



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 10:09 AM EDT

PDB ID : 5IY5 / pdb_00005iy5
Title : Electron transfer complex of cytochrome c and cytochrome c oxidase at 2.0 angstrom resolution
Authors : Shimada, S.; Baba, J.; Aoe, S.; Shimada, A.; Yamashita, E.; Tsukihara, T.
Deposited on : 2016-03-24
Resolution : 2.00 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

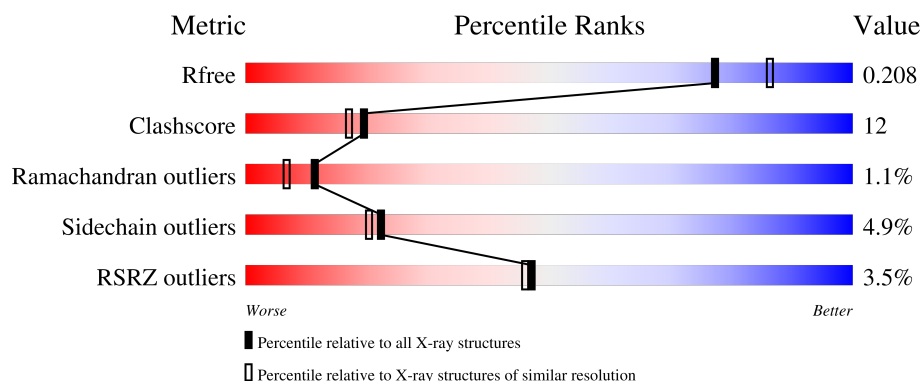
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	80% 18% •
1	N	514	84% 14% •
2	B	227	2% 71% 23% 5%
2	O	227	79% 15% 5%
3	C	259	2% 79% 20% •

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Mol	Chain	Length	Quality of chain
3	P	259	
4	D	144	
4	Q	144	
5	E	105	
5	R	105	
6	F	98	
6	S	98	
7	G	84	
7	T	84	
8	H	79	
8	U	79	
9	I	73	
9	V	73	
10	J	58	
10	W	58	
11	K	49	
11	X	49	
12	L	46	
12	Y	46	
13	M	43	
13	Z	43	
14	1	105	
14	2	105	

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
1	FME	A	1	-	X	-	-
17	NA	P	302	-	-	-	X
26	CDL	G	101	-	-	X	-
26	CDL	T	101	-	-	X	-
27	UNL	C	310	-	-	X	-
27	UNL	N	601	-	-	X	-
27	UNL	P	308	-	-	X	-
27	UNL	P	310	-	-	X	-
28	PSC	V	101	-	-	X	-
29	ZN	S	101	-	-	X	-
9	SAC	I	1	-	X	-	-

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 34765 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	11	0
			4084	2731	628	685	40			
1	N	514	Total	C	N	O	S	0	8	0
			4065	2717	627	683	38			

- 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	2	0
			1836	1192	283	343	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	6	0
			2149	1437	343	355	14			
3	P	259	Total	C	N	O	S	0	5	0
			2143	1433	342	354	14			

- 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	0	0
			1195	777	196	218	4			
4	Q	144	Total	C	N	O	S	0	1	0
			1203	782	199	218	4			

- 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	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 subunit 5B, mitochondrial.

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 subunit 6A2, mitochondrial.

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

- 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	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 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	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 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 a protein called Cytochrome c.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	1	105	Total	C	N	O	S	0	0	0
			826	526	144	152	4			
14	2	105	Total	C	N	O	S	0	0	0
			826	526	144	152	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	0	ACE	-	acetylation	UNP P00004
2	0	ACE	-	acetylation	UNP P00004

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

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

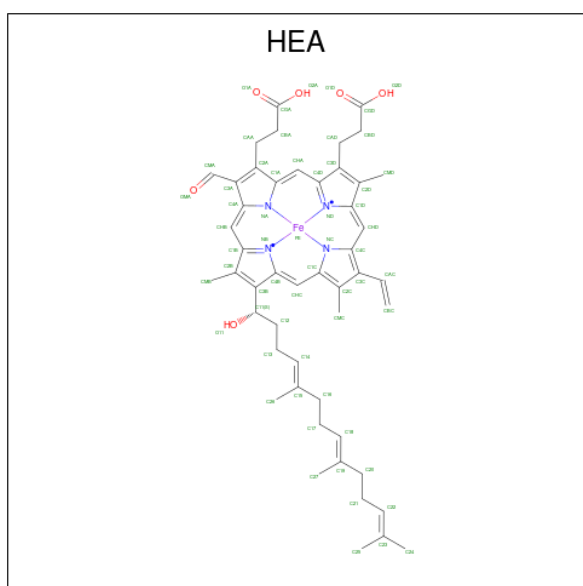
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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

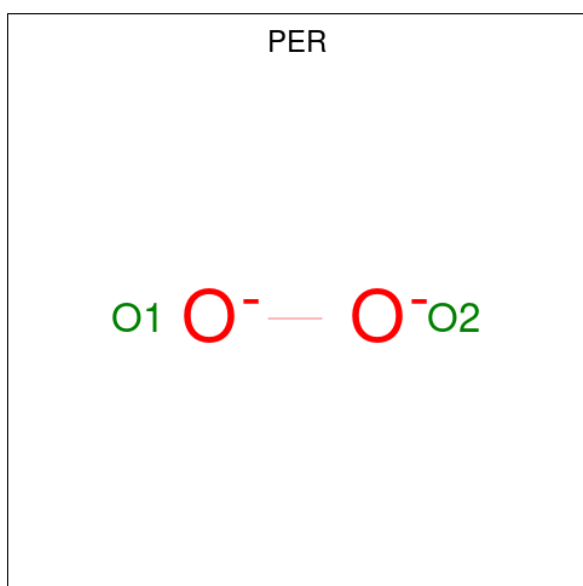
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	1	Total Na 1 1	0	0
17	C	1	Total Na 1 1	0	0
17	N	1	Total Na 1 1	0	0
17	P	1	Total Na 1 1	0	0

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



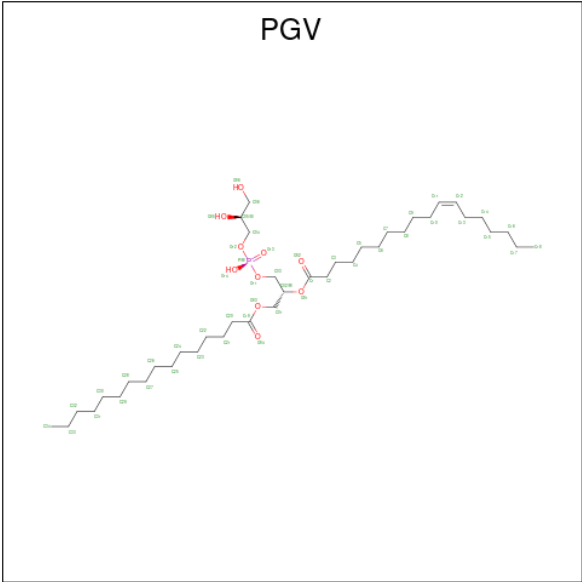
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	A	1	Total	C	Fe	N	O	0	1
			69	58	1	4	6		
18	A	1	Total	C	Fe	N	O	0	0
			60	49	1	4	6		
18	N	1	Total	C	Fe	N	O	0	1
			69	58	1	4	6		
18	N	1	Total	C	Fe	N	O	0	0
			60	49	1	4	6		

- Molecule 19 is PEROXIDE ION (CCD ID: PER) (formula: O₂).



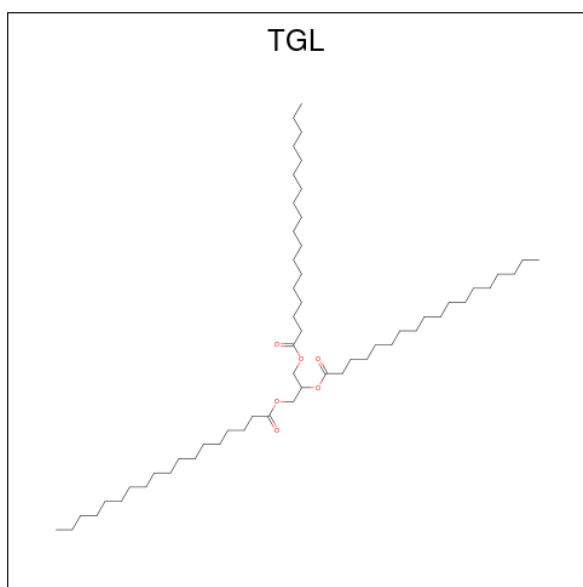
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	1	Total	O	0	0
			2	2		
19	N	1	Total	O	0	0
			2	2		

- 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: C₄₀H₇₇O₁₀P).



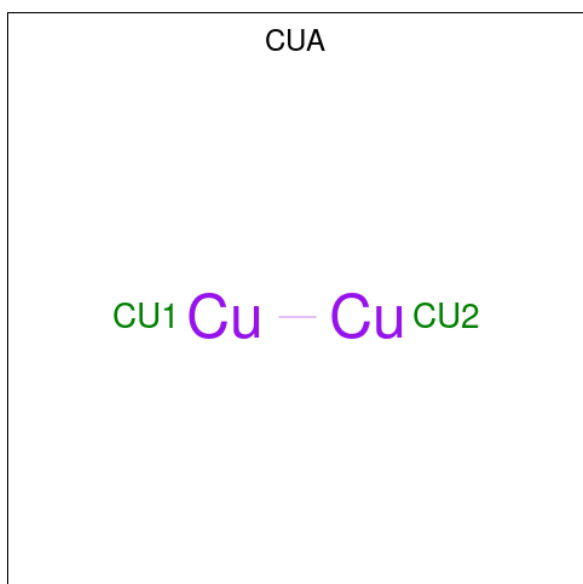
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
20	A	1	Total	C	O	P	0	0
			51	40	10	1		
20	A	1	Total	C	O	P	0	0
			51	40	10	1		
20	C	1	Total	C	O	P	0	0
			51	40	10	1		
20	C	1	Total	C	O	P	0	0
			51	40	10	1		
20	N	1	Total	C	O	P	0	0
			51	40	10	1		
20	P	1	Total	C	O	P	0	0
			51	40	10	1		
20	P	1	Total	C	O	P	0	0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

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



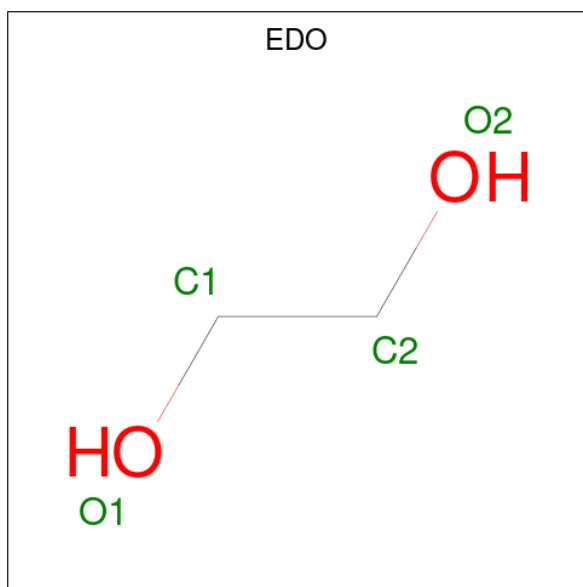
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	B	1	Total	C	O	0	0
			63	57	6		
21	D	1	Total	C	O	0	0
			63	57	6		
21	L	1	Total	C	O	0	0
			63	57	6		
21	N	1	Total	C	O	0	0
			63	57	6		
21	Q	1	Total	C	O	0	0
			63	57	6		

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



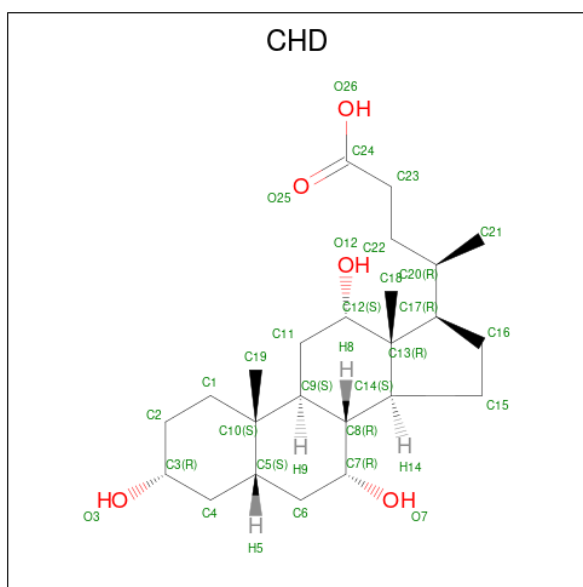
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
22	B	1	Total Cu 2 2	0	0
22	O	1	Total Cu 2 2	0	0

- Molecule 23 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



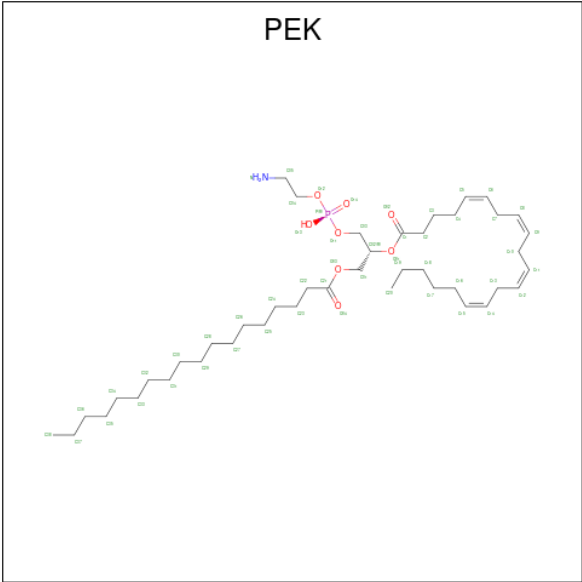
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	B	1	Total C O 4 2 2	0	0
23	C	1	Total C O 4 2 2	0	0
23	E	1	Total C O 4 2 2	0	0
23	F	1	Total C O 4 2 2	0	0
23	G	1	Total C O 4 2 2	0	0
23	I	1	Total C O 4 2 2	0	0
23	N	1	Total C O 4 2 2	0	0
23	N	1	Total C O 4 2 2	0	0
23	S	1	Total C O 4 2 2	0	0

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



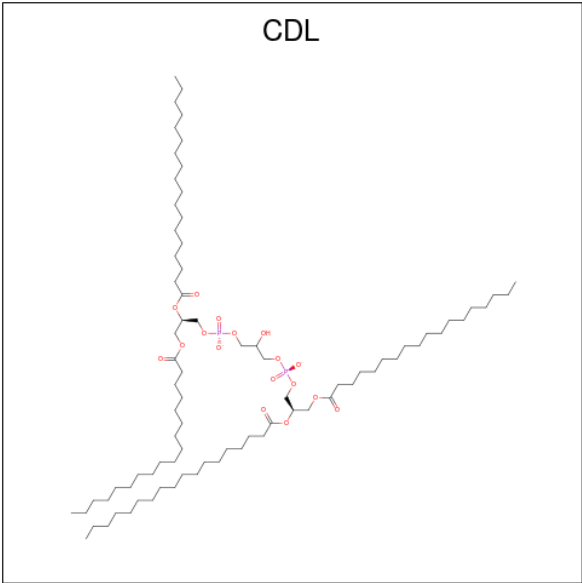
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	C	1	Total C O 29 24 5	0	0
24	C	1	Total C O 29 24 5	0	0
24	G	1	Total C O 29 24 5	0	0
24	J	1	Total C O 29 24 5	0	0
24	P	1	Total C O 29 24 5	0	0
24	P	1	Total C O 29 24 5	0	0
24	T	1	Total C O 29 24 5	0	0
24	W	1	Total C O 29 24 5	0	0

- 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: C₄₃H₇₈NO₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	C	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		

- Molecule 26 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



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		

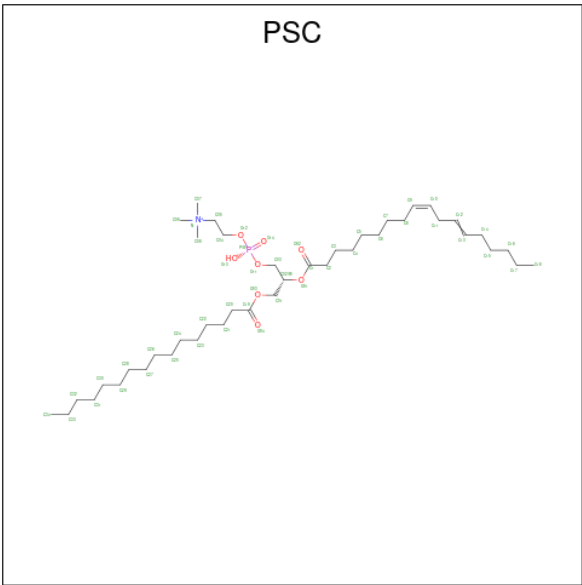
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
26	P	1	Total	C	O	P	0	0
			100	81	17	2		
26	T	1	Total	C	O	P	0	0
			100	81	17	2		

- Molecule 27 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	C	3	Total	C	0	0
			42	42		
27	J	1	Total	C	0	0
			10	10		
27	L	1	Total	C	0	0
			10	10		
27	N	4	Total	C	0	0
			63	63		
27	P	3	Total	C	0	0
			43	43		
27	T	1	Total	C	0	0
			18	18		
27	W	1	Total	C	0	0
			9	9		
27	Y	1	Total	C	0	0
			10	10		

- Molecule 28 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: C₄₂H₈₁NO₈P).

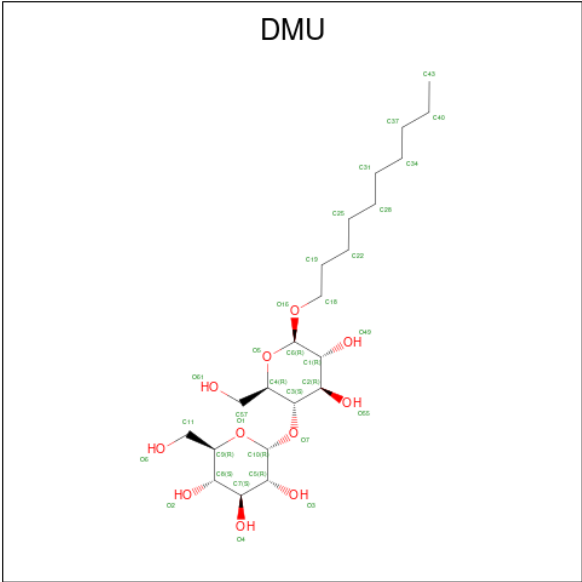


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
28	E	1	Total	C	N	O	P	0	0
			52	42	1	8	1		
28	V	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn).

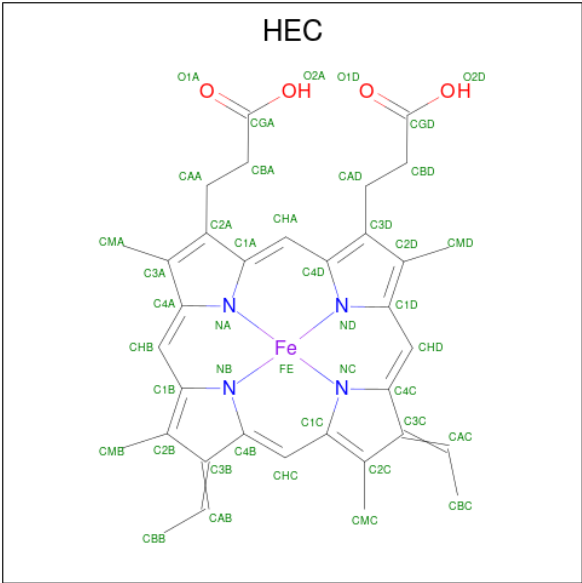
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	F	1	Total	Zn	0	0
			1	1		
29	S	1	Total	Zn	0	0
			1	1		

- Molecule 30 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



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

- Molecule 31 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
31	1	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
31	2	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 32 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	A	252	Total O 252 252	0	0
32	B	193	Total O 193 193	0	0
32	C	137	Total O 137 137	0	0
32	D	122	Total O 122 122	0	0
32	E	119	Total O 119 119	0	0
32	F	97	Total O 97 97	0	0
32	G	60	Total O 60 60	0	0
32	H	76	Total O 76 76	0	0
32	I	49	Total O 49 49	0	0
32	J	30	Total O 30 30	0	0
32	K	29	Total O 29 29	0	0
32	L	33	Total O 33 33	0	0
32	M	26	Total O 26 26	0	0
32	N	229	Total O 229 229	0	0
32	O	141	Total O 141 141	0	0
32	P	110	Total O 110 110	0	0
32	Q	99	Total O 99 99	0	0
32	R	83	Total O 83 83	0	0
32	S	95	Total O 95 95	0	0
32	T	41	Total O 41 41	0	0
32	U	54	Total O 54 54	0	0

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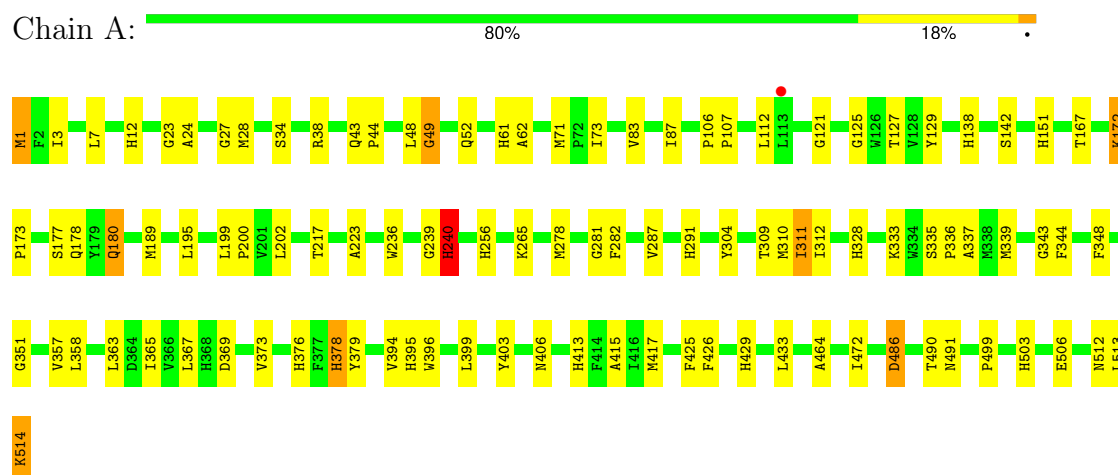
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	V	17	Total 17	O 17	0	0
32	W	10	Total 10	O 10	0	0
32	X	17	Total 17	O 17	0	0
32	Y	21	Total 21	O 21	0	0
32	Z	16	Total 16	O 16	0	0
32	1	53	Total 53	O 53	0	0
32	2	28	Total 28	O 28	0	0

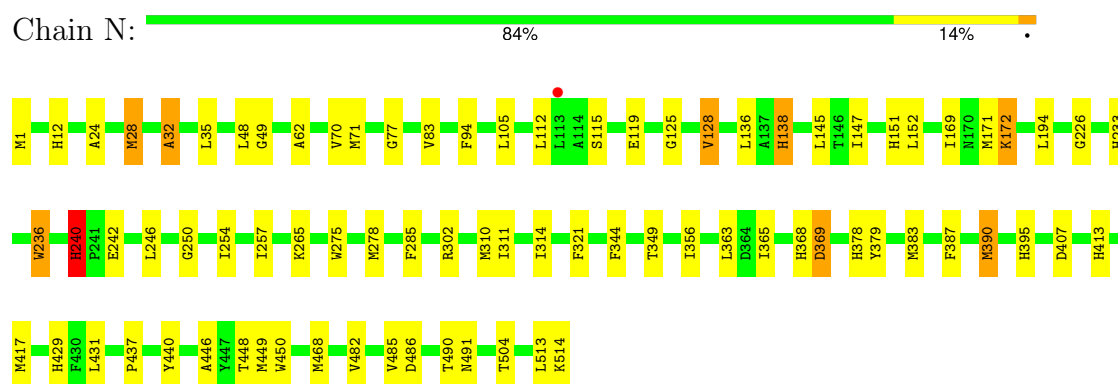
3 Residue-property plots

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 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.

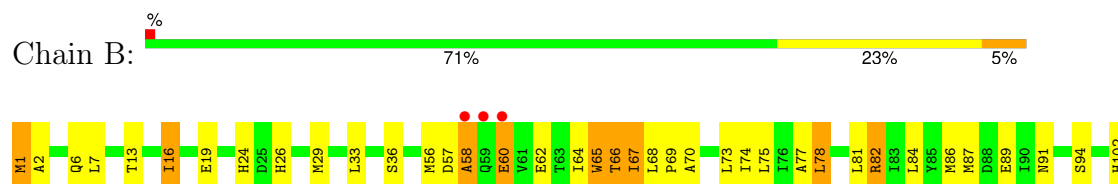
• Molecule 1: Cytochrome c oxidase subunit 1



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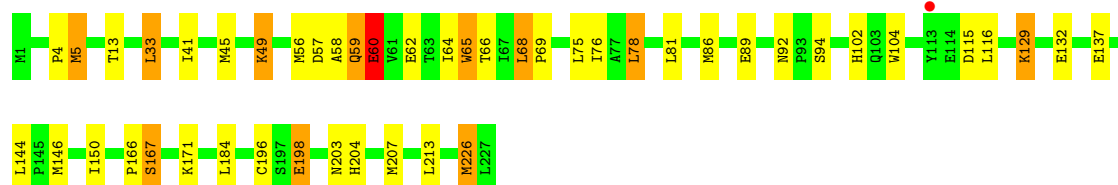
• Molecule 2: Cytochrome c oxidase subunit 2





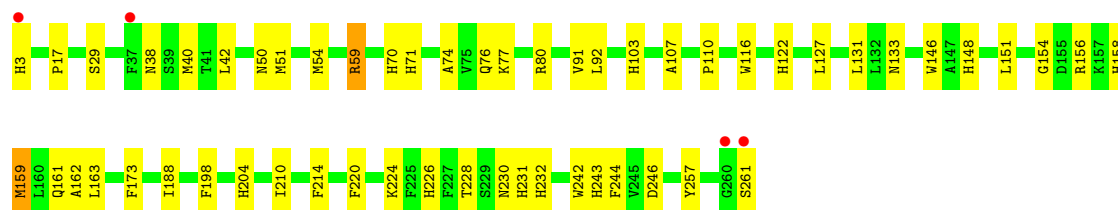
• Molecule 2: Cytochrome c oxidase subunit 2

Chain O: 79% 15% 5%



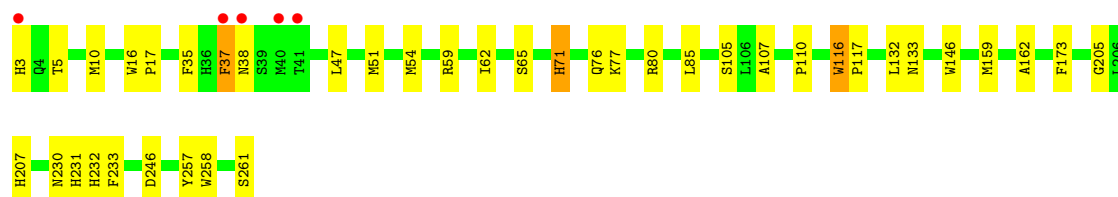
• Molecule 3: Cytochrome c oxidase subunit 3

Chain C: 79% 20% 2%



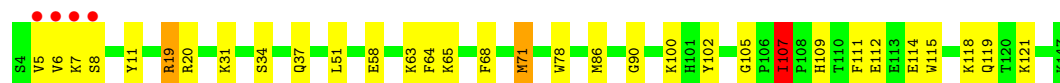
• Molecule 3: Cytochrome c oxidase subunit 3

Chain P: 85% 14% 2%



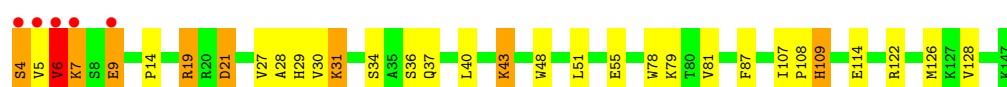
• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial

Chain D: 78% 20% 3%



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

Chain Q: 78% 16% 6%



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

Chain E:  90% 9%



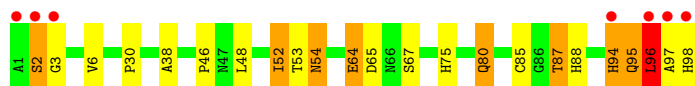
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial

Chain R:  88% 12%



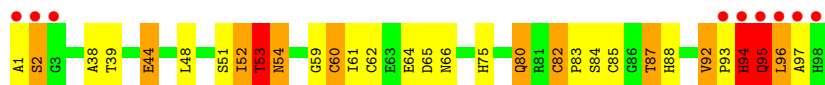
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial

Chain F:  7% 77% 14% 8%



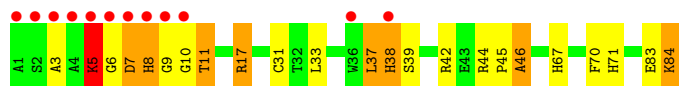
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial

Chain S:  9% 68% 18% 10%



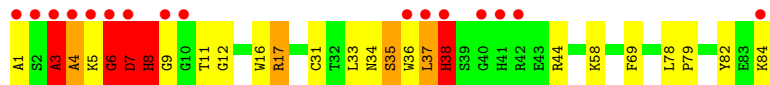
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial

Chain G:  14% 73% 17% 10%



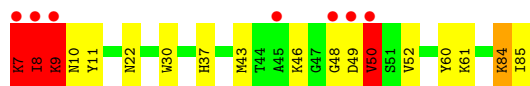
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial

Chain T:  19% 69% 20% 5% 6%

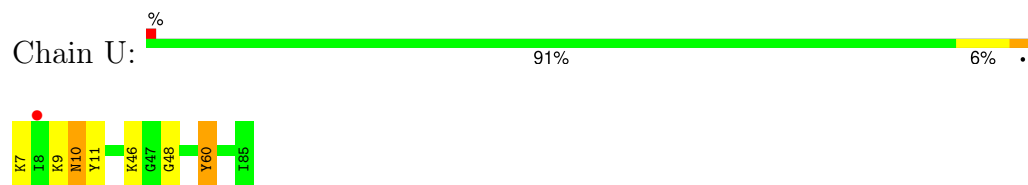


- Molecule 8: Cytochrome c oxidase subunit 6B1

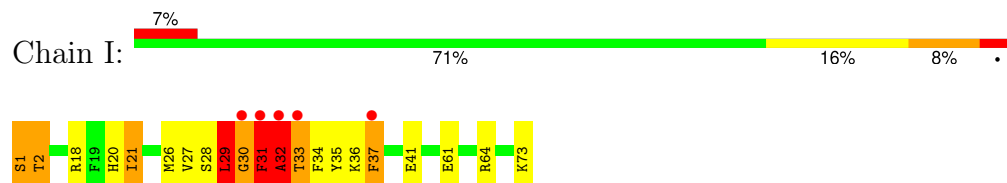
Chain H:  9% 77% 16% 5%



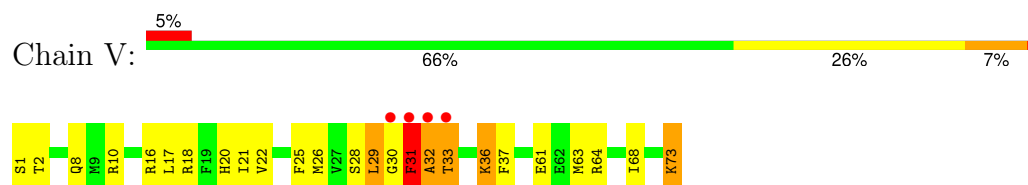
- Molecule 8: Cytochrome c oxidase subunit 6B1



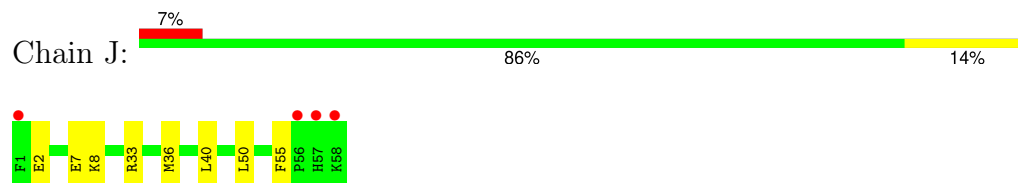
- Molecule 9: Cytochrome c oxidase subunit 6C



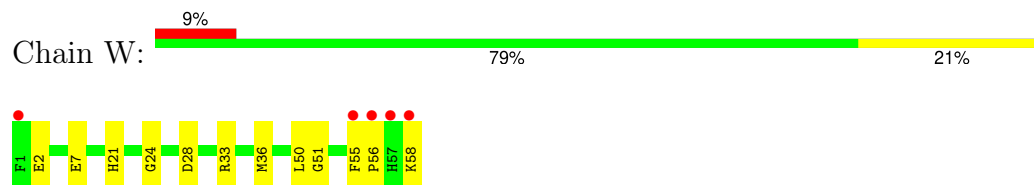
- Molecule 9: Cytochrome c oxidase subunit 6C



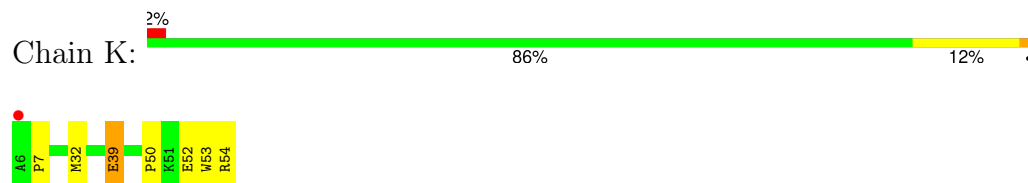
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



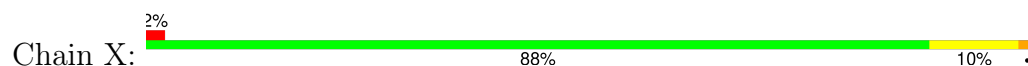
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



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

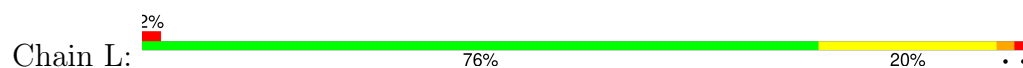


- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial

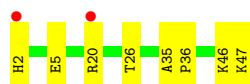
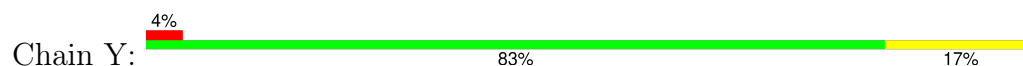




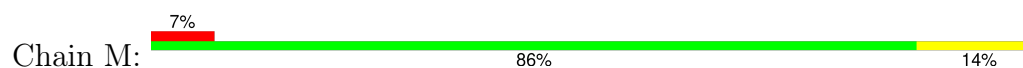
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



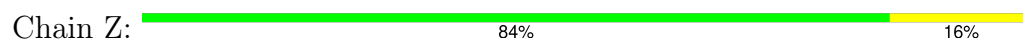
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



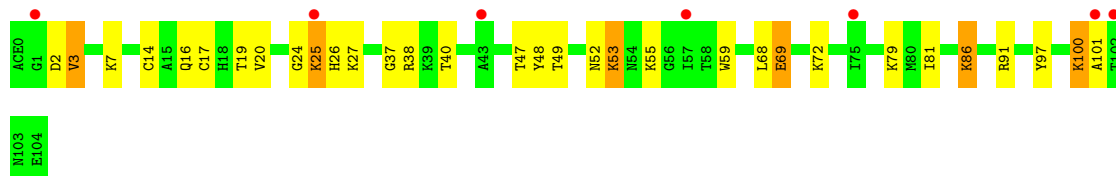
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial



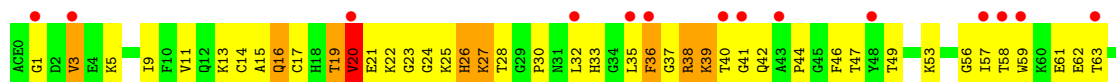
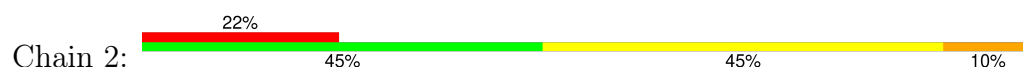
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial

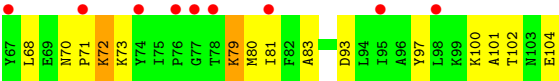


- Molecule 14: Cytochrome c



- Molecule 14: Cytochrome c





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	113.29Å 183.87Å 148.93Å 90.00° 102.12° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 40.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (40.00-2.00) 99.4 (40.00-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0048	Depositor
R, R_{free}	0.167 , 0.207 0.168 , 0.208	Depositor DCC
R_{free} test set	19991 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 62.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	34765	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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: HEA, CDL, NA, SAC, PEK, ZN, DMU, UNL, CU, TGL, CUA, MG, EDO, FME, PSC, PER, ACE, CHD, PGV, HEC, TPO

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	1.66	45/4244 (1.1%)	1.27	13/5793 (0.2%)
1	N	1.50	29/4214 (0.7%)	1.22	18/5754 (0.3%)
2	B	1.55	13/1878 (0.7%)	1.28	6/2558 (0.2%)
2	O	1.29	6/1860 (0.3%)	1.16	4/2534 (0.2%)
3	C	1.53	20/2247 (0.9%)	1.13	8/3070 (0.3%)
3	P	1.42	9/2238 (0.4%)	1.08	3/3058 (0.1%)
4	D	1.48	6/1229 (0.5%)	1.29	7/1658 (0.4%)
4	Q	1.31	6/1240 (0.5%)	1.18	3/1672 (0.2%)
5	E	1.36	1/871 (0.1%)	1.12	0/1182
5	R	1.27	2/871 (0.2%)	1.15	0/1182
6	F	1.53	6/765 (0.8%)	1.32	5/1038 (0.5%)
6	S	1.55	8/765 (1.0%)	1.58	14/1038 (1.3%)
7	G	1.50	3/690 (0.4%)	1.20	1/937 (0.1%)
7	T	1.56	6/690 (0.9%)	1.29	6/937 (0.6%)
8	H	1.56	6/682 (0.9%)	1.45	6/921 (0.7%)
8	U	1.24	0/682	1.19	0/921
9	I	1.36	2/605 (0.3%)	1.37	4/802 (0.5%)
9	V	1.13	1/605 (0.2%)	1.18	1/802 (0.1%)
10	J	1.22	0/471	1.14	2/636 (0.3%)
10	W	1.14	1/471 (0.2%)	1.13	3/636 (0.5%)
11	K	1.35	0/398	1.17	1/546 (0.2%)
11	X	1.11	0/398	1.17	1/546 (0.2%)
12	L	1.45	2/393 (0.5%)	1.13	0/526
12	Y	1.29	0/393	1.20	0/526
13	M	1.25	0/345	1.23	1/470 (0.2%)
13	Z	1.25	2/345 (0.6%)	1.29	0/470
14	1	1.00	0/840	1.16	5/1120 (0.4%)
14	2	0.98	0/840	1.14	1/1120 (0.1%)
All	All	1.44	174/31270 (0.6%)	1.22	113/42453 (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	1
1	N	0	1
6	S	0	2
8	H	0	2
9	V	0	2
All	All	0	8

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	83	VAL	CA-CB	12.01	1.60	1.54
1	A	378	HIS	ND1-CE1	10.96	1.43	1.32
8	H	8	ILE	N-CA	10.40	1.59	1.46
1	A	61	HIS	ND1-CE1	10.00	1.42	1.32
1	A	378	HIS	CG-CD2	9.73	1.46	1.35

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	S	82	CYS	CA-C-N	-11.55	108.50	119.82
6	S	82	CYS	C-N-CA	-11.55	108.50	119.82
8	H	9	LYS	CA-CB-CG	-11.23	91.63	114.10
9	I	29	LEU	N-CA-C	-10.64	99.65	111.14
8	H	9	LYS	O-C-N	8.69	134.15	122.59

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	HIS	Sidechain
8	H	8	ILE	Peptide
8	H	9	LYS	Peptide
1	N	240	HIS	Sidechain
6	S	94	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4084	0	4069	69	0
1	N	4065	0	4046	50	0
2	B	1836	0	1843	47	0
2	O	1824	0	1833	43	0
3	C	2149	0	2075	26	0
3	P	2143	0	2067	32	0
4	D	1195	0	1183	19	0
4	Q	1203	0	1196	30	0
5	E	852	0	845	8	0
5	R	852	0	845	6	0
6	F	748	0	728	25	0
6	S	748	0	729	27	0
7	G	675	0	643	22	0
7	T	675	0	644	29	0
8	H	662	0	623	37	0
8	U	662	0	623	8	0
9	I	601	0	613	40	0
9	V	601	0	613	21	0
10	J	460	0	459	7	0
10	W	460	0	459	13	0
11	K	384	0	366	5	0
11	X	384	0	366	8	0
12	L	380	0	380	13	0
12	Y	380	0	380	6	0
13	M	335	0	352	1	0
13	Z	335	0	352	4	0
14	1	826	0	849	26	0
14	2	826	0	848	40	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	N	1	0	0	0	0
17	P	1	0	0	0	0
18	A	129	0	88	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	N	129	0	88	9	0
19	A	2	0	0	0	0
19	N	2	0	0	1	0
20	A	102	0	152	9	0
20	C	102	0	152	14	0
20	N	51	0	76	1	0
20	P	102	0	152	10	0
21	B	63	0	110	6	0
21	D	63	0	110	13	0
21	L	63	0	110	20	0
21	N	63	0	110	2	0
21	Q	63	0	110	10	0
22	B	2	0	0	0	0
22	O	2	0	0	0	0
23	B	4	0	6	0	0
23	C	4	0	6	0	0
23	E	4	0	6	1	0
23	F	4	0	6	0	0
23	G	4	0	6	0	0
23	I	4	0	6	0	0
23	N	8	0	12	0	0
23	S	4	0	6	0	0
24	C	58	0	78	4	0
24	G	29	0	39	0	0
24	J	29	0	38	5	0
24	P	58	0	78	2	0
24	T	29	0	39	1	0
24	W	29	0	37	5	0
25	C	53	0	77	7	0
25	P	53	0	77	3	0
26	C	100	0	156	15	0
26	G	100	0	156	23	0
26	P	100	0	156	12	0
26	T	100	0	156	24	0
27	C	42	0	0	4	0
27	J	10	0	0	1	0
27	L	10	0	0	1	0
27	N	63	0	0	2	0
27	P	43	0	0	6	0
27	T	18	0	0	1	0
27	W	9	0	0	1	0
27	Y	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	E	52	0	80	19	0
28	V	52	0	80	21	0
29	F	1	0	0	0	0
29	S	1	0	0	2	0
30	M	33	0	42	1	0
30	Z	33	0	42	1	0
31	1	43	0	31	3	0
31	2	43	0	30	4	0
32	1	53	0	0	7	0
32	2	28	0	0	7	0
32	A	252	0	0	19	0
32	B	193	0	0	6	0
32	C	137	0	0	8	0
32	D	122	0	0	7	0
32	E	119	0	0	6	0
32	F	97	0	0	2	2
32	G	60	0	0	11	0
32	H	76	0	0	7	0
32	I	49	0	0	5	0
32	J	30	0	0	3	0
32	K	29	0	0	1	0
32	L	33	0	0	1	0
32	M	26	0	0	2	0
32	N	229	0	0	6	0
32	O	141	0	0	3	0
32	P	110	0	0	9	0
32	Q	99	0	0	7	0
32	R	83	0	0	1	0
32	S	95	0	0	5	0
32	T	41	0	0	3	0
32	U	54	0	0	4	2
32	V	17	0	0	2	0
32	W	10	0	0	0	0
32	X	17	0	0	3	0
32	Y	21	0	0	0	0
32	Z	16	0	0	0	0
All	All	34765	0	32733	753	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 753 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)
27:C:310:UNL:C4	27:C:310:UNL:C6	1.76	1.36
32:A:927:HOH:O	26:T:101:CDL:H412	1.17	1.28
5:E:79:LYS:HE3	32:E:387:HOH:O	1.31	1.24
27:W:102:UNL:C5	27:W:102:UNL:C4	2.17	1.23
1:A:486:ASP:OD2	4:D:19:ARG:HD2	1.32	1.21

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:F:266:HOH:O	32:U:148:HOH:O[1_455]	2.11	0.09
32:F:276:HOH:O	32:U:141:HOH:O[1_455]	2.14	0.06

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	524/514 (102%)	510 (97%)	14 (3%)	0	100	100
1	N	520/514 (101%)	504 (97%)	16 (3%)	0	100	100
2	B	227/227 (100%)	217 (96%)	9 (4%)	1 (0%)	30	27
2	O	225/227 (99%)	216 (96%)	8 (4%)	1 (0%)	30	27
3	C	263/259 (102%)	259 (98%)	4 (2%)	0	100	100
3	P	262/259 (101%)	256 (98%)	5 (2%)	1 (0%)	30	27
4	D	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
4	Q	143/144 (99%)	136 (95%)	5 (4%)	2 (1%)	9	4
5	E	103/105 (98%)	102 (99%)	1 (1%)	0	100	100
5	R	103/105 (98%)	102 (99%)	1 (1%)	0	100	100
6	F	96/98 (98%)	90 (94%)	4 (4%)	2 (2%)	5	2
6	S	96/98 (98%)	90 (94%)	3 (3%)	3 (3%)	3	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	81/84 (96%)	65 (80%)	10 (12%)	6 (7%)	1	0
7	T	81/84 (96%)	64 (79%)	10 (12%)	7 (9%)	0	0
8	H	77/79 (98%)	70 (91%)	4 (5%)	3 (4%)	2	1
8	U	77/79 (98%)	73 (95%)	3 (4%)	1 (1%)	9	5
9	I	71/73 (97%)	67 (94%)	1 (1%)	3 (4%)	2	0
9	V	71/73 (97%)	65 (92%)	4 (6%)	2 (3%)	4	1
10	J	56/58 (97%)	56 (100%)	0	0	100	100
10	W	56/58 (97%)	55 (98%)	0	1 (2%)	6	3
11	K	47/49 (96%)	47 (100%)	0	0	100	100
11	X	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
12	L	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
12	Y	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
13	M	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
13	Z	41/43 (95%)	41 (100%)	0	0	100	100
14	1	103/105 (98%)	90 (87%)	11 (11%)	2 (2%)	6	3
14	2	103/105 (98%)	81 (79%)	15 (15%)	7 (7%)	1	0
All	All	3744/3768 (99%)	3557 (95%)	145 (4%)	42 (1%)	11	7

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	2	SER
6	F	96	LEU
7	G	3	ALA
7	G	7	ASP
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	437/426 (103%)	430 (98%)	7 (2%)	55	62
1	N	433/426 (102%)	425 (98%)	8 (2%)	51	58
2	B	212/210 (101%)	205 (97%)	7 (3%)	33	34
2	O	210/210 (100%)	193 (92%)	17 (8%)	11	7
3	C	230/224 (103%)	224 (97%)	6 (3%)	40	44
3	P	229/224 (102%)	226 (99%)	3 (1%)	61	68
4	D	128/128 (100%)	122 (95%)	6 (5%)	23	22
4	Q	129/128 (101%)	120 (93%)	9 (7%)	14	10
5	E	92/92 (100%)	90 (98%)	2 (2%)	45	50
5	R	92/92 (100%)	89 (97%)	3 (3%)	33	34
6	F	81/81 (100%)	76 (94%)	5 (6%)	16	13
6	S	81/81 (100%)	73 (90%)	8 (10%)	7	4
7	G	67/67 (100%)	61 (91%)	6 (9%)	9	6
7	T	67/67 (100%)	62 (92%)	5 (8%)	12	9
8	H	71/71 (100%)	64 (90%)	7 (10%)	7	4
8	U	71/71 (100%)	70 (99%)	1 (1%)	59	66
9	I	57/57 (100%)	50 (88%)	7 (12%)	4	3
9	V	57/57 (100%)	51 (90%)	6 (10%)	6	4
10	J	49/49 (100%)	48 (98%)	1 (2%)	48	54
10	W	49/49 (100%)	46 (94%)	3 (6%)	17	14
11	K	39/39 (100%)	37 (95%)	2 (5%)	21	19
11	X	39/39 (100%)	38 (97%)	1 (3%)	40	44
12	L	39/39 (100%)	35 (90%)	4 (10%)	7	4
12	Y	39/39 (100%)	36 (92%)	3 (8%)	12	8
13	M	37/37 (100%)	33 (89%)	4 (11%)	6	3
13	Z	37/37 (100%)	35 (95%)	2 (5%)	20	17
14	1	86/86 (100%)	78 (91%)	8 (9%)	8	5
14	2	86/86 (100%)	69 (80%)	17 (20%)	1	0
All	All	3244/3212 (101%)	3086 (95%)	158 (5%)	22	20

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	T	38	HIS
14	2	16	GLN
9	V	8	GLN
12	Y	20	ARG
14	2	38	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
8	U	10	ASN
8	U	31	GLN
14	1	103	ASN
10	J	57	HIS
10	J	29	ASN

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
7	TPO	G	11	7	8,10,11	1.88	2 (25%)	10,14,16	1.09	0
9	SAC	I	1	9	7,8,9	2.20	2 (28%)	7,9,11	1.88	2 (28%)
1	FME	N	1	1	8,9,10	0.75	0	8,9,11	6.18	6 (75%)
2	FME	B	1	2	8,9,10	2.30	3 (37%)	8,9,11	7.75	4 (50%)
9	SAC	V	1	9	7,8,9	2.45	2 (28%)	7,9,11	1.56	2 (28%)
2	FME	O	1	2	8,9,10	0.83	0	8,9,11	0.87	0
7	TPO	T	11	7	8,10,11	2.24	2 (25%)	10,14,16	1.36	1 (10%)
1	FME	A	1	1	8,9,10	1.31	1 (12%)	8,9,11	5.61	6 (75%)

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	G	11	7	-	6/9/11/13	-
9	SAC	I	1	9	-	6/7/8/10	-
1	FME	N	1	1	-	4/7/9/11	-
2	FME	B	1	2	-	1/7/9/11	-
9	SAC	V	1	9	-	2/7/8/10	-
2	FME	O	1	2	-	0/7/9/11	-
7	TPO	T	11	7	-	5/9/11/13	-
1	FME	A	1	1	-	4/7/9/11	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	FME	CA-N	5.13	1.54	1.46
9	V	1	SAC	OAC-C1A	4.93	1.34	1.23
9	I	1	SAC	OAC-C1A	4.77	1.33	1.23
9	V	1	SAC	CA-N	3.89	1.52	1.46
7	T	11	TPO	P-O1P	3.74	1.62	1.50

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	FME	CA-N-CN	-20.68	91.02	122.82
1	N	1	FME	CA-N-CN	-15.59	98.84	122.82
1	A	1	FME	CA-N-CN	-13.93	101.39	122.82
1	A	1	FME	CB-CA-N	6.22	121.85	110.52
2	B	1	FME	O1-CN-N	5.94	140.65	125.32

There are no chirality outliers.

5 of 28 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-OG1
7	G	11	TPO	CA-CB-OG1-P

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	11	TPO	2	0
9	I	1	SAC	1	0
2	B	1	FME	2	0
1	A	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 76 ligands modelled in this entry, 10 are monoatomic and 15 are unknown - leaving 51 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	P	303	-	52,52,52	1.00	4 (7%)	55,57,57	0.93	2 (3%)
26	CDL	C	306	-	99,99,99	1.47	12 (12%)	105,111,111	1.43	10 (9%)
18	HEA	N	606	19,1	67,67,67	2.17	23 (34%)	81,103,103	1.51	16 (19%)
24	CHD	G	102	-	32,32,32	1.16	2 (6%)	51,51,51	1.98	12 (23%)
18	HEA	A	604[B]	-	67,67,67	1.82	22 (32%)	81,103,103	1.78	21 (25%)
21	TGL	N	608	-	62,62,62	1.53	8 (12%)	65,65,65	2.13	14 (21%)
23	EDO	B	303	-	3,3,3	0.73	0	2,2,2	0.40	0
31	HEC	1	201	14	46,50,50	1.65	6 (13%)	58,82,82	1.62	13 (22%)
20	PGV	P	305	-	50,50,50	1.30	2 (4%)	53,56,56	1.41	6 (11%)
21	TGL	B	301	-	62,62,62	1.50	8 (12%)	65,65,65	1.90	13 (20%)
23	EDO	N	613	-	3,3,3	0.55	0	2,2,2	0.31	0
26	CDL	T	101	-	99,99,99	1.51	12 (12%)	105,111,111	1.50	15 (14%)
18	HEA	N	605[B]	-	67,67,67	1.91	21 (31%)	81,103,103	1.84	21 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CHD	P	301	-	32,32,32	1.11	2 (6%)	51,51,51	1.85	13 (25%)
26	CDL	G	101	-	99,99,99	1.51	12 (12%)	105,111,111	1.37	13 (12%)
26	CDL	P	306	-	99,99,99	1.50	13 (13%)	105,111,111	1.23	10 (9%)
23	EDO	N	614	-	3,3,3	0.39	0	2,2,2	0.50	0
19	PER	A	606	18,15	1,1,1	0.54	0	-		
25	PEK	C	303	-	52,52,52	0.97	2 (3%)	55,57,57	1.21	5 (9%)
24	CHD	P	307	-	32,32,32	0.64	0	51,51,51	2.36	19 (37%)
18	HEA	A	604[A]	-	67,67,67	1.82	23 (34%)	81,103,103	1.81	20 (24%)
22	CUA	O	301	2	0,1,1	-	-	-		
21	TGL	D	201	-	62,62,62	1.44	6 (9%)	65,65,65	1.53	8 (12%)
20	PGV	P	304	-	50,50,50	0.83	2 (4%)	53,56,56	1.18	6 (11%)
21	TGL	Q	201	-	62,62,62	1.46	6 (9%)	65,65,65	1.32	9 (13%)
28	PSC	E	201	-	51,51,51	1.33	3 (5%)	57,59,59	1.52	9 (15%)
23	EDO	E	202	-	3,3,3	0.47	0	2,2,2	0.73	0
20	PGV	A	608	-	50,50,50	1.07	4 (8%)	53,56,56	1.31	6 (11%)
19	PER	N	607	18,15	1,1,1	0.84	0	-		
24	CHD	W	101	-	32,32,32	0.93	2 (6%)	51,51,51	3.14	23 (45%)
31	HEC	2	201	14	46,50,50	1.67	8 (17%)	58,82,82	1.45	7 (12%)
24	CHD	T	103	-	32,32,32	1.28	4 (12%)	51,51,51	2.00	19 (37%)
18	HEA	N	605[A]	-	67,67,67	1.92	21 (31%)	81,103,103	1.80	19 (23%)
20	PGV	A	607	-	50,50,50	1.13	2 (4%)	53,56,56	1.06	4 (7%)
23	EDO	I	101	-	3,3,3	0.60	0	2,2,2	0.32	0
24	CHD	C	301	-	32,32,32	1.33	4 (12%)	51,51,51	1.77	10 (19%)
18	HEA	A	605	19,1	67,67,67	2.08	22 (32%)	81,103,103	1.67	23 (28%)
24	CHD	J	101	-	32,32,32	0.90	1 (3%)	51,51,51	2.12	15 (29%)
21	TGL	L	101	-	62,62,62	1.61	6 (9%)	65,65,65	1.60	14 (21%)
24	CHD	C	307	-	32,32,32	0.93	1 (3%)	51,51,51	3.48	26 (50%)
23	EDO	G	103	-	3,3,3	0.79	0	2,2,2	0.67	0
28	PSC	V	101	-	51,51,51	1.22	3 (5%)	57,59,59	1.32	5 (8%)
23	EDO	C	311	-	3,3,3	0.58	0	2,2,2	0.34	0
30	DMU	Z	101	-	34,34,34	0.75	1 (2%)	45,45,45	1.08	4 (8%)
20	PGV	C	304	-	50,50,50	0.82	2 (4%)	53,56,56	1.35	8 (15%)
20	PGV	C	305	-	50,50,50	1.42	4 (8%)	53,56,56	1.44	7 (13%)
23	EDO	F	102	-	3,3,3	0.41	0	2,2,2	0.57	0
20	PGV	N	612	-	50,50,50	0.86	1 (2%)	53,56,56	1.23	5 (9%)
22	CUA	B	302	2	0,1,1	-	-	-		
30	DMU	M	101	-	34,34,34	0.74	0	45,45,45	1.76	10 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	EDO	S	102	-	3,3,3	0.61	0	2,2,2	0.81	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
25	PEK	P	303	-	-	20/56/56/56	-
26	CDL	C	306	-	-	61/110/110/110	-
18	HEA	N	606	19,1	-	6/36/76/76	-
24	CHD	G	102	-	-	3/9/74/74	0/4/4/4
18	HEA	A	604[B]	-	-	6/36/76/76	-
21	TGL	N	608	-	-	34/65/65/65	-
23	EDO	B	303	-	-	1/1/1/1	-
31	HEC	1	201	14	-	4/14/54/54	-
20	PGV	P	305	-	-	31/55/55/55	-
21	TGL	B	301	-	-	33/65/65/65	-
23	EDO	N	613	-	-	0/1/1/1	-
26	CDL	T	101	-	-	59/110/110/110	-
18	HEA	N	605[B]	-	-	8/36/76/76	-
24	CHD	P	301	-	-	2/9/74/74	0/4/4/4
26	CDL	G	101	-	-	57/110/110/110	-
26	CDL	P	306	-	-	65/110/110/110	-
23	EDO	N	614	-	-	1/1/1/1	-
25	PEK	C	303	-	-	19/56/56/56	-
24	CHD	P	307	-	-	5/9/74/74	0/4/4/4
18	HEA	A	604[A]	-	-	5/36/76/76	-
21	TGL	D	201	-	-	41/65/65/65	-
20	PGV	P	304	-	-	12/55/55/55	-
21	TGL	Q	201	-	-	35/65/65/65	-
28	PSC	E	201	-	-	36/55/55/55	-
23	EDO	E	202	-	-	1/1/1/1	-
20	PGV	A	608	-	-	12/55/55/55	-
24	CHD	W	101	-	-	8/9/74/74	0/4/4/4
31	HEC	2	201	14	-	10/14/54/54	-
24	CHD	T	103	-	-	2/9/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	HEA	N	605[A]	-	-	6/36/76/76	-
20	PGV	A	607	-	-	29/55/55/55	-
23	EDO	I	101	-	-	0/1/1/1	-
24	CHD	C	301	-	-	2/9/74/74	0/4/4/4
18	HEA	A	605	19,1	-	7/36/76/76	-
24	CHD	J	101	-	-	7/9/74/74	0/4/4/4
21	TGL	L	101	-	-	47/65/65/65	-
24	CHD	C	307	-	-	8/9/74/74	0/4/4/4
23	EDO	G	103	-	-	0/1/1/1	-
28	PSC	V	101	-	-	34/55/55/55	-
23	EDO	C	311	-	-	1/1/1/1	-
30	DMU	Z	101	-	-	4/19/59/59	0/2/2/2
20	PGV	C	304	-	-	19/55/55/55	-
20	PGV	C	305	-	-	25/55/55/55	-
23	EDO	F	102	-	-	0/1/1/1	-
20	PGV	N	612	-	-	9/55/55/55	-
30	DMU	M	101	-	-	6/19/59/59	0/2/2/2
23	EDO	S	102	-	-	0/1/1/1	-

The worst 5 of 275 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	L	101	TGL	OG2-CB1	6.99	1.54	1.34
20	C	305	PGV	O01-C1	5.87	1.50	1.34
21	L	101	TGL	OG3-CC1	5.79	1.50	1.33
28	E	201	PSC	O01-C1	5.63	1.50	1.34
28	V	101	PSC	O01-C1	5.59	1.50	1.34

The worst 5 of 460 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	C	307	CHD	C10-C9-C8	9.97	122.96	111.84
24	W	101	CHD	C17-C13-C12	9.97	126.64	117.67
24	C	307	CHD	C6-C5-C4	-7.60	102.55	111.23
24	W	101	CHD	C13-C17-C20	7.38	128.43	119.48
24	C	307	CHD	C4-C5-C10	7.20	120.33	112.66

There are no chirality outliers.

5 of 781 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	A	604[A]	HEA	C2A-C3A-CMA-OMA
18	A	604[B]	HEA	C2A-C3A-CMA-OMA
18	A	605	HEA	C2A-C3A-CMA-OMA
18	N	605[A]	HEA	C2A-C3A-CMA-OMA
18	N	605[B]	HEA	C2A-C3A-CMA-OMA

There are no ring outliers.

38 monomers are involved in 249 short contacts:

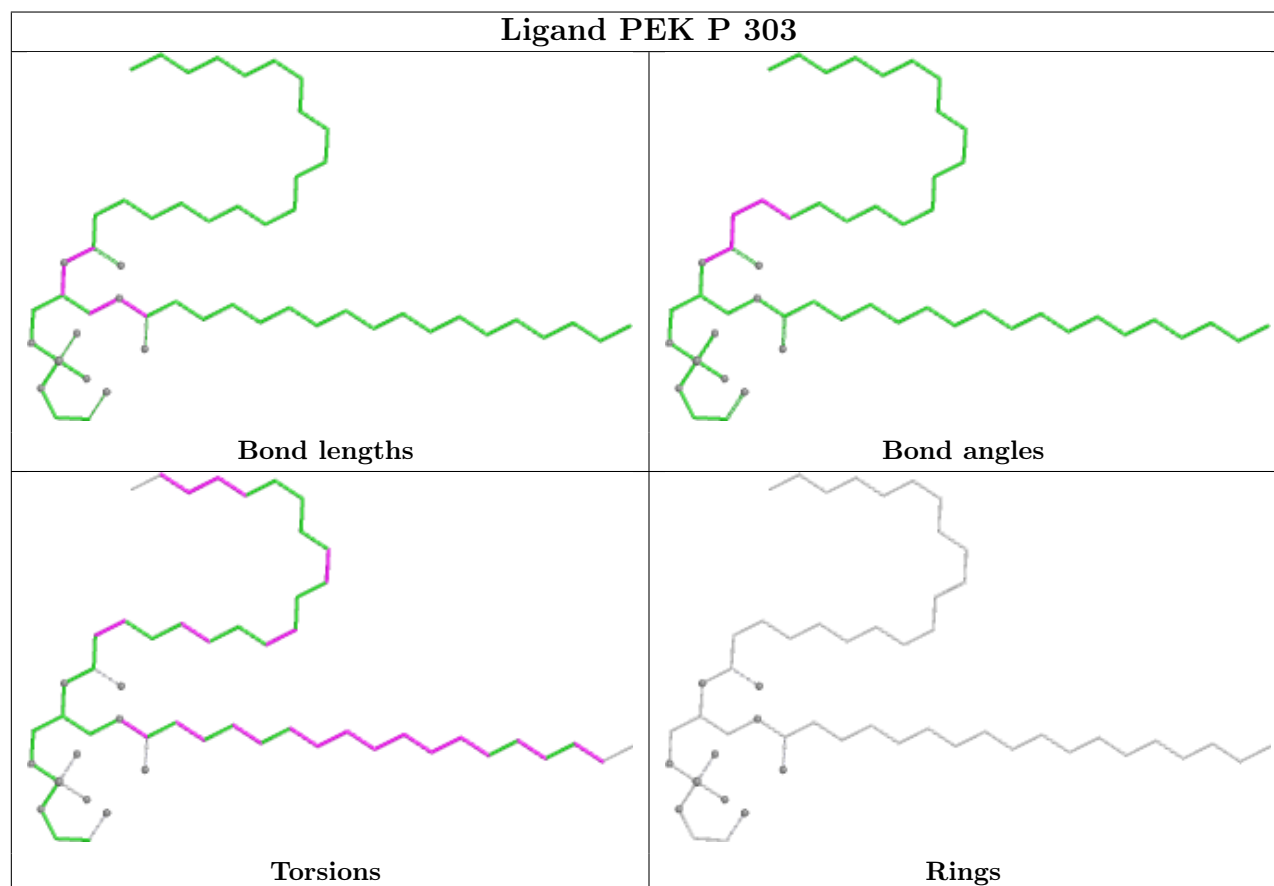
Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	P	303	PEK	3	0
26	C	306	CDL	15	0
18	N	606	HEA	1	0
18	A	604[B]	HEA	7	0
21	N	608	TGL	2	0
31	1	201	HEC	3	0
20	P	305	PGV	4	0
21	B	301	TGL	6	0
26	T	101	CDL	24	0
18	N	605[B]	HEA	7	0
24	P	301	CHD	1	0
26	G	101	CDL	23	0
26	P	306	CDL	12	0
25	C	303	PEK	7	0
24	P	307	CHD	1	0
21	D	201	TGL	13	0
20	P	304	PGV	6	0
21	Q	201	TGL	10	0
28	E	201	PSC	19	0
23	E	202	EDO	1	0
20	A	608	PGV	4	0
19	N	607	PER	1	0
24	W	101	CHD	5	0
31	2	201	HEC	4	0
24	T	103	CHD	1	0
18	N	605[A]	HEA	1	0
20	A	607	PGV	5	0
24	C	301	CHD	1	0
18	A	605	HEA	3	0
24	J	101	CHD	5	0
21	L	101	TGL	20	0
24	C	307	CHD	3	0
28	V	101	PSC	21	0

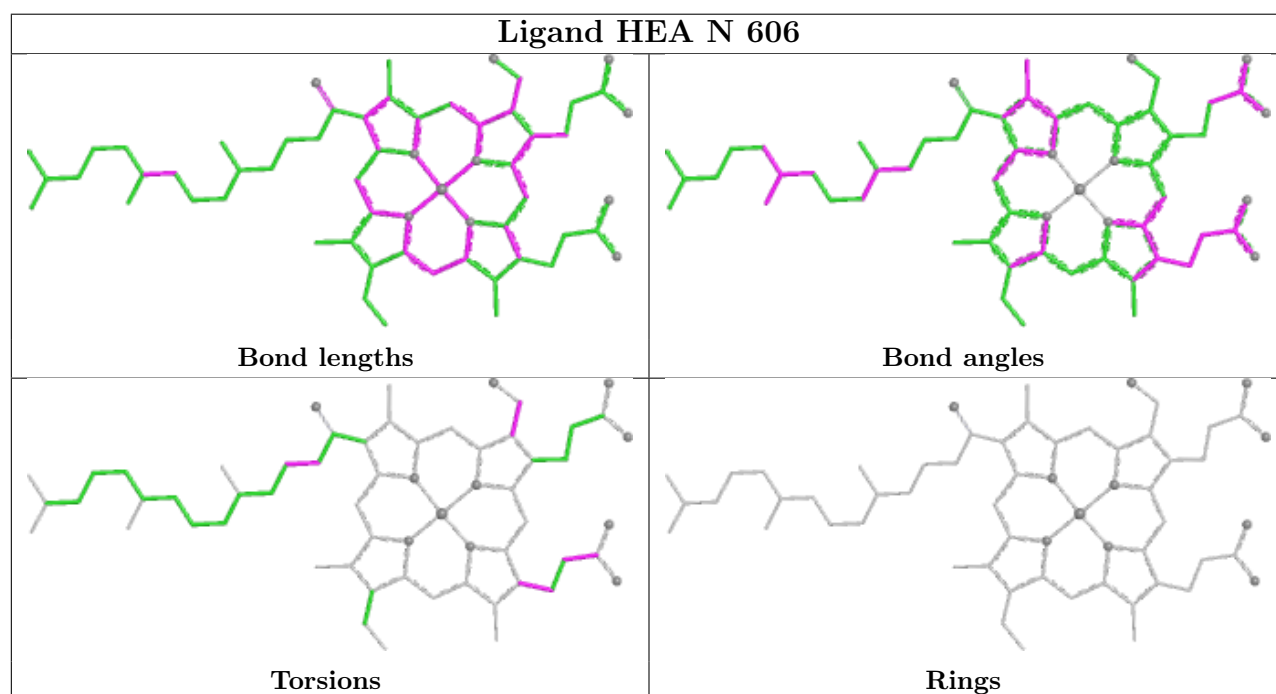
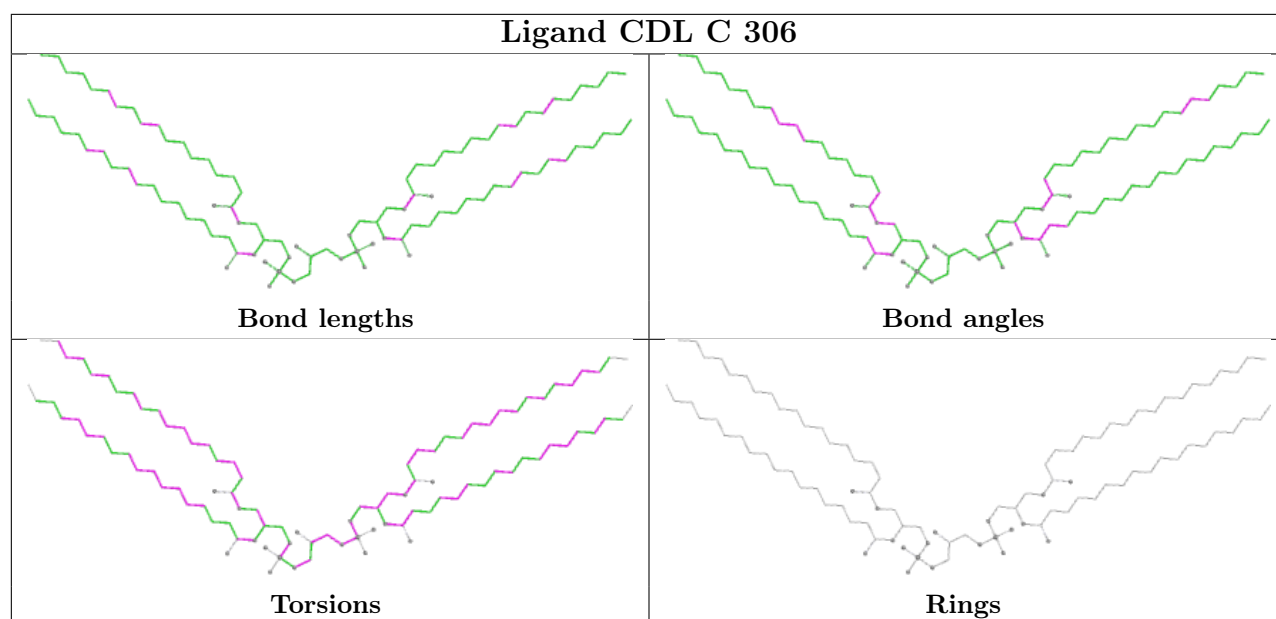
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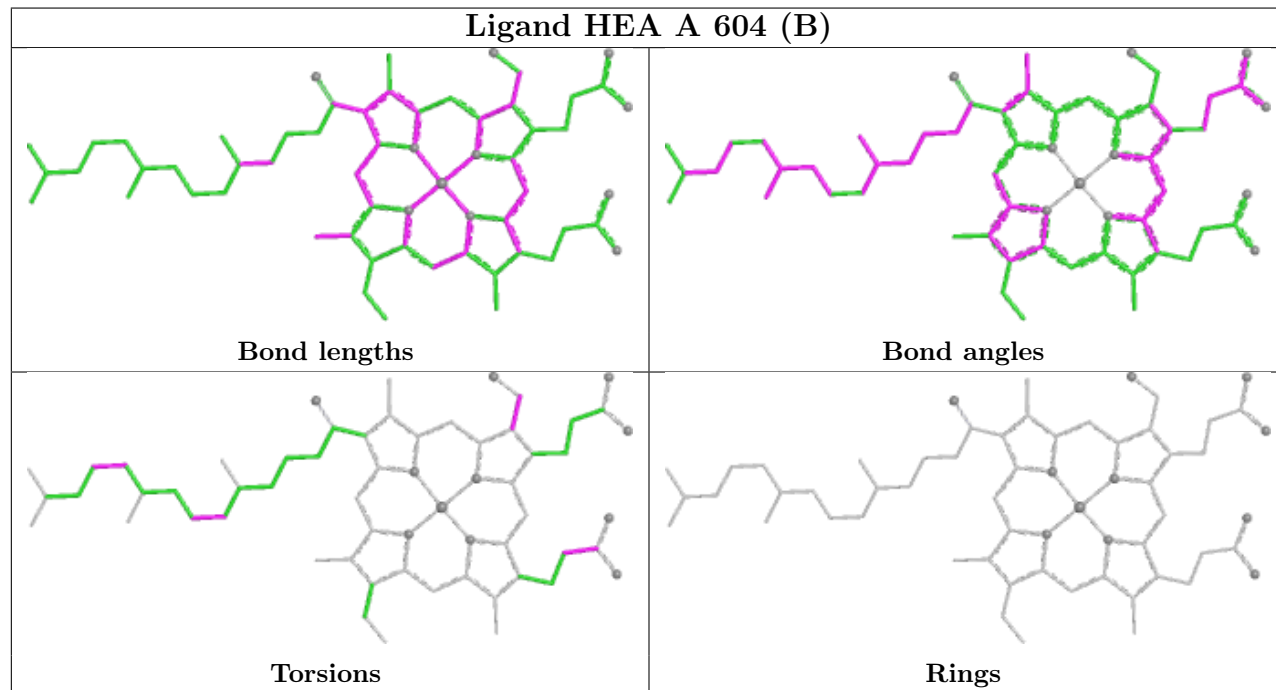
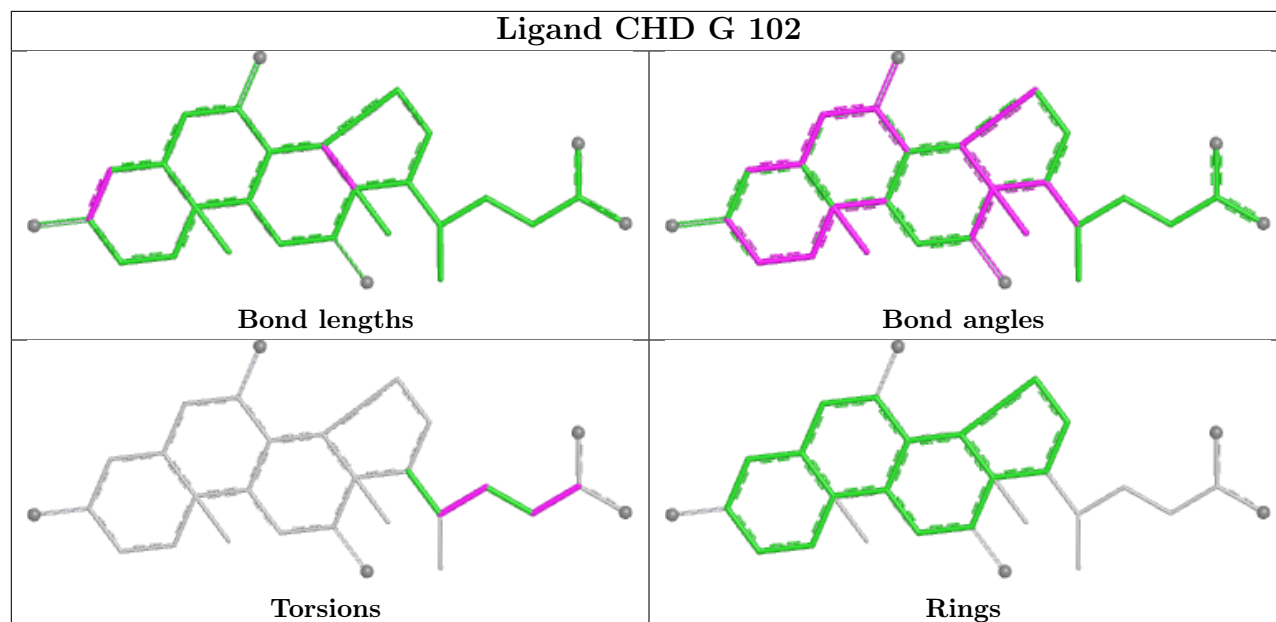
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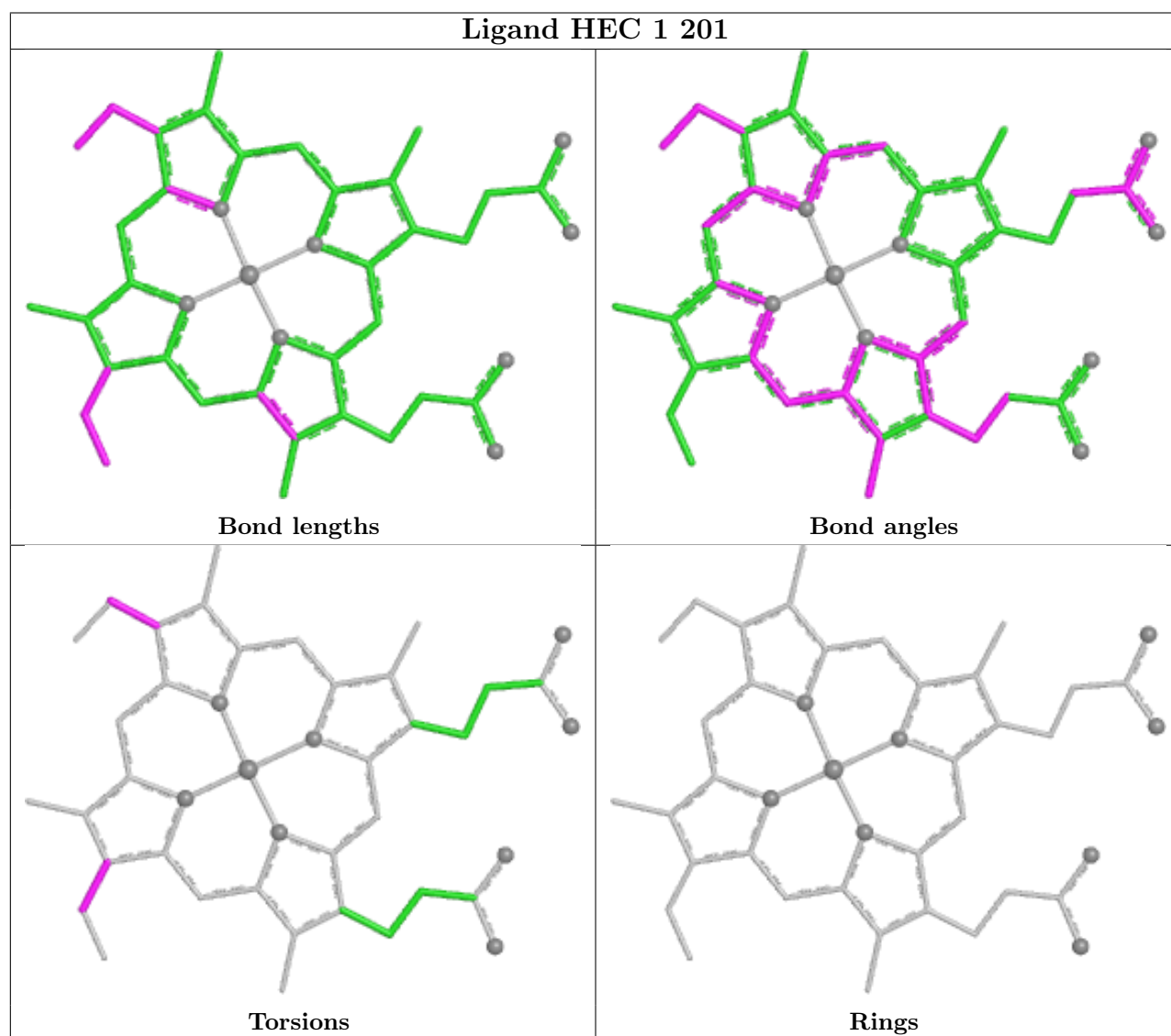
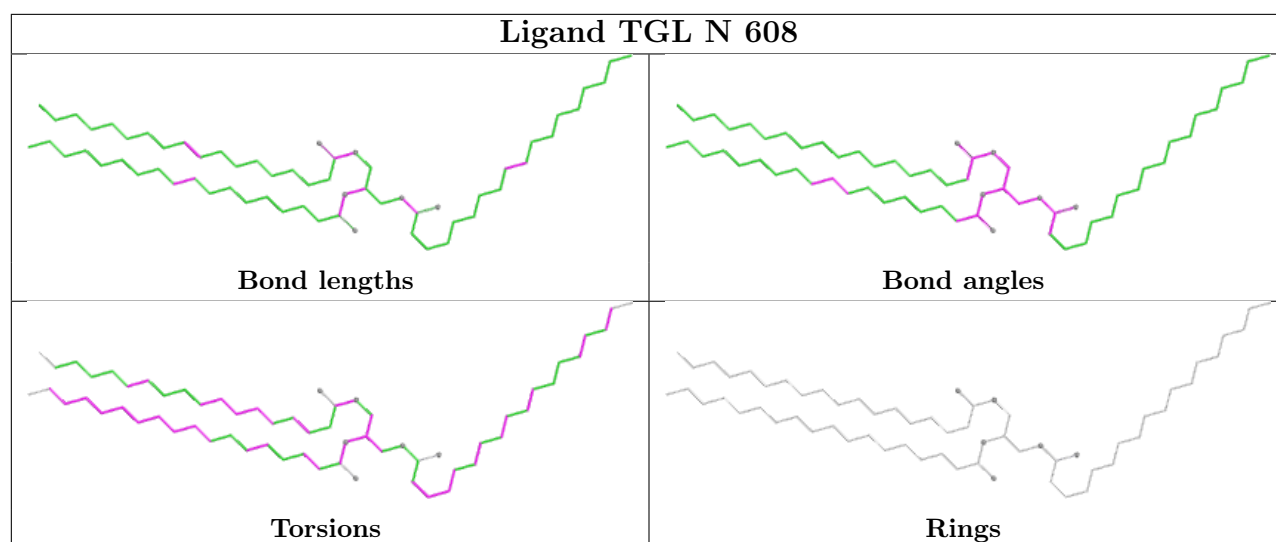
Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	Z	101	DMU	1	0
20	C	304	PGV	5	0
20	C	305	PGV	9	0
20	N	612	PGV	1	0
30	M	101	DMU	1	0

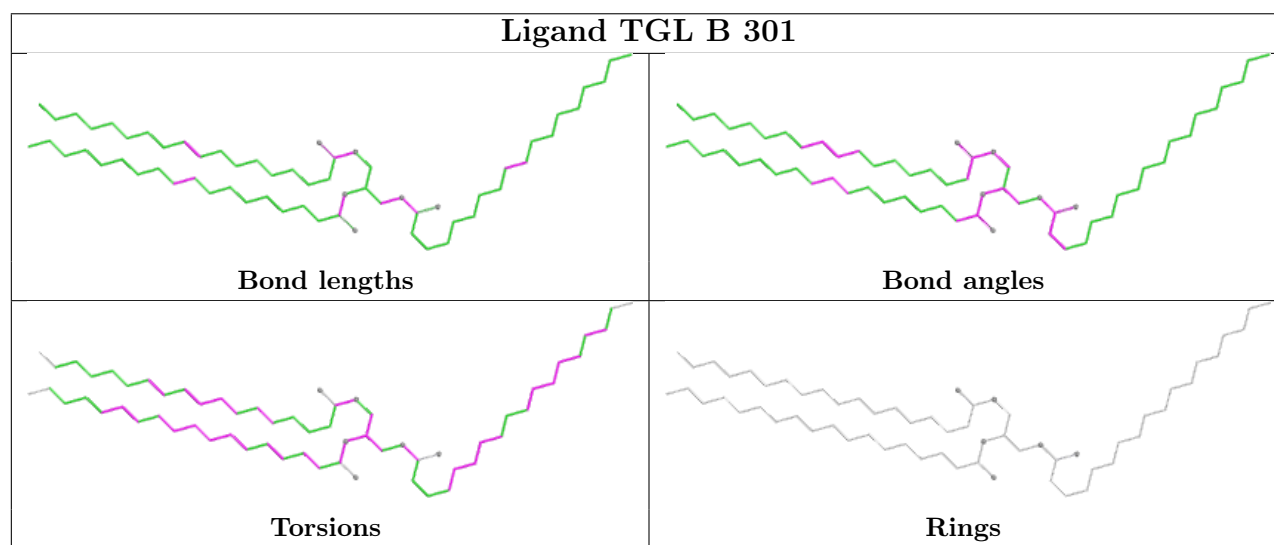
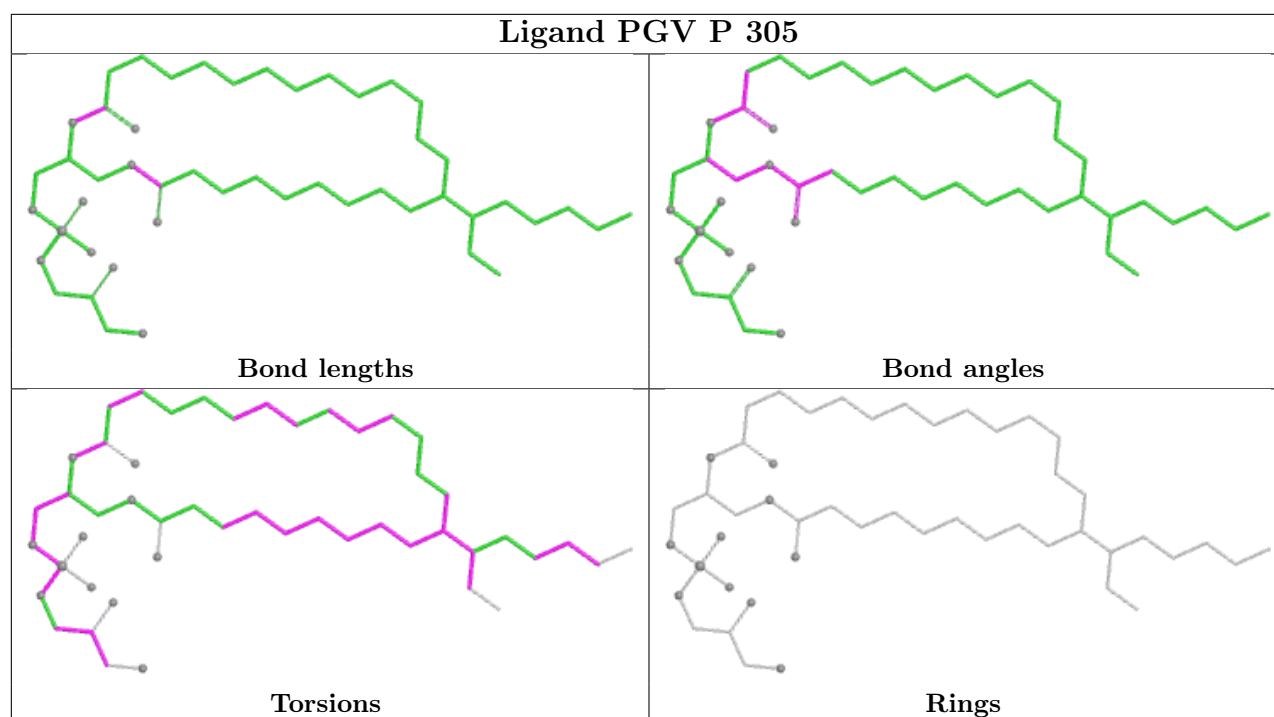
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

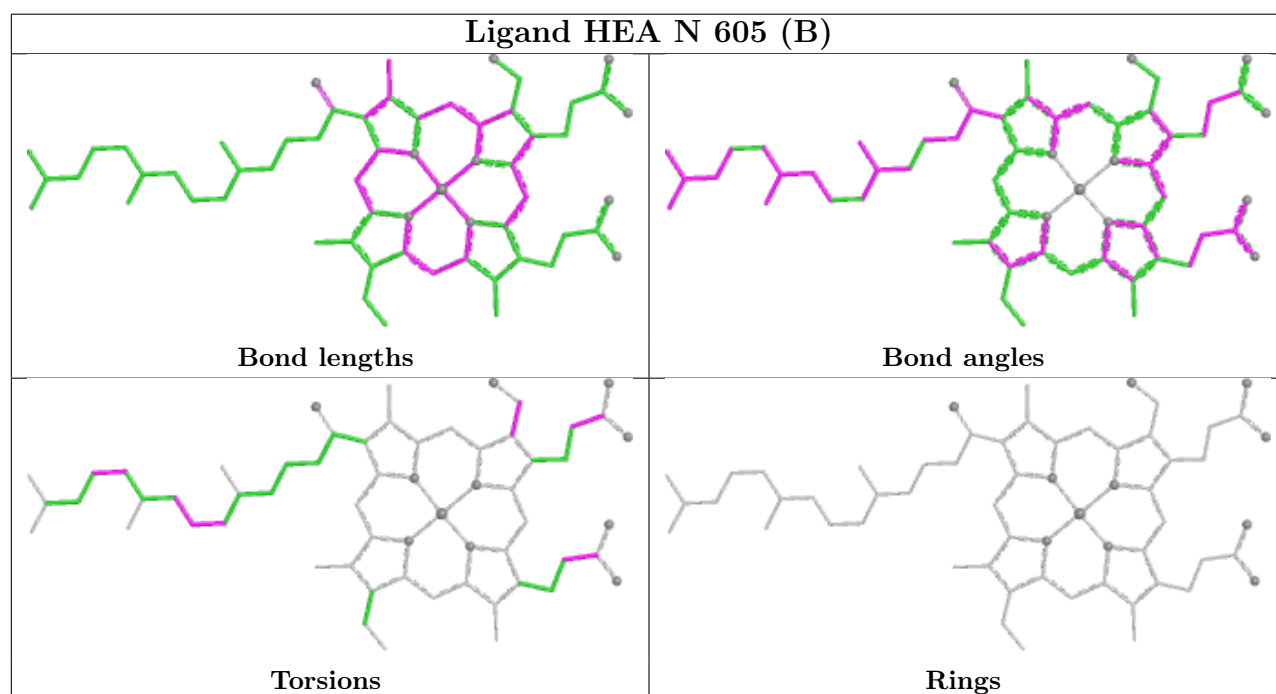
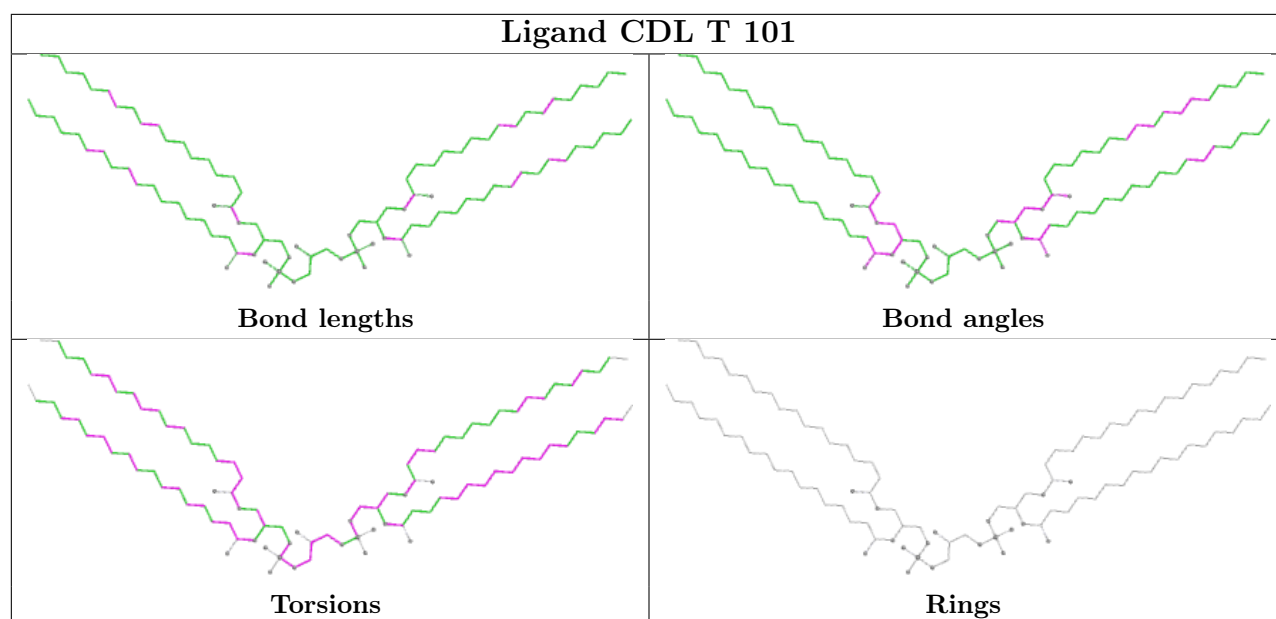


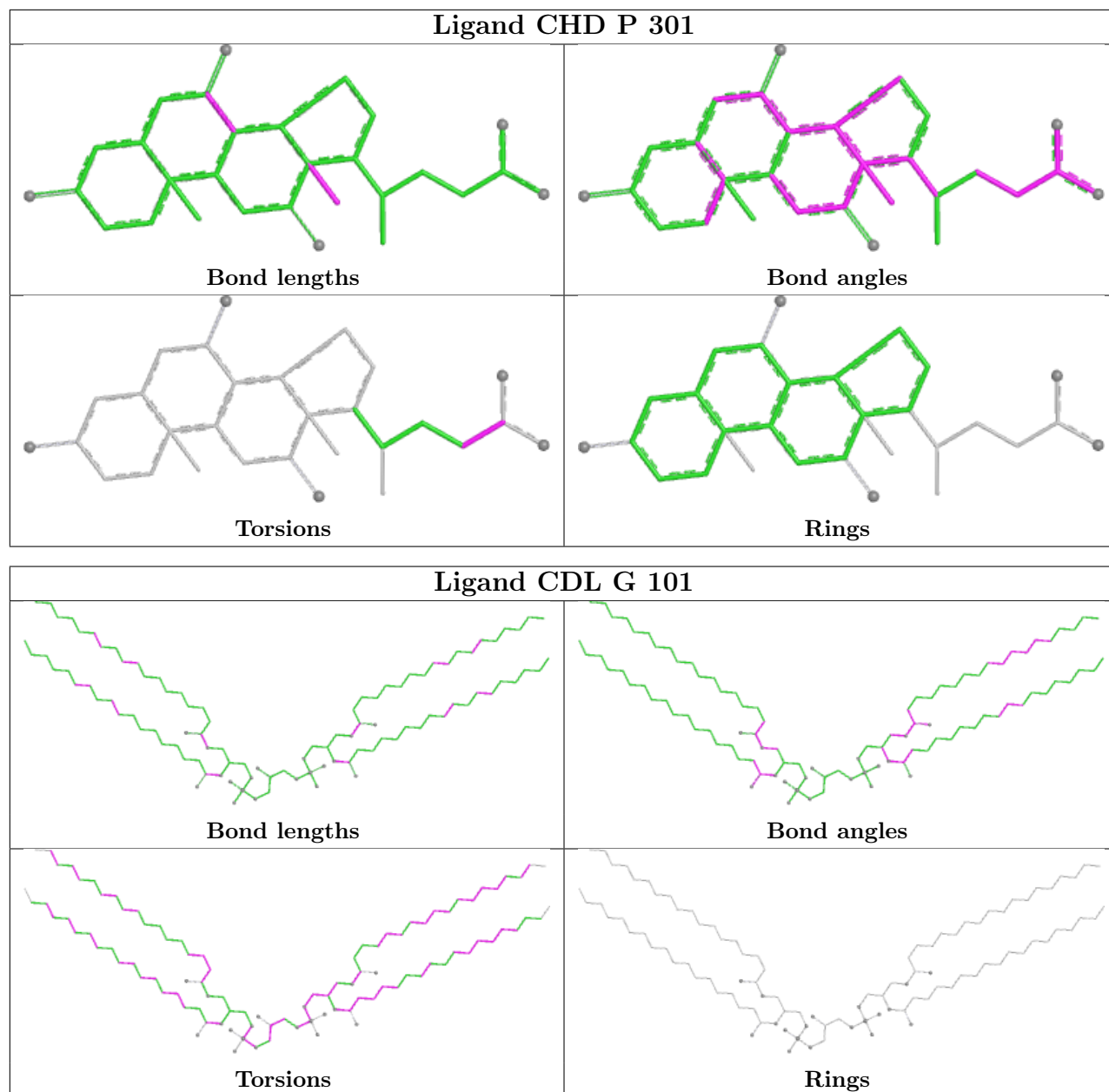


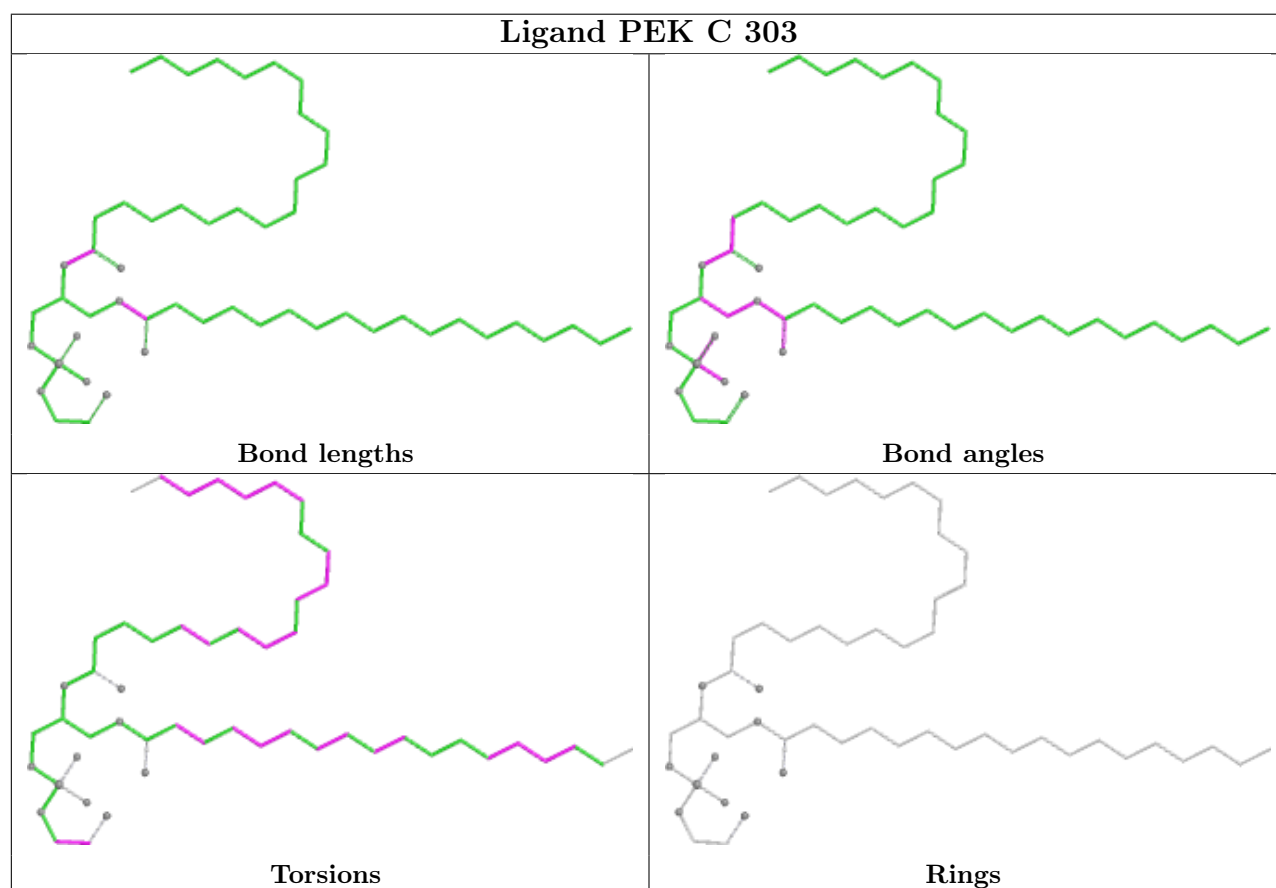
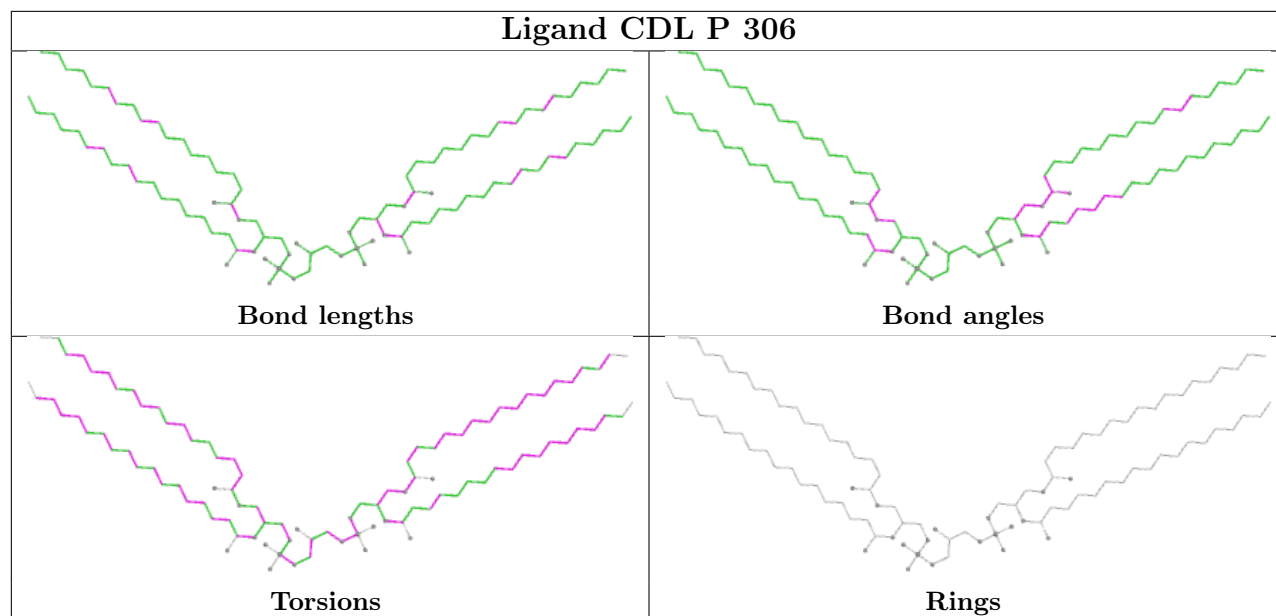


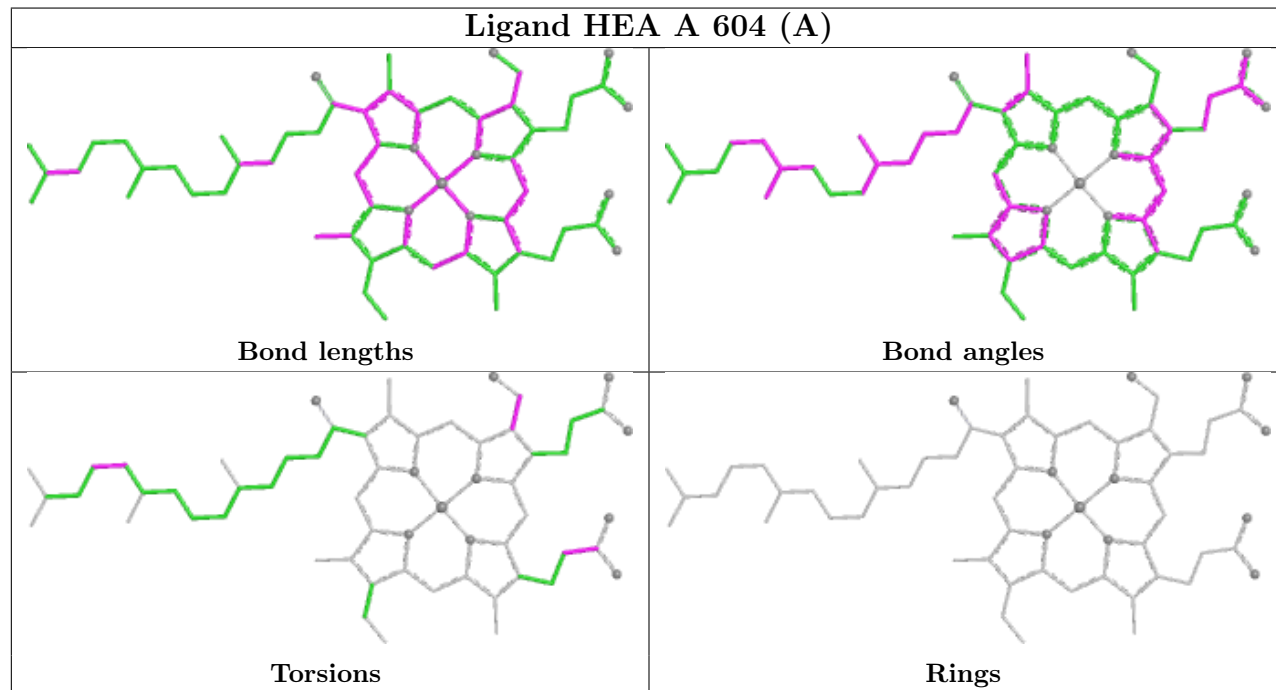
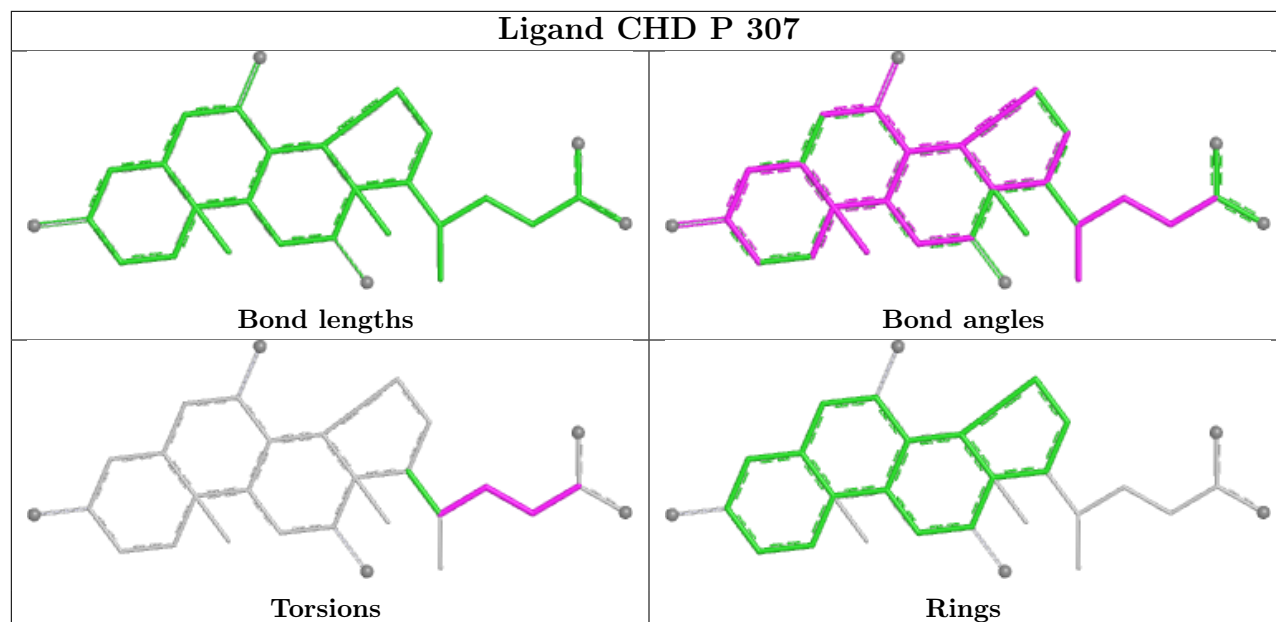


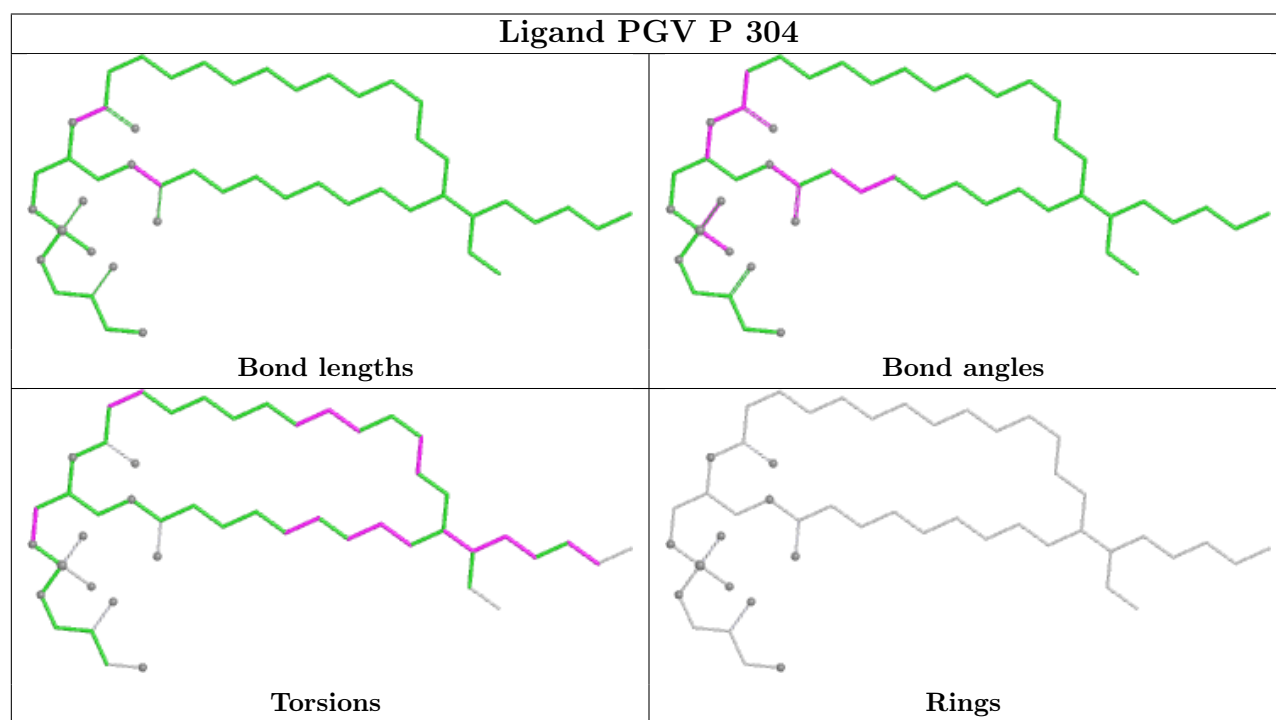
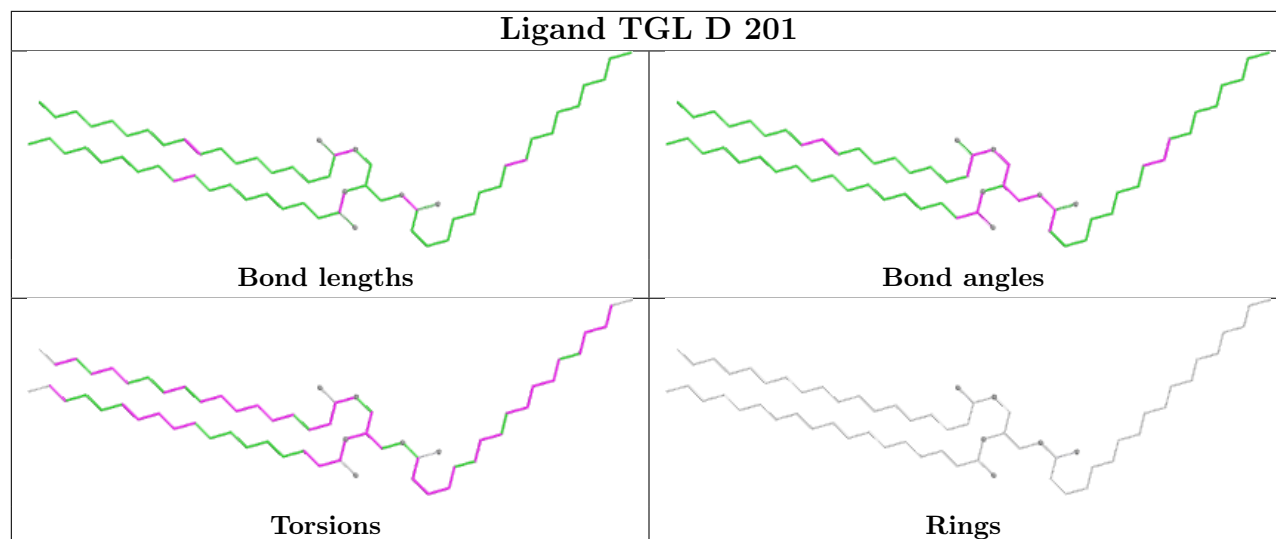


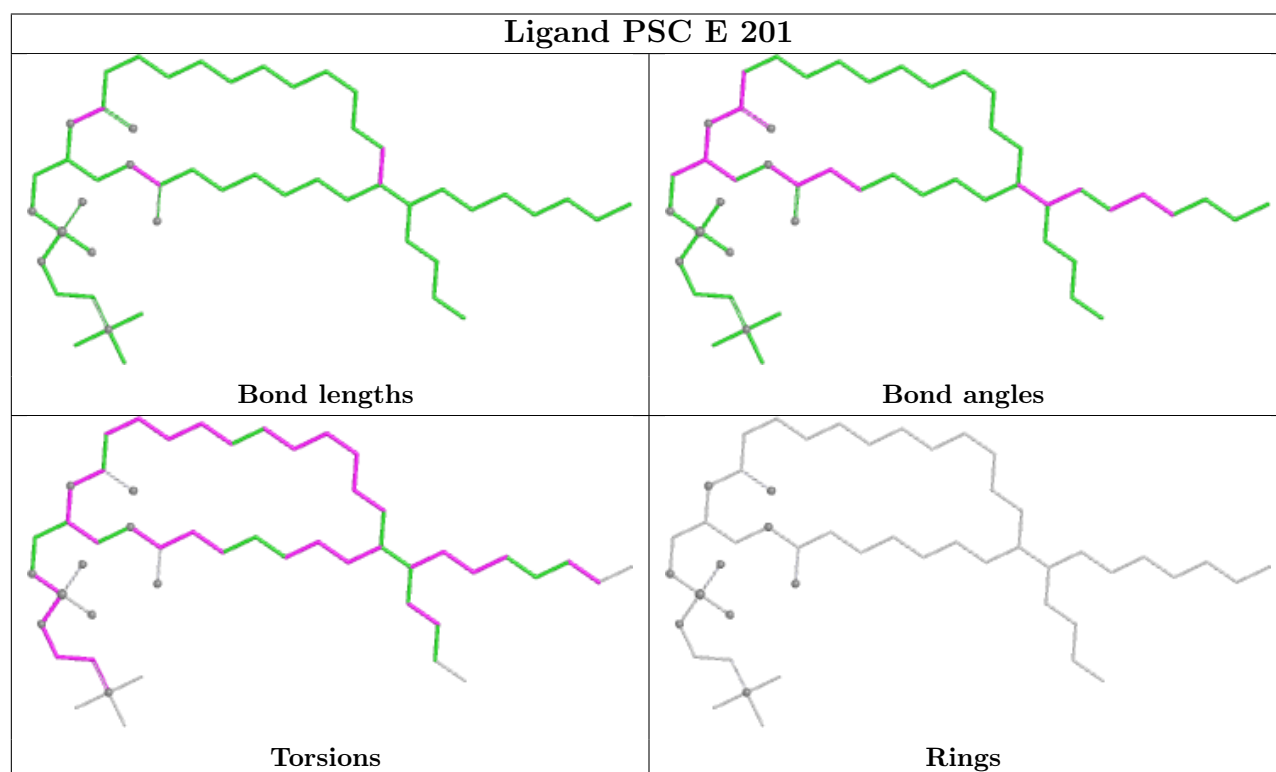
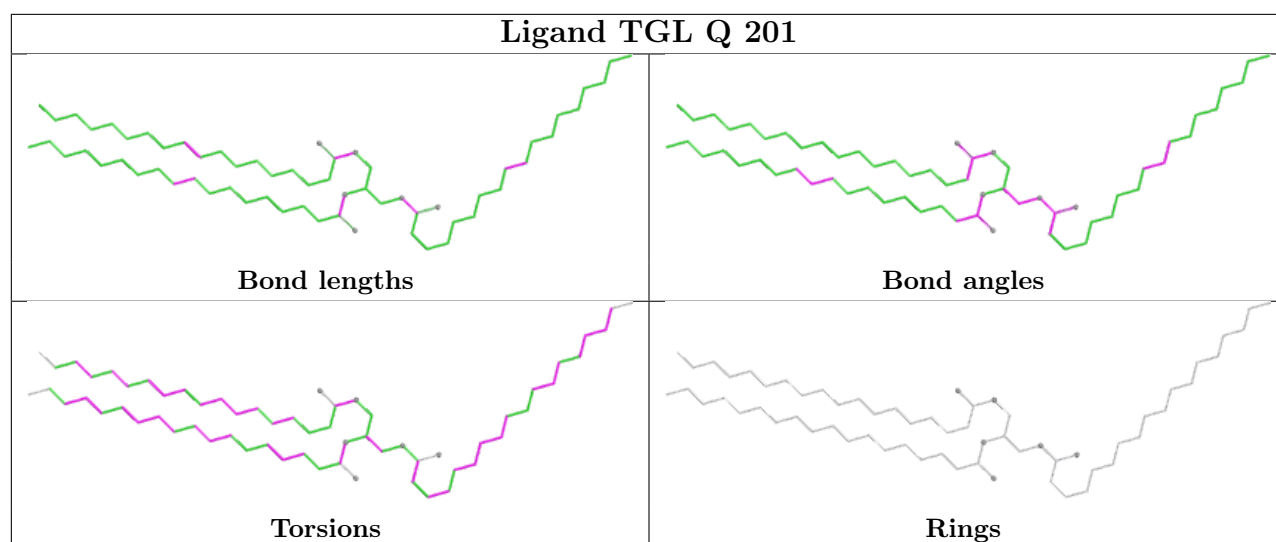


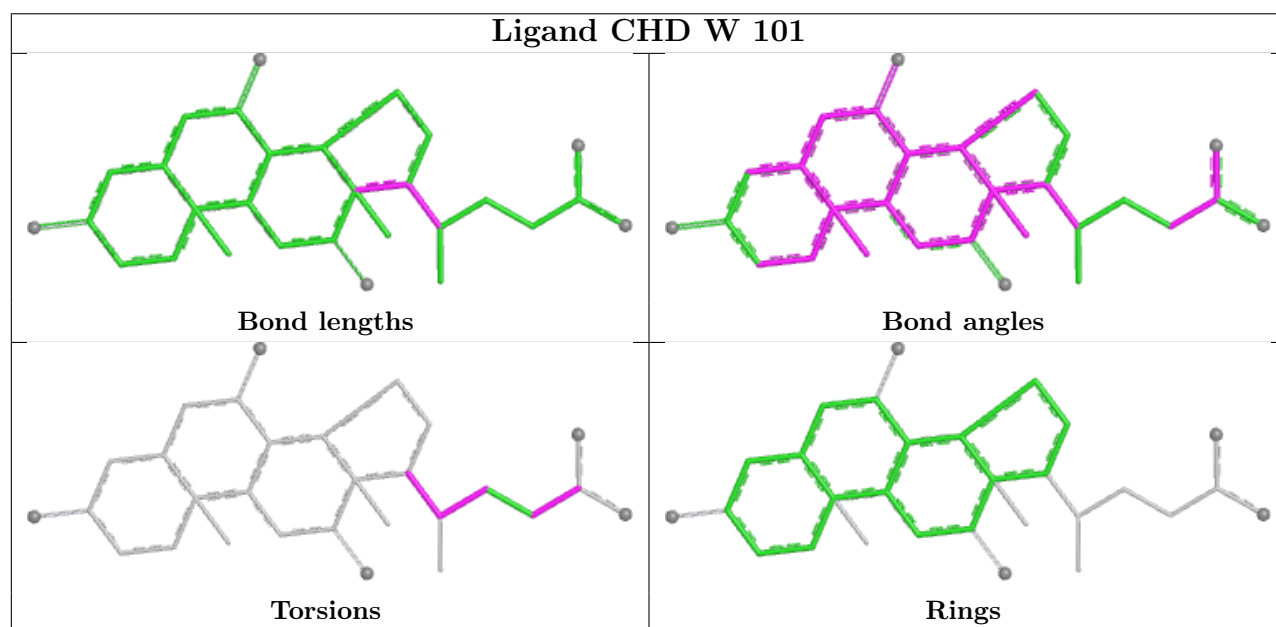
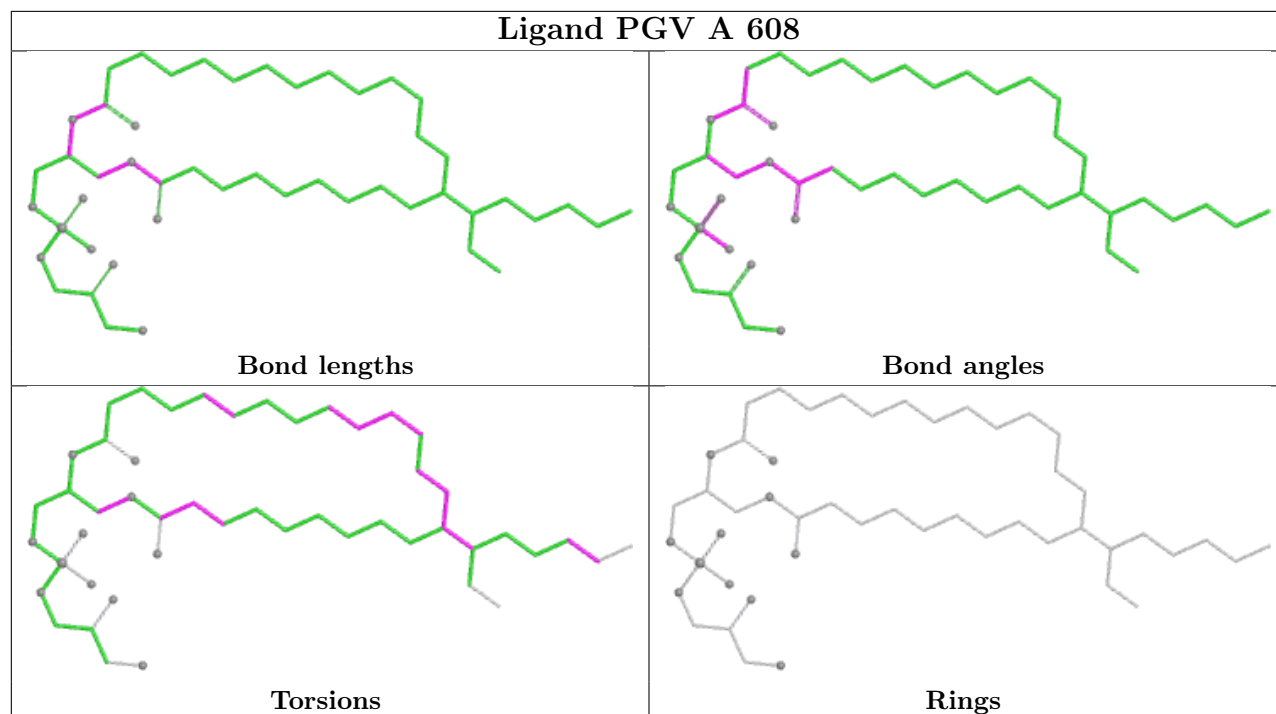




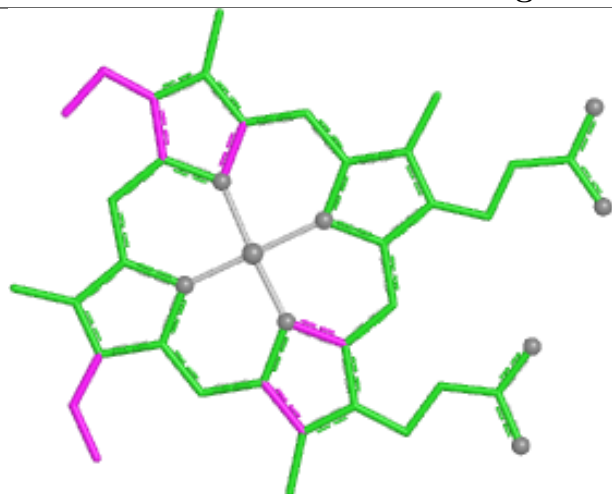




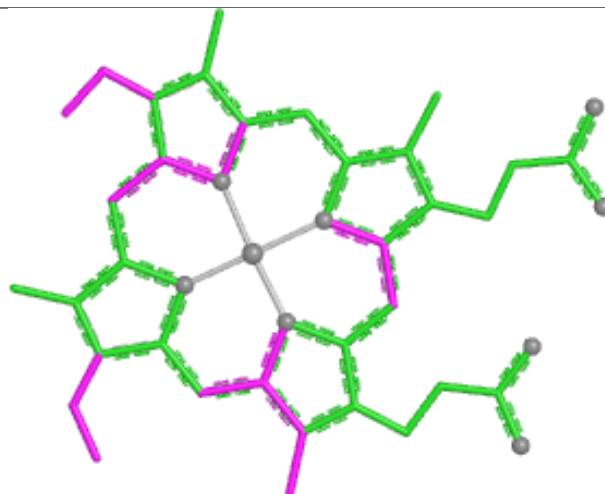




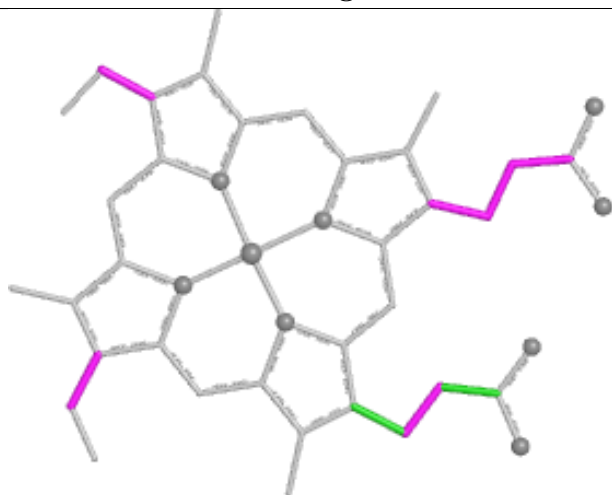
Ligand HEC 2 201



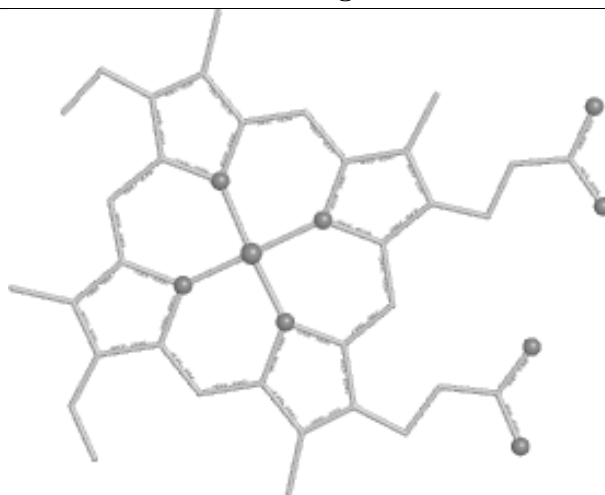
Bond lengths



Bond angles

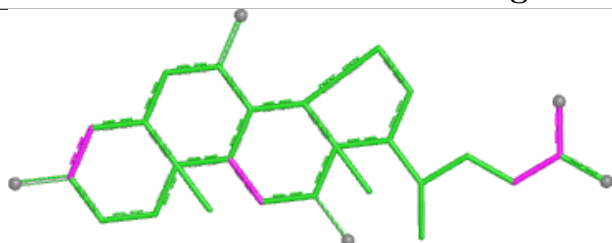


Torsions

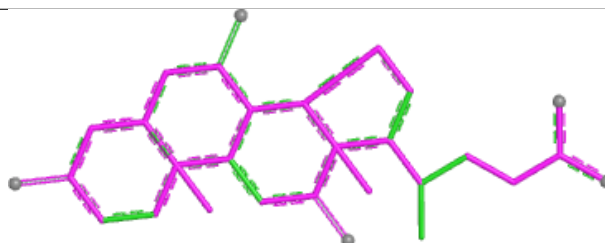


Rings

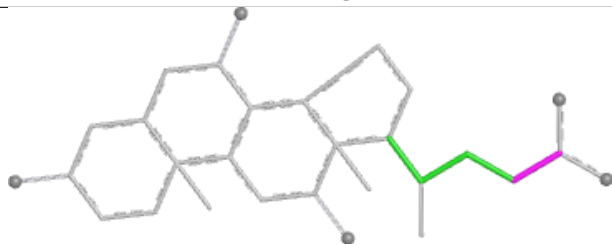
Ligand CHD T 103



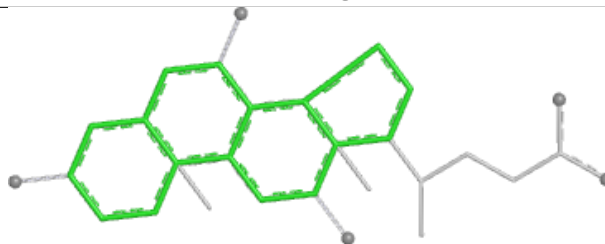
Bond lengths



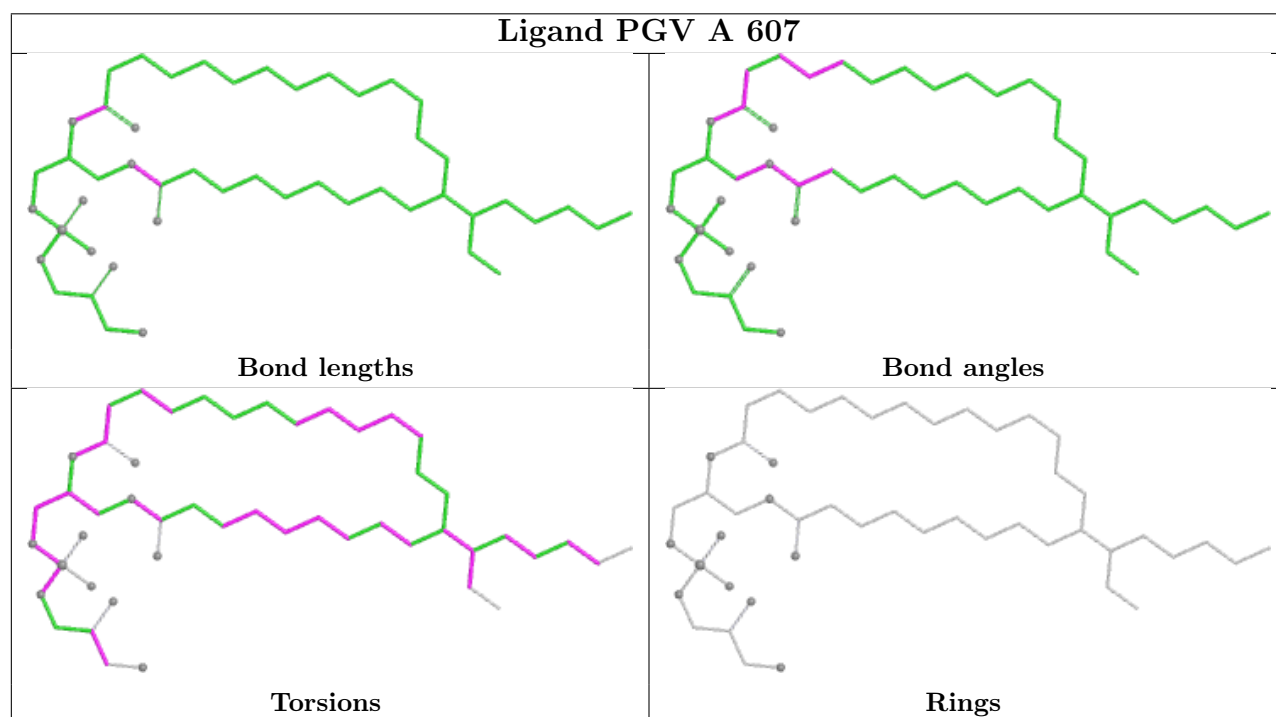
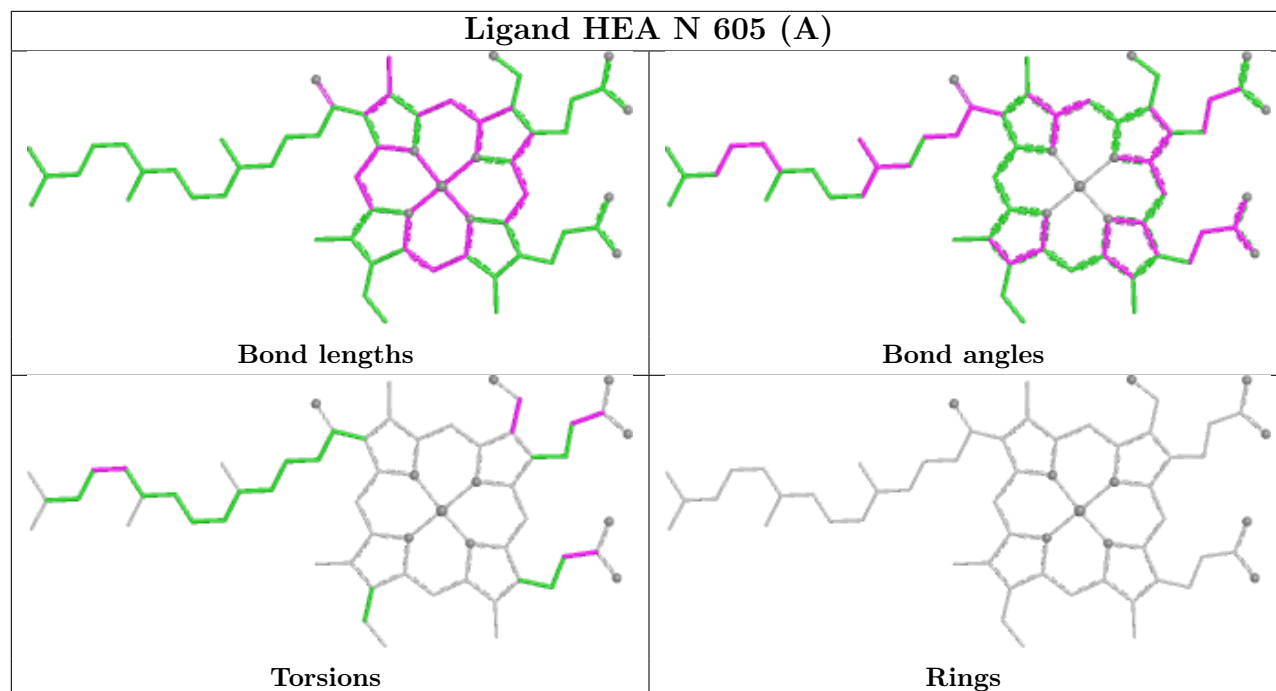
Bond angles

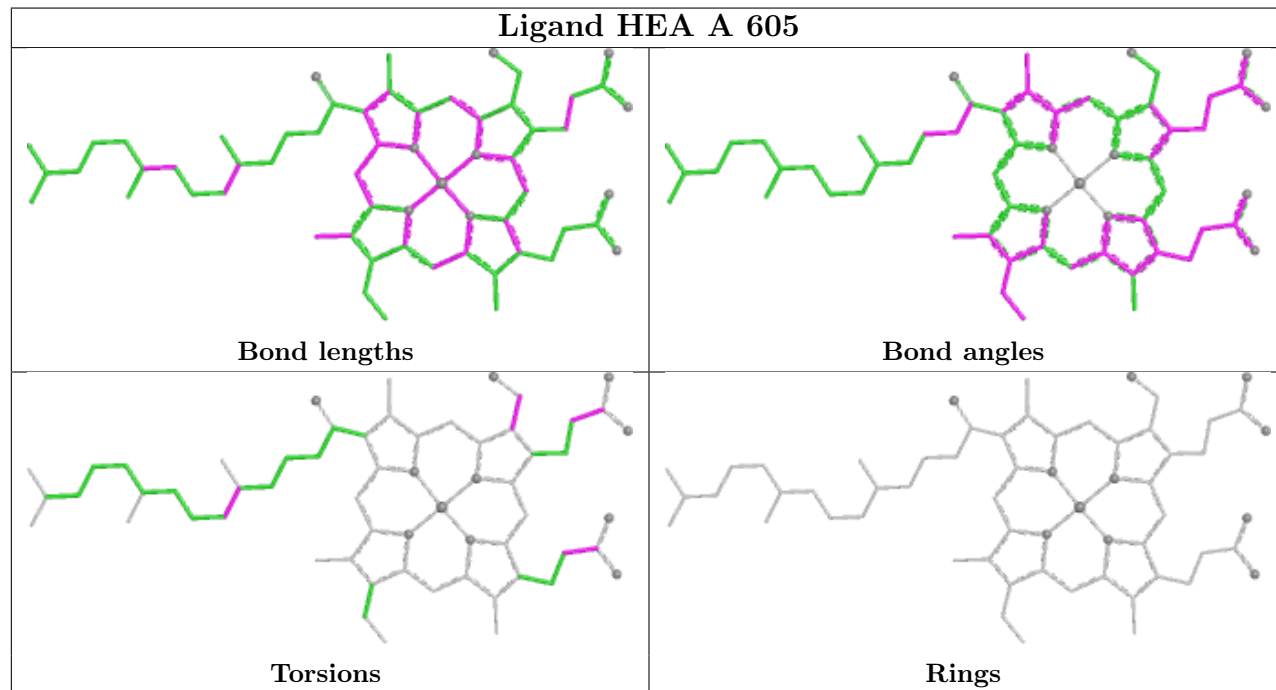
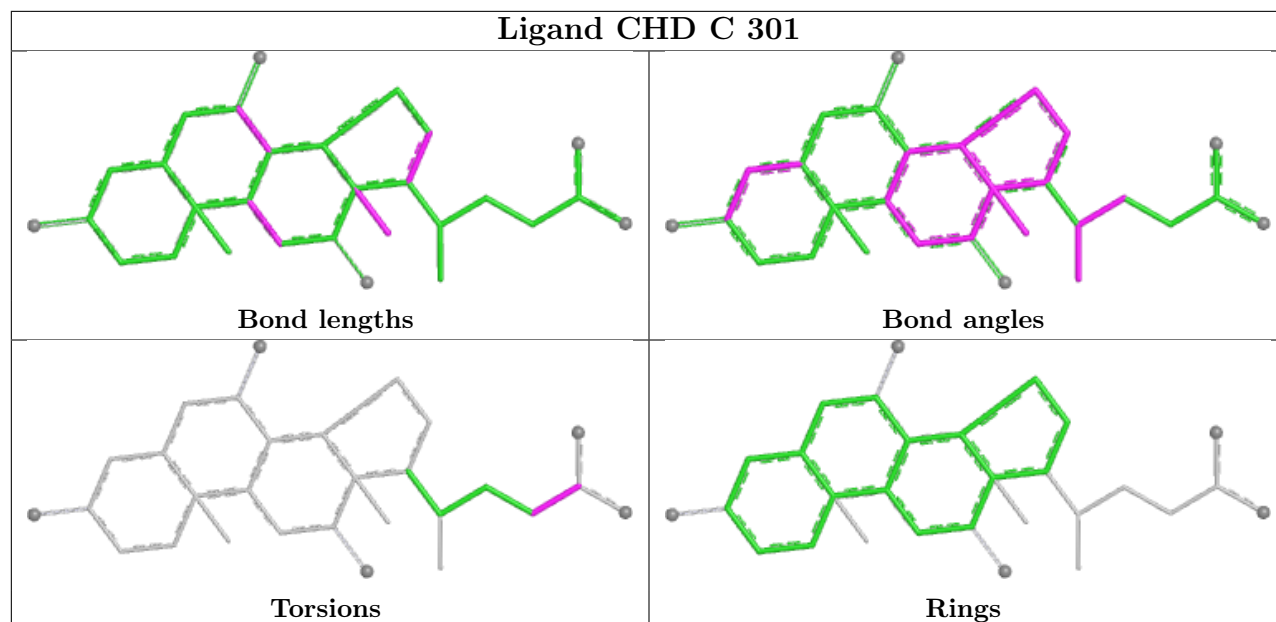


Torsions

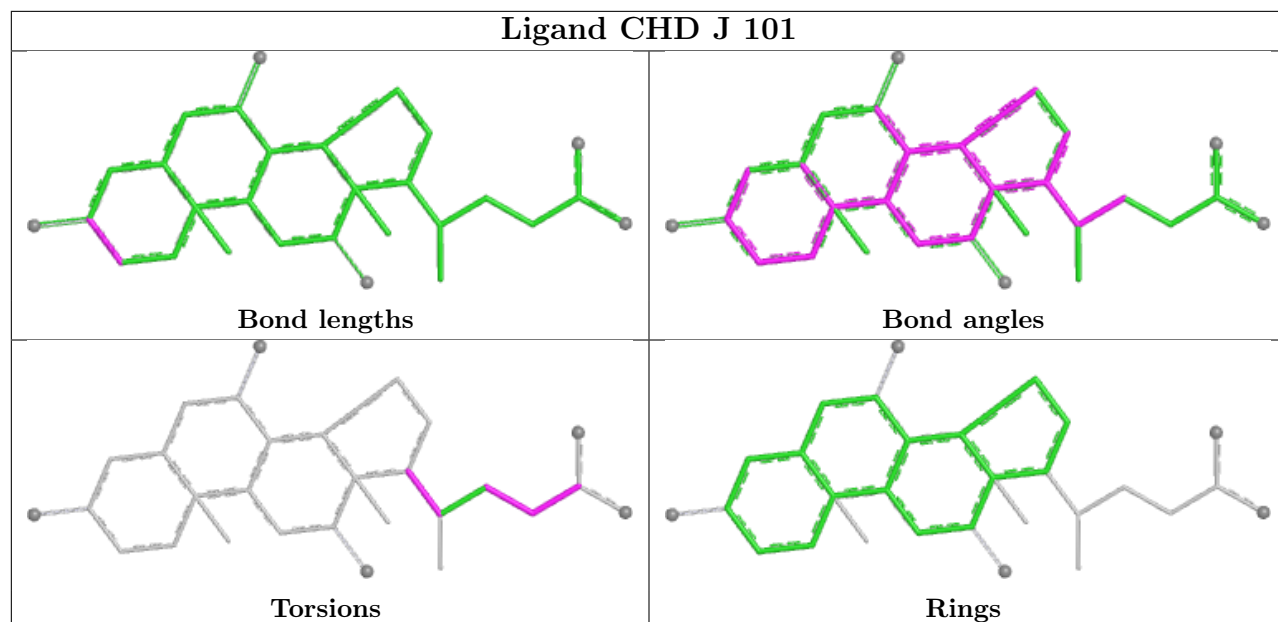


Rings

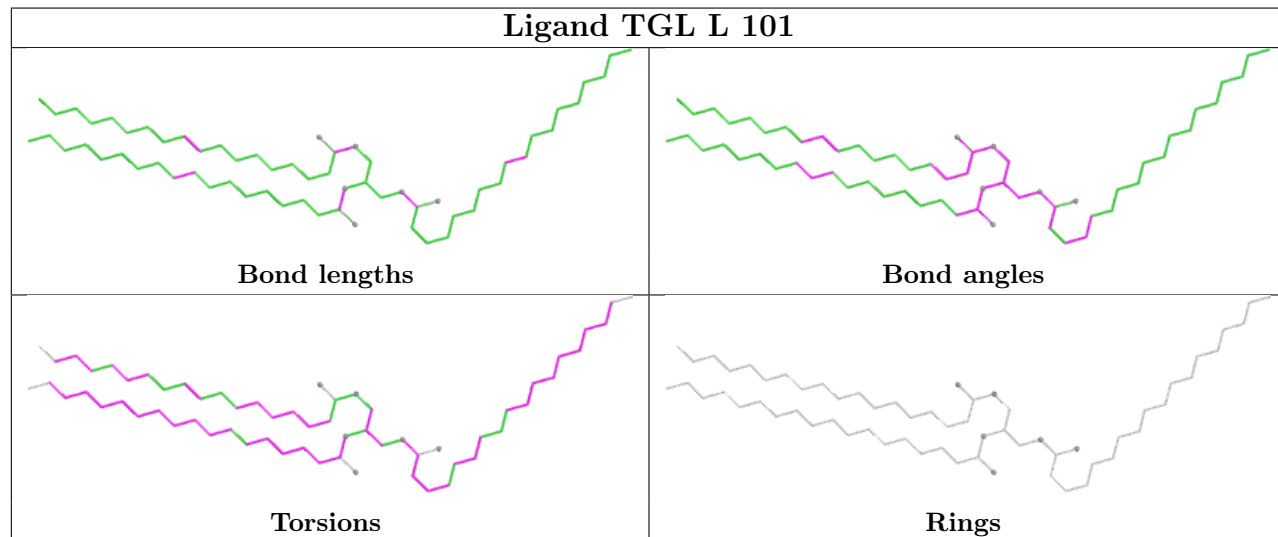


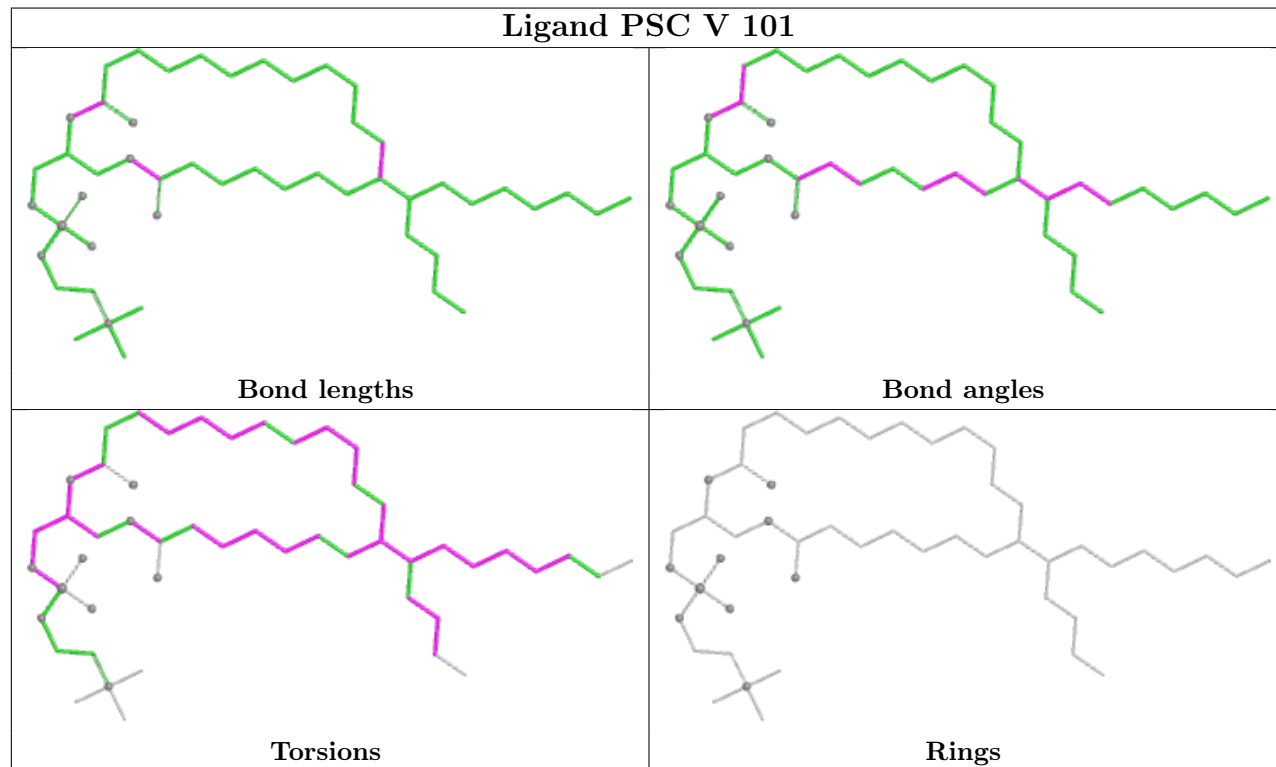
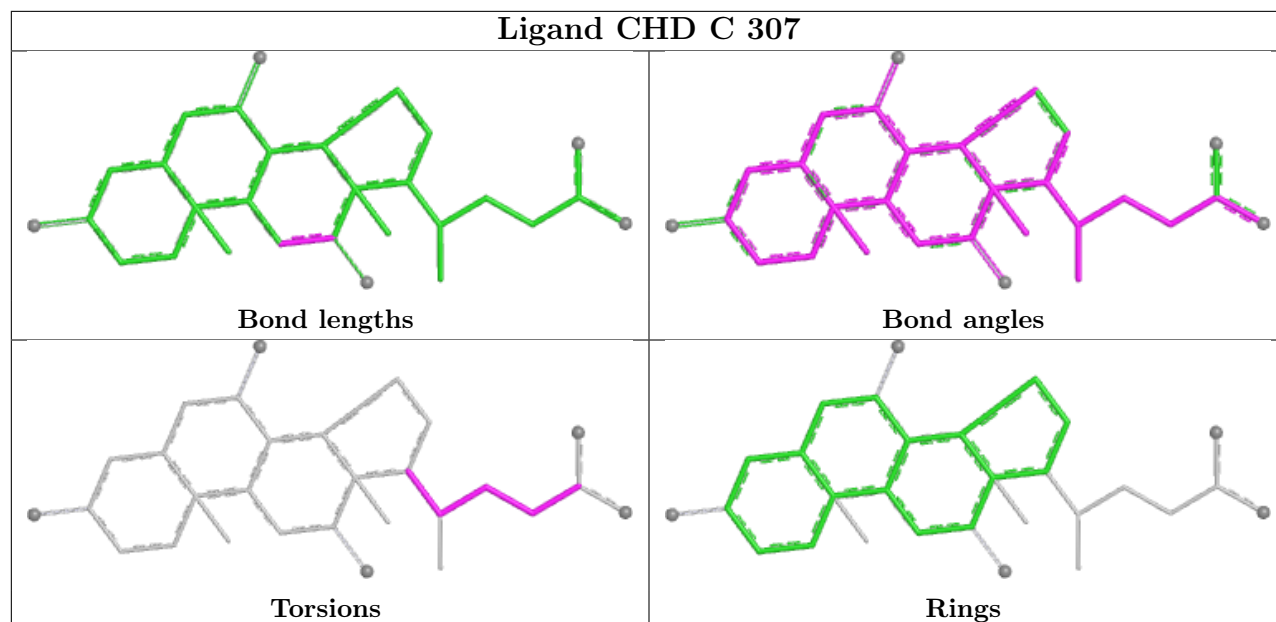


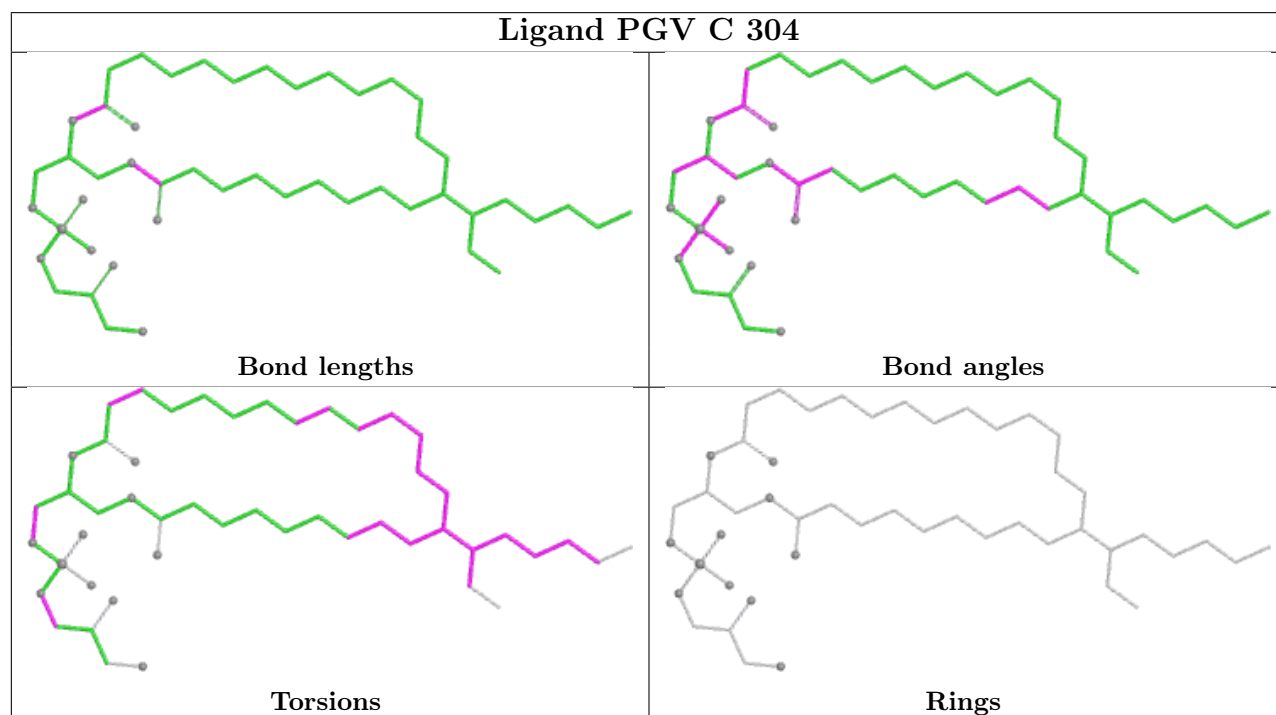
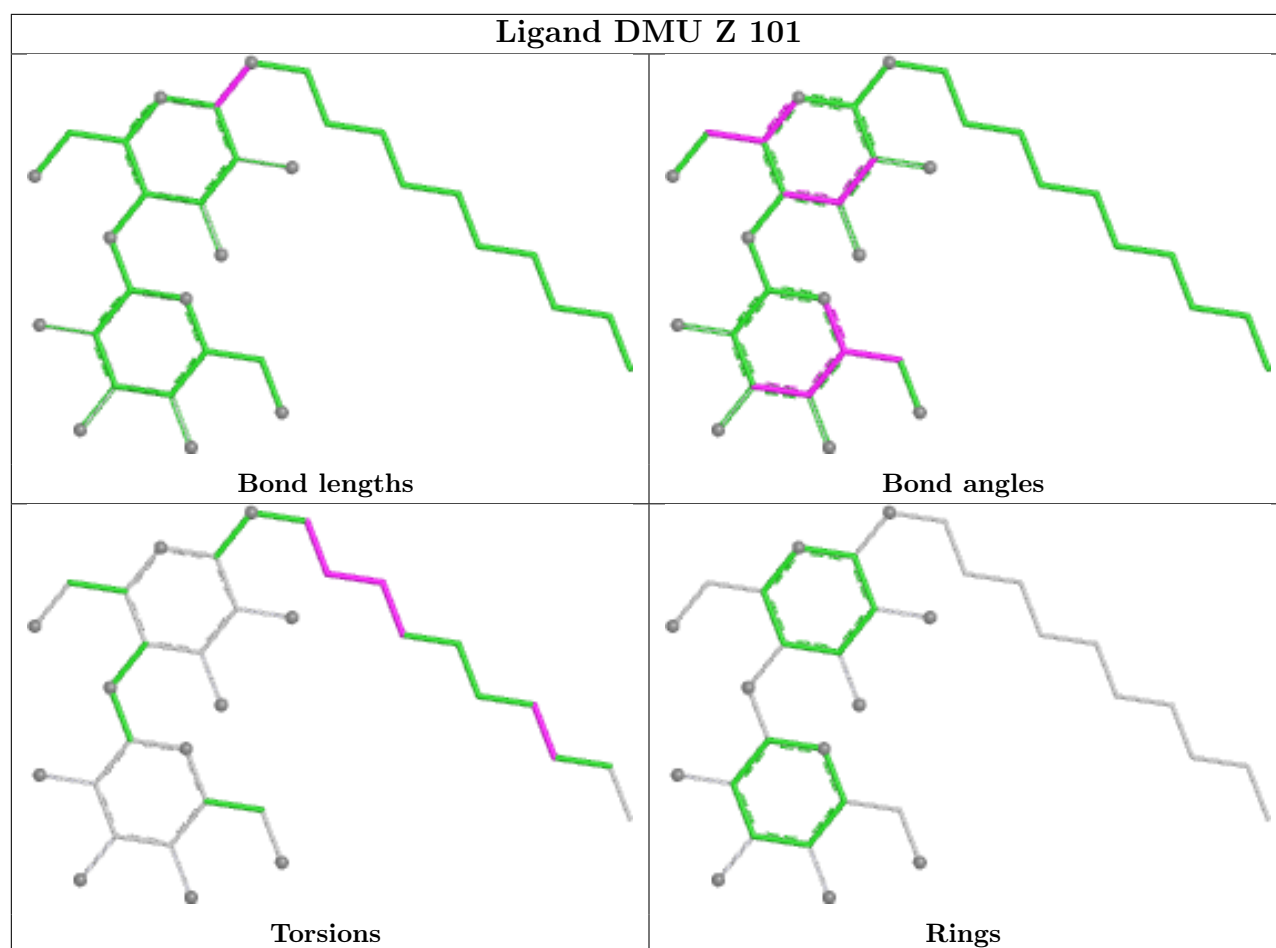
Ligand CHD J 101

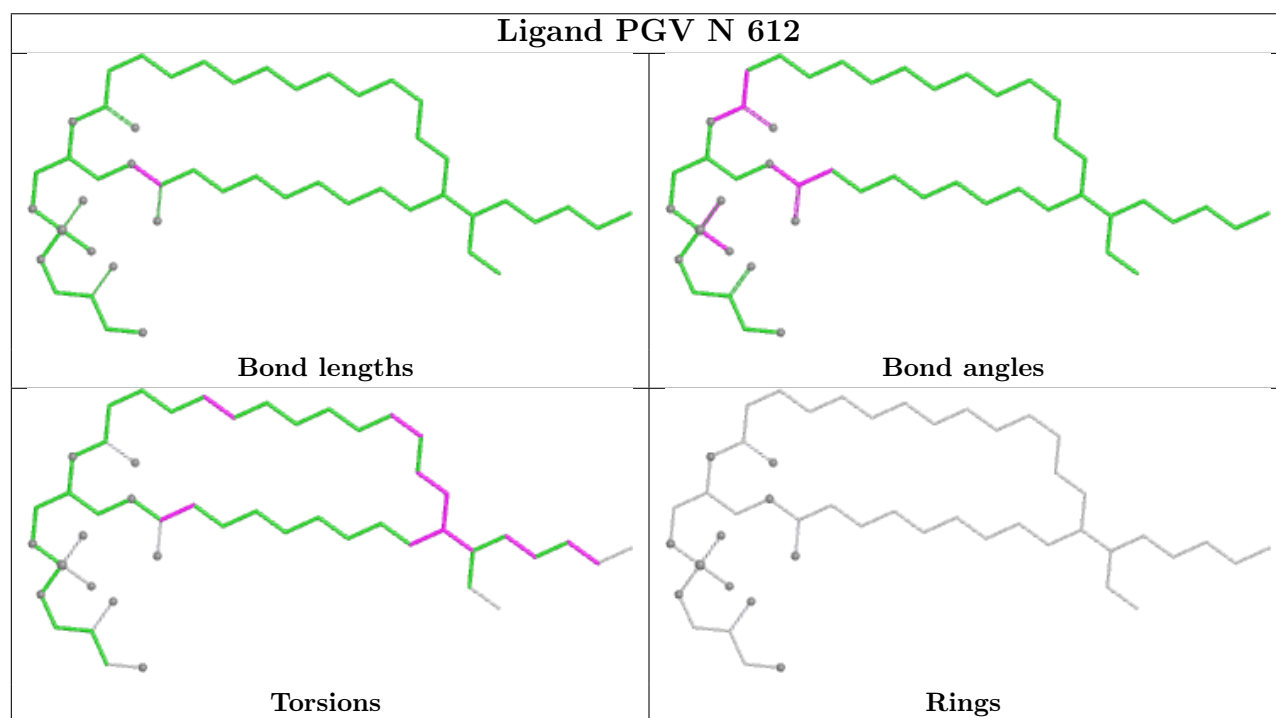
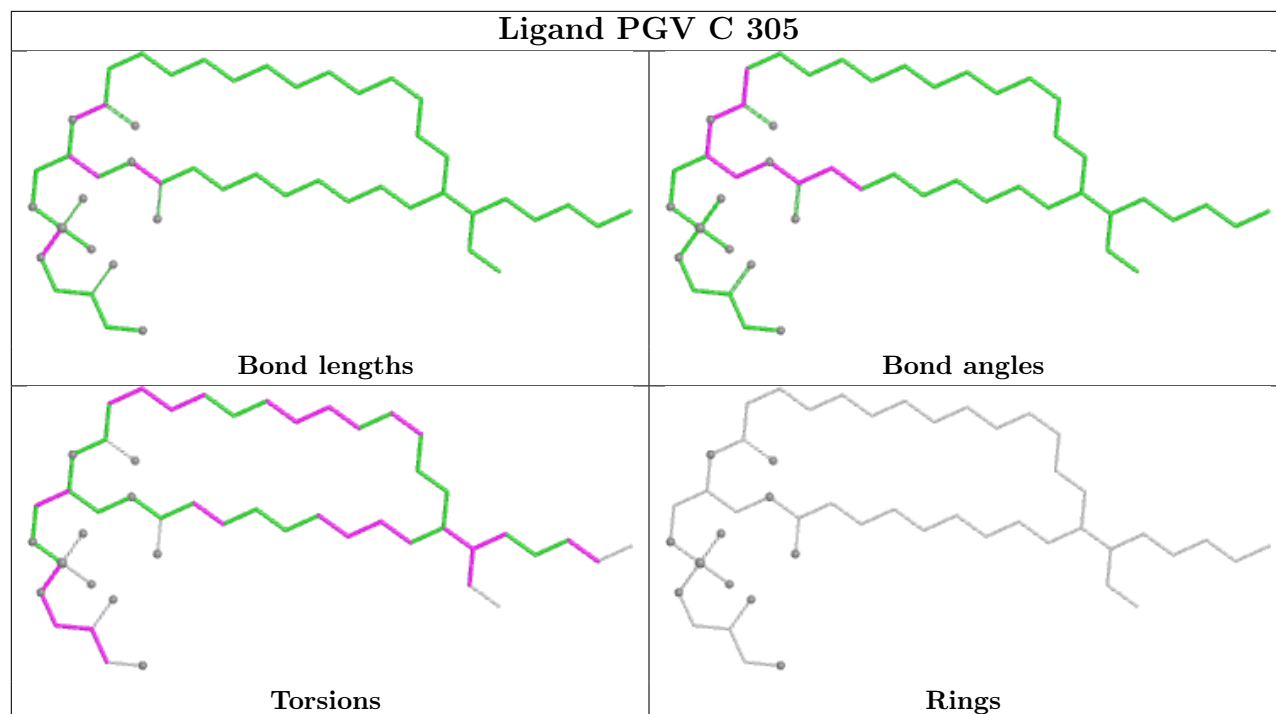


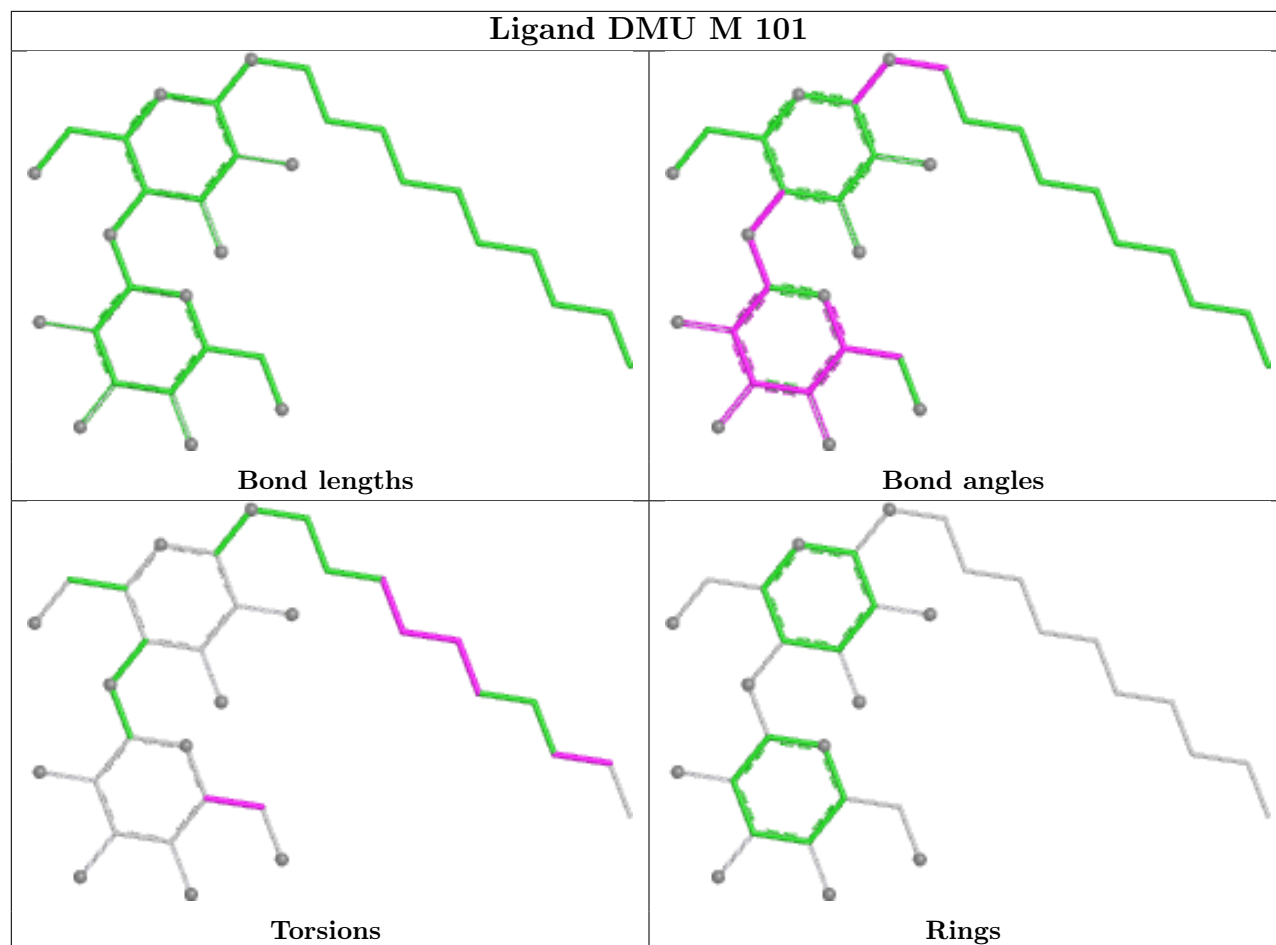
Ligand TGL L 101











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%)	-0.76	1 (0%) 91 90	11, 30, 39, 74	11 (2%)
1	N	513/514 (99%)	-0.58	1 (0%) 91 90	18, 36, 48, 71	8 (1%)
2	B	226/227 (99%)	-0.49	3 (1%) 75 74	15, 35, 59, 109	2 (0%)
2	O	226/227 (99%)	-0.07	1 (0%) 88 88	34, 49, 78, 98	0
3	C	259/259 (100%)	-0.52	4 (1%) 72 71	16, 35, 48, 83	6 (2%)
3	P	259/259 (100%)	-0.38	5 (1%) 66 66	17, 38, 52, 87	5 (1%)
4	D	144/144 (100%)	-0.34	4 (2%) 55 54	30, 38, 63, 144	0
4	Q	144/144 (100%)	-0.01	5 (3%) 47 46	22, 50, 81, 139	1 (0%)
5	E	105/105 (100%)	-0.52	0 100 100	30, 38, 62, 134	0
5	R	105/105 (100%)	-0.62	0 100 100	33, 41, 62, 123	0
6	F	98/98 (100%)	-0.14	7 (7%) 22 20	30, 40, 95, 141	0
6	S	98/98 (100%)	0.14	9 (9%) 14 13	32, 45, 106, 141	0
7	G	83/84 (98%)	0.39	12 (14%) 6 5	34, 44, 116, 138	0
7	T	83/84 (98%)	0.49	16 (19%) 3 3	31, 47, 111, 136	0
8	H	79/79 (100%)	-0.05	7 (8%) 15 14	33, 43, 90, 106	0
8	U	79/79 (100%)	-0.10	1 (1%) 75 74	38, 49, 69, 137	0
9	I	72/73 (98%)	-0.05	5 (6%) 23 21	33, 46, 66, 79	0
9	V	72/73 (98%)	0.38	4 (5%) 30 29	36, 63, 85, 111	0
10	J	58/58 (100%)	-0.04	4 (6%) 23 21	36, 46, 75, 135	0
10	W	58/58 (100%)	0.08	5 (8%) 16 15	39, 53, 84, 144	0
11	K	49/49 (100%)	-0.24	1 (2%) 65 64	35, 42, 58, 70	0
11	X	49/49 (100%)	0.06	1 (2%) 65 64	47, 58, 77, 78	0
12	L	46/46 (100%)	-0.46	1 (2%) 62 61	30, 38, 59, 104	0
12	Y	46/46 (100%)	-0.24	2 (4%) 40 39	36, 46, 69, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	43/43 (100%)	-0.18	3 (6%) 22 21	32, 40, 79, 127	0
13	Z	43/43 (100%)	-0.11	0 100 100	36, 50, 81, 108	0
14	1	104/105 (99%)	0.77	7 (6%) 24 22	45, 90, 118, 125	0
14	2	104/105 (99%)	1.33	23 (22%) 2 2	67, 115, 139, 147	0
All	All	3758/3768 (99%)	-0.26	132 (3%) 47 46	11, 40, 98, 147	33 (0%)

The worst 5 of 132 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	S	1	ALA	9.7
6	F	1	ALA	7.8
7	G	3	ALA	6.8
8	H	8	ILE	6.5
4	Q	5	VAL	6.4

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	SAC	V	1	9/10	0.51	0.18	131,137,150,153	0
9	SAC	I	1	9/10	0.60	0.15	98,106,110,119	0
7	TPO	G	11	11/12	0.62	0.17	81,97,160,160	0
7	TPO	T	11	11/12	0.76	0.21	85,109,117,125	0
1	FME	A	1	10/11	0.89	0.13	40,52,71,88	0
1	FME	N	1	10/11	0.92	0.11	43,61,73,95	0
2	FME	B	1	10/11	0.97	0.08	30,35,39,51	0
2	FME	O	1	10/11	0.97	0.08	49,56,65,78	0

6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
17	NA	C	302	1/1	0.62	0.40	59,59,59,59	0
17	NA	P	302	1/1	0.72	0.42	57,57,57,57	0
20	PGV	C	305	51/51	0.76	0.21	55,80,122,138	0
24	CHD	W	101	29/29	0.77	0.21	73,114,126,130	0
20	PGV	P	305	51/51	0.78	0.19	54,86,135,150	0
27	UNL	P	309	16/-	0.78	0.25	70,79,89,95	0
26	CDL	T	101	100/100	0.80	0.21	61,95,153,161	0
24	CHD	C	307	29/29	0.81	0.19	73,85,93,99	0
20	PGV	A	607	51/51	0.82	0.19	44,84,151,159	0
26	CDL	G	101	100/100	0.82	0.21	58,103,158,163	0
21	TGL	D	201	63/63	0.83	0.19	47,70,101,105	0
26	CDL	P	306	100/100	0.84	0.19	49,97,149,159	0
21	TGL	Q	201	63/63	0.84	0.22	52,82,104,109	0
27	UNL	C	308	18/-	0.84	0.19	55,66,77,81	0
27	UNL	C	309	17/-	0.84	0.21	60,71,87,90	0
21	TGL	N	608	63/63	0.84	0.18	51,73,104,115	0
28	PSC	E	201	52/52	0.84	0.18	50,79,162,163	0
28	PSC	V	101	52/52	0.84	0.18	49,77,145,166	0
27	UNL	J	102	10/-	0.85	0.30	61,65,77,92	0
21	TGL	L	101	63/63	0.85	0.21	45,70,98,107	0
24	CHD	P	307	29/29	0.86	0.13	71,80,88,95	0
27	UNL	Y	101	10/-	0.86	0.24	69,76,86,94	0
27	UNL	C	310	7/-	0.86	0.29	41,64,76,83	0
24	CHD	J	101	29/29	0.86	0.15	61,75,106,109	0
27	UNL	N	609	16/-	0.87	0.20	54,59,79,85	0
27	UNL	N	610	18/-	0.87	0.17	51,59,69,70	0
27	UNL	L	102	10/-	0.87	0.25	61,75,82,86	0
30	DMU	Z	101	33/33	0.87	0.11	55,76,107,113	0
23	EDO	E	202	4/4	0.88	0.12	57,61,68,79	0
27	UNL	T	102	18/-	0.88	0.19	47,66,85,92	0
27	UNL	W	102	9/-	0.88	0.24	59,62,79,82	0
27	UNL	N	601	17/-	0.88	0.18	52,60,83,85	0
26	CDL	C	306	100/100	0.88	0.17	51,86,124,152	0
21	TGL	B	301	63/63	0.88	0.18	33,68,103,114	0
27	UNL	N	611	12/-	0.88	0.19	48,56,68,69	0
27	UNL	P	308	20/-	0.89	0.16	58,64,72,73	0
23	EDO	I	101	4/4	0.90	0.17	55,59,63,72	0

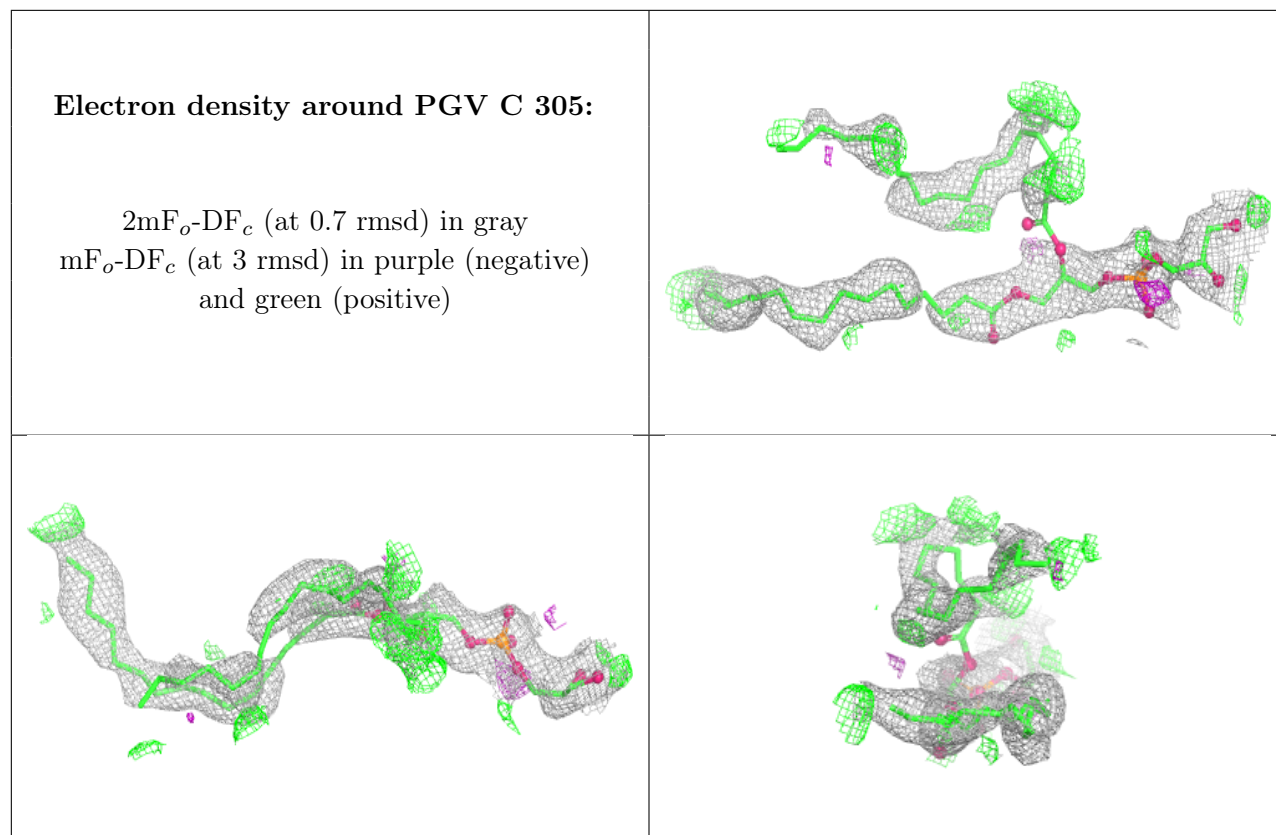
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
27	UNL	P	310	7/-	0.91	0.23	53,60,76,88	0
24	CHD	P	301	29/29	0.93	0.09	40,45,52,55	0
24	CHD	C	301	29/29	0.94	0.07	34,40,48,53	0
31	HEC	2	201	43/43	0.94	0.12	79,101,135,149	0
25	PEK	C	303	53/53	0.95	0.12	34,48,88,97	0
23	EDO	N	614	4/4	0.95	0.11	56,59,63,85	0
30	DMU	M	101	33/33	0.95	0.08	40,46,62,65	0
24	CHD	T	103	29/29	0.95	0.07	30,36,42,53	0
23	EDO	S	102	4/4	0.95	0.10	44,45,46,53	0
16	MG	A	602	1/1	0.96	0.08	36,36,36,36	0
23	EDO	G	103	4/4	0.96	0.10	37,39,49,51	0
16	MG	N	603	1/1	0.96	0.07	42,42,42,42	0
24	CHD	G	102	29/29	0.96	0.07	35,38,43,52	0
23	EDO	C	311	4/4	0.96	0.09	48,51,51,52	0
31	HEC	1	201	43/43	0.96	0.10	57,81,94,99	0
25	PEK	P	303	53/53	0.96	0.11	39,53,94,101	0
20	PGV	P	304	51/51	0.97	0.09	30,46,73,76	0
20	PGV	C	304	51/51	0.97	0.09	31,38,95,103	0
20	PGV	A	608	51/51	0.97	0.09	29,41,68,74	0
23	EDO	B	303	4/4	0.98	0.05	30,31,33,36	0
20	PGV	N	612	51/51	0.98	0.08	33,43,70,80	0
23	EDO	N	613	4/4	0.98	0.06	38,38,39,41	0
19	PER	N	607	2/2	0.98	0.10	36,36,36,48	0
23	EDO	F	102	4/4	0.98	0.07	45,47,49,49	0
19	PER	A	606	2/2	0.99	0.09	40,40,40,54	0
17	NA	N	604	1/1	0.99	0.03	45,45,45,45	0
17	NA	A	603	1/1	0.99	0.07	31,31,31,31	0
18	HEA	A	604[A]	60/60	0.99	0.06	23,28,38,40	9
18	HEA	A	604[B]	60/60	0.99	0.06	23,28,35,40	9
22	CUA	O	301	2/2	0.99	0.04	42,42,42,43	0
29	ZN	S	101	1/1	0.99	0.05	37,37,37,37	0
18	HEA	A	605	60/60	0.99	0.04	22,26,33,39	0
18	HEA	N	605[A]	60/60	0.99	0.06	32,38,47,50	9
18	HEA	N	605[B]	60/60	0.99	0.06	32,38,44,47	9
18	HEA	N	606	60/60	0.99	0.05	27,33,41,47	0
15	CU	A	601	1/1	1.00	0.01	29,29,29,29	0
15	CU	N	602	1/1	1.00	0.01	35,35,35,35	0
29	ZN	F	101	1/1	1.00	0.01	36,36,36,36	0
22	CUA	B	302	2/2	1.00	0.01	27,27,27,29	0

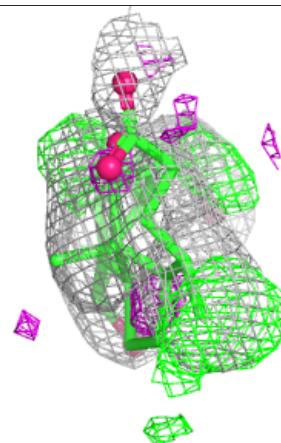
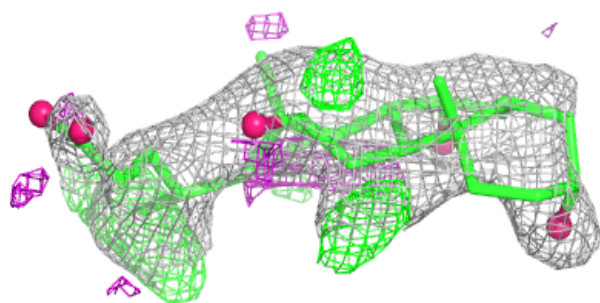
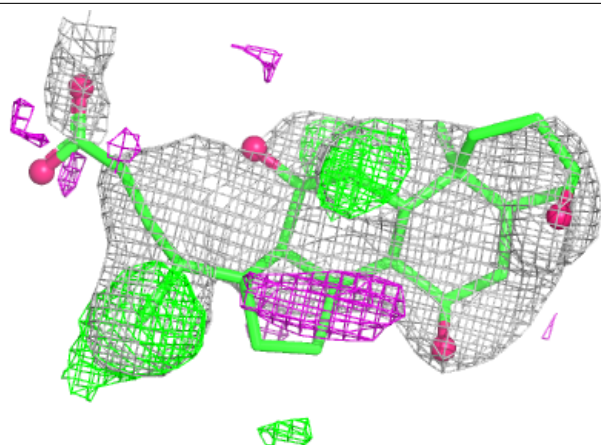
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

orientation to approximate a three-dimensional view.

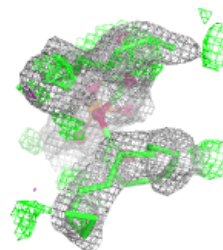
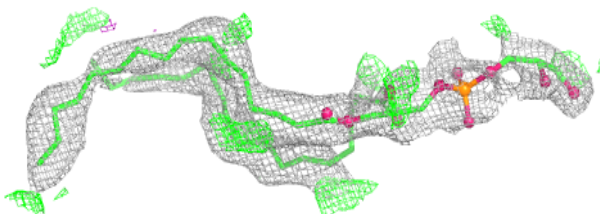
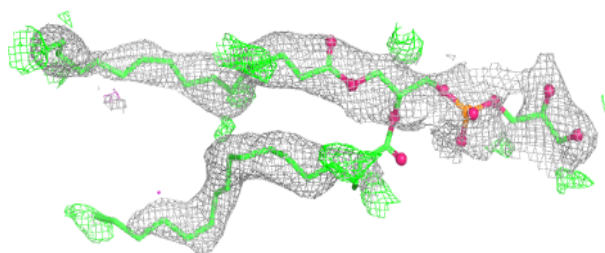


Electron density around CHD W 101:

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

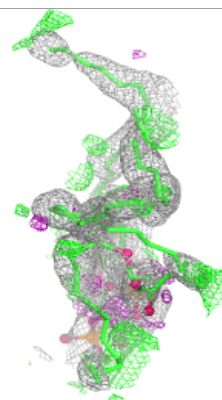
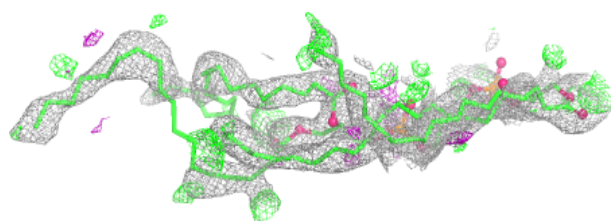
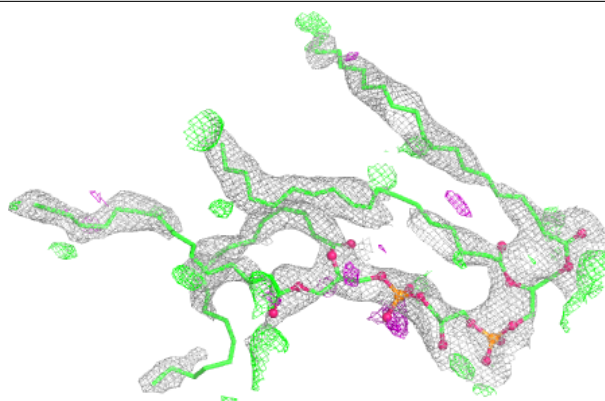
**Electron density around PGV P 305:**

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

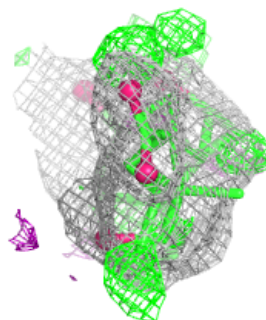
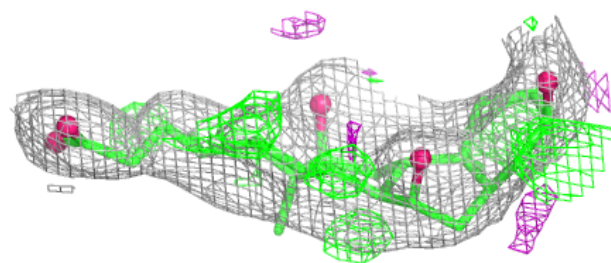
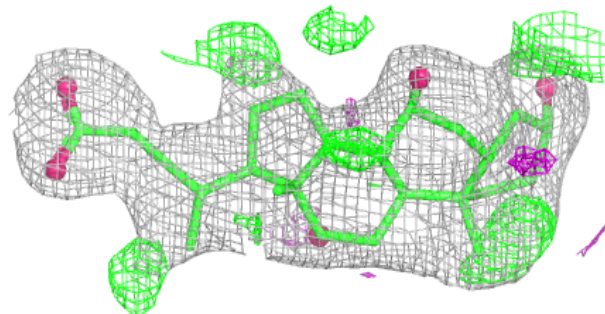


Electron density around CDL T 101:

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

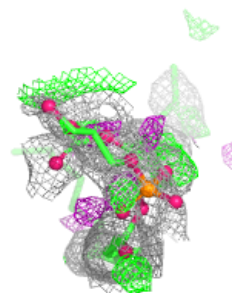
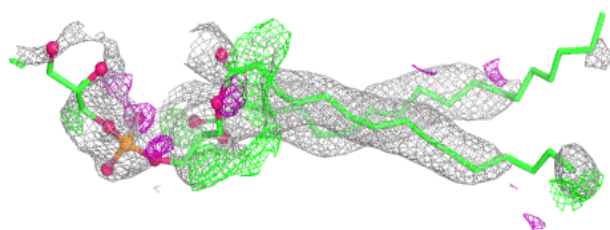
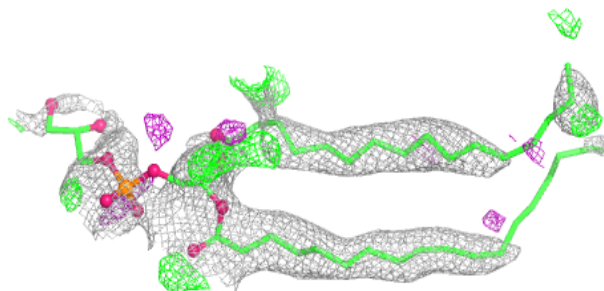
**Electron density around CHD C 307:**

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

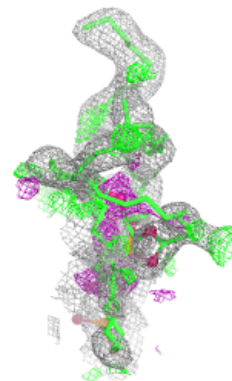
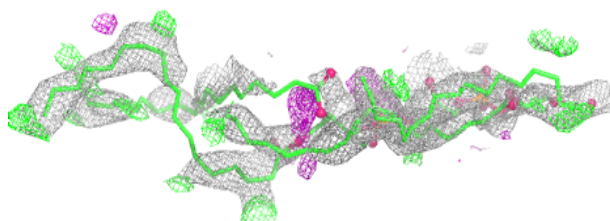
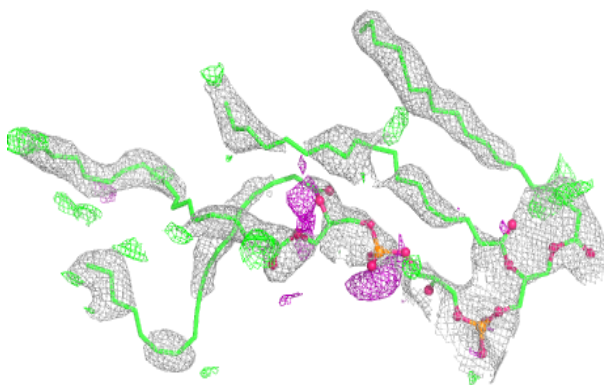


Electron density around PGV A 607:

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

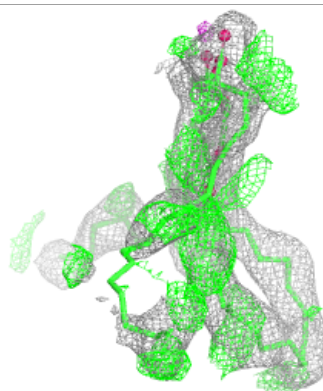
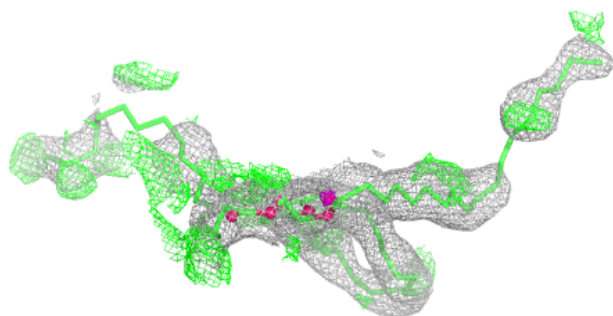
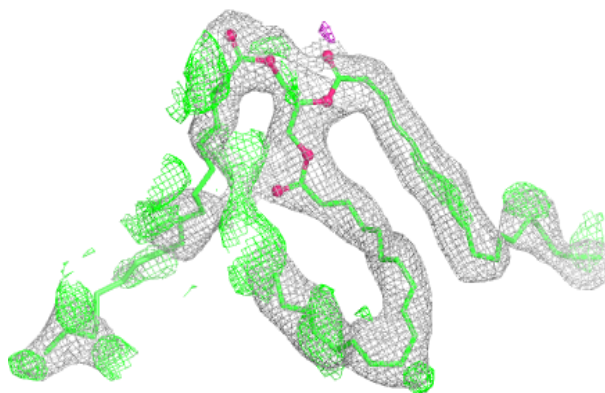
**Electron density around CDL G 101:**

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

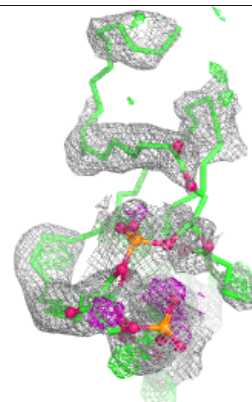
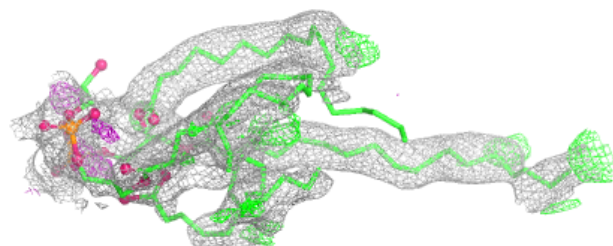
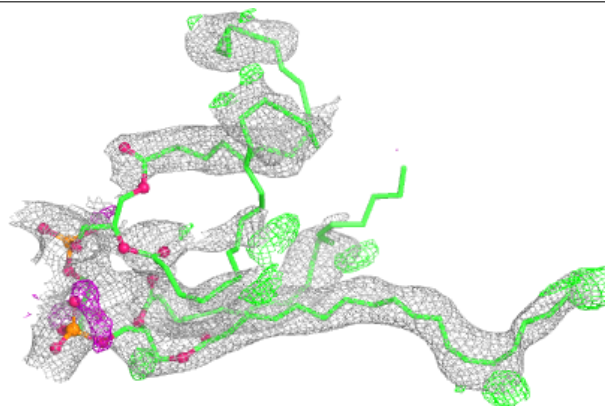


Electron density around TGL D 201:

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

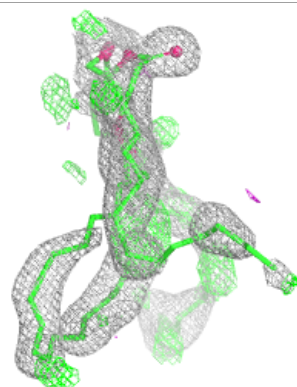
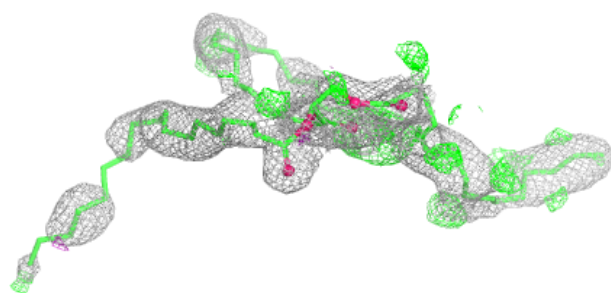
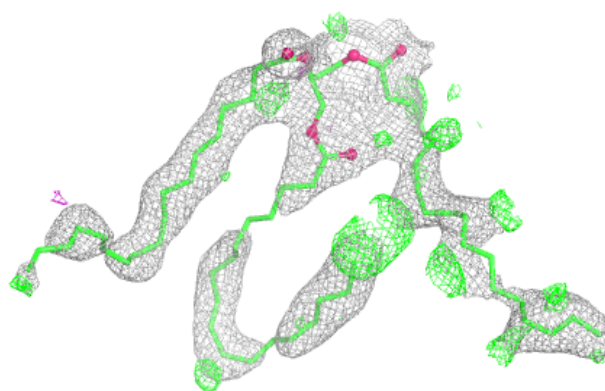
**Electron density around CDL P 306:**

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

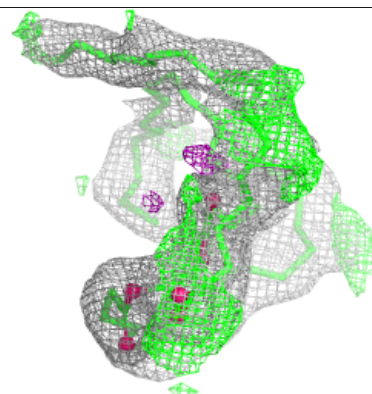
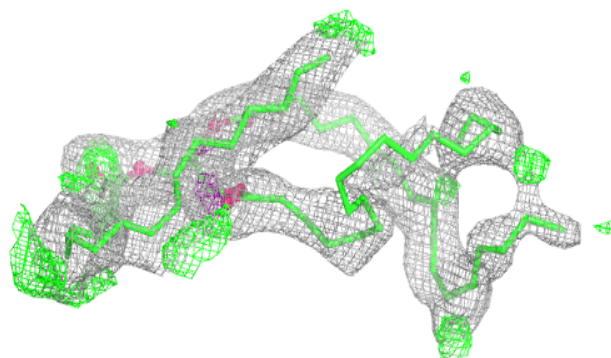
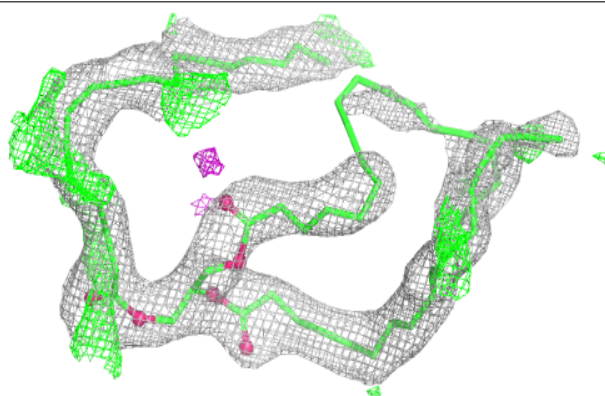


Electron density around TGL Q 201:

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

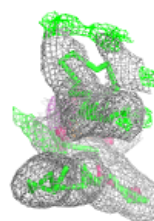
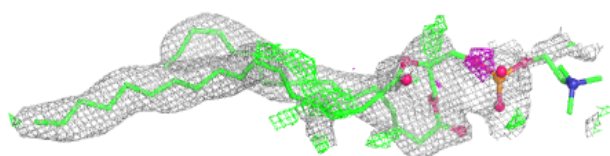
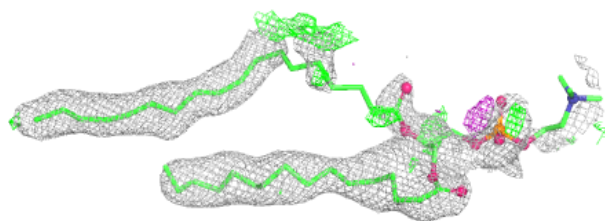
**Electron density around TGL N 608:**

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

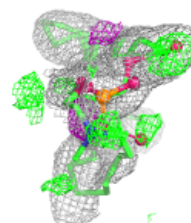
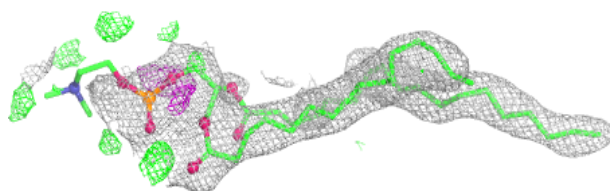
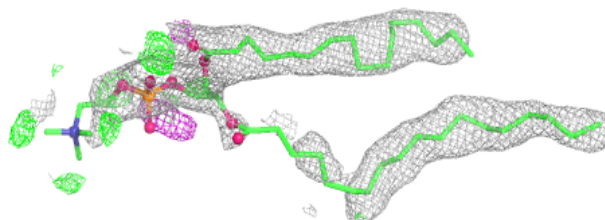


Electron density around PSC E 201:

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

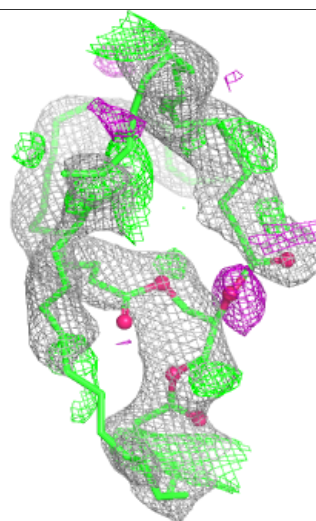
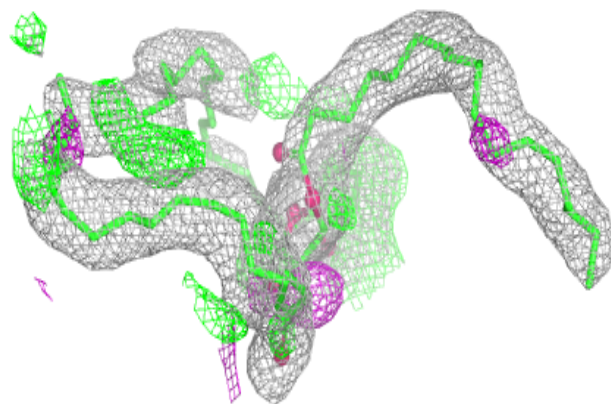
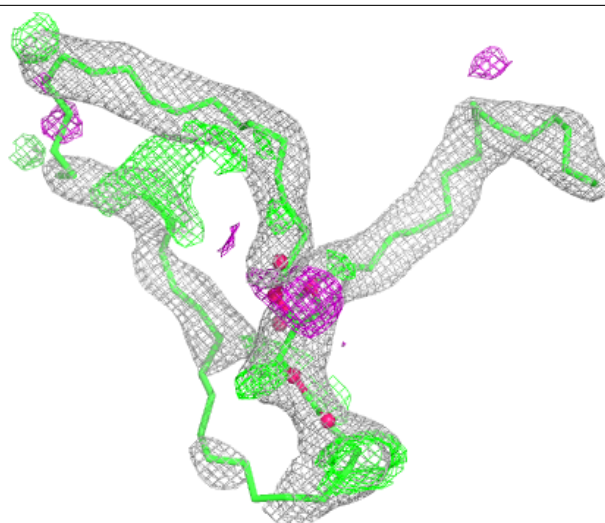
**Electron density around PSC V 101:**

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



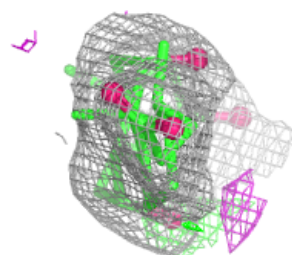
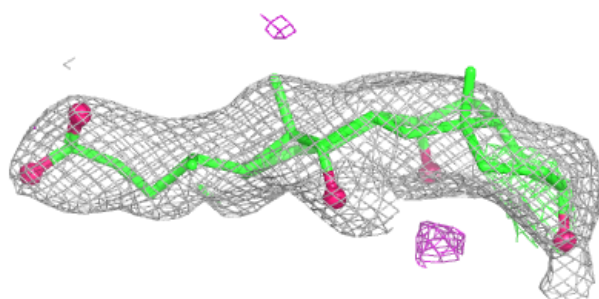
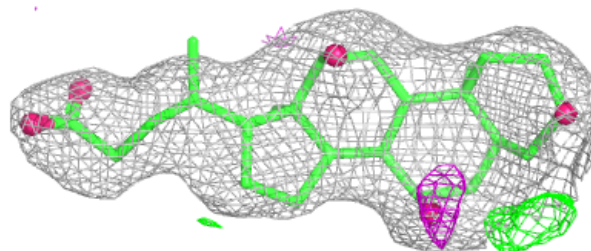
Electron density around TGL L 101:

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

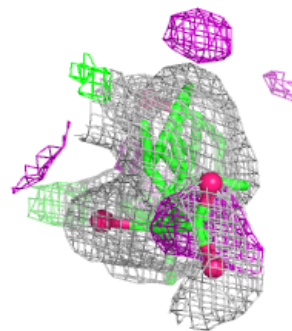
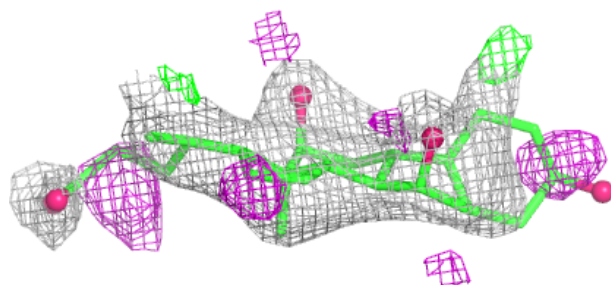
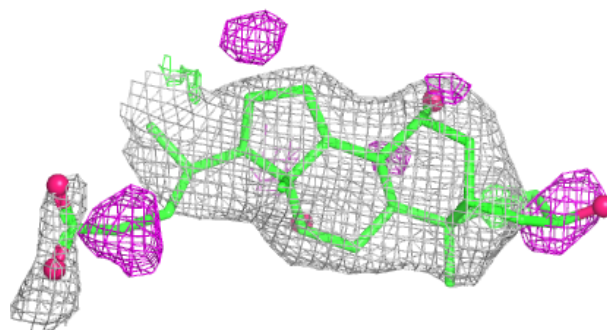


Electron density around CHD P 307:

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

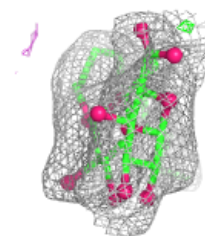
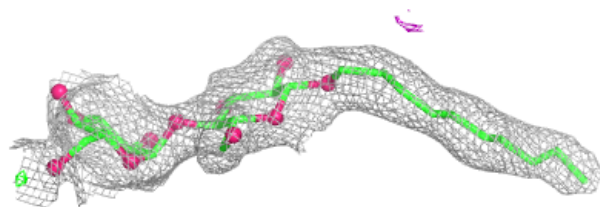
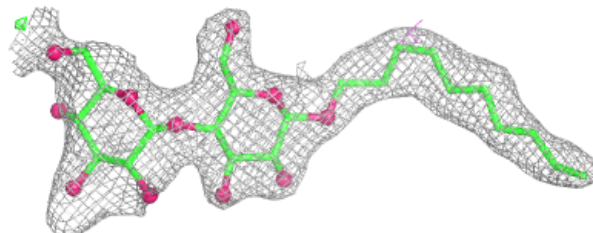
**Electron density around CHD J 101:**

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

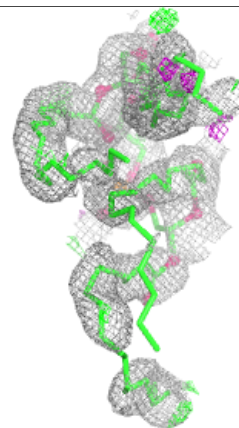
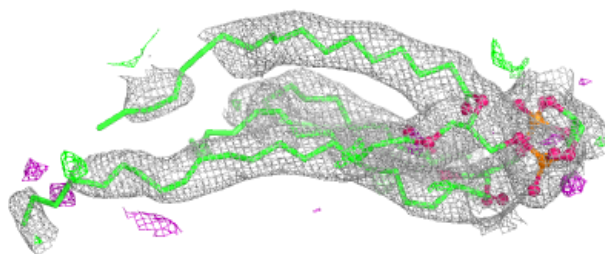
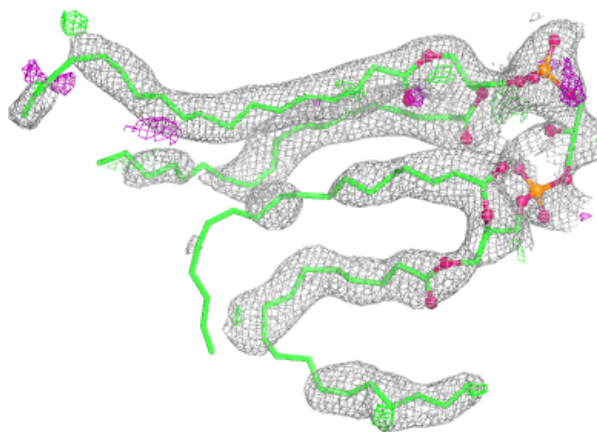


Electron density around DMU Z 101:

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

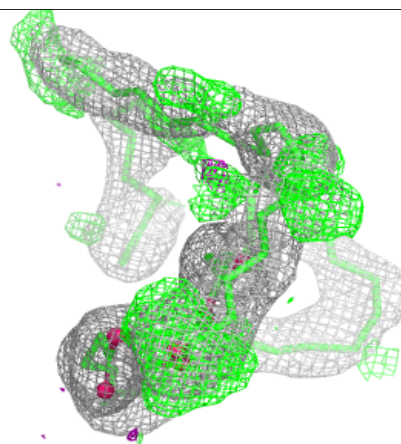
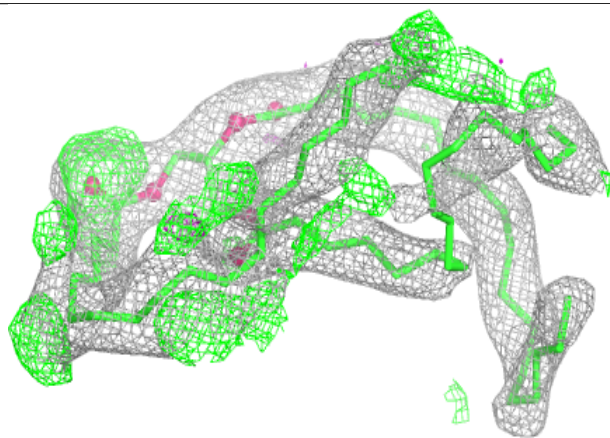
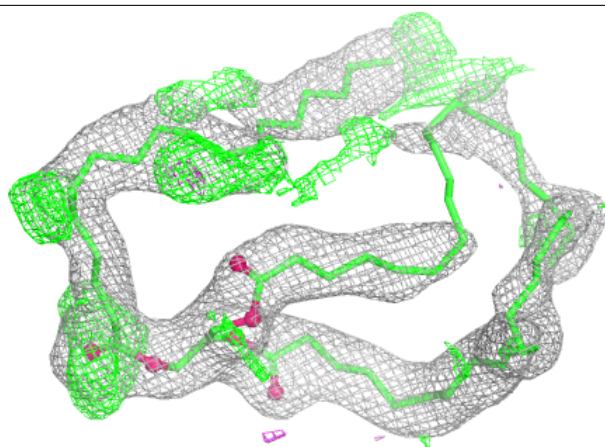
**Electron density around CDL C 306:**

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

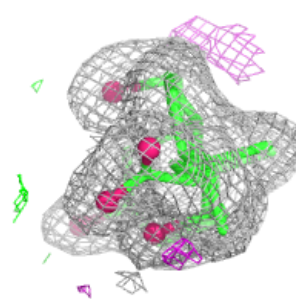
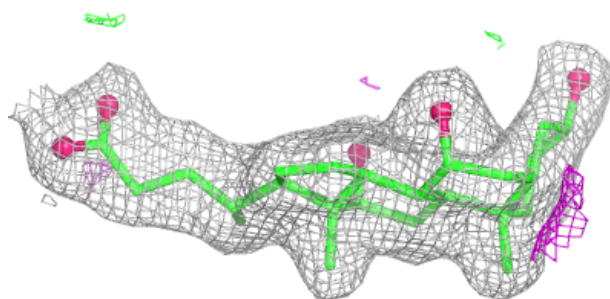
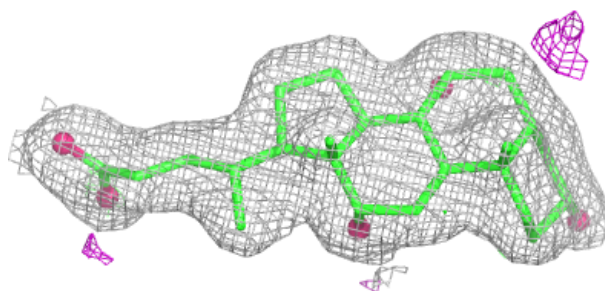


Electron density around TGL B 301:

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

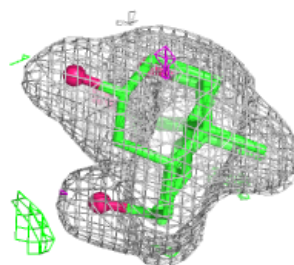
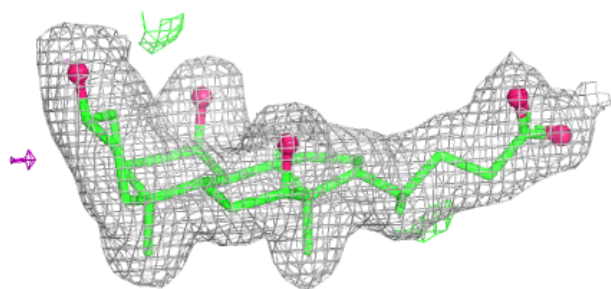
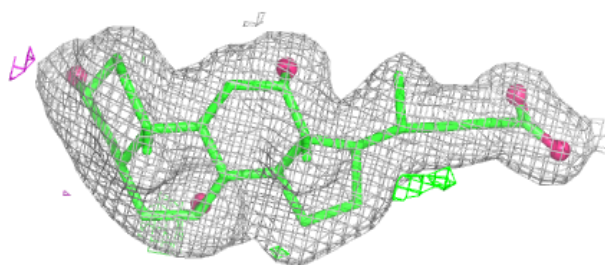
**Electron density around CHD P 301:**

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

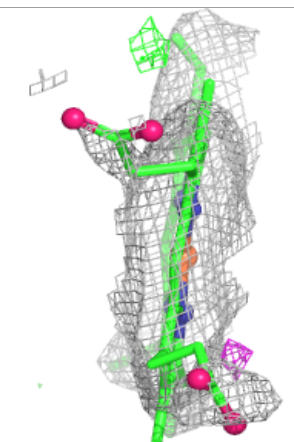
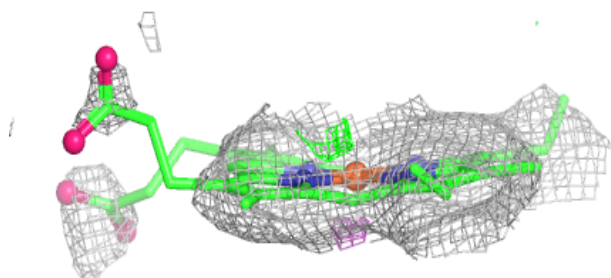
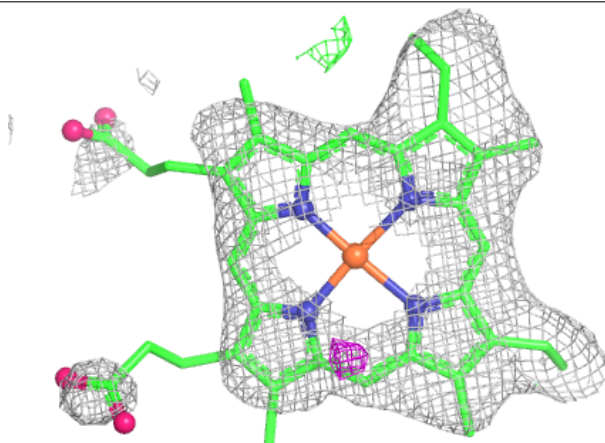


Electron density around CHD C 301:

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

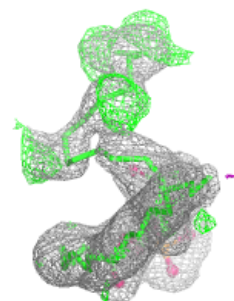
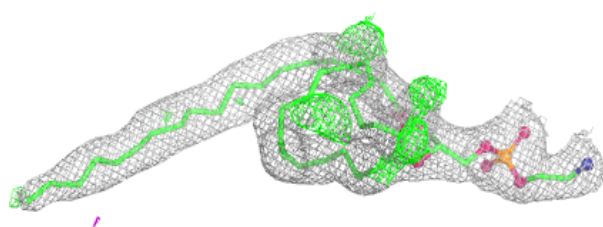
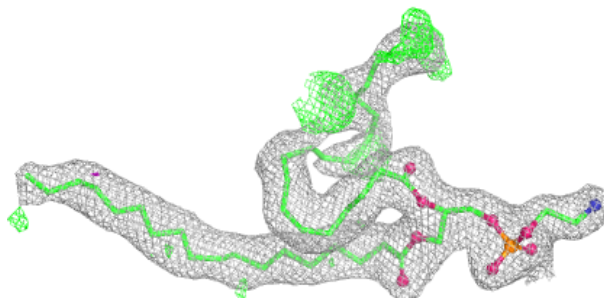
**Electron density around HEC 2 201:**

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

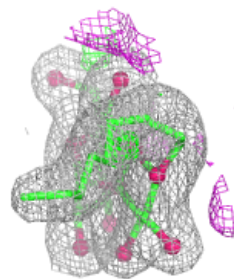
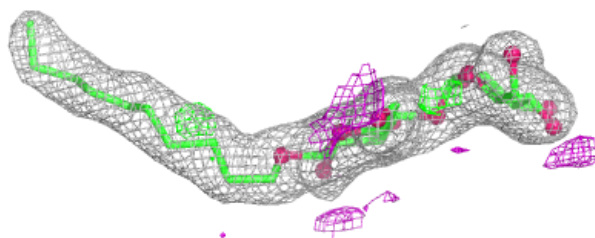
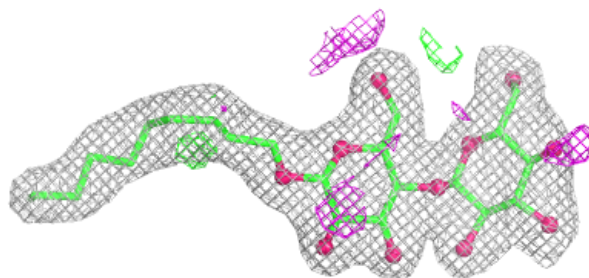


Electron density around PEK C 303:

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

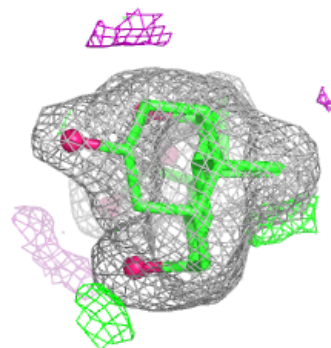
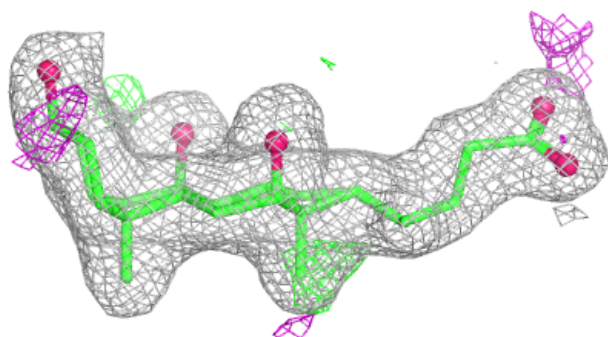
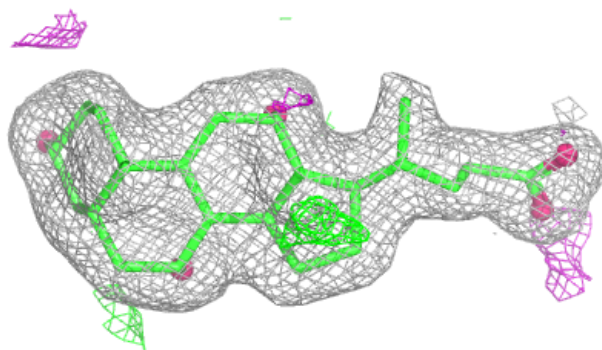
**Electron density around DMU M 101:**

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

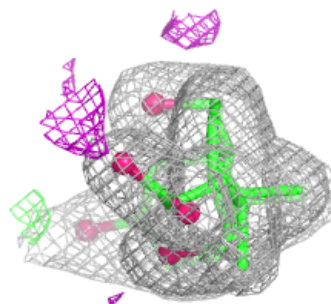
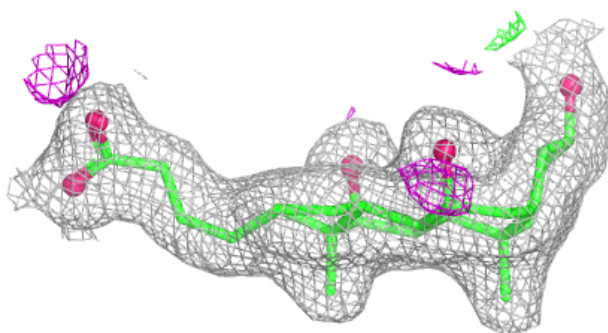
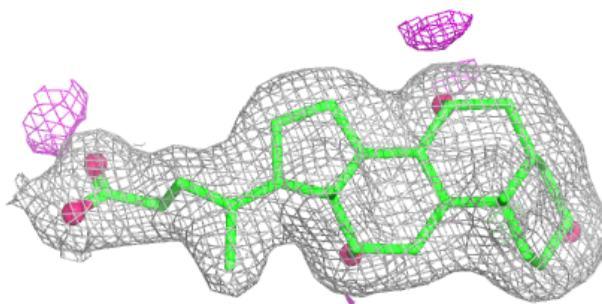


Electron density around CHD T 103:

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

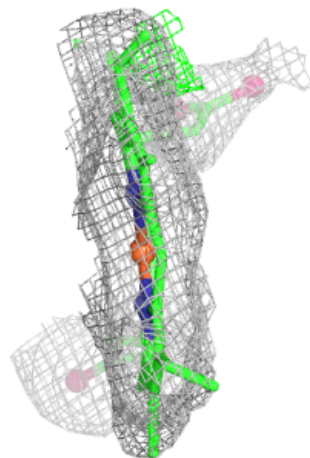
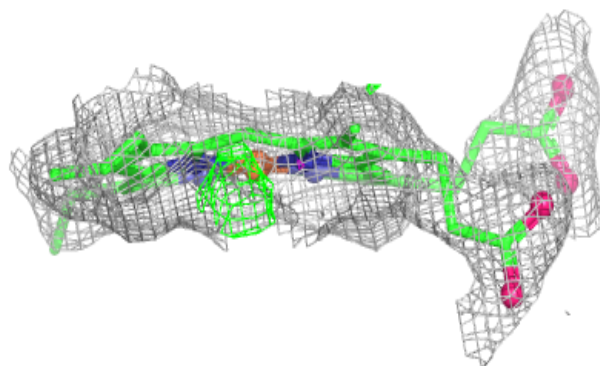
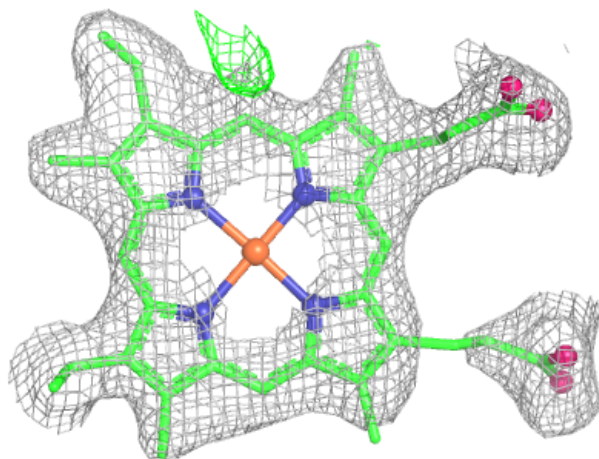
**Electron density around CHD G 102:**

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



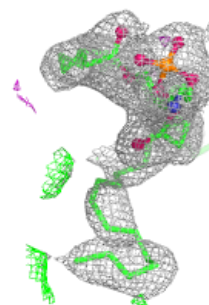
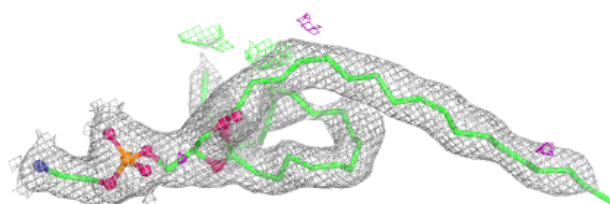
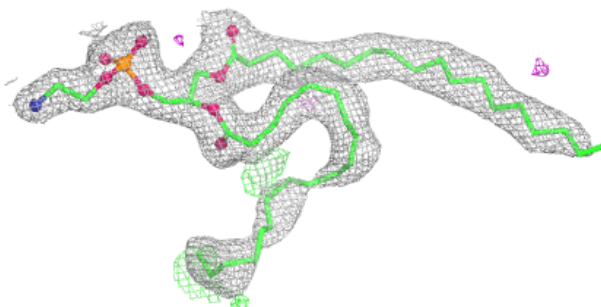
Electron density around HEC 1 201:

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

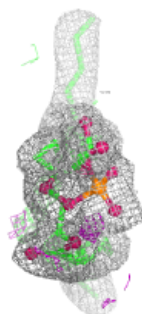
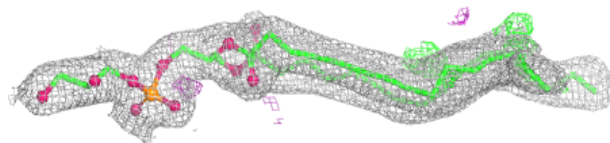
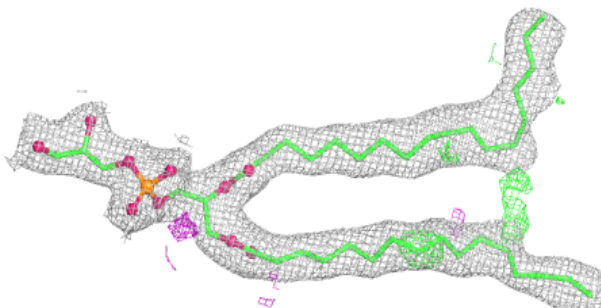


Electron density around PEK P 303:

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

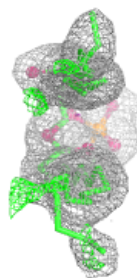
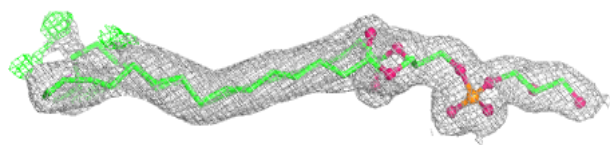
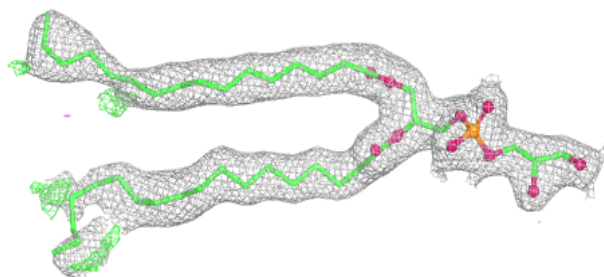
**Electron density around PGV P 304:**

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

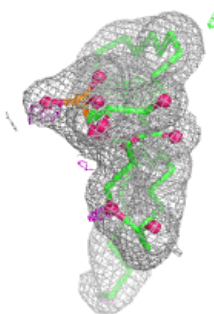
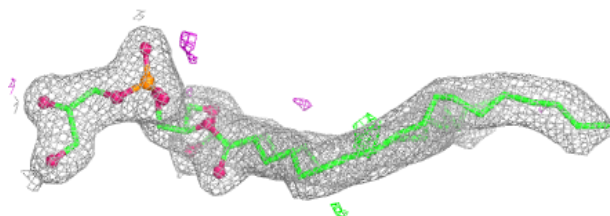
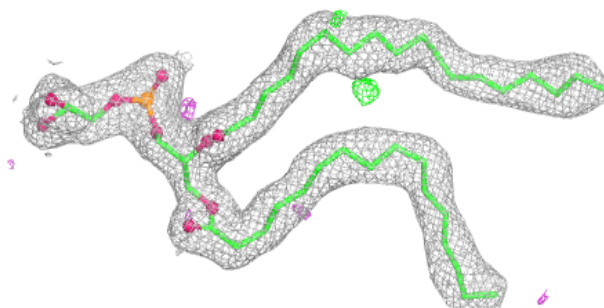


Electron density around PGV C 304:

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

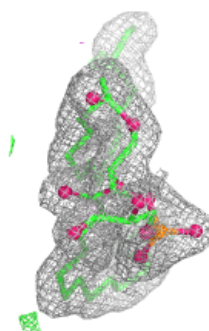
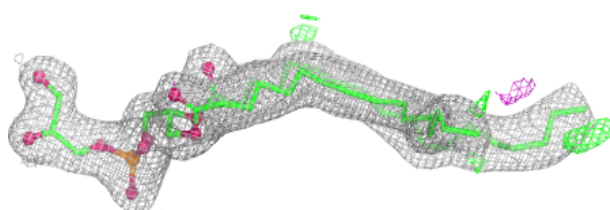
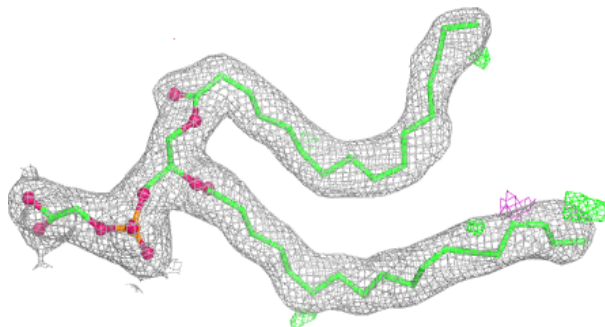
**Electron density around PGV A 608:**

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

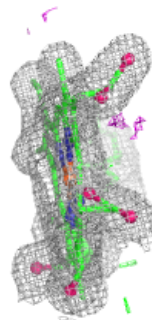
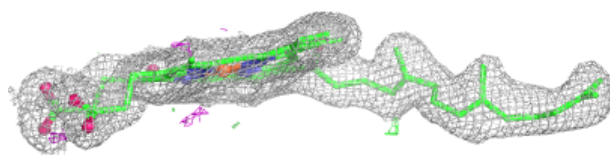
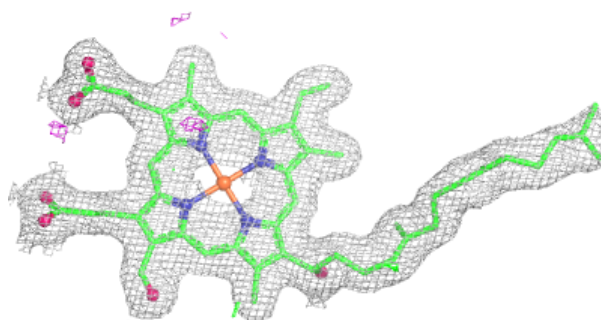


Electron density around PGV N 612:

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

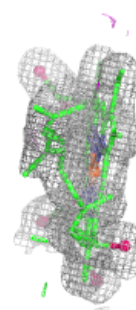
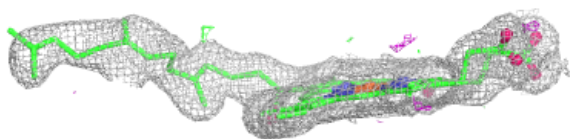
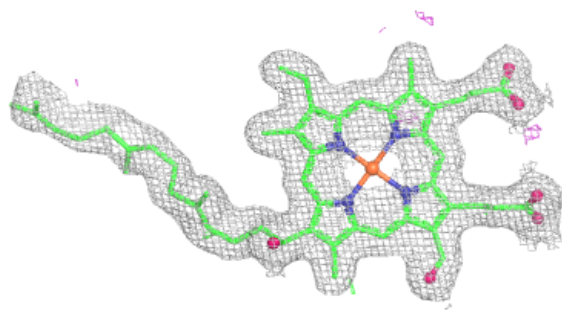
**Electron density around HEA A 604 (A):**

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

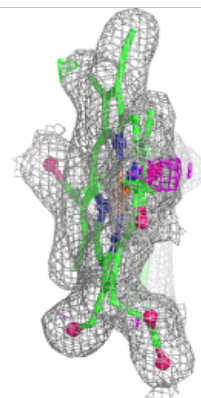
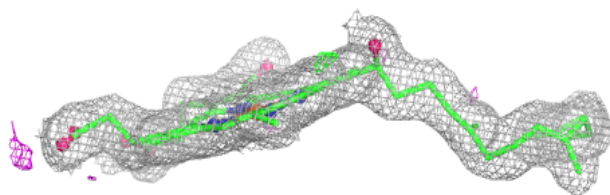
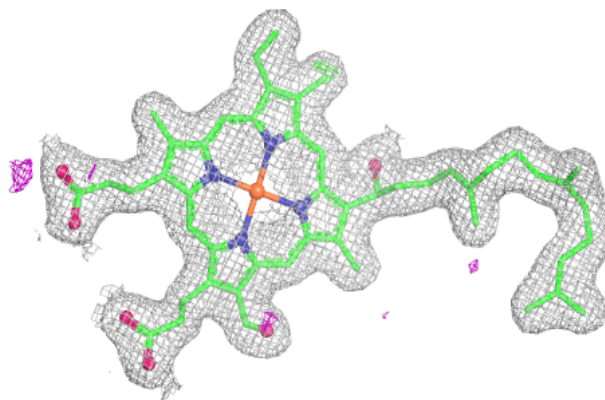


Electron density around HEA A 604 (B):

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

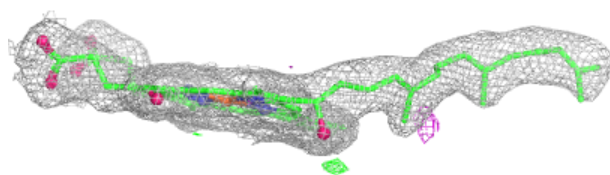
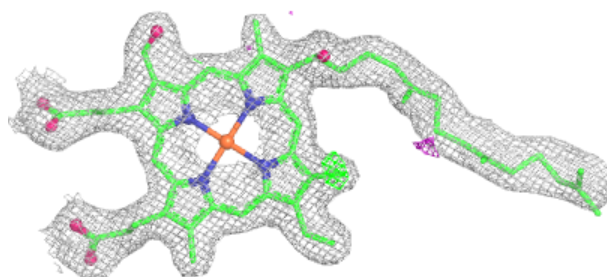
**Electron density around HEA A 605:**

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

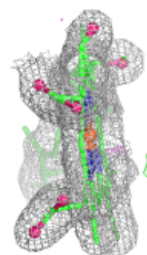
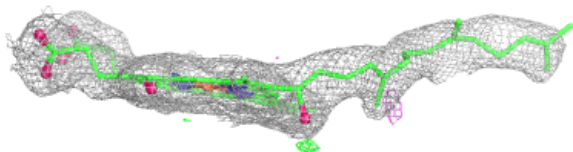
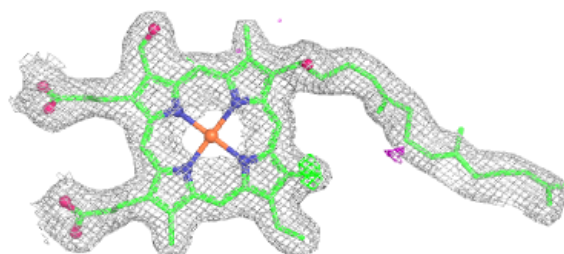


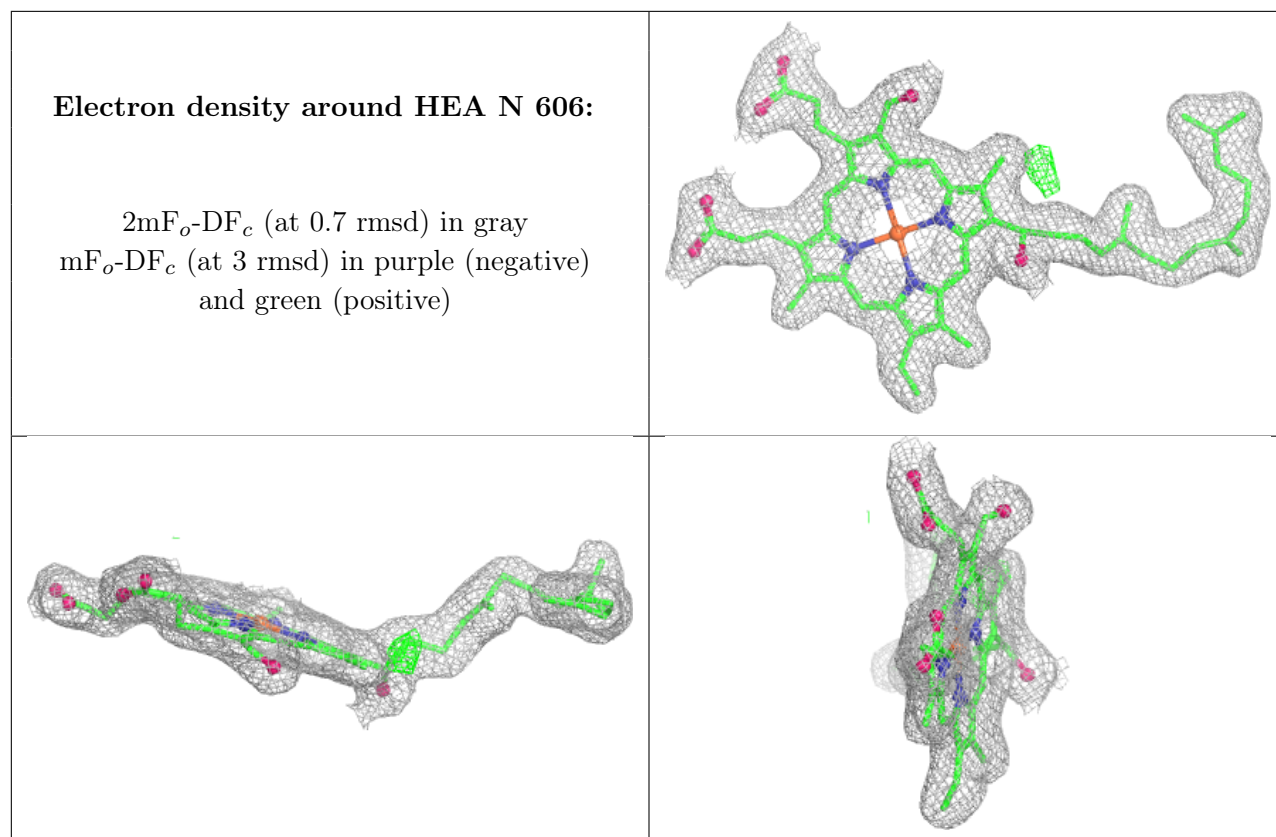
Electron density around HEA N 605 (A):

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

**Electron density around HEA N 605 (B):**

$2mF_o-DF_c$ (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.