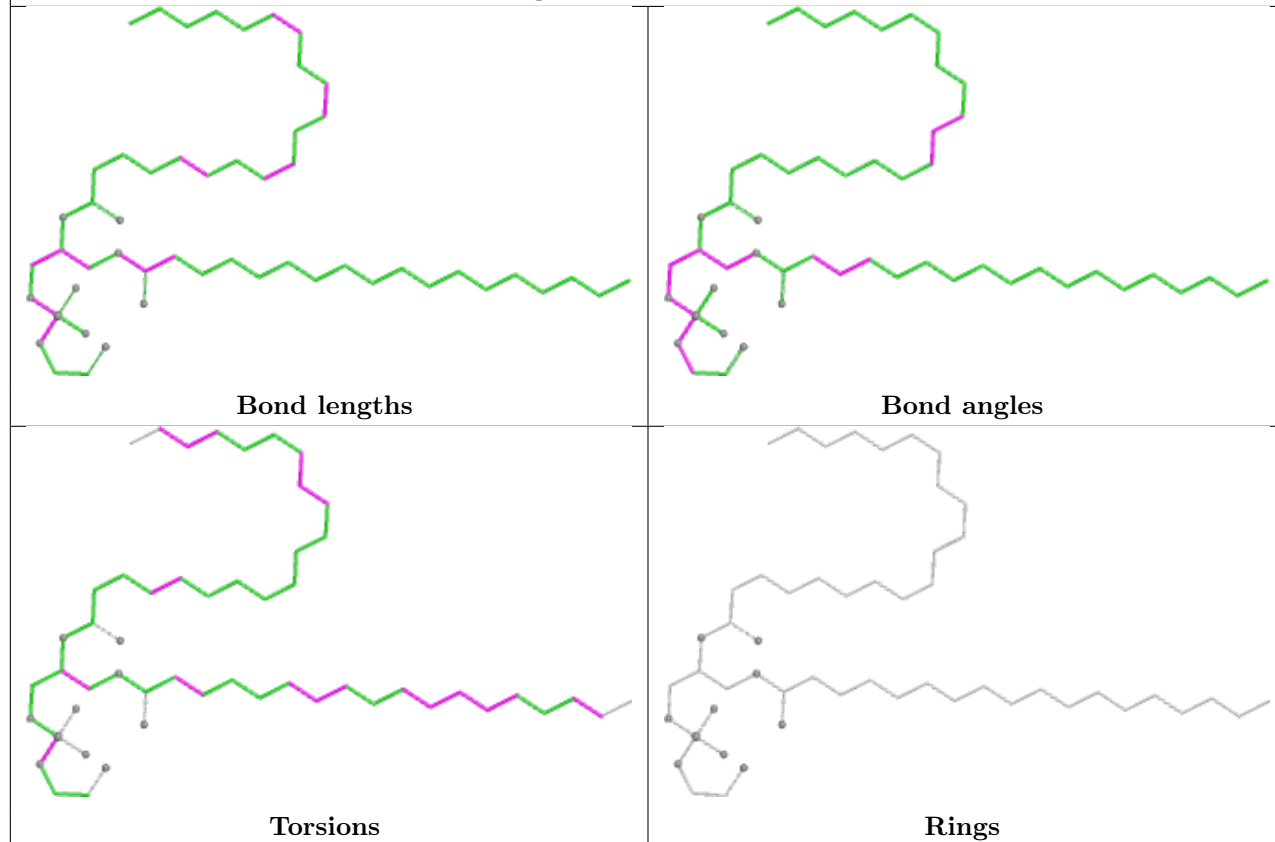
Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	G	269	CDL	21	0
20	P	1268	PGV	2	0
22	O	1230	PSC	15	0
19	Q	1523	TGL	7	0
26	T	1269	CDL	19	0
22	B	230	PSC	14	0
20	A	524	PGV	8	0
20	P	1267	PGV	5	0
25	P	1265	PEK	7	0
20	N	1266	PGV	1	0
19	L	522	TGL	23	0
20	N	1524	PGV	9	0
26	C	270	CDL	17	0
18	N	516	HEA	1	0

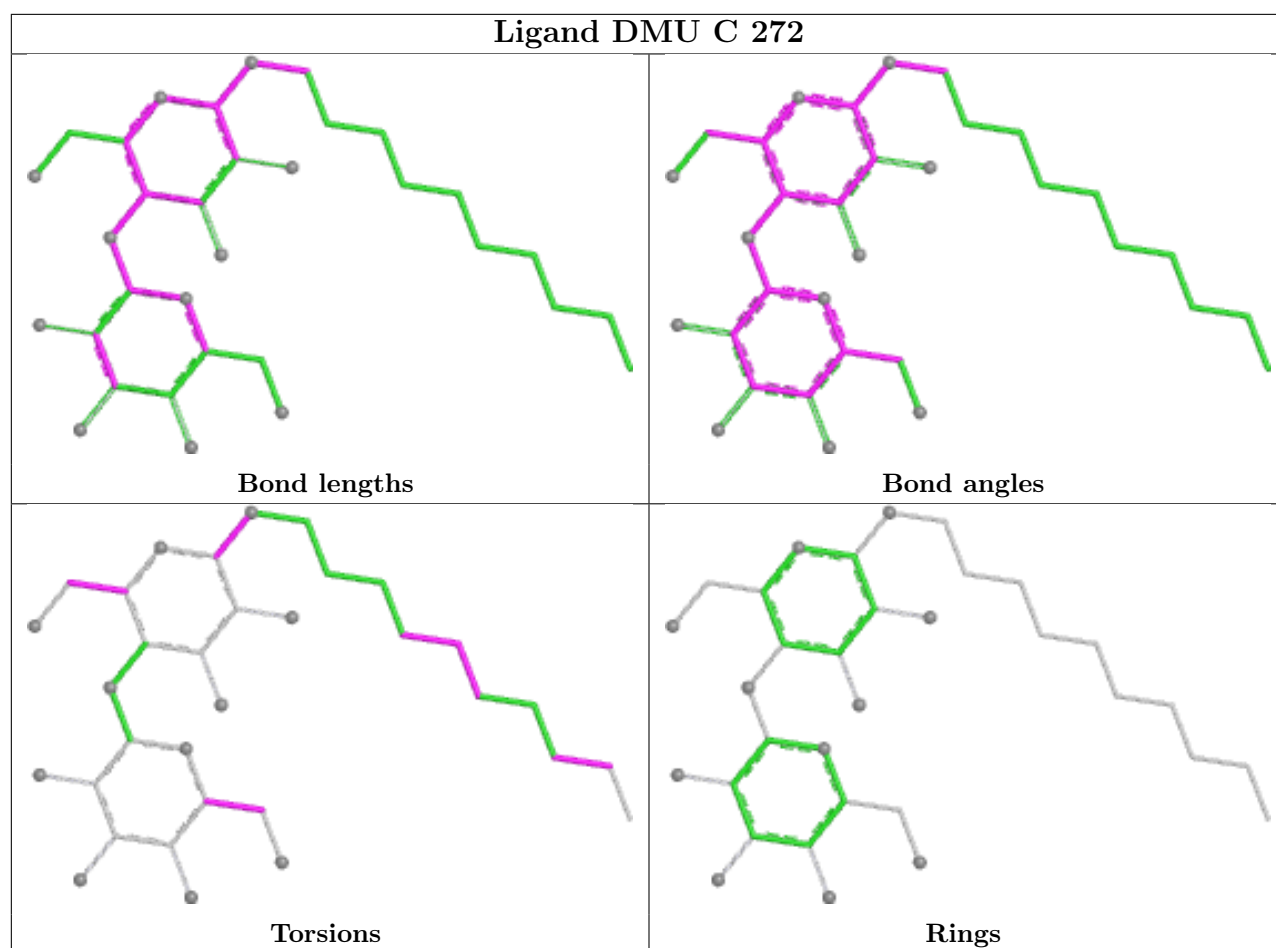
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

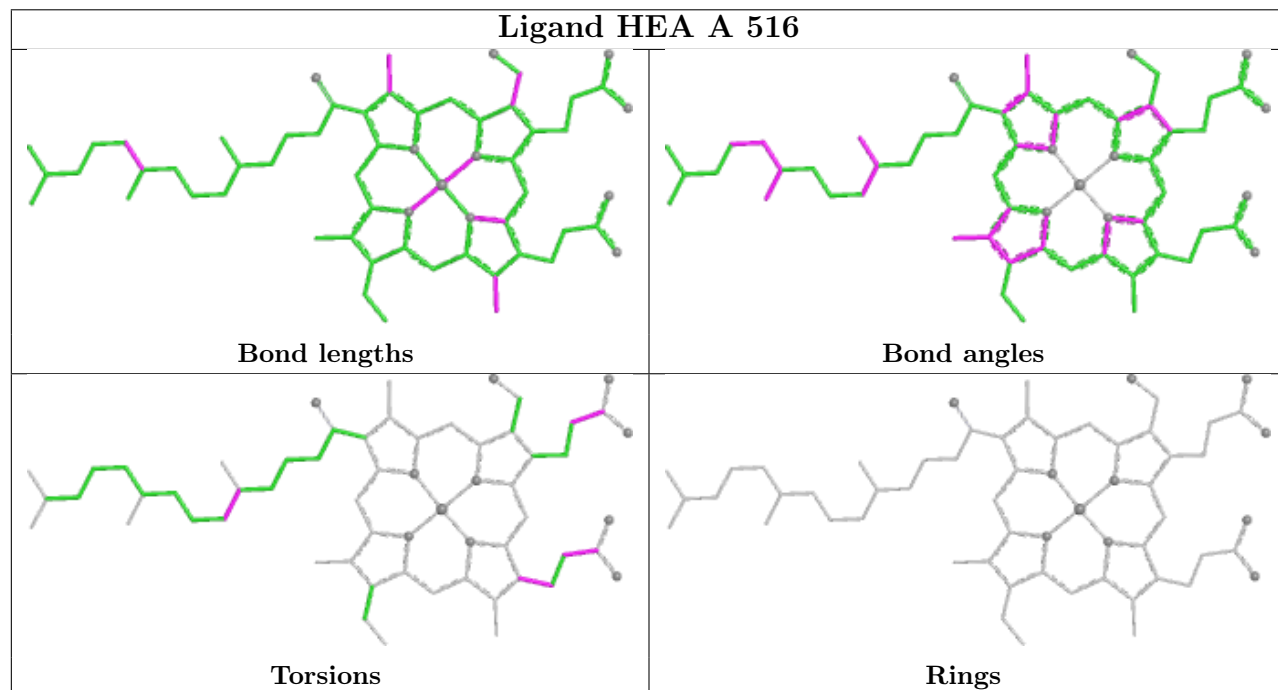
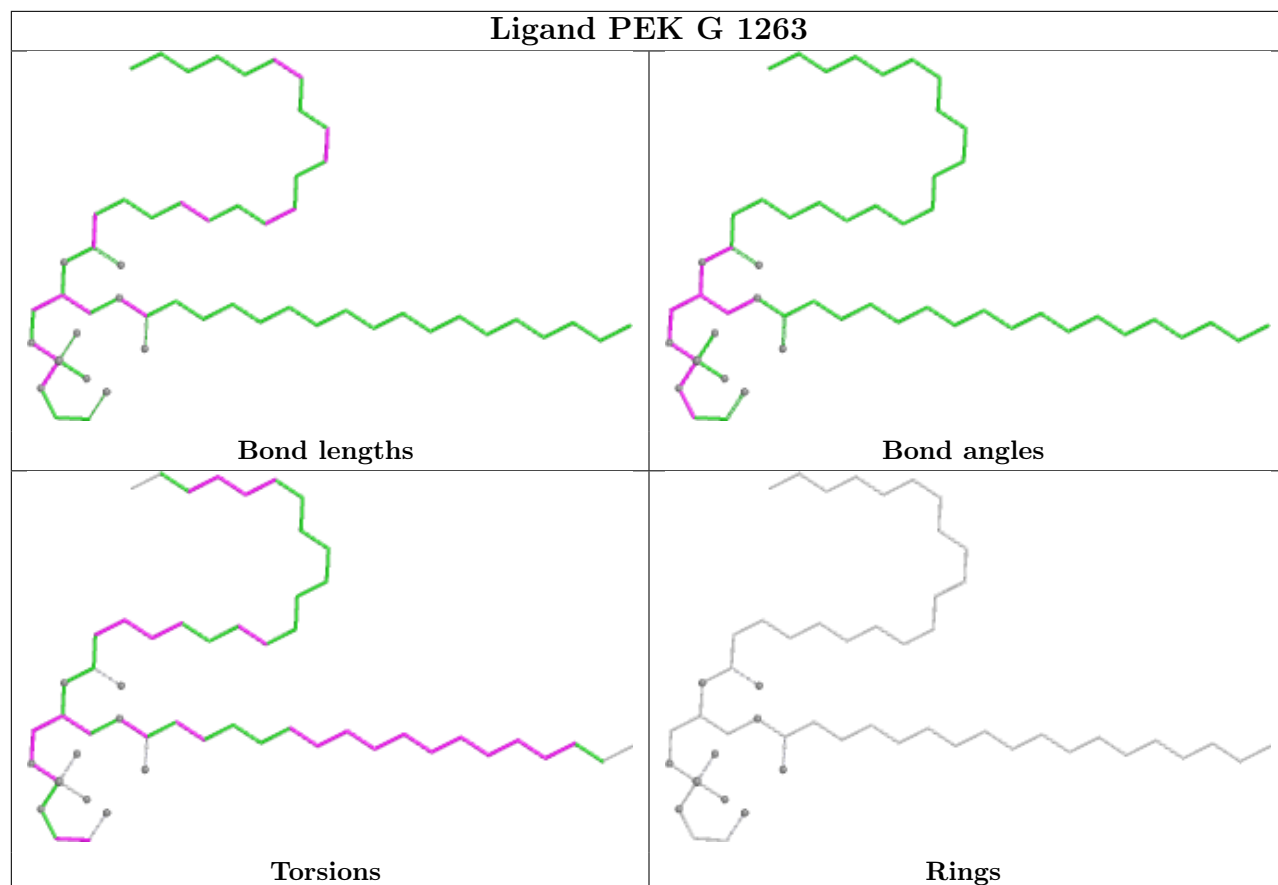
Ligand PEK C 264

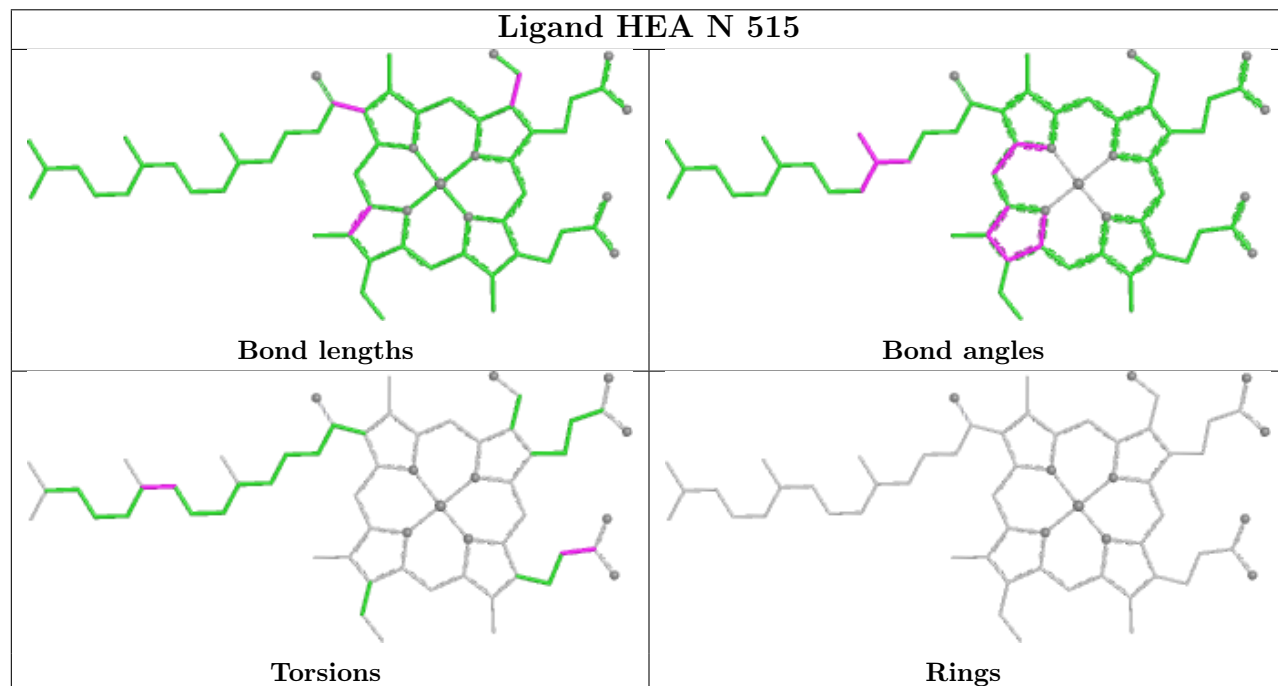
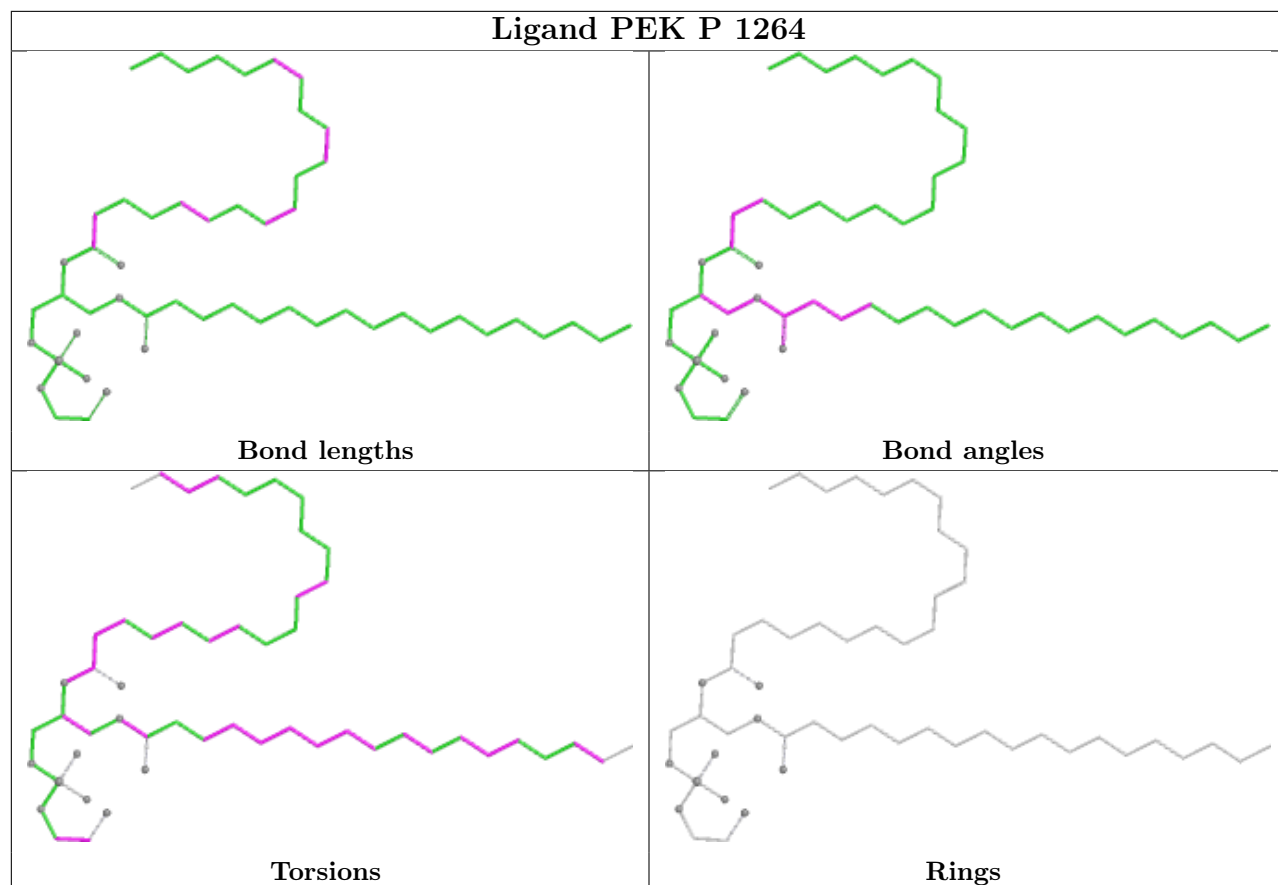


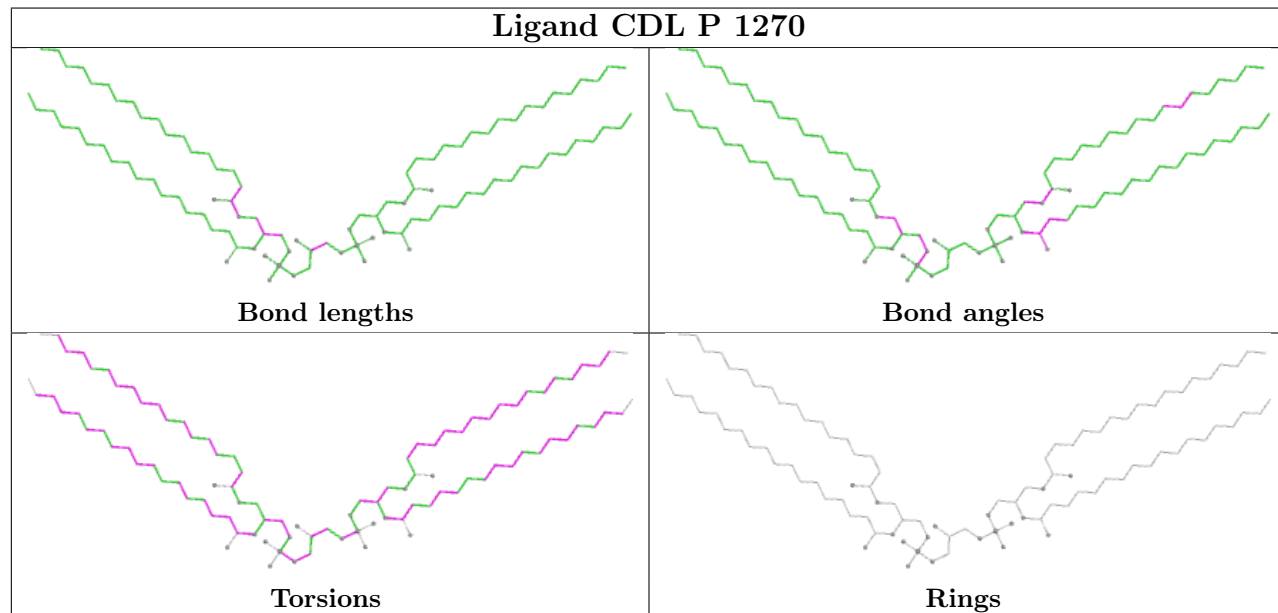
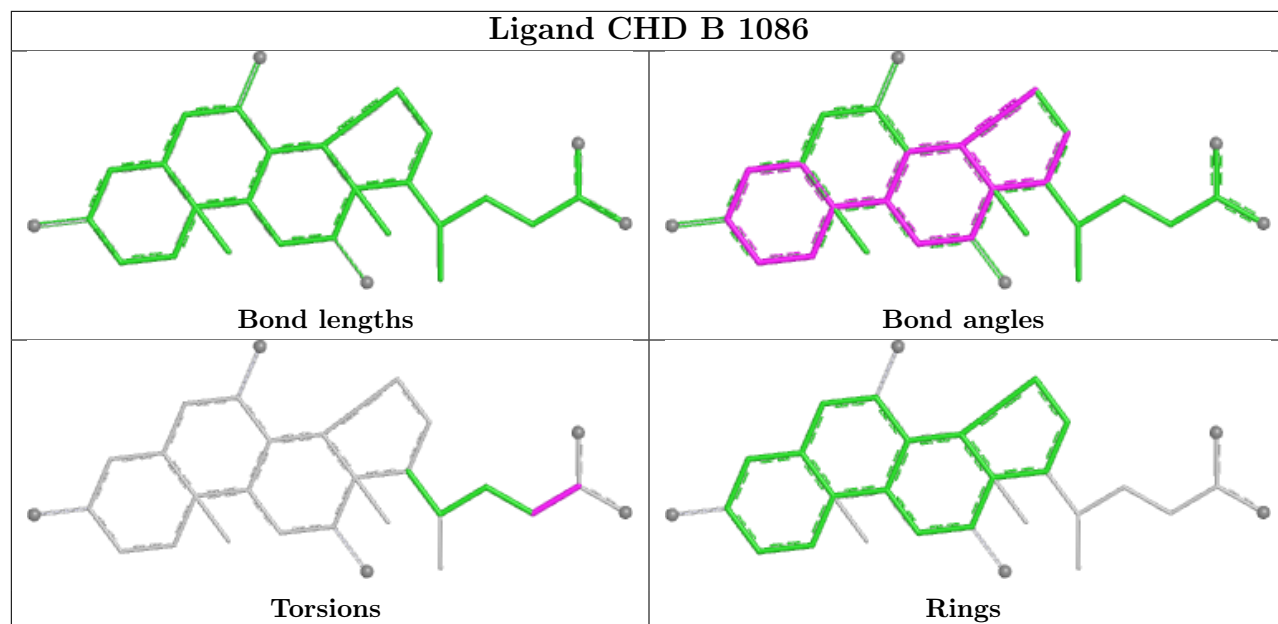
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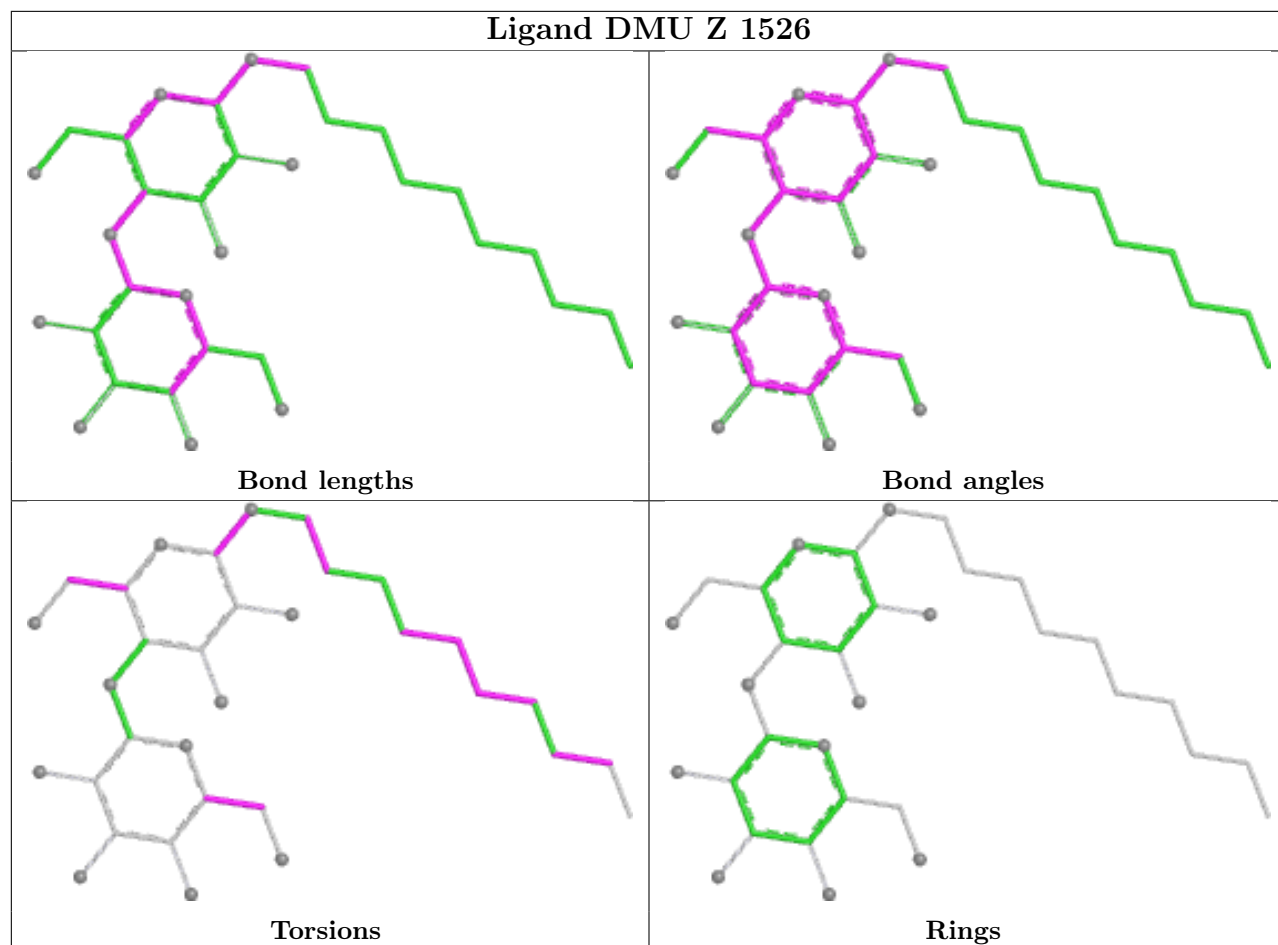




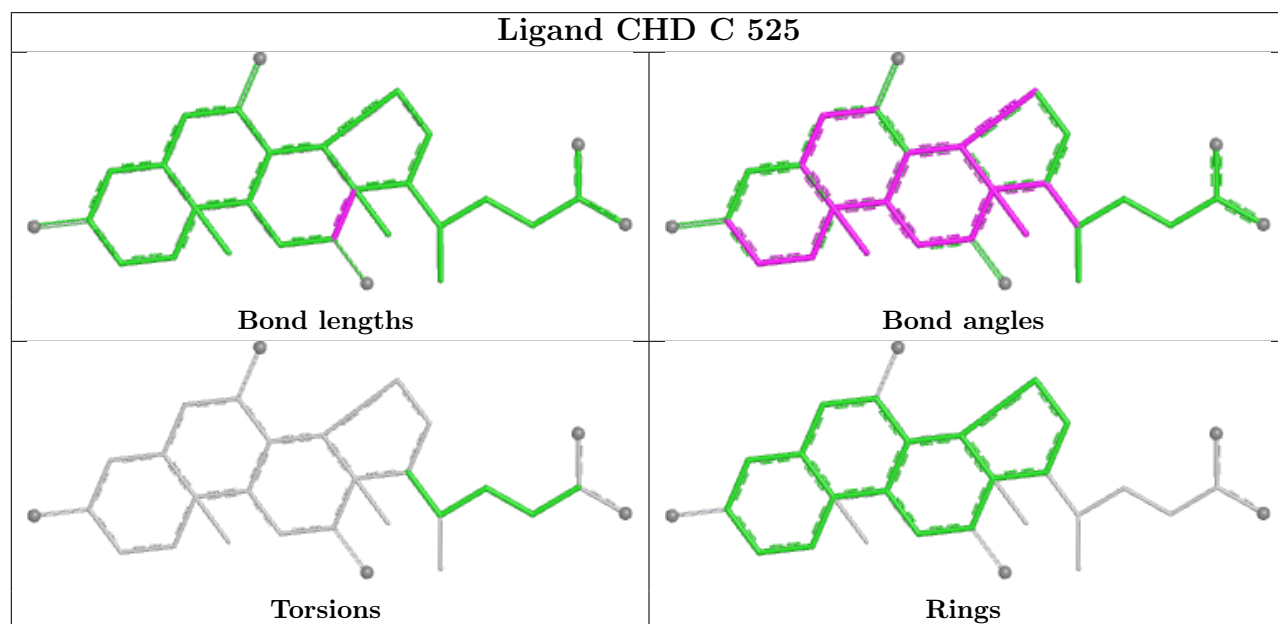


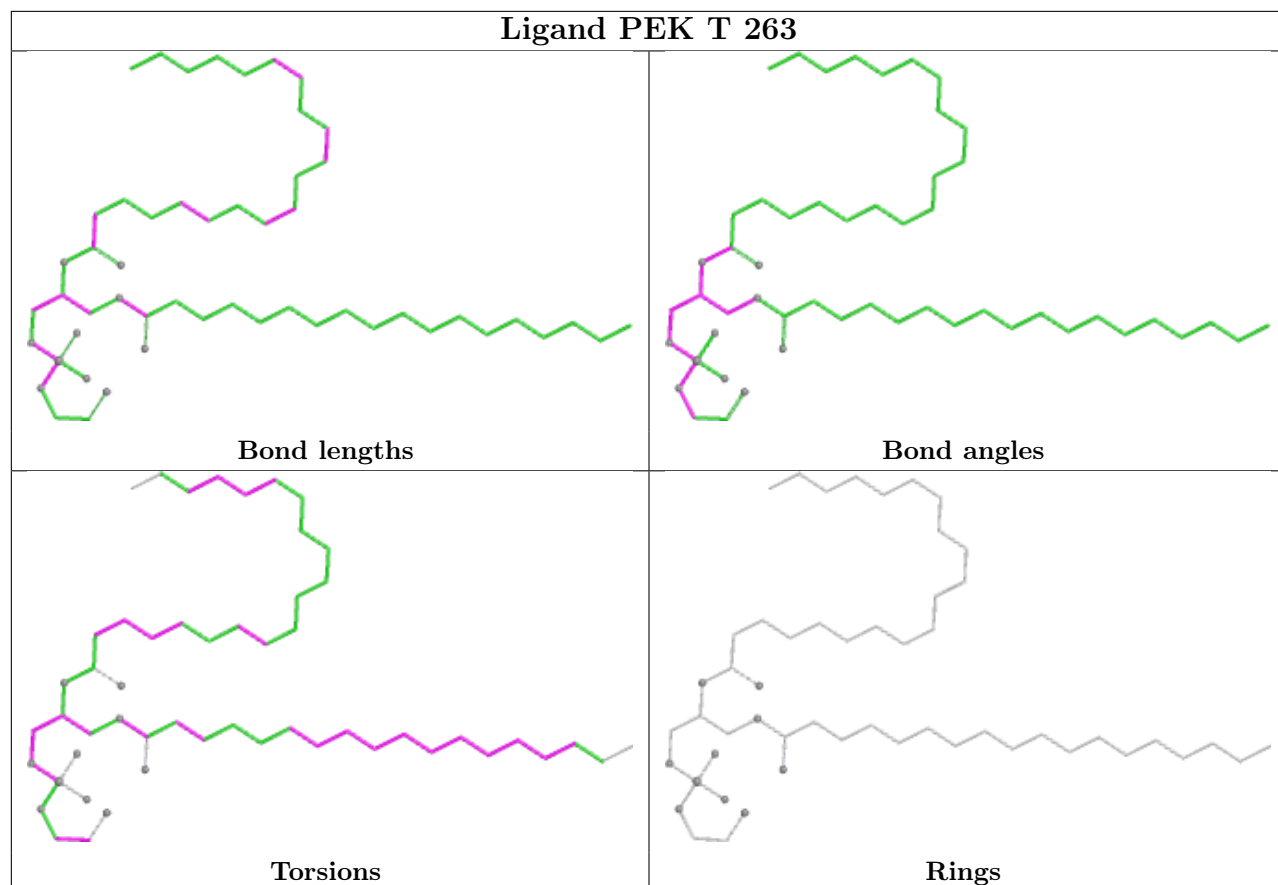
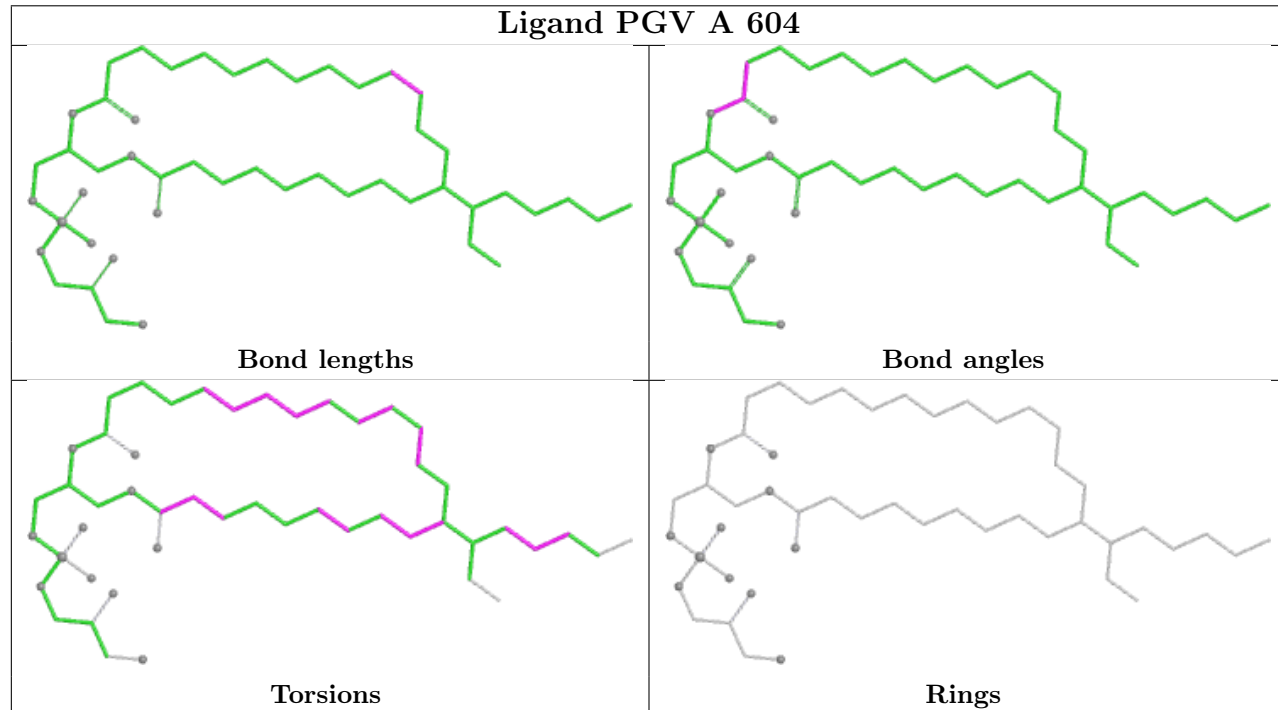


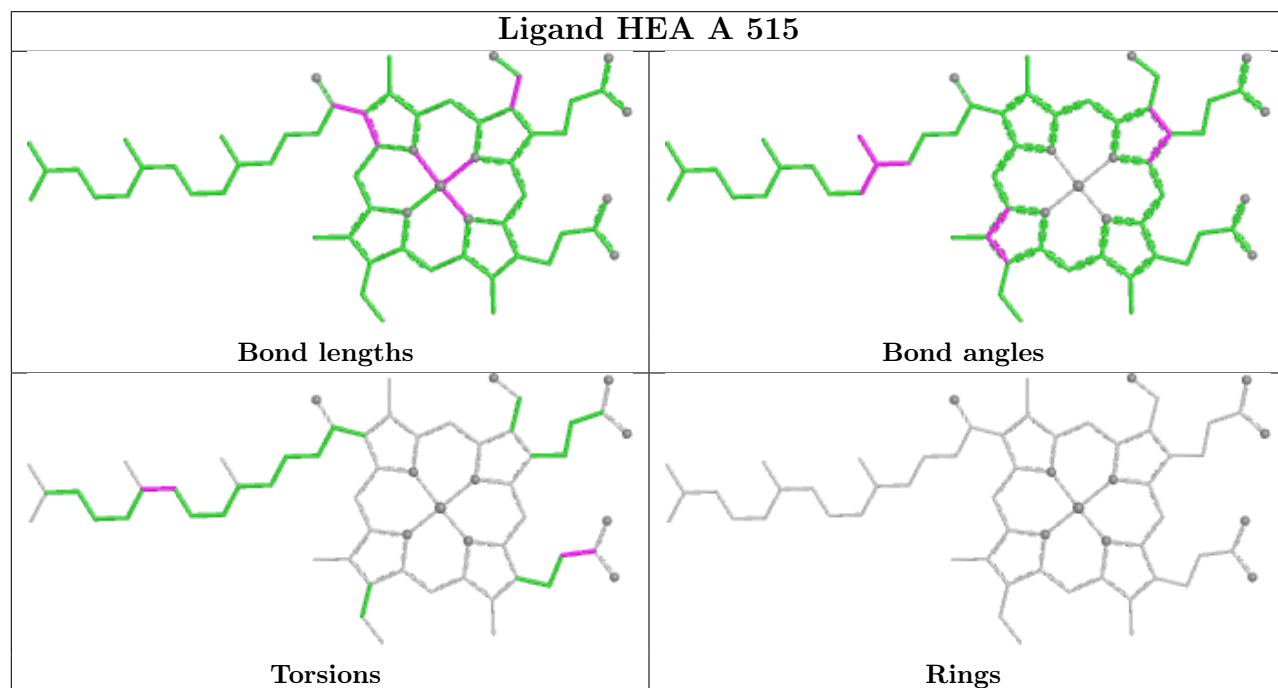
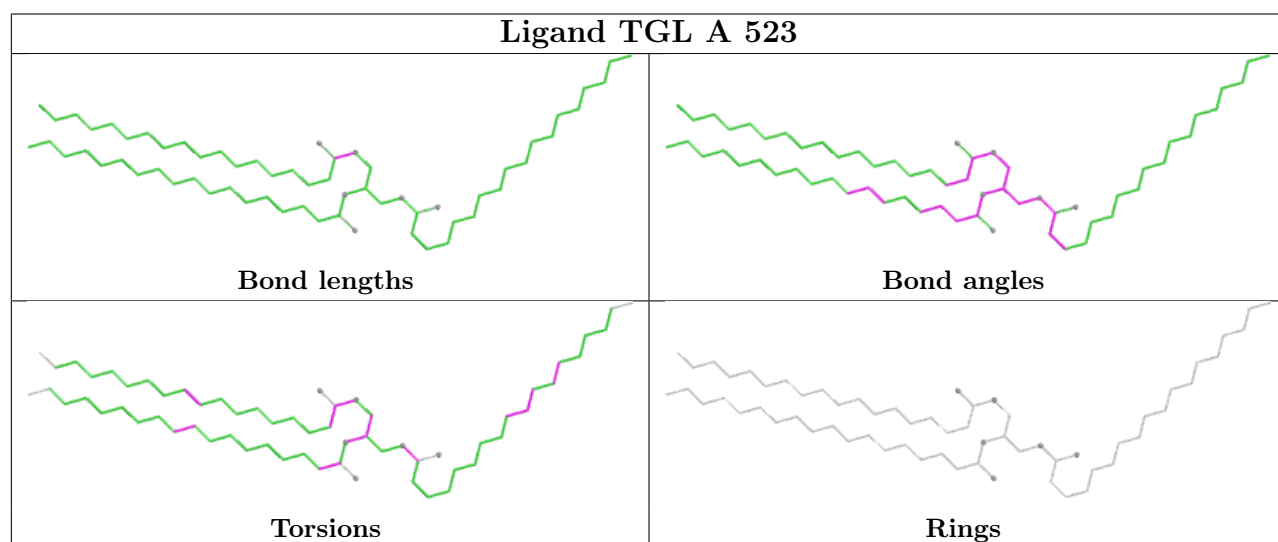
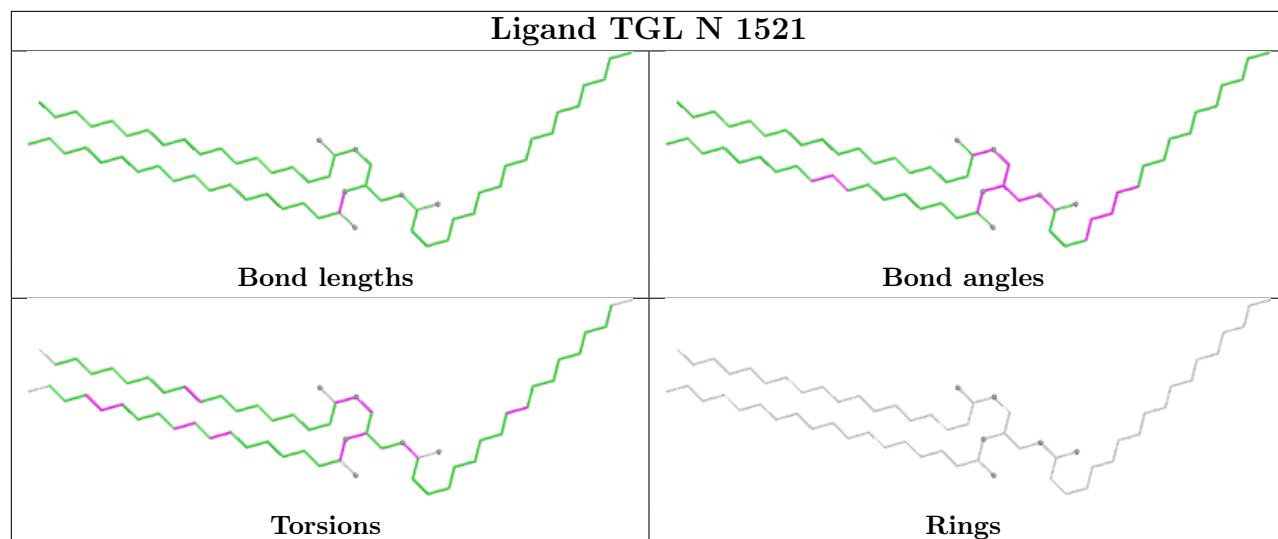
Ligand DMU Z 1526

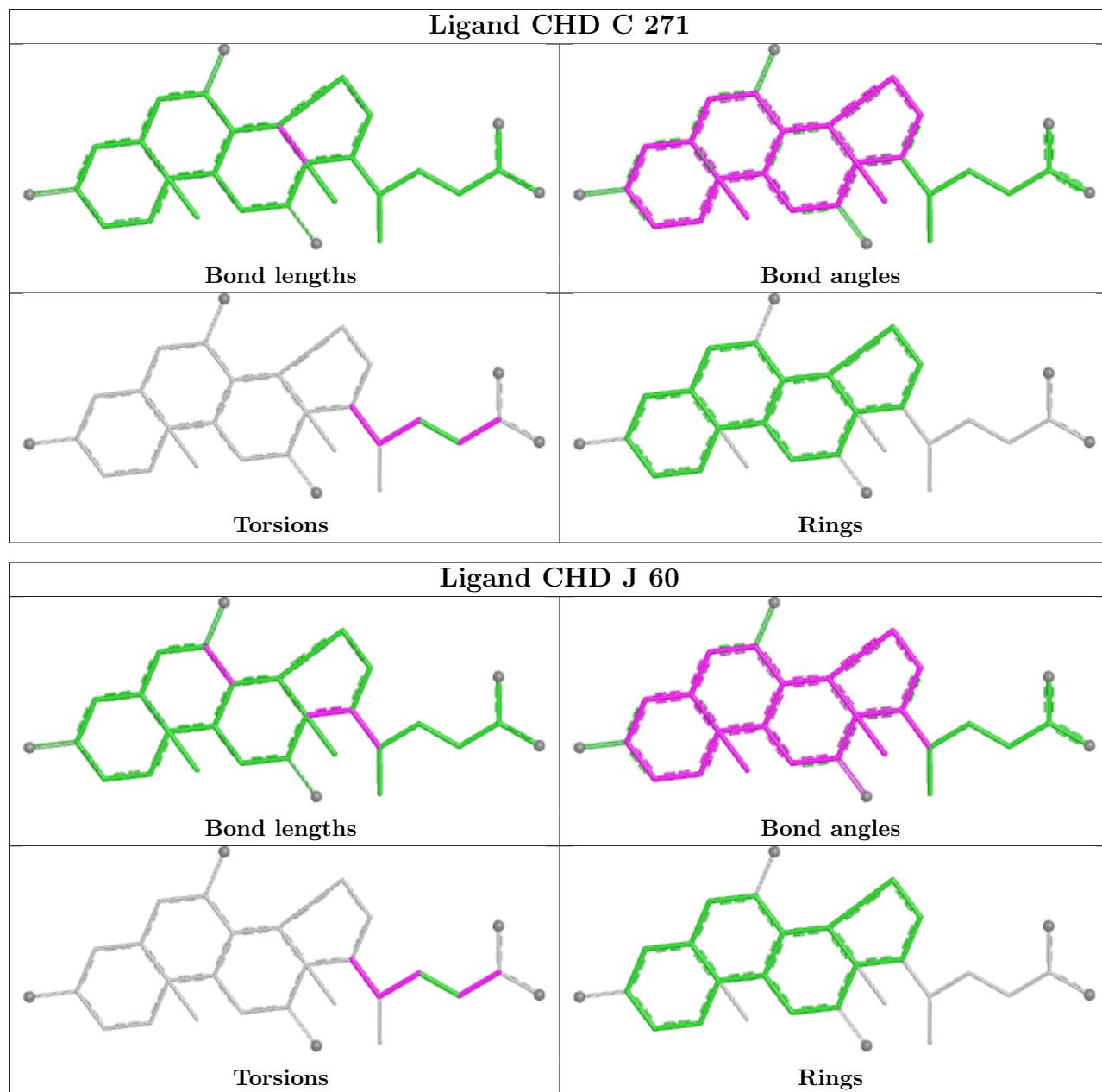


Ligand CHD C 525

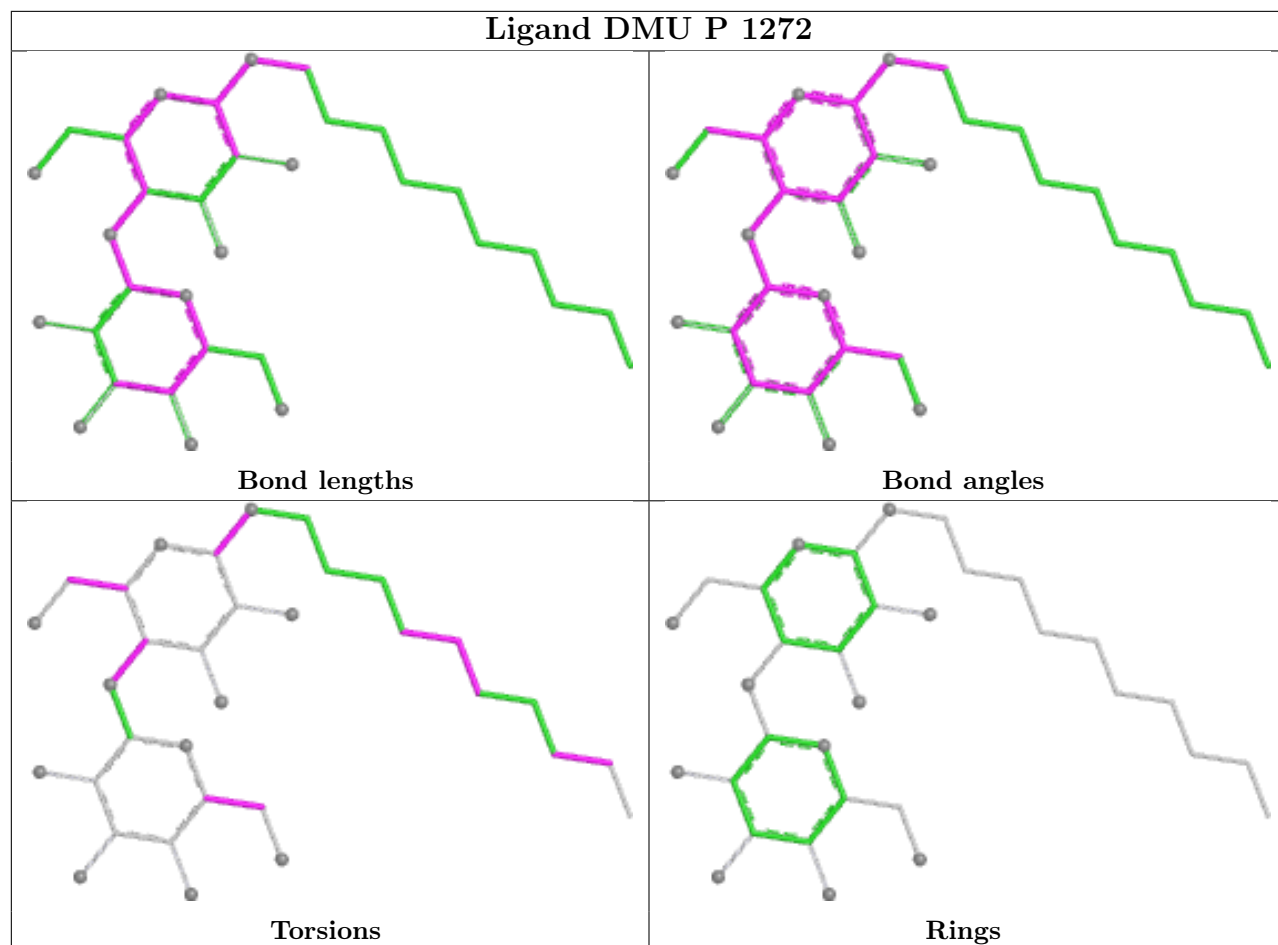


Ligand PEK T 263**Ligand PGV A 604**

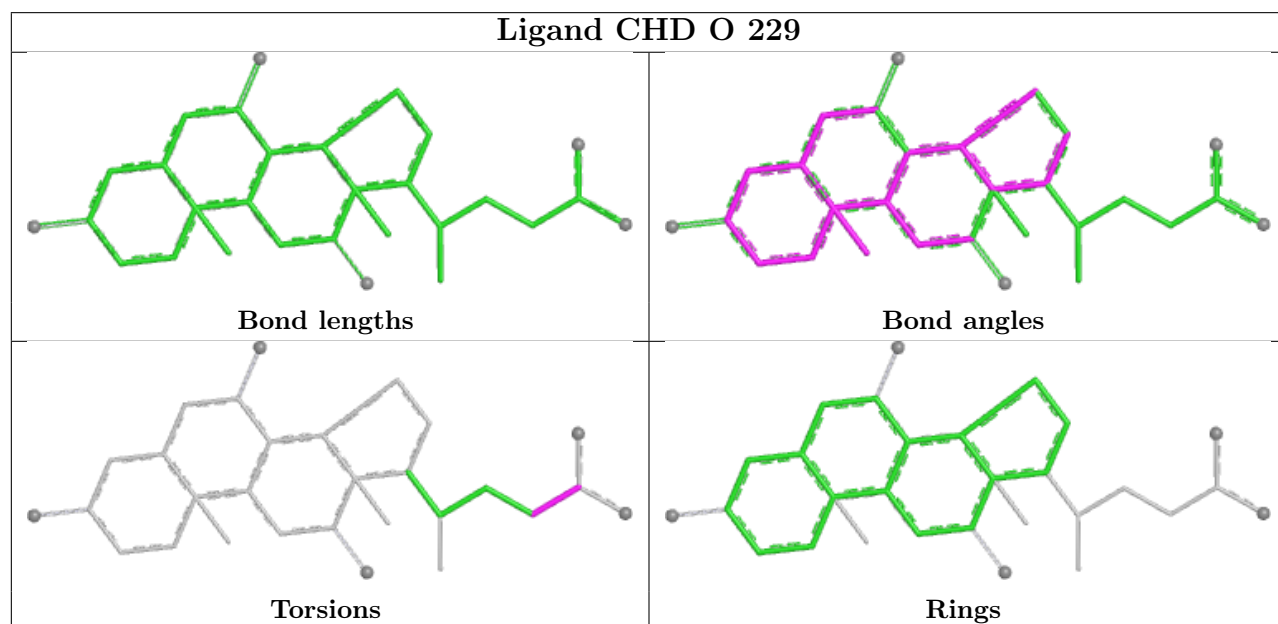


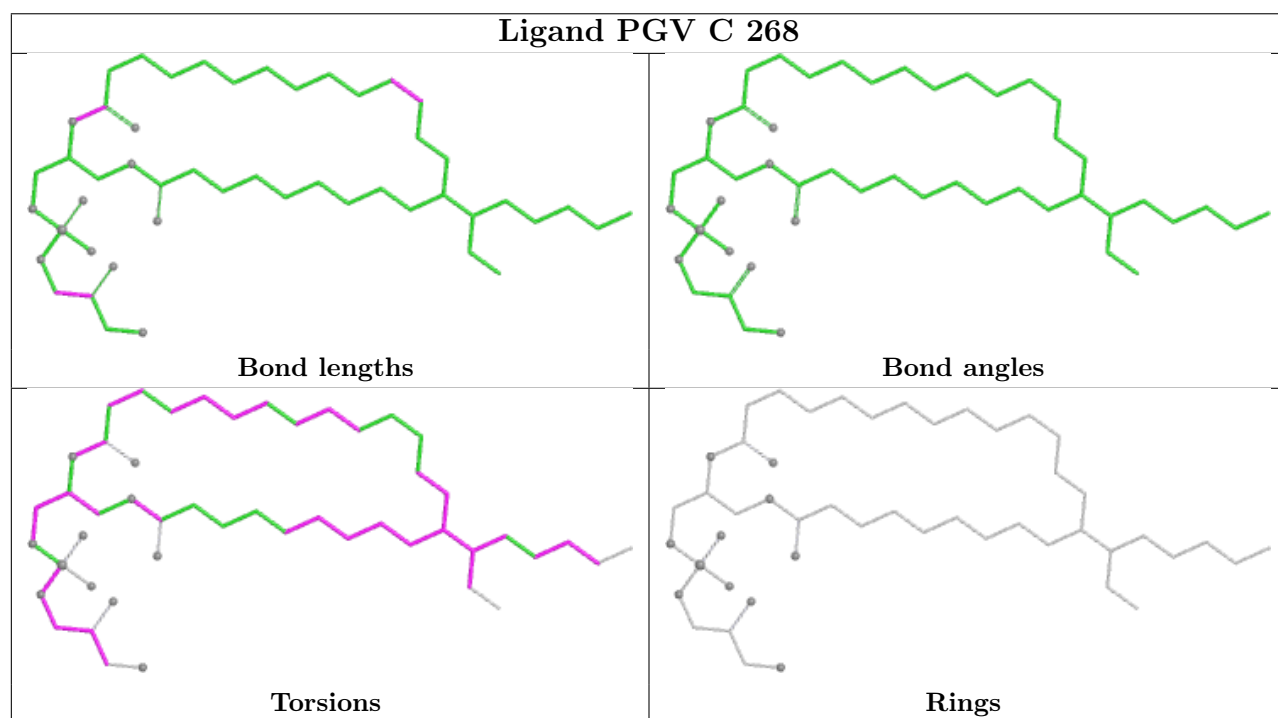
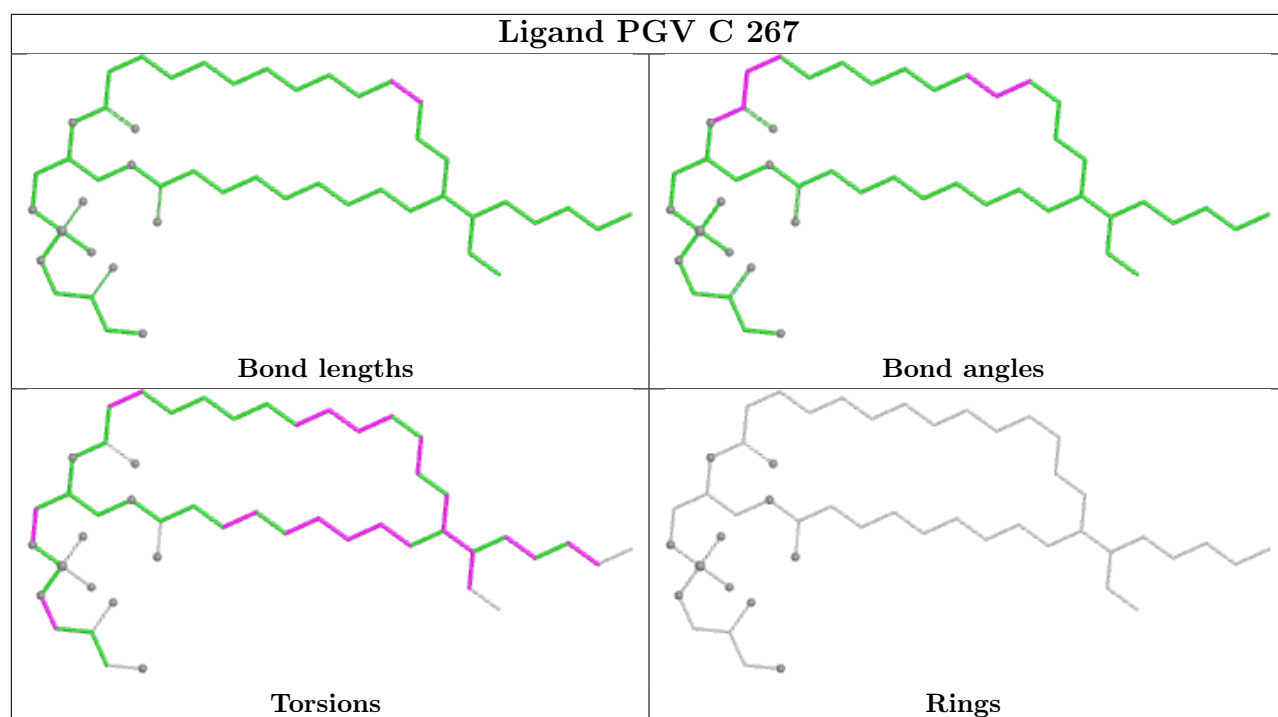


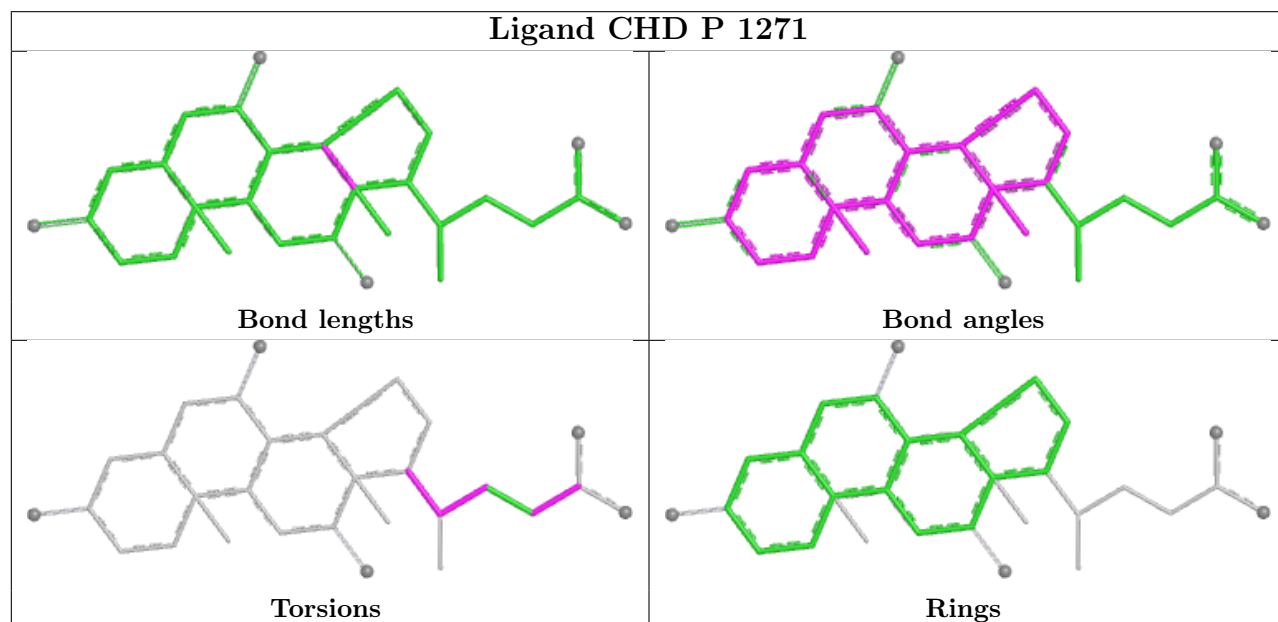
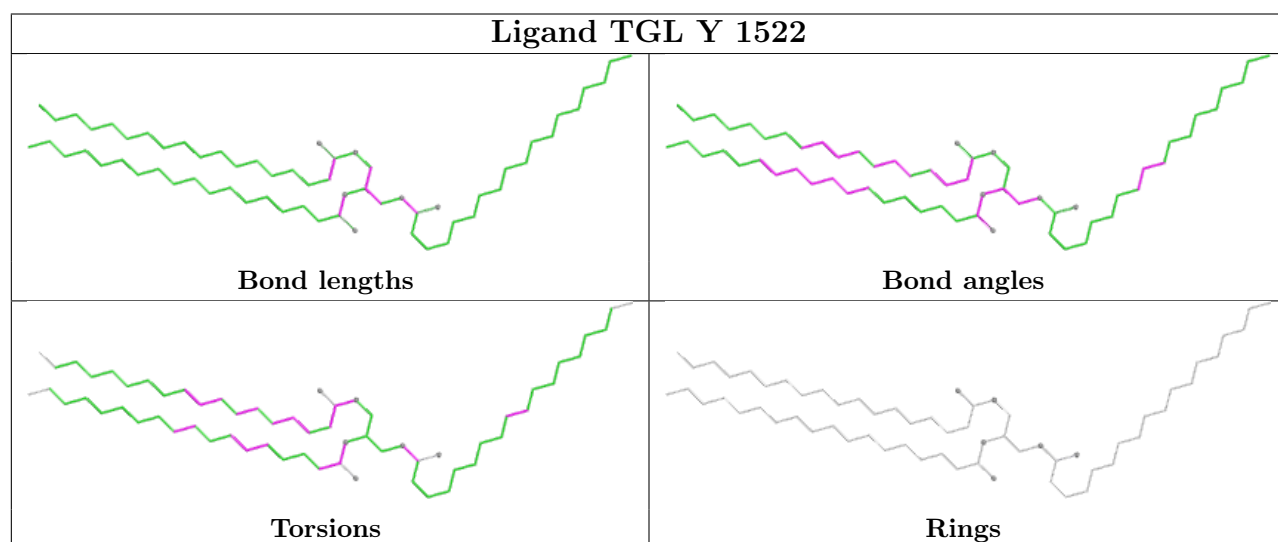
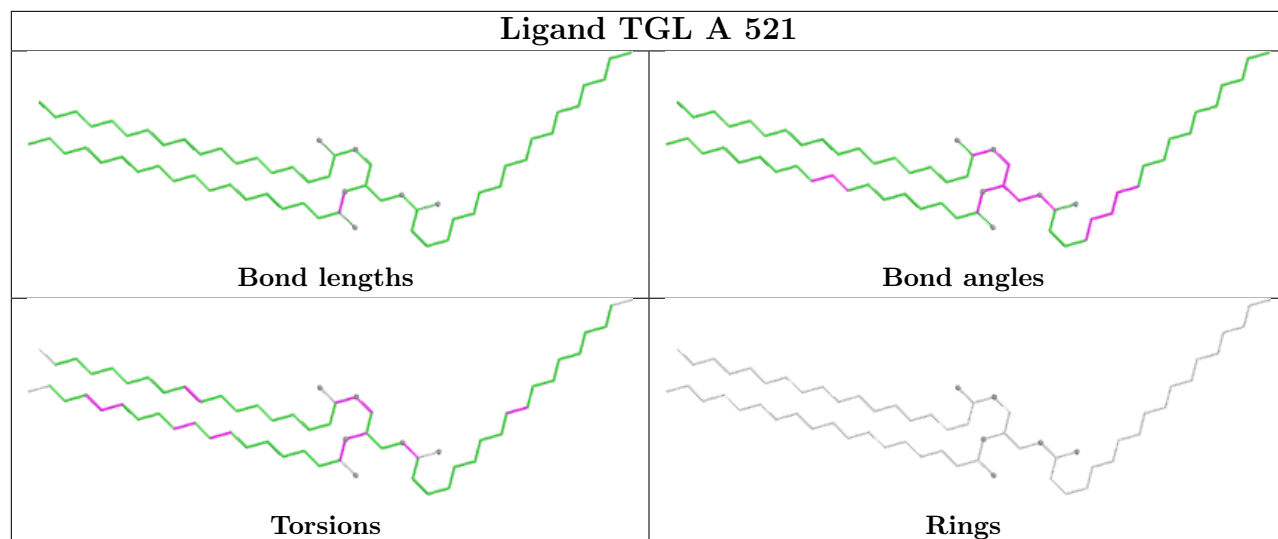
Ligand DMU P 1272



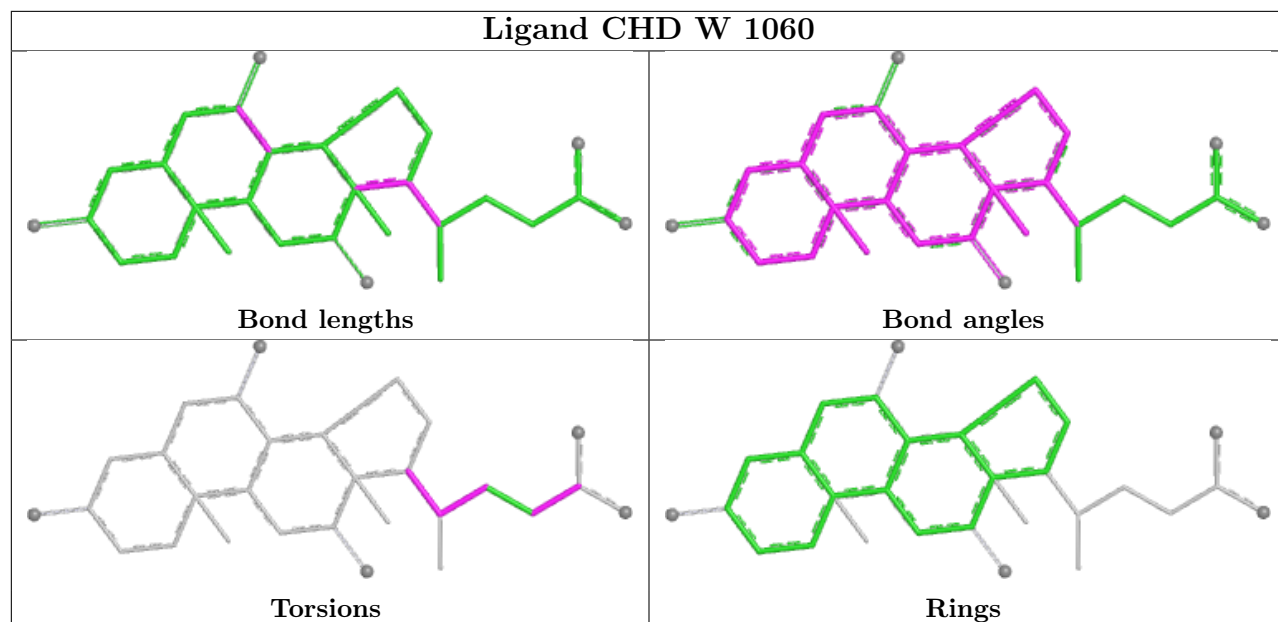
Ligand CHD O 229



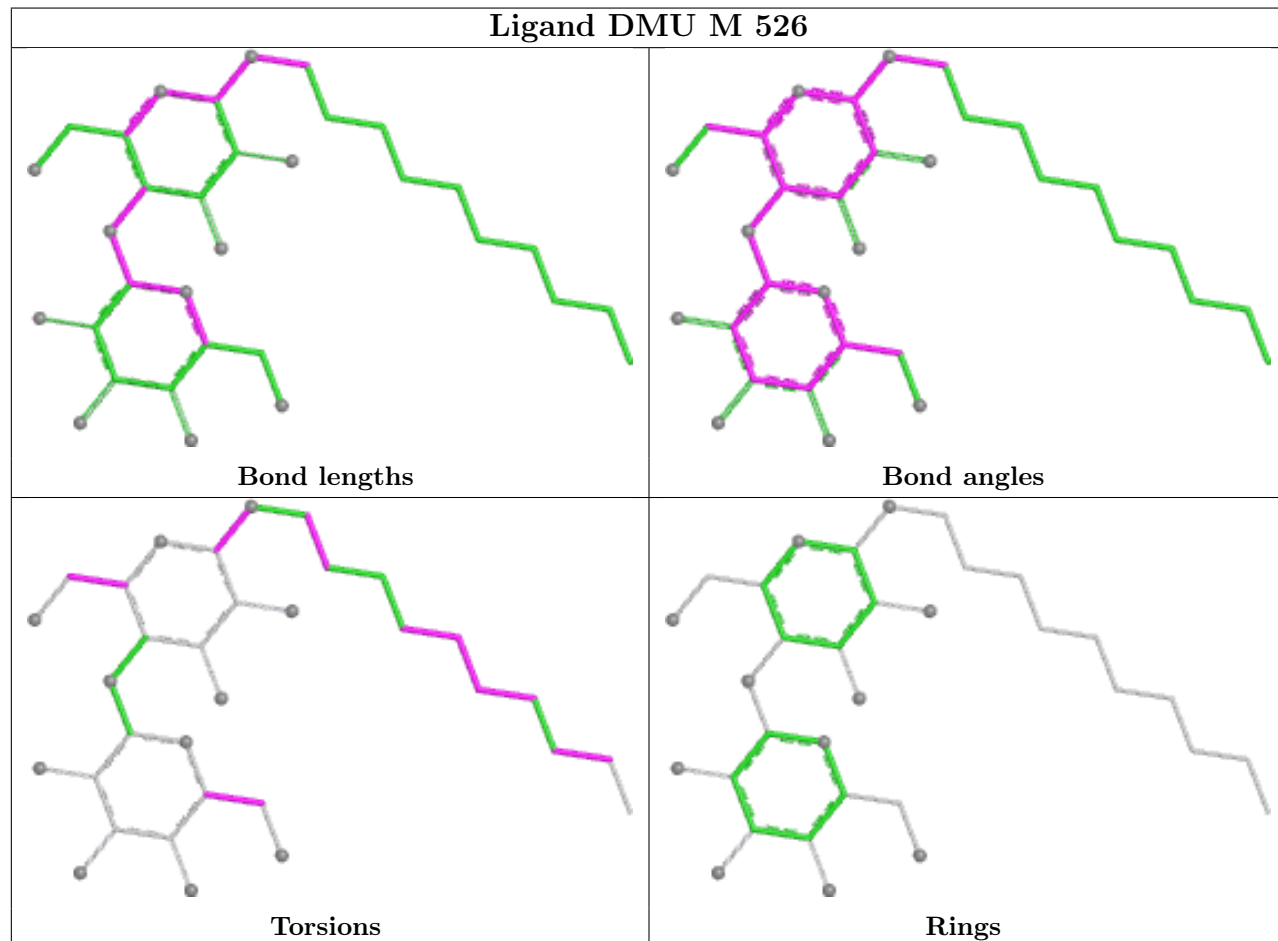


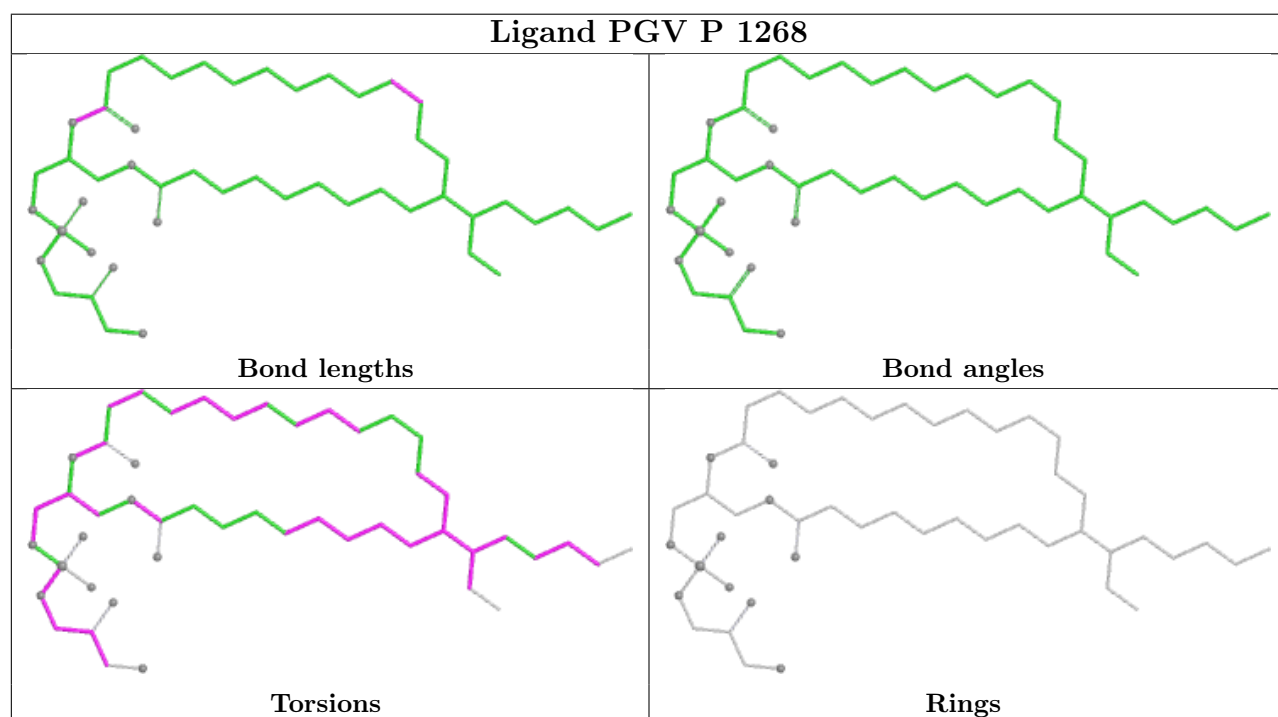
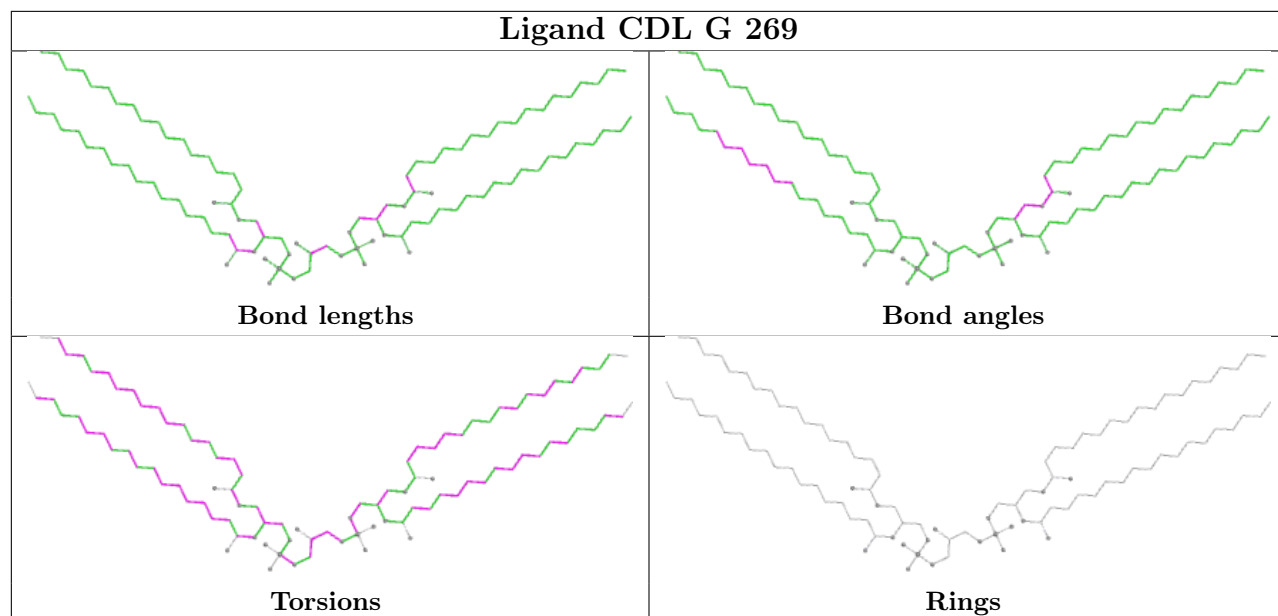


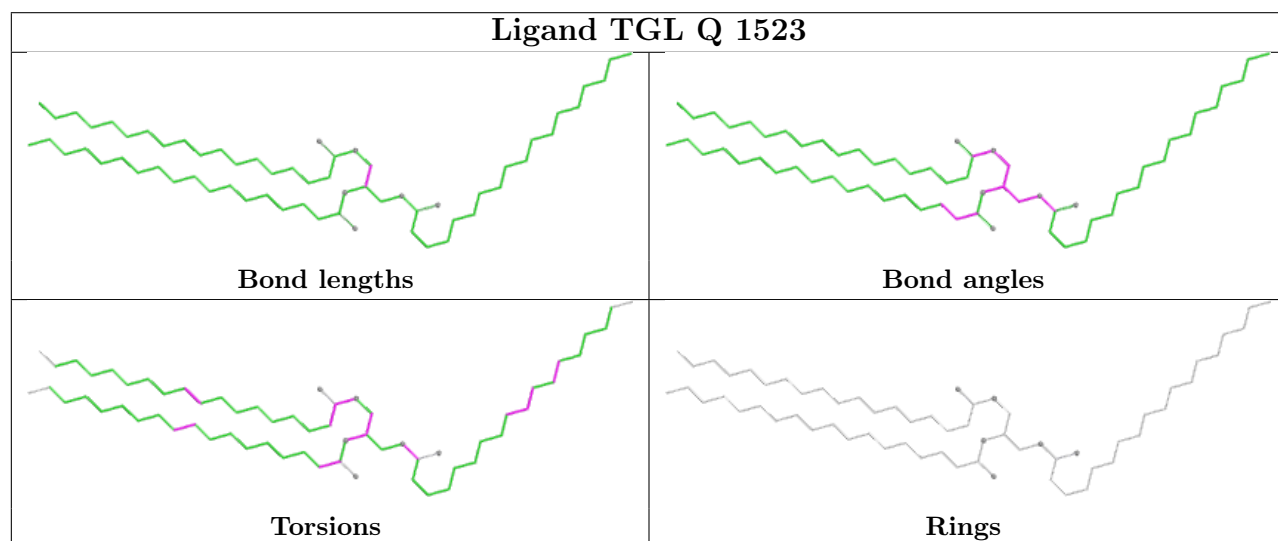
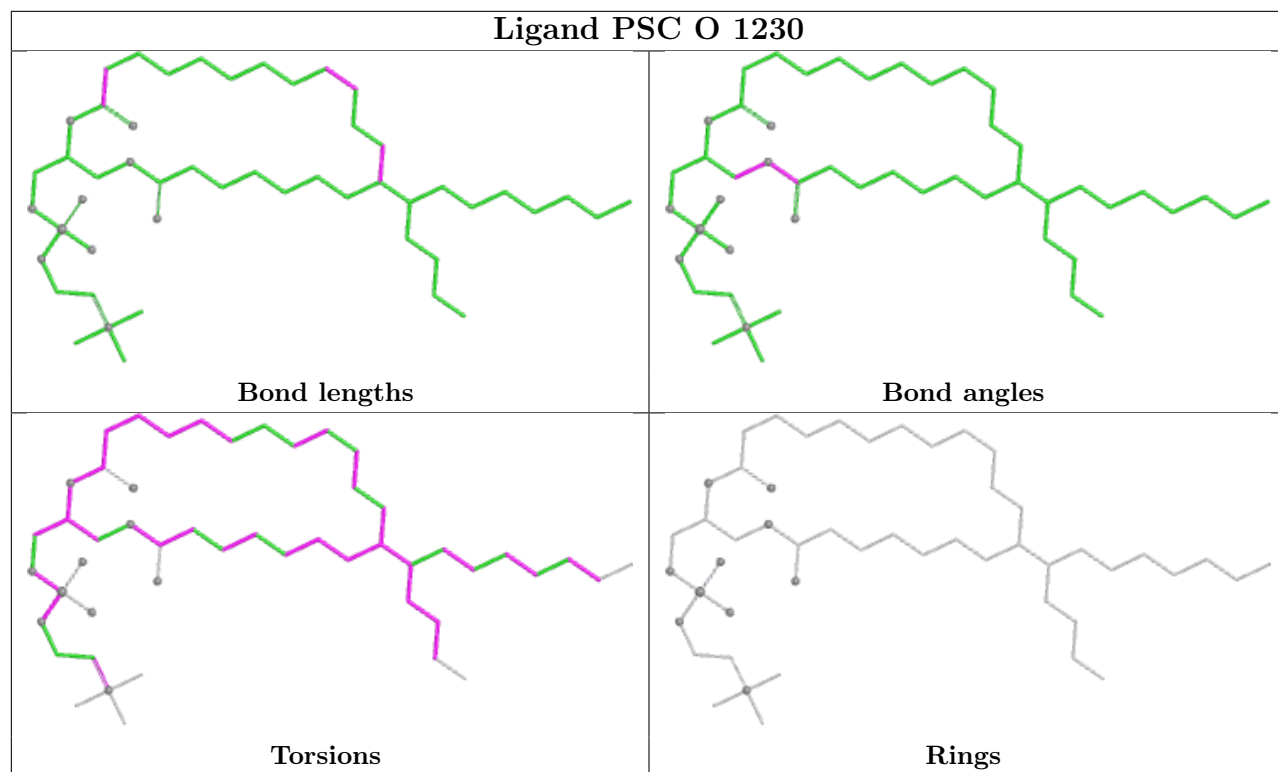
Ligand CHD W 1060

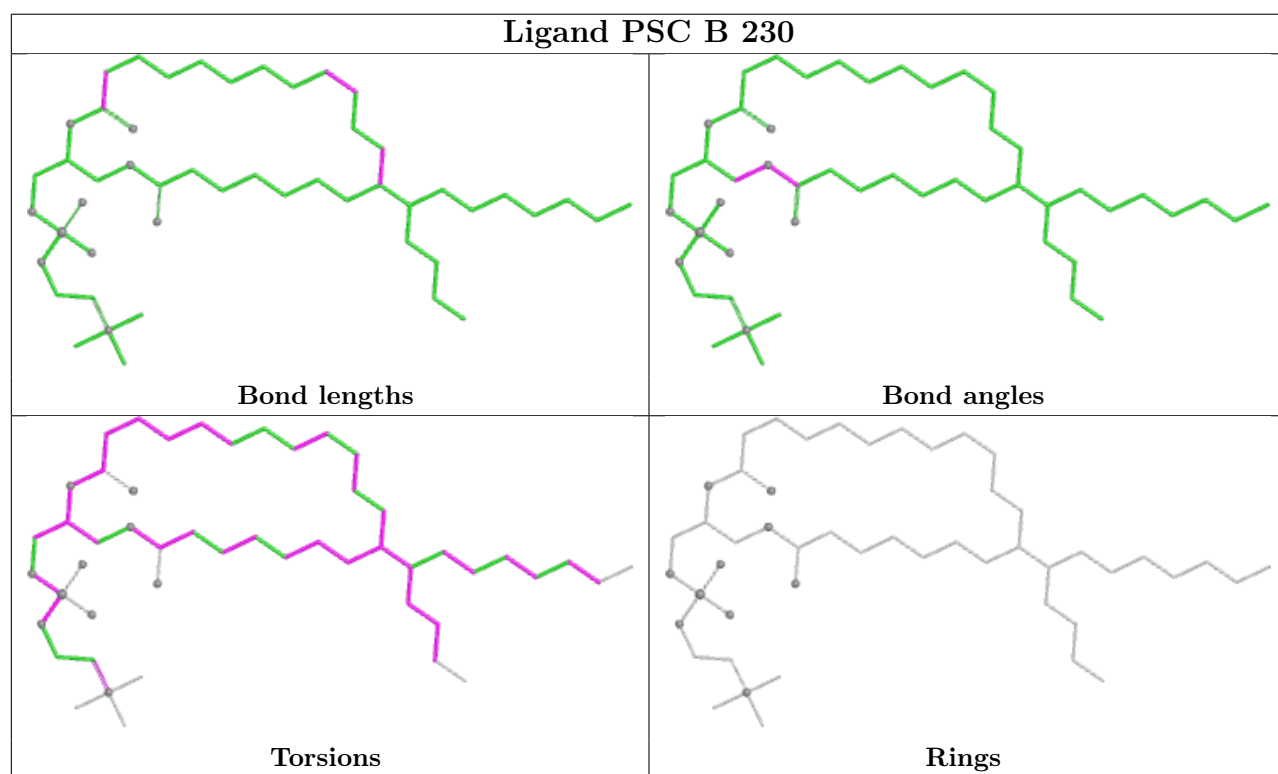
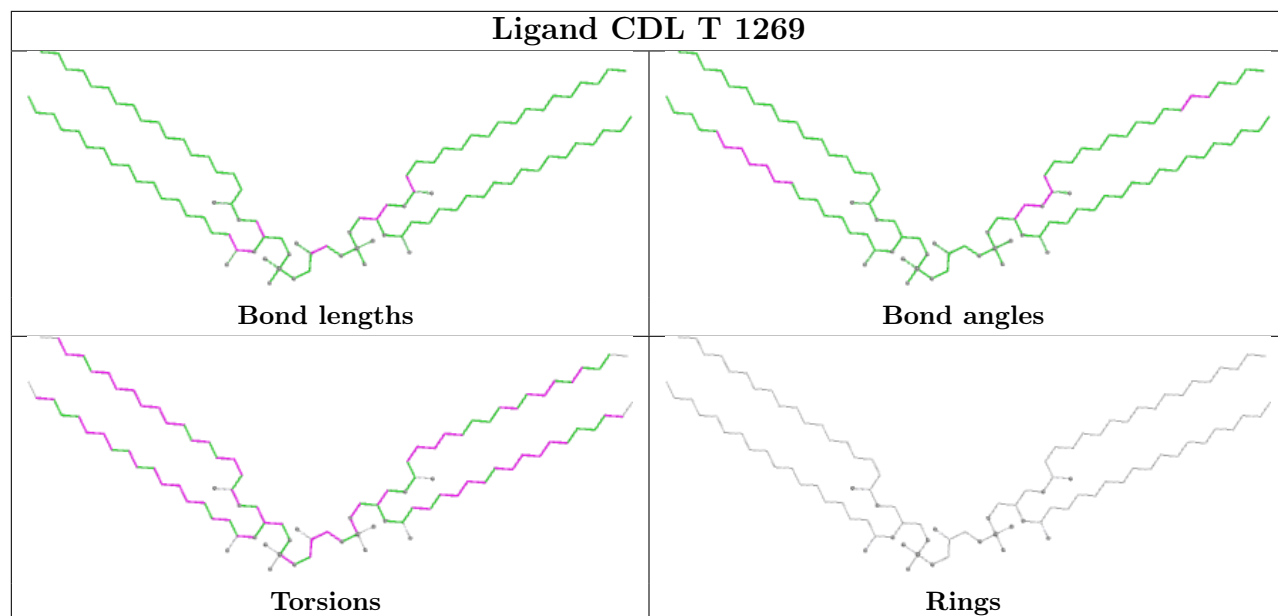


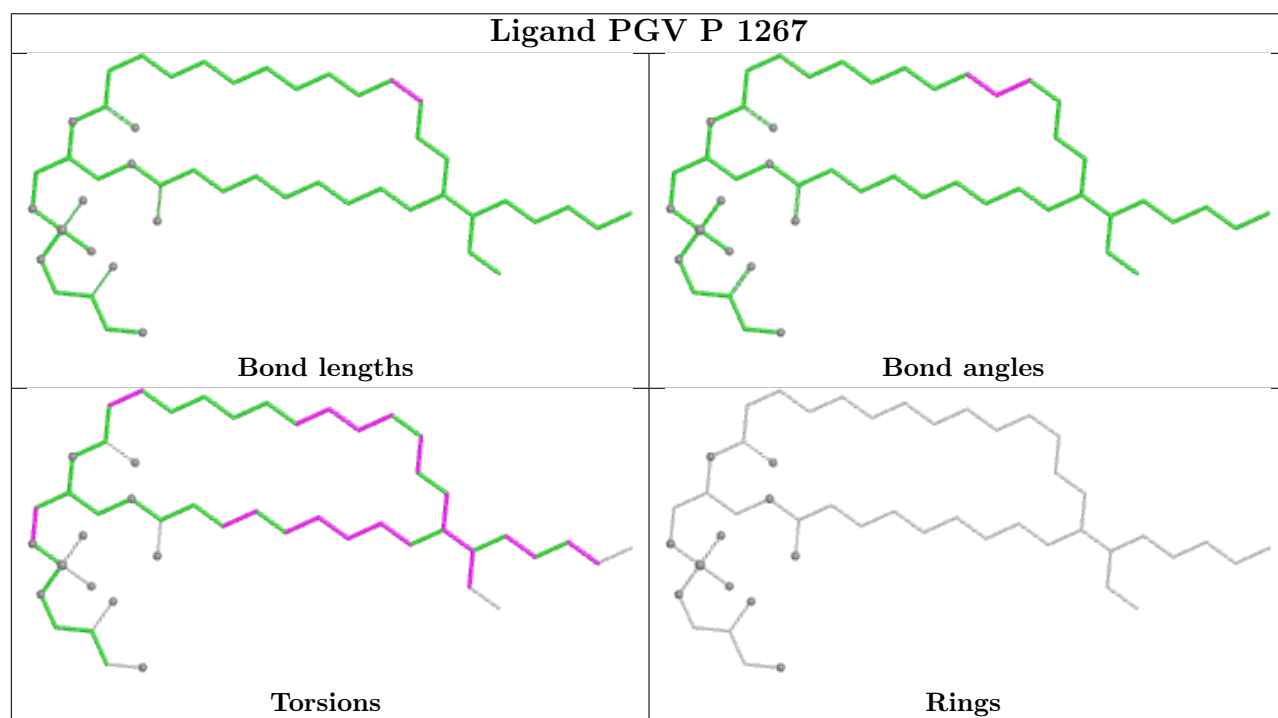
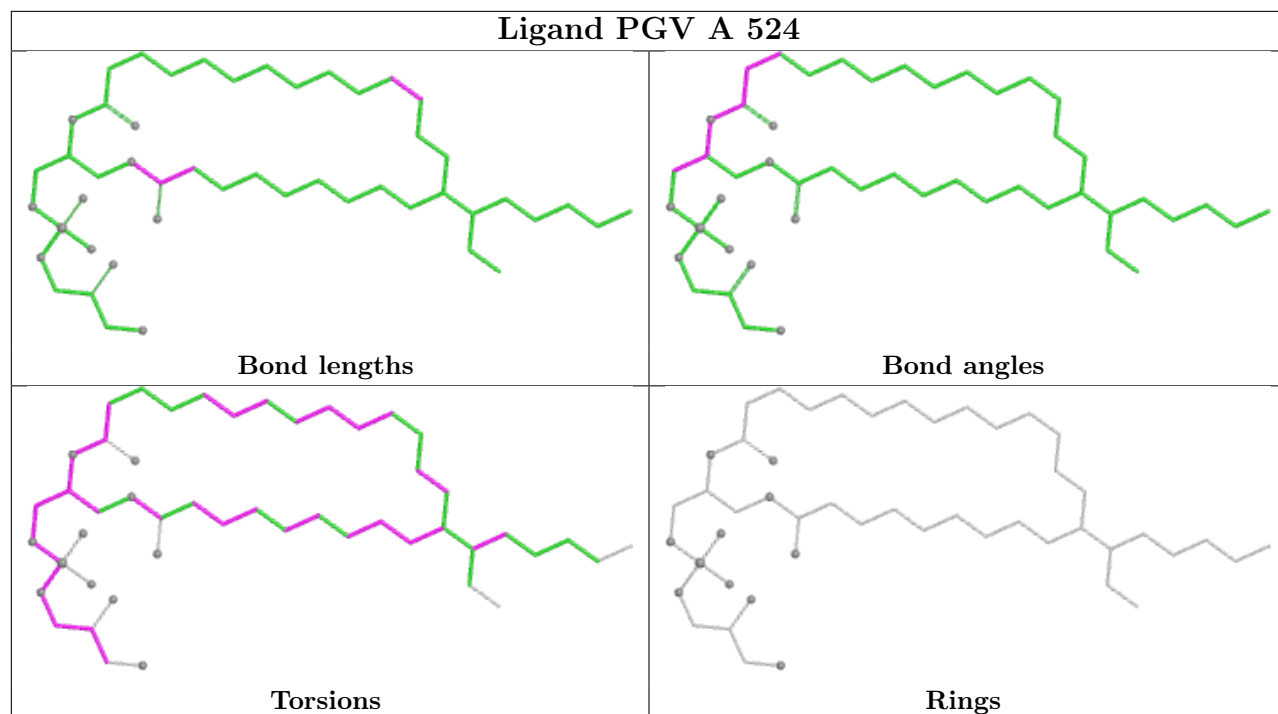
Ligand DMU M 526



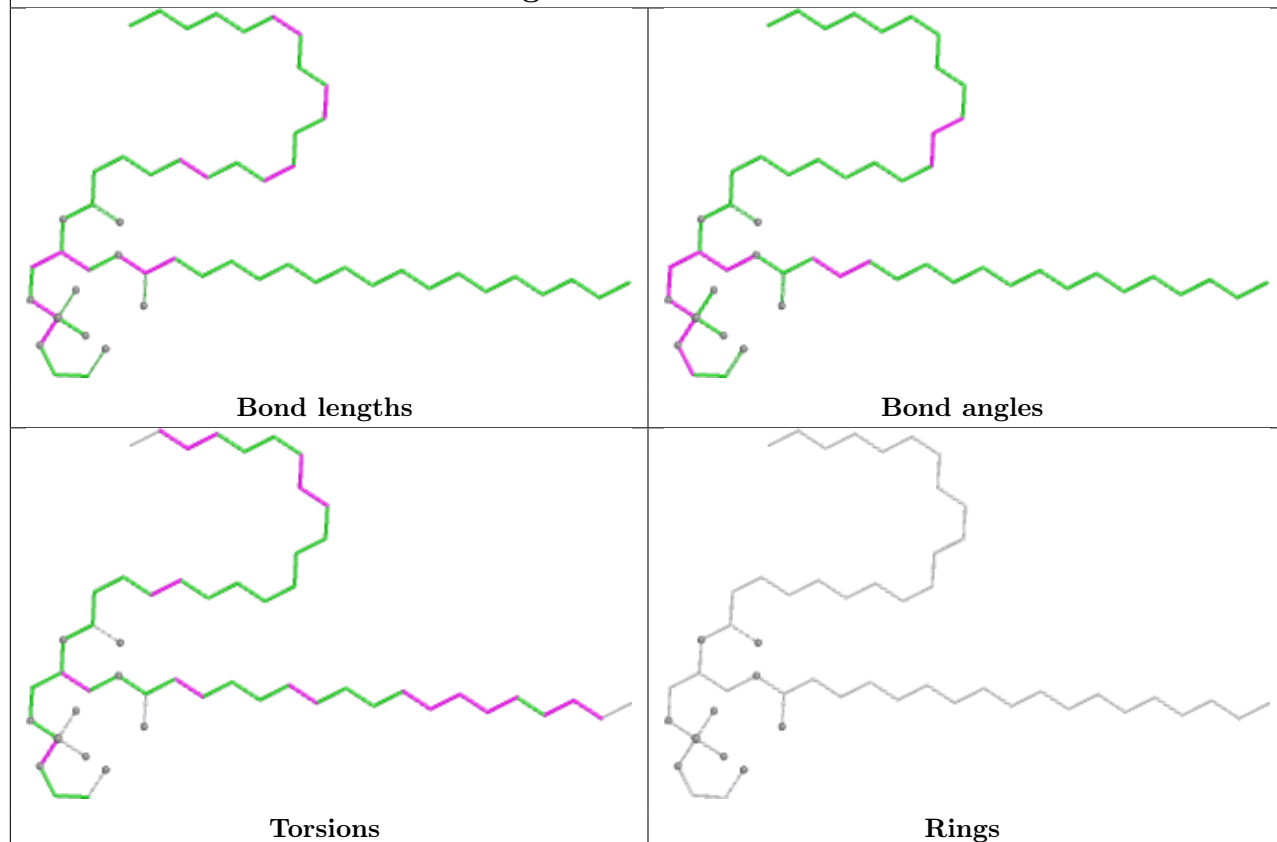




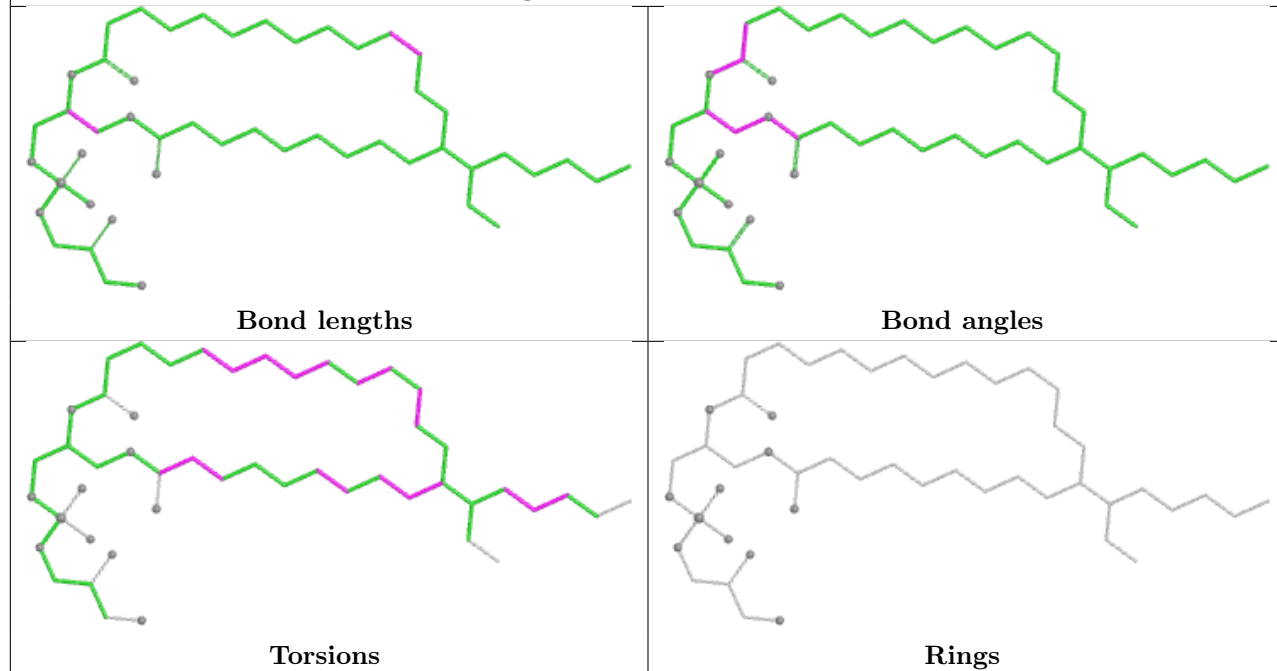


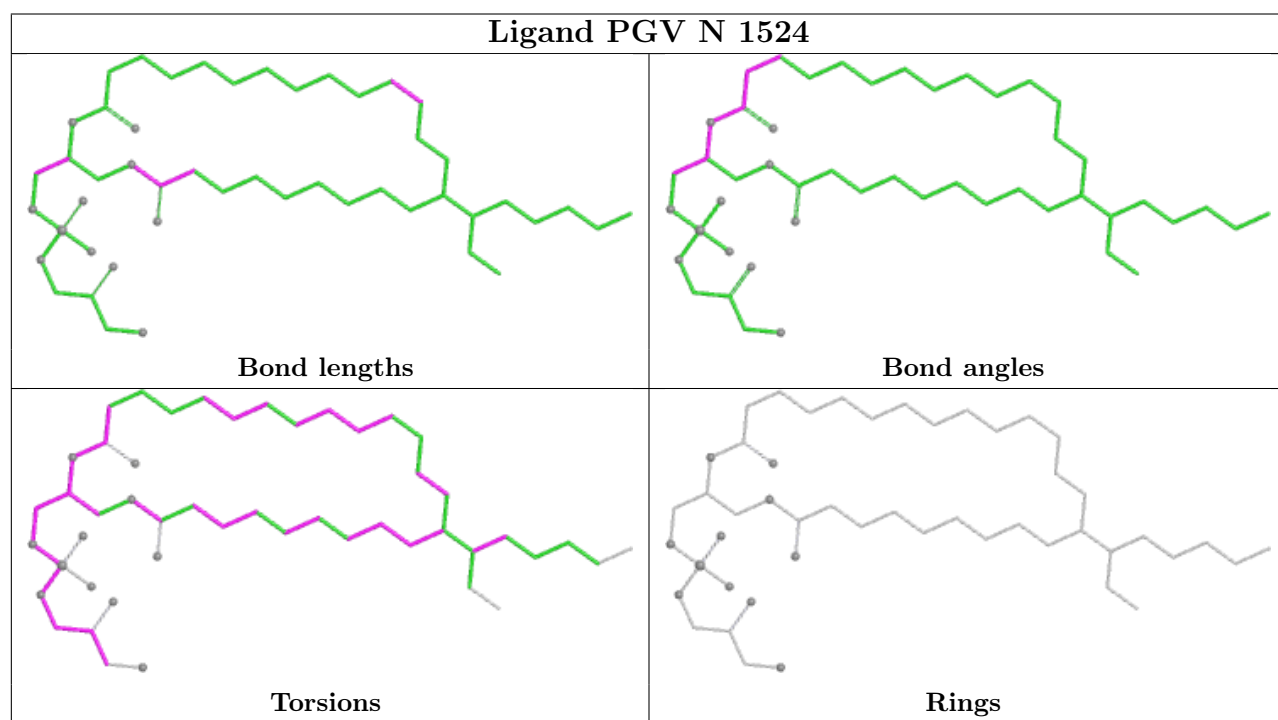
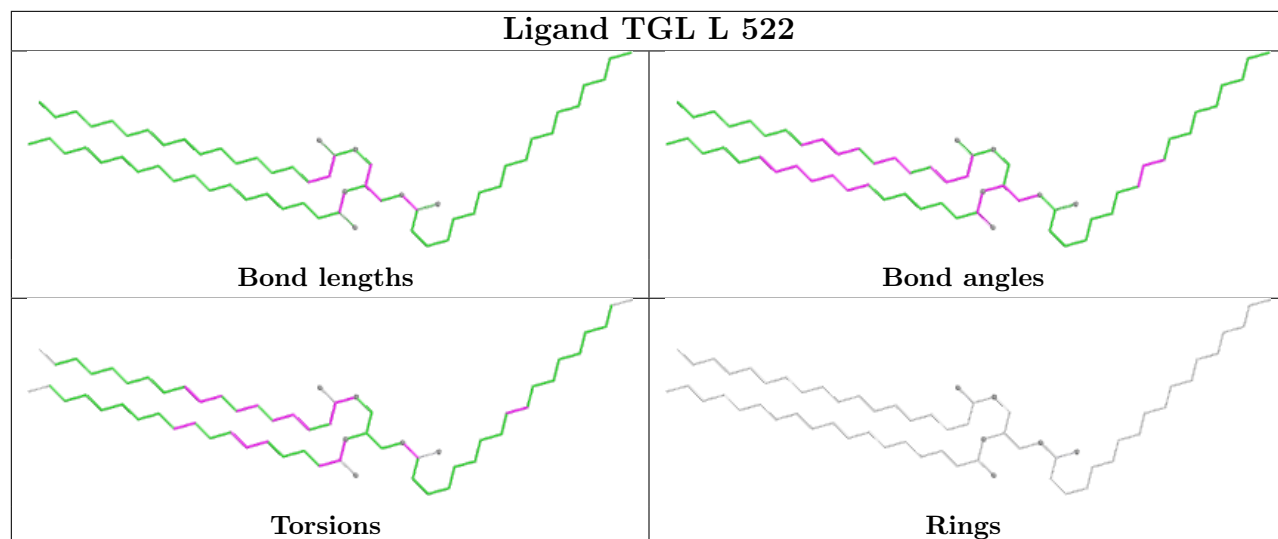


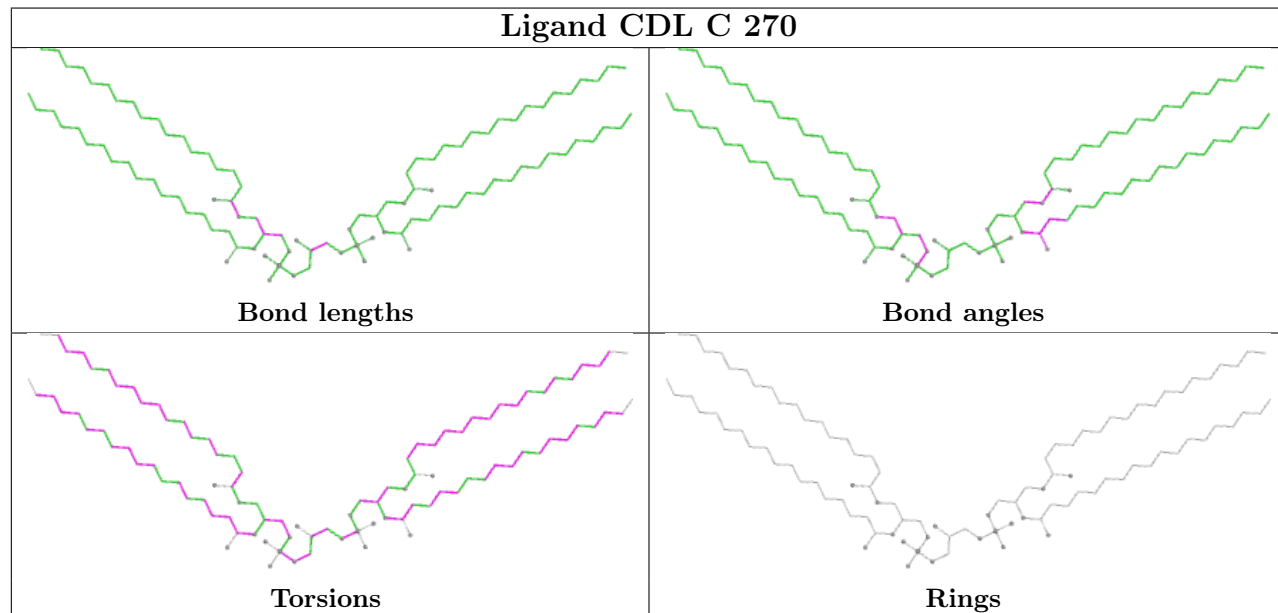
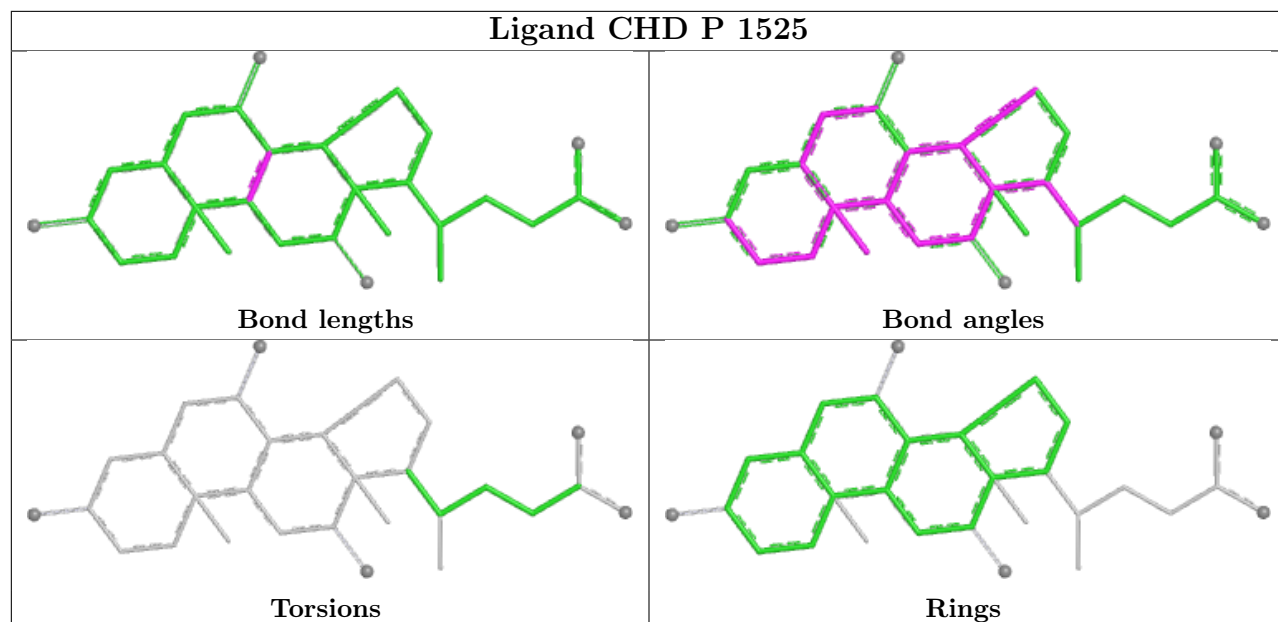
Ligand PEK P 1265

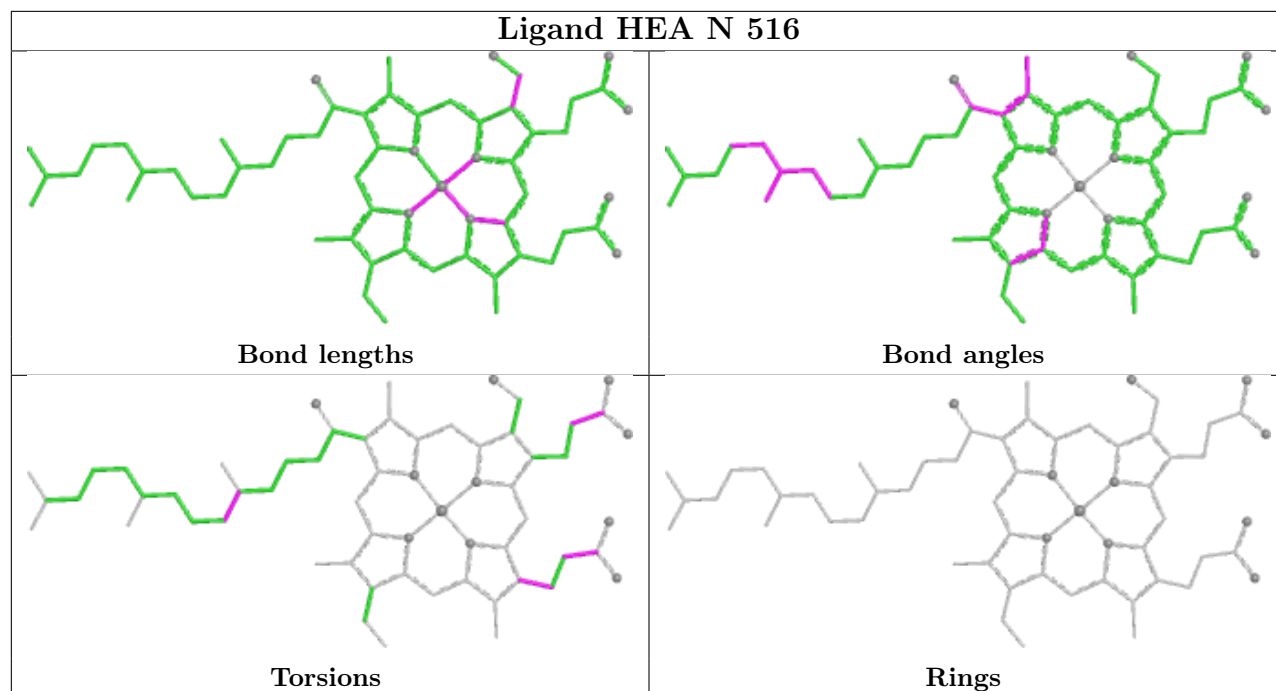


Ligand PGV N 1266









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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.