



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 10:51 PM UTC

PDB ID : 5X1F / pdb_00005x1f
Title : CO bound cytochrome c oxidase without pump laser irradiation at 278K
Authors : Shimada, A.; Kubo, M.; Baba, S.; Yamashita, K.; Hirata, K.; Ueno, G.; Nomura, T.; Kimura, T.; Shinzawa-Itoh, K.; Baba, J.; Hatano, K.; Eto, Y.; Miyamoto, A.; Murakami, H.; Kumasaka, T.; Owada, S.; Tono, K.; Yabashi, M.; Yamaguchi, Y.; Yanagisawa, S.; Sakaguchi, M.; Ogura, T.; Komiya, R.; Yan, J.; Yamashita, E.; Yamamoto, M.; Ago, H.; Yoshikawa, S.; Tsukihara, T.
Deposited on : 2017-01-25
Resolution : 2.20 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

<https://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)

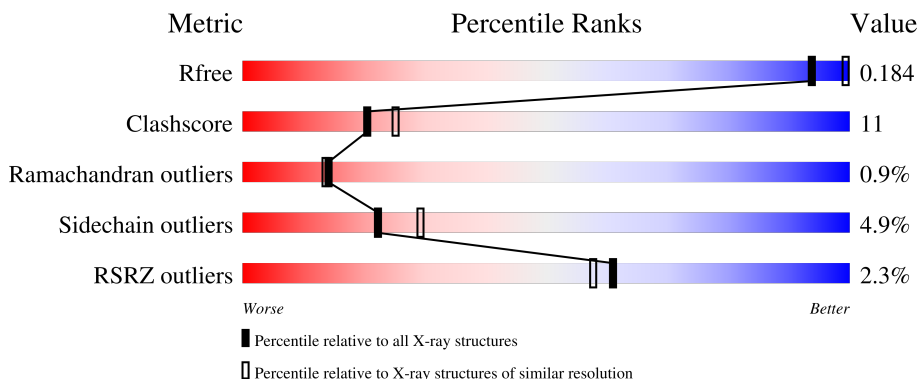
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

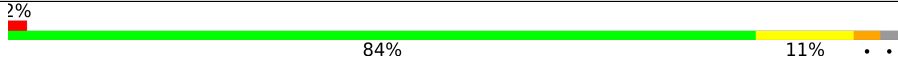
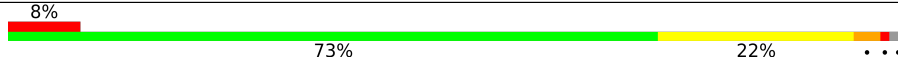
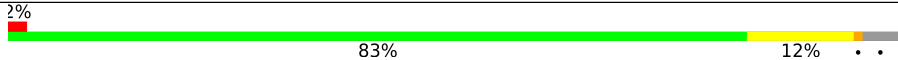
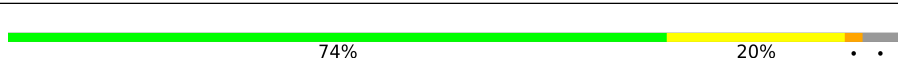
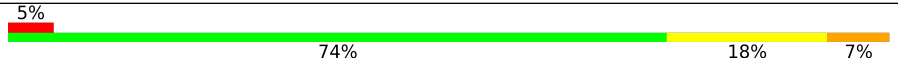
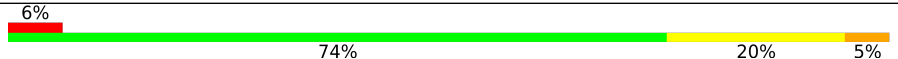
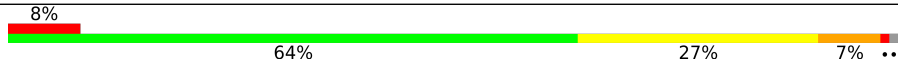
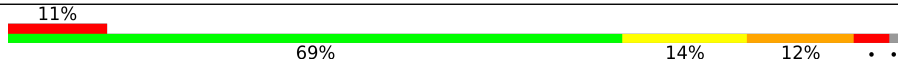
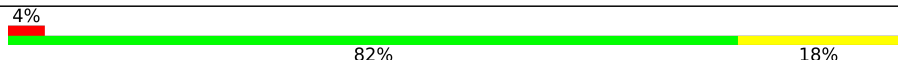
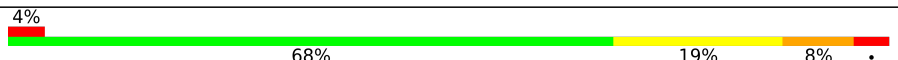
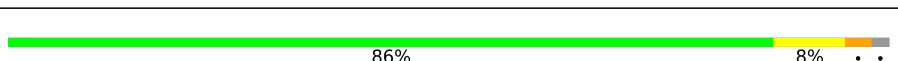
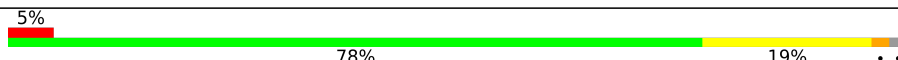
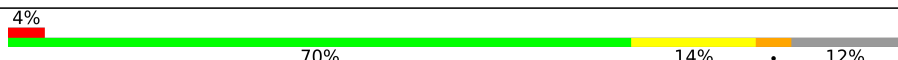
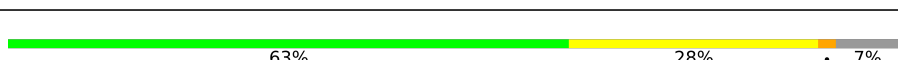
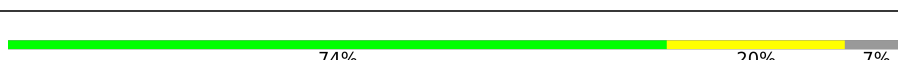
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	82% 17% .
1	N	514	76% 22% .
2	B	227	76% 19% ..

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
2	O	227	
3	C	261	
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	CMO	N	606	-	-	X	-
21	EDO	A	613	-	-	X	-
21	EDO	C	312	-	-	X	-
21	EDO	I	101	-	-	X	-
26	UNX	C	301	-	-	-	X

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 32099 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	1	0
			4030	2694	623	678	35			
1	N	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			

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

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

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

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

- Molecule 4 is a protein called Cytochrome c oxidase subunit 4 isoform 1, 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	0	0
			1195	777	196	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			

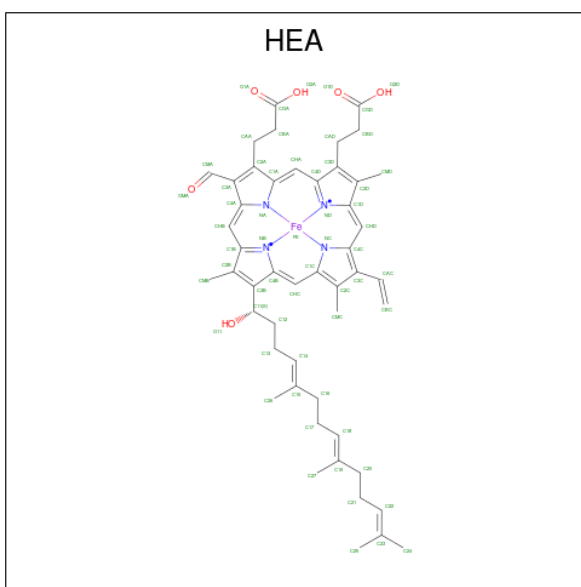
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

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 HEME-A (CCD ID: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



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		

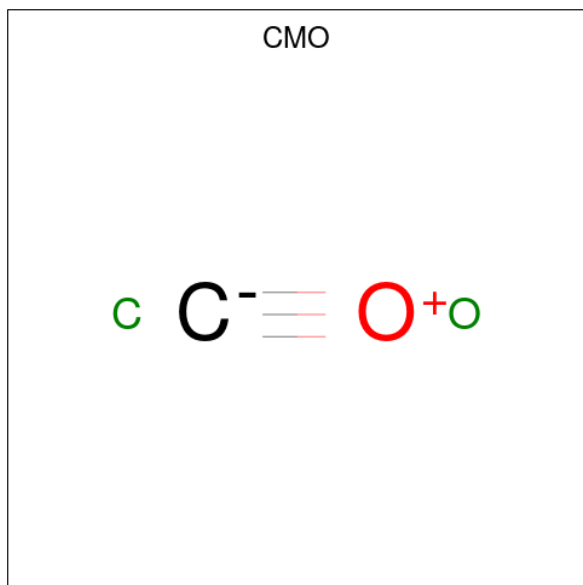
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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).

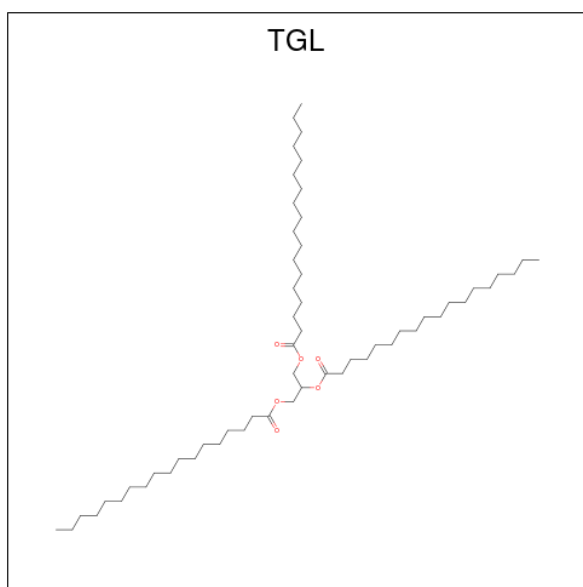
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Na	0	0
			1	1		
17	N	1	Total	Na	0	0
			1	1		

- Molecule 18 is CARBON MONOXIDE (CCD ID: CMO) (formula: CO).



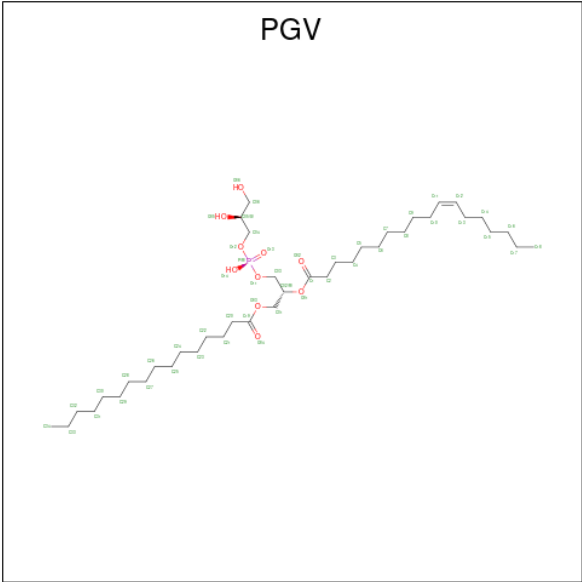
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	A	1	Total	C	O	0	0
			2	1	1		
18	N	1	Total	C	O	0	0
			2	1	1		

- Molecule 19 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: C₅₇H₁₁₀O₆).



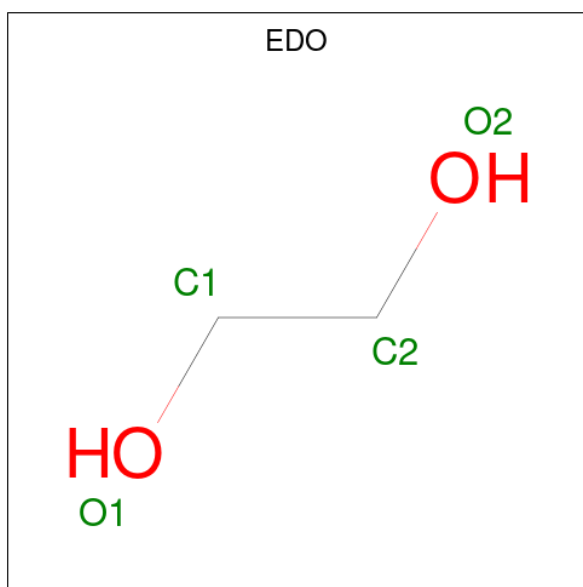
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	A	1	Total	C	O	0	0
			63	57	6		
19	D	1	Total	C	O	0	0
			63	57	6		
19	L	1	Total	C	O	0	0
			63	57	6		
19	N	1	Total	C	O	0	0
			63	57	6		
19	Q	1	Total	C	O	0	0
			63	57	6		
19	Y	1	Total	C	O	0	0
			63	57	6		

- Molecule 20 is (1R)-2-{{[[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: 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	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	Z	1	Total	C	O	P	0	0
			51	40	10	1		

- Molecule 21 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



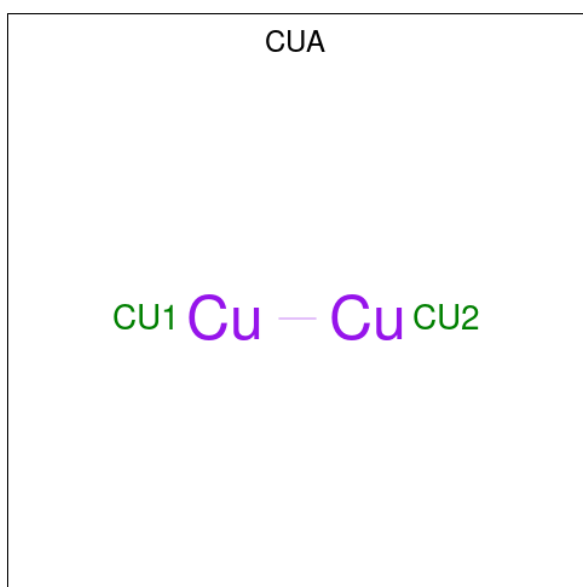
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	B	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	F	1	Total	C	O	0	0
			4	2	2		
21	G	1	Total	C	O	0	0
			4	2	2		
21	I	1	Total	C	O	0	0
			4	2	2		
21	K	1	Total	C	O	0	0
			4	2	2		
21	K	1	Total	C	O	0	0
			4	2	2		

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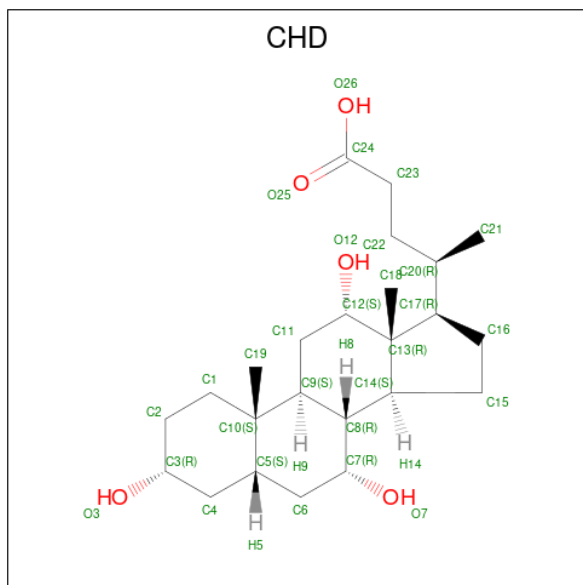
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
21	K	1	Total C O 4 2 2	0	0
21	L	1	Total C O 4 2 2	0	0
21	L	1	Total C O 4 2 2	0	0
21	N	1	Total C O 4 2 2	0	0
21	N	1	Total C O 4 2 2	0	0
21	N	1	Total C O 4 2 2	0	0
21	P	1	Total C O 4 2 2	0	0
21	P	1	Total C O 4 2 2	0	0
21	S	1	Total C O 4 2 2	0	0
21	T	1	Total C O 4 2 2	0	0
21	X	1	Total C O 4 2 2	0	0

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



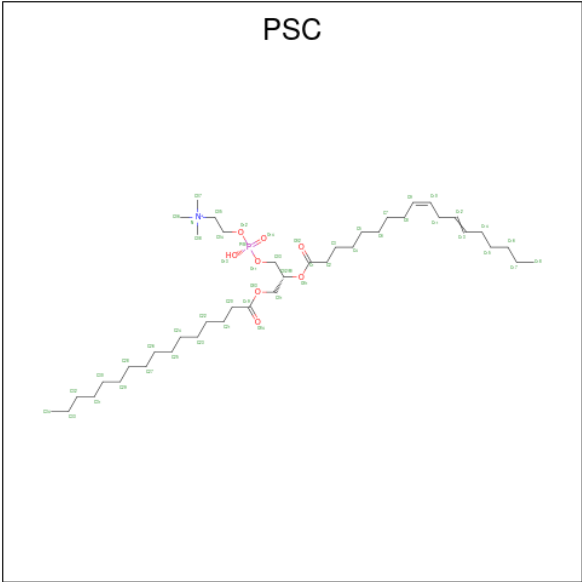
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
22	B	1	Total Cu 2 2	0	0
22	O	1	Total Cu 2 2	0	0

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



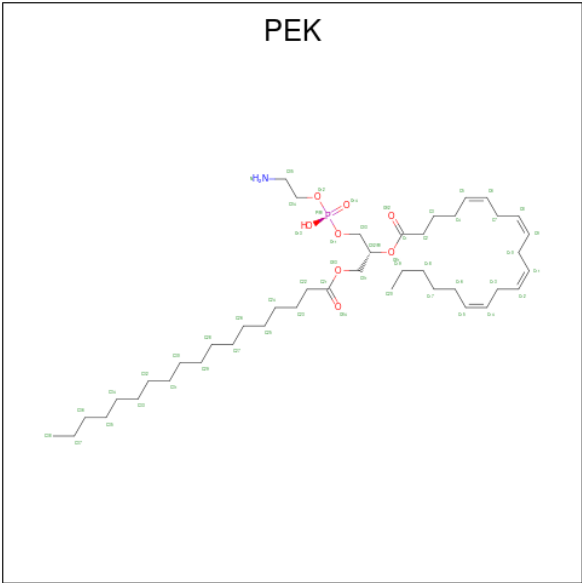
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	B	1	Total C O 29 24 5	0	0
23	C	1	Total C O 29 24 5	0	0
23	C	1	Total C O 29 24 5	0	0
23	G	1	Total C O 29 24 5	0	0
23	J	1	Total C O 29 24 5	0	0
23	P	1	Total C O 29 24 5	0	0
23	P	1	Total C O 29 24 5	0	0
23	W	1	Total C O 29 24 5	0	0

- Molecule 24 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: $C_{42}H_{81}NO_8P$).



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

- Molecule 25 is (1S)-2-[[[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYL)OXY]METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (CCD ID: PEK) (formula: C₄₃H₇₈NO₈P).



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

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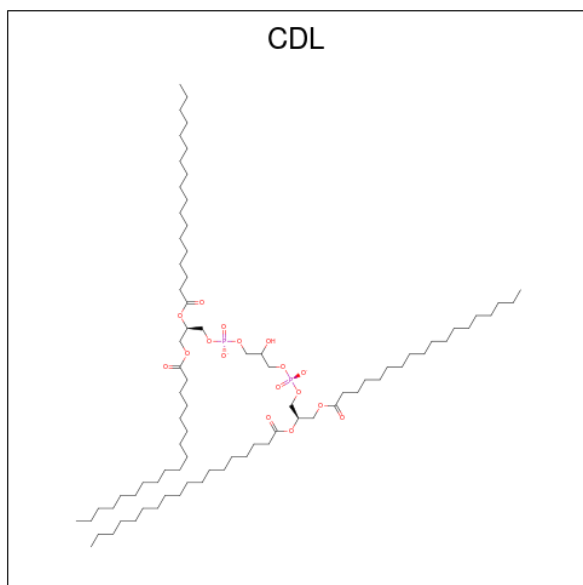
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
25	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	C	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
25	T	1	Total	C	N	O	P	0	0
			53	43	1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

- Molecule 26 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	C	1	Total	X	0	0
			1	1		
26	P	1	Total	X	0	0
			1	1		

- Molecule 27 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



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

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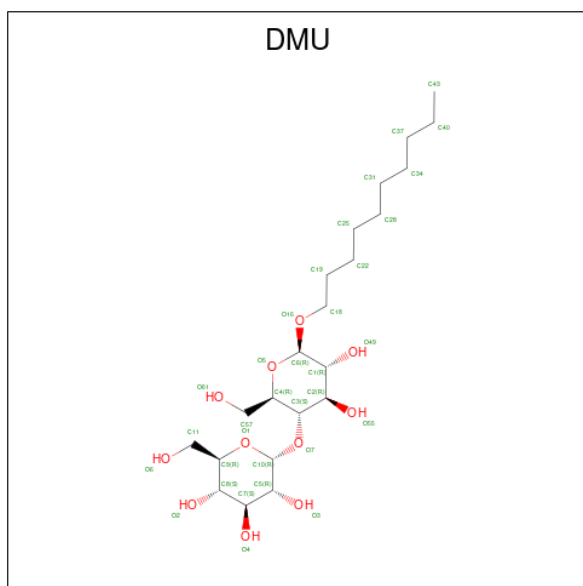
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
27	P	1	Total	C	O	P	0	0
			100	81	17	2		
27	T	1	Total	C	O	P	0	0
			100	81	17	2		

- 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 DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: $C_{22}H_{42}O_{11}$).



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

- Molecule 30 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
30	A	170	Total O 170 170	0	0
30	B	113	Total O 114 114	0	1
30	C	85	Total O 85 85	0	0
30	D	80	Total O 80 80	0	0
30	E	30	Total O 30 30	0	0
30	F	54	Total O 54 54	0	0
30	G	33	Total O 33 33	0	0
30	H	42	Total O 42 42	0	0
30	I	22	Total O 22 22	0	0
30	J	19	Total O 19 19	0	0
30	K	26	Total O 26 26	0	0
30	L	20	Total O 20 20	0	0
30	M	20	Total O 20 20	0	0
30	N	164	Total O 164 164	0	0
30	O	95	Total O 96 96	0	1
30	P	74	Total O 74 74	0	0
30	Q	43	Total O 43 43	0	0
30	R	39	Total O 39 39	0	0
30	S	54	Total O 54 54	0	0
30	T	35	Total O 35 35	0	0
30	U	30	Total O 30 30	0	0
30	V	22	Total O 22 22	0	0

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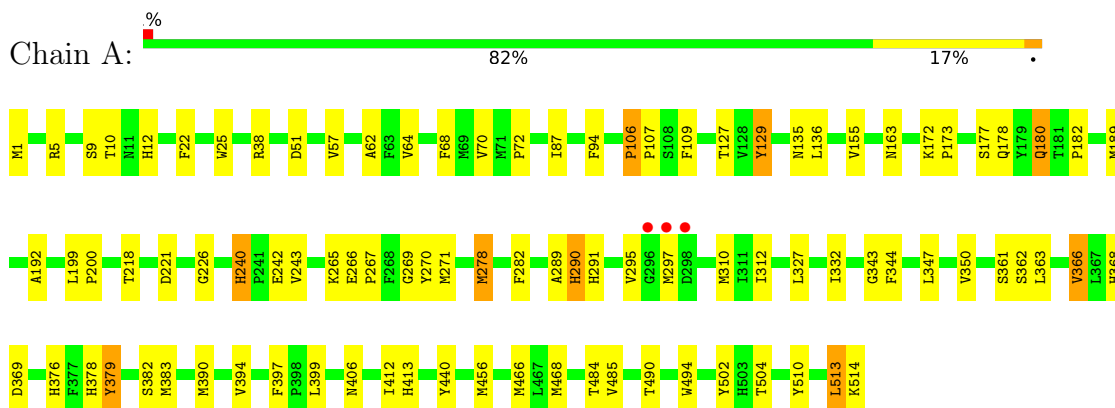
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	W	21	Total 21	O 21	0	0
30	X	12	Total 12	O 12	0	0
30	Y	14	Total 14	O 14	0	0
30	Z	7	Total 7	O 7	0	0

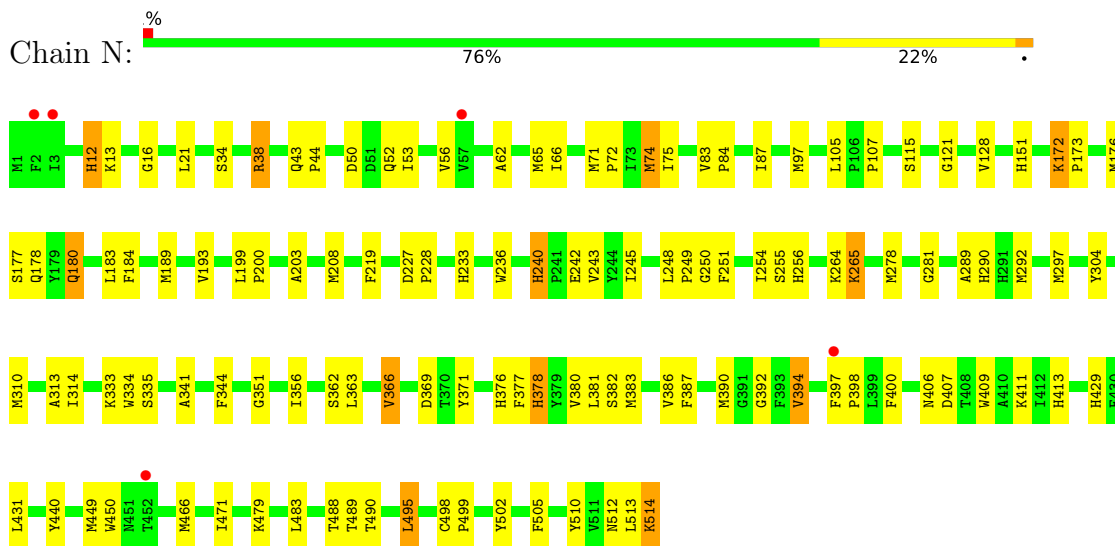
3 Residue-property plots

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.

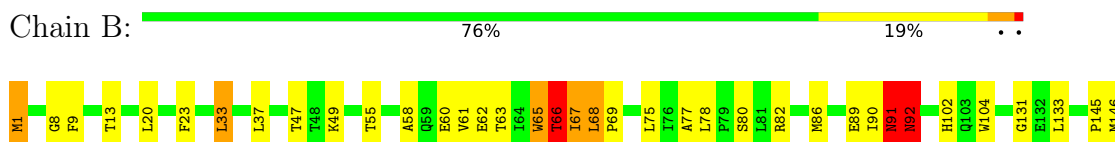
• Molecule 1: Cytochrome c oxidase subunit 1



• Molecule 1: Cytochrome c oxidase subunit 1

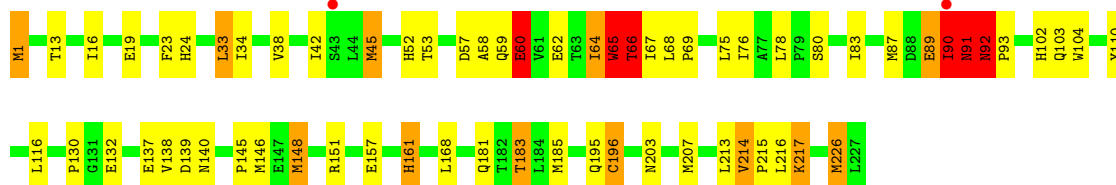


• Molecule 2: Cytochrome c oxidase subunit 2

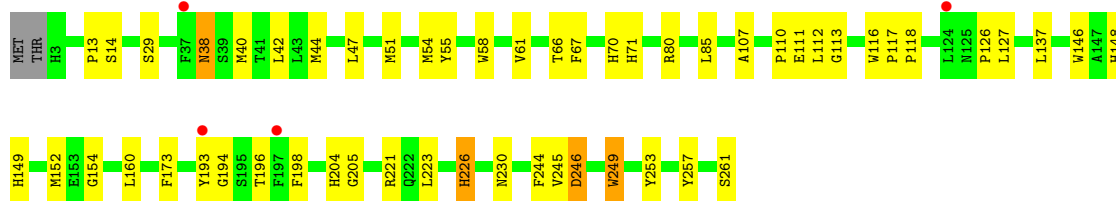
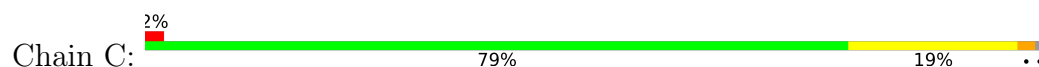




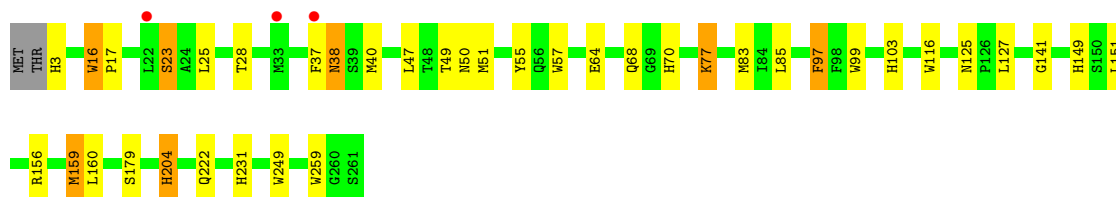
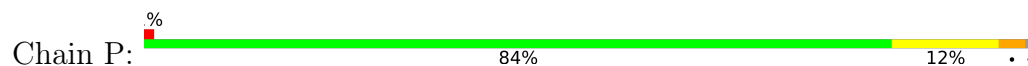
• Molecule 2: Cytochrome c oxidase subunit 2



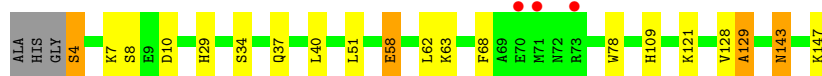
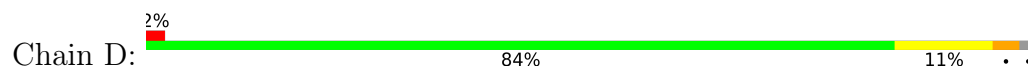
• Molecule 3: Cytochrome c oxidase subunit 3



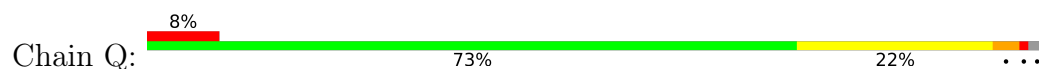
• Molecule 3: Cytochrome c oxidase subunit 3

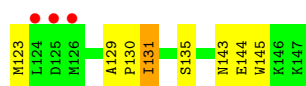


• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial

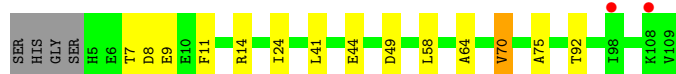
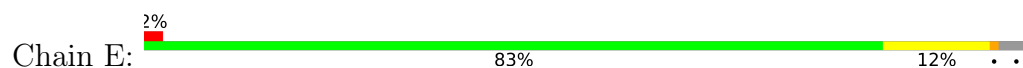


• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial





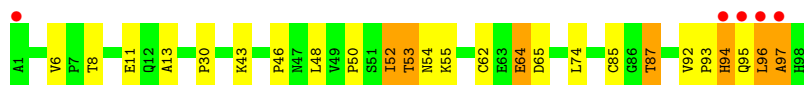
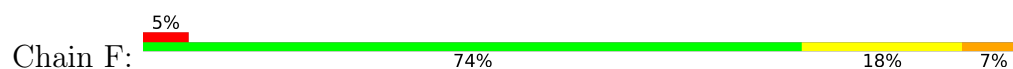
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



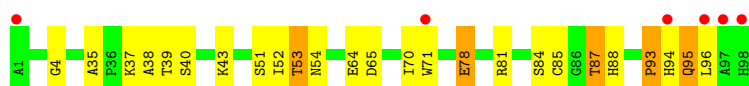
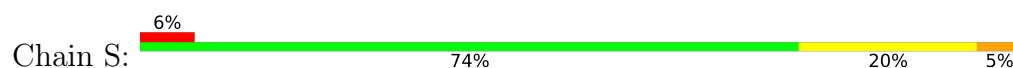
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



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



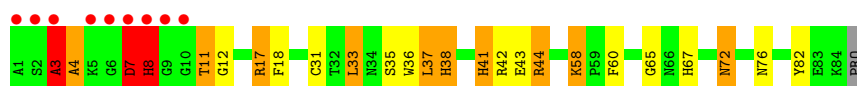
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



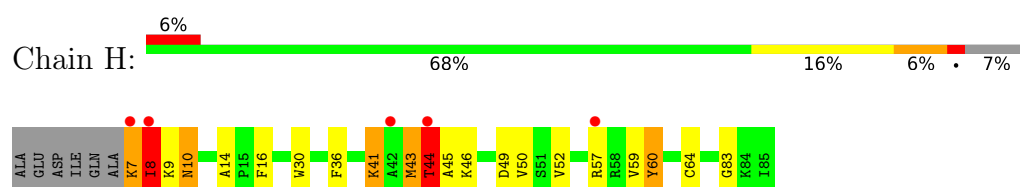
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



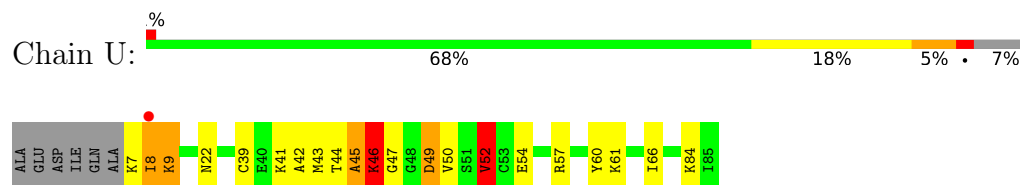
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



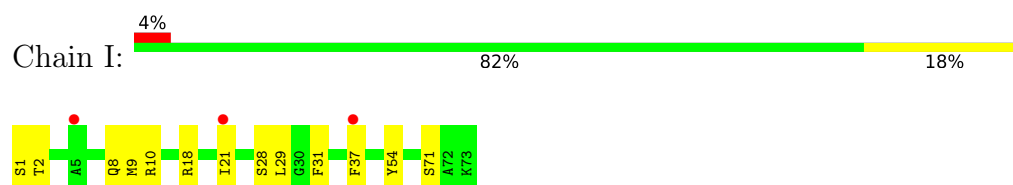
- Molecule 8: Cytochrome c oxidase subunit 6B1



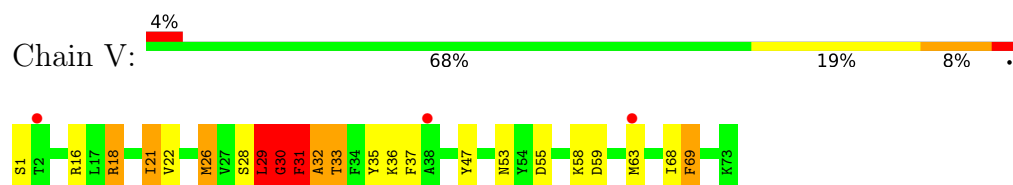
- Molecule 8: Cytochrome c oxidase subunit 6B1



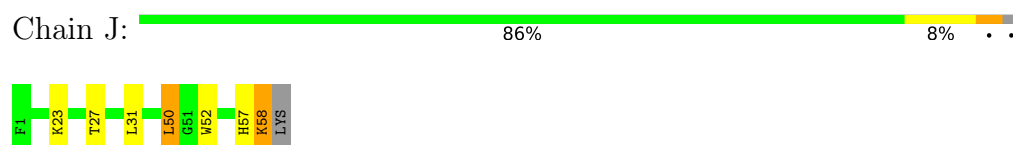
- Molecule 9: Cytochrome c oxidase subunit 6C



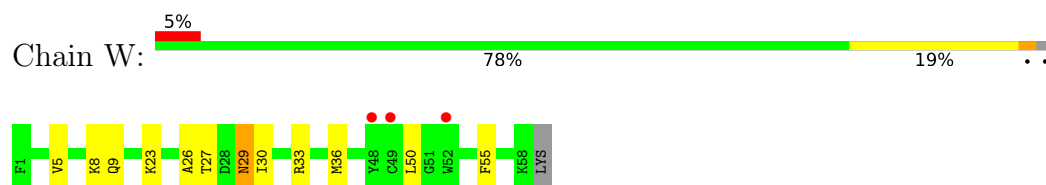
- Molecule 9: Cytochrome c oxidase subunit 6C



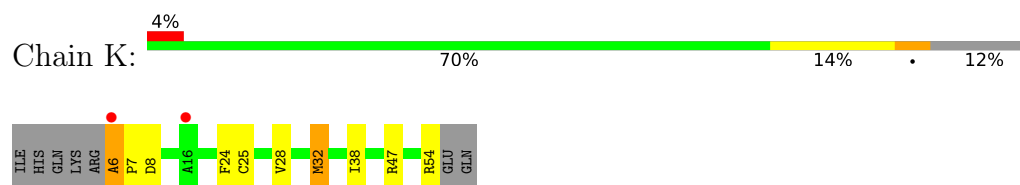
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



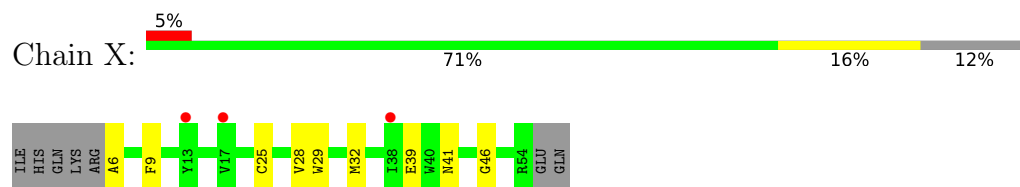
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



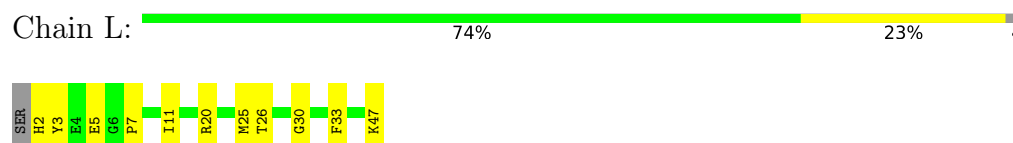
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



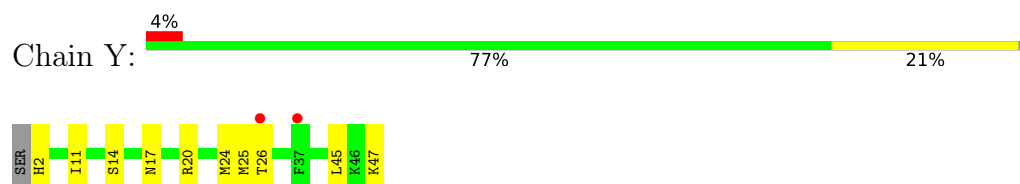
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



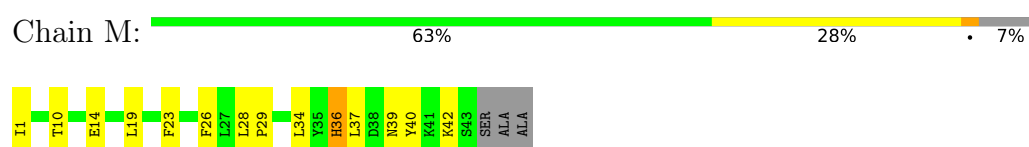
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



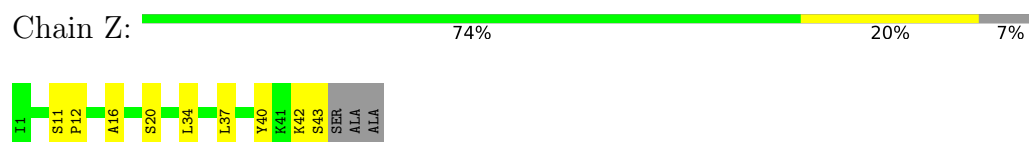
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



- 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	184.81Å 208.49Å 177.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.20 25.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.9 (25.00-2.20) 96.9 (25.00-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.8.0048	Depositor
R, R_{free}	0.172 , 0.209 (Not available) , 0.184	Depositor DCC
R_{free} test set	17153 reflections (1.36%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.036 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	32099	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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: DMU, ZN, CMO, CUA, FME, SAC, CDL, CU, NA, TGL, PGV, HEA, EDO, CHD, PSC, PEK, UNX, MG, 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	1.45	20/4164 (0.5%)	1.24	12/5689 (0.2%)
1	N	1.38	15/4156 (0.4%)	1.24	15/5678 (0.3%)
2	B	1.33	7/1860 (0.4%)	1.27	9/2534 (0.4%)
2	O	1.24	10/1860 (0.5%)	1.25	5/2534 (0.2%)
3	C	1.41	8/2197 (0.4%)	1.23	9/3005 (0.3%)
3	P	1.37	9/2197 (0.4%)	1.18	8/3005 (0.3%)
4	D	1.20	3/1229 (0.2%)	1.15	2/1658 (0.1%)
4	Q	1.00	1/1229 (0.1%)	1.09	2/1658 (0.1%)
5	E	1.16	0/871	1.15	2/1182 (0.2%)
5	R	1.05	1/871 (0.1%)	1.12	2/1182 (0.2%)
6	F	1.31	0/765	1.28	3/1038 (0.3%)
6	S	1.22	1/765 (0.1%)	1.28	4/1038 (0.4%)
7	G	1.42	2/690 (0.3%)	1.28	8/937 (0.9%)
7	T	1.33	2/690 (0.3%)	1.21	4/937 (0.4%)
8	H	1.20	0/682	1.25	5/921 (0.5%)
8	U	1.06	0/682	1.22	5/921 (0.5%)
9	I	1.08	0/605	1.21	2/802 (0.2%)
9	V	0.93	0/605	1.31	3/802 (0.4%)
10	J	1.11	0/471	1.13	0/636
10	W	1.01	0/471	1.11	1/636 (0.2%)
11	K	1.20	0/398	1.17	3/546 (0.5%)
11	X	0.99	0/398	1.20	2/546 (0.4%)
12	L	1.26	0/393	1.27	2/526 (0.4%)
12	Y	1.14	0/393	1.16	0/526
13	M	1.20	1/345 (0.3%)	1.17	1/470 (0.2%)
13	Z	1.10	0/345	1.21	1/470 (0.2%)
All	All	1.29	80/29332 (0.3%)	1.22	110/39877 (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
2	B	0	1
2	O	0	2
6	S	0	1
7	G	0	1
7	T	0	1
9	V	0	2
All	All	0	8

The worst 5 of 80 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	204	HIS	ND1-CE1	10.76	1.43	1.32
1	N	290	HIS	CG-CD2	7.79	1.44	1.35
1	N	378	HIS	ND1-CE1	7.50	1.40	1.32
2	B	204	HIS	CG-CD2	7.44	1.44	1.35
1	A	350	VAL	CA-C	7.34	1.61	1.52

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	V	31	PHE	N-CA-C	-17.88	91.94	111.07
7	T	3	ALA	N-CA-C	11.40	125.97	108.42
1	N	172	LYS	CA-C-N	-9.01	113.08	119.66
1	N	172	LYS	C-N-CA	-9.01	113.08	119.66
7	G	57	THR	N-CA-C	-8.21	103.41	113.50

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	91	ASN	Peptide
7	G	10	GLY	Peptide
2	O	90	ILE	Peptide
2	O	91	ASN	Peptide
6	S	93	PRO	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	4030	0	4008	69	0
1	N	4027	0	4001	91	0
2	B	1824	0	1833	38	0
2	O	1824	0	1833	58	0
3	C	2110	0	2027	36	0
3	P	2110	0	2027	26	0
4	D	1195	0	1183	21	0
4	Q	1195	0	1183	33	0
5	E	852	0	845	8	0
5	R	852	0	845	13	0
6	F	748	0	728	27	0
6	S	748	0	728	12	0
7	G	675	0	643	32	0
7	T	675	0	644	25	0
8	H	662	0	623	17	0
8	U	662	0	623	20	0
9	I	601	0	613	8	0
9	V	601	0	613	31	0
10	J	460	0	459	5	0
10	W	460	0	459	9	0
11	K	384	0	366	11	0
11	X	384	0	366	9	0
12	L	380	0	380	14	0
12	Y	380	0	380	16	0
13	M	335	0	352	12	0
13	Z	335	0	352	3	0
14	A	120	0	108	7	0
14	N	120	0	108	8	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	2	0	0	1	0
18	N	2	0	0	2	0
19	A	63	0	110	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	D	63	0	110	10	0
19	L	63	0	110	11	0
19	N	63	0	110	4	0
19	Q	63	0	110	6	0
19	Y	63	0	110	16	0
20	A	102	0	152	7	0
20	C	102	0	152	8	0
20	N	102	0	152	5	0
20	P	51	0	76	1	0
20	Z	51	0	76	5	0
21	A	16	0	24	11	0
21	B	4	0	6	0	0
21	C	16	0	24	5	0
21	F	4	0	6	3	0
21	G	4	0	6	0	0
21	I	4	0	6	5	0
21	K	12	0	18	0	0
21	L	8	0	12	1	0
21	N	12	0	18	0	0
21	P	8	0	12	2	0
21	S	4	0	6	1	0
21	T	4	0	6	1	0
21	X	4	0	6	0	0
22	B	2	0	0	0	0
22	O	2	0	0	0	0
23	B	29	0	39	1	0
23	C	58	0	78	1	0
23	G	29	0	39	0	0
23	J	29	0	39	1	0
23	P	58	0	78	5	0
23	W	29	0	39	2	0
24	B	52	0	80	2	0
24	O	52	0	80	5	0
25	B	53	0	77	1	0
25	C	106	0	154	4	0
25	G	106	0	154	9	0
25	T	53	0	77	4	0
26	C	1	0	0	0	0
26	P	1	0	0	1	0
27	C	100	0	156	10	0
27	G	100	0	156	16	0
27	P	100	0	156	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	T	100	0	156	16	0
28	F	1	0	0	0	0
28	S	1	0	0	0	0
29	M	33	0	42	0	0
29	Z	33	0	42	1	0
30	A	170	0	0	27	0
30	B	114	0	0	10	0
30	C	85	0	0	13	0
30	D	80	0	0	5	0
30	E	30	0	0	2	0
30	F	54	0	0	4	0
30	G	33	0	0	6	0
30	H	42	0	0	7	0
30	I	22	0	0	2	0
30	J	19	0	0	1	0
30	K	26	0	0	4	0
30	L	20	0	0	6	0
30	M	20	0	0	4	0
30	N	164	0	0	22	0
30	O	96	0	0	19	0
30	P	74	0	0	4	0
30	Q	43	0	0	7	0
30	R	39	0	0	6	0
30	S	54	0	0	2	0
30	T	35	0	0	8	0
30	U	30	0	0	2	0
30	V	22	0	0	0	0
30	W	21	0	0	1	0
30	X	12	0	0	6	0
30	Y	14	0	0	1	0
30	Z	7	0	0	2	0
All	All	32099	0	31390	695	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 11.

The worst 5 of 695 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)
13:M:26:PHE:HB2	30:M:201:HOH:O	1.24	1.26
1:N:466:MET:HG2	30:N:795:HOH:O	1.35	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:14:ALA:HB2	30:H:107:HOH:O	1.33	1.25
11:X:28:VAL:HG13	30:X:205:HOH:O	1.35	1.22
1:N:466:MET:HA	30:N:795:HOH:O	1.40	1.21

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	513/514 (100%)	500 (98%)	13 (2%)	0	100	100
1	N	512/514 (100%)	499 (98%)	12 (2%)	1 (0%)	43	51
2	B	225/227 (99%)	218 (97%)	6 (3%)	1 (0%)	30	34
2	O	225/227 (99%)	216 (96%)	6 (3%)	3 (1%)	9	8
3	C	257/261 (98%)	251 (98%)	6 (2%)	0	100	100
3	P	257/261 (98%)	248 (96%)	8 (3%)	1 (0%)	30	34
4	D	142/147 (97%)	139 (98%)	3 (2%)	0	100	100
4	Q	142/147 (97%)	132 (93%)	8 (6%)	2 (1%)	9	7
5	E	103/109 (94%)	101 (98%)	2 (2%)	0	100	100
5	R	103/109 (94%)	100 (97%)	3 (3%)	0	100	100
6	F	96/98 (98%)	83 (86%)	9 (9%)	4 (4%)	2	1
6	S	96/98 (98%)	89 (93%)	4 (4%)	3 (3%)	3	1
7	G	81/85 (95%)	70 (86%)	8 (10%)	3 (4%)	2	1
7	T	81/85 (95%)	70 (86%)	6 (7%)	5 (6%)	1	0
8	H	77/85 (91%)	68 (88%)	6 (8%)	3 (4%)	2	1
8	U	77/85 (91%)	69 (90%)	6 (8%)	2 (3%)	4	2
9	I	71/73 (97%)	69 (97%)	1 (1%)	1 (1%)	9	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	V	71/73 (97%)	64 (90%)	4 (6%)	3 (4%)	2	1
10	J	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
10	W	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
11	K	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
11	X	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
12	L	44/47 (94%)	44 (100%)	0	0	100	100
12	Y	44/47 (94%)	41 (93%)	3 (7%)	0	100	100
13	M	41/46 (89%)	40 (98%)	0	1 (2%)	4	3
13	Z	41/46 (89%)	39 (95%)	2 (5%)	0	100	100
All	All	3505/3614 (97%)	3351 (96%)	121 (4%)	33 (1%)	14	14

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	94	HIS
6	F	96	LEU
6	F	97	ALA
7	G	4	ALA
8	H	8	ILE

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	427/426 (100%)	412 (96%)	15 (4%)	32	43
1	N	426/426 (100%)	412 (97%)	14 (3%)	33	45
2	B	210/210 (100%)	201 (96%)	9 (4%)	26	35
2	O	210/210 (100%)	191 (91%)	19 (9%)	9	9
3	C	224/226 (99%)	221 (99%)	3 (1%)	61	76
3	P	224/226 (99%)	221 (99%)	3 (1%)	61	76
4	D	128/129 (99%)	121 (94%)	7 (6%)	19	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Q	128/129 (99%)	120 (94%)	8 (6%)	16	19
5	E	92/95 (97%)	90 (98%)	2 (2%)	45	61
5	R	92/95 (97%)	85 (92%)	7 (8%)	12	14
6	F	81/81 (100%)	78 (96%)	3 (4%)	30	41
6	S	81/81 (100%)	74 (91%)	7 (9%)	10	10
7	G	67/68 (98%)	65 (97%)	2 (3%)	36	49
7	T	67/68 (98%)	58 (87%)	9 (13%)	4	3
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%)	53 (93%)	4 (7%)	14	16
9	V	57/57 (100%)	51 (90%)	6 (10%)	6	6
10	J	49/50 (98%)	45 (92%)	4 (8%)	10	12
10	W	49/50 (98%)	45 (92%)	4 (8%)	10	12
11	K	39/46 (85%)	37 (95%)	2 (5%)	21	27
11	X	39/46 (85%)	39 (100%)	0	100	100
12	L	39/40 (98%)	36 (92%)	3 (8%)	12	13
12	Y	39/40 (98%)	38 (97%)	1 (3%)	40	55
13	M	37/38 (97%)	35 (95%)	2 (5%)	20	25
13	Z	37/38 (97%)	34 (92%)	3 (8%)	11	12
All	All	3041/3082 (99%)	2892 (95%)	149 (5%)	22	29

5 of 149 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	S	54	ASN
10	W	29	ASN
6	S	96	LEU
8	U	46	LYS
9	I	21	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	180	GLN

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Mol	Chain	Res	Type
8	U	22	ASN
2	O	181	GLN
7	T	76	ASN
5	R	94	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$
1	FME	N	1	1	8,9,10	0.62	0	8,9,11	1.24	0
7	TPO	T	11	7	8,10,11	1.65	2 (25%)	10,14,16	1.28	2 (20%)
9	SAC	V	1	9	7,8,9	1.36	1 (14%)	7,9,11	1.84	1 (14%)
7	TPO	G	11	7	8,10,11	2.18	2 (25%)	10,14,16	0.97	0
1	FME	A	1	1	8,9,10	0.59	0	8,9,11	1.33	2 (25%)
9	SAC	I	1	9	7,8,9	1.14	1 (14%)	7,9,11	1.57	2 (28%)
2	FME	B	1	2	8,9,10	1.07	1 (12%)	8,9,11	1.05	0
2	FME	O	1	2	8,9,10	1.12	1 (12%)	8,9,11	1.30	1 (12%)

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
1	FME	N	1	1	-	3/7/9/11	-
7	TPO	T	11	7	-	7/9/11/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	SAC	V	1	9	-	3/7/8/10	-
7	TPO	G	11	7	-	3/9/11/13	-
1	FME	A	1	1	-	4/7/9/11	-
9	SAC	I	1	9	-	4/7/8/10	-
2	FME	B	1	2	-	1/7/9/11	-
2	FME	O	1	2	-	0/7/9/11	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	11	TPO	P-OG1	3.80	1.66	1.59
7	G	11	TPO	P-O1P	3.57	1.61	1.50
9	V	1	SAC	CA-N	3.40	1.51	1.46
7	T	11	TPO	P-O1P	2.82	1.59	1.50
9	I	1	SAC	CA-N	2.72	1.50	1.46

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	V	1	SAC	C-CA-N	4.08	117.36	109.50
9	I	1	SAC	C-CA-N	3.24	115.75	109.50
1	A	1	FME	C-CA-N	2.66	114.63	109.50
7	T	11	TPO	CG2-CB-CA	2.50	118.14	113.26
7	T	11	TPO	O2P-P-OG1	2.25	114.64	105.85

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	C-CA-CB-CG
7	G	11	TPO	N-CA-CB-OG1
7	G	11	TPO	CA-CB-OG1-P
9	I	1	SAC	C2A-C1A-N-CA
9	I	1	SAC	OAC-C1A-N-CA

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	T	11	TPO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	FME	1	0
2	O	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 79 ligands modelled in this entry, 8 are monoatomic and 2 are unknown - leaving 69 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	$\# Z > 2$
21	EDO	C	311	-	3,3,3	0.40	0	2,2,2	0.53	0
21	EDO	A	610	-	3,3,3	0.61	0	2,2,2	0.38	0
23	CHD	C	305	-	32,32,32	1.07	3 (9%)	51,51,51	1.68	10 (19%)
29	DMU	Z	102	-	34,34,34	0.45	0	45,45,45	1.61	9 (20%)
29	DMU	M	101	-	34,34,34	0.60	1 (2%)	45,45,45	1.14	4 (8%)
20	PGV	N	608	-	50,50,50	1.11	2 (4%)	53,56,56	1.34	5 (9%)
21	EDO	N	610	-	3,3,3	0.70	0	2,2,2	0.05	0
21	EDO	F	102	-	3,3,3	0.59	0	2,2,2	0.27	0
27	CDL	C	303	-	99,99,99	1.50	13 (13%)	105,111,111	1.20	7 (6%)
19	TGL	L	101	-	62,62,62	1.22	3 (4%)	65,65,65	1.60	9 (13%)
14	HEA	A	602	1	67,67,67	2.13	21 (31%)	81,103,103	1.95	22 (27%)
14	HEA	N	602	18,1	67,67,67	2.12	22 (32%)	81,103,103	1.91	23 (28%)
19	TGL	Y	101	-	62,62,62	1.27	3 (4%)	65,65,65	1.28	7 (10%)
21	EDO	B	305	-	3,3,3	0.55	0	2,2,2	0.16	0
21	EDO	P	306	-	3,3,3	0.70	0	2,2,2	0.49	0
19	TGL	D	201	-	62,62,62	1.25	4 (6%)	65,65,65	1.26	6 (9%)
23	CHD	P	304	-	32,32,32	0.79	1 (3%)	51,51,51	1.64	12 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CHD	G	104	-	32,32,32	0.97	1 (3%)	51,51,51	1.63	14 (27%)
14	HEA	N	601	1	67,67,67	2.15	26 (38%)	81,103,103	1.42	9 (11%)
27	CDL	P	303	-	99,99,99	1.48	12 (12%)	105,111,111	1.29	11 (10%)
18	CMO	A	606	15	0,1,1	-	-	-	-	-
21	EDO	K	102	-	3,3,3	0.41	0	2,2,2	0.56	0
20	PGV	A	609	-	50,50,50	1.15	2 (4%)	53,56,56	1.11	6 (11%)
21	EDO	A	612	-	3,3,3	0.58	0	2,2,2	0.55	0
23	CHD	J	101	-	32,32,32	1.05	1 (3%)	51,51,51	2.18	20 (39%)
18	CMO	N	606	14	0,1,1	-	-	-	-	-
21	EDO	C	309	-	3,3,3	0.69	0	2,2,2	0.28	0
21	EDO	I	101	-	3,3,3	0.70	0	2,2,2	0.28	0
21	EDO	K	103	-	3,3,3	0.48	0	2,2,2	0.46	0
21	EDO	N	612	-	3,3,3	0.68	0	2,2,2	0.56	0
25	PEK	C	308	-	52,52,52	1.04	2 (3%)	55,57,57	1.00	3 (5%)
23	CHD	P	305	-	32,32,32	0.99	0	51,51,51	1.92	10 (19%)
20	PGV	C	307	-	50,50,50	1.07	2 (4%)	53,56,56	1.00	3 (5%)
21	EDO	P	307	-	3,3,3	0.56	0	2,2,2	0.14	0
22	CUA	O	301	2,30	0,1,1	-	-	-	-	-
20	PGV	N	607	-	50,50,50	0.97	2 (4%)	53,56,56	1.30	5 (9%)
24	PSC	O	302	-	51,51,51	1.25	3 (5%)	57,59,59	1.13	4 (7%)
20	PGV	A	608	-	50,50,50	0.89	3 (6%)	53,56,56	1.43	7 (13%)
25	PEK	C	306	-	52,52,52	1.14	2 (3%)	55,57,57	1.12	5 (9%)
20	PGV	P	302	-	50,50,50	0.89	3 (6%)	53,56,56	1.29	9 (16%)
14	HEA	A	601	1	67,67,67	1.95	21 (31%)	81,103,103	1.94	22 (27%)
20	PGV	Z	101	-	50,50,50	1.13	2 (4%)	53,56,56	1.13	4 (7%)
25	PEK	B	304	-	52,52,52	1.19	2 (3%)	55,57,57	1.07	3 (5%)
21	EDO	C	312	-	3,3,3	0.48	0	2,2,2	0.17	0
27	CDL	T	102	-	99,99,99	1.43	12 (12%)	105,111,111	1.24	10 (9%)
23	CHD	C	304	-	32,32,32	0.73	0	51,51,51	2.40	18 (35%)
21	EDO	N	611	-	3,3,3	0.53	0	2,2,2	0.12	0
25	PEK	G	101	-	52,52,52	0.87	3 (5%)	55,57,57	1.41	5 (9%)
19	TGL	A	607	-	62,62,62	1.23	4 (6%)	65,65,65	1.53	7 (10%)
21	EDO	G	105	-	3,3,3	0.56	0	2,2,2	0.31	0
21	EDO	K	101	-	3,3,3	0.49	0	2,2,2	0.38	0
23	CHD	B	302	-	32,32,32	1.00	2 (6%)	51,51,51	1.67	15 (29%)
24	PSC	B	303	-	51,51,51	1.20	3 (5%)	57,59,59	1.07	2 (3%)
27	CDL	G	102	-	99,99,99	1.45	12 (12%)	105,111,111	1.28	12 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	PEK	G	103	-	52,52,52	1.15	2 (3%)	55,57,57	1.10	4 (7%)
19	TGL	N	609	-	62,62,62	1.19	3 (4%)	65,65,65	1.38	9 (13%)
21	EDO	A	611	-	3,3,3	0.46	0	2,2,2	0.35	0
21	EDO	C	310	-	3,3,3	0.47	0	2,2,2	0.33	0
21	EDO	L	103	-	3,3,3	0.55	0	2,2,2	0.03	0
21	EDO	X	101	-	3,3,3	0.54	0	2,2,2	0.17	0
21	EDO	A	613	-	3,3,3	0.52	0	2,2,2	0.43	0
21	EDO	S	102	-	3,3,3	0.78	0	2,2,2	0.27	0
22	CUA	B	301	2,30	0,1,1	-	-	-	-	-
25	PEK	T	101	-	52,52,52	0.99	3 (5%)	55,57,57	1.19	5 (9%)
20	PGV	C	302	-	50,50,50	0.89	2 (4%)	53,56,56	1.17	6 (11%)
21	EDO	L	102	-	3,3,3	0.43	0	2,2,2	0.46	0
23	CHD	W	101	-	32,32,32	0.84	0	51,51,51	2.20	21 (41%)
19	TGL	Q	201	-	62,62,62	1.22	3 (4%)	65,65,65	1.02	6 (9%)
21	EDO	T	103	-	3,3,3	0.64	0	2,2,2	0.14	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
21	EDO	C	311	-	-	1/1/1/1	-
21	EDO	A	610	-	-	0/1/1/1	-
23	CHD	C	305	-	-	0/9/74/74	0/4/4/4
29	DMU	Z	102	-	-	7/19/59/59	0/2/2/2
29	DMU	M	101	-	-	7/19/59/59	0/2/2/2
20	PGV	N	608	-	-	23/55/55/55	-
21	EDO	N	610	-	-	0/1/1/1	-
21	EDO	F	102	-	-	0/1/1/1	-
27	CDL	C	303	-	-	65/110/110/110	-
19	TGL	L	101	-	-	34/65/65/65	-
14	HEA	A	602	1	-	6/36/76/76	-
14	HEA	N	602	18,1	-	9/36/76/76	-
19	TGL	Y	101	-	-	37/65/65/65	-
21	EDO	B	305	-	-	0/1/1/1	-
21	EDO	P	306	-	-	0/1/1/1	-
19	TGL	D	201	-	-	29/65/65/65	-
23	CHD	P	304	-	-	4/9/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CHD	G	104	-	-	3/9/74/74	0/4/4/4
14	HEA	N	601	1	-	4/36/76/76	-
27	CDL	P	303	-	-	71/110/110/110	-
21	EDO	K	102	-	-	1/1/1/1	-
20	PGV	A	609	-	-	28/55/55/55	-
21	EDO	A	612	-	-	1/1/1/1	-
23	CHD	J	101	-	-	7/9/74/74	0/4/4/4
21	EDO	I	101	-	-	1/1/1/1	-
21	EDO	C	309	-	-	0/1/1/1	-
21	EDO	K	103	-	-	1/1/1/1	-
21	EDO	N	612	-	-	0/1/1/1	-
25	PEK	C	308	-	-	31/56/56/56	-
23	CHD	P	305	-	-	3/9/74/74	0/4/4/4
20	PGV	C	307	-	-	32/55/55/55	-
21	EDO	P	307	-	-	1/1/1/1	-
20	PGV	N	607	-	-	11/55/55/55	-
24	PSC	O	302	-	-	23/55/55/55	-
20	PGV	A	608	-	-	20/55/55/55	-
25	PEK	C	306	-	-	25/56/56/56	-
20	PGV	P	302	-	-	12/55/55/55	-
14	HEA	A	601	1	-	4/36/76/76	-
20	PGV	Z	101	-	-	32/55/55/55	-
25	PEK	B	304	-	-	36/56/56/56	-
21	EDO	C	312	-	-	1/1/1/1	-
27	CDL	T	102	-	-	54/110/110/110	-
23	CHD	C	304	-	-	8/9/74/74	0/4/4/4
21	EDO	N	611	-	-	1/1/1/1	-
25	PEK	G	101	-	-	21/56/56/56	-
19	TGL	A	607	-	-	35/65/65/65	-
21	EDO	G	105	-	-	0/1/1/1	-
21	EDO	K	101	-	-	0/1/1/1	-
23	CHD	B	302	-	-	3/9/74/74	0/4/4/4
24	PSC	B	303	-	-	30/55/55/55	-
27	CDL	G	102	-	-	59/110/110/110	-
25	PEK	G	103	-	-	36/56/56/56	-
19	TGL	N	609	-	-	41/65/65/65	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	EDO	A	611	-	-	1/1/1/1	-
21	EDO	C	310	-	-	0/1/1/1	-
21	EDO	L	103	-	-	1/1/1/1	-
21	EDO	X	101	-	-	0/1/1/1	-
21	EDO	A	613	-	-	0/1/1/1	-
21	EDO	S	102	-	-	0/1/1/1	-
25	PEK	T	101	-	-	22/56/56/56	-
20	PGV	C	302	-	-	20/55/55/55	-
21	EDO	L	102	-	-	1/1/1/1	-
23	CHD	W	101	-	-	8/9/74/74	0/4/4/4
19	TGL	Q	201	-	-	34/65/65/65	-
21	EDO	T	103	-	-	1/1/1/1	-

The worst 5 of 206 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	602	HEA	FE-ND	6.67	2.15	1.94
19	L	101	TGL	OG2-CB1	5.99	1.51	1.34
19	Y	101	TGL	OG3-CC1	5.84	1.50	1.33
19	N	609	TGL	OG2-CB1	5.82	1.50	1.34
19	Y	101	TGL	OG2-CB1	5.48	1.49	1.34

The worst 5 of 369 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	101	CHD	C13-C17-C20	7.23	128.24	119.48
23	J	101	CHD	C13-C17-C20	7.03	128.00	119.48
19	L	101	TGL	OG2-CB1-CB2	6.97	126.57	111.48
23	P	305	CHD	C18-C13-C12	-6.89	102.16	109.06
19	N	609	TGL	OG2-CB1-CB2	6.39	125.31	111.48

There are no chirality outliers.

5 of 946 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	602	HEA	C2A-C3A-CMA-OMA
14	N	601	HEA	C2A-C3A-CMA-OMA
14	N	602	HEA	C2A-C3A-CMA-OMA
14	N	602	HEA	C4A-C3A-CMA-OMA
19	D	201	TGL	CB2-CB1-OG2-CG2

There are no ring outliers.

46 monomers are involved in 199 short contacts:

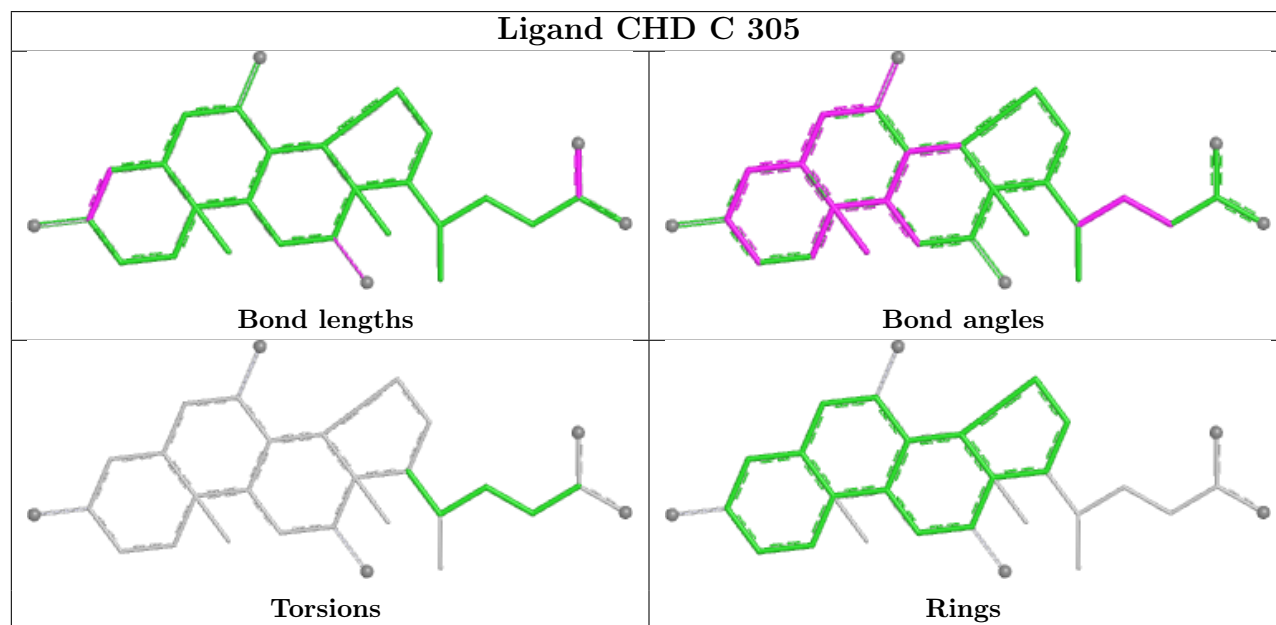
Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	Z	102	DMU	1	0
20	N	608	PGV	5	0
21	F	102	EDO	3	0
27	C	303	CDL	10	0
19	L	101	TGL	11	0
14	A	602	HEA	1	0
14	N	602	HEA	4	0
19	Y	101	TGL	16	0
19	D	201	TGL	10	0
23	P	304	CHD	4	0
14	N	601	HEA	4	0
27	P	303	CDL	6	0
18	A	606	CMO	1	0
20	A	609	PGV	7	0
21	A	612	EDO	2	0
23	J	101	CHD	1	0
18	N	606	CMO	2	0
21	C	309	EDO	1	0
21	I	101	EDO	5	0
25	C	308	PEK	3	0
23	P	305	CHD	1	0
20	C	307	PGV	5	0
21	P	307	EDO	2	0
24	O	302	PSC	5	0
25	C	306	PEK	1	0
20	P	302	PGV	1	0
14	A	601	HEA	6	0
20	Z	101	PGV	5	0
25	B	304	PEK	1	0
21	C	312	EDO	4	0
27	T	102	CDL	16	0
23	C	304	CHD	1	0
25	G	101	PEK	6	0
23	B	302	CHD	1	0
24	B	303	PSC	2	0
27	G	102	CDL	16	0
25	G	103	PEK	3	0
19	N	609	TGL	4	0
21	L	103	EDO	1	0
21	A	613	EDO	9	0

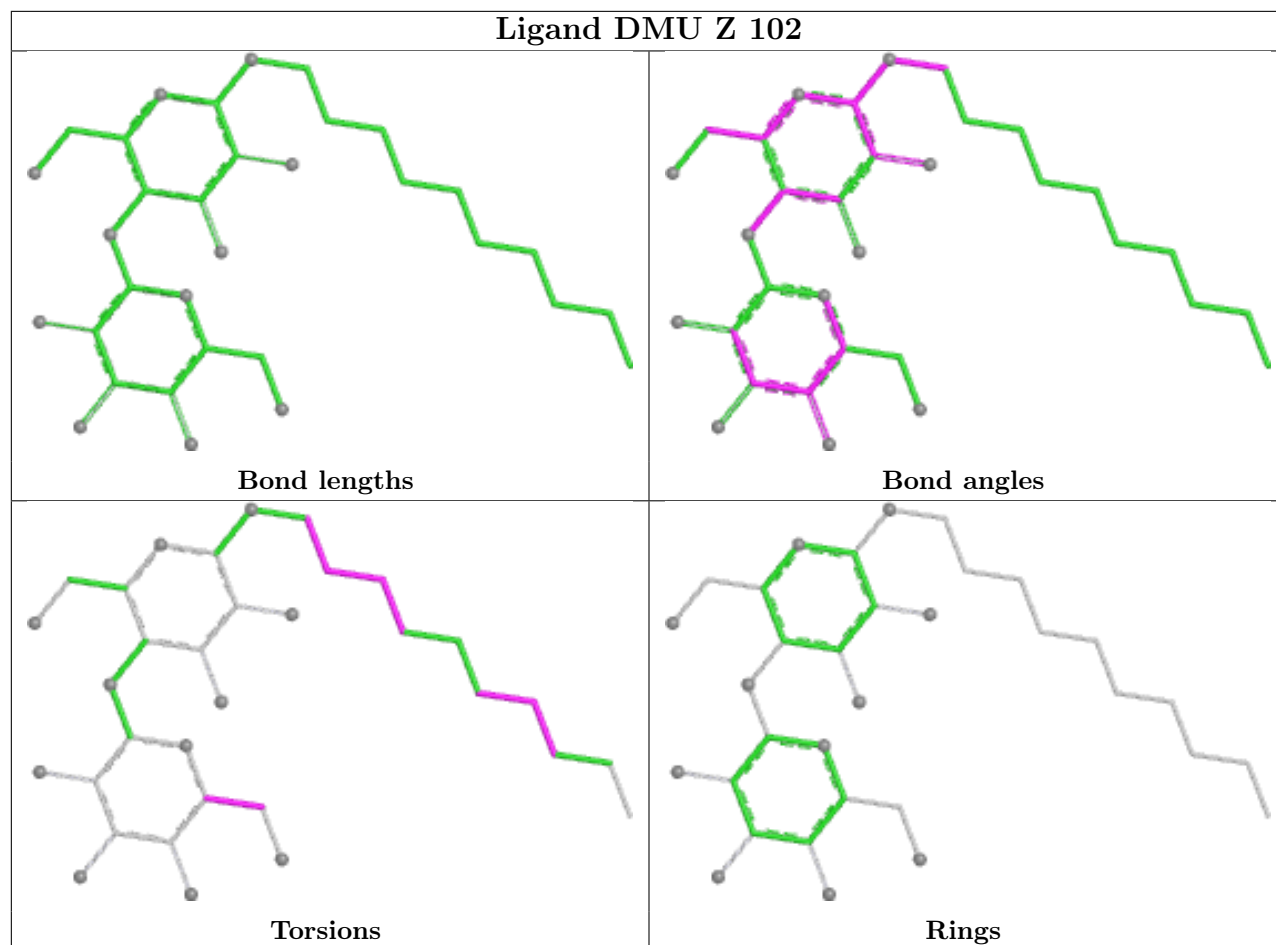
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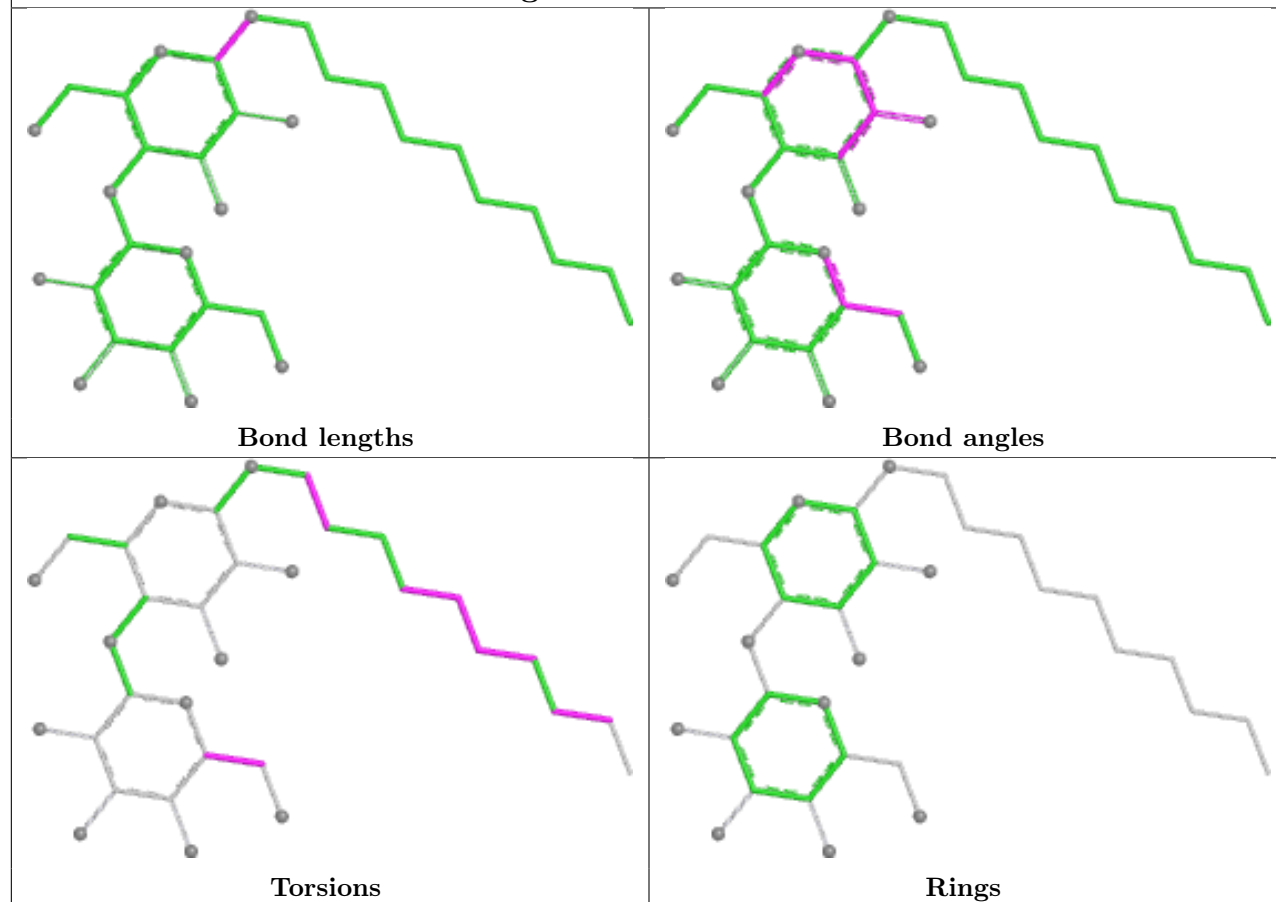
Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	S	102	EDO	1	0
25	T	101	PEK	4	0
20	C	302	PGV	3	0
23	W	101	CHD	2	0
19	Q	201	TGL	6	0
21	T	103	EDO	1	0

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.

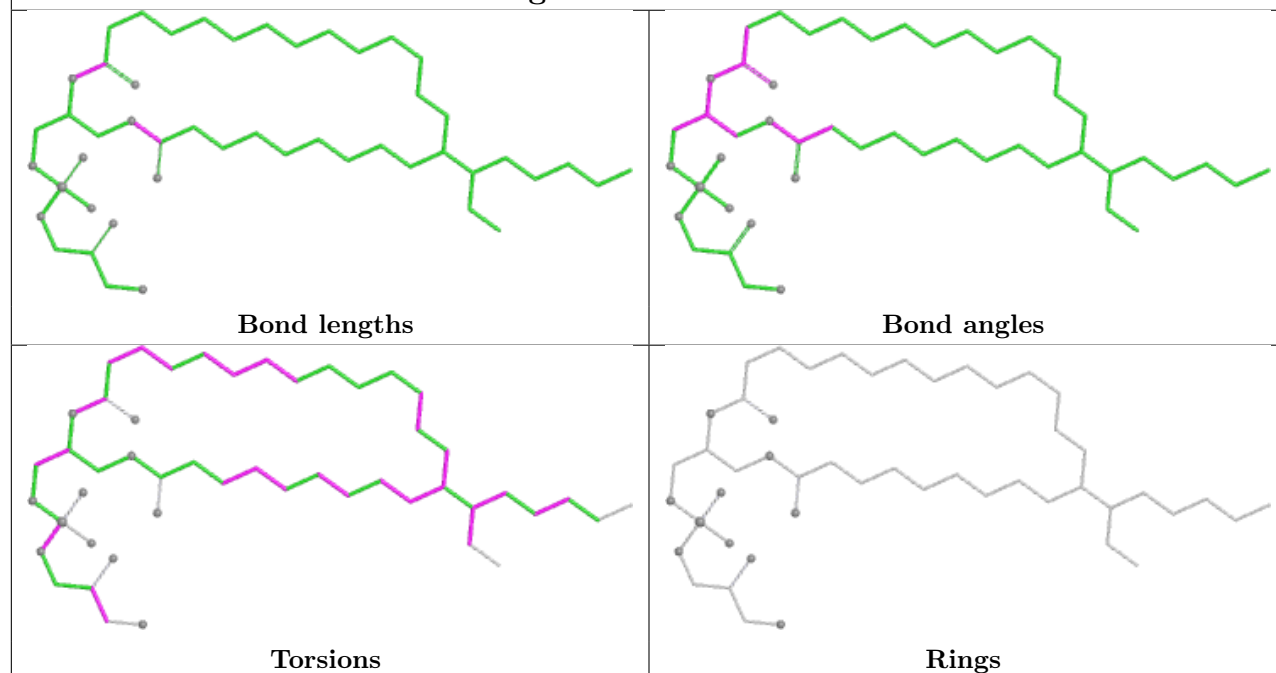


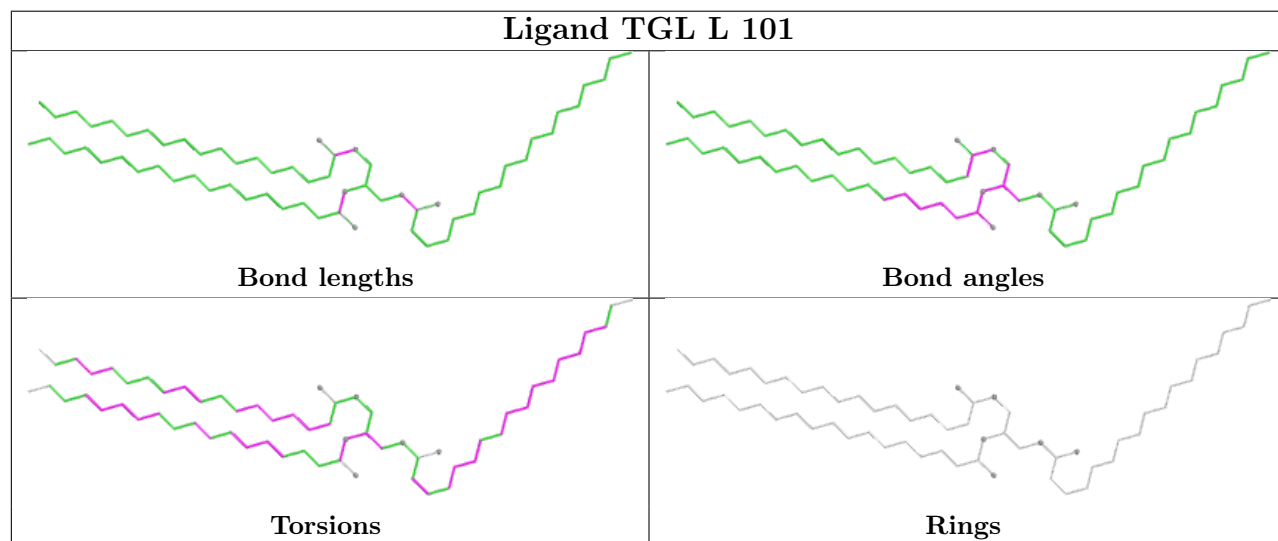
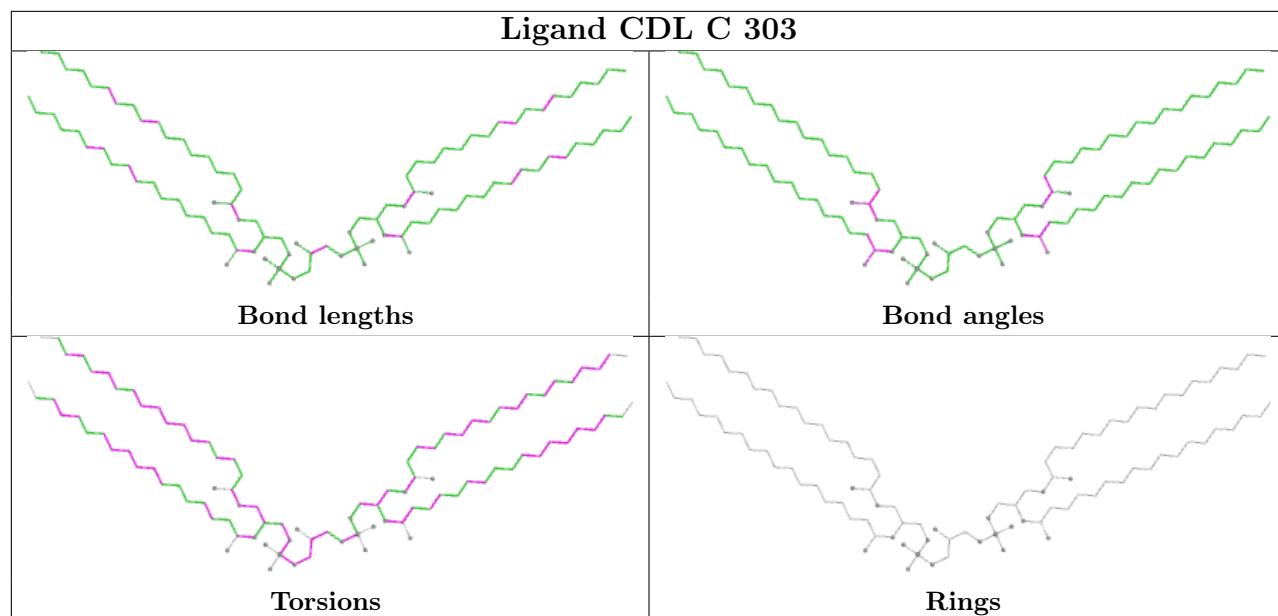


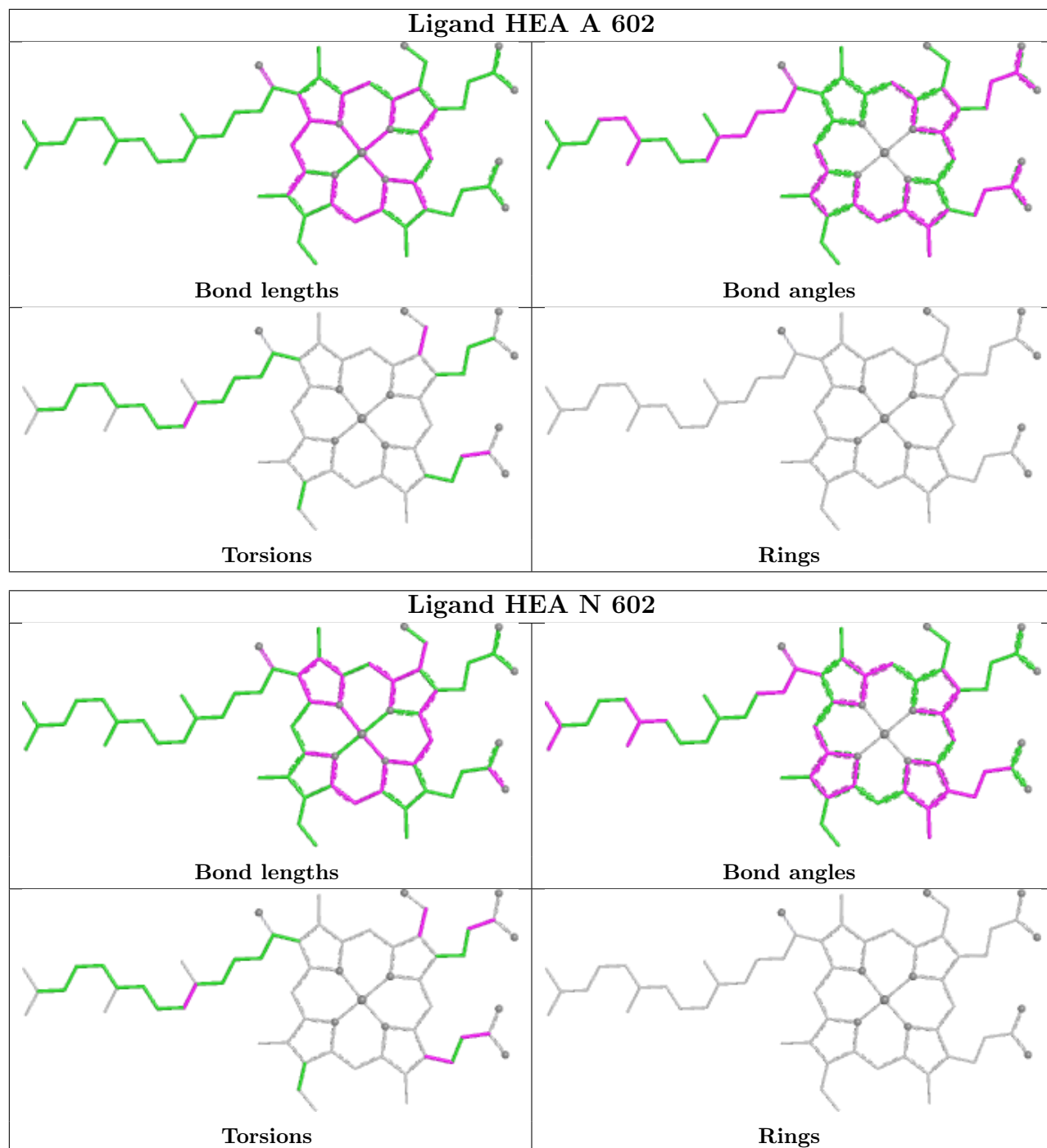
Ligand DMU M 101

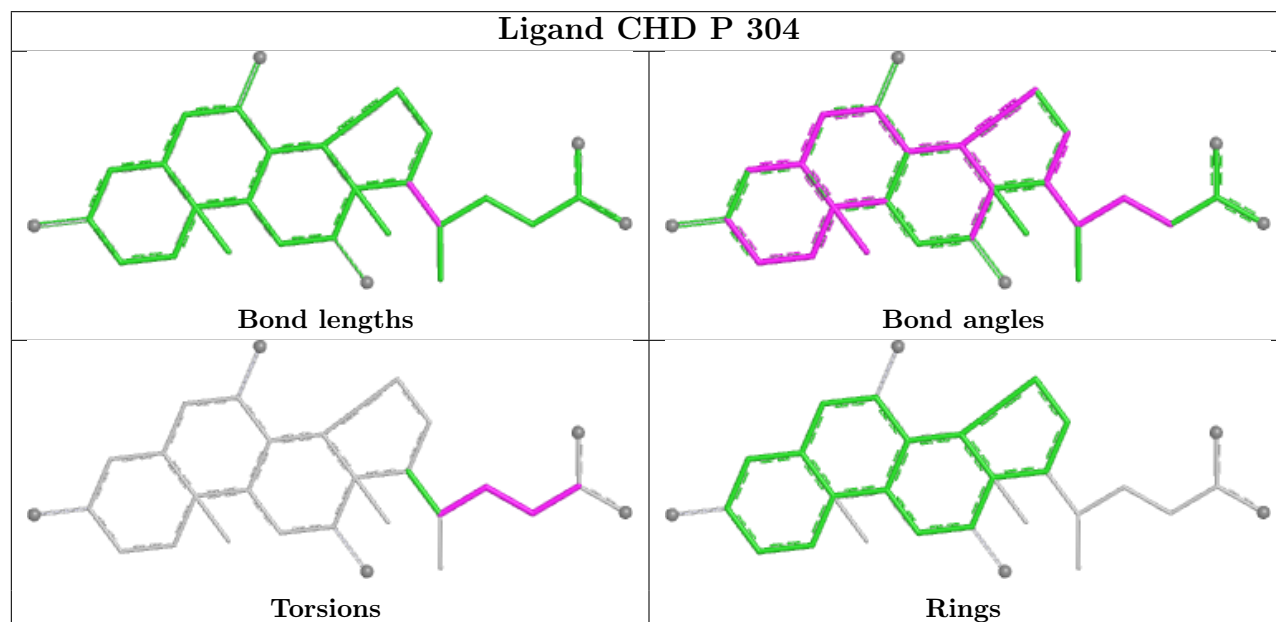
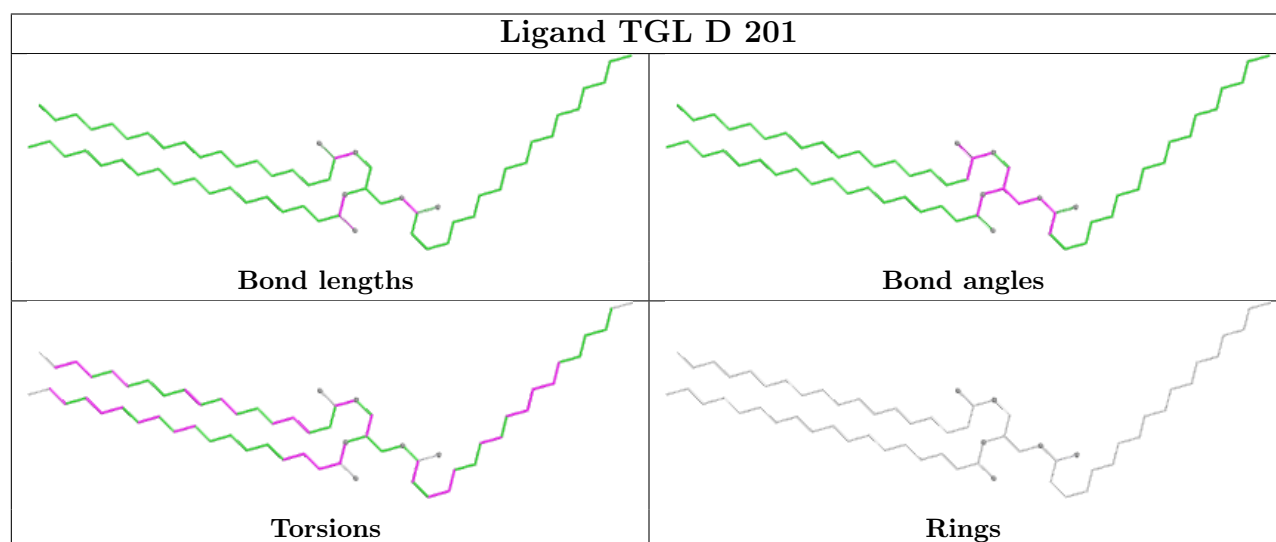
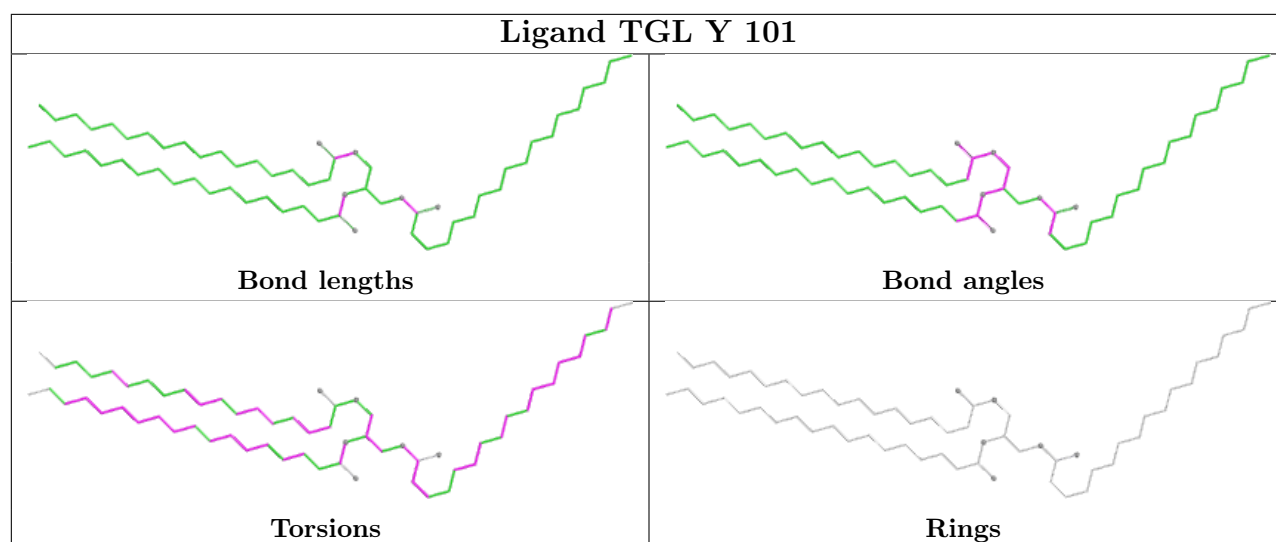


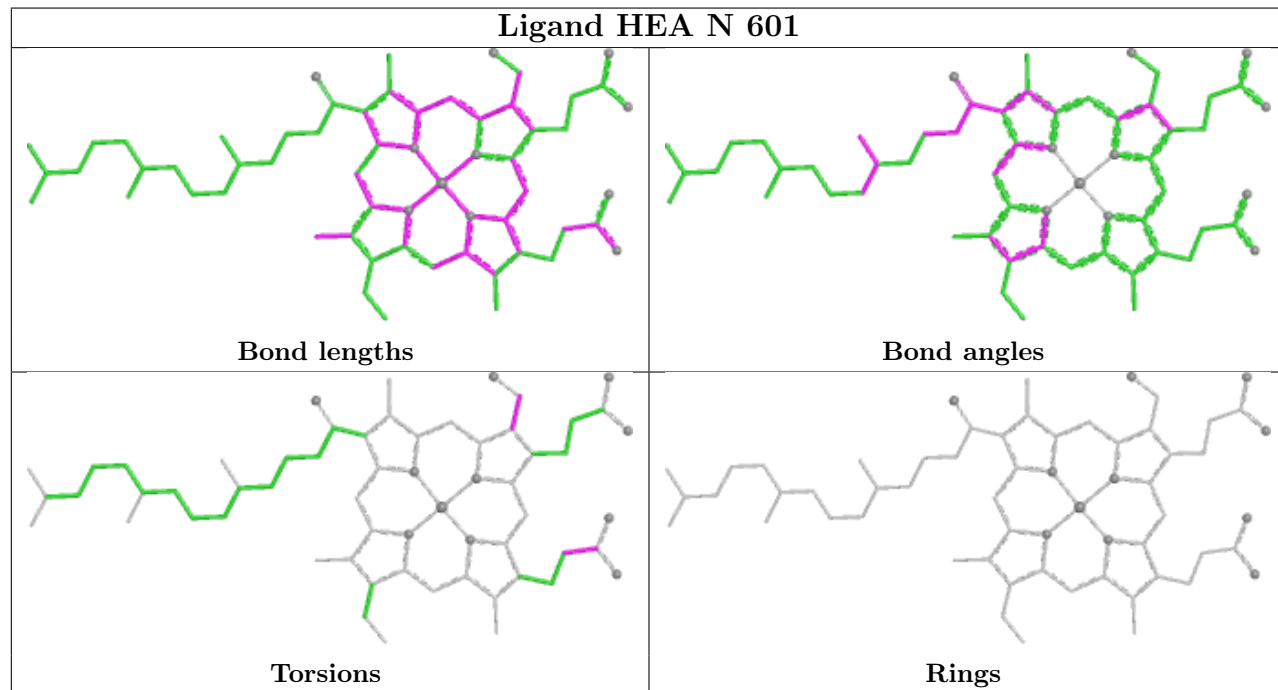
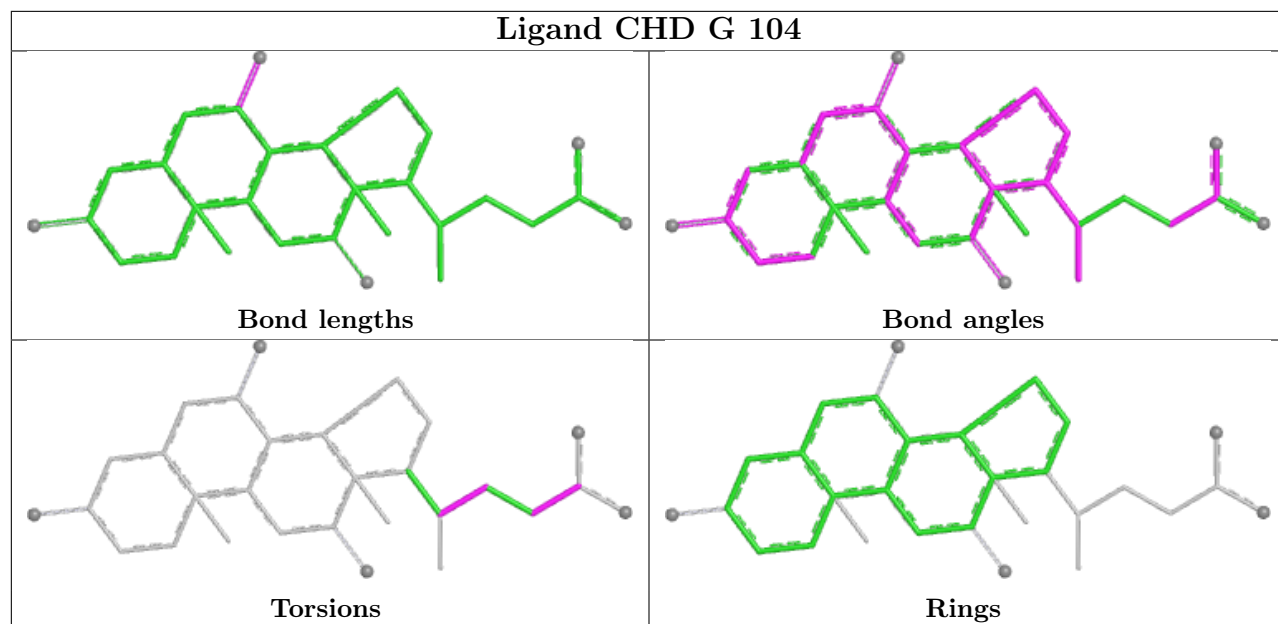
Ligand PGV N 608

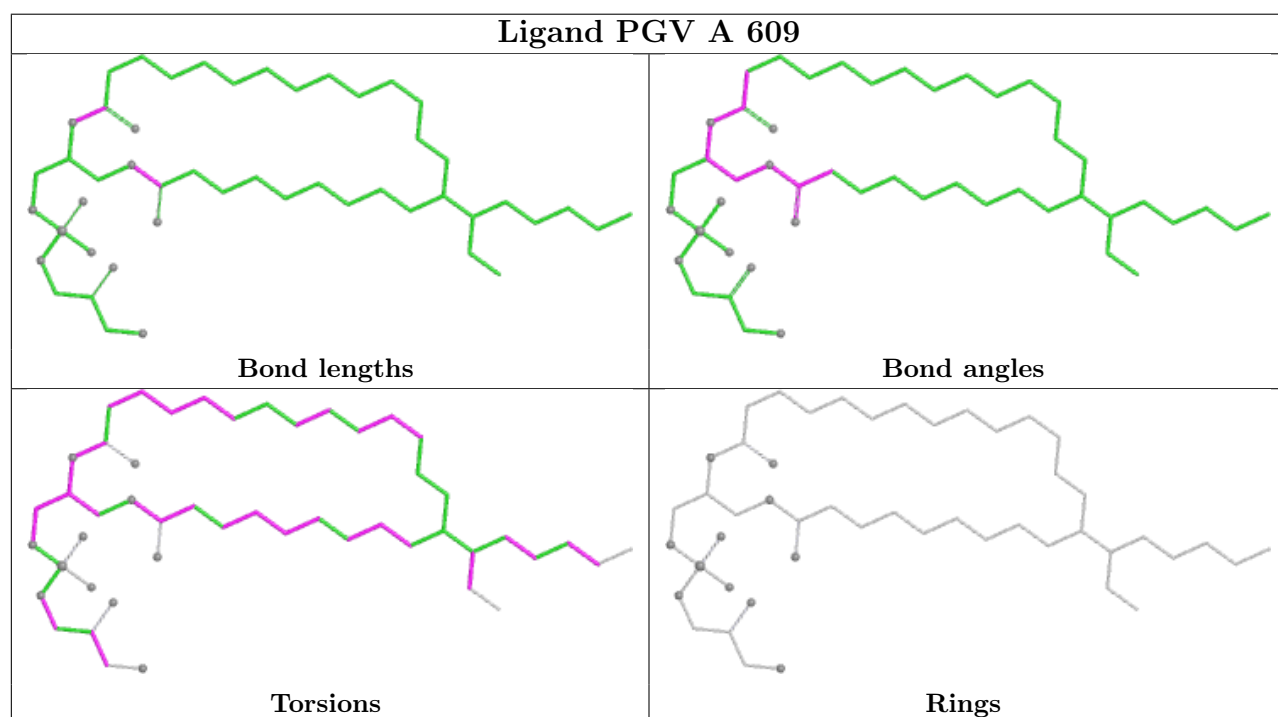
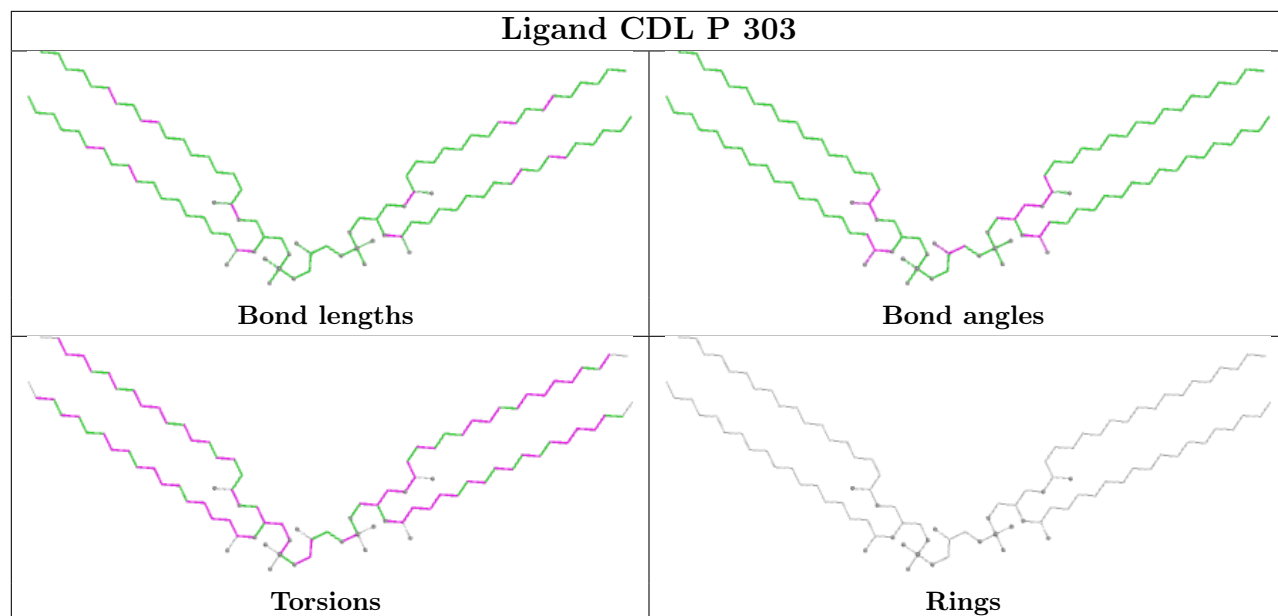




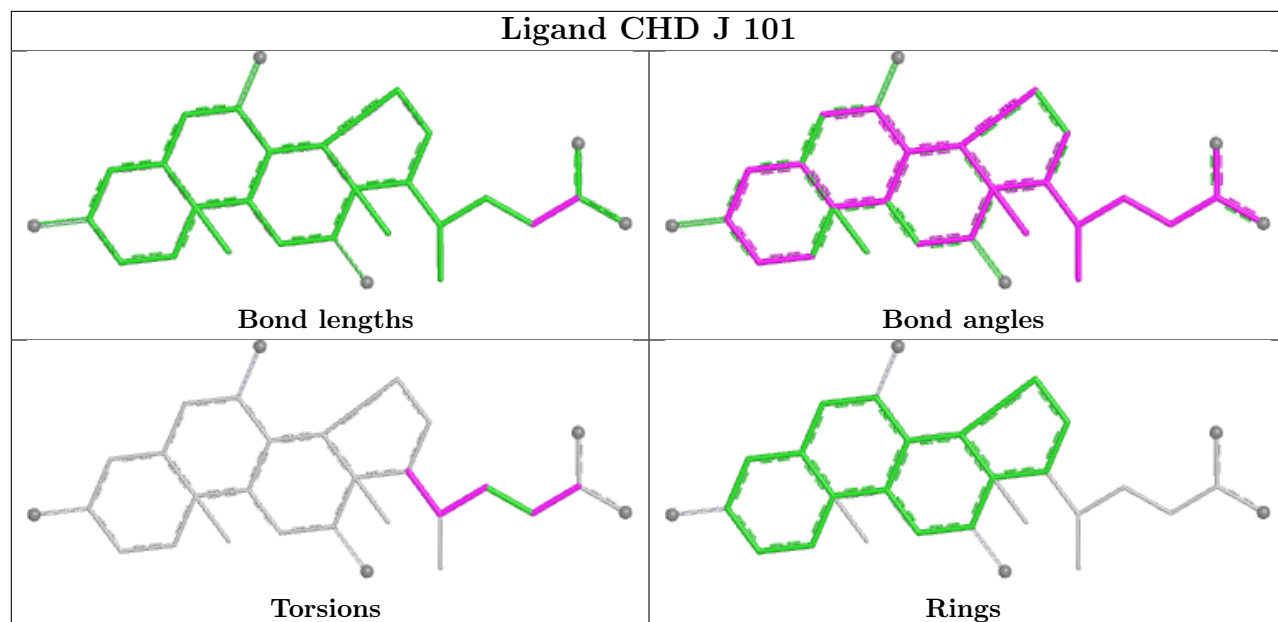




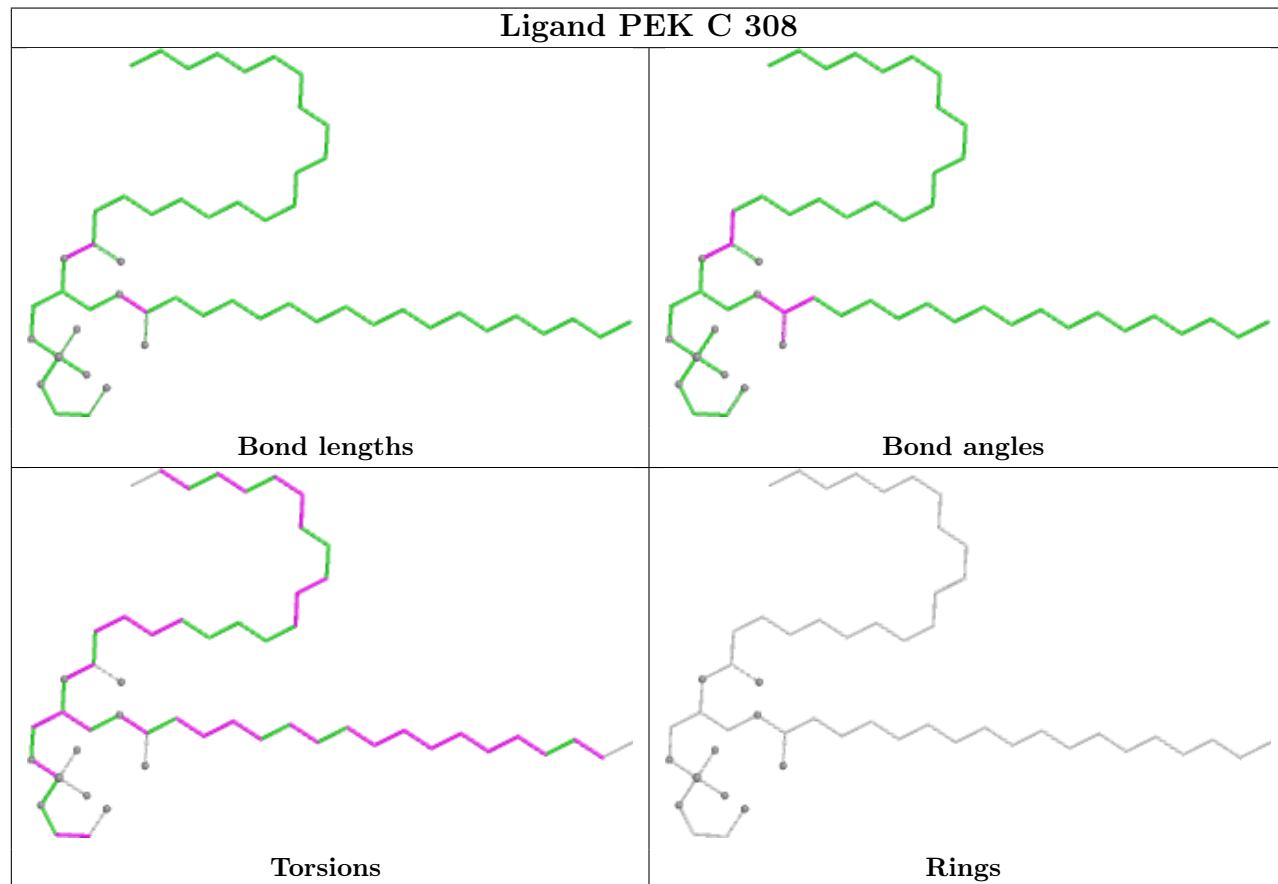


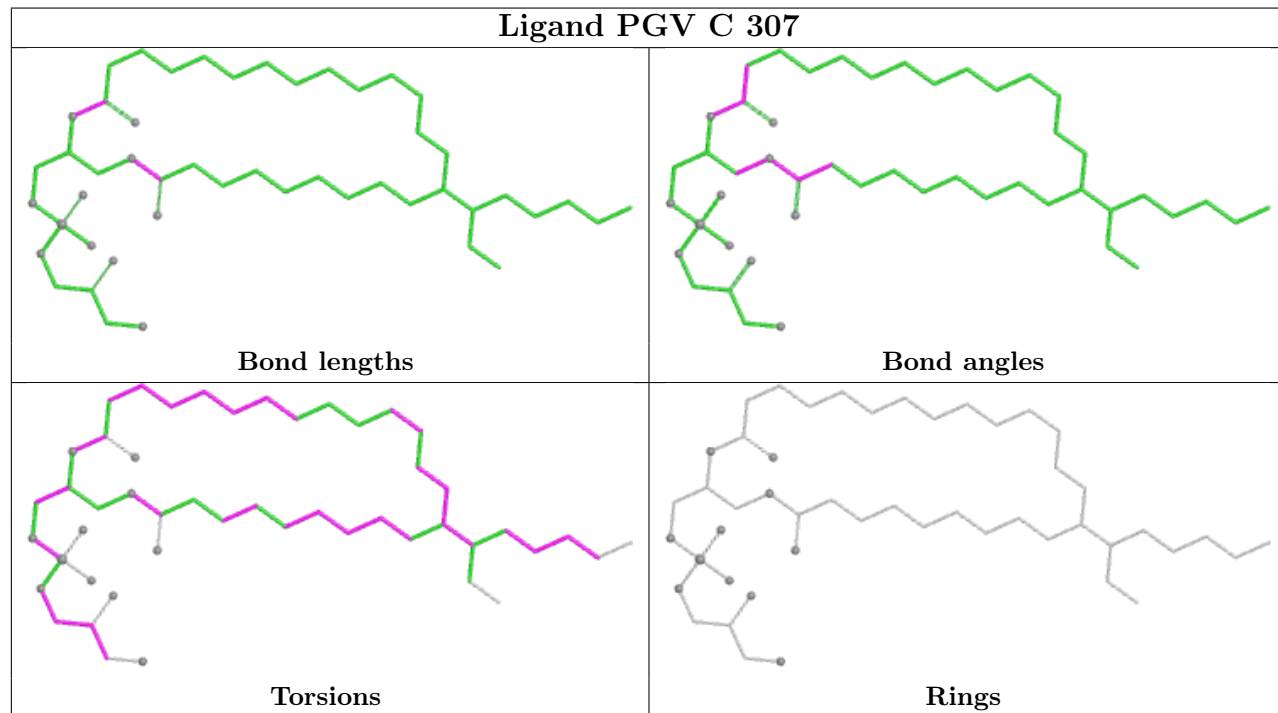
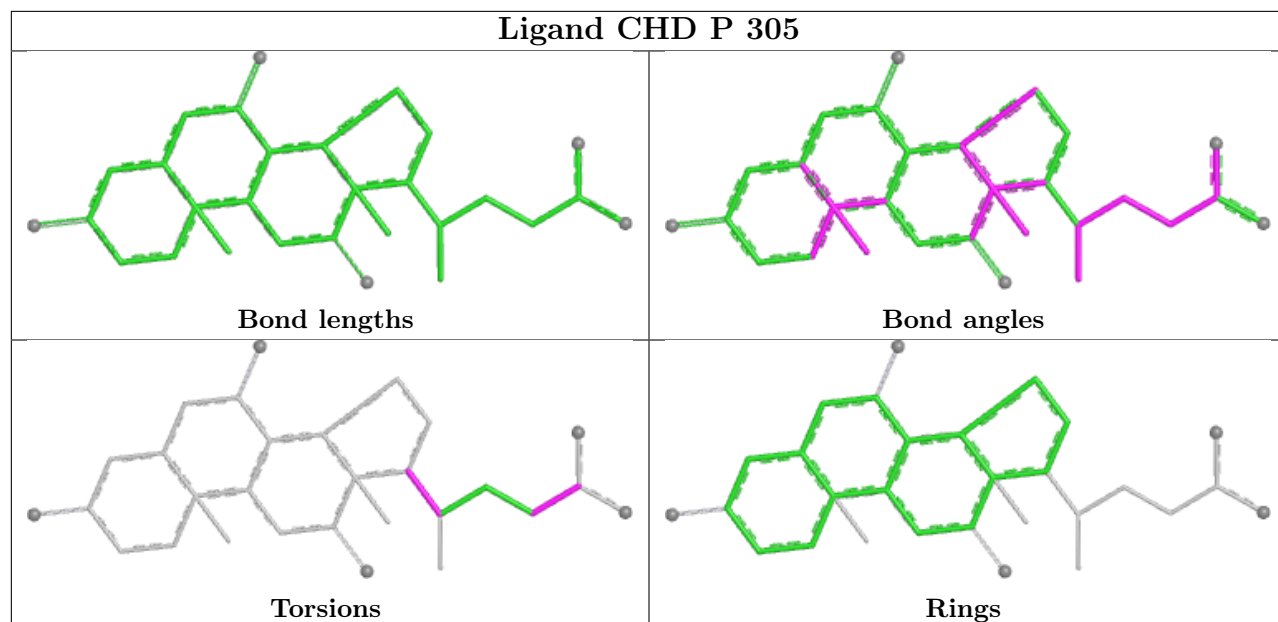


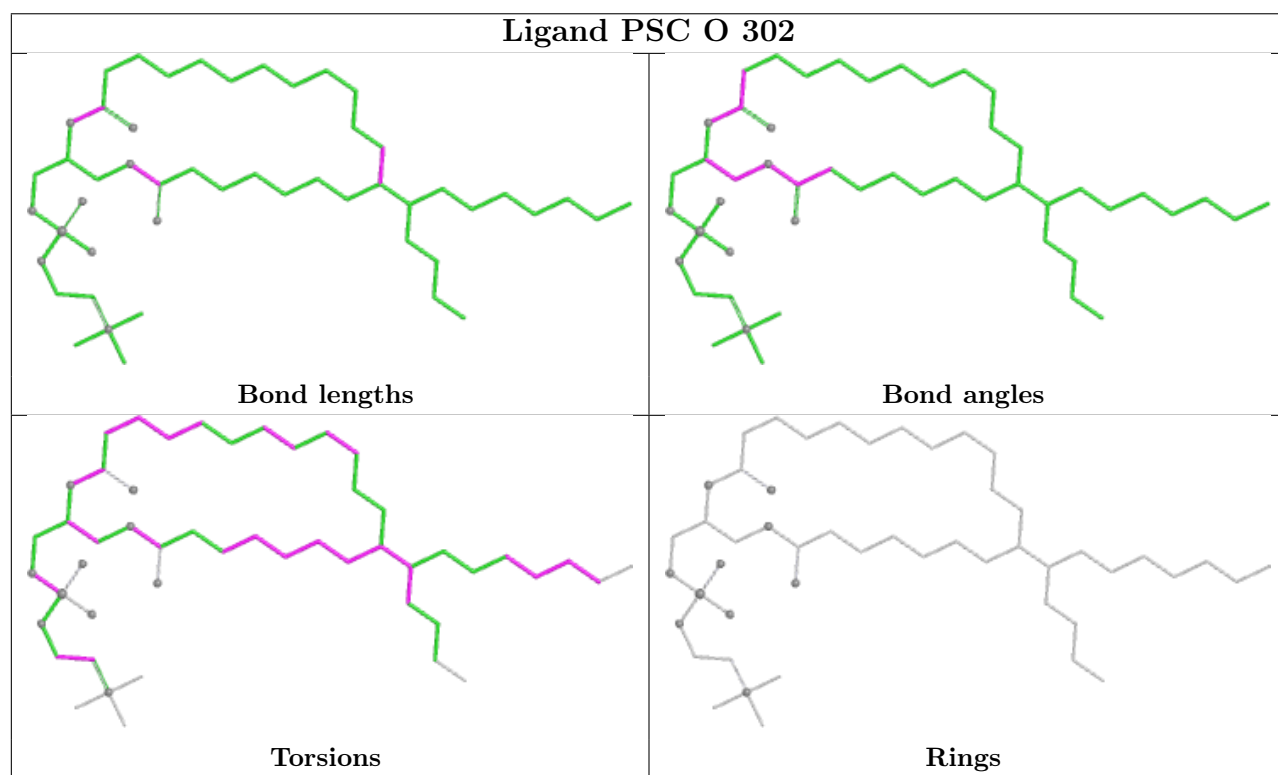
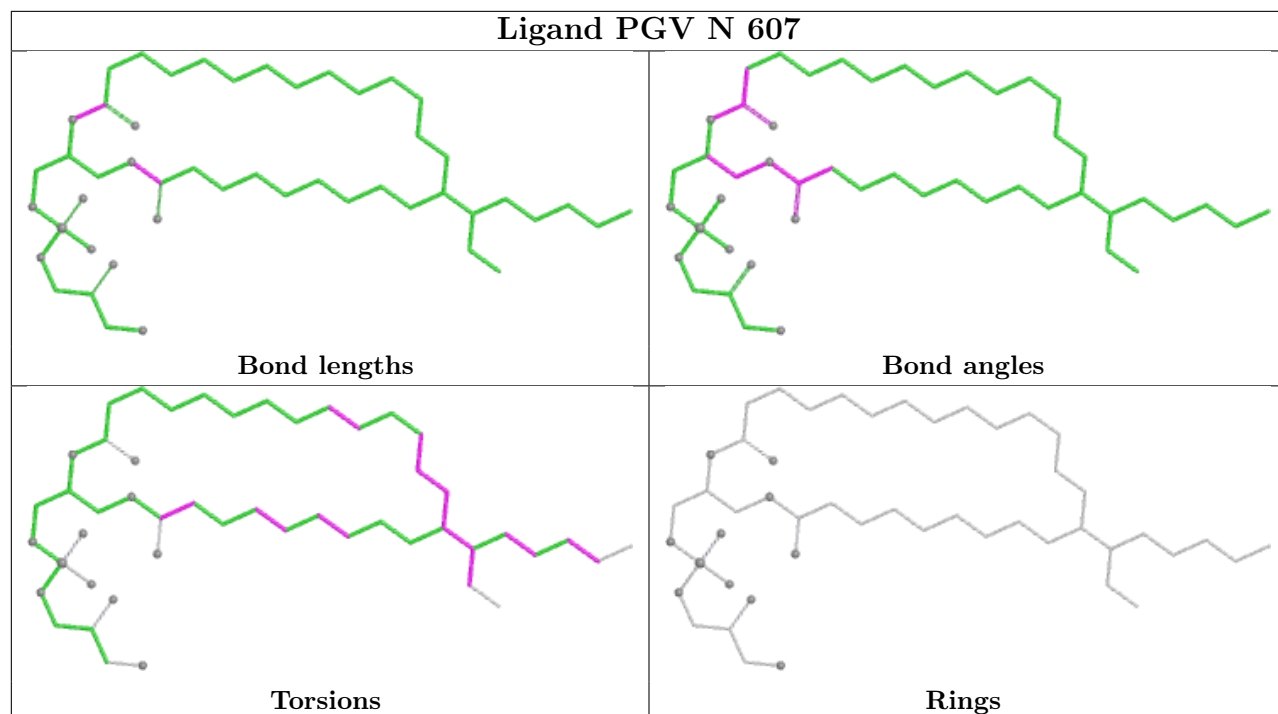
Ligand CHD J 101

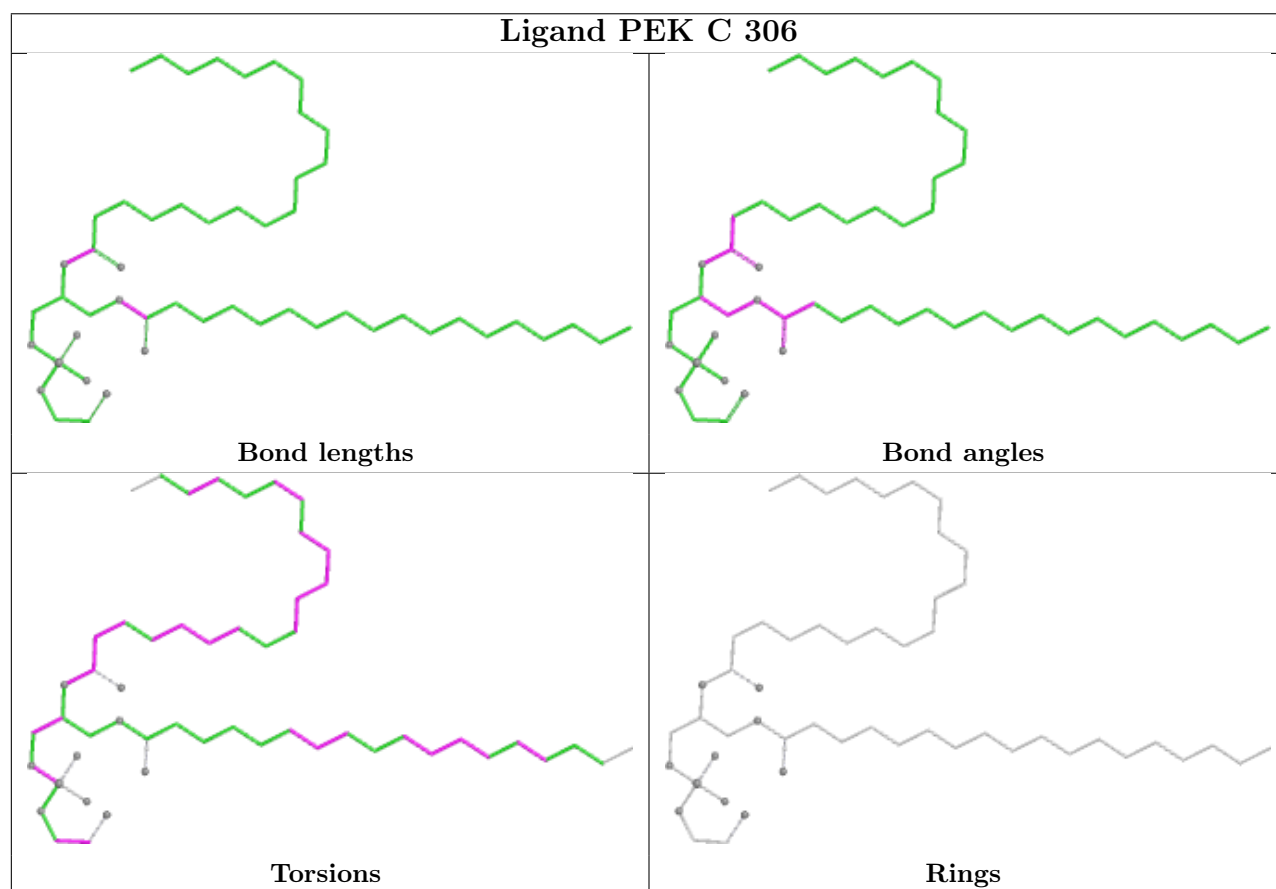
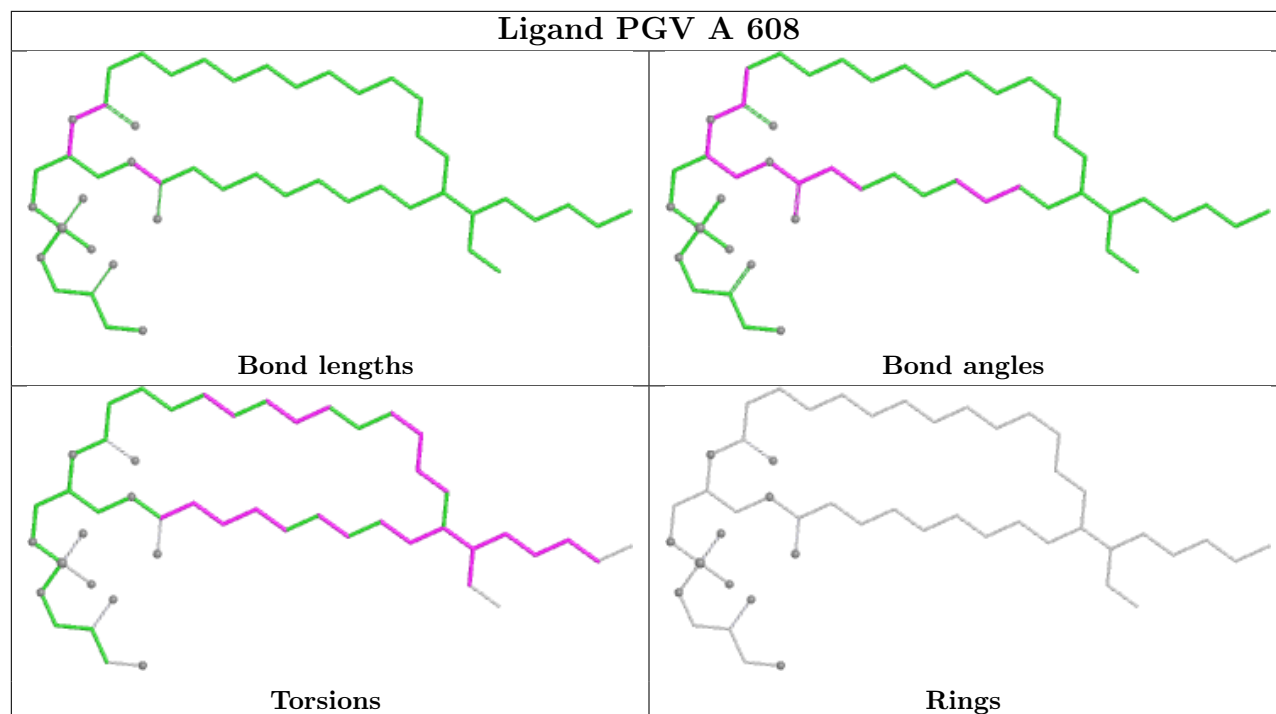


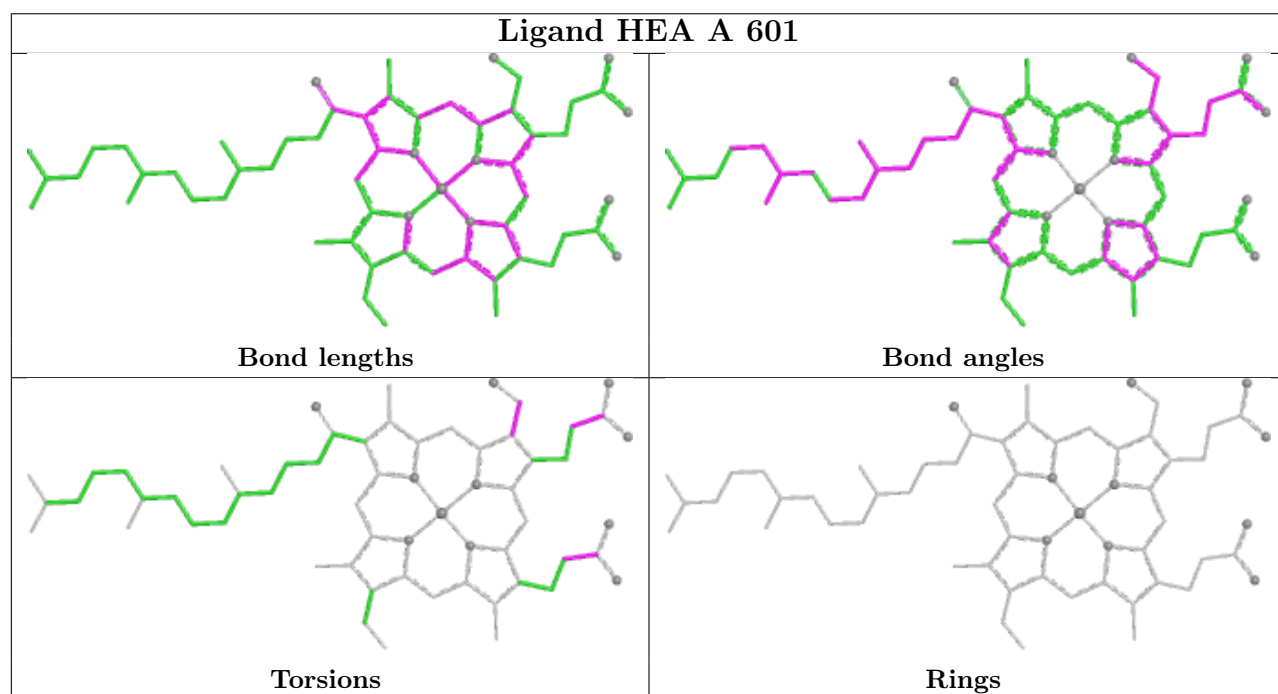
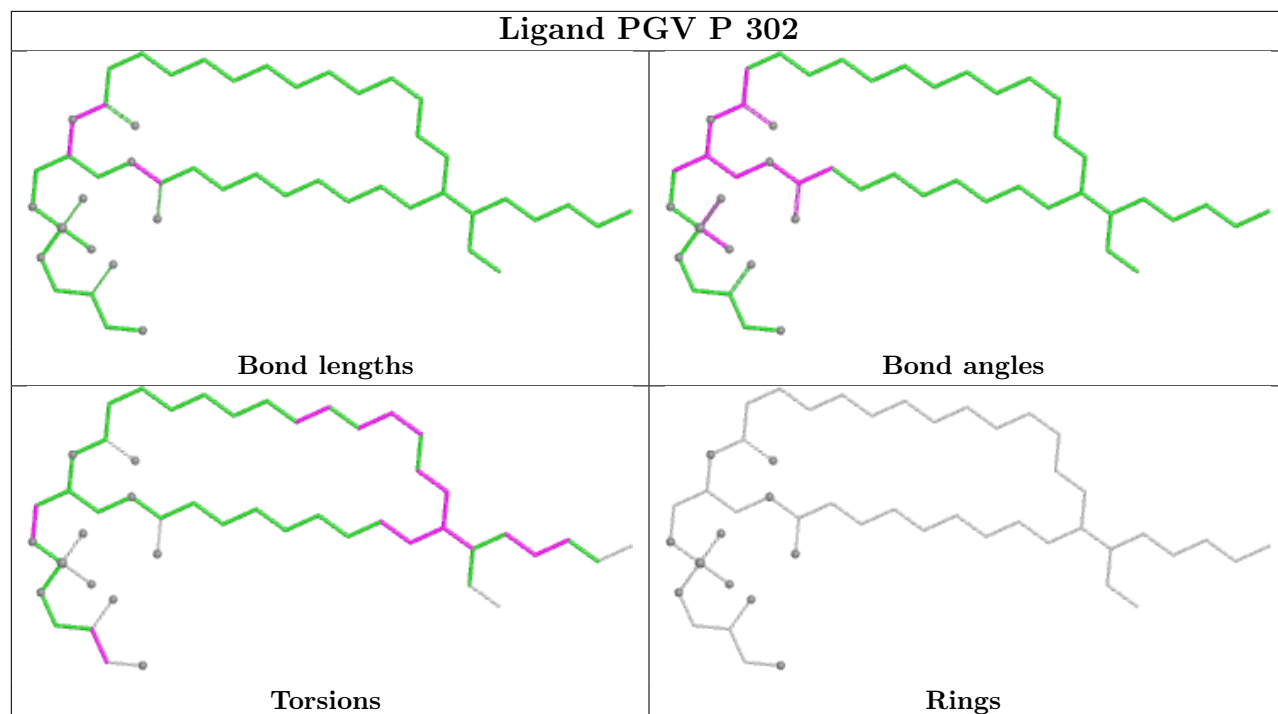
Ligand PEK C 308

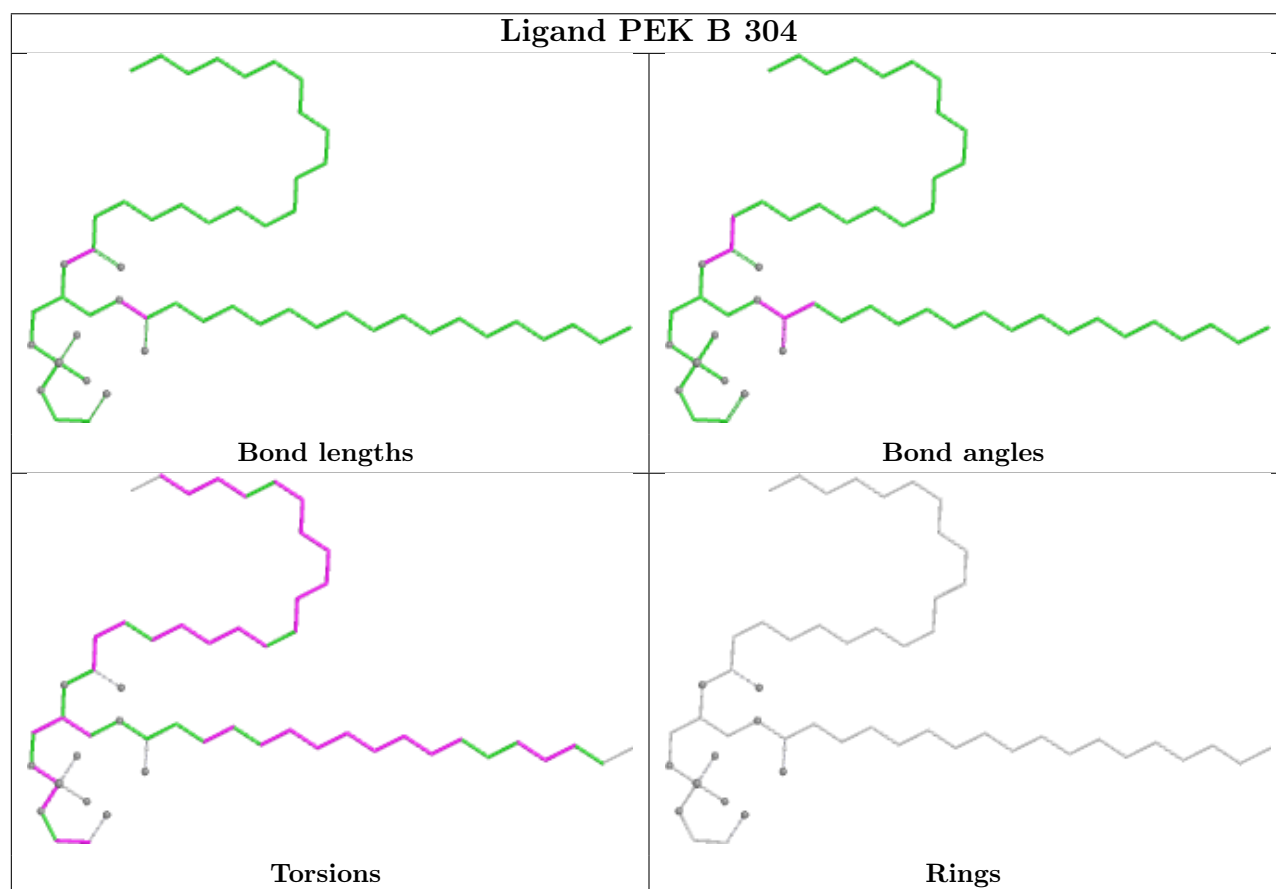
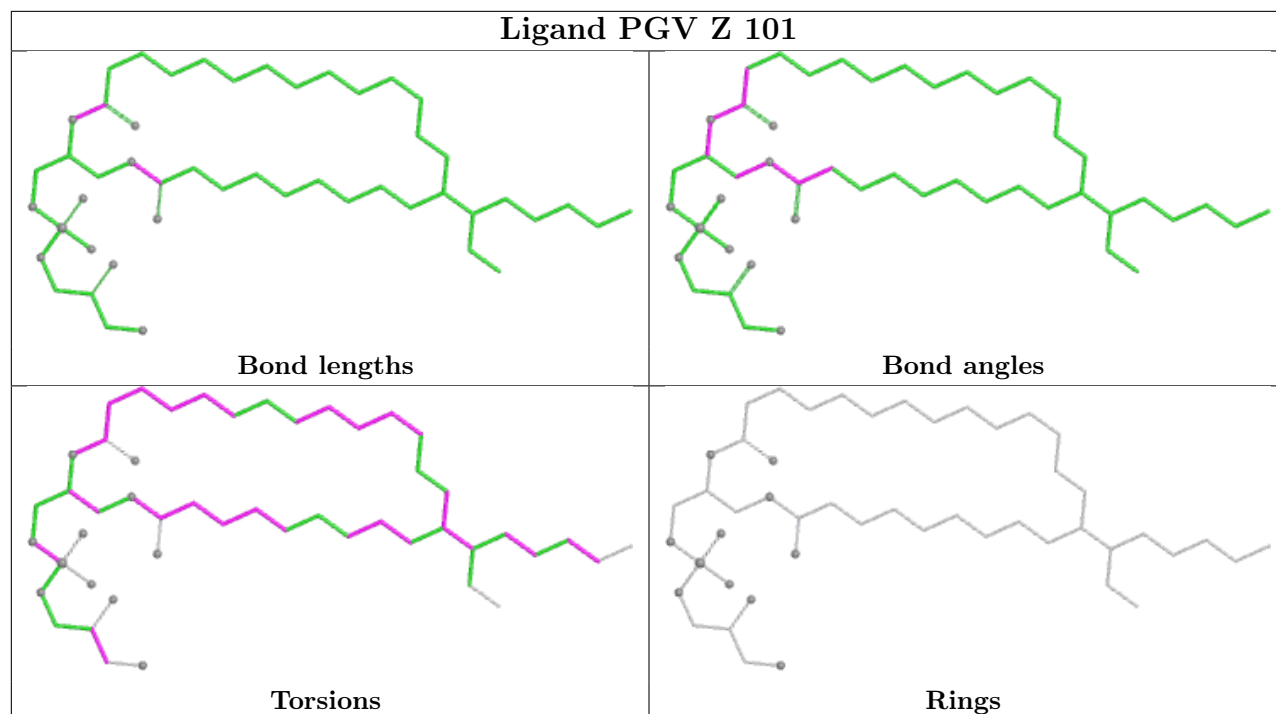


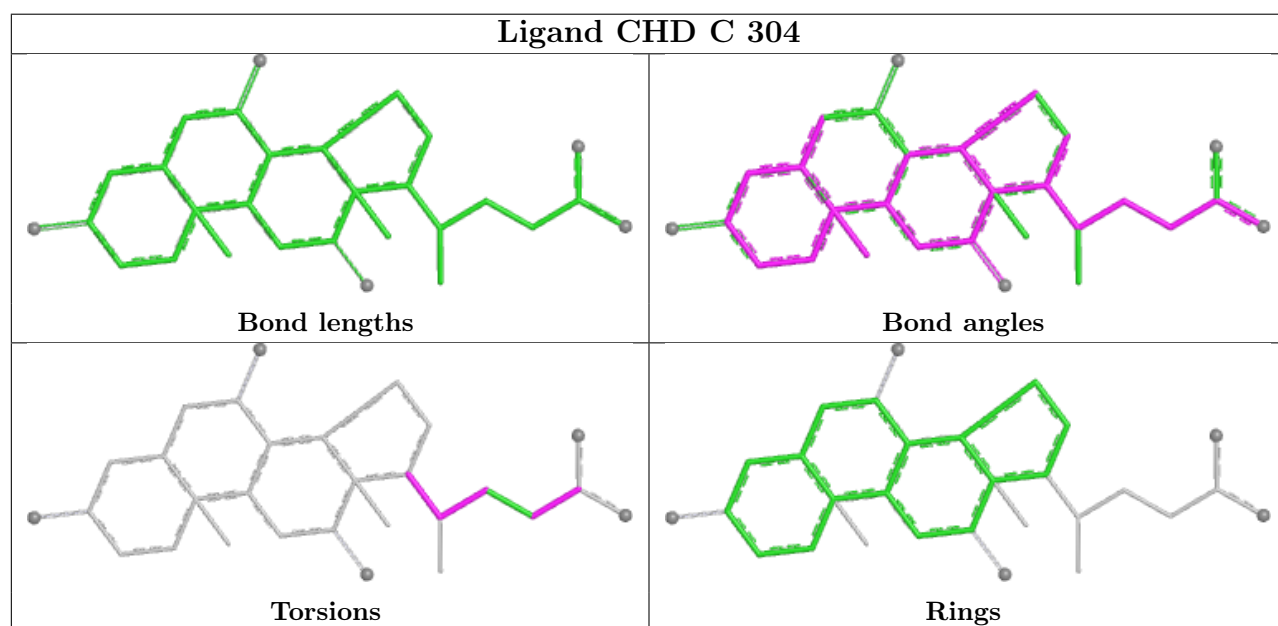
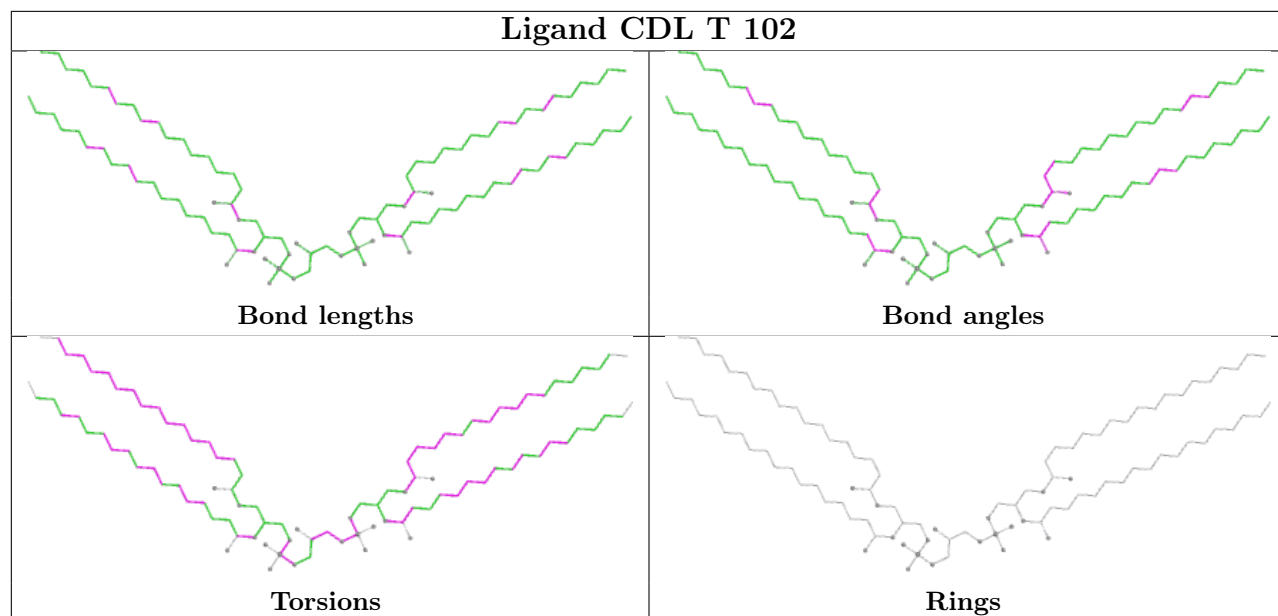


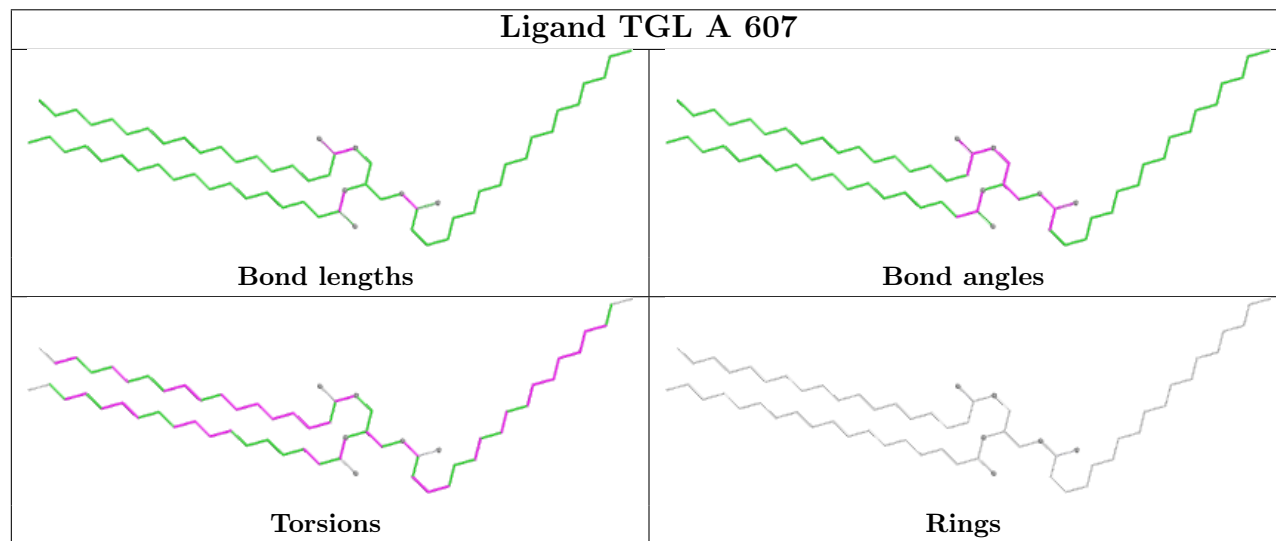
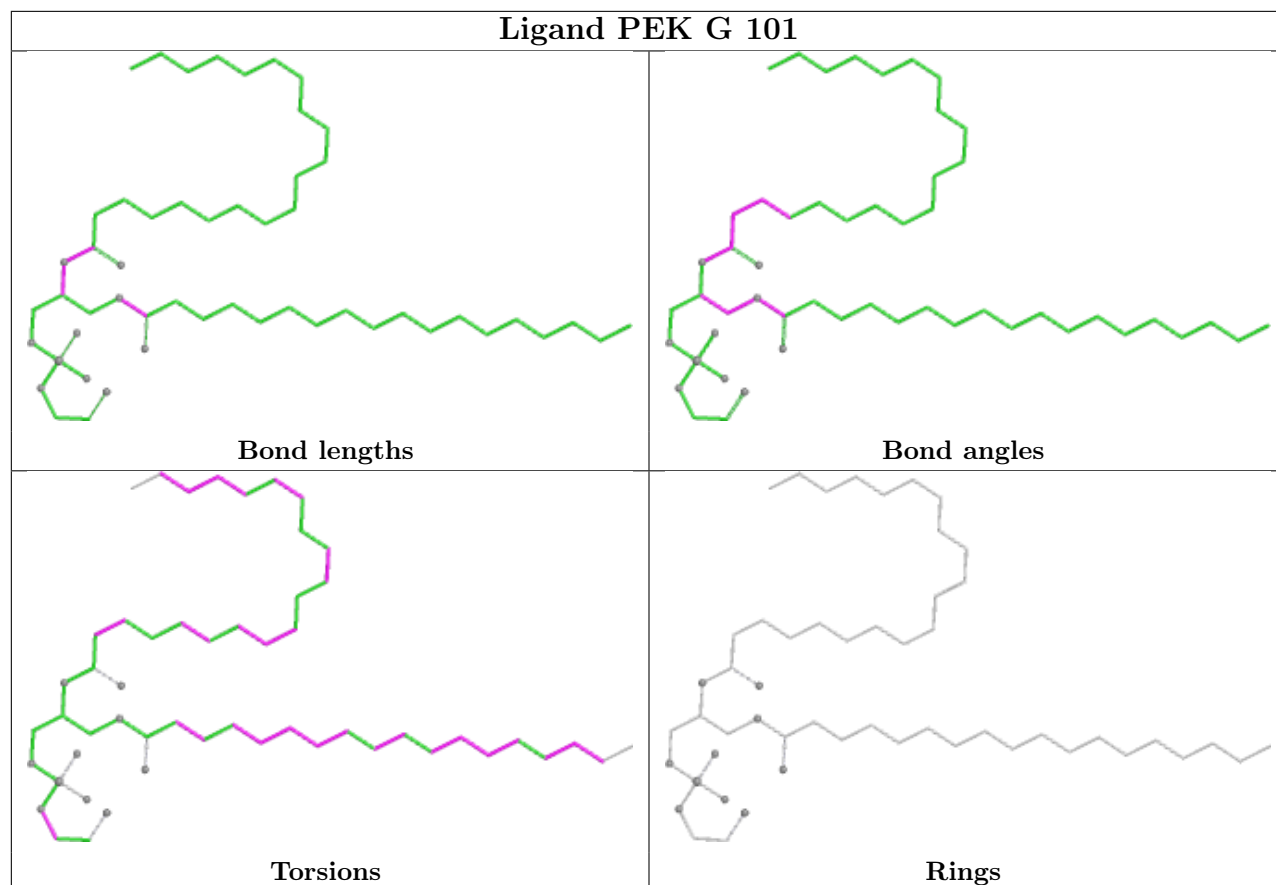


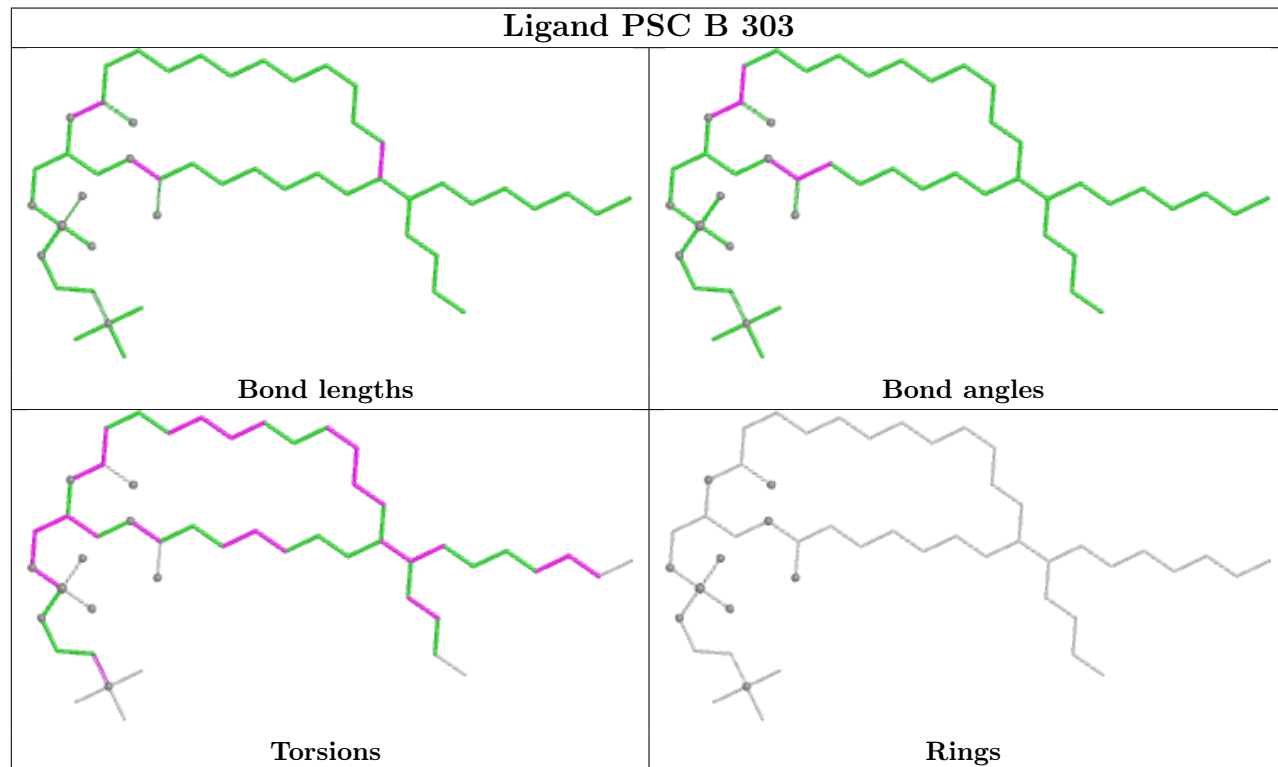
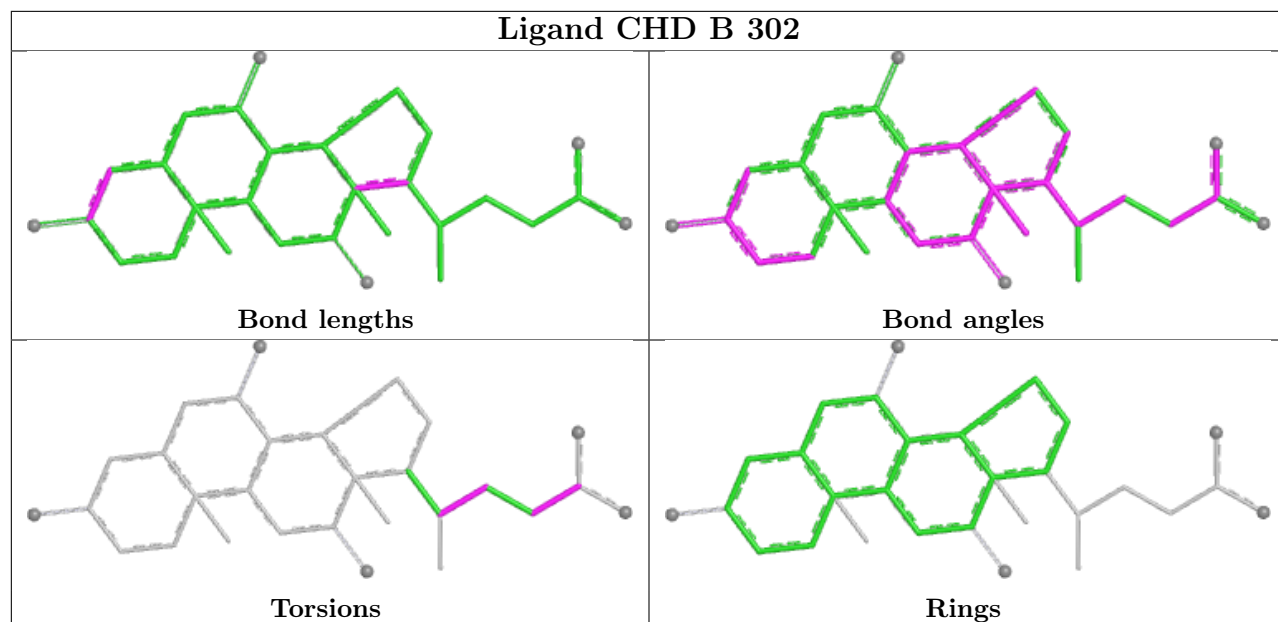


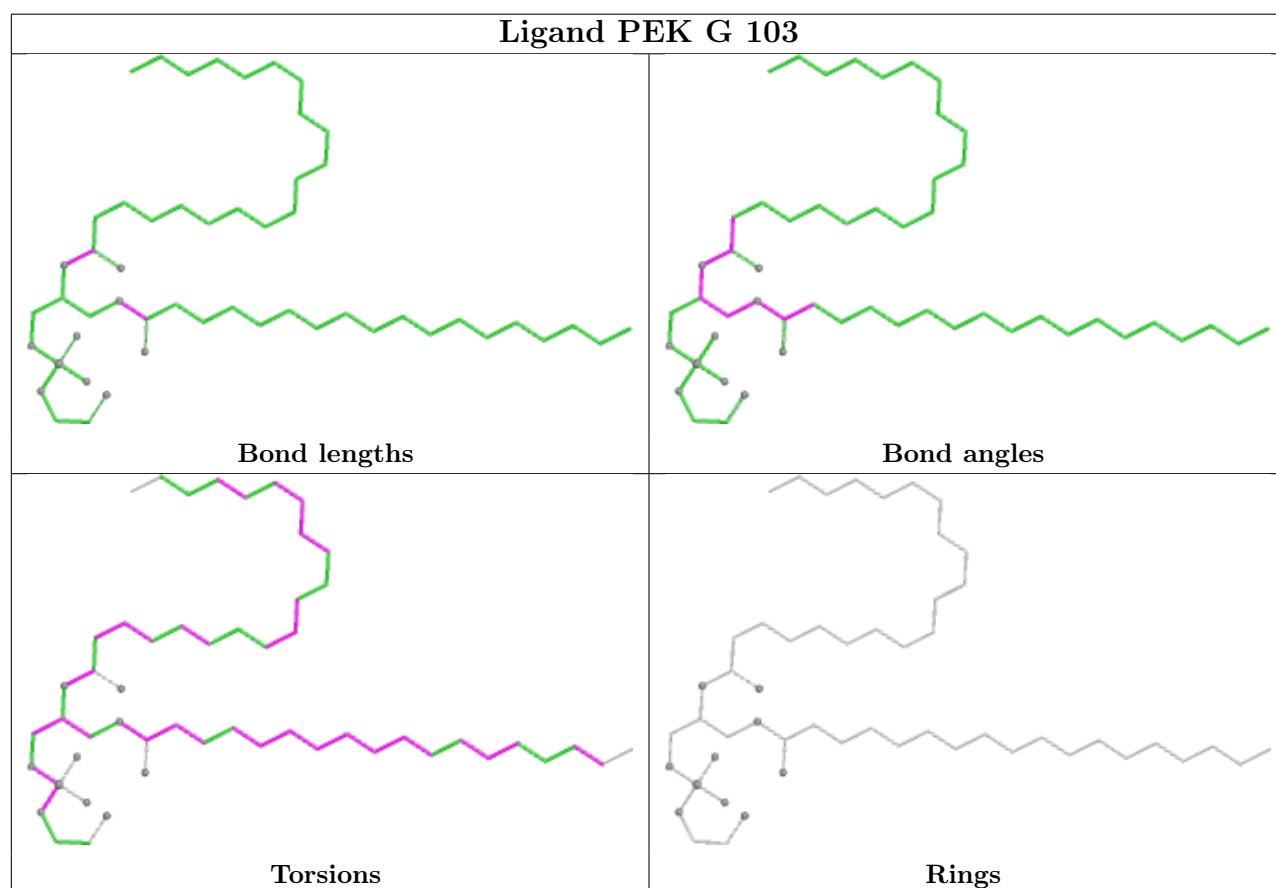
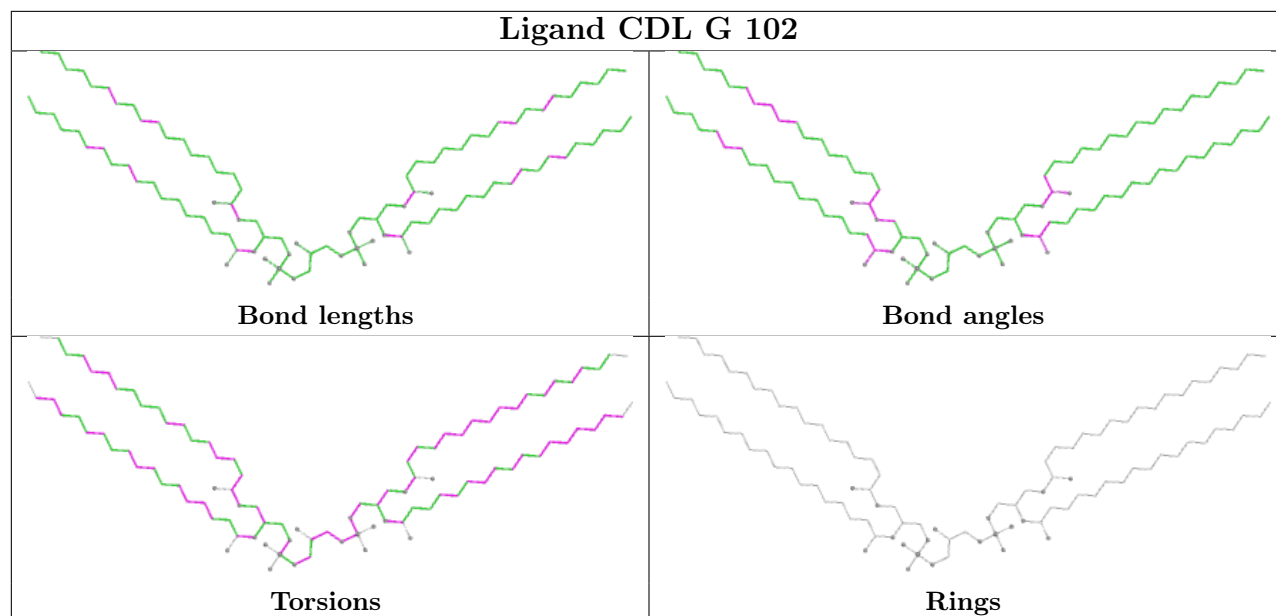


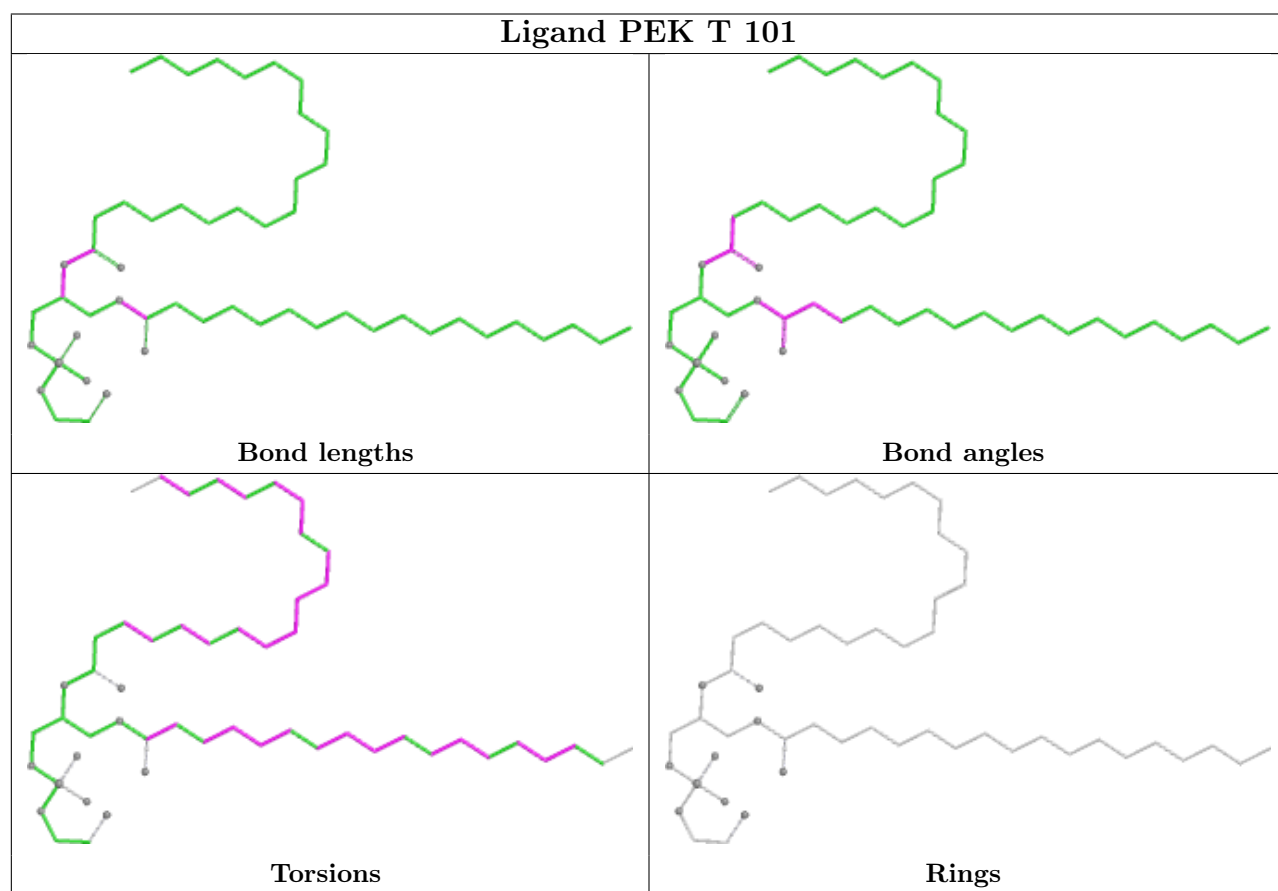
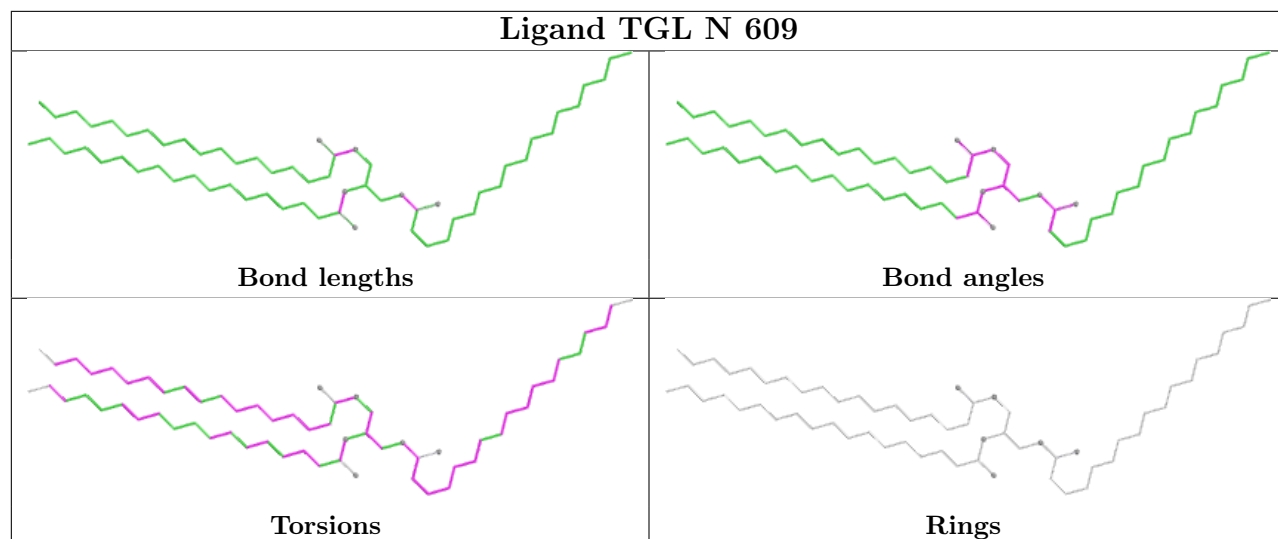


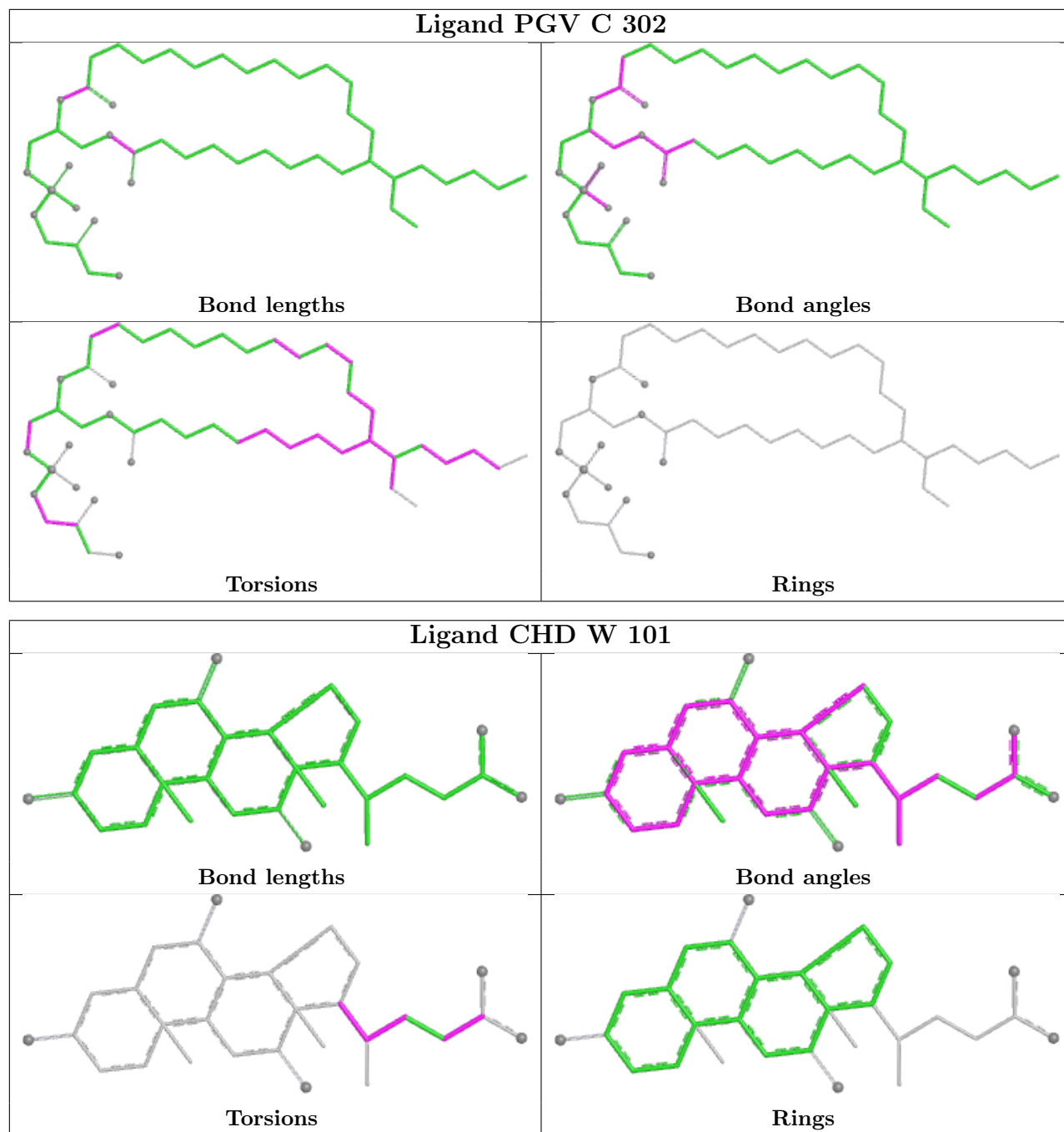


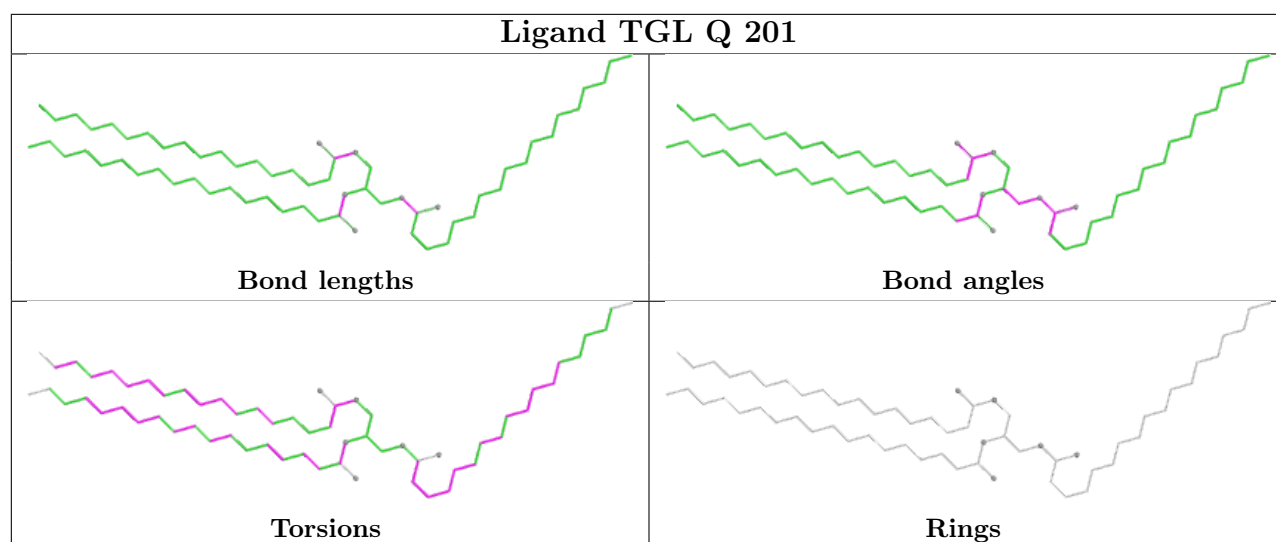












5.7 Other polymers [i](#)

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%)	-0.50	3 (0%) 85 83	33, 42, 53, 87	1 (0%)
1	N	513/514 (99%)	-0.26	5 (0%) 79 77	40, 48, 63, 83	0
2	B	226/227 (99%)	-0.39	0 100 100	38, 49, 73, 112	0
2	O	226/227 (99%)	-0.22	2 (0%) 81 79	45, 56, 89, 138	0
3	C	259/261 (99%)	-0.33	4 (1%) 72 69	38, 46, 65, 117	0
3	P	259/261 (99%)	-0.16	3 (1%) 76 74	41, 51, 69, 107	0
4	D	144/147 (97%)	-0.26	3 (2%) 63 60	43, 54, 77, 115	0
4	Q	144/147 (97%)	0.33	12 (8%) 17 15	54, 71, 118, 159	0
5	E	105/109 (96%)	-0.14	2 (1%) 66 63	44, 54, 88, 136	0
5	R	105/109 (96%)	-0.34	0 100 100	49, 65, 91, 133	0
6	F	98/98 (100%)	-0.12	5 (5%) 33 30	41, 55, 135, 155	0
6	S	98/98 (100%)	0.08	6 (6%) 27 24	47, 62, 126, 160	0
7	G	83/85 (97%)	0.33	7 (8%) 17 14	44, 56, 142, 157	0
7	T	83/85 (97%)	0.27	9 (10%) 11 8	45, 61, 144, 158	0
8	H	79/85 (92%)	0.07	5 (6%) 26 23	44, 57, 123, 140	0
8	U	79/85 (92%)	-0.03	1 (1%) 75 73	51, 65, 132, 156	0
9	I	72/73 (98%)	-0.15	3 (4%) 40 37	48, 62, 88, 114	0
9	V	72/73 (98%)	0.19	3 (4%) 40 37	50, 73, 105, 147	0
10	J	58/59 (98%)	-0.07	0 100 100	45, 59, 101, 140	0
10	W	58/59 (98%)	0.33	3 (5%) 33 29	51, 70, 110, 156	0
11	K	49/56 (87%)	0.16	2 (4%) 41 38	50, 60, 82, 106	0
11	X	49/56 (87%)	0.31	3 (6%) 27 24	59, 71, 95, 119	0
12	L	46/47 (97%)	-0.41	0 100 100	43, 49, 68, 107	0
12	Y	46/47 (97%)	0.06	2 (4%) 40 36	51, 62, 90, 132	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	43/46 (93%)	-0.11	0 100 100	43, 51, 80, 150	0
13	Z	43/46 (93%)	-0.05	0 100 100	57, 66, 100, 154	0
All	All	3550/3614 (98%)	-0.18	83 (2%) 61 58	33, 53, 94, 160	1 (0%)

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	G	3	ALA	7.5
7	G	5	LYS	7.1
4	Q	6	VAL	6.3
4	Q	5	VAL	6.1
10	W	48	TYR	5.8

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	G	11	11/12	0.43	0.15	100,128,158,158	0
7	TPO	T	11	11/12	0.60	0.15	110,133,150,157	0
9	SAC	I	1	9/10	0.70	0.11	105,118,134,139	0
9	SAC	V	1	9/10	0.74	0.13	139,151,162,164	0
1	FME	N	1	10/11	0.81	0.17	75,79,131,135	0
1	FME	A	1	10/11	0.91	0.14	53,68,109,123	0
2	FME	O	1	10/11	0.97	0.09	50,55,65,65	0
2	FME	B	1	10/11	0.98	0.07	46,51,52,55	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
26	UNX	C	301	1/1	0.64	0.52	19,19,19,19	1
27	CDL	G	102	100/100	0.78	0.24	78,118,150,150	0
19	TGL	D	201	63/63	0.80	0.25	60,99,130,145	0
19	TGL	Q	201	63/63	0.80	0.29	72,107,141,149	0
27	CDL	T	102	100/100	0.80	0.26	64,118,150,150	0
21	EDO	C	309	4/4	0.81	0.13	74,80,83,84	0
25	PEK	B	304	53/53	0.82	0.21	58,127,150,150	0
20	PGV	N	608	51/51	0.83	0.19	70,109,144,150	0
25	PEK	C	308	53/53	0.83	0.21	68,122,150,150	0
19	TGL	A	607	63/63	0.83	0.22	53,93,127,141	0
21	EDO	N	611	4/4	0.83	0.23	79,84,87,95	0
23	CHD	W	101	29/29	0.83	0.17	85,138,150,150	0
27	CDL	P	303	100/100	0.84	0.16	55,127,150,150	0
23	CHD	J	101	29/29	0.84	0.14	79,102,129,130	0
25	PEK	C	306	53/53	0.85	0.20	63,117,150,150	0
19	TGL	N	609	63/63	0.85	0.20	57,100,138,150	0
25	PEK	G	103	53/53	0.85	0.16	68,116,150,150	0
20	PGV	Z	101	51/51	0.85	0.26	63,121,150,150	0
27	CDL	C	303	100/100	0.85	0.17	57,114,156,159	0
20	PGV	A	609	51/51	0.85	0.22	64,103,157,158	0
24	PSC	O	302	52/52	0.85	0.23	67,130,150,150	0
21	EDO	C	312	4/4	0.85	0.15	92,93,108,109	0
20	PGV	C	307	51/51	0.86	0.17	57,105,146,150	0
21	EDO	I	101	4/4	0.86	0.16	72,74,89,95	0
19	TGL	Y	101	63/63	0.86	0.21	70,105,147,150	0
21	EDO	S	102	4/4	0.86	0.15	71,73,74,87	0
23	CHD	P	304	29/29	0.87	0.11	73,92,104,114	0
21	EDO	K	103	4/4	0.87	0.18	91,97,99,99	0
21	EDO	T	103	4/4	0.88	0.15	87,92,97,100	0
24	PSC	B	303	52/52	0.88	0.20	71,129,150,150	0
19	TGL	L	101	63/63	0.88	0.21	53,87,129,144	0
21	EDO	L	103	4/4	0.88	0.16	76,83,84,90	0
21	EDO	C	311	4/4	0.89	0.09	74,76,81,97	0
21	EDO	A	613	4/4	0.89	0.16	56,63,74,80	0
21	EDO	P	306	4/4	0.90	0.17	69,70,80,84	0
23	CHD	C	304	29/29	0.90	0.09	74,98,117,117	0
21	EDO	P	307	4/4	0.90	0.08	88,89,91,94	0
21	EDO	K	101	4/4	0.90	0.14	84,86,93,96	0
29	DMU	Z	102	33/33	0.90	0.10	64,81,111,121	0
21	EDO	N	610	4/4	0.92	0.12	63,71,74,75	0
21	EDO	A	611	4/4	0.93	0.16	81,81,82,88	0
21	EDO	N	612	4/4	0.93	0.10	52,61,67,68	0

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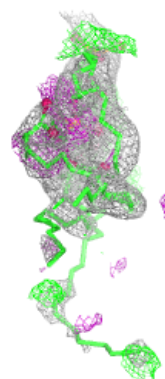
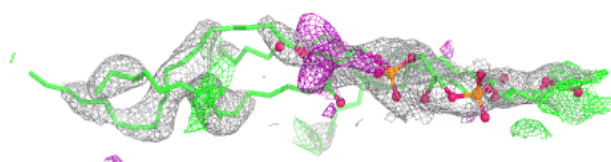
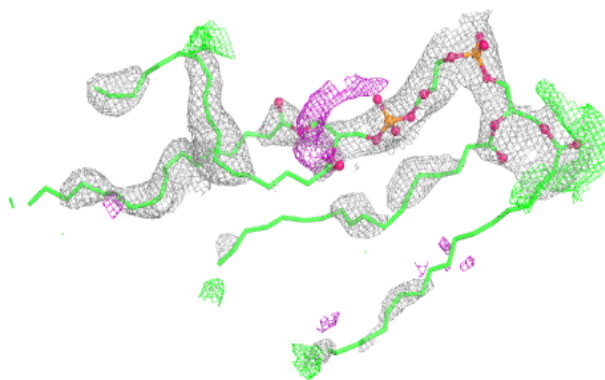
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
21	EDO	A	612	4/4	0.94	0.25	58,59,71,78	0
21	EDO	F	102	4/4	0.94	0.11	63,64,72,80	0
21	EDO	K	102	4/4	0.94	0.10	82,82,86,89	0
21	EDO	X	101	4/4	0.94	0.13	88,102,104,111	0
26	UNX	P	301	1/1	0.95	0.21	23,23,23,23	1
21	EDO	L	102	4/4	0.95	0.10	78,80,81,83	0
29	DMU	M	101	33/33	0.95	0.09	56,69,89,103	0
23	CHD	P	305	29/29	0.95	0.07	42,47,53,53	0
23	CHD	C	305	29/29	0.96	0.06	41,46,54,59	0
23	CHD	G	104	29/29	0.96	0.07	39,46,50,64	0
21	EDO	G	105	4/4	0.96	0.15	59,70,73,73	0
21	EDO	C	310	4/4	0.96	0.12	63,69,77,80	0
21	EDO	B	305	4/4	0.97	0.23	52,56,62,66	0
21	EDO	A	610	4/4	0.97	0.09	44,47,55,57	0
20	PGV	C	302	51/51	0.97	0.09	41,54,96,101	0
25	PEK	G	101	53/53	0.97	0.12	44,65,105,130	0
20	PGV	P	302	51/51	0.97	0.10	40,58,132,137	0
25	PEK	T	101	53/53	0.97	0.10	48,72,118,128	0
20	PGV	N	607	51/51	0.97	0.10	41,60,86,93	0
23	CHD	B	302	29/29	0.98	0.06	40,47,52,65	0
18	CMO	A	606	2/2	0.98	0.10	34,34,34,48	0
18	CMO	N	606	2/2	0.98	0.10	43,43,43,49	0
20	PGV	A	608	51/51	0.98	0.07	38,57,76,78	0
14	HEA	A	601	60/60	0.98	0.06	31,41,59,66	0
14	HEA	N	601	60/60	0.98	0.07	41,50,67,74	0
14	HEA	N	602	60/60	0.98	0.06	38,44,52,56	0
16	MG	N	604	1/1	0.98	0.03	46,46,46,46	0
17	NA	N	605	1/1	0.99	0.03	52,52,52,52	0
14	HEA	A	602	60/60	0.99	0.06	34,38,45,54	0
17	NA	A	605	1/1	0.99	0.03	43,43,43,43	0
22	CUA	O	301	2/2	0.99	0.06	55,55,55,57	0
15	CU	A	603	1/1	1.00	0.01	39,39,39,39	0
15	CU	N	603	1/1	1.00	0.02	45,45,45,45	0
28	ZN	F	101	1/1	1.00	0.03	52,52,52,52	0
28	ZN	S	101	1/1	1.00	0.02	56,56,56,56	0
22	CUA	B	301	2/2	1.00	0.02	43,43,43,44	0
16	MG	A	604	1/1	1.00	0.01	39,39,39,39	0

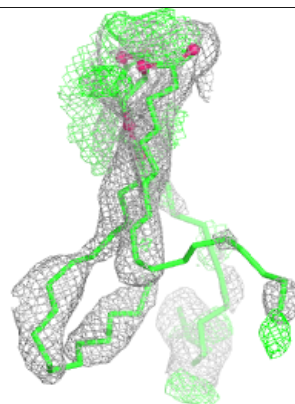
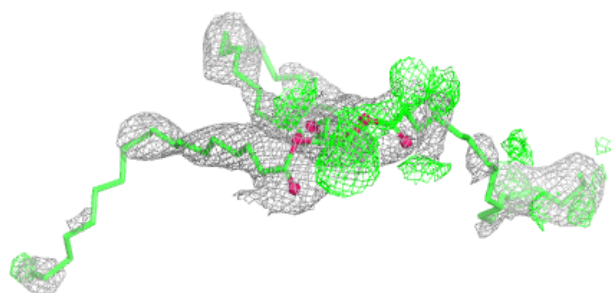
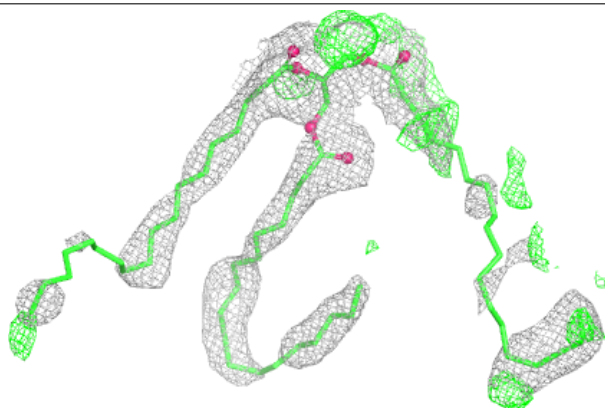
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CDL 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)

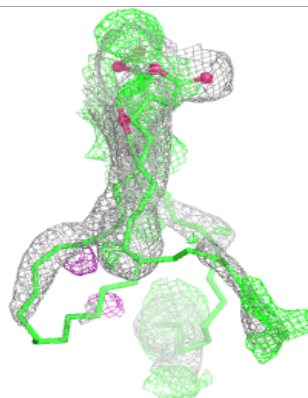
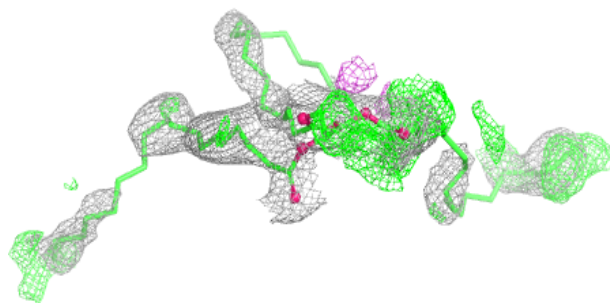
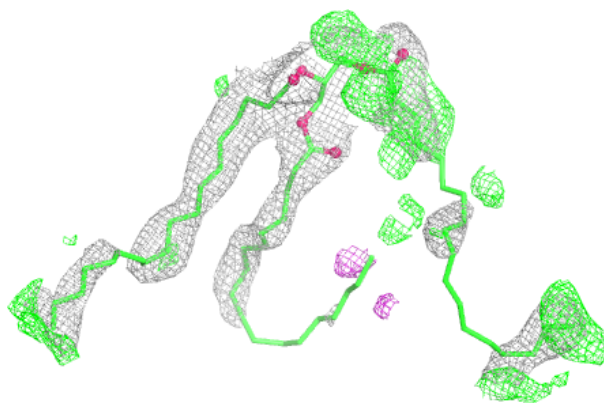
**Electron density around TGL D 201:**

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

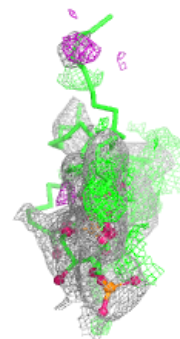
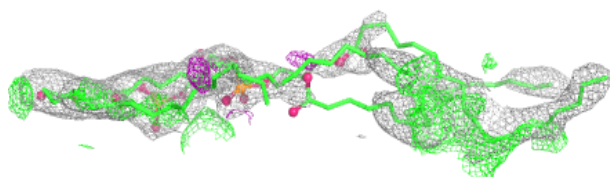
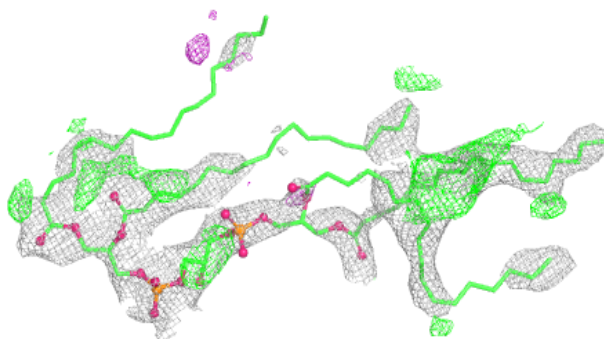


Electron density around TGL Q 201:

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

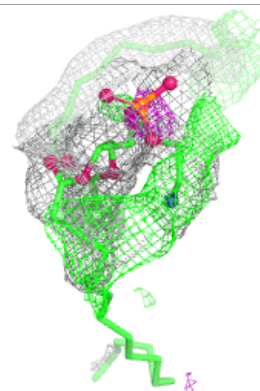
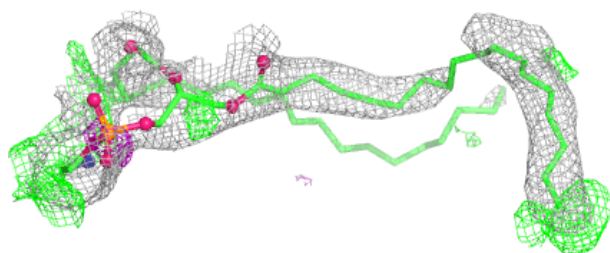
**Electron density around CDL T 102:**

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

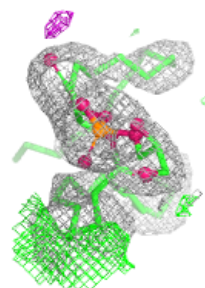
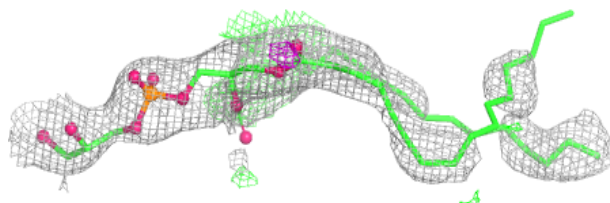
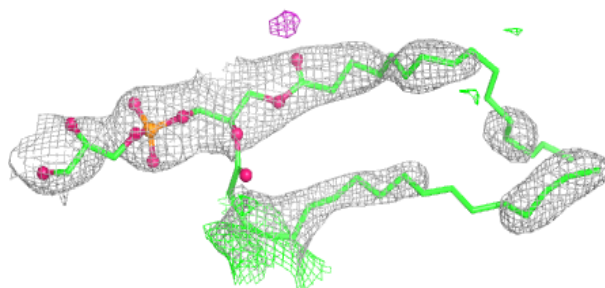


Electron density around PEK B 304:

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

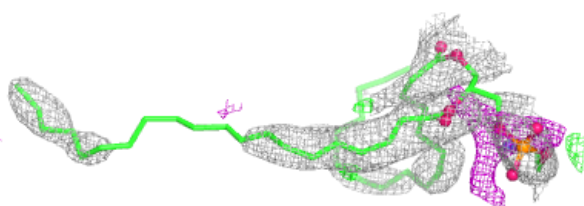
**Electron density around PGV N 608:**

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

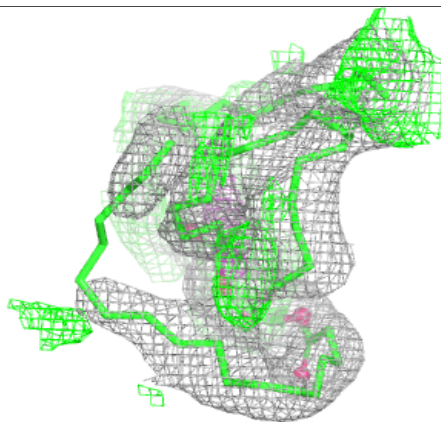
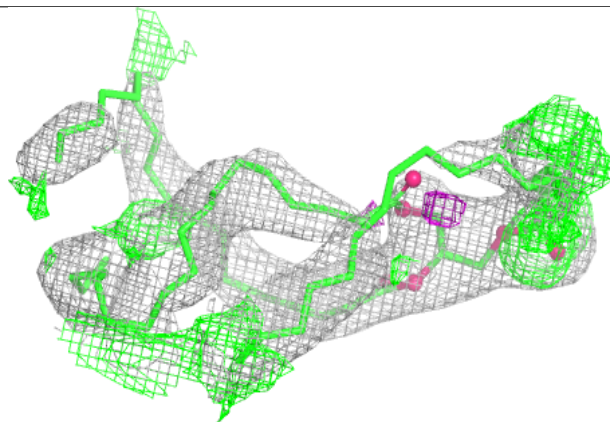
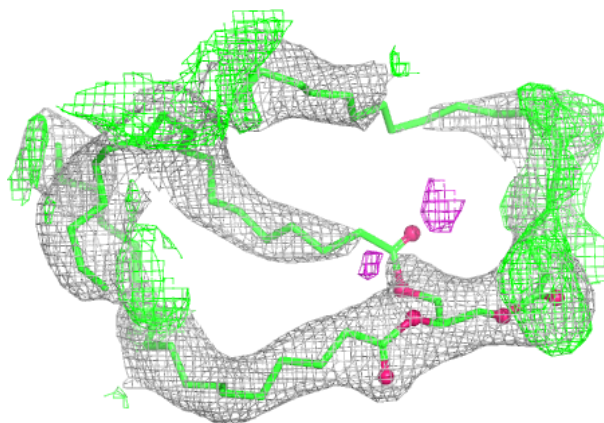


Electron density around PEK C 308:

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

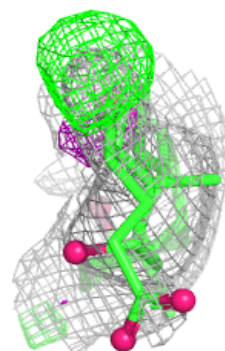
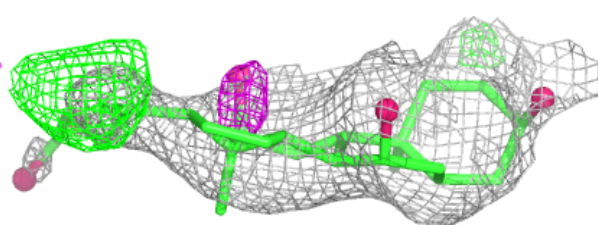
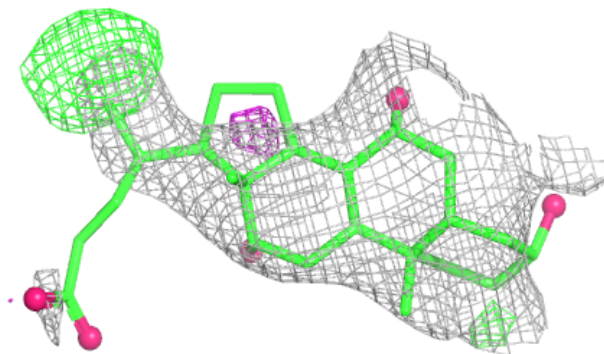
**Electron density around TGL A 607:**

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

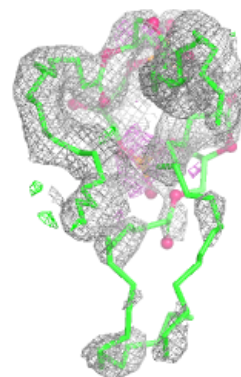
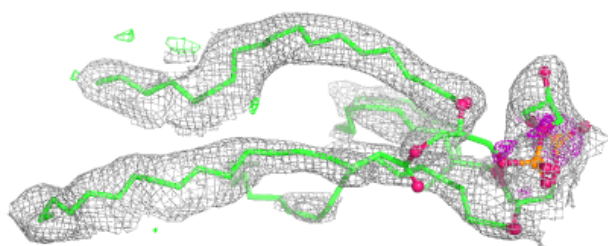
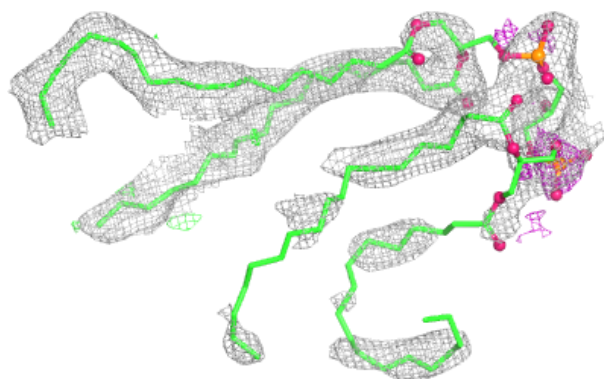


Electron density around CHD W 101:

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

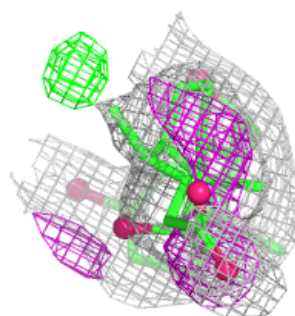
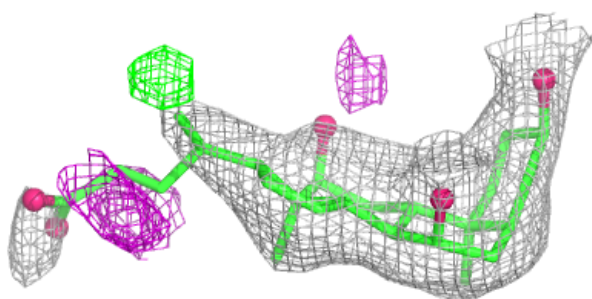
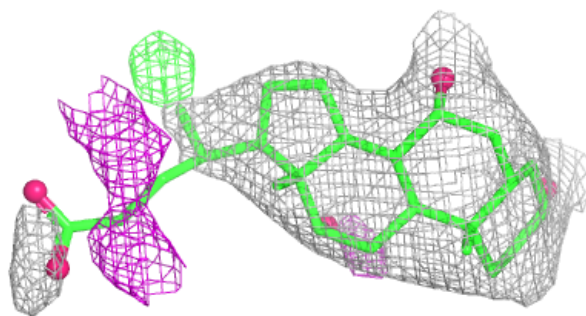
**Electron density around CDL P 303:**

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

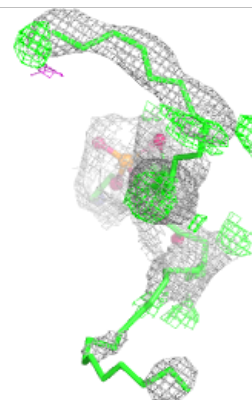
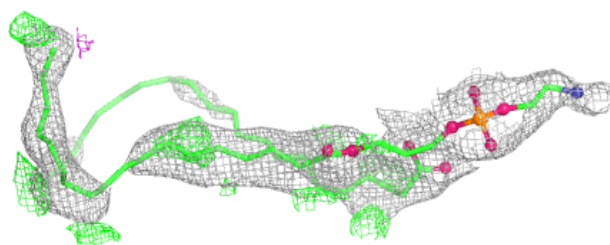
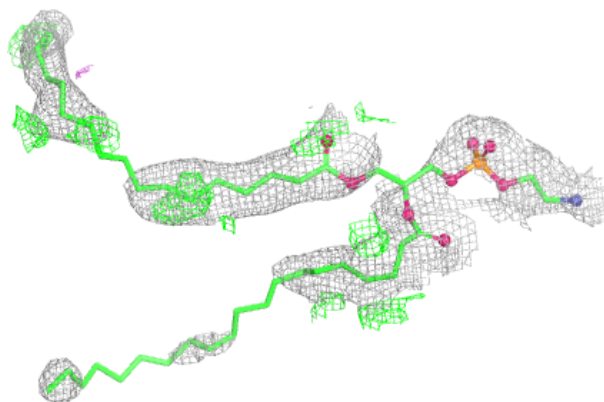


Electron density around CHD J 101:

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

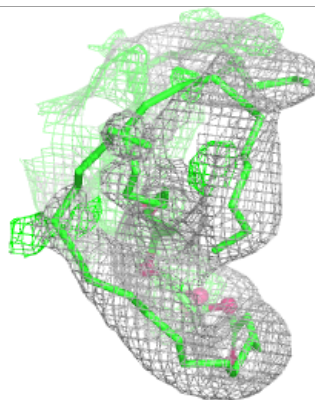
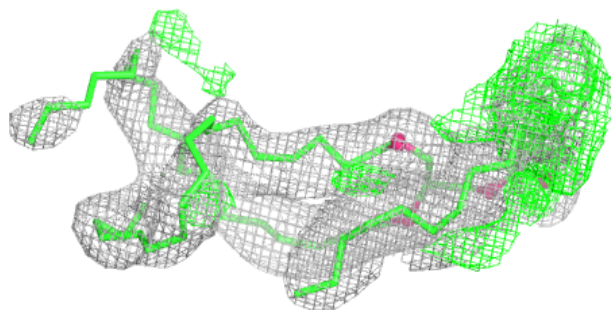
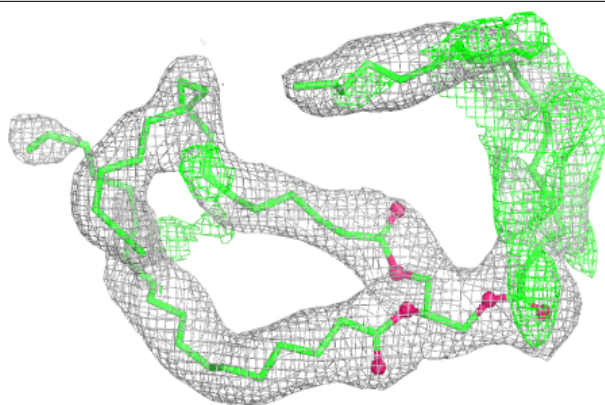
**Electron density around PEK C 306:**

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



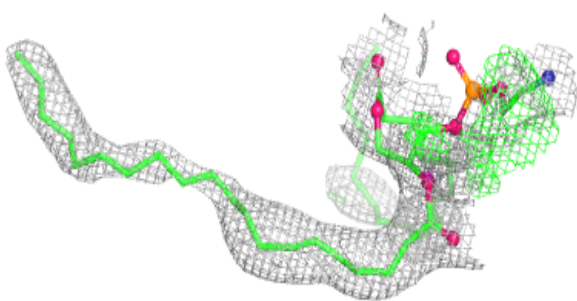
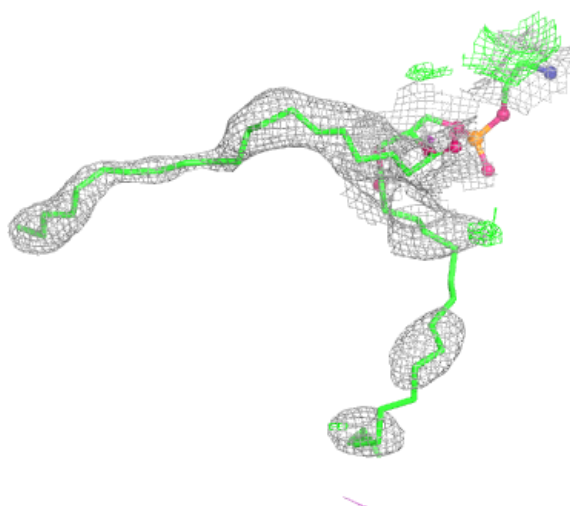
Electron density around TGL N 609:

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



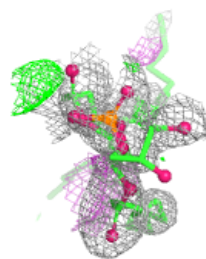
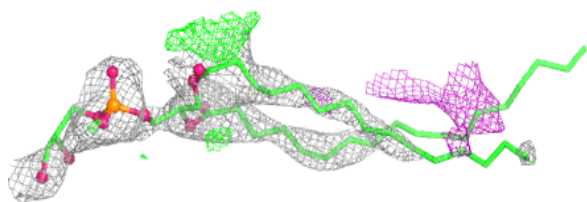
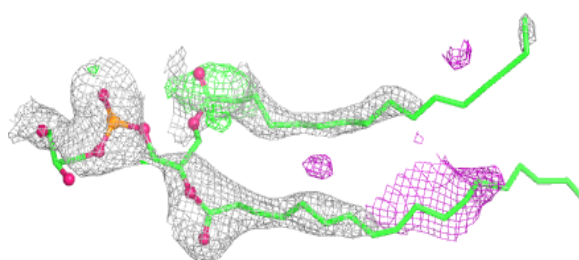
Electron density around PEK G 103:

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

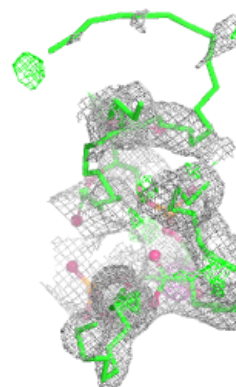
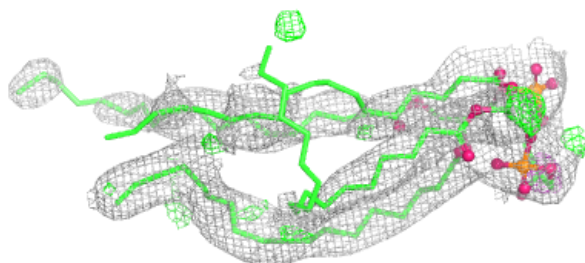
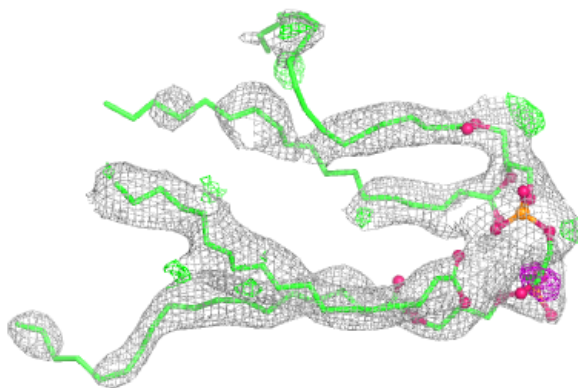


Electron density around PGV Z 101:

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

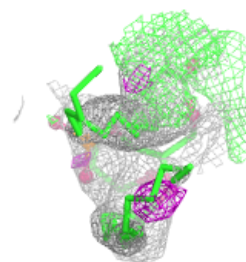
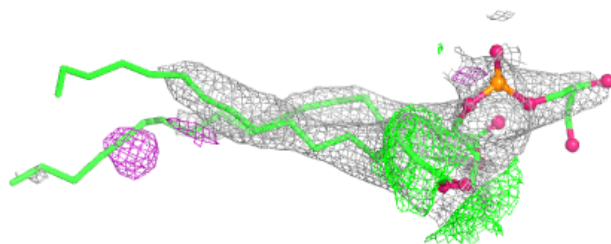
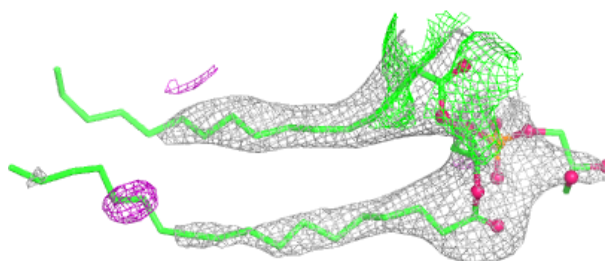
**Electron density around CDL C 303:**

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

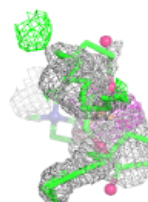
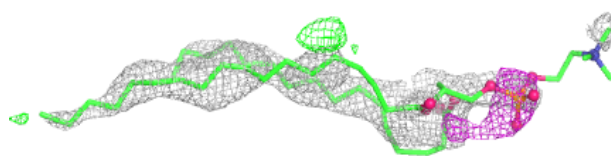
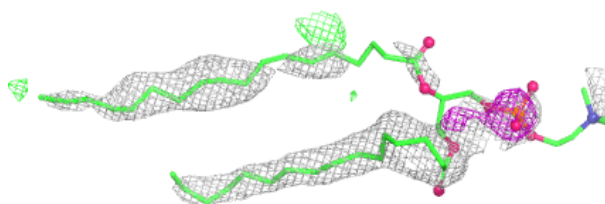


Electron density around PGV A 609:

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

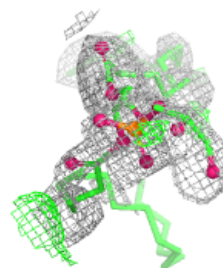
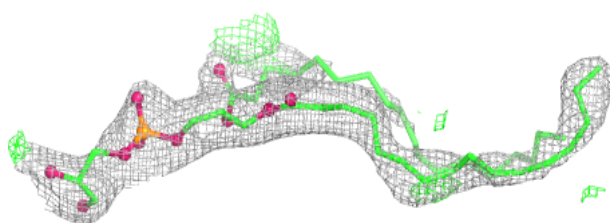
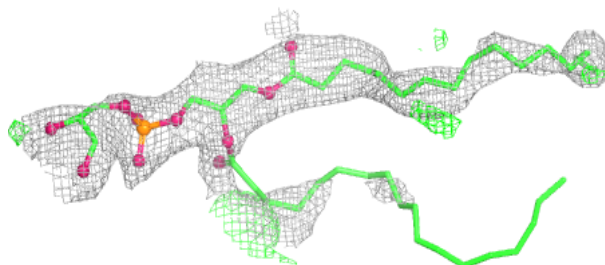
**Electron density around PSC O 302:**

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



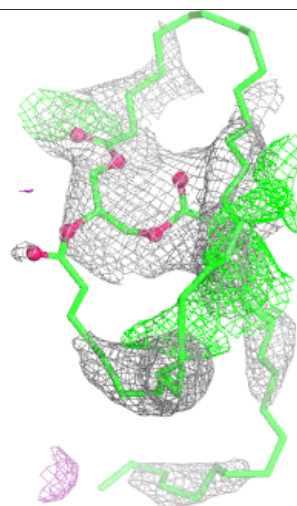
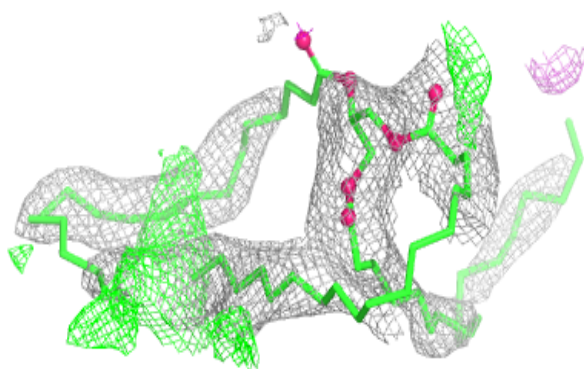
Electron density around PGV C 307:

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



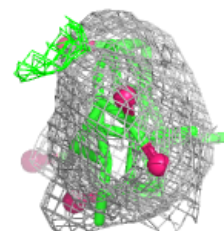
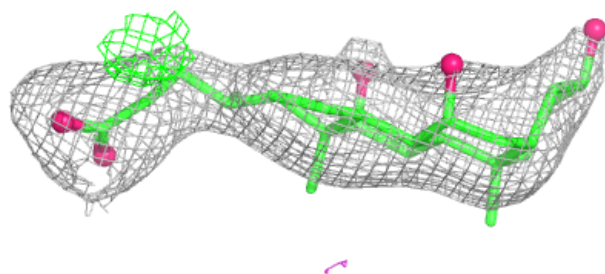
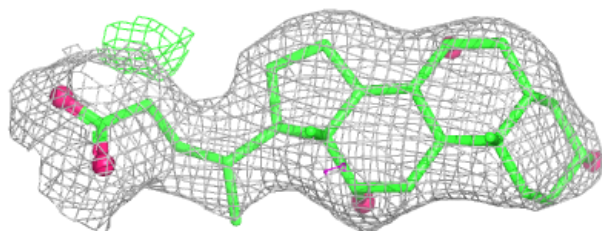
Electron density around TGL Y 101:

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

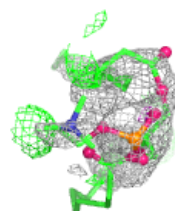
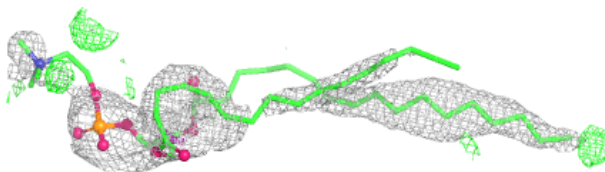
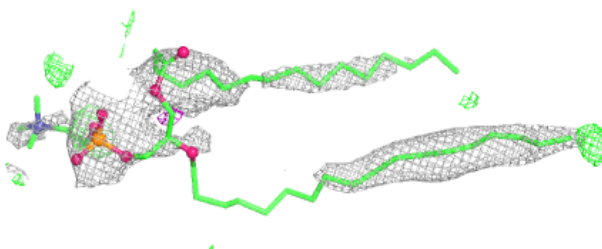


Electron density around CHD P 304:

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

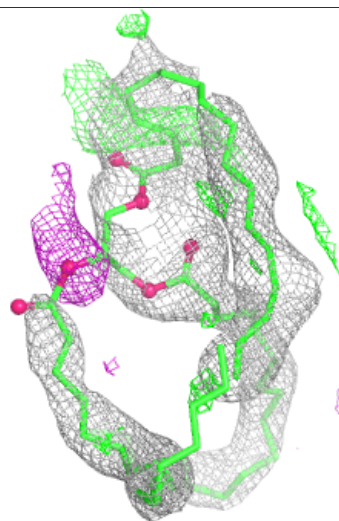
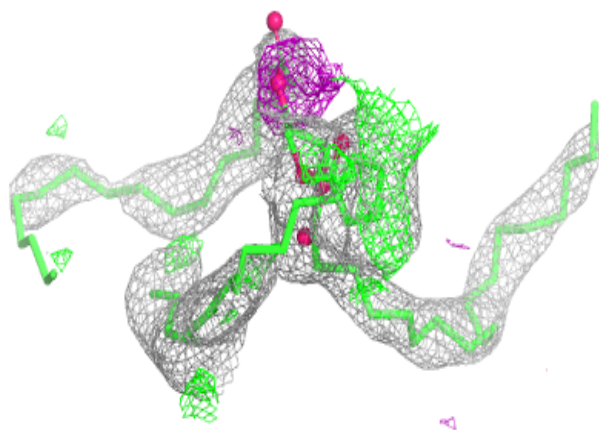
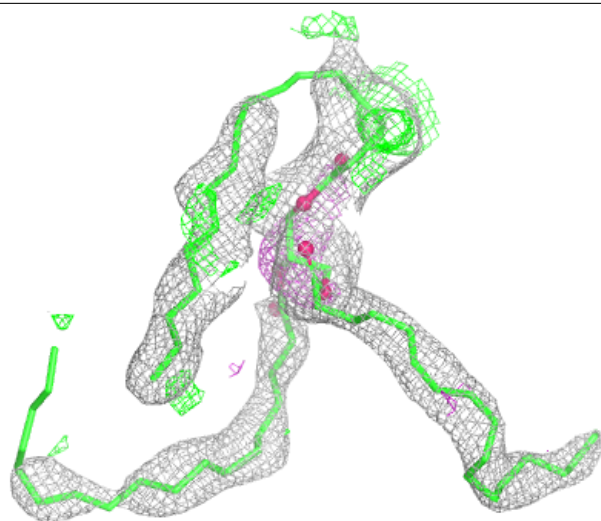
**Electron density around PSC B 303:**

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



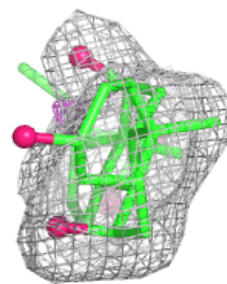
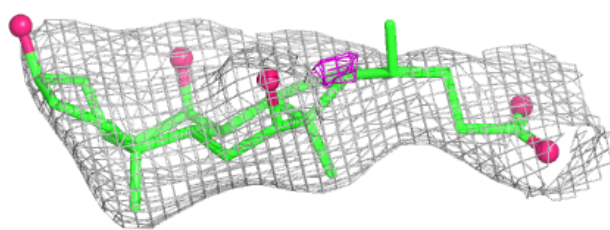
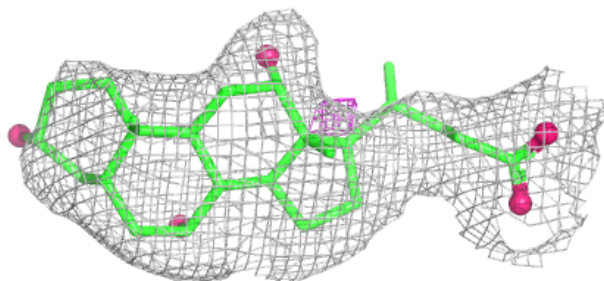
Electron density around TGL L 101:

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

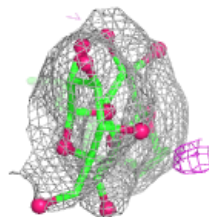
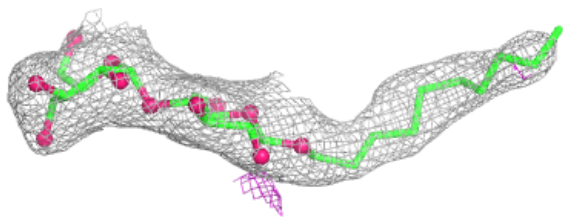
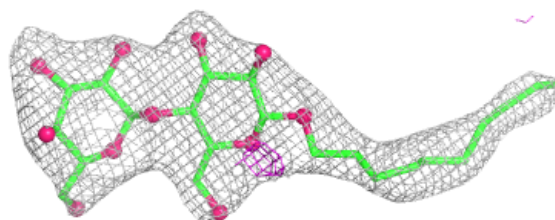


Electron density around CHD C 304:

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

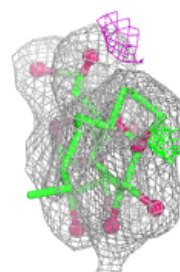
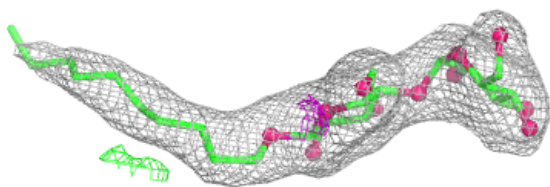
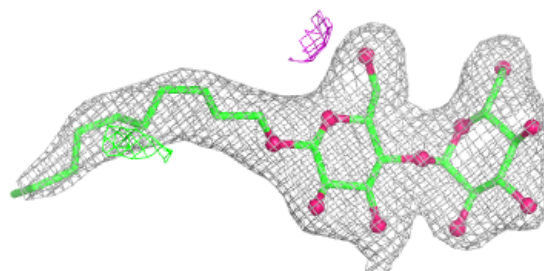
**Electron density around DMU Z 102:**

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

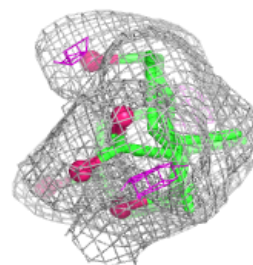
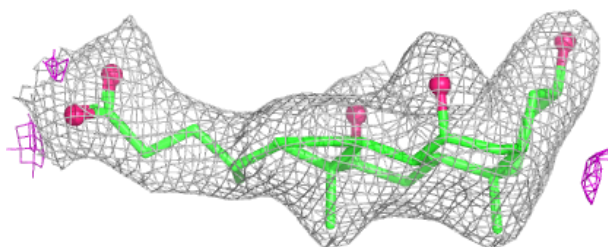
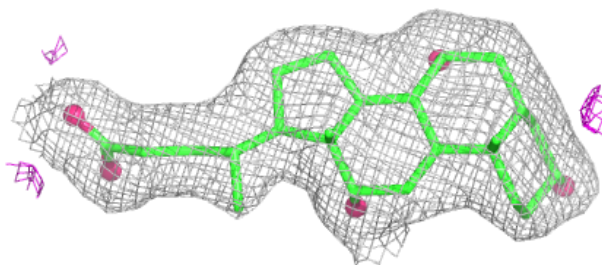


Electron density around DMU M 101:

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

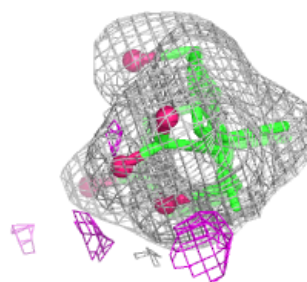
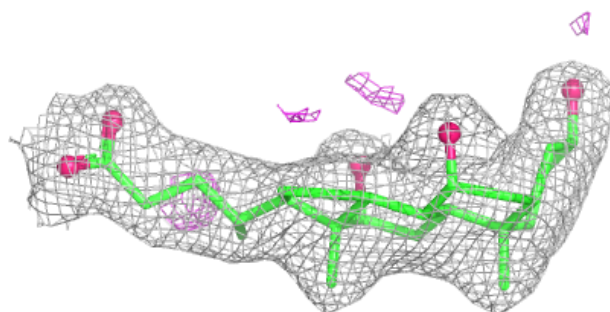
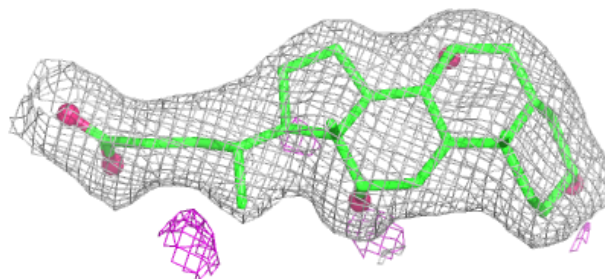
**Electron density around CHD P 305:**

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

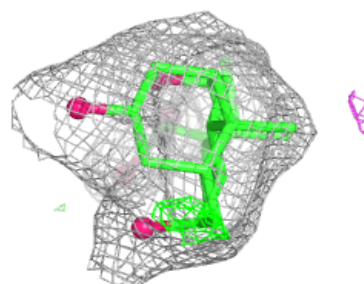
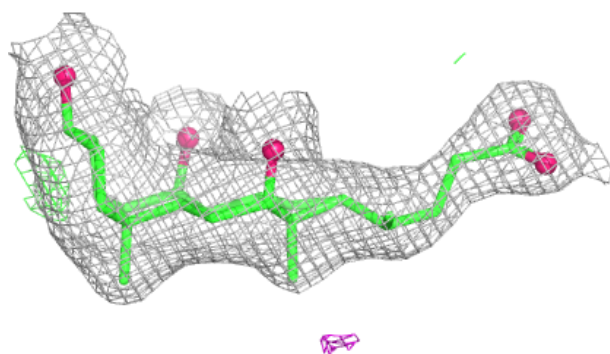
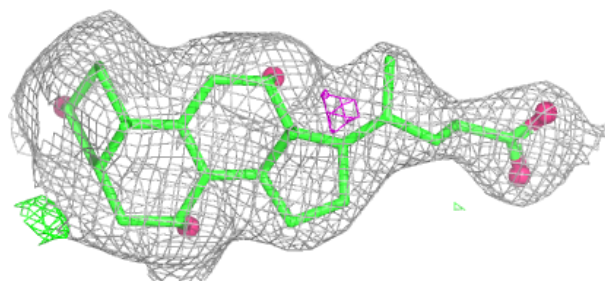


Electron density around CHD C 305:

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

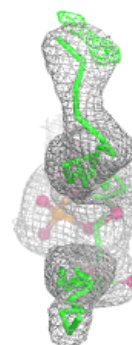
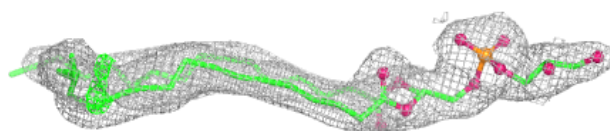
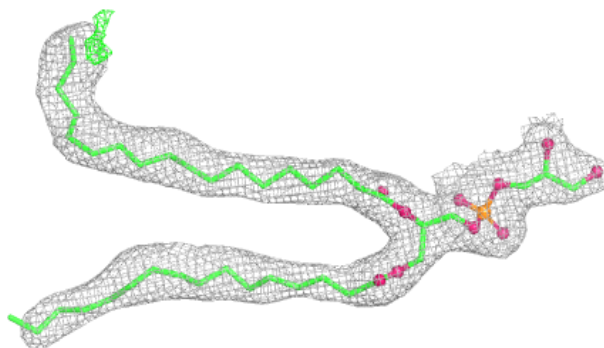
**Electron density around CHD G 104:**

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

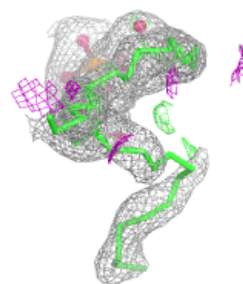
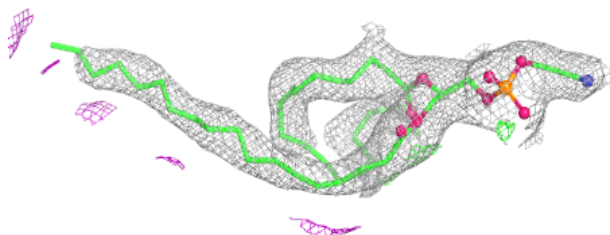
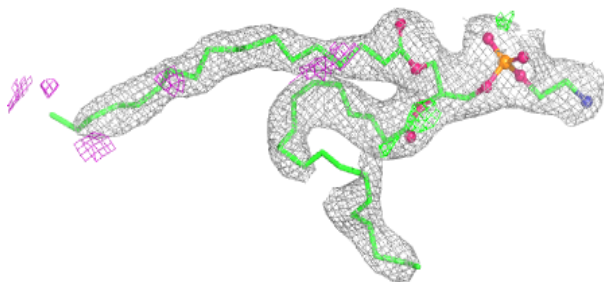


Electron density around PGV C 302:

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

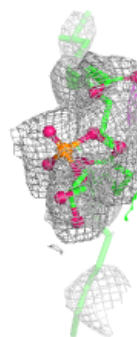
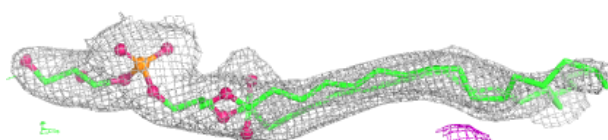
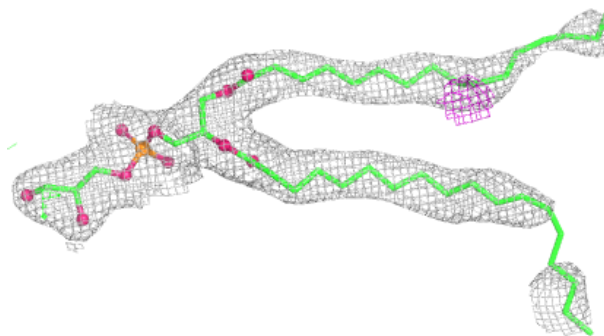
**Electron density around PEK G 101:**

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

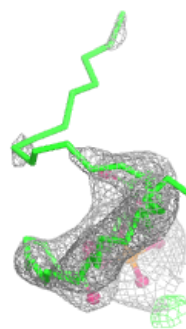
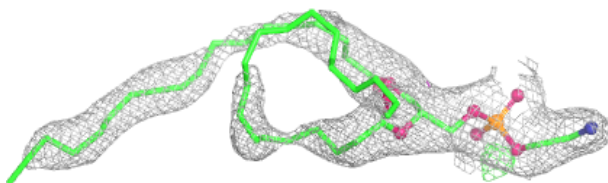
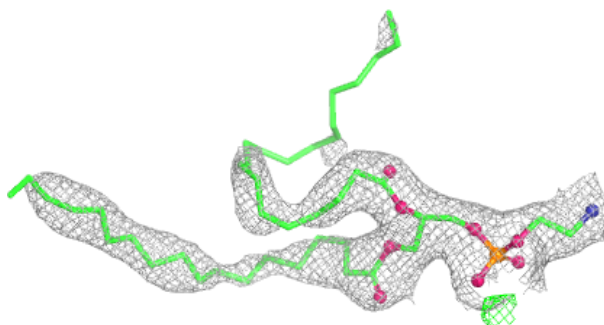


Electron density around PGV P 302:

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

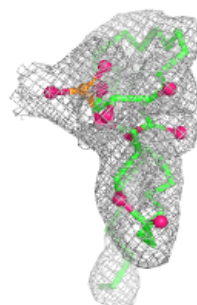
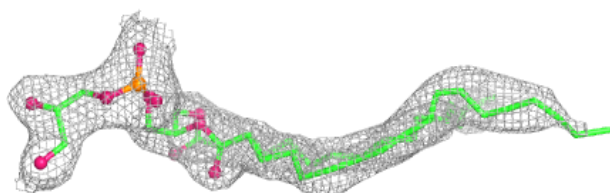
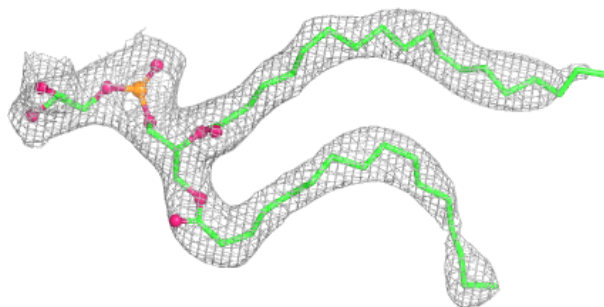
**Electron density around PEK T 101:**

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

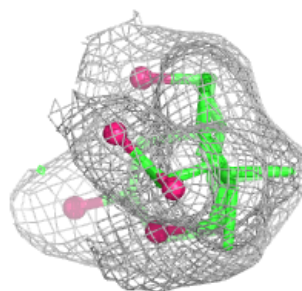
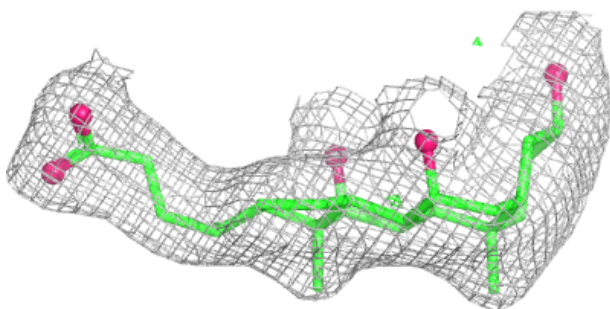
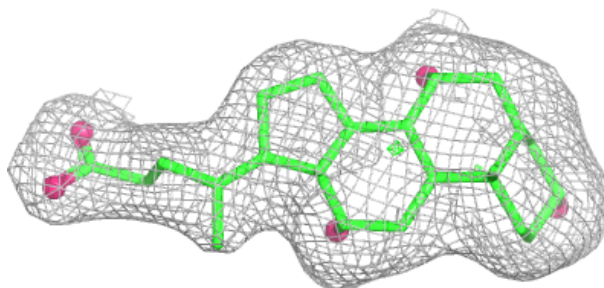


Electron density around PGV N 607:

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

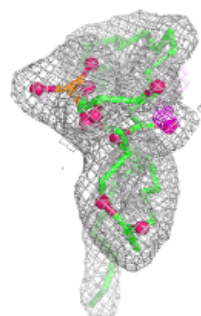
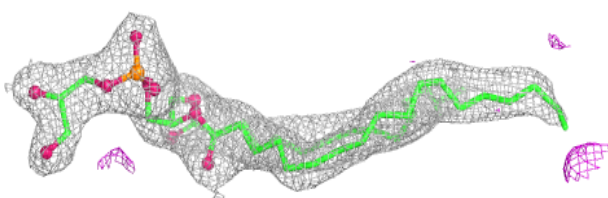
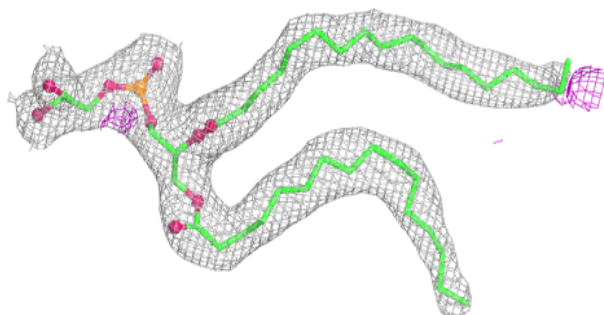
**Electron density around CHD B 302:**

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

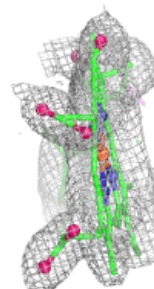
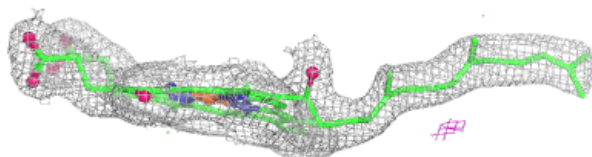
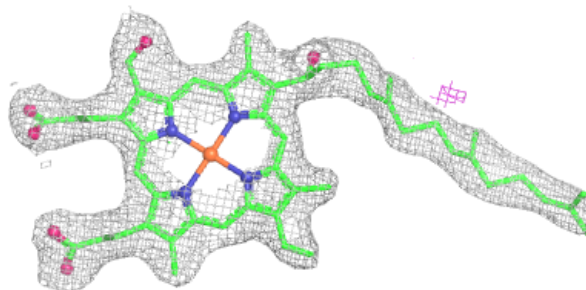


Electron density around PGV A 608:

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

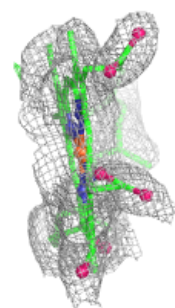
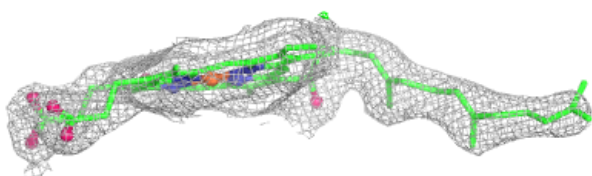
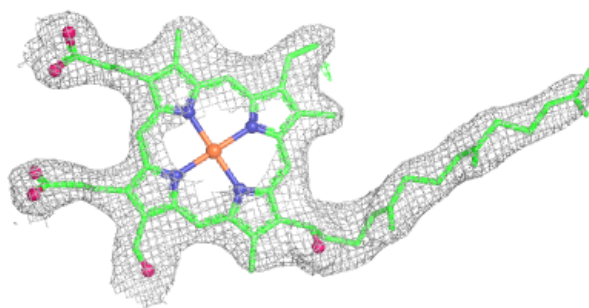
**Electron density around HEA A 601:**

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

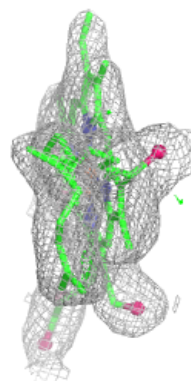
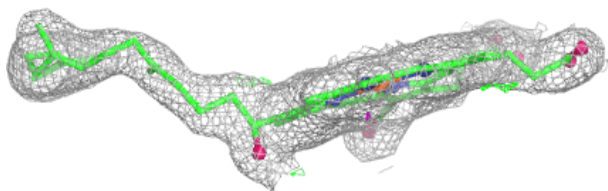
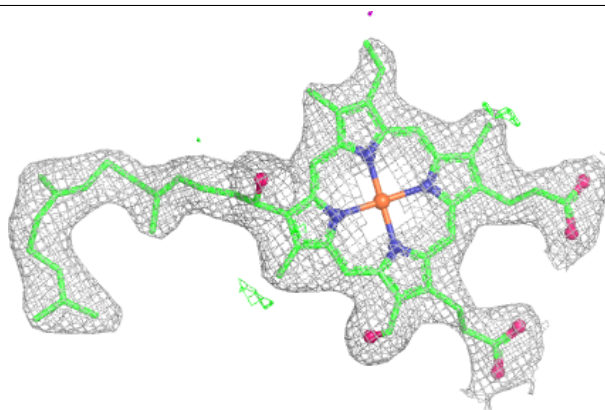


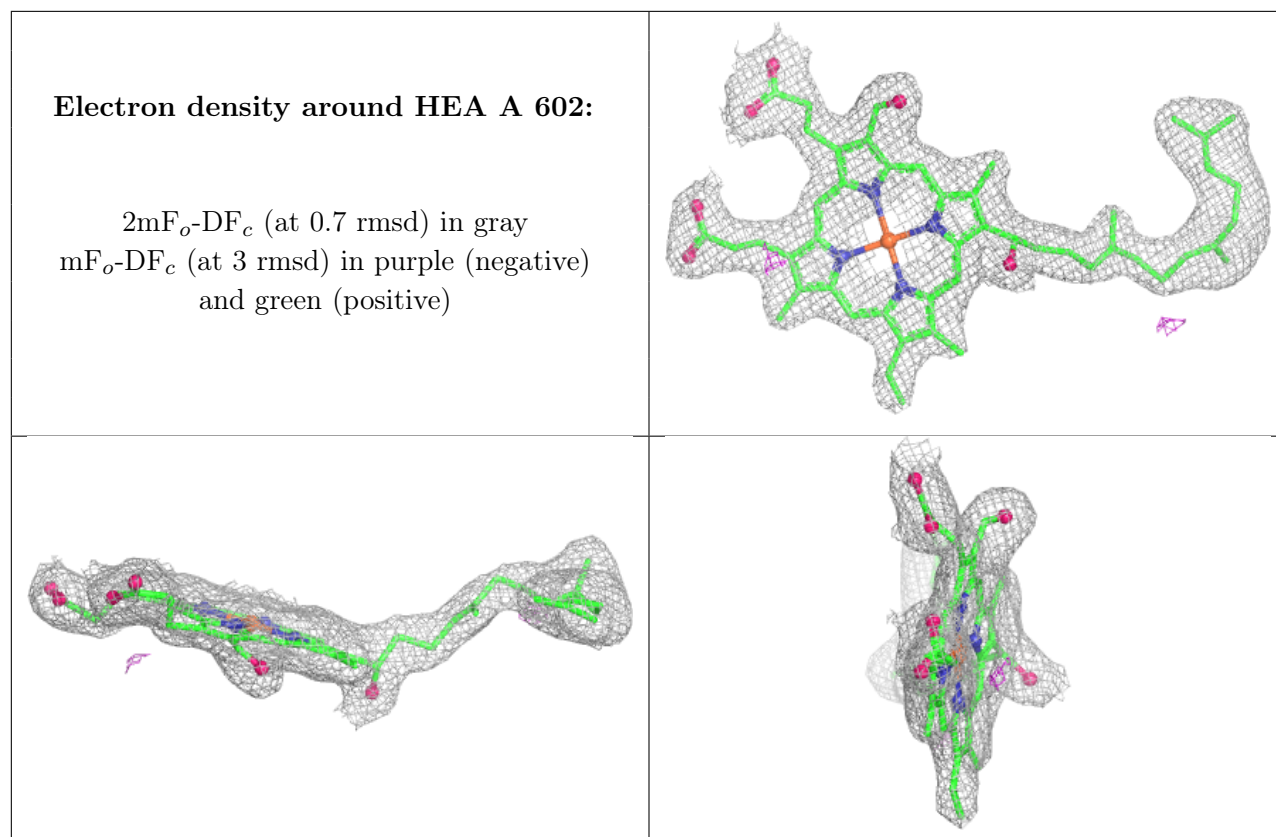
Electron density around HEA N 601:

$2mF_o-DF_c$ (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.