



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:18 AM UTC

PDB ID : 7TII / pdb_00007tii
Title : Annealed structure of oxidized bovine cytochrome c oxidase with reduced metal centers induced by synchrotron X-ray exposure
Authors : Ishigami, I.; Rousseau, D.L.; Yeh, S.-R.; Russi, S.; Cohen, A.
Deposited on : 2022-01-13
Resolution : 2.45 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

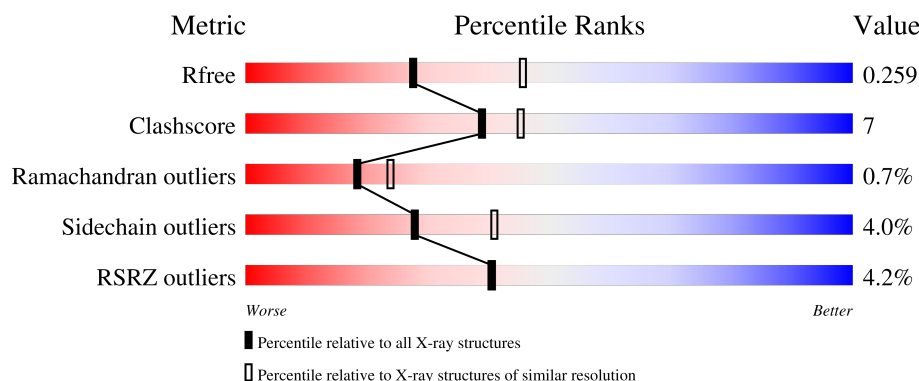
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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.



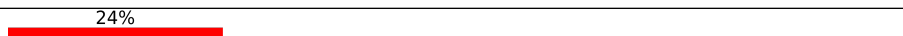
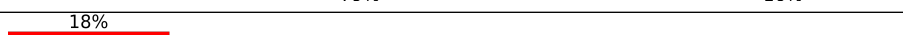
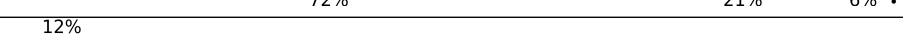
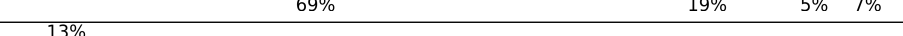
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	514	0.2% 82% 16% .
1	N	514	0.2% 83% 16% .
2	B	227	2% 80% 19% .
2	O	227	4% 80% 19% .
3	C	261	0.2% 87% 11% ..

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Mol	Chain	Length	Quality of chain
3	P	261	
4	D	147	
4	Q	147	
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
18	PGV	A	607	X	-	-	-
19	EDO	S	103	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
26	CHD	W	102	X	-	-	-

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 32401 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	20	0
			4181	2791	646	703	41			
1	N	514	Total	C	N	O	S	0	21	0
			4188	2795	647	704	42			

- 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	6	0
			1874	1216	289	350	19			
2	O	227	Total	C	N	O	S	0	5	0
			1870	1215	289	348	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	8	0
			2174	1451	345	364	14			
3	P	259	Total	C	N	O	S	0	8	0
			2173	1451	344	363	15			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	144	Total	C	N	O	S	0	6	0
			1249	814	206	224	5			
4	Q	144	Total	C	N	O	S	0	1	0
			1203	782	197	219	5			

- Molecule 5 is a protein called Cytochrome c oxidase subunit 5A, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	105	Total	C	N	O	S	0	1	0
			863	550	148	163	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 subunit 5B, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	5	0
			789	489	142	152	6			
6	S	98	Total	C	N	O	S	0	1	0
			755	468	135	147	5			

- Molecule 7 is a protein called Cytochrome c oxidase subunit 6A2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
7	G	84	Total 686	C 440	N 130	O 114	P 1	S 1	0	1	0
7	T	84	Total 706	C 454	N 133	O 117	P 1	S 1	0	3	0

- Molecule 8 is a protein called Cytochrome c oxidase subunit 6B1.

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 subunit 6C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	72	Total	C	N	O	S	0	0	0
			592	385	106	97	4			
9	V	72	Total	C	N	O	S	0	1	0
			600	390	107	98	5			

- Molecule 10 is a protein called Cytochrome c oxidase subunit 7A1, mitochondrial.

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 subunit 7B, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	49	Total	C	N	O	S	0	1	0
			391	255	66	68	2			
11	X	49	Total	C	N	O	S	0	1	0
			391	255	66	68	2			

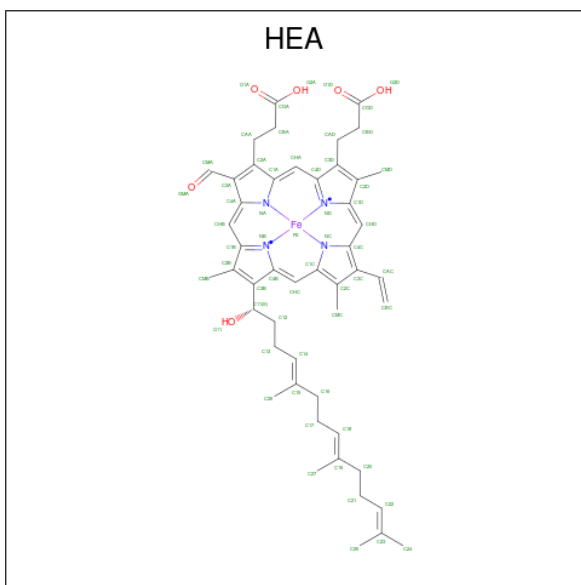
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

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 subunit 8B, mitochondrial.

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 HEME-A (CCD ID: HEA) (formula: $C_{49}H_{56}FeN_4O_6$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 15 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

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

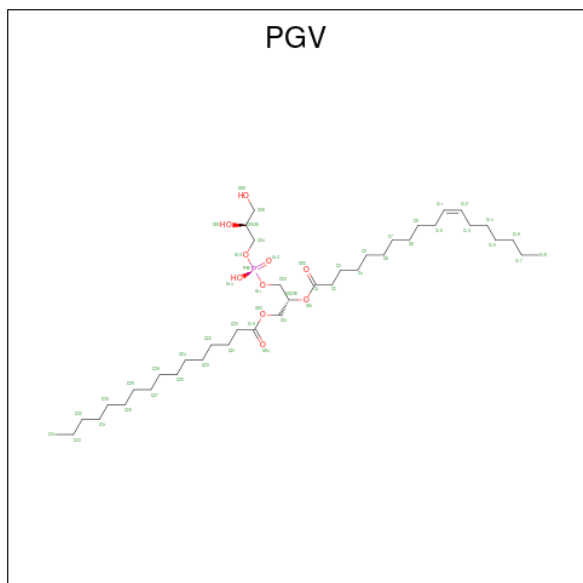
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 17 is SODIUM ION (CCD ID: NA) (formula: Na).

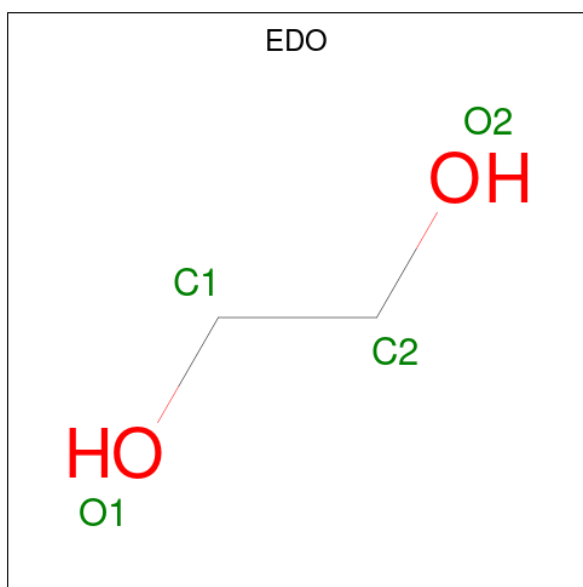
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Na	0	0
			1	1		
17	N	1	Total	Na	0	0
			1	1		

- Molecule 18 is (1R)-2-{{[[[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P) (labeled as "Ligand of Interest" by depositor).



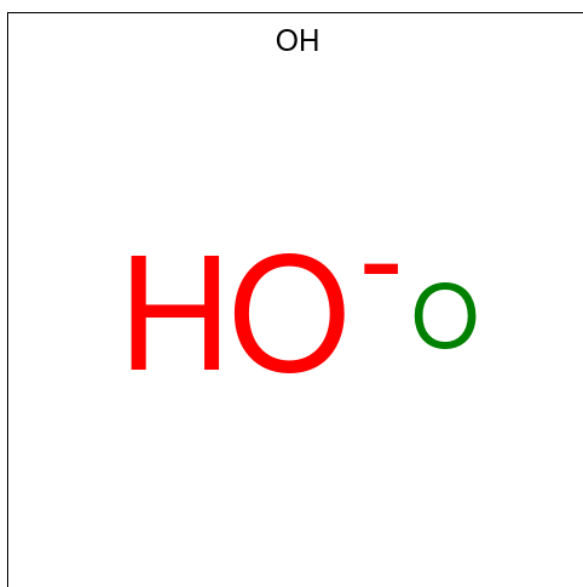
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
18	A	1	Total	C	O	P	0	0
			51	40	10	1		
18	A	1	Total	C	O	P	0	0
			51	40	10	1		
18	C	1	Total	C	O	P	0	0
			51	40	10	1		
18	C	1	Total	C	O	P	0	0
			51	40	10	1		
18	P	1	Total	C	O	P	0	0
			51	40	10	1		
18	P	1	Total	C	O	P	0	0
			51	40	10	1		
18	P	1	Total	C	O	P	0	0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

- Molecule 19 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



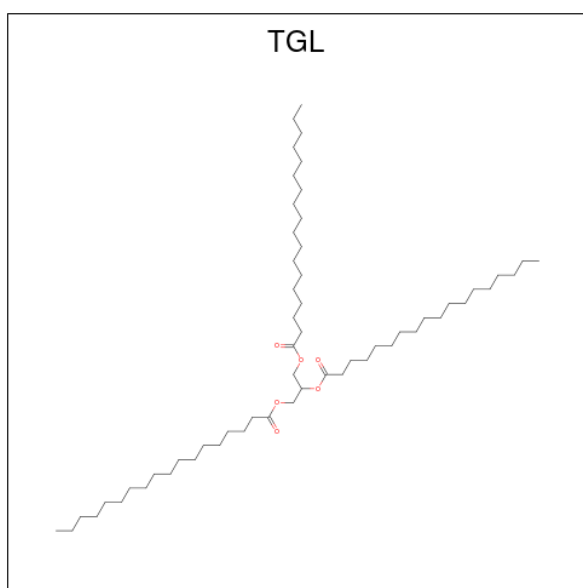
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	A	1	Total	C	O	0	0
			4	2	2		
19	A	1	Total	C	O	0	0
			4	2	2		
19	C	1	Total	C	O	0	0
			4	2	2		
19	G	1	Total	C	O	0	0
			4	2	2		
19	N	1	Total	C	O	0	0
			4	2	2		
19	S	1	Total	C	O	0	0
			4	2	2		
19	S	1	Total	C	O	0	0
			4	2	2		
19	T	1	Total	C	O	0	0
			4	2	2		

- Molecule 20 is HYDROXIDE ION (CCD ID: OH) (formula: HO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	A	1	Total	O		0	0
			1	1			
20	N	1	Total	O		0	0
			1	1			

- Molecule 21 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: C₅₇H₁₁₀O₆).



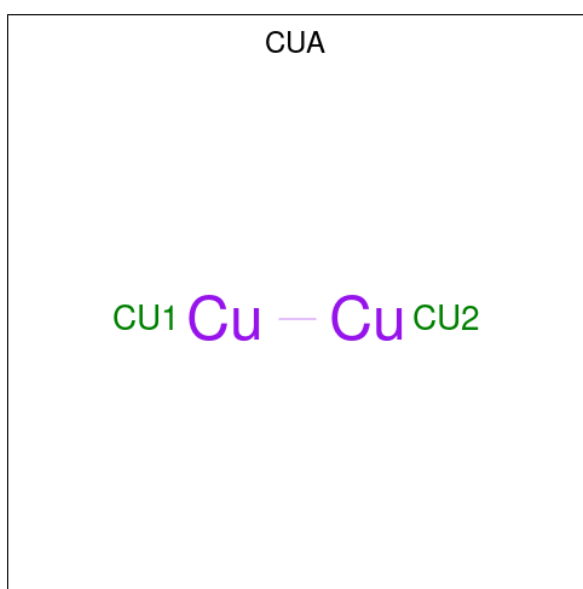
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	B	1	Total	C	O	0	0
			63	57	6		
21	D	1	Total	C	O	0	0
			63	57	6		

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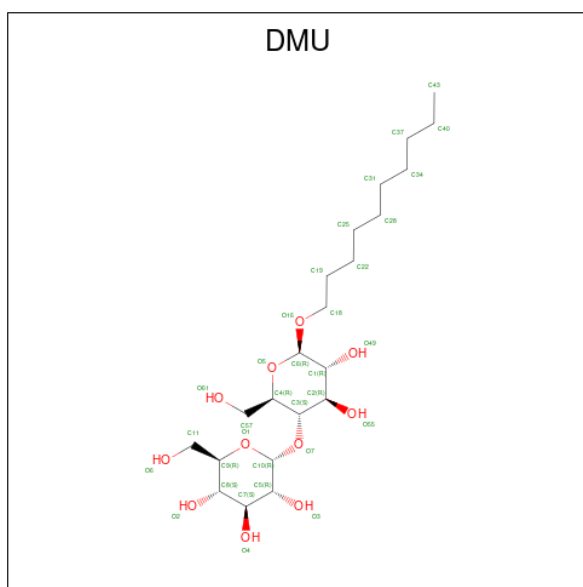
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	L	1	Total	C	O	0	0
			63	57	6		
21	N	1	Total	C	O	0	0
			63	57	6		
21	Q	1	Total	C	O	0	0
			63	57	6		
21	Y	1	Total	C	O	0	0
			63	57	6		

- Molecule 22 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



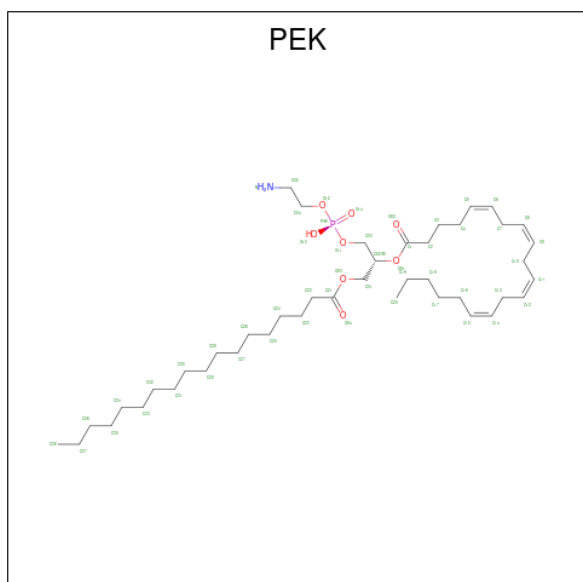
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	B	1	Total	Cu	0	0
			2	2		
22	O	1	Total	Cu	0	0
			2	2		

- Molecule 23 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



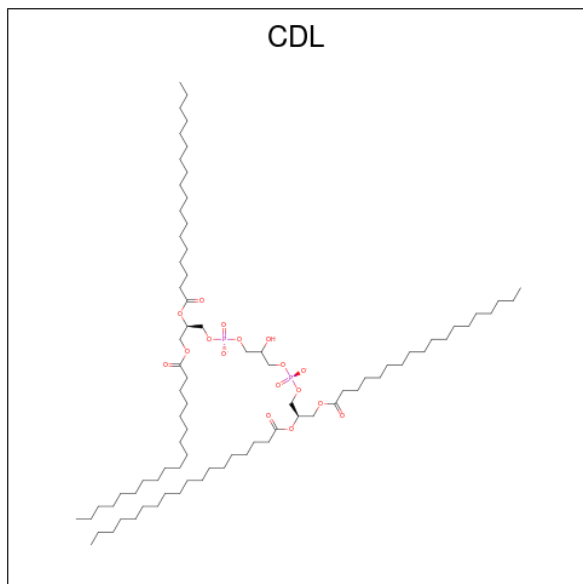
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
23	C	1	Total 33	C 22	O 11	0	0
23	D	1	Total 33	C 22	O 11	0	0
23	W	1	Total 33	C 22	O 11	0	0
23	Z	1	Total 33	C 22	O 11	0	0

- Molecule 24 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: $C_{43}H_{78}NO_8P$).



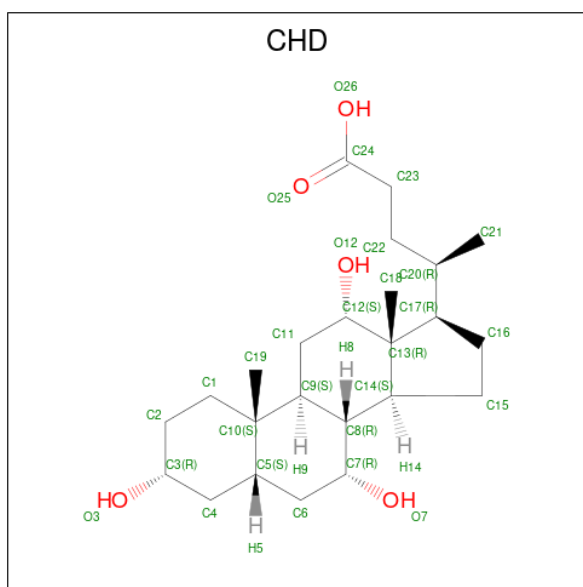
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
24	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
24	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
24	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
24	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
24	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		

- Molecule 25 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



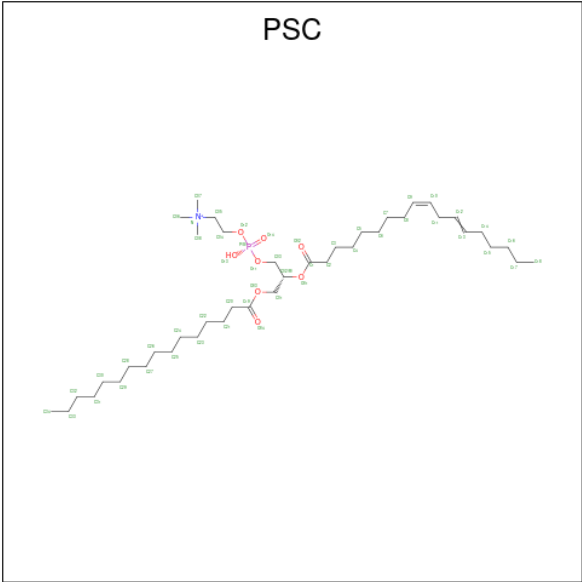
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
25	C	1	Total	C	O	P	0	0
			100	81	17	2		
25	G	1	Total	C	O	P	0	0
			100	81	17	2		
25	P	1	Total	C	O	P	0	0
			100	81	17	2		
25	T	1	Total	C	O	P	0	0
			100	81	17	2		

- Molecule 26 is CHOLIC ACID (CCD ID: CHD) (formula: $C_{24}H_{40}O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	C	1	Total C O 29 24 5	0	0
26	C	1	Total C O 29 24 5	0	0
26	G	1	Total C O 29 24 5	0	0
26	J	1	Total C O 29 24 5	0	0
26	P	1	Total C O 29 24 5	0	0
26	P	1	Total C O 29 24 5	0	0
26	T	1	Total C O 29 24 5	0	0
26	W	1	Total C O 29 24 5	0	0

- Molecule 27 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (CCD ID: PSC) (formula: $C_{42}H_{81}NO_8P$) (labeled as "Ligand of Interest" by depositor).

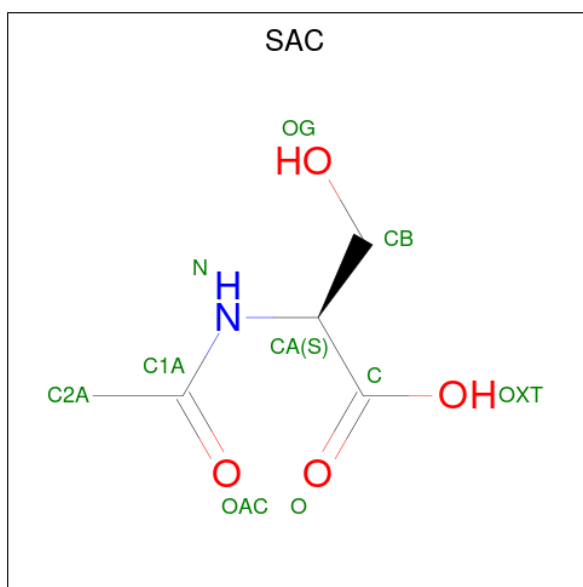


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
27	E	1	Total	C	N	O	P	0	0
			52	42	1	8	1		
27	O	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

- Molecule 28 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 29 is N-ACETYL-SERINE (CCD ID: SAC) (formula: C₅H₉NO₄) (labeled as "Lig- and of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
29	I	1	Total	C	N	O	0	0
			9	5	1	3		
29	V	1	Total	C	N	O	0	0
			9	5	1	3		

- Molecule 30 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	A	130	Total	O	0	0
			130	130		
30	B	88	Total	O	0	0
			88	88		
30	C	54	Total	O	0	0
			54	54		
30	D	53	Total	O	0	0
			53	53		
30	E	35	Total	O	0	0
			35	35		
30	F	39	Total	O	0	0
			39	39		
30	G	31	Total	O	0	0
			31	31		
30	H	22	Total	O	0	0
			22	22		
30	I	19	Total	O	0	0
			19	19		
30	J	8	Total	O	0	0
			8	8		

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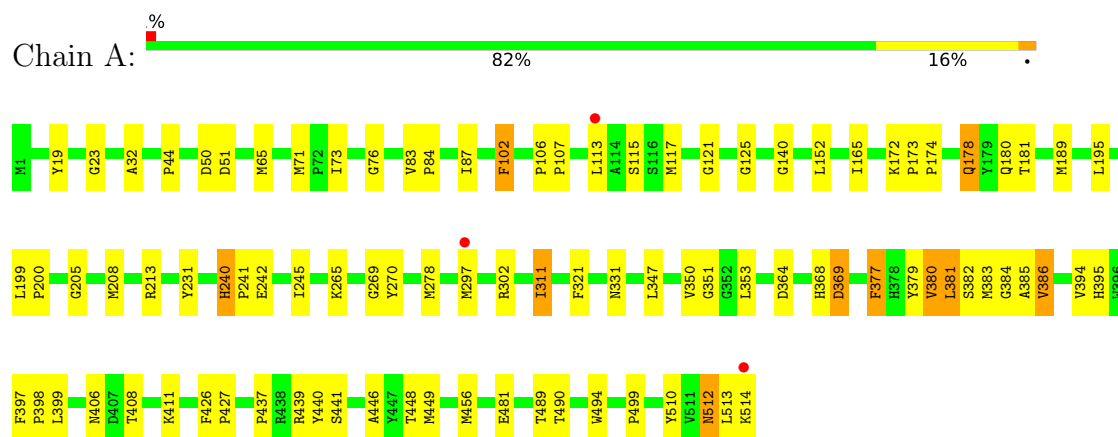
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	K	13	Total 13	O 13	0	0
30	L	14	Total 14	O 14	0	0
30	M	14	Total 14	O 14	0	0
30	N	114	Total 114	O 114	0	0
30	O	64	Total 64	O 64	0	0
30	P	54	Total 54	O 54	0	0
30	Q	16	Total 16	O 16	0	0
30	R	19	Total 19	O 19	0	0
30	S	41	Total 41	O 41	0	0
30	T	30	Total 30	O 30	0	0
30	U	18	Total 18	O 18	0	0
30	V	9	Total 9	O 9	0	0
30	W	10	Total 10	O 10	0	0
30	X	1	Total 1	O 1	0	0
30	Y	11	Total 11	O 11	0	0
30	Z	7	Total 7	O 7	0	0

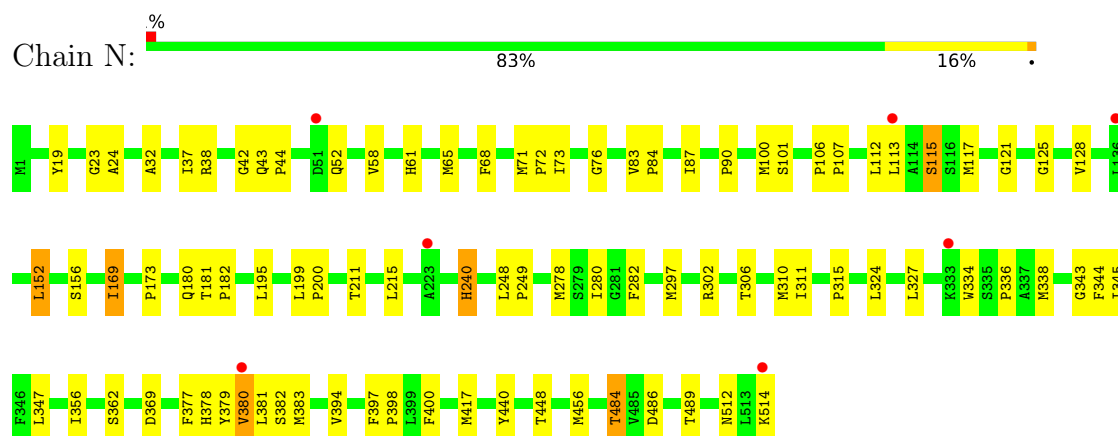
3 Residue-property plots [i](#)

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.

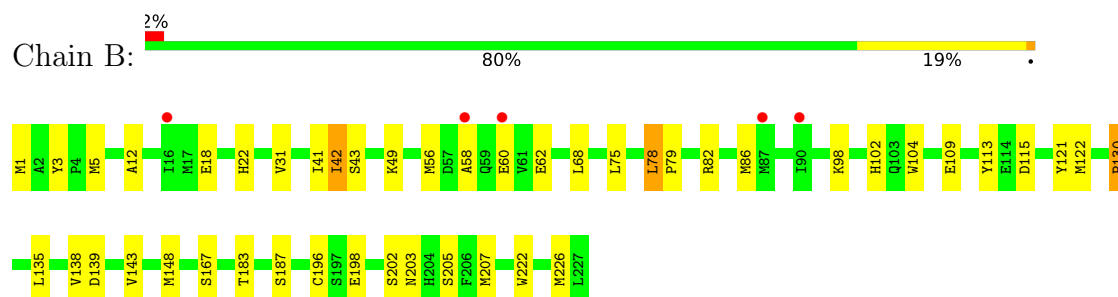
• Molecule 1: Cytochrome c oxidase subunit 1



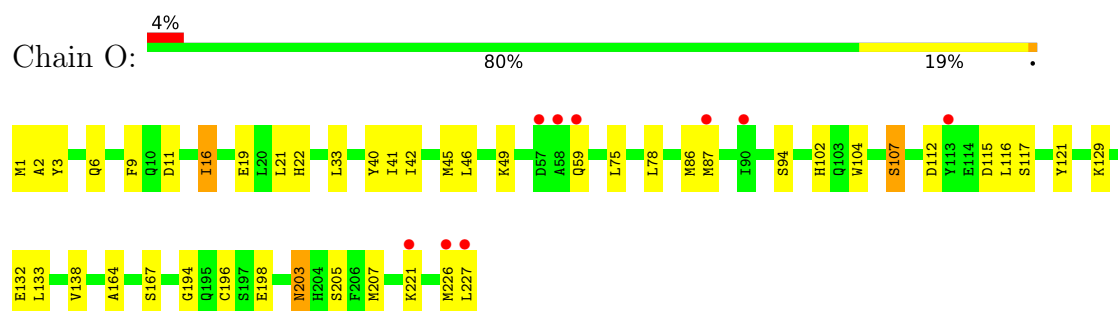
• Molecule 1: Cytochrome c oxidase subunit 1



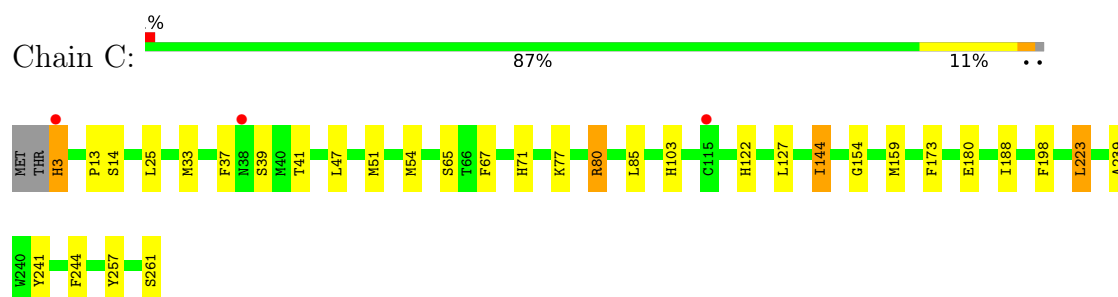
• Molecule 2: Cytochrome c oxidase subunit 2



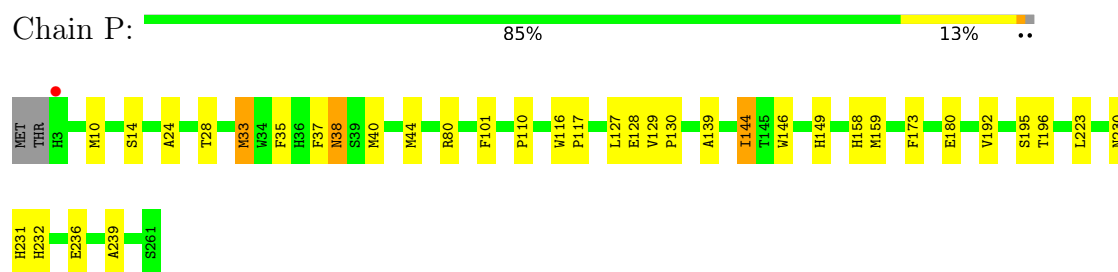
- Molecule 2: Cytochrome c oxidase subunit 2



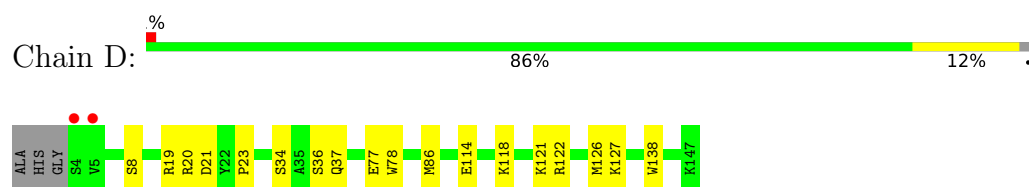
- Molecule 3: Cytochrome c oxidase subunit 3



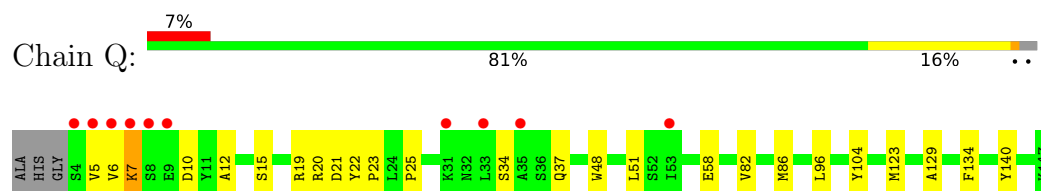
- Molecule 3: Cytochrome c oxidase subunit 3



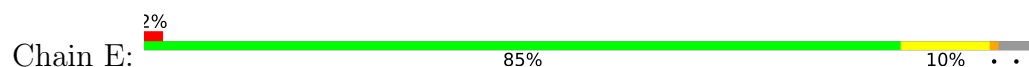
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial

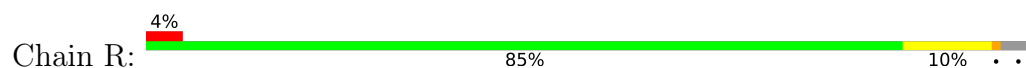


- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial

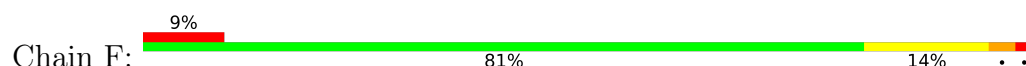




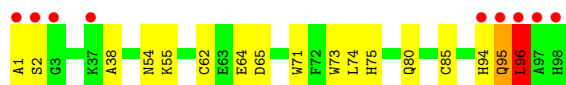
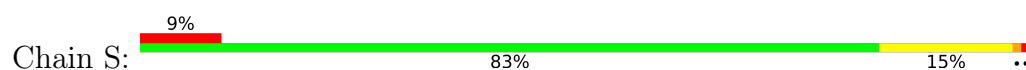
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



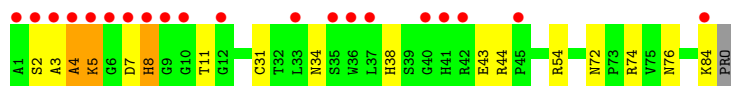
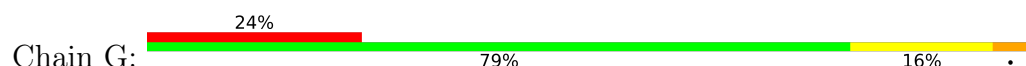
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



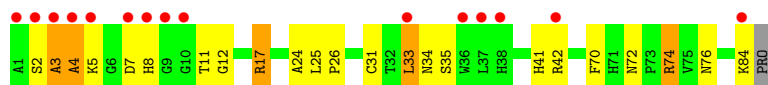
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



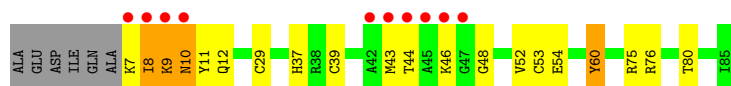
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



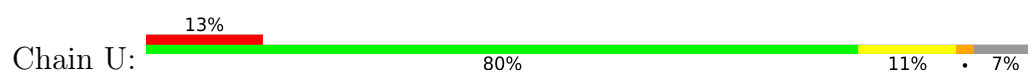
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



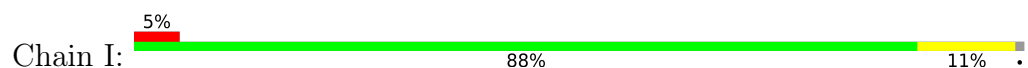
- Molecule 8: Cytochrome c oxidase subunit 6B1



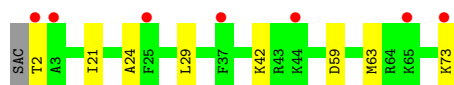
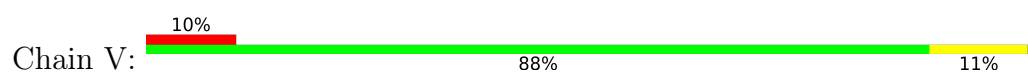
- Molecule 8: Cytochrome c oxidase subunit 6B1



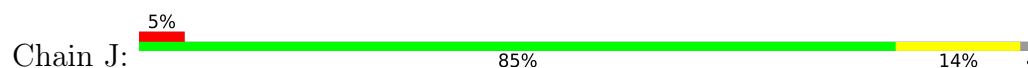
- Molecule 9: Cytochrome c oxidase subunit 6C



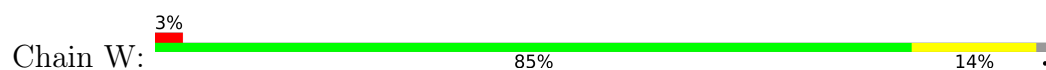
- Molecule 9: Cytochrome c oxidase subunit 6C



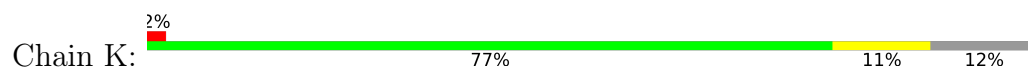
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



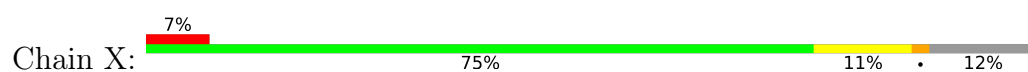
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



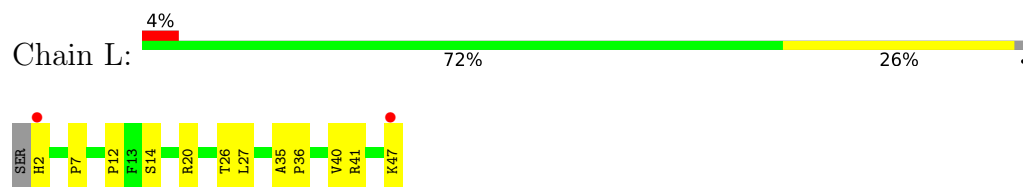
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



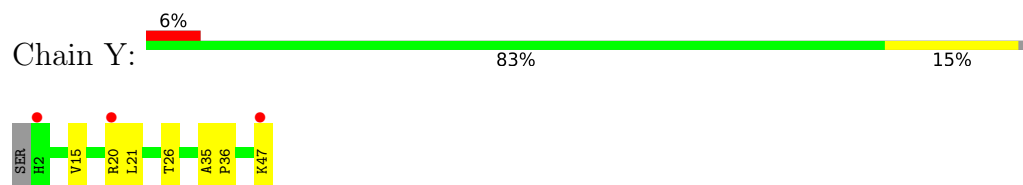
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



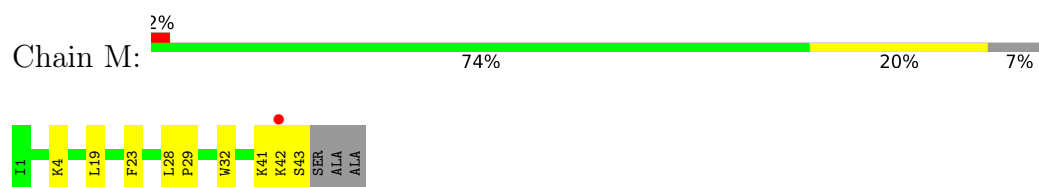
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



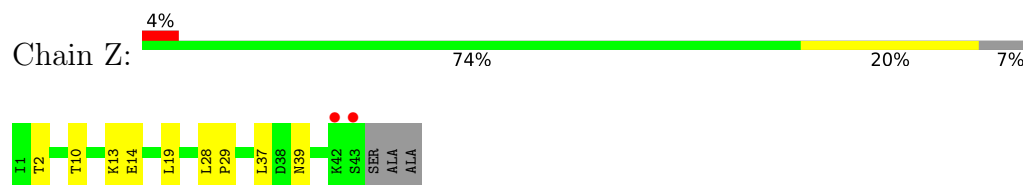
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial



- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	178.04Å 182.63Å 205.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.30 – 2.45 39.30 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.30-2.45) 99.9 (39.30-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.206 , 0.253 0.215 , 0.259	Depositor DCC
R_{free} test set	12054 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	32401	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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

5.1 Standard geometry

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

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	1.00	1/4311 (0.0%)	1.39	8/5884 (0.1%)
1	N	1.01	1/4318 (0.0%)	1.42	4/5893 (0.1%)
2	B	1.04	1/1912 (0.1%)	1.41	1/2603 (0.0%)
2	O	1.03	1/1908 (0.1%)	1.38	0/2599
3	C	0.96	0/2261	1.42	2/3090 (0.1%)
3	P	0.96	0/2260	1.41	1/3088 (0.0%)
4	D	1.03	0/1284	1.38	0/1730
4	Q	1.02	0/1237	1.52	3/1668 (0.2%)
5	E	1.02	0/882	1.45	0/1196
5	R	0.99	0/871	1.50	0/1182
6	F	1.08	0/806	1.37	3/1093 (0.3%)
6	S	1.07	0/772	1.36	0/1048
7	G	1.03	0/702	1.32	0/953
7	T	1.01	0/724	1.36	0/984
8	H	0.96	0/682	1.48	0/921
8	U	1.02	0/682	1.50	0/921
9	I	0.98	0/605	1.60	1/802 (0.1%)
9	V	1.00	0/613	1.58	0/812
10	J	0.99	0/471	1.50	0/636
10	W	0.99	0/471	1.50	2/636 (0.3%)
11	K	1.05	0/405	1.45	0/556
11	X	1.05	0/405	1.45	1/556 (0.2%)
12	L	0.98	0/393	1.44	0/526
12	Y	0.99	0/393	1.33	1/526 (0.2%)
13	M	1.00	0/345	1.48	0/470
13	Z	0.99	0/345	1.51	0/470
All	All	1.01	4/30058 (0.0%)	1.43	27/40843 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	198	GLU	C-O	7.09	1.32	1.23
1	N	240	HIS	CE1-NE2	6.29	1.38	1.32
2	O	198	GLU	C-O	5.44	1.30	1.23
1	A	174	PRO	C-O	-5.31	1.17	1.24

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	HIS	CA-CB-CG	-8.27	105.53	113.80
3	C	122	HIS	CB-CA-C	7.51	118.46	110.65
1	N	240	HIS	CA-CB-CG	-7.40	106.40	113.80
1	A	439	ARG	CB-CA-C	6.31	121.48	111.51
11	X	49	THR	CB-CA-C	6.24	117.25	110.08

There are no chirality outliers.

There are no planarity outliers.

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	4181	0	4161	82	0
1	N	4188	0	4166	78	0
2	B	1874	0	1869	25	0
2	O	1870	0	1867	36	0
3	C	2174	0	2082	26	0
3	P	2173	0	2083	28	0
4	D	1249	0	1242	15	0
4	Q	1203	0	1191	16	0
5	E	863	0	857	8	0
5	R	852	0	845	6	0
6	F	789	0	769	14	0
6	S	755	0	734	14	0
7	G	686	0	651	10	0
7	T	706	0	664	18	0
8	H	662	0	623	16	0
8	U	662	0	623	5	0
9	I	592	0	604	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	V	600	0	612	6	0
10	J	460	0	459	5	0
10	W	460	0	459	3	0
11	K	391	0	374	5	0
11	X	391	0	374	2	0
12	L	380	0	380	9	0
12	Y	380	0	380	3	0
13	M	335	0	352	7	0
13	Z	335	0	352	4	0
14	A	120	0	108	9	0
14	N	120	0	108	10	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	N	1	0	0	0	0
18	A	102	0	152	5	0
18	C	102	0	152	0	0
18	P	153	0	228	7	0
18	Z	51	0	76	2	0
19	A	8	0	12	1	0
19	C	4	0	6	1	0
19	G	4	0	6	1	0
19	N	4	0	6	0	0
19	S	8	0	12	5	0
19	T	4	0	6	0	0
20	A	1	0	0	0	0
20	N	1	0	0	0	0
21	B	63	0	110	0	0
21	D	63	0	110	4	0
21	L	63	0	110	4	0
21	N	63	0	110	0	0
21	Q	63	0	110	0	0
21	Y	63	0	110	2	0
22	B	2	0	0	0	0
22	O	2	0	0	0	0
23	C	33	0	42	6	0
23	D	33	0	42	0	0
23	W	33	0	42	7	0
23	Z	33	0	42	0	0
24	C	106	0	154	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	G	53	0	77	3	0
24	T	159	0	231	6	0
25	C	100	0	156	2	0
25	G	100	0	156	4	0
25	P	100	0	156	2	0
25	T	100	0	156	7	0
26	C	58	0	78	2	0
26	G	29	0	39	0	0
26	J	29	0	39	0	0
26	P	58	0	78	1	0
26	T	29	0	39	1	0
26	W	29	0	39	1	0
27	E	52	0	80	6	0
27	O	52	0	80	2	0
28	F	1	0	0	0	0
28	S	1	0	0	0	0
29	I	9	0	8	0	0
29	V	9	0	8	1	0
30	A	130	0	0	3	0
30	B	88	0	0	0	0
30	C	54	0	0	2	0
30	D	53	0	0	1	0
30	E	35	0	0	2	0
30	F	39	0	0	1	0
30	G	31	0	0	3	0
30	H	22	0	0	2	0
30	I	19	0	0	2	0
30	J	8	0	0	0	0
30	K	13	0	0	1	0
30	L	14	0	0	2	0
30	M	14	0	0	2	0
30	N	114	0	0	2	0
30	O	64	0	0	2	0
30	P	54	0	0	4	0
30	Q	16	0	0	0	0
30	R	19	0	0	0	0
30	S	41	0	0	1	0
30	T	30	0	0	5	0
30	U	18	0	0	0	0
30	V	9	0	0	0	0
30	W	10	0	0	0	0
30	X	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Y	11	0	0	0	0
30	Z	7	0	0	0	0
All	All	32401	0	32047	435	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 7.

The worst 5 of 435 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)
1:N:297[B]:MET:SD	1:N:302[B]:ARG:HG2	1.77	1.22
3:P:40[B]:MET:O	3:P:44[B]:MET:HG3	1.57	1.03
1:A:379[A]:TYR:HA	1:A:383[A]:MET:HE3	1.44	1.00
1:A:51:ASP:OD2	1:A:441:SER:OG	1.78	0.99
8:H:9:LYS:HB3	30:H:121:HOH:O	1.65	0.95

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	532/514 (104%)	507 (95%)	24 (4%)	1 (0%)	43	54
1	N	533/514 (104%)	514 (96%)	19 (4%)	0	100	100
2	B	231/227 (102%)	218 (94%)	12 (5%)	1 (0%)	30	37
2	O	230/227 (101%)	213 (93%)	16 (7%)	1 (0%)	30	37
3	C	265/261 (102%)	258 (97%)	7 (3%)	0	100	100
3	P	265/261 (102%)	256 (97%)	7 (3%)	2 (1%)	16	20
4	D	148/147 (101%)	142 (96%)	6 (4%)	0	100	100
4	Q	143/147 (97%)	132 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	104/109 (95%)	103 (99%)	1 (1%)	0	100	100
5	R	103/109 (94%)	101 (98%)	2 (2%)	0	100	100
6	F	101/98 (103%)	92 (91%)	4 (4%)	5 (5%)	1	0
6	S	97/98 (99%)	88 (91%)	8 (8%)	1 (1%)	12	14
7	G	82/85 (96%)	64 (78%)	14 (17%)	4 (5%)	1	0
7	T	84/85 (99%)	71 (84%)	9 (11%)	4 (5%)	2	0
8	H	77/85 (91%)	66 (86%)	9 (12%)	2 (3%)	4	2
8	U	77/85 (91%)	69 (90%)	7 (9%)	1 (1%)	9	9
9	I	70/73 (96%)	67 (96%)	3 (4%)	0	100	100
9	V	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
10	J	56/59 (95%)	56 (100%)	0	0	100	100
10	W	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
11	K	48/56 (86%)	46 (96%)	2 (4%)	0	100	100
11	X	48/56 (86%)	45 (94%)	2 (4%)	1 (2%)	5	4
12	L	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
12	Y	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
13	M	41/46 (89%)	39 (95%)	1 (2%)	1 (2%)	4	3
13	Z	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
All	All	3591/3614 (99%)	3393 (94%)	174 (5%)	24 (1%)	18	24

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	95	GLN
6	F	96	LEU
6	F	97	ALA
7	G	4	ALA
7	G	8	HIS

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	444/426 (104%)	431 (97%)	13 (3%)	37	52
1	N	445/426 (104%)	432 (97%)	13 (3%)	37	52
2	B	216/210 (103%)	205 (95%)	11 (5%)	21	31
2	O	215/210 (102%)	202 (94%)	13 (6%)	17	26
3	C	232/226 (103%)	221 (95%)	11 (5%)	23	35
3	P	232/226 (103%)	223 (96%)	9 (4%)	28	42
4	D	134/129 (104%)	130 (97%)	4 (3%)	36	51
4	Q	129/129 (100%)	124 (96%)	5 (4%)	28	42
5	E	93/95 (98%)	90 (97%)	3 (3%)	34	49
5	R	92/95 (97%)	89 (97%)	3 (3%)	33	48
6	F	86/81 (106%)	83 (96%)	3 (4%)	32	46
6	S	82/81 (101%)	78 (95%)	4 (5%)	22	33
7	G	68/68 (100%)	62 (91%)	6 (9%)	9	10
7	T	70/68 (103%)	64 (91%)	6 (9%)	10	11
8	H	71/75 (95%)	65 (92%)	6 (8%)	10	11
8	U	71/75 (95%)	65 (92%)	6 (8%)	10	11
9	I	57/57 (100%)	56 (98%)	1 (2%)	51	65
9	V	58/57 (102%)	56 (97%)	2 (3%)	32	47
10	J	49/50 (98%)	48 (98%)	1 (2%)	48	63
10	W	49/50 (98%)	46 (94%)	3 (6%)	17	24
11	K	40/46 (87%)	39 (98%)	1 (2%)	42	56
11	X	40/46 (87%)	37 (92%)	3 (8%)	12	16
12	L	39/40 (98%)	37 (95%)	2 (5%)	21	31
12	Y	39/40 (98%)	37 (95%)	2 (5%)	21	31
13	M	37/38 (97%)	37 (100%)	0	100	100
13	Z	37/38 (97%)	34 (92%)	3 (8%)	11	13
All	All	3125/3082 (101%)	2991 (96%)	134 (4%)	28	38

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	U	8	ILE

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Mol	Chain	Res	Type
8	U	60	TYR
12	Y	47	LYS
7	G	44	ARG
7	G	8	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	422	ASN
3	P	38	ASN
11	X	15	ASN
1	N	503	HIS
2	O	59	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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
7	TPO	T	11	7	8,10,11	0.80	0	10,14,16	1.03	0
2	FME	B	1	2	8,9,10	0.61	0	8,9,11	1.33	2 (25%)
1	FME	A	1	1	8,9,10	0.55	0	8,9,11	0.77	0
7	TPO	G	11	7	8,10,11	1.33	1 (12%)	10,14,16	0.86	0
2	FME	O	1	2	8,9,10	0.50	0	8,9,11	0.75	0
1	FME	N	1	1	8,9,10	0.47	0	8,9,11	0.87	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
7	TPO	T	11	7	-	5/9/11/13	-
2	FME	B	1	2	-	2/7/9/11	-
1	FME	A	1	1	-	4/7/9/11	-
7	TPO	G	11	7	-	6/9/11/13	-
2	FME	O	1	2	-	0/7/9/11	-
1	FME	N	1	1	-	2/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	11	TPO	P-OG1	3.27	1.65	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	FME	CA-N-CN	-2.70	118.68	122.82
2	B	1	FME	C-CA-N	2.14	113.62	109.50

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

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

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	T	11	TPO	2	0
2	O	1	FME	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 8 are monoatomic and 2 are modelled with single atom - leaving 54 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	$\# Z > 2$
19	EDO	S	102	-	3,3,3	0.18	0	2,2,2	0.18	0
18	PGV	A	607	-	50,50,50	0.36	0	53,56,56	0.51	0
26	CHD	P	306	-	32,32,32	0.66	0	51,51,51	1.03	5 (9%)
19	EDO	T	106	-	3,3,3	0.34	0	2,2,2	0.31	0
19	EDO	C	309	-	3,3,3	0.13	0	2,2,2	0.10	0
26	CHD	G	103	-	32,32,32	0.60	0	51,51,51	0.74	0
18	PGV	Z	101	-	50,50,50	0.40	0	53,56,56	0.78	2 (3%)
21	TGL	L	101	-	62,62,62	0.38	0	65,65,65	0.48	1 (1%)
22	CUA	O	301	2	0,1,1	-	-	-		
22	CUA	B	302	2	0,1,1	-	-	-		
18	PGV	P	303	-	50,50,50	0.31	0	53,56,56	0.49	0
18	PGV	C	303	-	50,50,50	0.35	0	53,56,56	0.63	1 (1%)
19	EDO	A	609	-	3,3,3	0.08	0	2,2,2	0.26	0
21	TGL	D	201	-	62,62,62	0.37	0	65,65,65	0.66	2 (3%)
26	CHD	P	305	-	32,32,32	0.63	0	51,51,51	0.75	0
23	DMU	W	101	-	34,34,34	2.03	9 (26%)	45,45,45	1.79	12 (26%)
27	PSC	E	201	-	51,51,51	0.33	0	57,59,59	0.42	0
18	PGV	P	302	-	50,50,50	0.39	0	53,56,56	0.44	0
14	HEA	A	602	1	67,67,67	2.34	27 (40%)	81,103,103	2.65	34 (41%)
24	PEK	T	102	-	52,52,52	0.28	0	55,57,57	0.62	1 (1%)
24	PEK	C	302	-	52,52,52	0.29	0	55,57,57	0.60	0
21	TGL	Y	101	-	62,62,62	0.34	0	65,65,65	0.31	0
23	DMU	C	301	-	34,34,34	1.63	6 (17%)	45,45,45	1.51	9 (20%)
29	SAC	I	101	-	7,8,9	0.53	0	7,9,11	1.30	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	CHD	T	101	-	32,32,32	0.58	0	51,51,51	0.92	0
25	CDL	C	304	-	99,99,99	0.38	0	105,111,111	0.40	0
24	PEK	G	102	-	52,52,52	0.34	0	55,57,57	0.46	0
25	CDL	T	105	-	99,99,99	0.34	0	105,111,111	0.42	0
14	HEA	N	602	1	67,67,67	2.26	28 (41%)	81,103,103	2.60	30 (37%)
24	PEK	T	103	-	52,52,52	0.36	0	55,57,57	0.51	0
18	PGV	C	308	-	50,50,50	0.48	0	53,56,56	0.52	0
19	EDO	S	103	-	3,3,3	0.18	0	2,2,2	0.09	0
19	EDO	N	607	-	3,3,3	0.16	0	2,2,2	0.22	0
21	TGL	N	606	-	62,62,62	0.34	0	65,65,65	0.43	0
27	PSC	O	302	-	51,51,51	0.35	0	57,59,59	0.50	1 (1%)
18	PGV	P	301	-	50,50,50	0.32	0	53,56,56	0.52	0
26	CHD	C	305	-	32,32,32	0.59	0	51,51,51	0.80	0
21	TGL	B	301	-	62,62,62	0.36	0	65,65,65	0.47	1 (1%)
26	CHD	J	101	-	32,32,32	0.73	0	51,51,51	1.08	3 (5%)
23	DMU	Z	102	-	34,34,34	1.09	3 (8%)	45,45,45	1.15	3 (6%)
24	PEK	T	104	-	52,52,52	0.41	0	55,57,57	0.57	1 (1%)
14	HEA	N	601	1	67,67,67	2.31	25 (37%)	81,103,103	2.44	27 (33%)
18	PGV	A	606	-	50,50,50	0.38	0	53,56,56	0.52	0
26	CHD	C	306	-	32,32,32	0.52	0	51,51,51	0.64	0
24	PEK	C	307	-	52,52,52	0.44	0	55,57,57	0.50	0
23	DMU	D	202	-	34,34,34	0.99	1 (2%)	45,45,45	1.52	6 (13%)
21	TGL	Q	201	-	62,62,62	0.38	0	65,65,65	0.50	2 (3%)
25	CDL	G	101	-	99,99,99	0.40	0	105,111,111	0.52	1 (0%)
14	HEA	A	601	1	67,67,67	2.53	27 (40%)	81,103,103	2.49	27 (33%)
29	SAC	V	101	-	7,8,9	0.54	0	7,9,11	1.01	1 (14%)
19	EDO	G	104	-	3,3,3	0.15	0	2,2,2	0.07	0
19	EDO	A	608	-	3,3,3	0.24	0	2,2,2	0.18	0
26	CHD	W	102	-	32,32,32	0.69	0	51,51,51	0.85	2 (3%)
25	CDL	P	304	-	99,99,99	0.38	0	105,111,111	0.46	1 (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
19	EDO	S	102	-	-	0/1/1/1	-
18	PGV	A	607	-	1/1/5/7	33/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	CHD	P	306	-	-	1/9/74/74	0/4/4/4
19	EDO	T	106	-	-	0/1/1/1	-
19	EDO	C	309	-	-	1/1/1/1	-
26	CHD	G	103	-	-	4/9/74/74	0/4/4/4
18	PGV	Z	101	-	-	30/55/55/55	-
21	TGL	L	101	-	-	38/65/65/65	-
18	PGV	P	303	-	-	13/55/55/55	-
18	PGV	C	303	-	-	13/55/55/55	-
19	EDO	A	609	-	-	0/1/1/1	-
21	TGL	D	201	-	-	35/65/65/65	-
26	CHD	P	305	-	-	6/9/74/74	0/4/4/4
23	DMU	W	101	-	-	5/19/59/59	0/2/2/2
27	PSC	E	201	-	-	24/55/55/55	-
18	PGV	P	302	-	-	22/55/55/55	-
14	HEA	A	602	1	-	5/36/76/76	-
24	PEK	T	102	-	-	16/56/56/56	-
24	PEK	C	302	-	-	12/56/56/56	-
21	TGL	Y	101	-	-	37/65/65/65	-
23	DMU	C	301	-	-	11/19/59/59	0/2/2/2
29	SAC	I	101	-	-	4/7/8/10	-
26	CHD	T	101	-	-	2/9/74/74	0/4/4/4
25	CDL	C	304	-	-	69/110/110/110	-
24	PEK	G	102	-	-	27/56/56/56	-
25	CDL	T	105	-	-	56/110/110/110	-
14	HEA	N	602	1	-	8/36/76/76	-
24	PEK	T	103	-	-	27/56/56/56	-
18	PGV	C	308	-	-	35/55/55/55	-
19	EDO	S	103	-	-	1/1/1/1	-
19	EDO	N	607	-	-	0/1/1/1	-
21	TGL	N	606	-	-	34/65/65/65	-
27	PSC	O	302	-	-	22/55/55/55	-
18	PGV	P	301	-	-	13/55/55/55	-
26	CHD	C	305	-	-	5/9/74/74	0/4/4/4
21	TGL	B	301	-	-	31/65/65/65	-
26	CHD	J	101	-	-	4/9/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	DMU	Z	102	-	-	5/19/59/59	0/2/2/2
24	PEK	T	104	-	-	22/56/56/56	-
14	HEA	N	601	1	-	8/36/76/76	-
18	PGV	A	606	-	-	11/55/55/55	-
26	CHD	C	306	-	-	0/9/74/74	0/4/4/4
24	PEK	C	307	-	-	23/56/56/56	-
23	DMU	D	202	-	-	10/19/59/59	0/2/2/2
21	TGL	Q	201	-	-	33/65/65/65	-
25	CDL	G	101	-	-	59/110/110/110	-
14	HEA	A	601	1	-	8/36/76/76	-
29	SAC	V	101	-	-	3/7/8/10	-
19	EDO	G	104	-	-	1/1/1/1	-
19	EDO	A	608	-	-	1/1/1/1	-
26	CHD	W	102	-	1/1/12/12	4/9/74/74	0/4/4/4
25	CDL	P	304	-	-	58/110/110/110	-

The worst 5 of 126 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	W	101	DMU	O16-C6	7.14	1.52	1.40
23	C	301	DMU	O16-C6	6.30	1.50	1.40
14	N	601	HEA	C3B-C2B	5.51	1.47	1.34
14	A	601	HEA	C3D-C2D	5.31	1.48	1.36
14	A	601	HEA	C11-C3B	-5.21	1.45	1.51

The worst 5 of 174 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	602	HEA	C3A-C2A-C1A	-7.78	99.68	107.05
14	N	602	HEA	C3A-C2A-C1A	-7.50	99.95	107.05
14	A	601	HEA	C13-C12-C11	-7.24	102.82	114.39
14	N	602	HEA	C2A-C1A-NA	7.23	117.30	110.32
14	N	602	HEA	C3D-C4D-ND	7.07	117.18	110.35

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
18	A	607	PGV	C05
26	W	102	CHD	C3

5 of 890 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	601	HEA	C2A-C3A-CMA-OMA
14	A	602	HEA	C2D-C3D-CAD-CBD
14	N	601	HEA	C2A-C3A-CMA-OMA
14	N	602	HEA	C2A-C3A-CMA-OMA
14	N	602	HEA	C4D-C3D-CAD-CBD

There are no ring outliers.

35 monomers are involved in 100 short contacts:

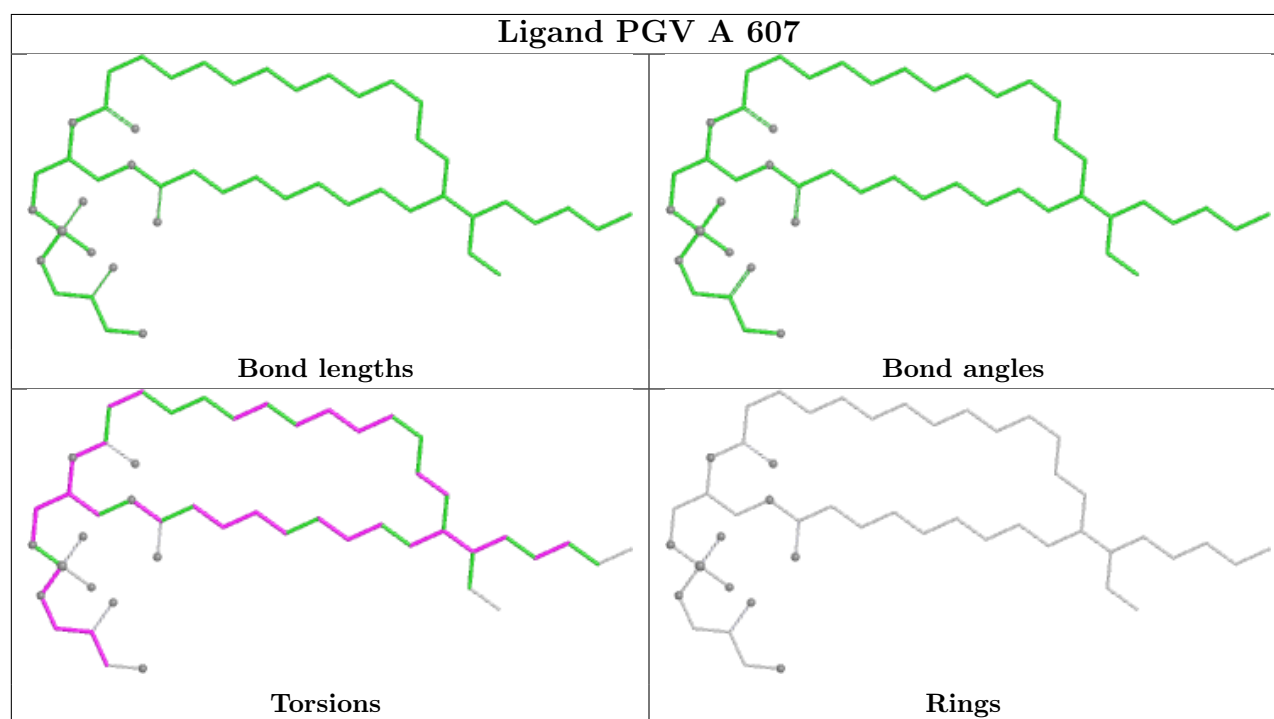
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	S	102	EDO	1	0
18	A	607	PGV	5	0
19	C	309	EDO	1	0
18	Z	101	PGV	2	0
21	L	101	TGL	4	0
18	P	303	PGV	1	0
21	D	201	TGL	4	0
26	P	305	CHD	1	0
23	W	101	DMU	7	0
27	E	201	PSC	6	0
18	P	302	PGV	1	0
14	A	602	HEA	5	0
24	T	102	PEK	4	0
24	C	302	PEK	1	0
21	Y	101	TGL	2	0
23	C	301	DMU	6	0
26	T	101	CHD	1	0
25	C	304	CDL	2	0
24	G	102	PEK	3	0
25	T	105	CDL	7	0
14	N	602	HEA	4	0
19	S	103	EDO	4	0
27	O	302	PSC	2	0
18	P	301	PGV	5	0
26	C	305	CHD	1	0
24	T	104	PEK	2	0
14	N	601	HEA	6	0
26	C	306	CHD	1	0
25	G	101	CDL	4	0
14	A	601	HEA	4	0
29	V	101	SAC	1	0

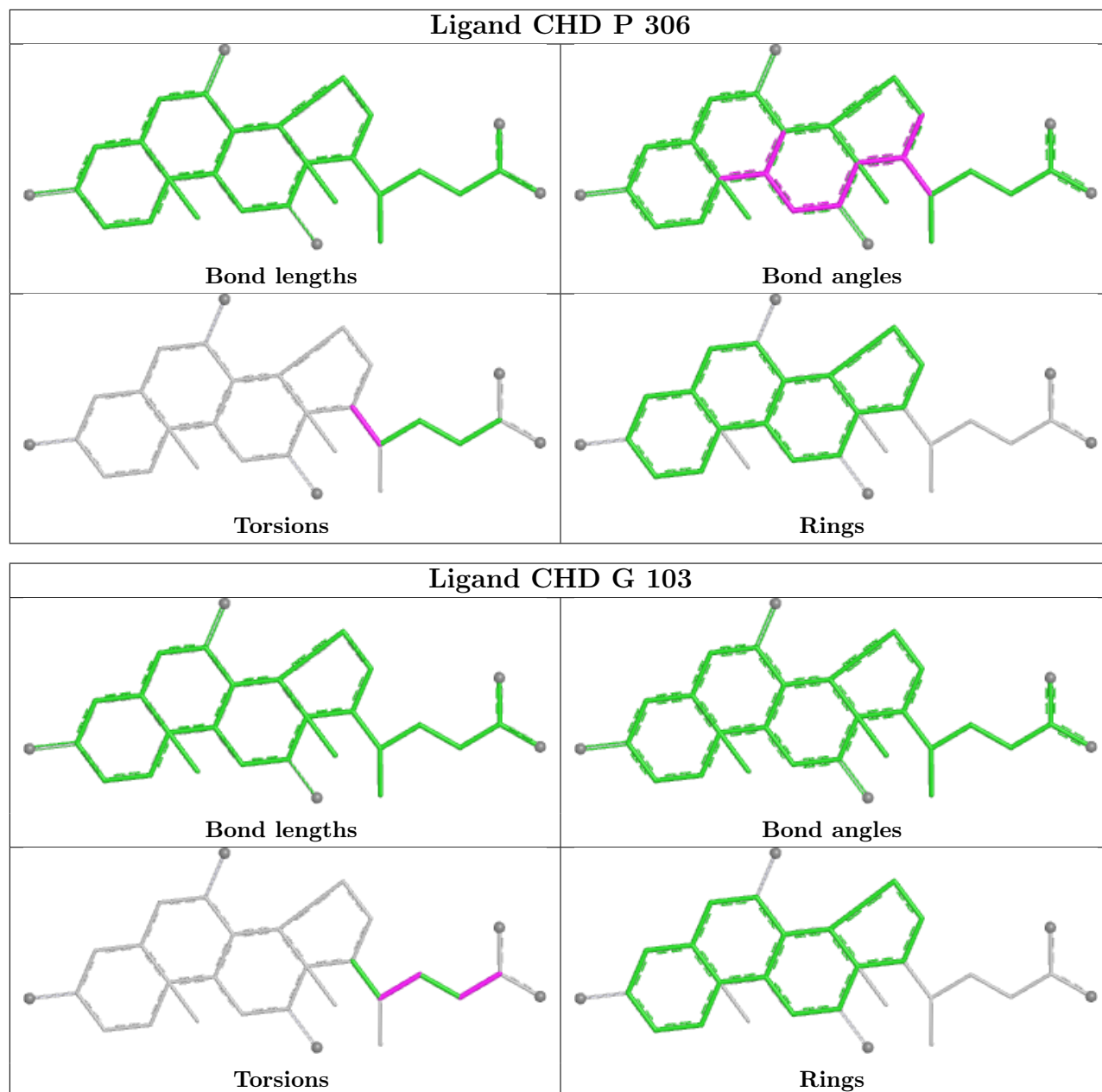
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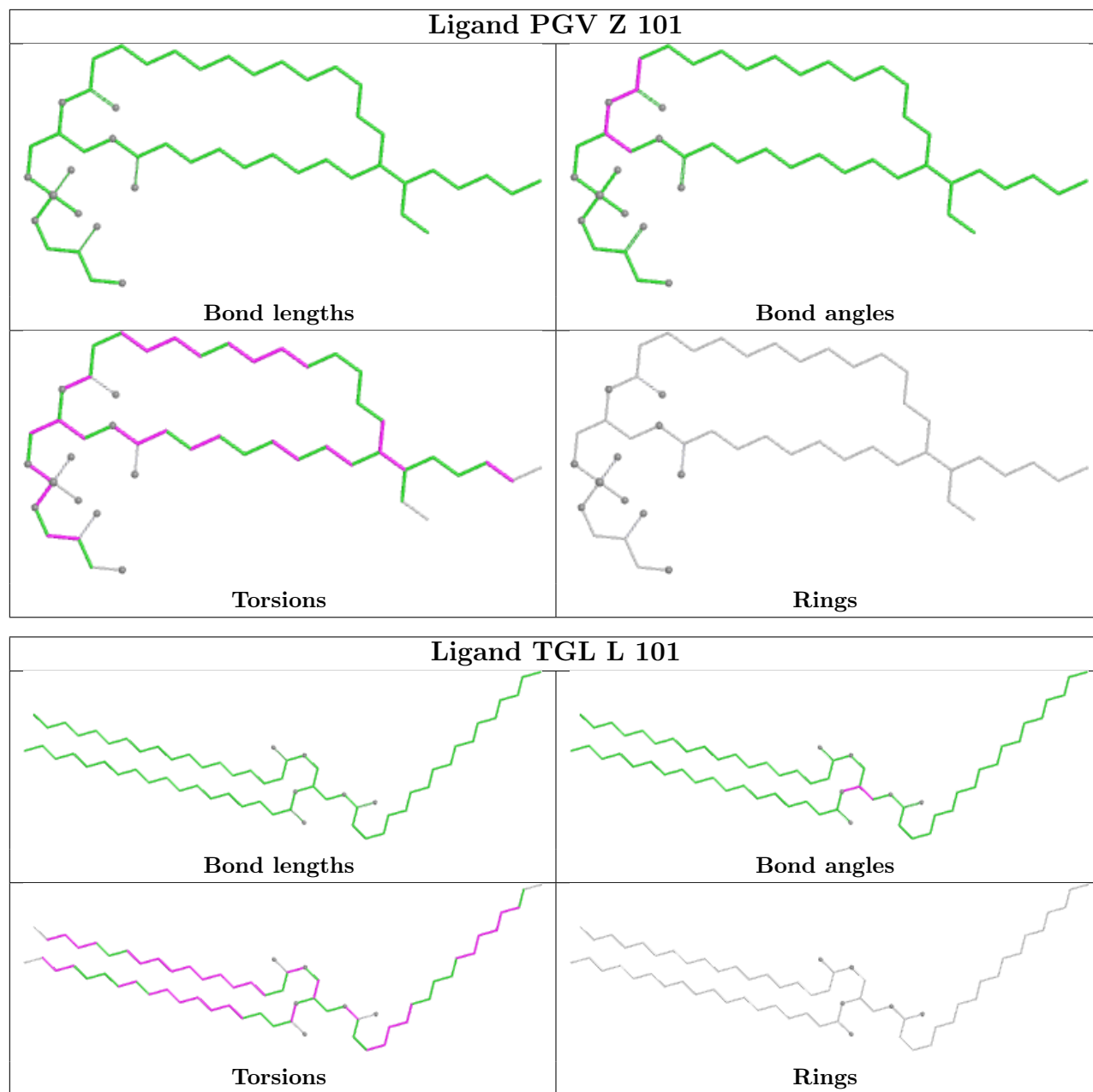
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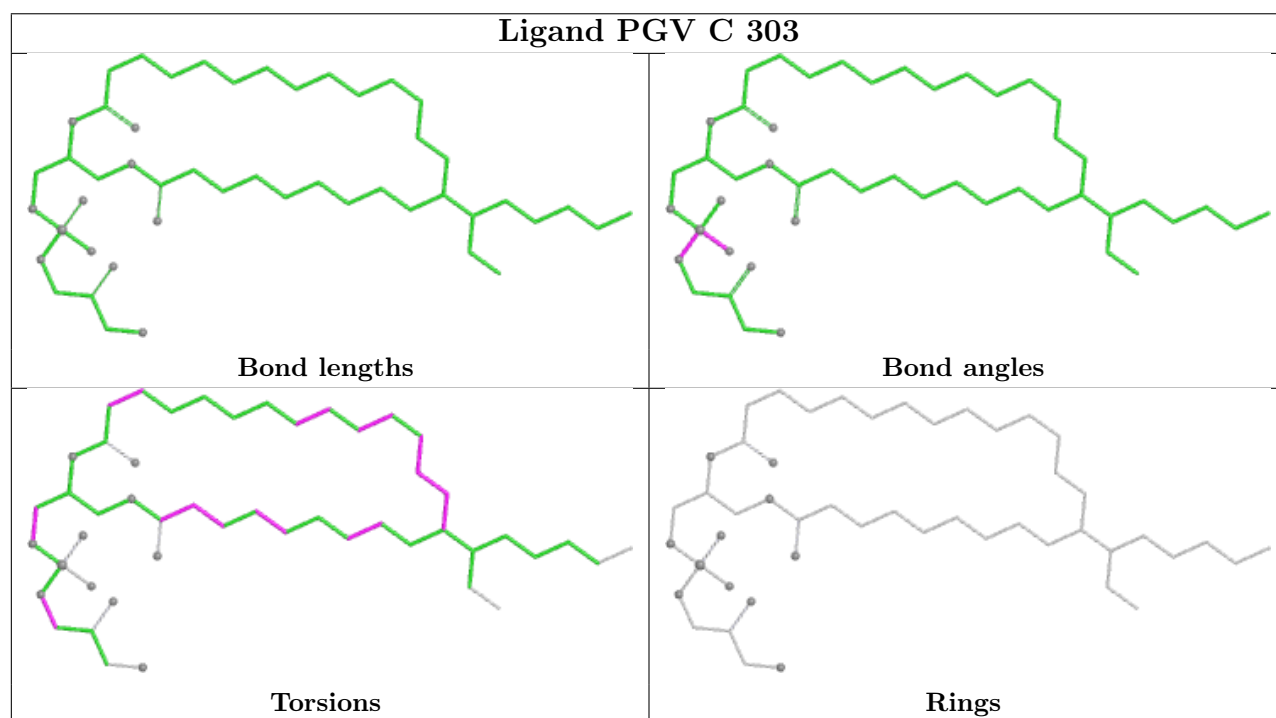
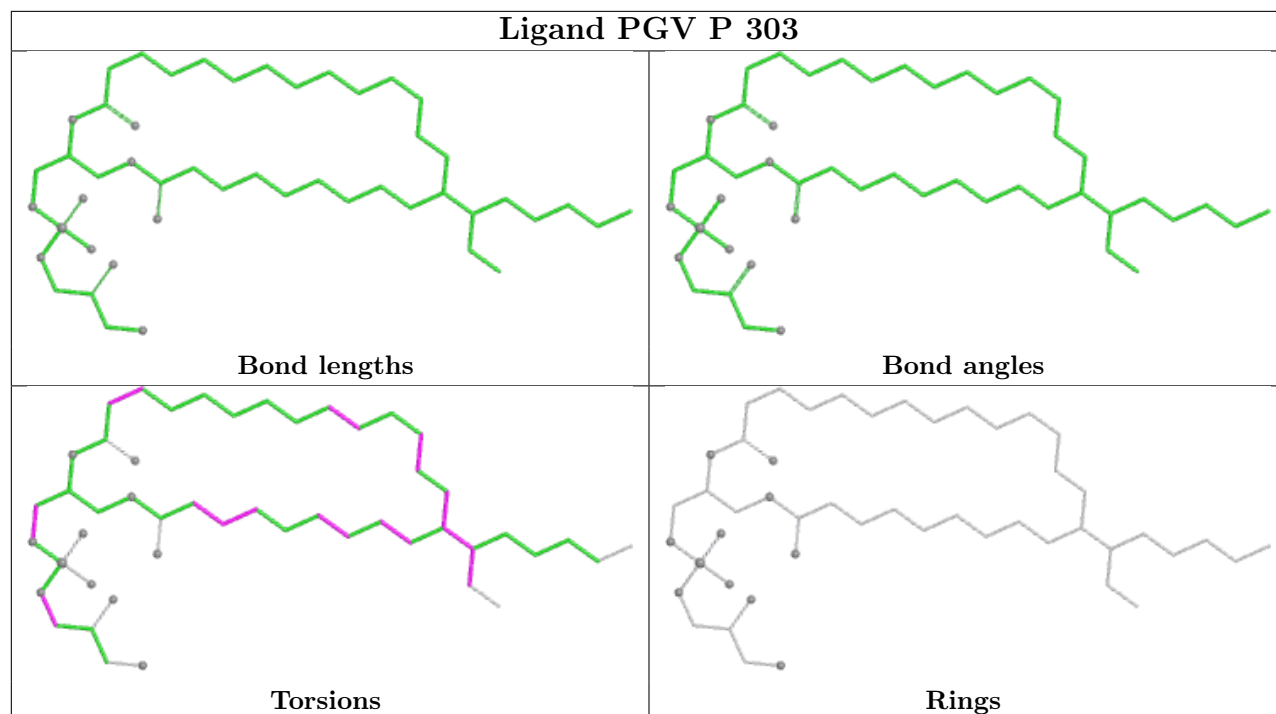
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	G	104	EDO	1	0
19	A	608	EDO	1	0
26	W	102	CHD	1	0
25	P	304	CDL	2	0

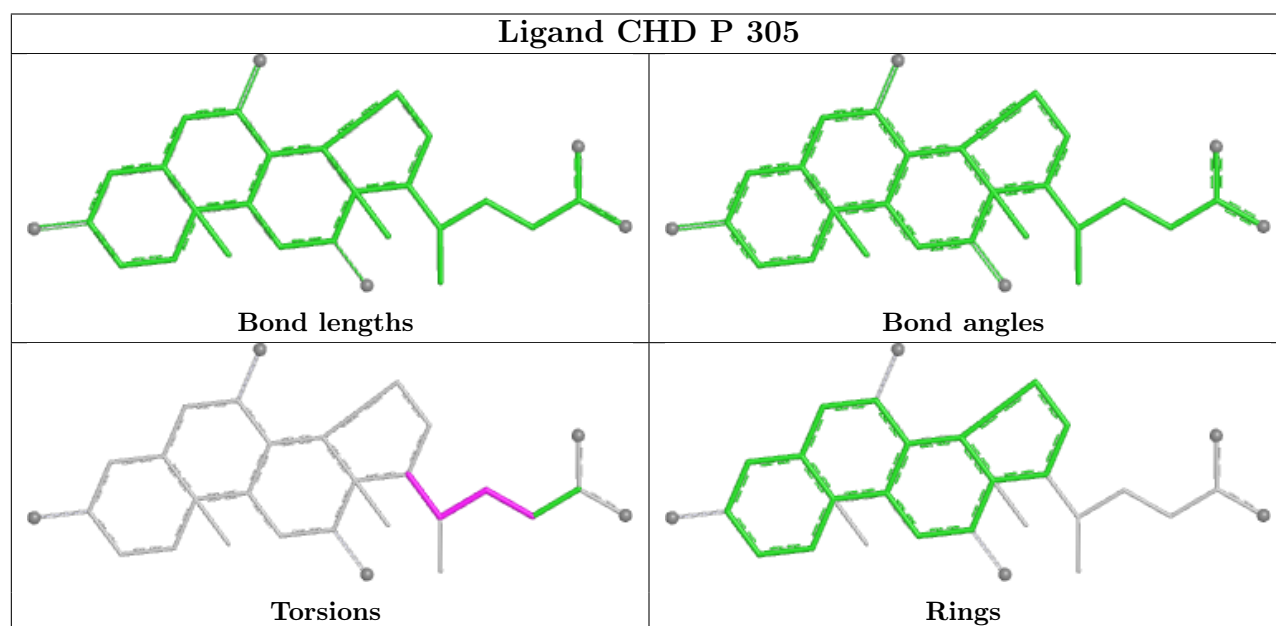
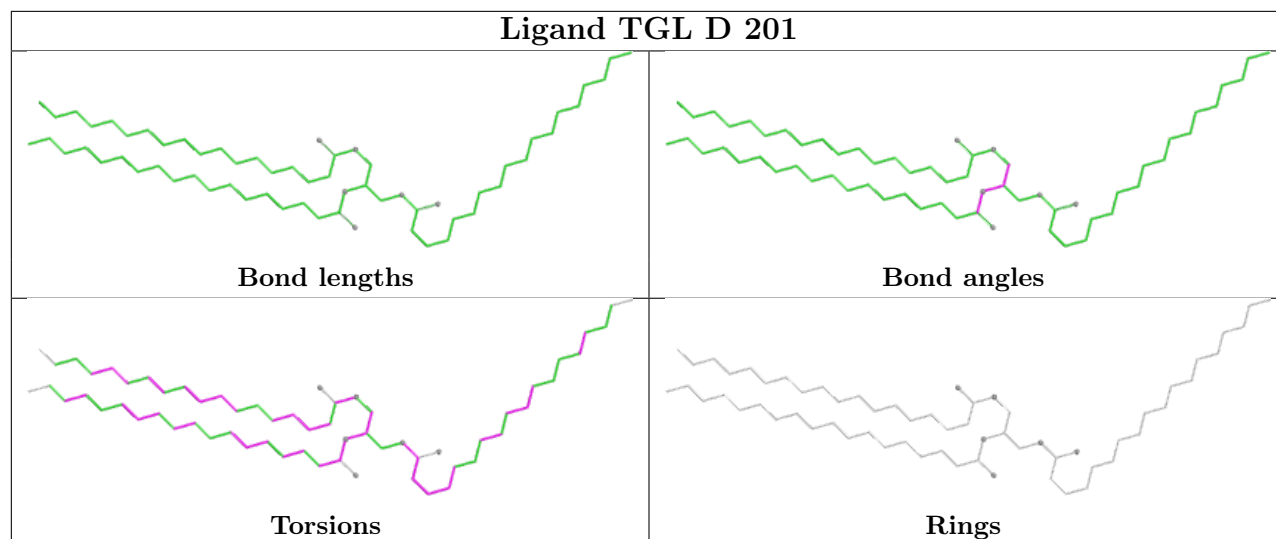
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

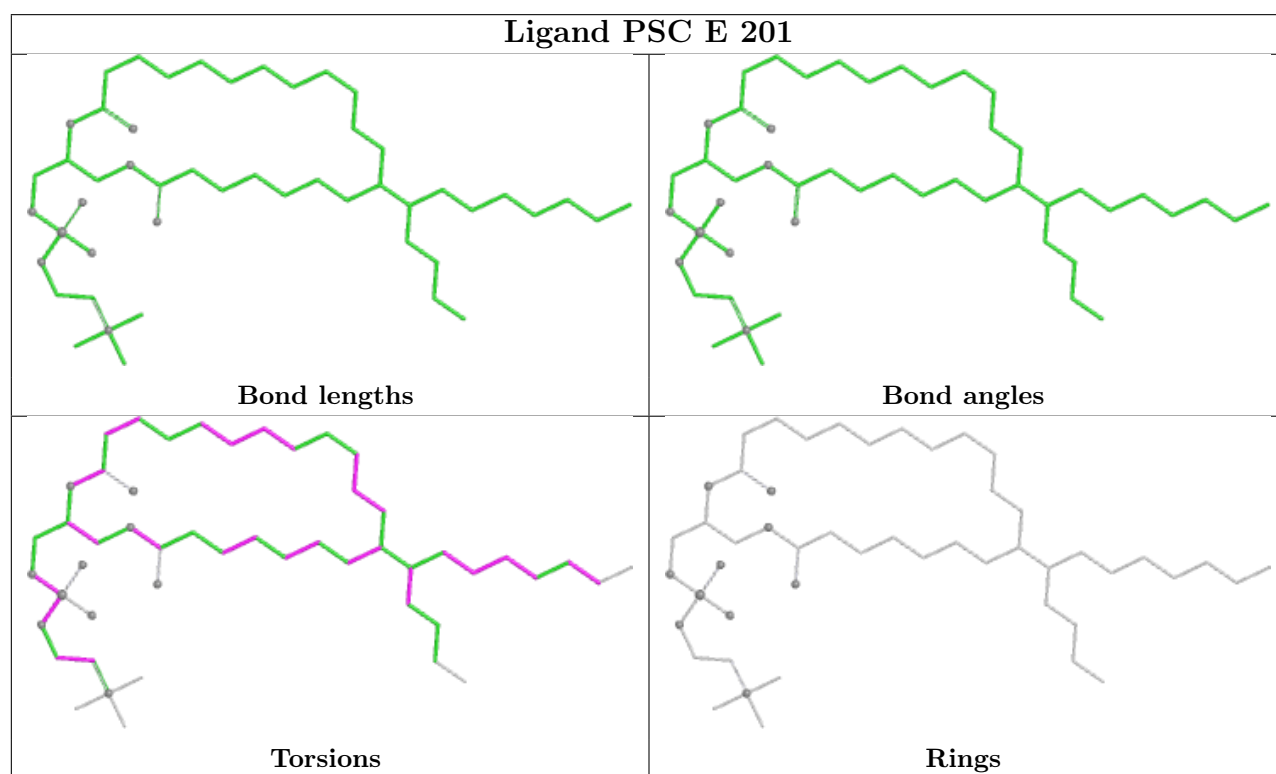
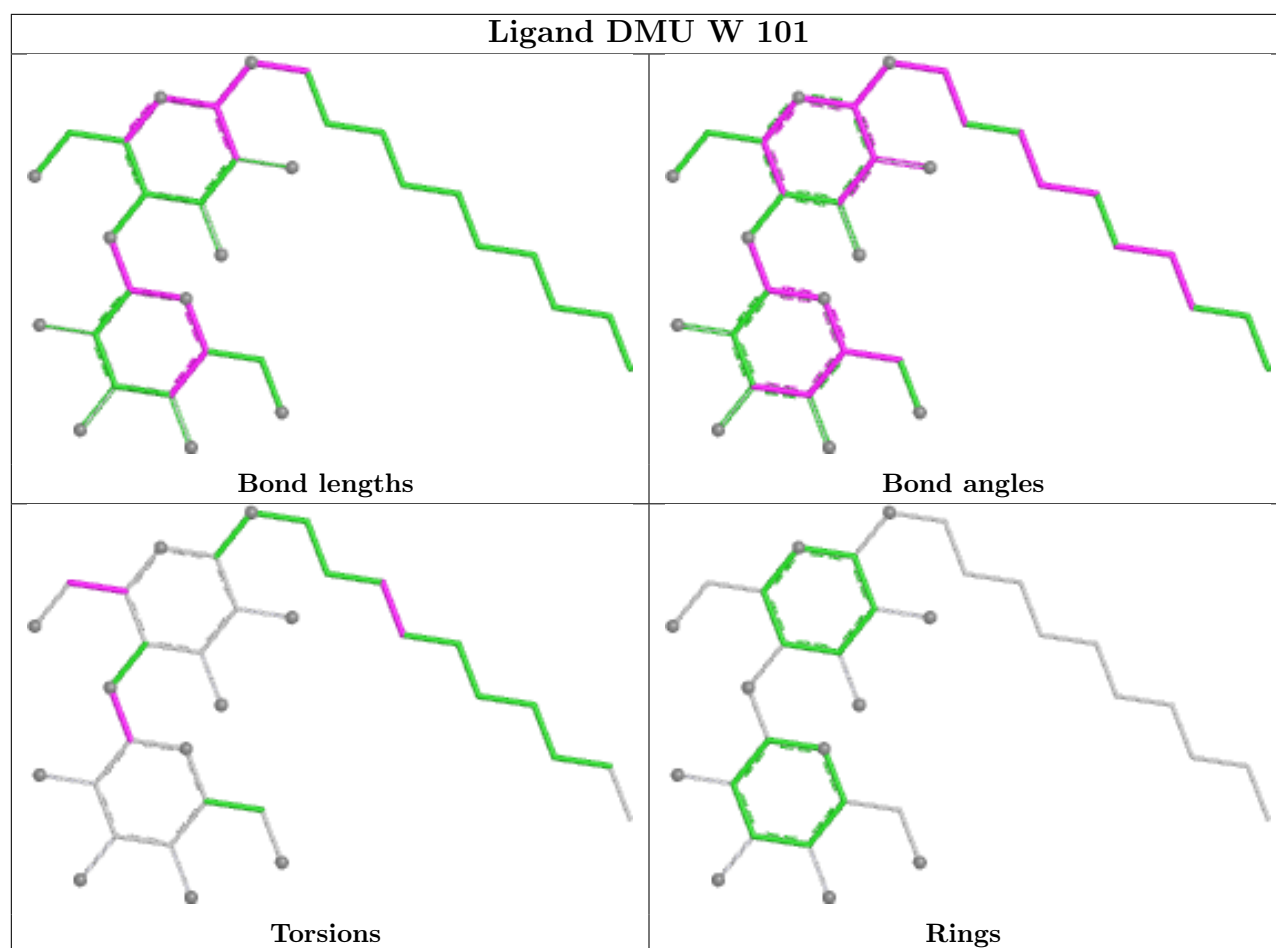


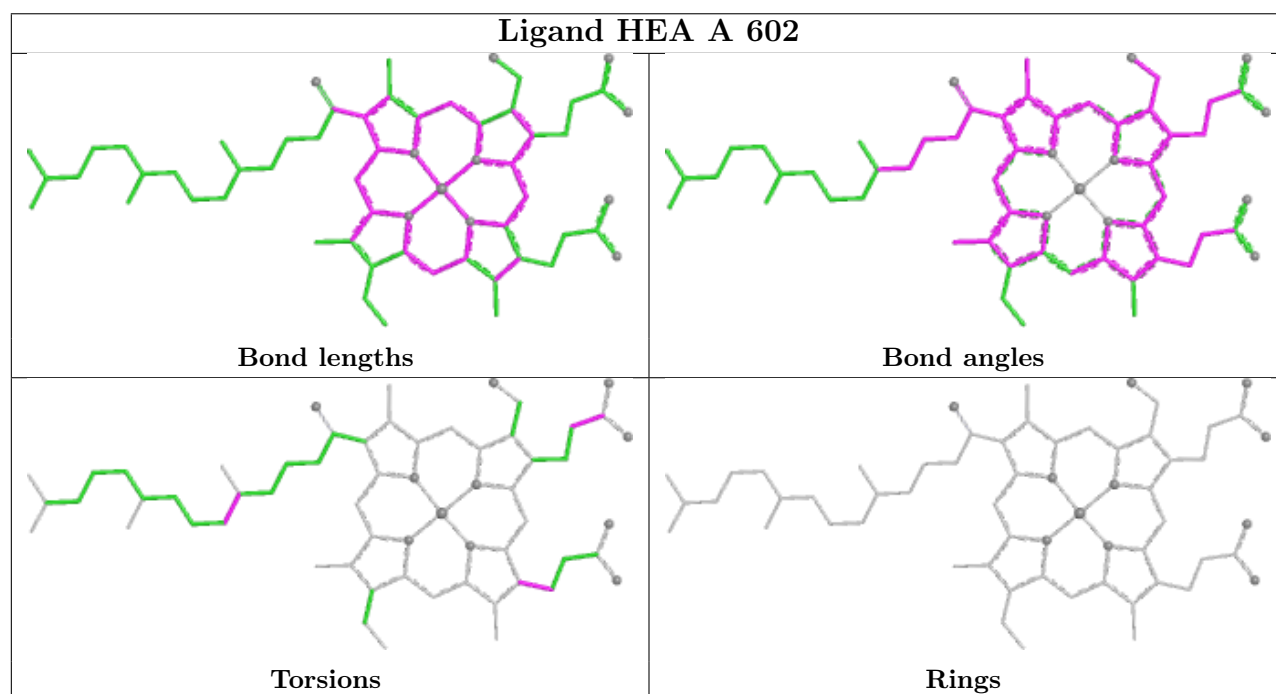
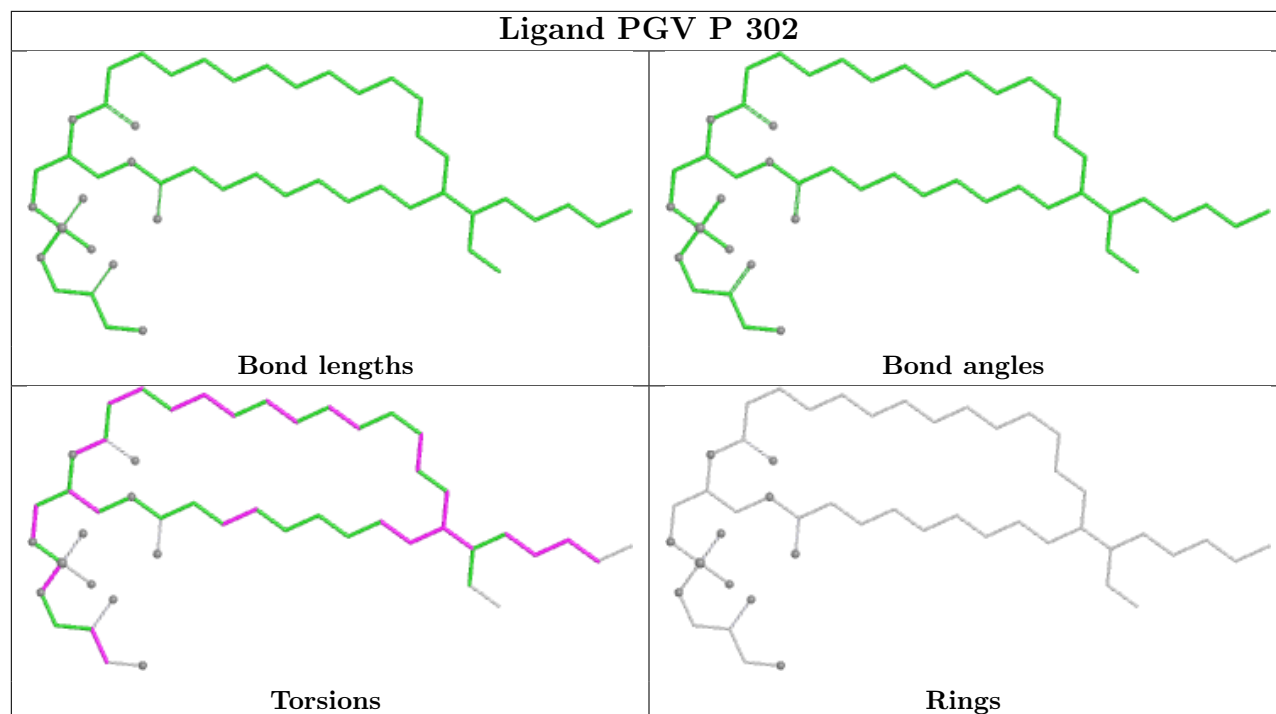




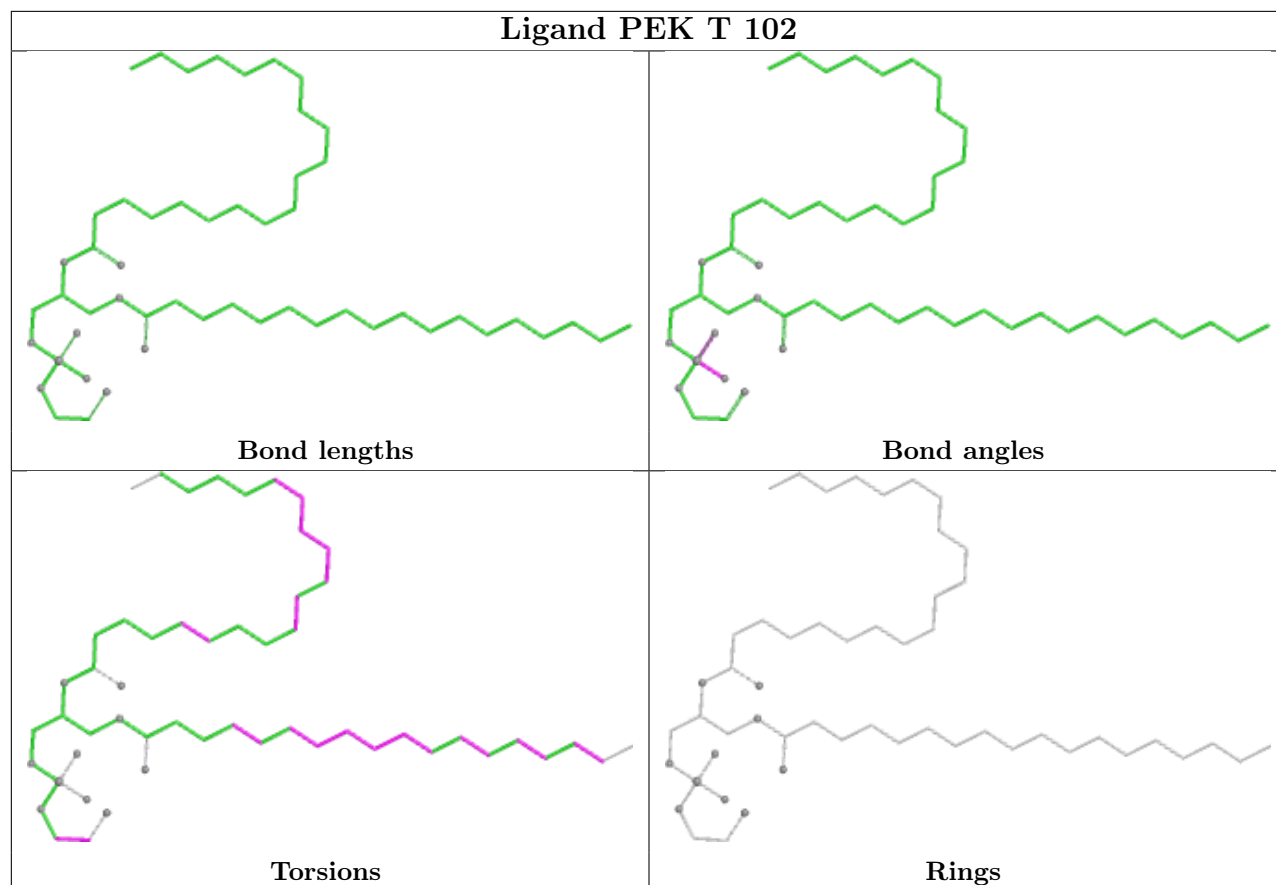




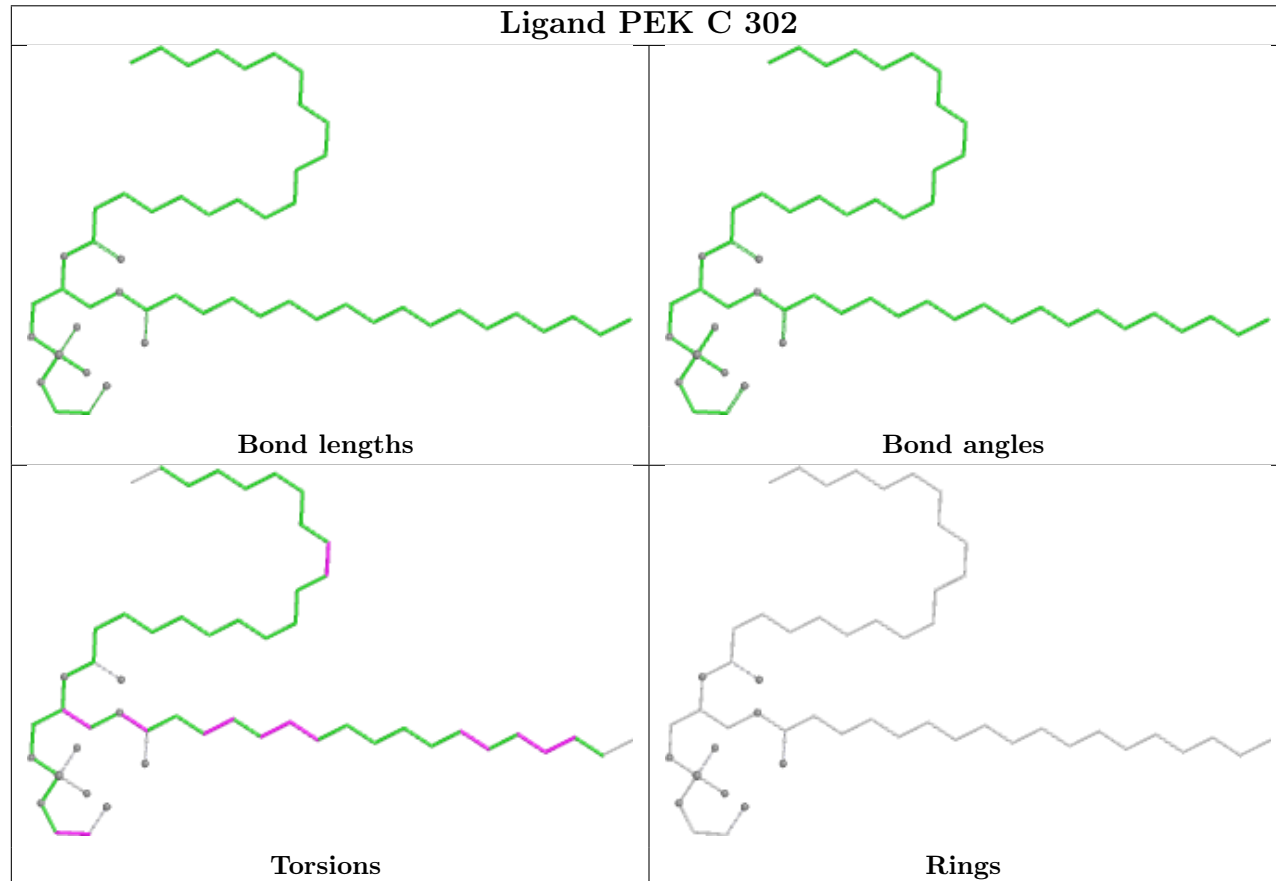


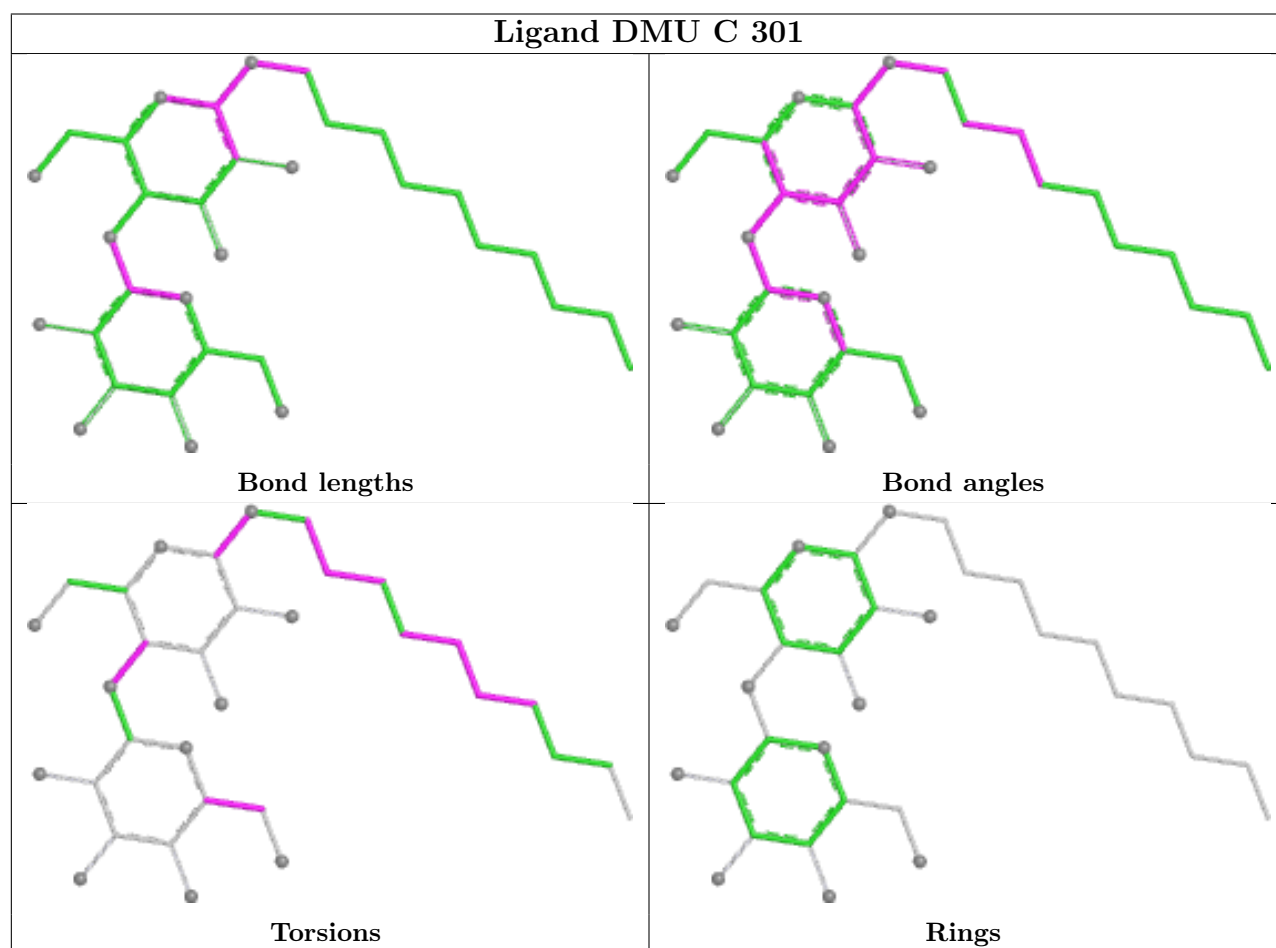
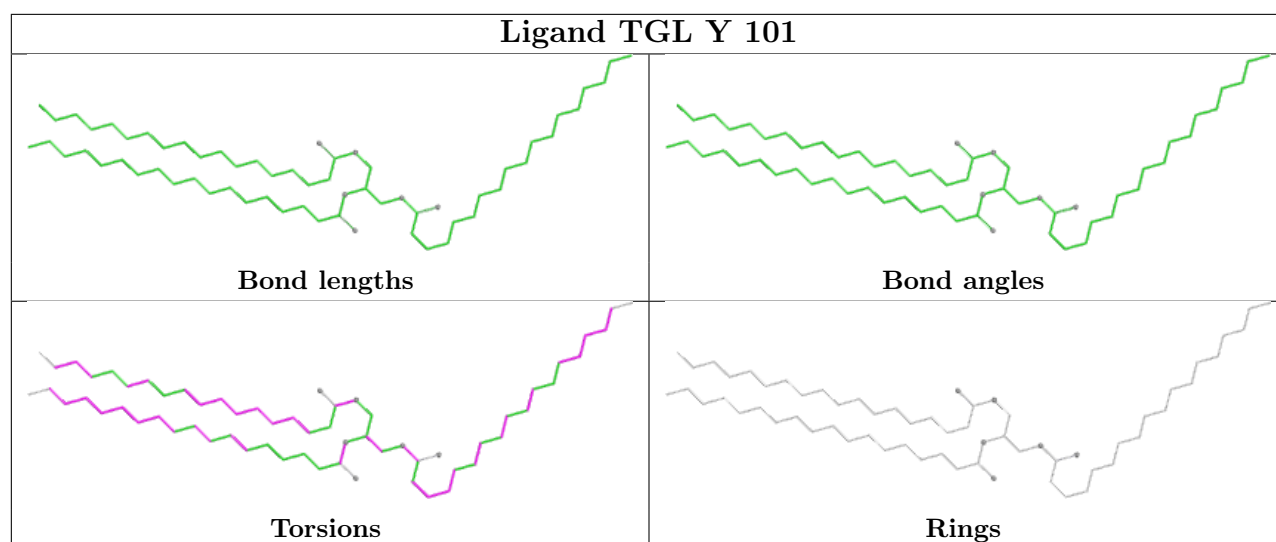


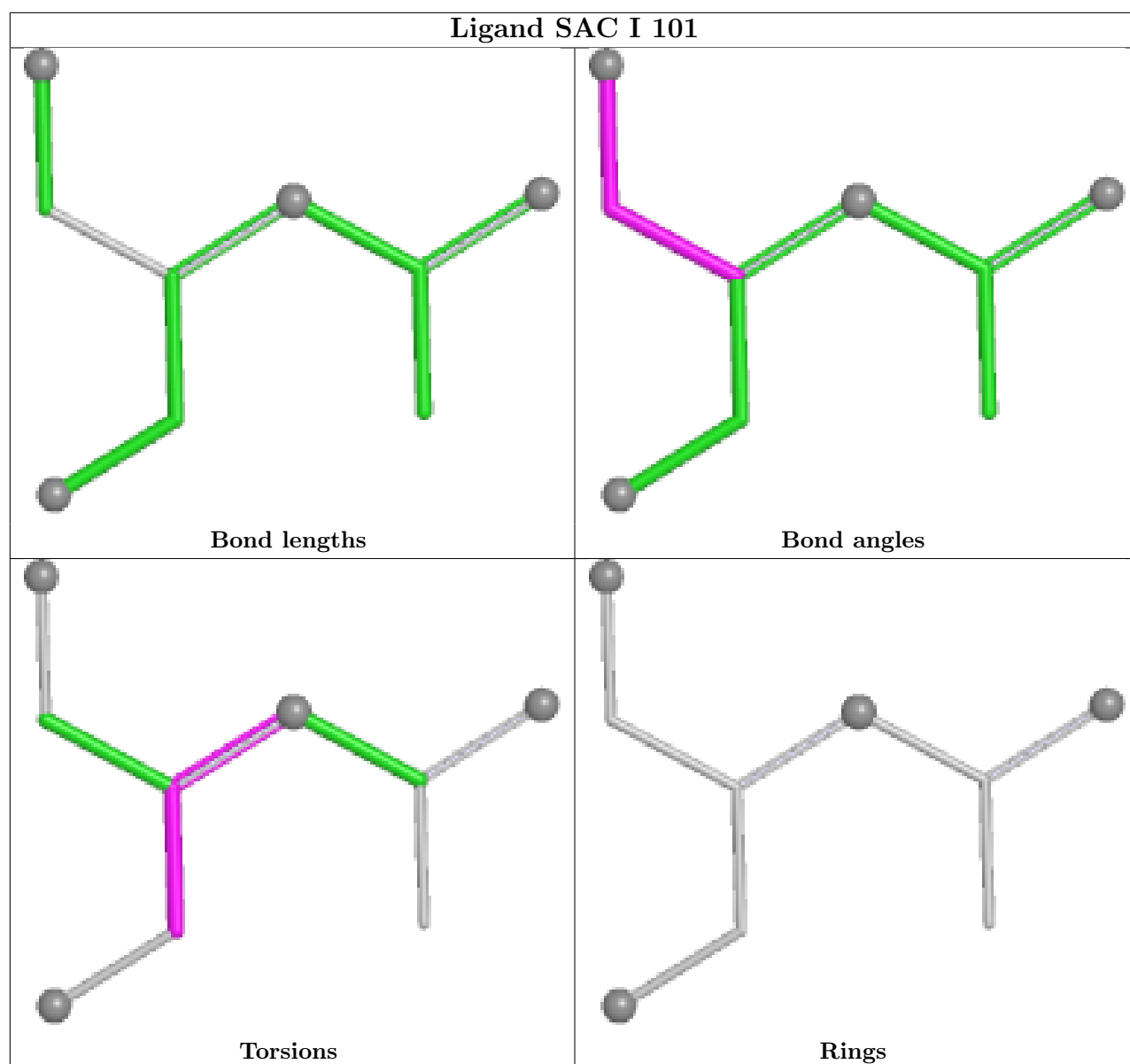
Ligand PEK T 102

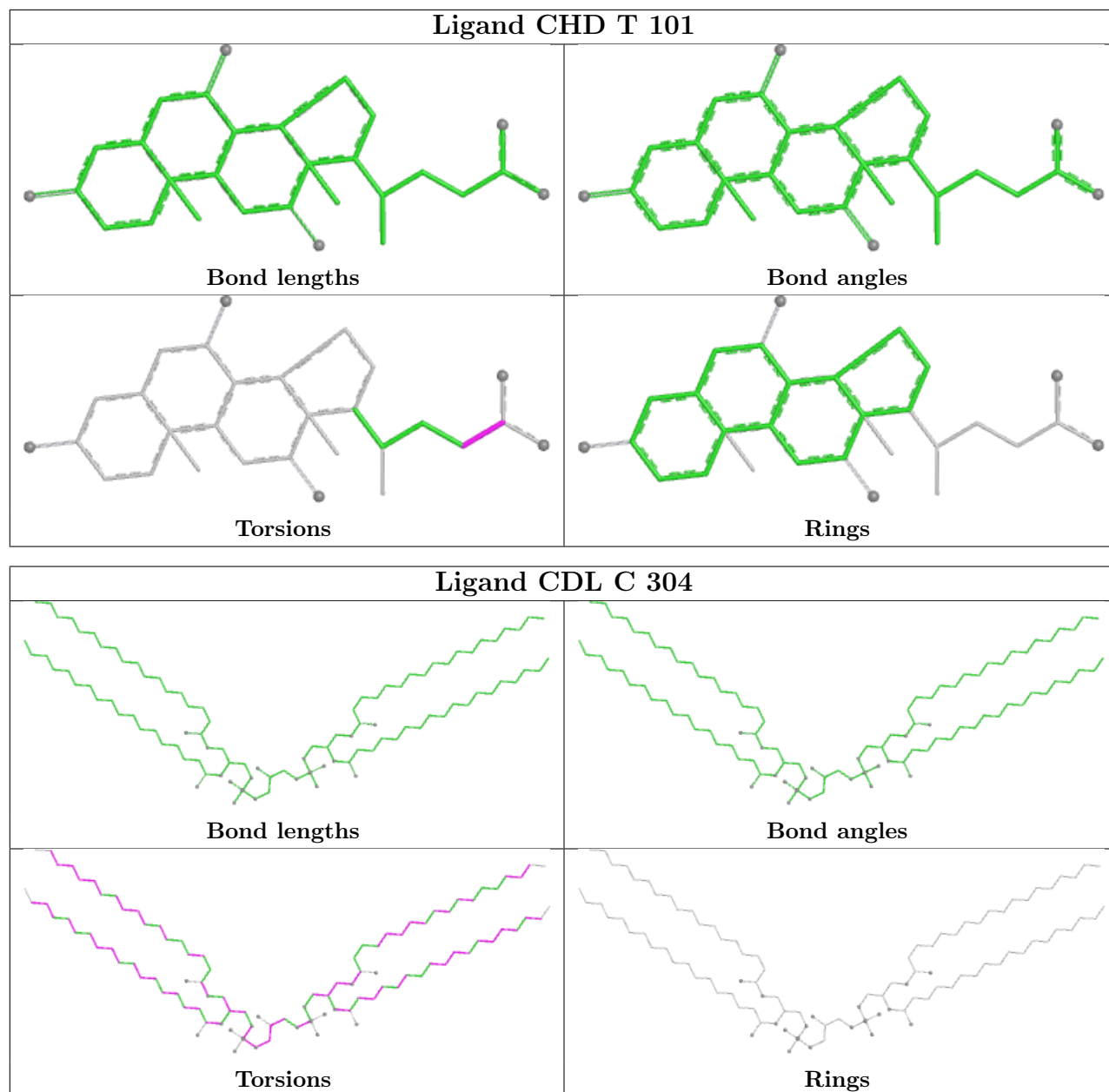


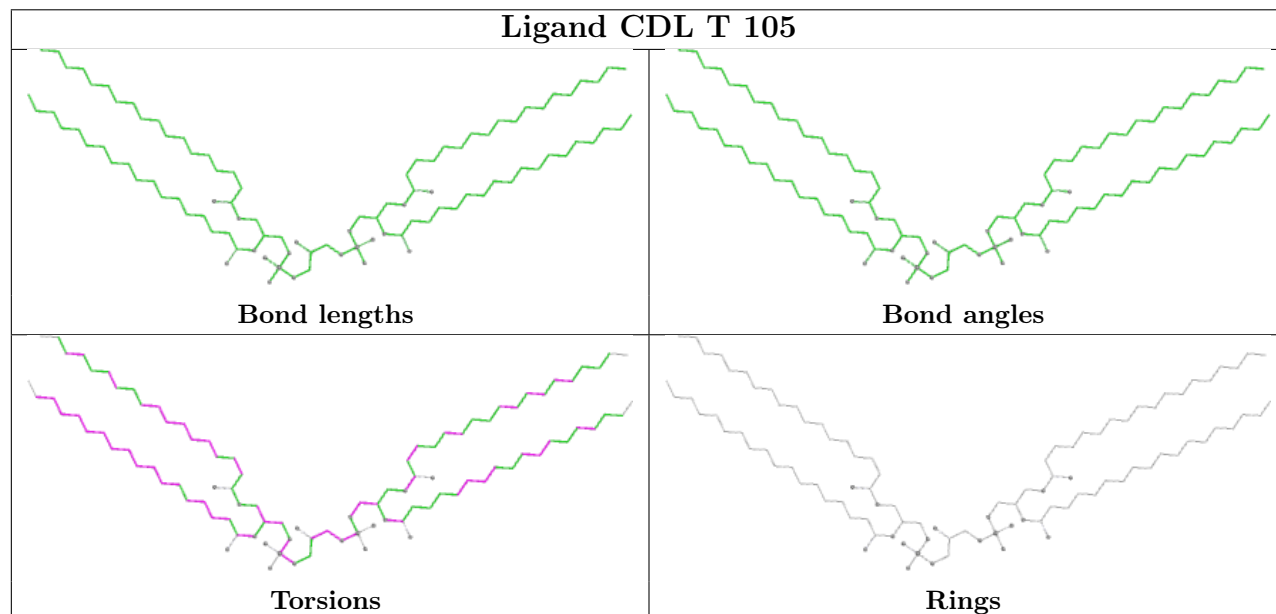
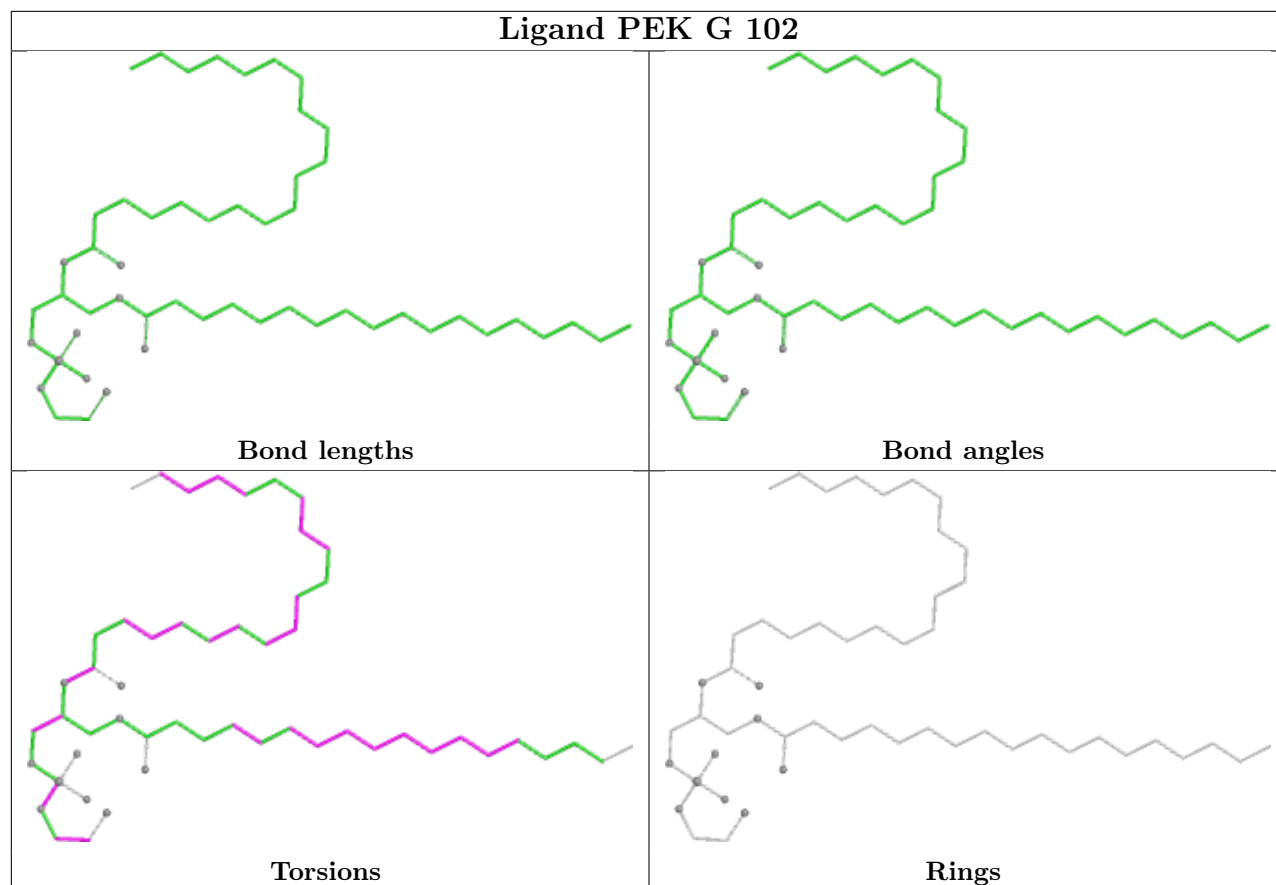
Ligand PEK C 302

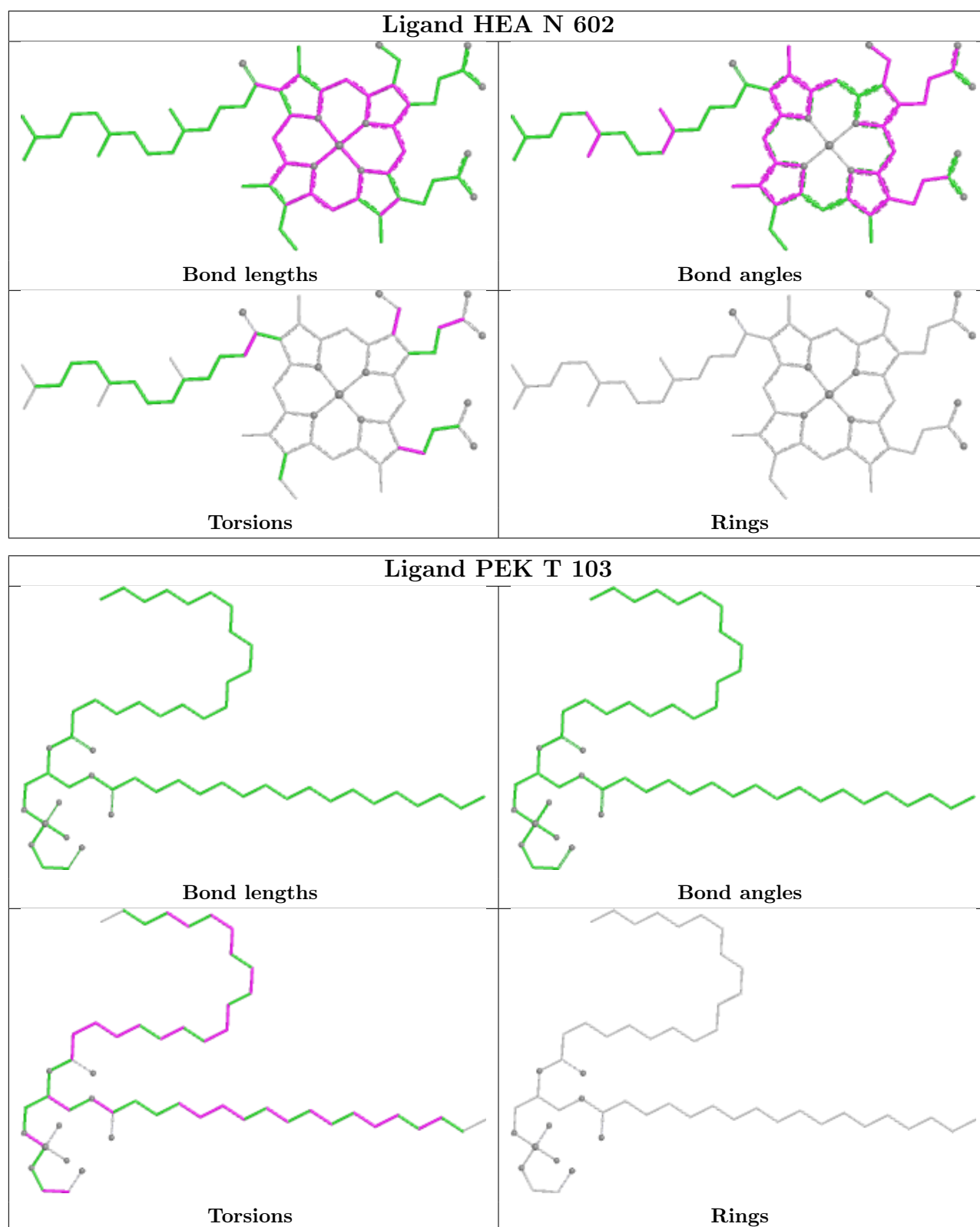


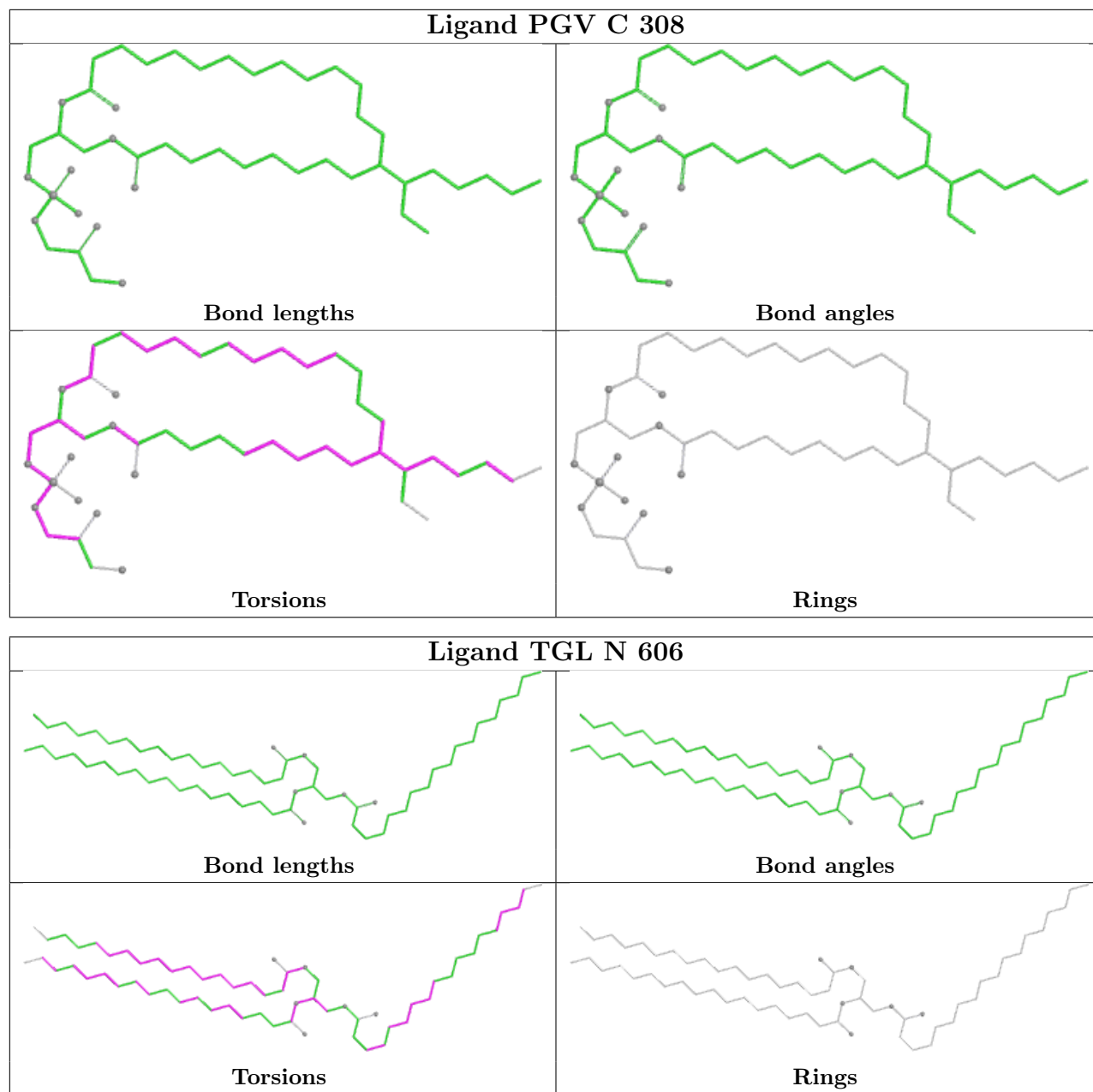




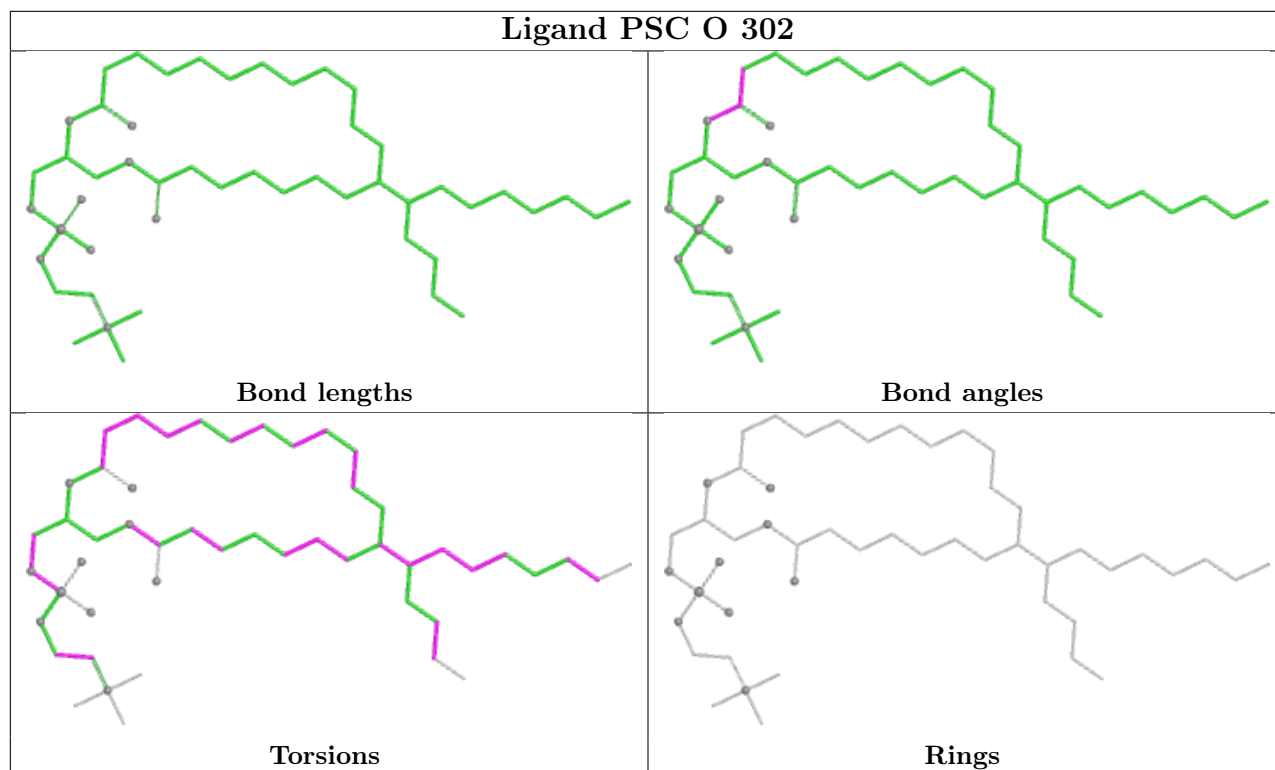




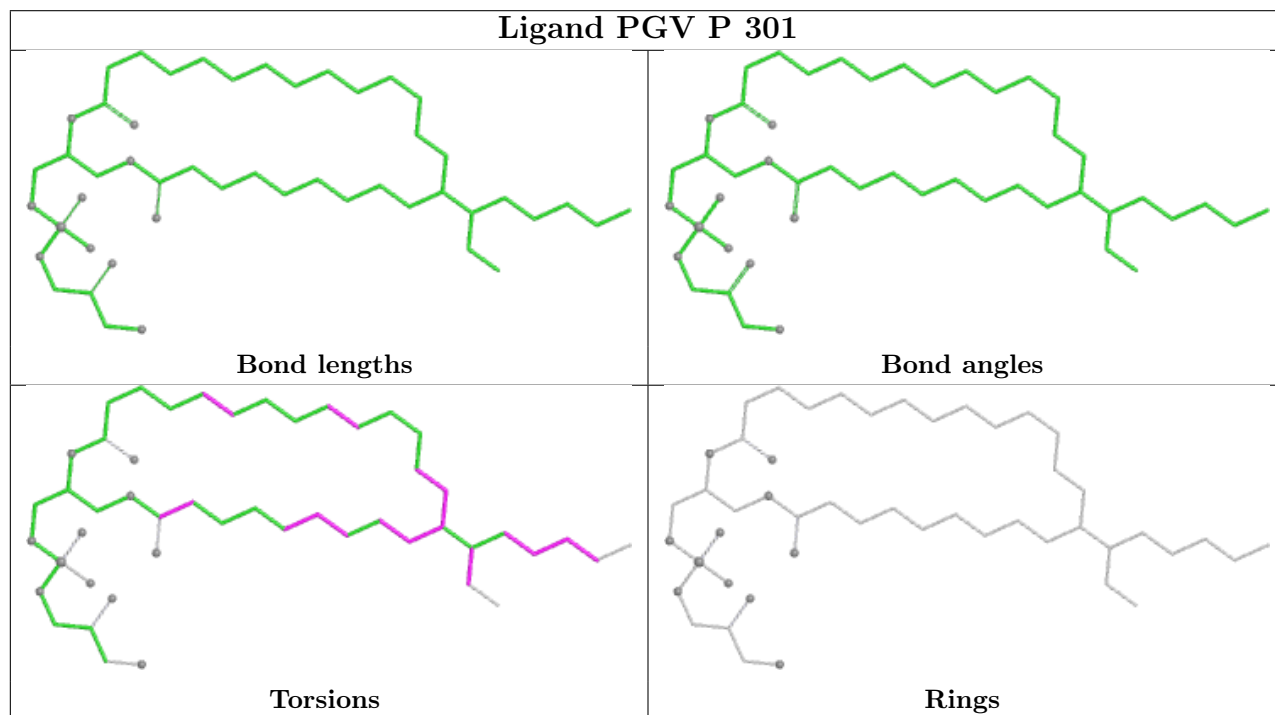


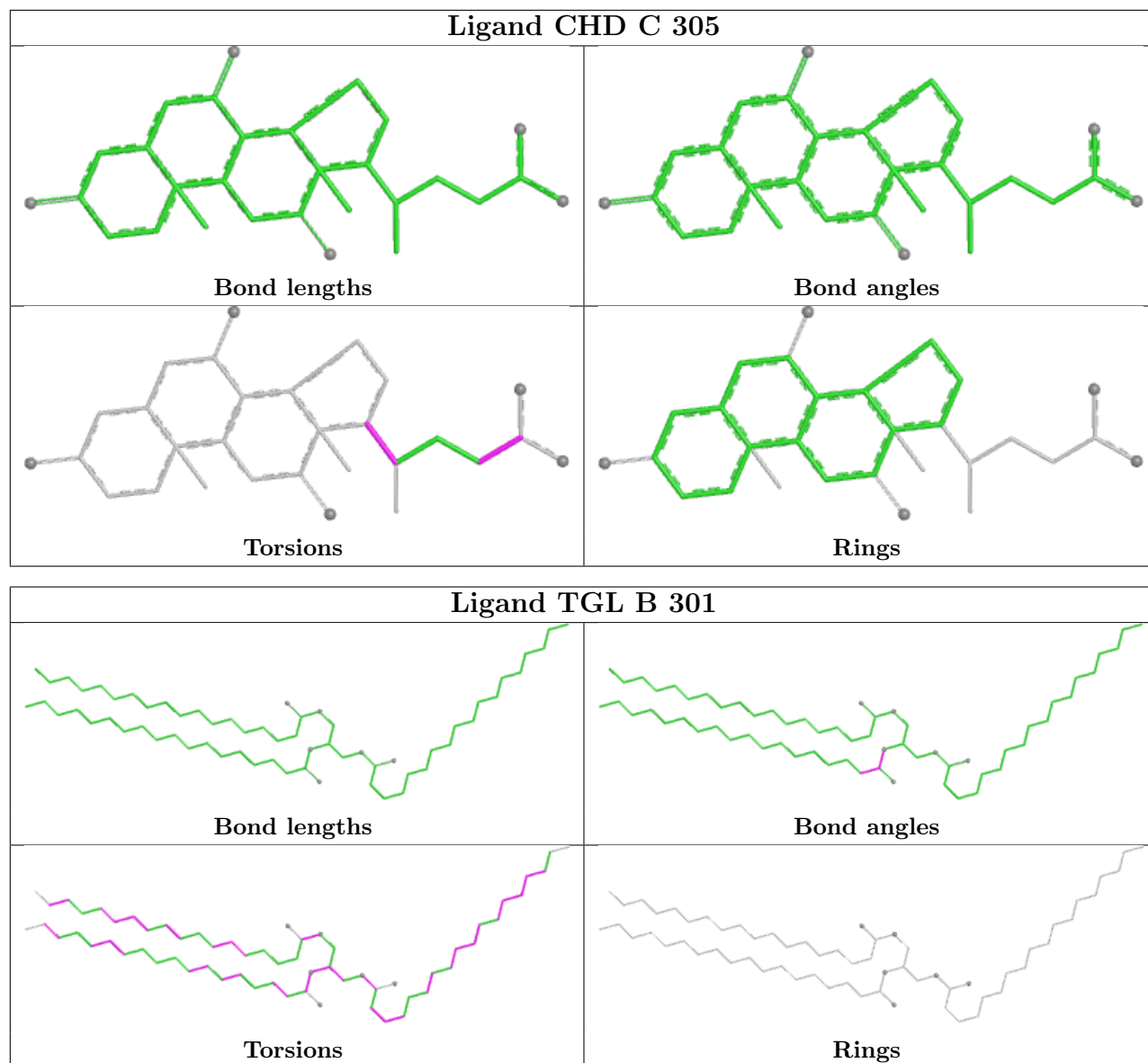


Ligand PSC O 302

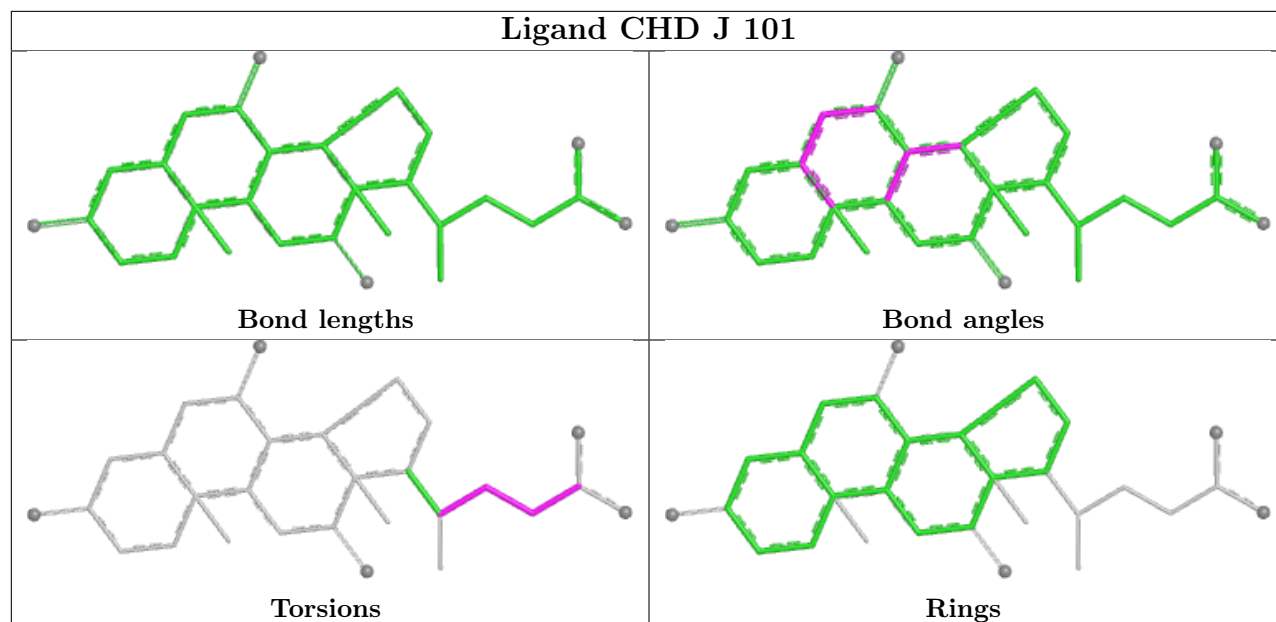


Ligand PGV P 301

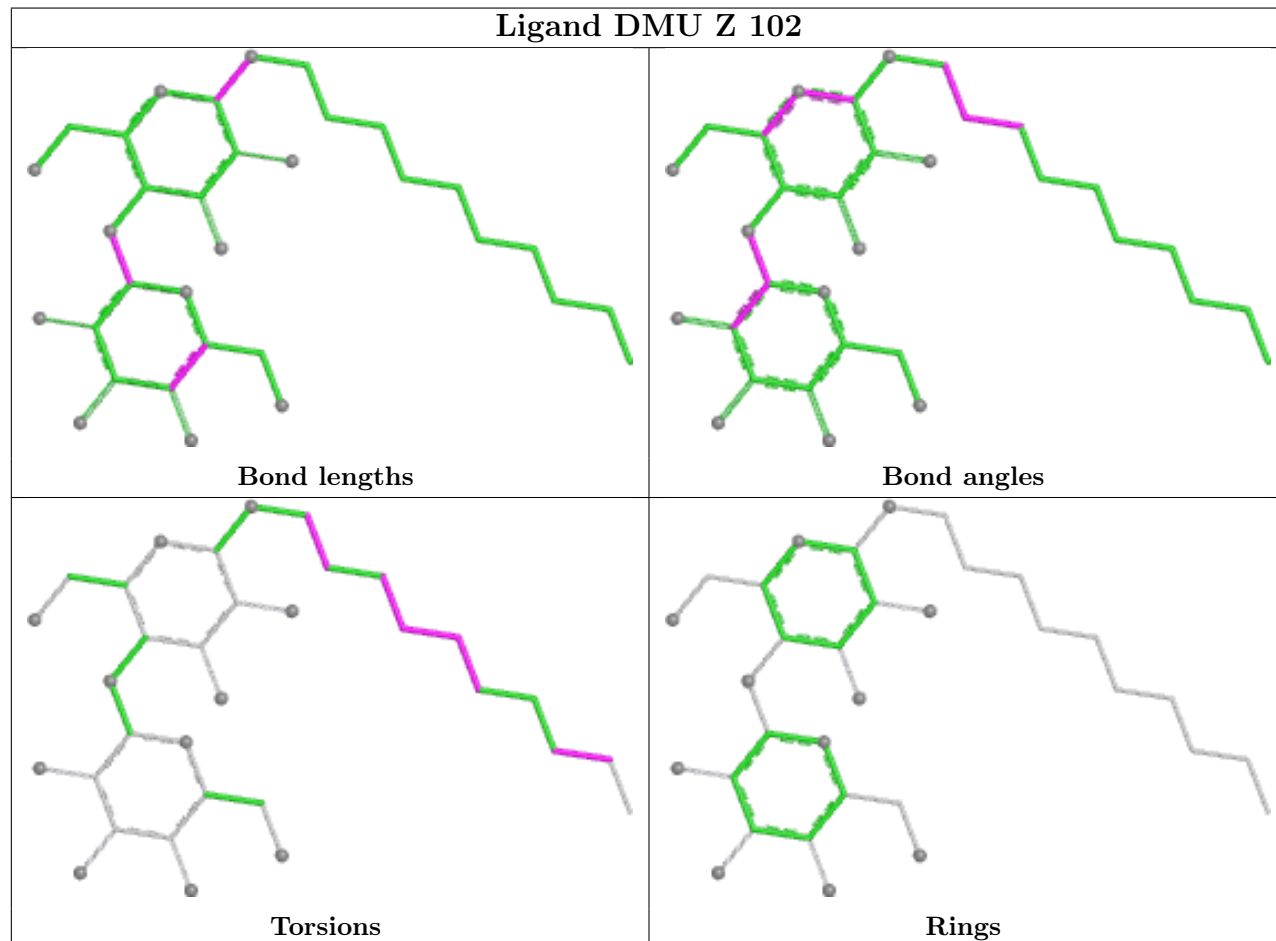


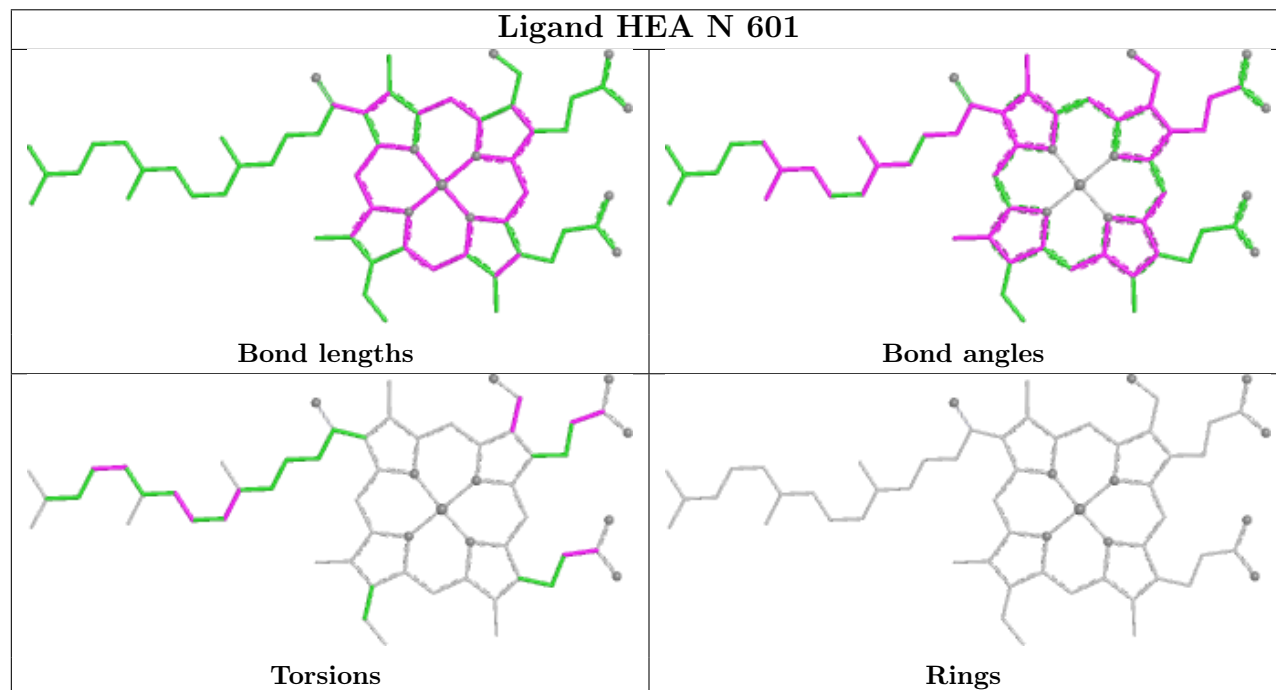
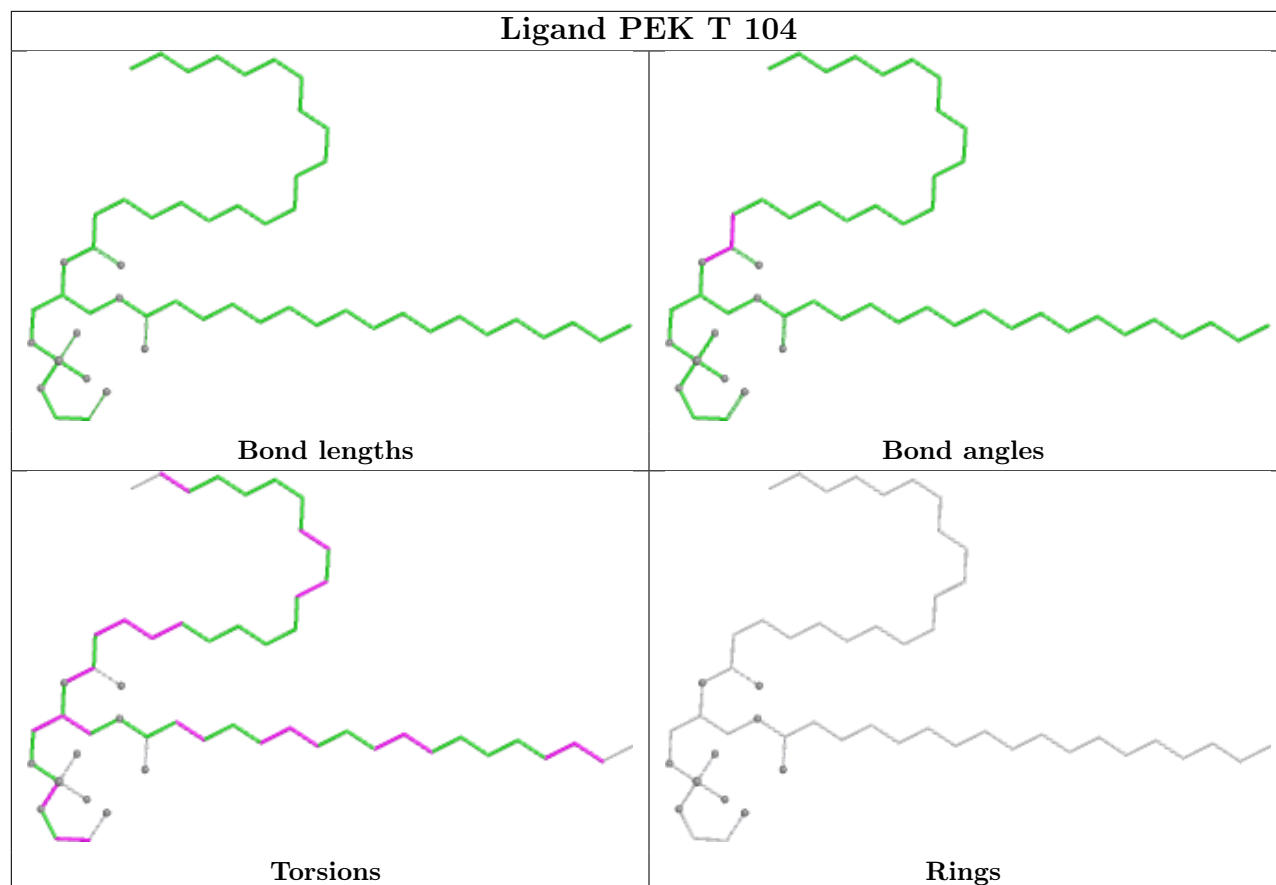


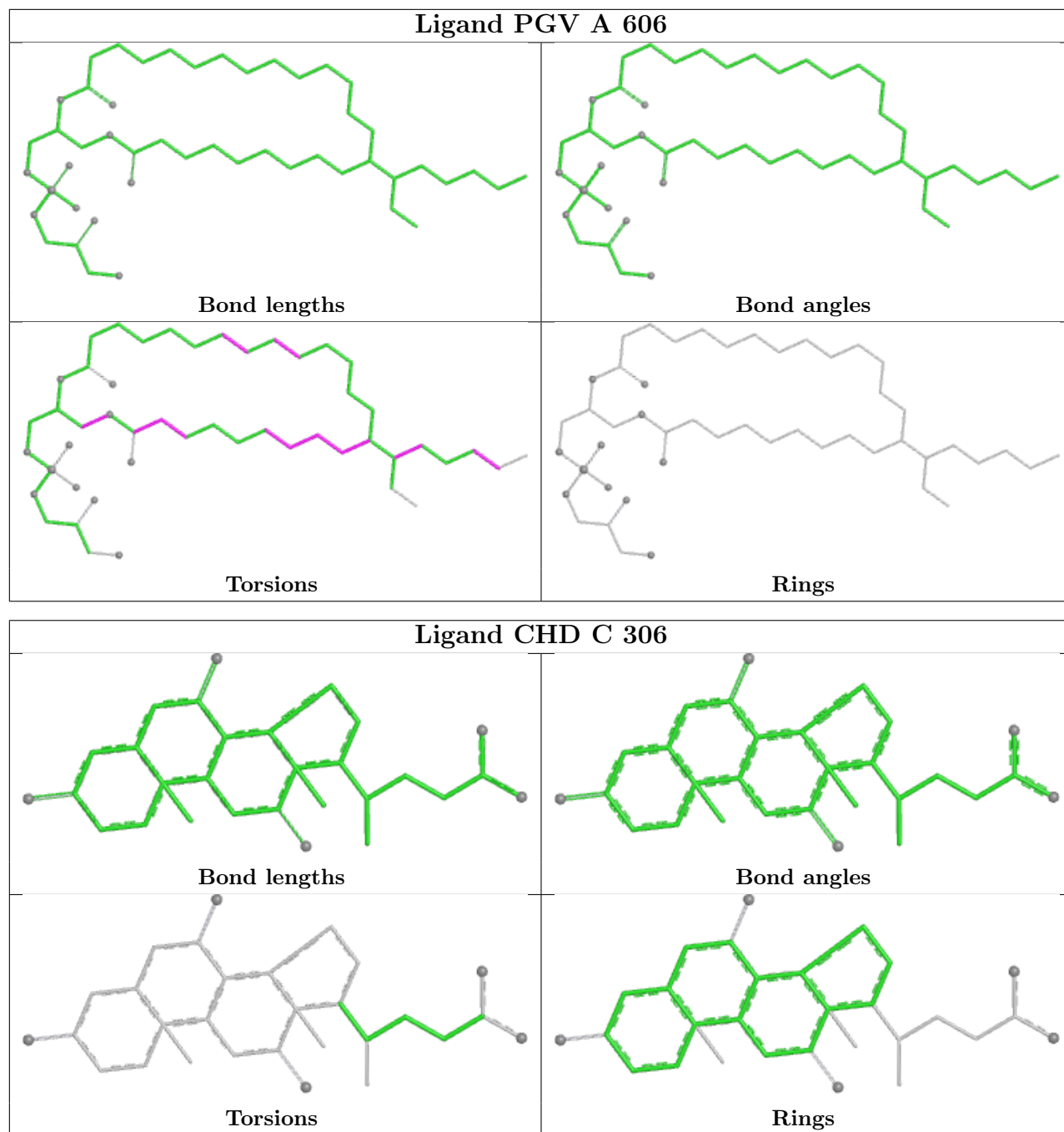
Ligand CHD J 101

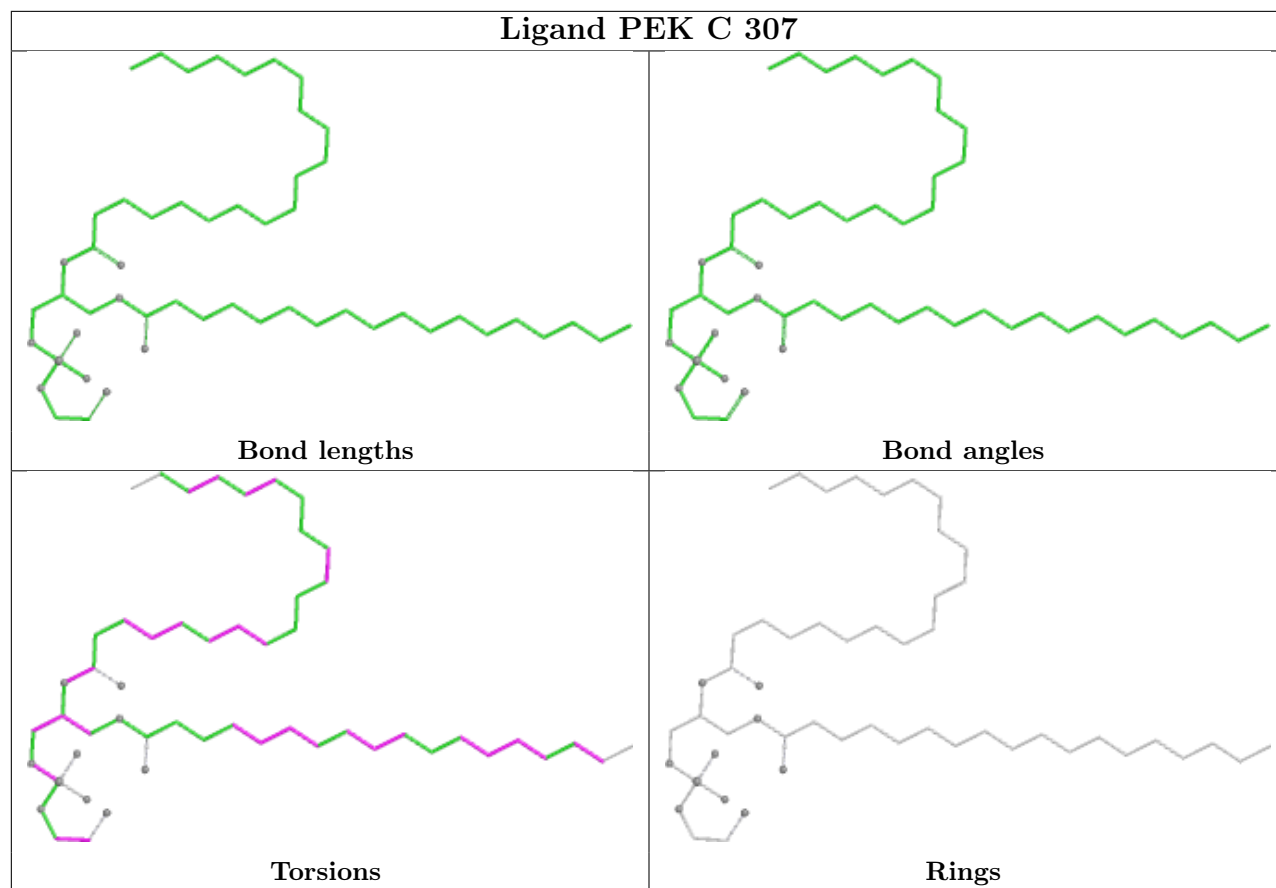


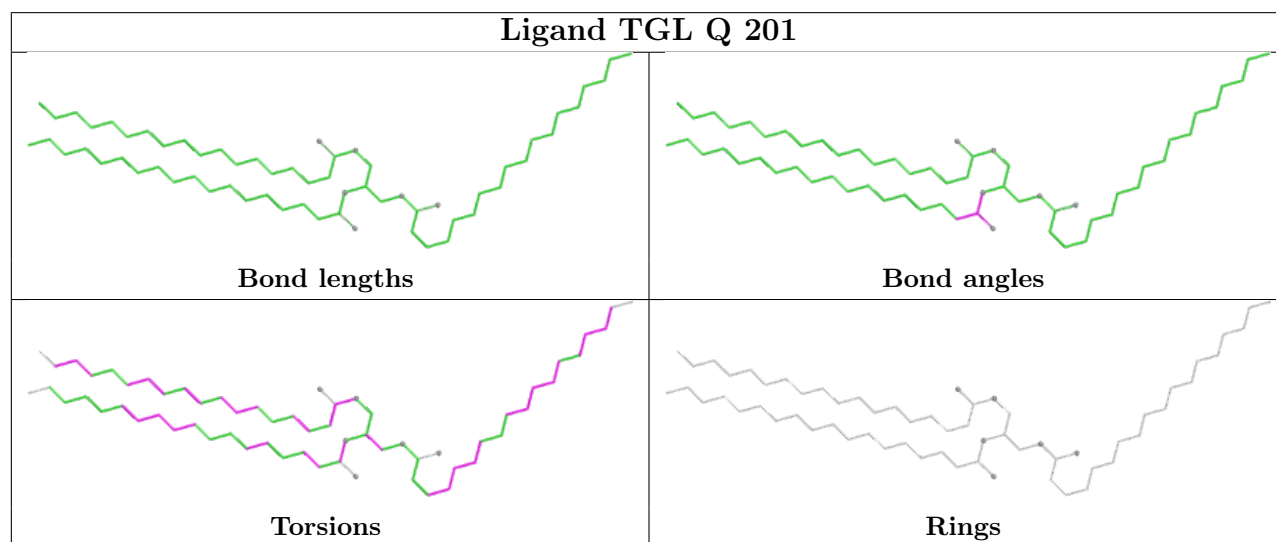
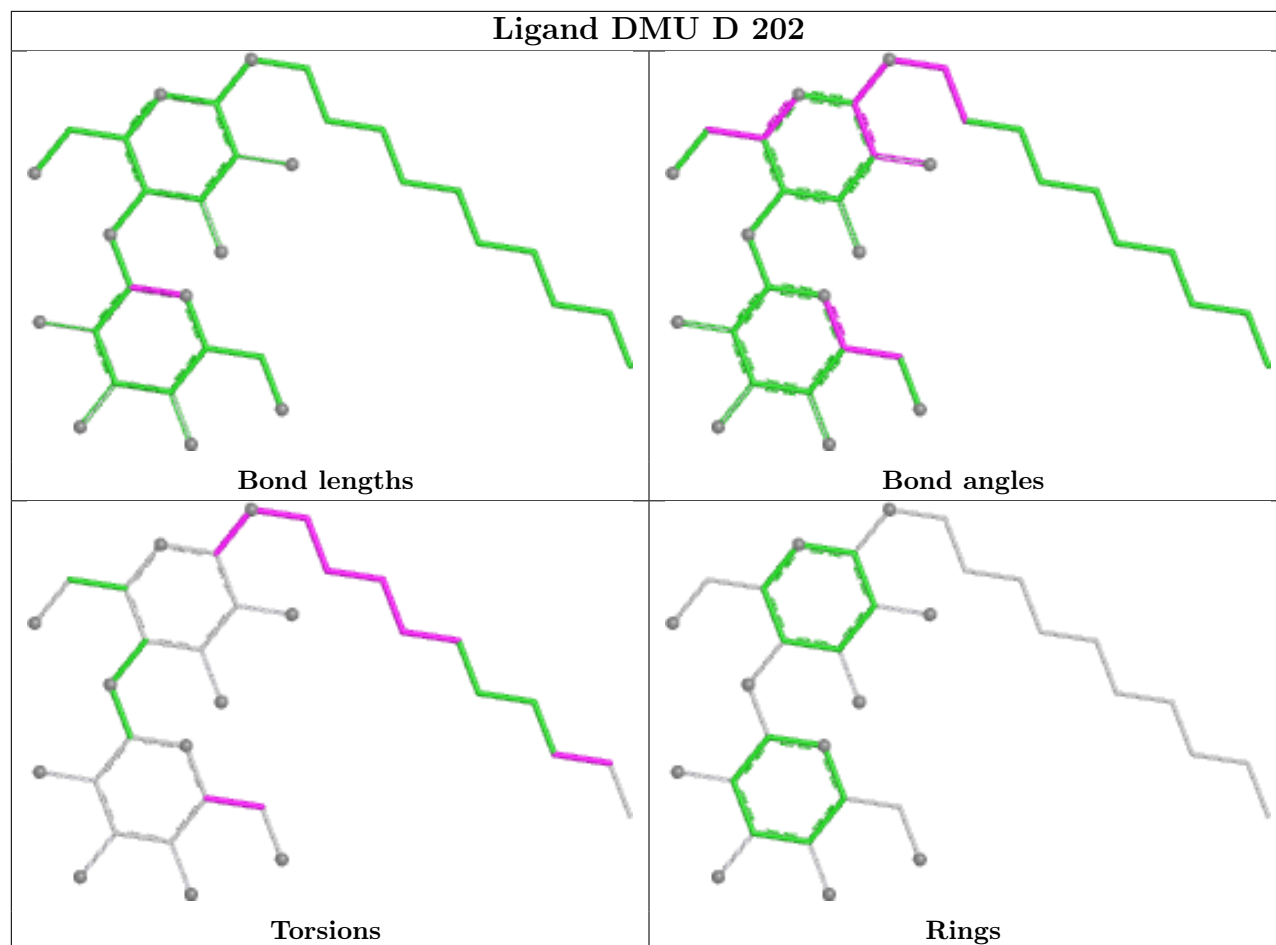
Ligand DMU Z 102

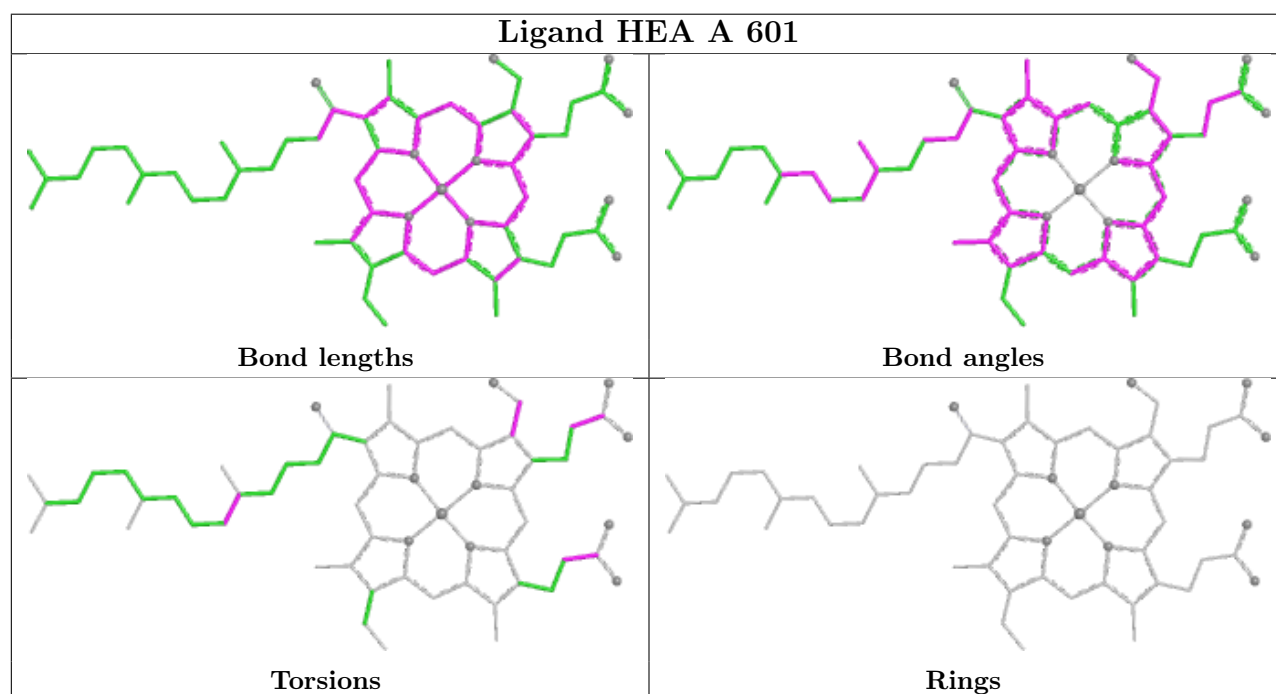
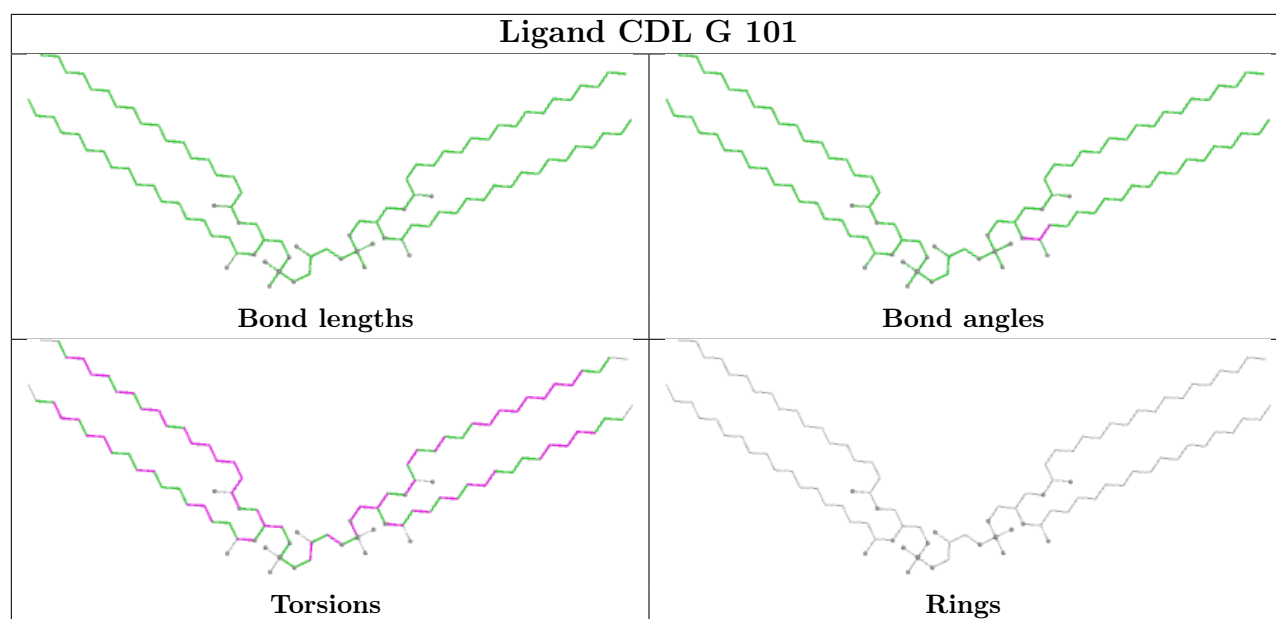


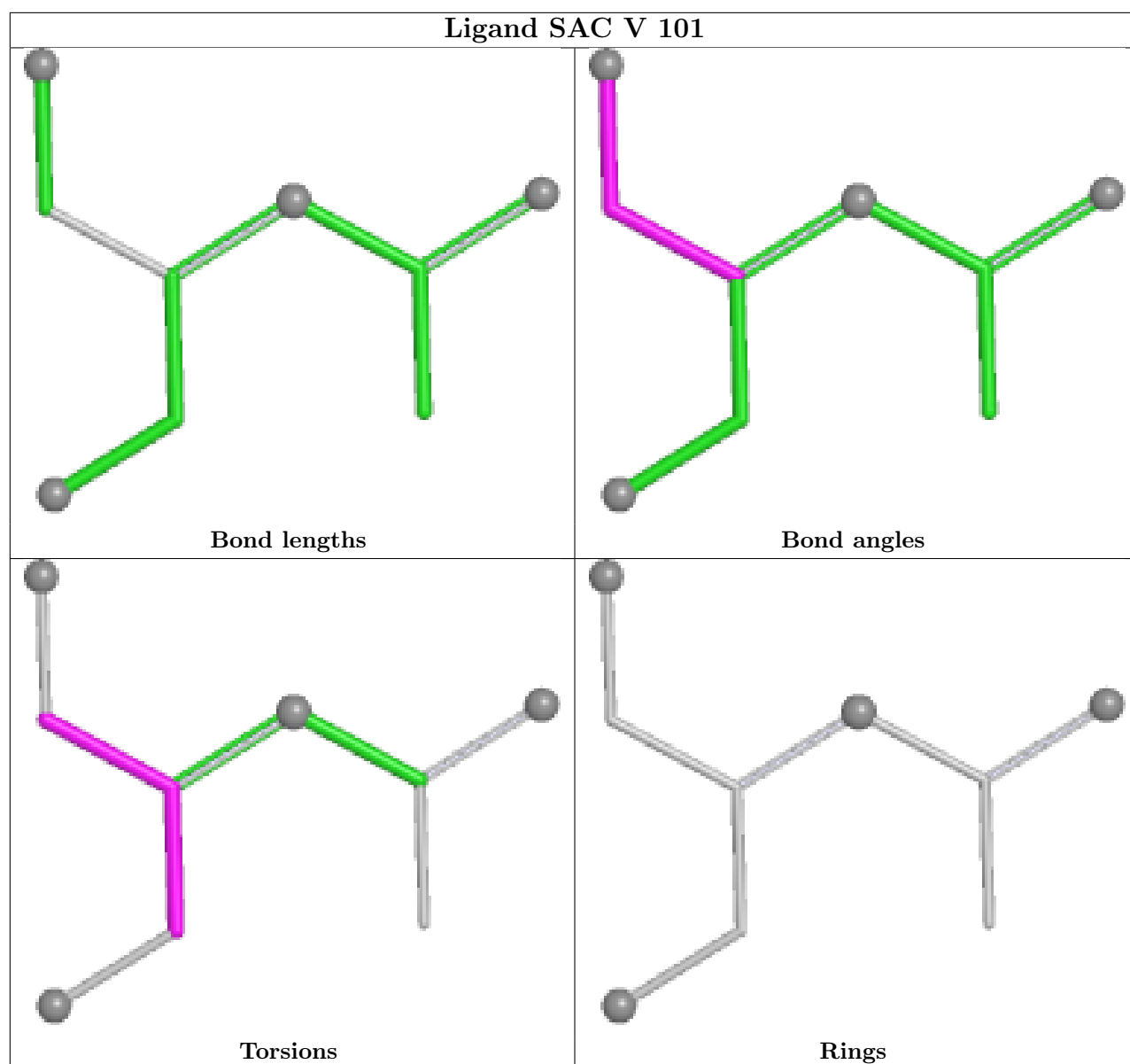


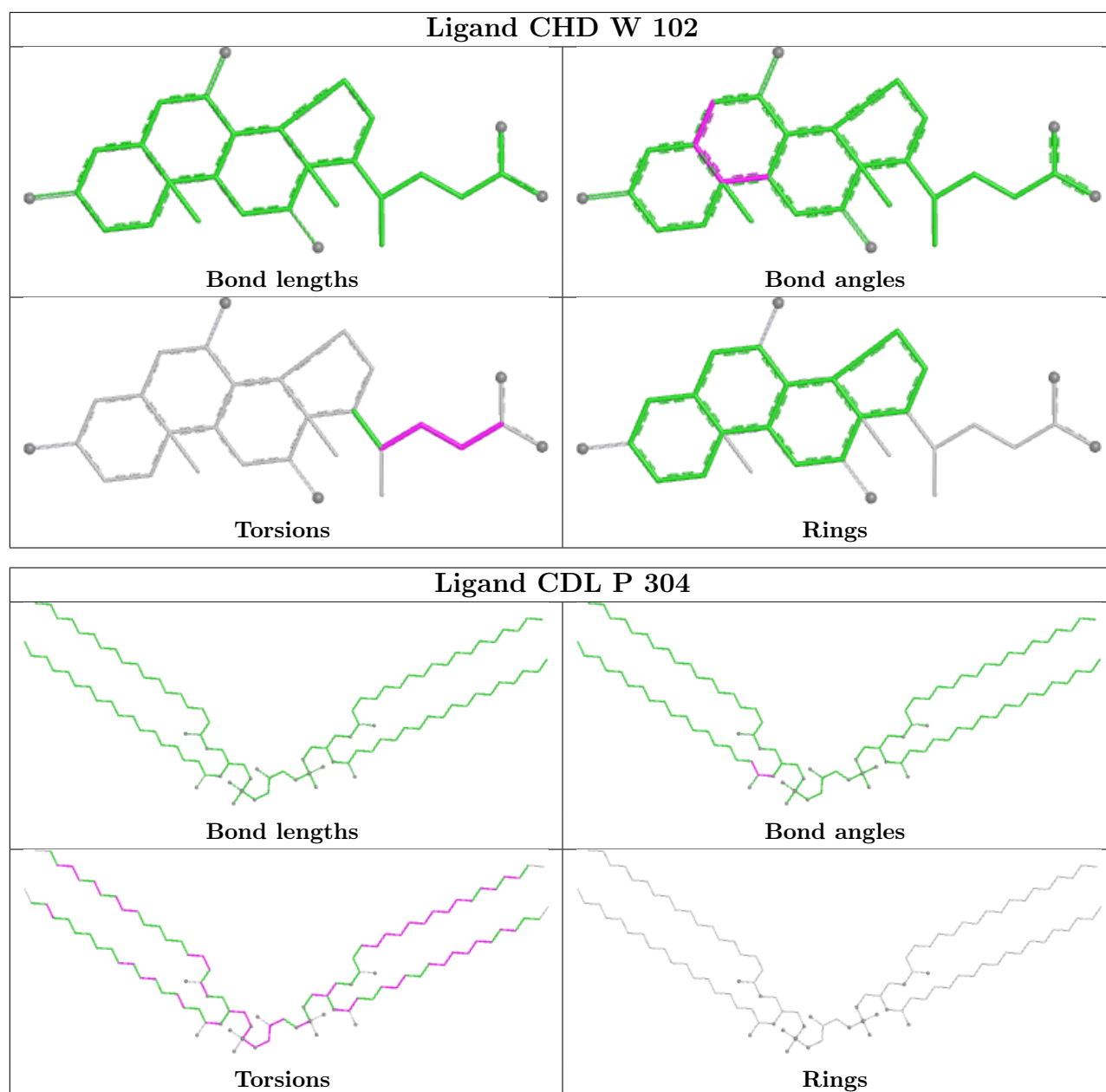












5.7 Other polymers [i](#)

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 ⓘ

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	513/514 (99%)	-0.35	3 (0%) 85 87	14, 32, 42, 77	20 (3%)
1	N	513/514 (99%)	-0.19	7 (1%) 73 75	16, 37, 48, 84	21 (4%)
2	B	226/227 (99%)	0.04	5 (2%) 62 64	22, 41, 77, 117	6 (2%)
2	O	226/227 (99%)	0.23	9 (3%) 42 41	19, 48, 79, 118	5 (2%)
3	C	259/261 (99%)	-0.32	3 (1%) 76 78	15, 37, 52, 96	8 (3%)
3	P	259/261 (99%)	-0.27	1 (0%) 88 89	15, 38, 55, 94	8 (3%)
4	D	144/147 (97%)	-0.11	2 (1%) 73 75	19, 43, 63, 83	6 (4%)
4	Q	144/147 (97%)	0.62	10 (6%) 23 20	24, 59, 90, 149	1 (0%)
5	E	105/109 (96%)	-0.16	2 (1%) 66 67	23, 44, 75, 122	1 (0%)
5	R	105/109 (96%)	0.17	4 (3%) 44 44	41, 52, 74, 119	0
6	F	98/98 (100%)	0.21	9 (9%) 14 12	19, 43, 111, 165	5 (5%)
6	S	98/98 (100%)	0.32	9 (9%) 14 12	21, 44, 133, 189	1 (1%)
7	G	83/85 (97%)	0.99	20 (24%) 2 1	17, 47, 124, 150	1 (1%)
7	T	83/85 (97%)	0.78	15 (18%) 3 3	19, 49, 111, 135	3 (3%)
8	H	79/85 (92%)	0.57	10 (12%) 8 6	35, 47, 114, 130	0
8	U	79/85 (92%)	0.82	11 (13%) 6 5	35, 52, 116, 152	0
9	I	72/73 (98%)	0.43	4 (5%) 30 27	36, 53, 92, 107	0
9	V	72/73 (98%)	0.67	7 (9%) 13 11	27, 62, 93, 107	1 (1%)
10	J	58/59 (98%)	0.03	3 (5%) 33 30	36, 47, 82, 128	0
10	W	58/59 (98%)	0.28	2 (3%) 48 48	38, 52, 84, 138	0
11	K	49/56 (87%)	0.14	1 (2%) 65 66	18, 48, 62, 76	1 (2%)
11	X	49/56 (87%)	0.55	4 (8%) 17 15	24, 57, 82, 100	1 (2%)
12	L	46/47 (97%)	-0.12	2 (4%) 40 39	33, 39, 56, 106	0
12	Y	46/47 (97%)	0.37	3 (6%) 25 22	36, 49, 71, 110	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	43/46 (93%)	-0.11	1 (2%) 61 63	30, 39, 69, 97	0
13	Z	43/46 (93%)	0.36	2 (4%) 36 35	43, 51, 95, 138	0
All	All	3550/3614 (98%)	0.05	149 (4%) 40 40	14, 41, 82, 189	89 (2%)

The worst 5 of 149 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	S	97	ALA	9.8
4	Q	5	VAL	9.5
7	T	36[A]	TRP	8.2
4	Q	6	VAL	7.8
7	T	3	ALA	7.3

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

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
7	TPO	T	11	11/12	0.62	0.24	116,120,142,143	0
7	TPO	G	11	11/12	0.66	0.28	110,125,150,150	0
1	FME	A	1	10/11	0.88	0.15	55,60,85,92	0
1	FME	N	1	10/11	0.93	0.13	51,63,84,88	0
2	FME	O	1	10/11	0.95	0.13	41,48,54,55	0
2	FME	B	1	10/11	0.96	0.12	33,40,47,61	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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($\text{\AA}^2$)	Q<0.9
29	SAC	I	101	9/10	0.46	0.29	80,104,115,123	0
29	SAC	V	101	9/10	0.52	0.24	118,130,141,147	0
23	DMU	W	101	33/33	0.74	0.19	59,104,124,144	0
27	PSC	O	302	52/52	0.76	0.32	54,111,177,203	0
21	TGL	N	606	63/63	0.77	0.34	61,94,161,172	0
18	PGV	P	302	51/51	0.77	0.31	69,104,137,150	0
27	PSC	E	201	52/52	0.77	0.29	66,112,177,181	0
18	PGV	C	308	51/51	0.78	0.27	60,93,116,126	0
25	CDL	G	101	100/100	0.78	0.32	70,109,164,179	0
18	PGV	Z	101	51/51	0.79	0.27	51,98,124,137	0
21	TGL	Q	201	63/63	0.79	0.32	69,98,120,131	0
23	DMU	C	301	33/33	0.79	0.19	60,111,136,138	0
24	PEK	G	102	53/53	0.80	0.27	56,120,164,170	0
24	PEK	T	103	53/53	0.80	0.29	54,124,165,170	0
24	PEK	C	307	53/53	0.80	0.27	57,90,174,186	0
25	CDL	P	304	100/100	0.80	0.29	58,109,142,159	0
21	TGL	Y	101	63/63	0.81	0.29	55,84,128,139	0
21	TGL	B	301	63/63	0.81	0.30	61,88,159,165	0
21	TGL	L	101	63/63	0.82	0.27	47,73,104,111	0
25	CDL	T	105	100/100	0.82	0.29	76,115,154,202	0
19	EDO	G	104	4/4	0.82	0.16	51,58,59,59	0
24	PEK	T	104	53/53	0.83	0.28	51,98,170,183	0
18	PGV	A	607	51/51	0.83	0.24	52,87,123,134	0
21	TGL	D	201	63/63	0.84	0.25	52,80,107,110	0
25	CDL	C	304	100/100	0.85	0.24	52,101,131,139	0
26	CHD	J	101	29/29	0.85	0.15	59,70,95,96	0
19	EDO	T	106	4/4	0.88	0.15	42,51,51,56	0
19	EDO	C	309	4/4	0.89	0.15	54,54,57,61	0
26	CHD	W	102	29/29	0.90	0.12	64,77,91,94	0
26	CHD	P	305	29/29	0.91	0.11	53,61,66,72	0
26	CHD	C	305	29/29	0.91	0.11	52,63,72,74	0
23	DMU	Z	102	33/33	0.91	0.11	55,63,88,90	0
19	EDO	S	102	4/4	0.92	0.12	59,59,60,61	0
23	DMU	D	202	33/33	0.92	0.10	44,50,69,72	0
24	PEK	T	102	53/53	0.93	0.16	34,56,92,98	0
19	EDO	A	608	4/4	0.93	0.14	31,37,38,43	0
19	EDO	A	609	4/4	0.93	0.10	54,57,57,58	0
24	PEK	C	302	53/53	0.94	0.14	38,57,85,94	0
26	CHD	T	101	29/29	0.95	0.08	32,36,40,49	0
26	CHD	C	306	29/29	0.95	0.07	31,37,41,41	0
18	PGV	C	303	51/51	0.96	0.11	31,45,80,81	0
26	CHD	P	306	29/29	0.96	0.07	32,38,42,43	0
18	PGV	P	303	51/51	0.96	0.11	29,47,84,86	0

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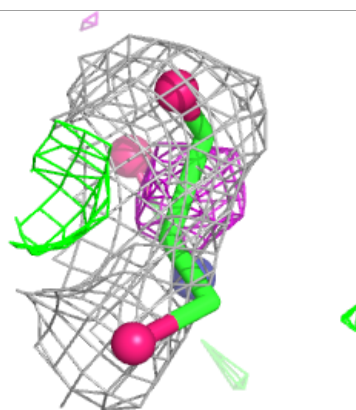
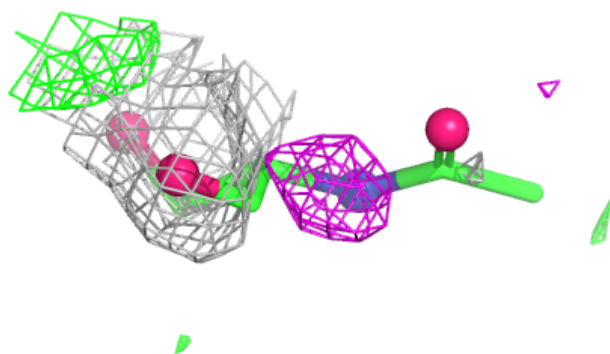
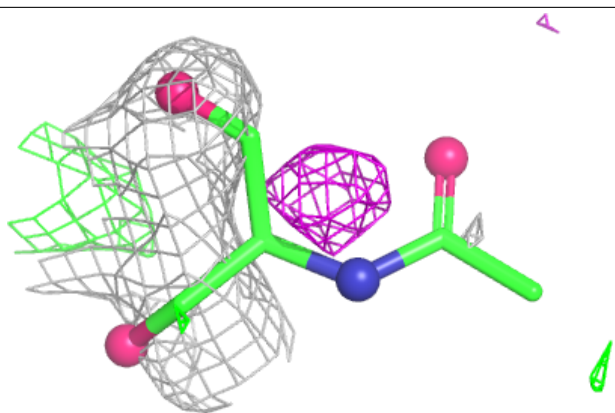
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
18	PGV	A	606	51/51	0.96	0.11	27,41,71,81	0
19	EDO	N	607	4/4	0.96	0.06	37,37,37,38	0
18	PGV	P	301	51/51	0.96	0.11	30,50,72,75	0
26	CHD	G	103	29/29	0.96	0.07	34,36,39,41	0
19	EDO	S	103	4/4	0.96	0.09	45,49,49,51	0
14	HEA	A	601	60/60	0.97	0.08	29,35,47,50	0
16	MG	N	604	1/1	0.98	0.05	34,34,34,34	0
17	NA	N	605	1/1	0.98	0.06	35,35,35,35	0
14	HEA	A	602	60/60	0.98	0.07	25,32,40,42	0
14	HEA	N	601	60/60	0.98	0.09	31,39,53,57	0
14	HEA	N	602	60/60	0.98	0.07	30,34,47,52	0
17	NA	A	605	1/1	0.99	0.10	32,32,32,32	0
16	MG	A	604	1/1	0.99	0.04	29,29,29,29	0
22	CUA	B	302	2/2	0.99	0.02	29,29,29,31	0
22	CUA	O	301	2/2	0.99	0.03	36,36,36,38	0
20	OH	A	610	1/1	0.99	0.12	26,26,26,26	1
20	OH	N	608	1/1	0.99	0.17	27,27,27,27	1
28	ZN	F	101	1/1	1.00	0.01	36,36,36,36	0
28	ZN	S	101	1/1	1.00	0.02	40,40,40,40	0
15	CU	A	603	1/1	1.00	0.01	32,32,32,32	0
15	CU	N	603	1/1	1.00	0.04	36,36,36,36	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.

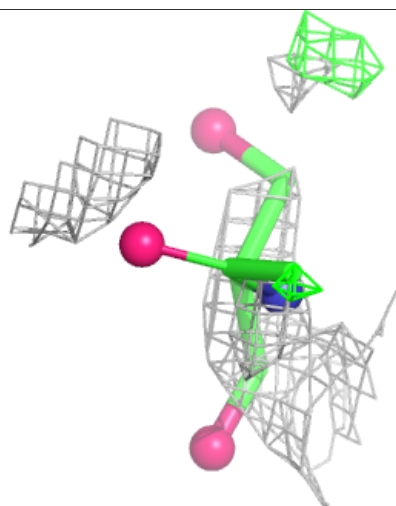
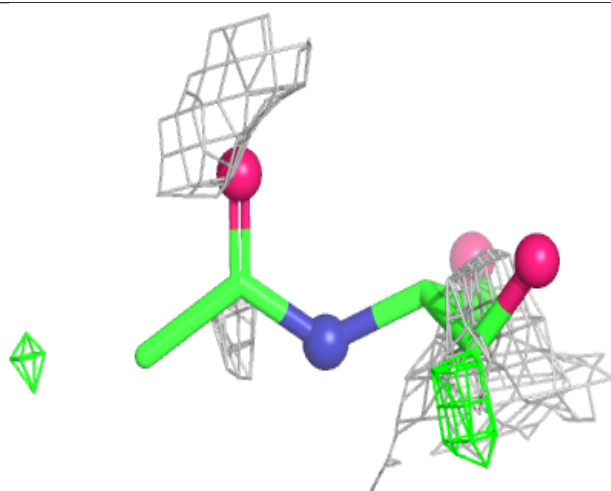
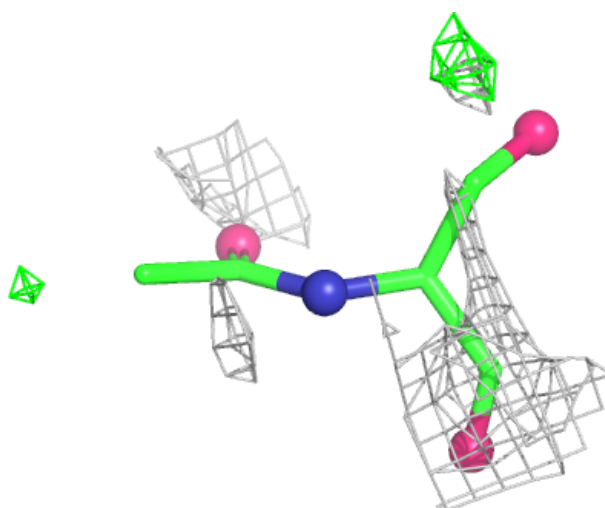
Electron density around SAC I 101:

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



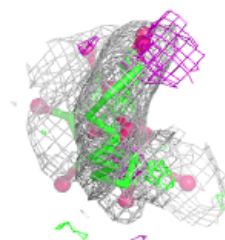
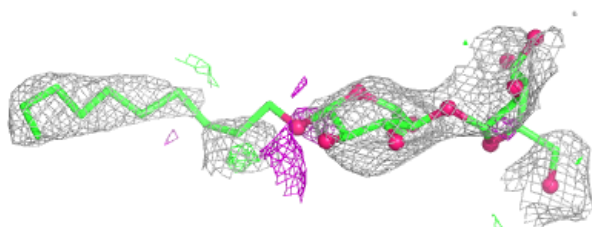
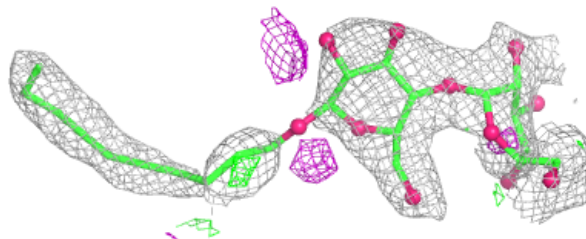
Electron density around SAC V 101:

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and green (positive)

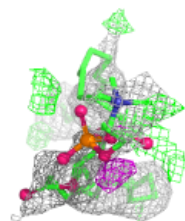
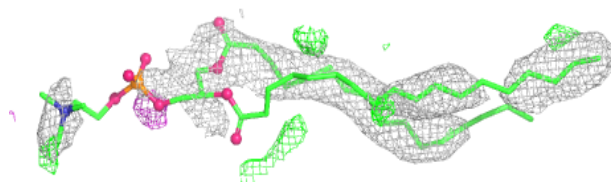
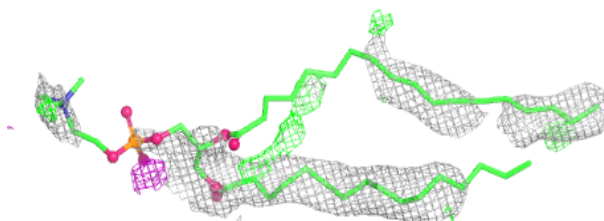


Electron density around DMU W 101:

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

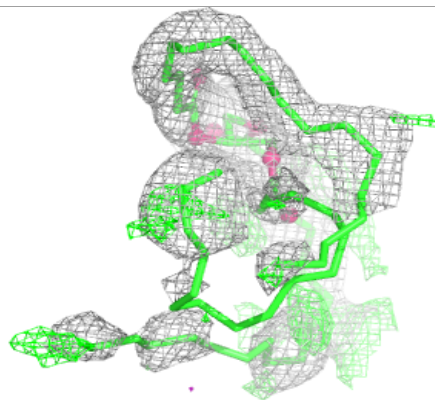
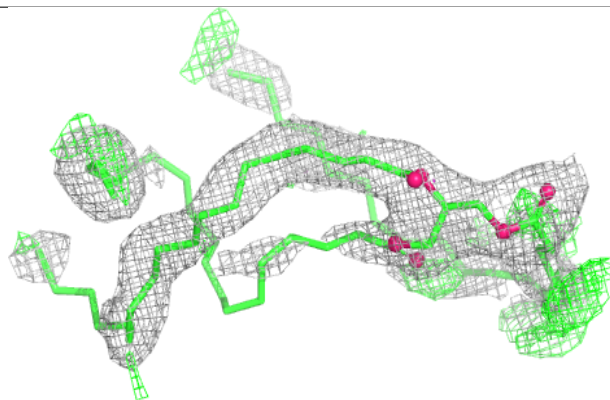
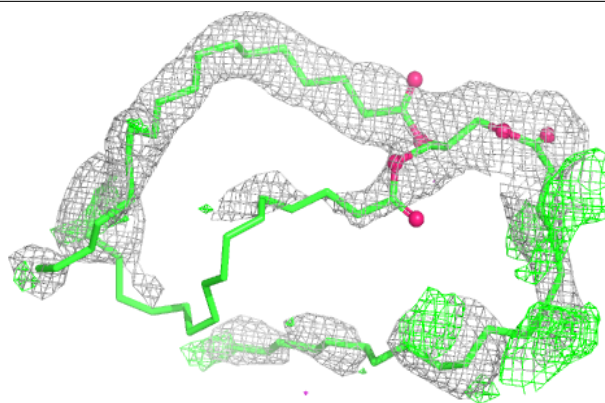
**Electron density around PSC O 302:**

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

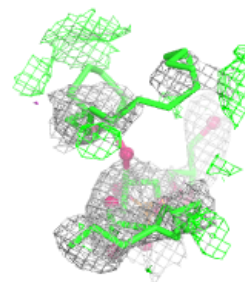
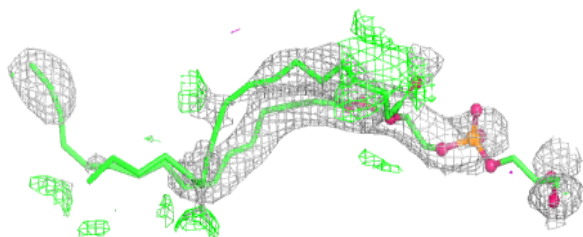
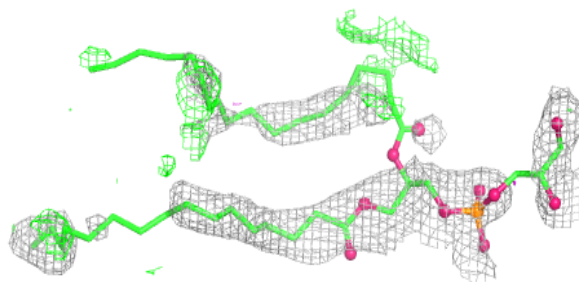


Electron density around TGL N 606:

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

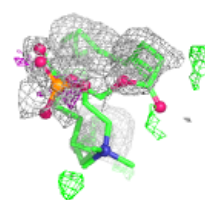
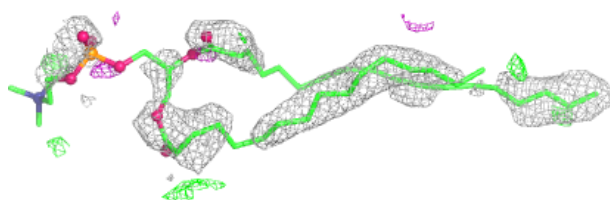
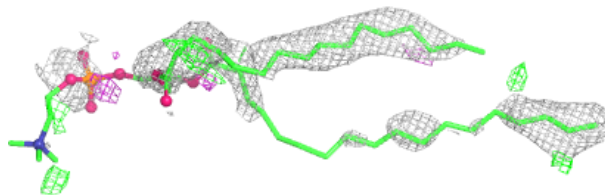
**Electron density around PGV P 302:**

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

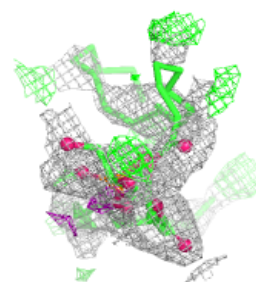
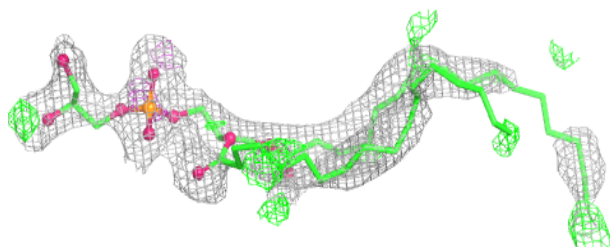
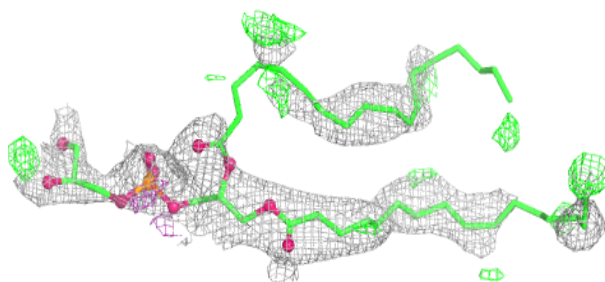


Electron density around PSC E 201:

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

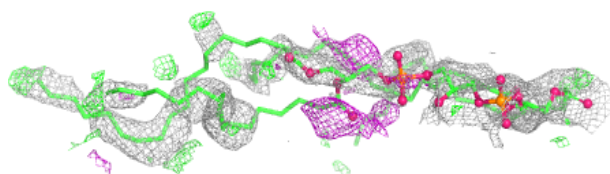
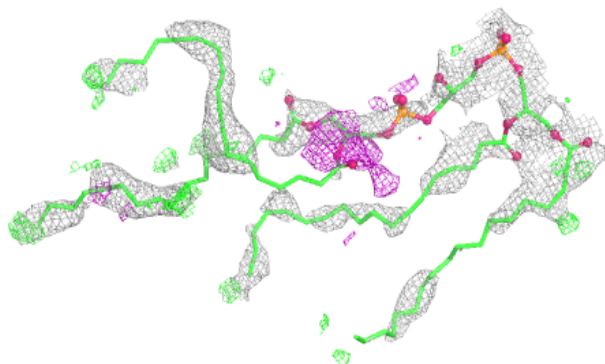
**Electron density around PGV C 308:**

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

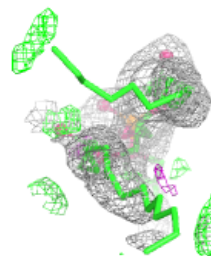
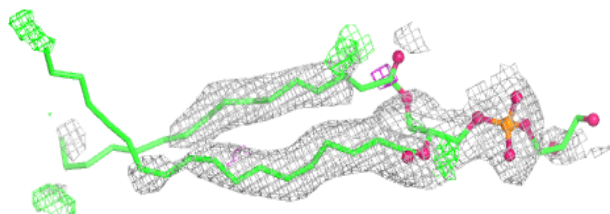
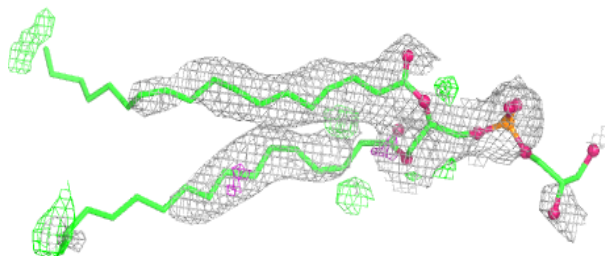


Electron density around CDL G 101:

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

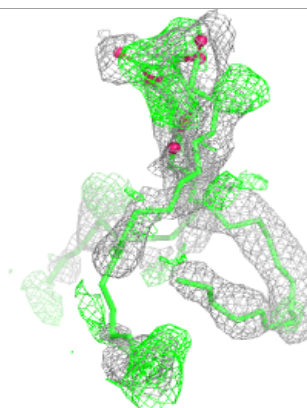
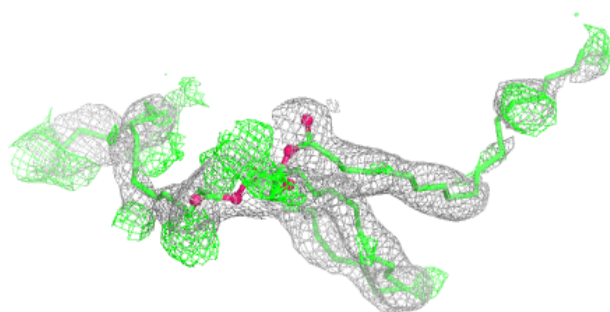
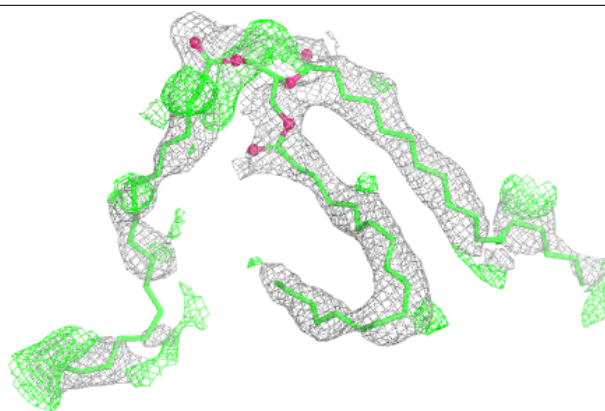
**Electron density around PGV Z 101:**

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

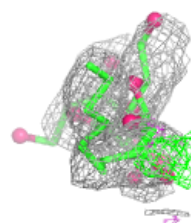
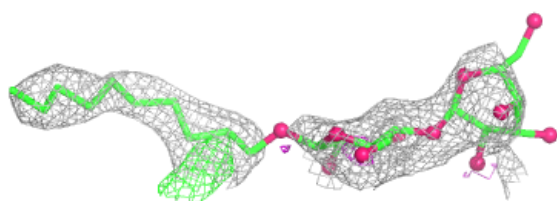
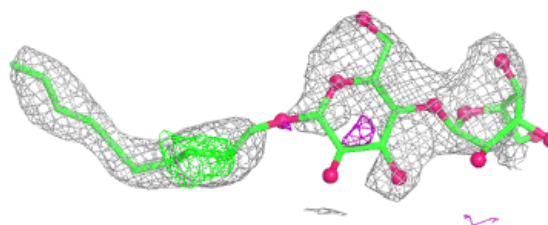


Electron density around TGL Q 201:

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

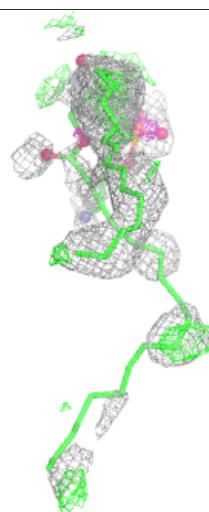
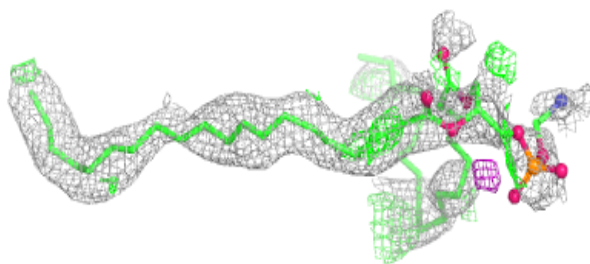
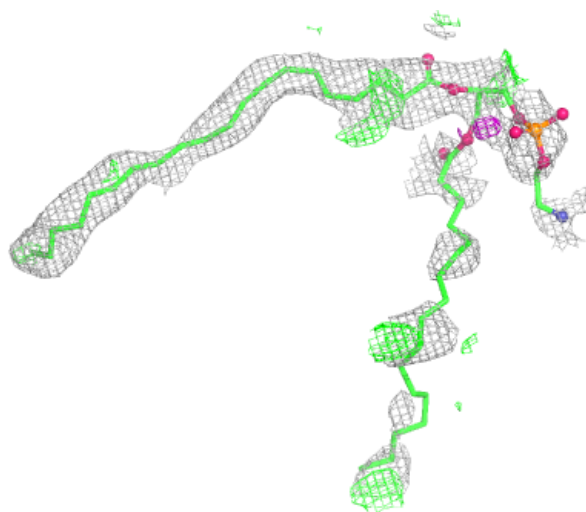
**Electron density around DMU C 301:**

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



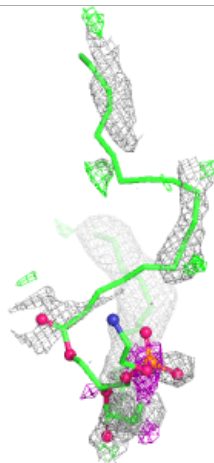
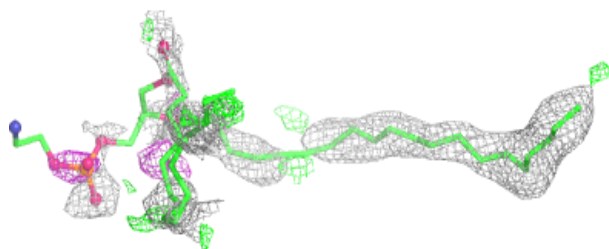
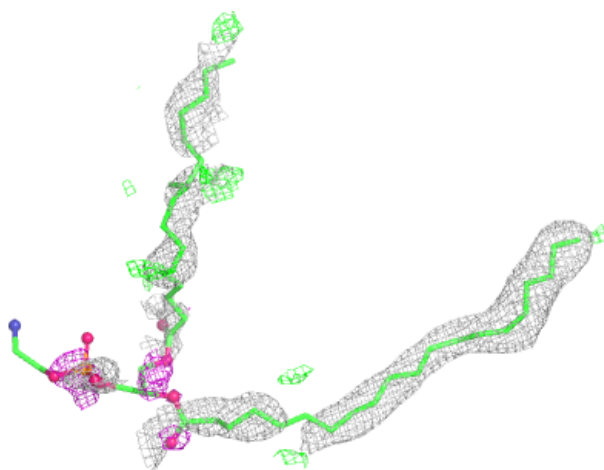
Electron density around PEK G 102:

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



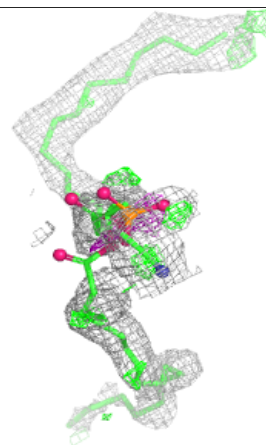
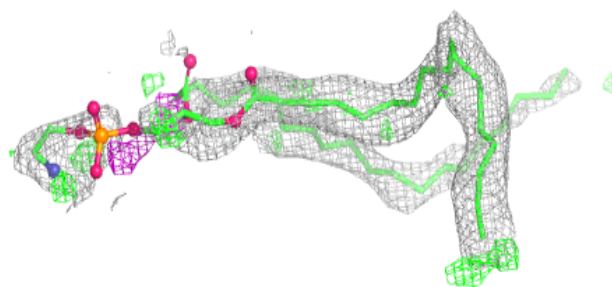
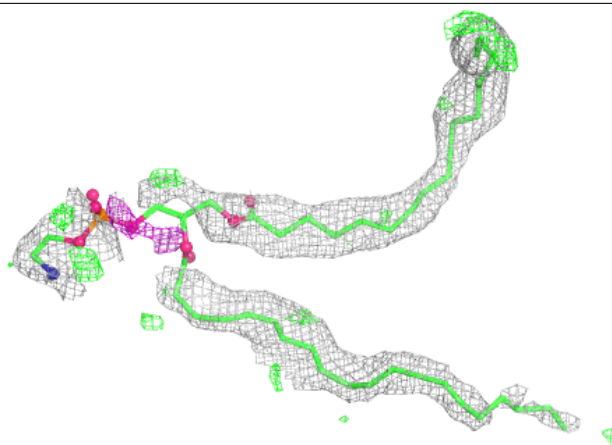
Electron density around PEK T 103:

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



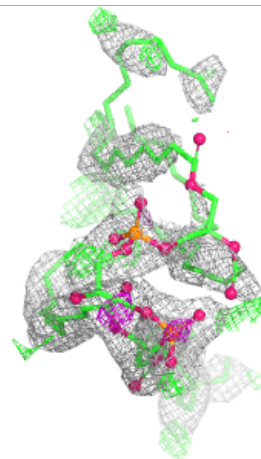
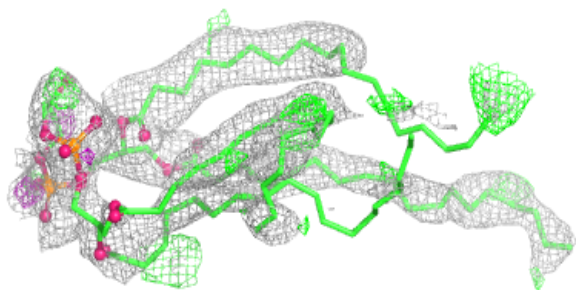
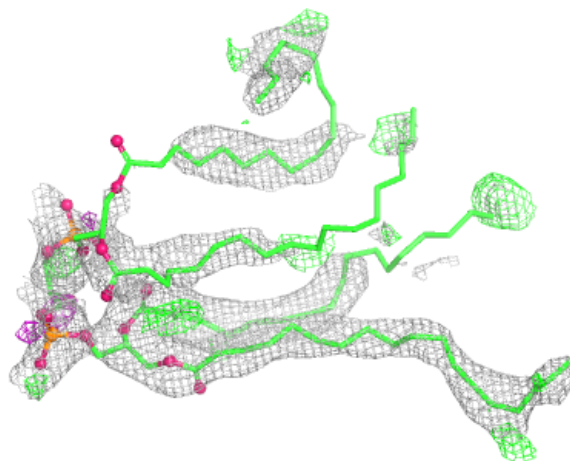
Electron density around PEK C 307:

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



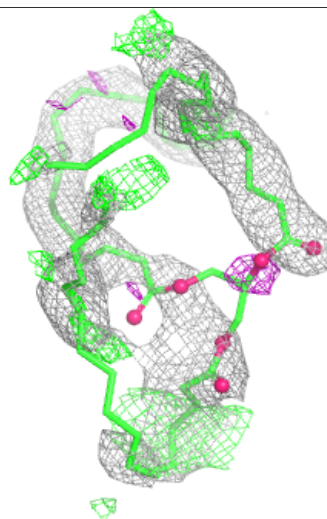
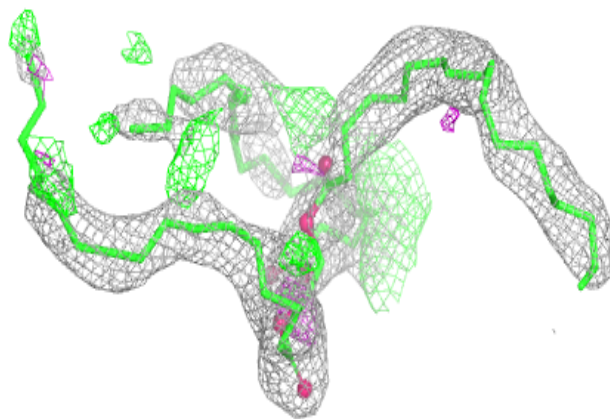
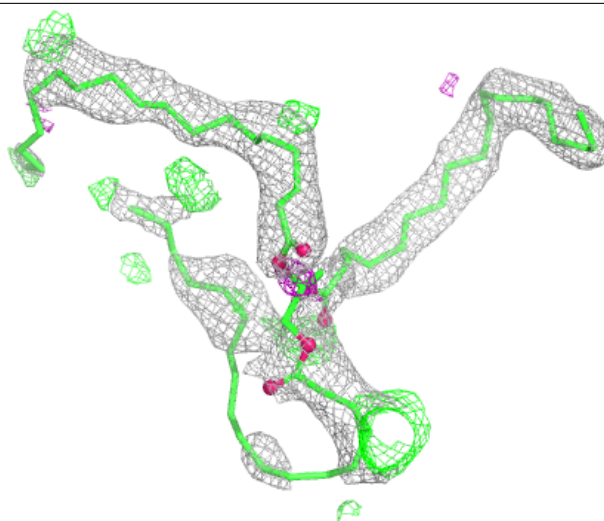
Electron density around CDL P 304:

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



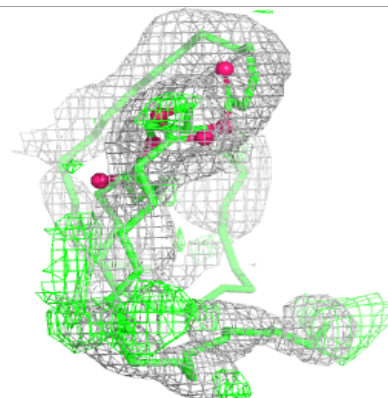
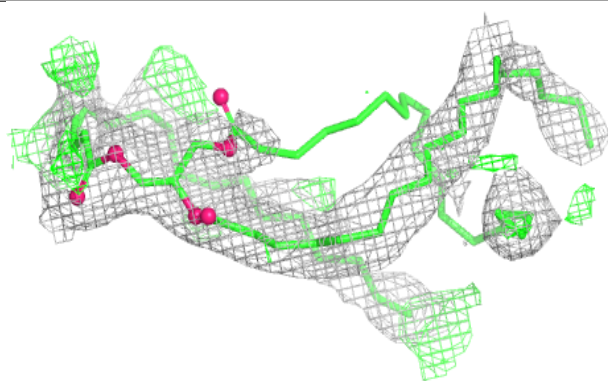
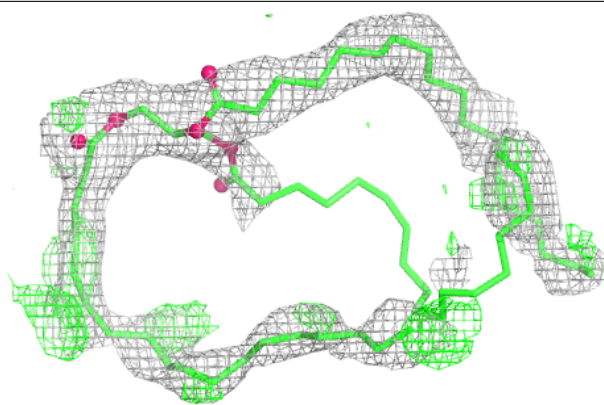
Electron density around TGL Y 101:

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



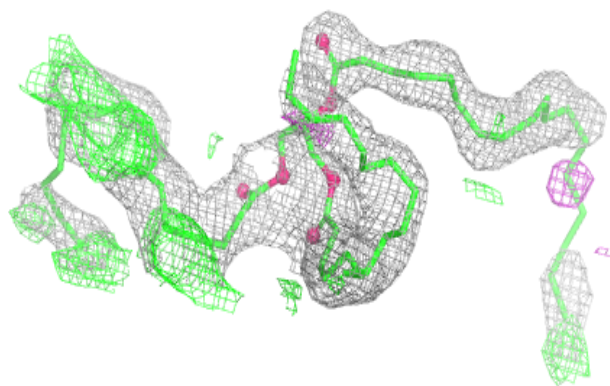
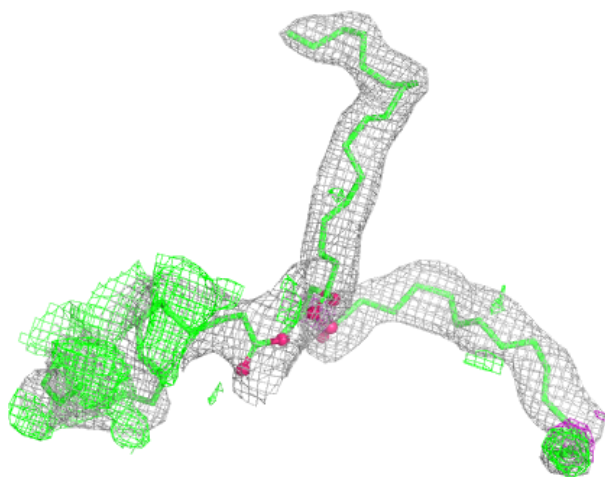
Electron density around TGL B 301:

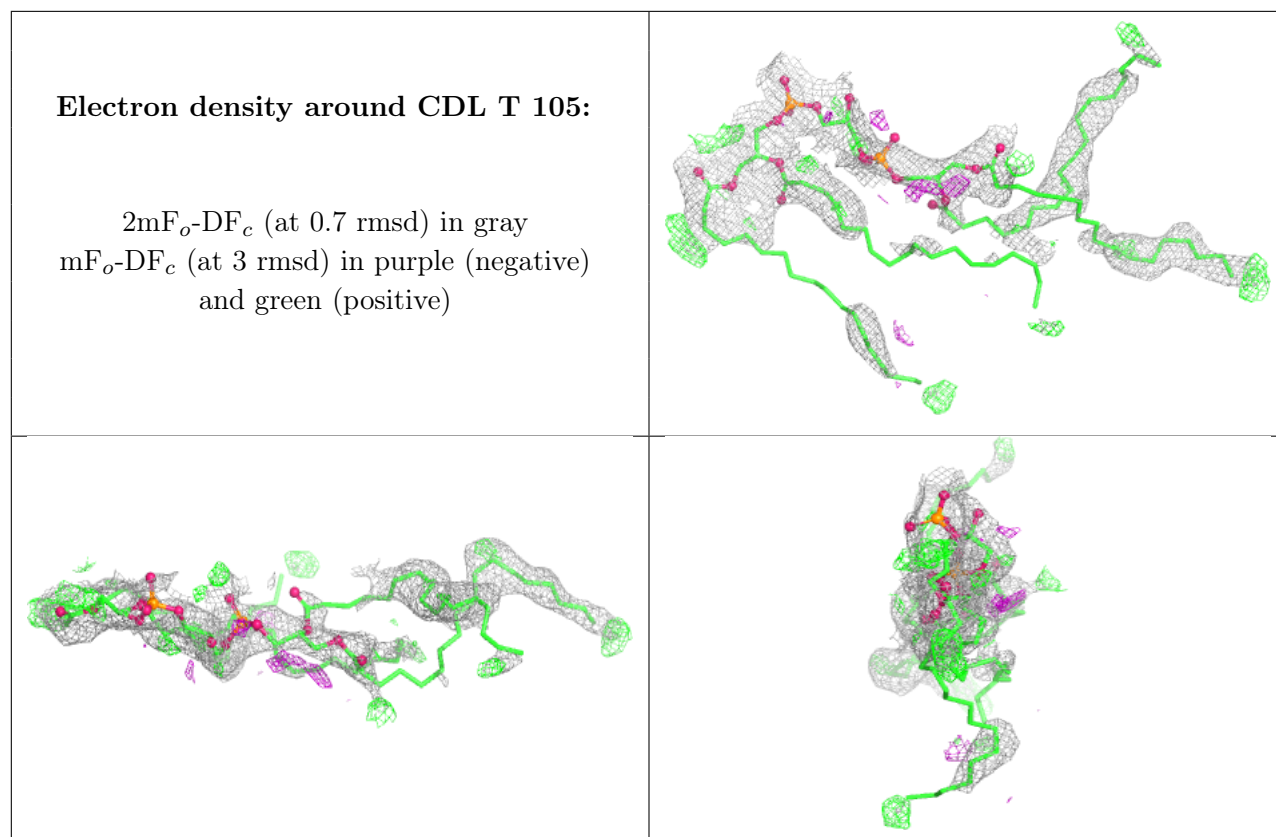
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around TGL L 101:

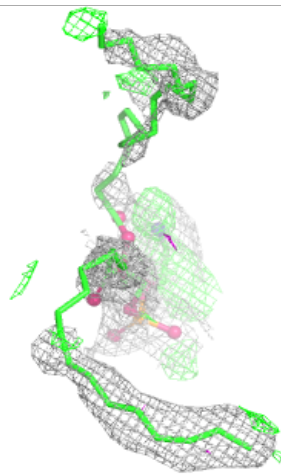
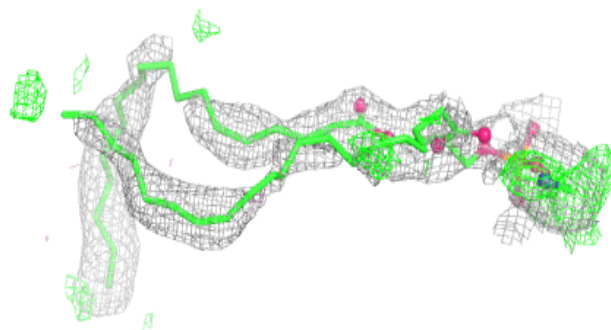
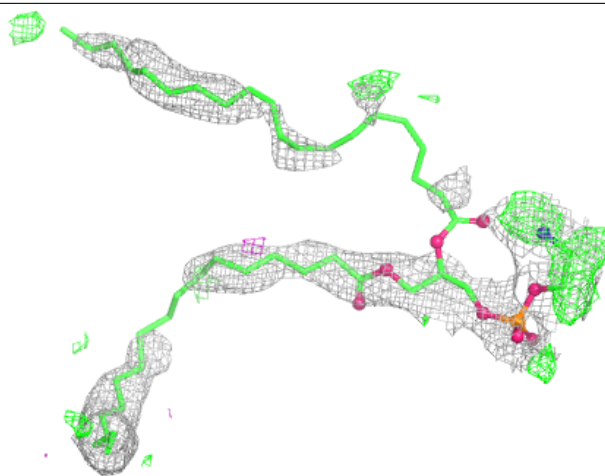
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





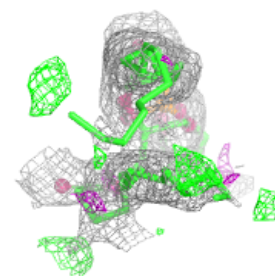
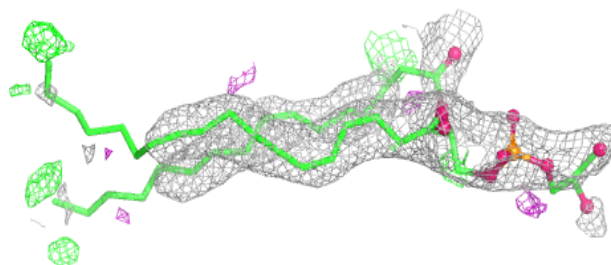
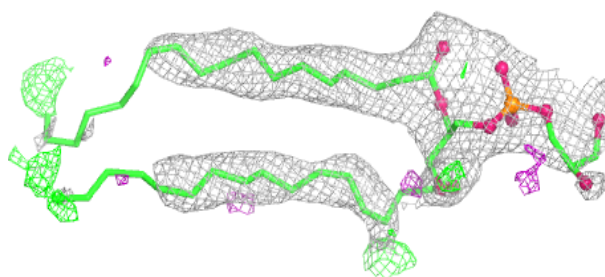
Electron density around PEK T 104:

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

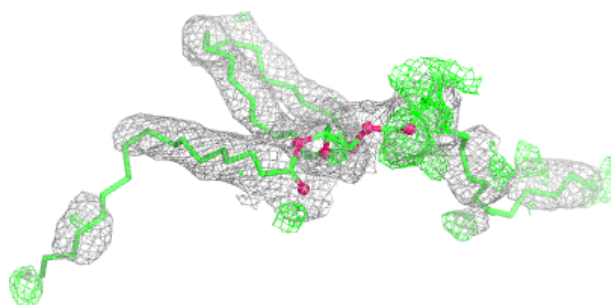
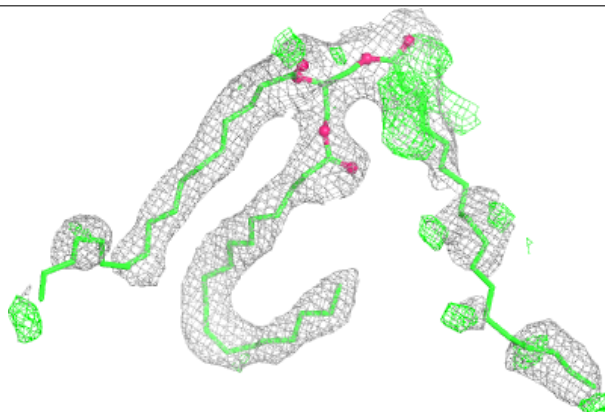


Electron density around PGV A 607:

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

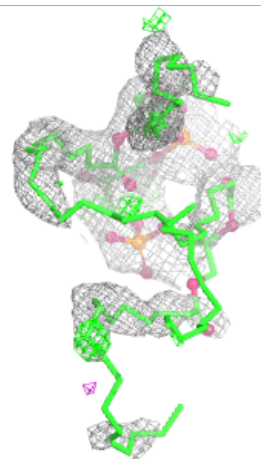
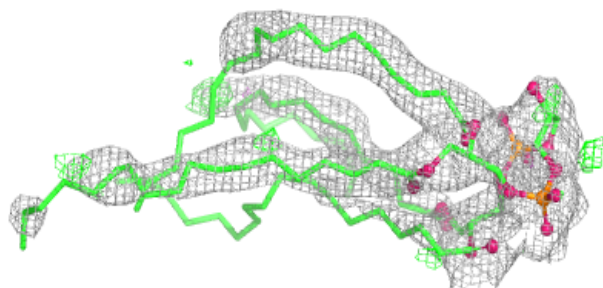
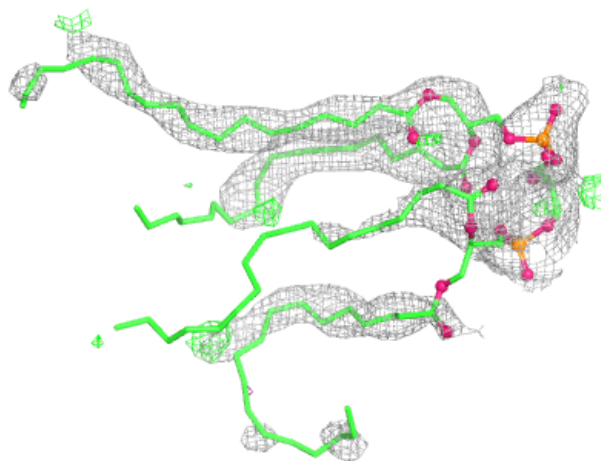
**Electron density around TGL D 201:**

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



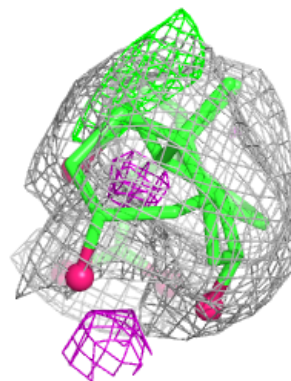
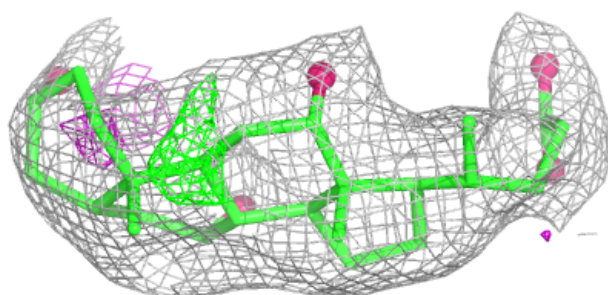
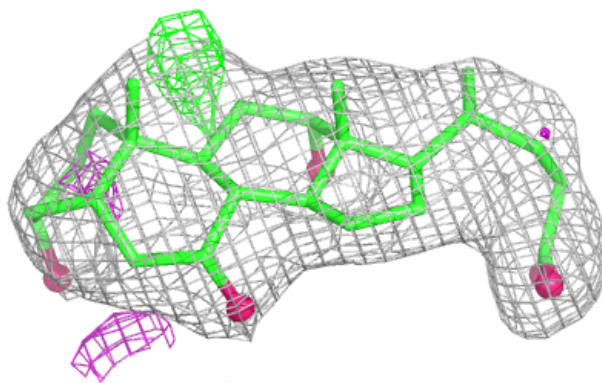
Electron density around CDL C 304:

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

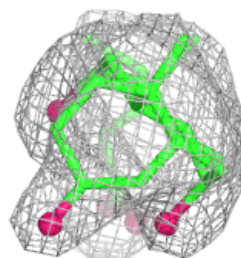
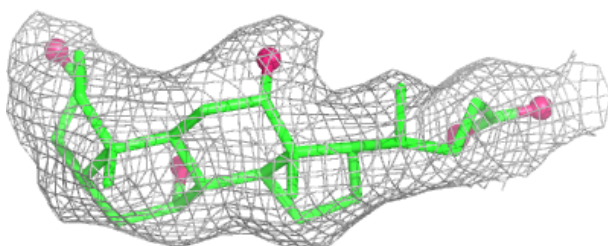
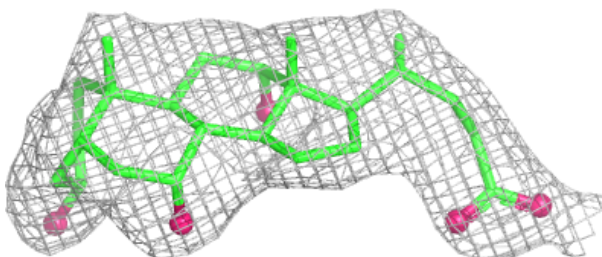


Electron density around CHD J 101:

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

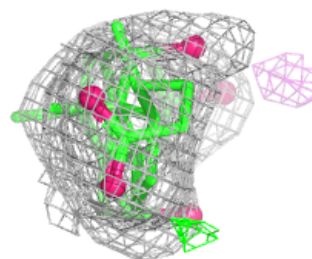
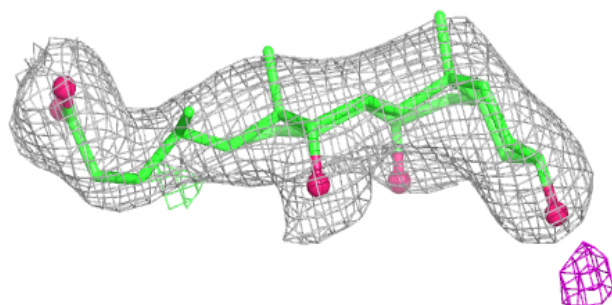
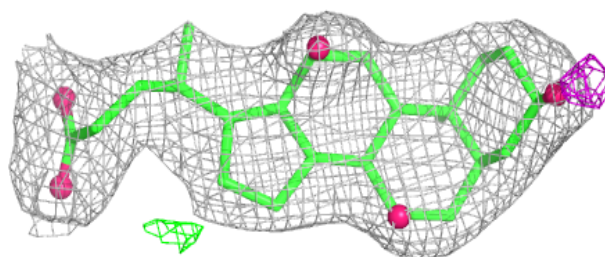
**Electron density around CHD W 102:**

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

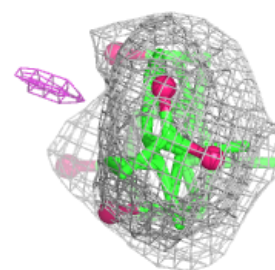
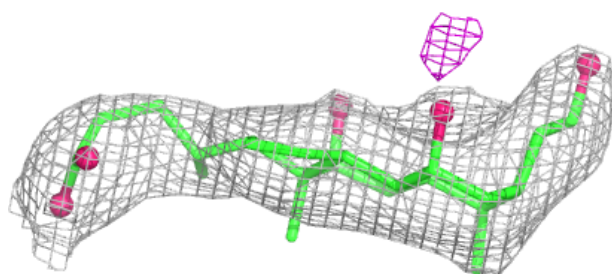
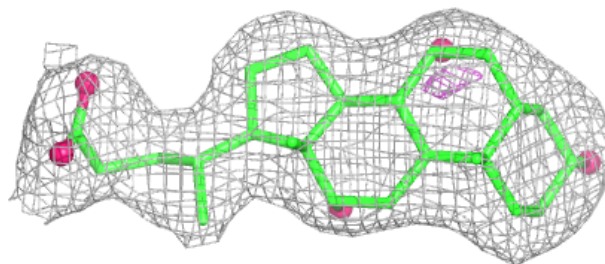


Electron density around CHD P 305:

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

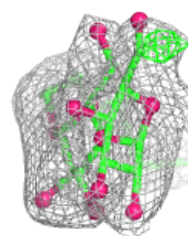
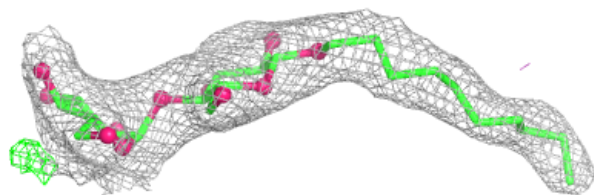
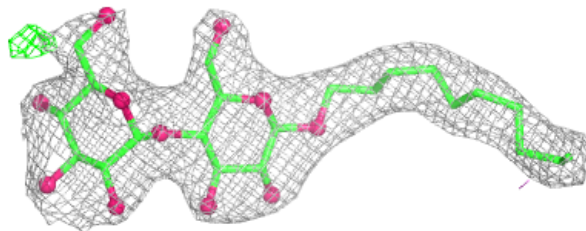
**Electron density around CHD C 305:**

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

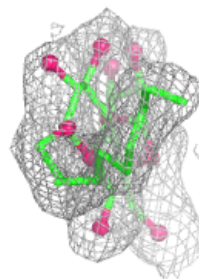
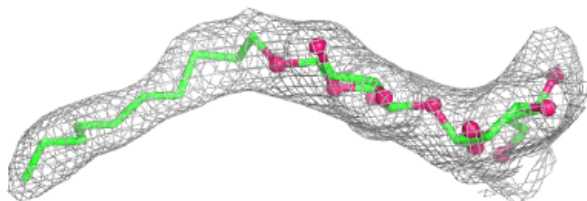
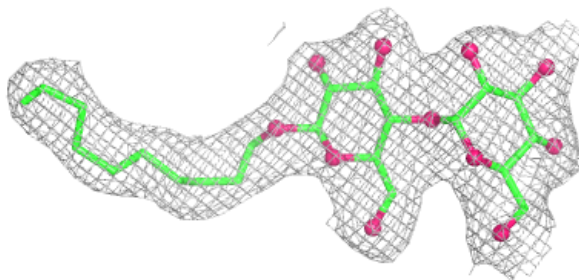


Electron density around DMU Z 102:

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

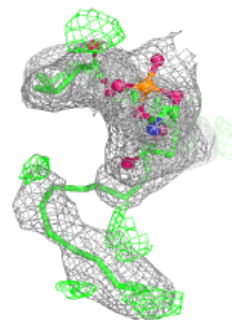
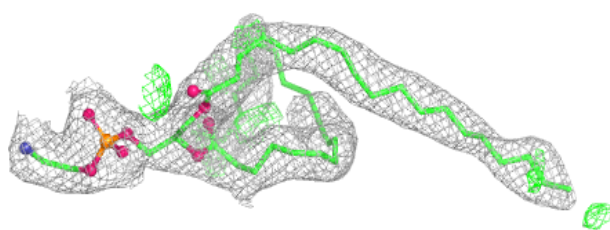
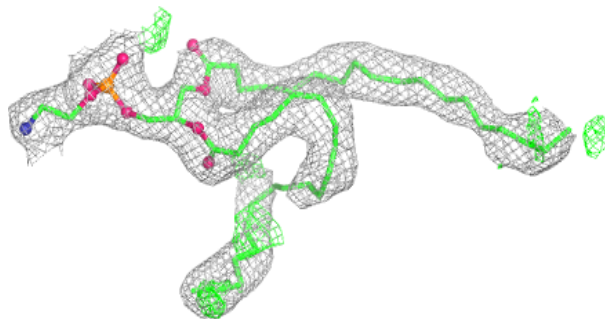
**Electron density around DMU D 202:**

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

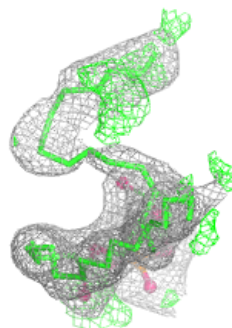
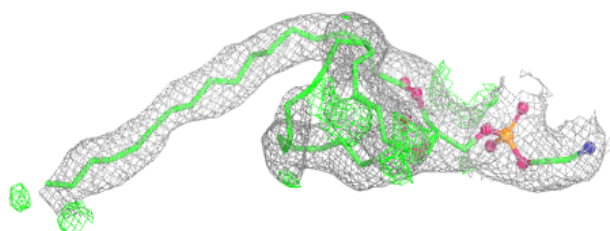
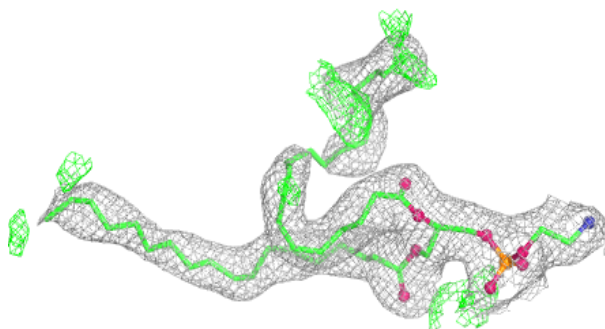


Electron density around PEK T 102:

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

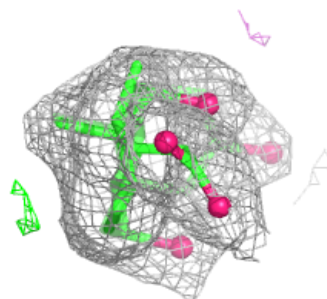
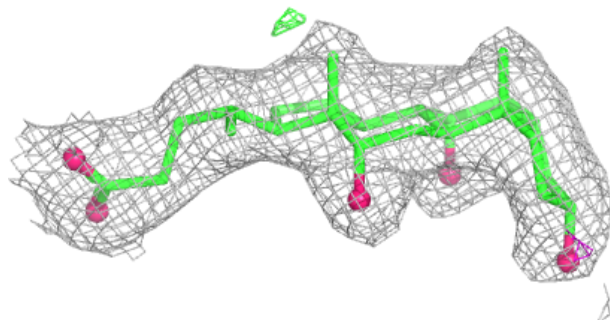
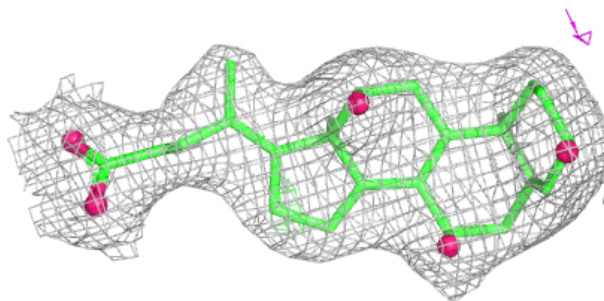
**Electron density around PEK C 302:**

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

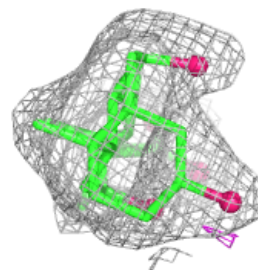
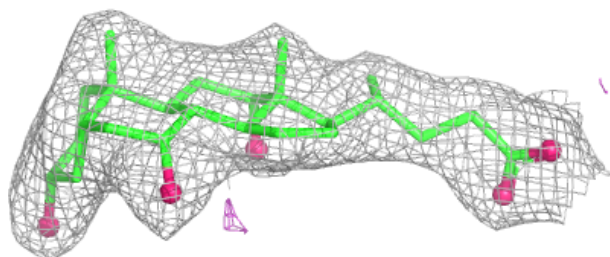
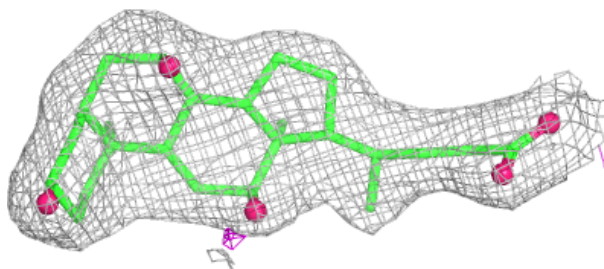


Electron density around CHD T 101:

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

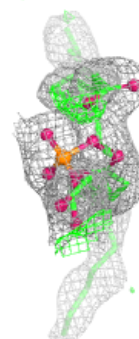
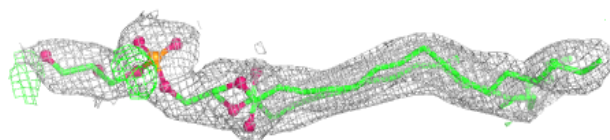
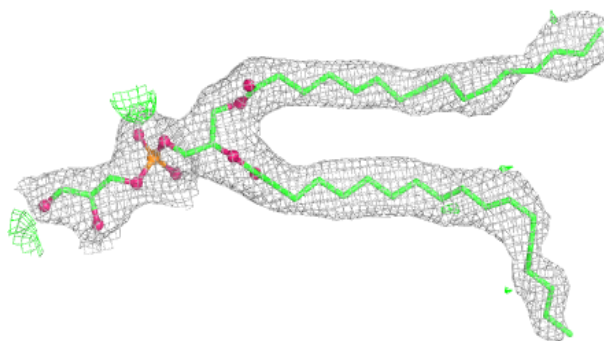
**Electron density around CHD C 306:**

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

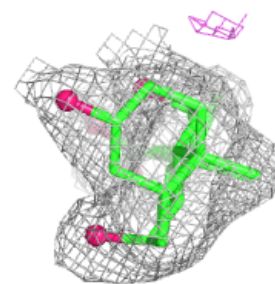
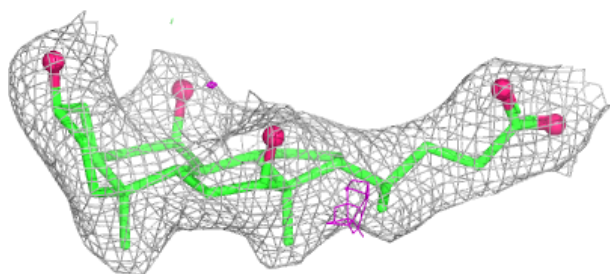
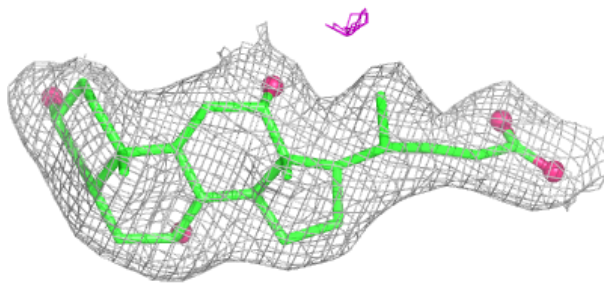


Electron density around PGV C 303:

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

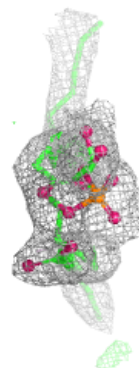
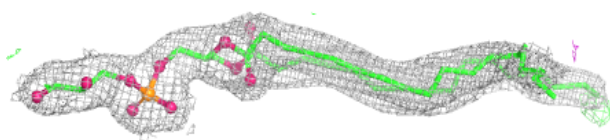
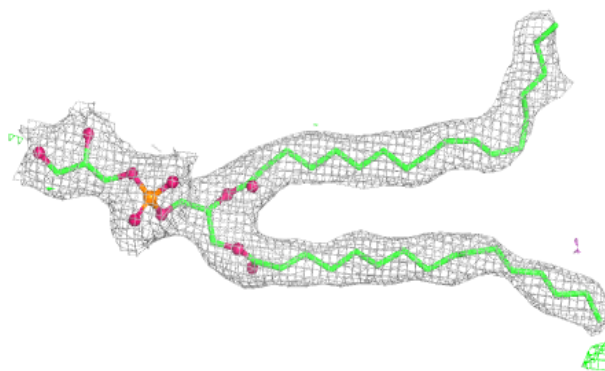
**Electron density around CHD P 306:**

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

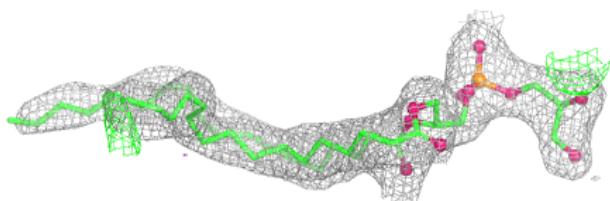
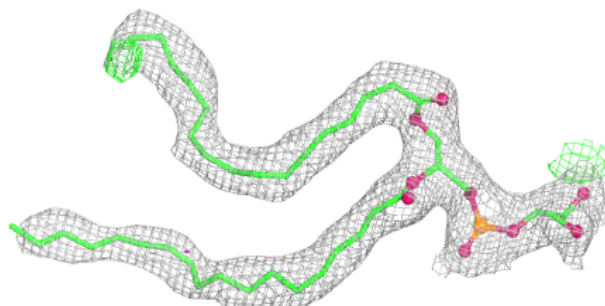


Electron density around PGV P 303:

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

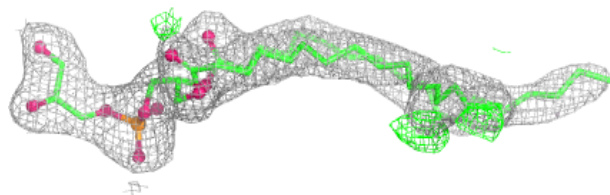
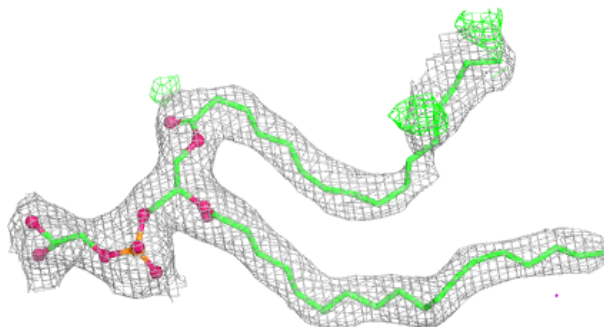
**Electron density around PGV A 606:**

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

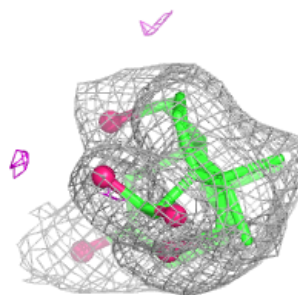
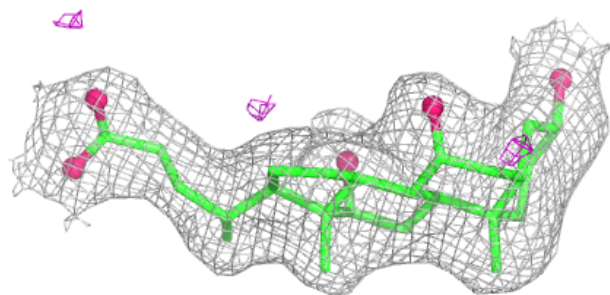
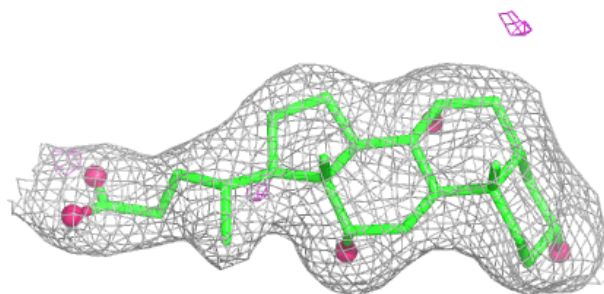


Electron density around PGV P 301:

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

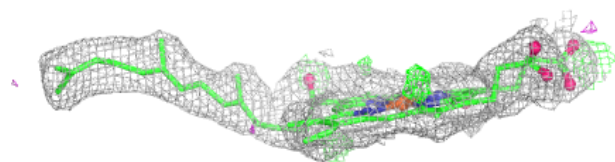
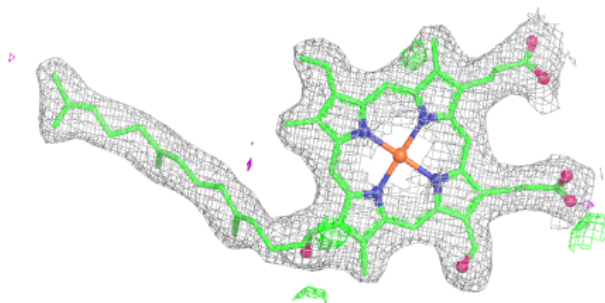
**Electron density around CHD G 103:**

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

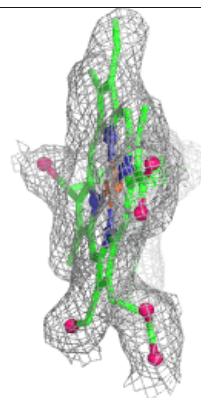
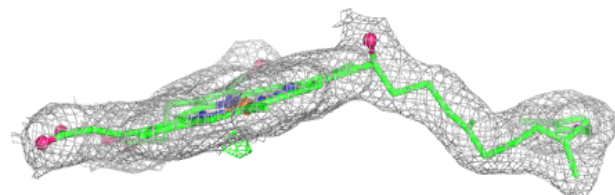
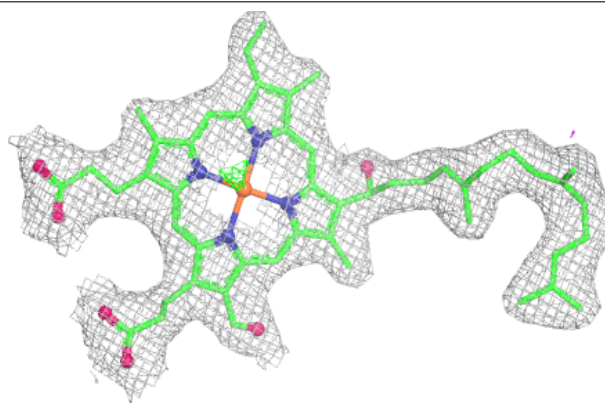


Electron density around HEA A 601:

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

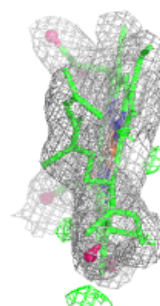
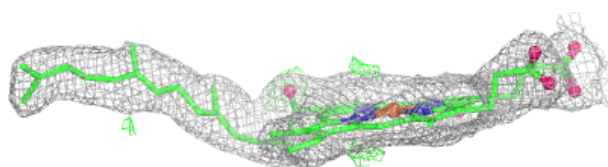
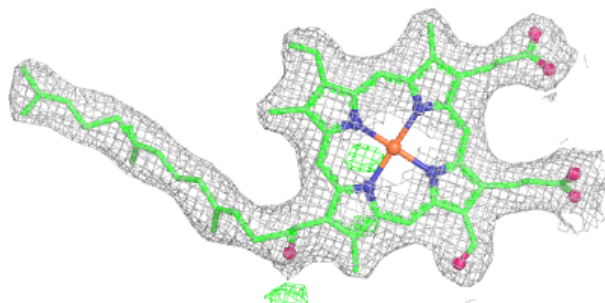
**Electron density around HEA A 602:**

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

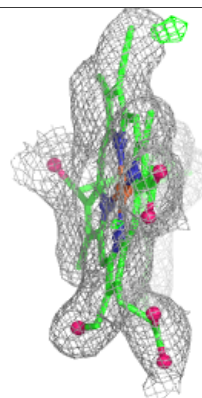
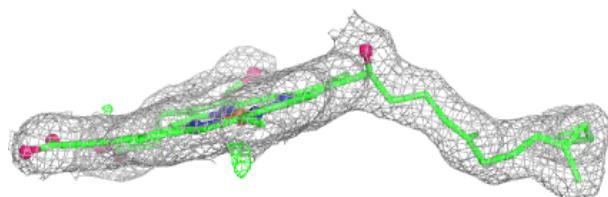
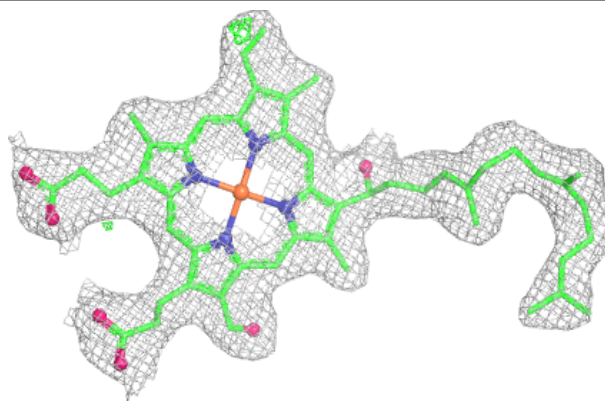


Electron density around HEA N 601:

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

**Electron density around HEA N 602:**

$2mF_o-DF_c$ (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.