



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 23, 2026 – 07:48 PM UTC

PDB ID : 7D5X / pdb_00007d5x
Title : Bovine heart cytochrome c oxidase in a catalytic intermediate, IO10, at 1.74 angstrom resolution
Authors : Tsukihara, T.; Shimada, A.
Deposited on : 2020-09-28
Resolution : 1.74 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

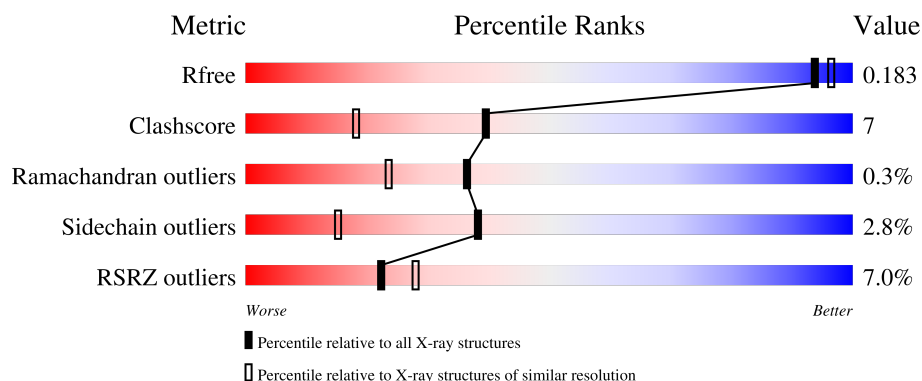
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	2% 88% 11%
1	N	514	2% 88% 12%
2	B	227	7% 84% 16%
2	O	227	6% 81% 17%
3	C	259	% 90% 10%

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Mol	Chain	Length	Quality of chain
3	P	259	90% 10% .
4	D	144	4% 91% 8% .
4	Q	144	13% 89% 10% .
5	E	105	5% 94% 6%
5	R	105	4% 94% 6%
6	F	94	6% 85% 13% .
6	S	94	6% 82% 16% ..
7	G	84	27% 87% 11% .
7	T	84	26% 86% 14%
8	H	79	15% 89% 8% ..
8	U	79	18% 87% 9% .
9	I	73	23% 95% 5%
9	V	73	27% 89% 11%
10	J	58	12% 83% 14% .
10	W	58	7% 95% ..
11	K	49	8% 92% 6% .
11	X	49	20% 90% 8% .
12	L	46	9% 78% 17% .
12	Y	46	11% 83% 15% .
13	M	43	7% 88% 12%
13	Z	43	12% 86% 14%

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 33923 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	34	0
			4183	2789	644	711	39			
1	N	514	Total	C	N	O	S	0	28	0
			4174	2782	645	709	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	14	0
			1867	1214	284	349	20			
2	O	227	Total	C	N	O	S	0	9	0
			1853	1204	283	346	20			

- 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	12	0
			2143	1430	341	358	14			
3	P	259	Total	C	N	O	S	0	8	0
			2131	1420	340	357	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	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	94	Total	C	N	O	S	0	0	0
			716	444	127	140	5			
6	S	94	Total	C	N	O	S	0	0	0
			716	444	127	140	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	S	0	0	0
			672	431	129	111	1			
7	T	84	Total	C	N	O	S	0	0	0
			672	431	129	111	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
			461	297	78	83	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	58	Total	C	N	O	S	0	0	0
			461	297	78	83	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
			385	250	65	68	2			
11	X	49	Total	C	N	O	S	0	0	0
			385	250	65	68	2			

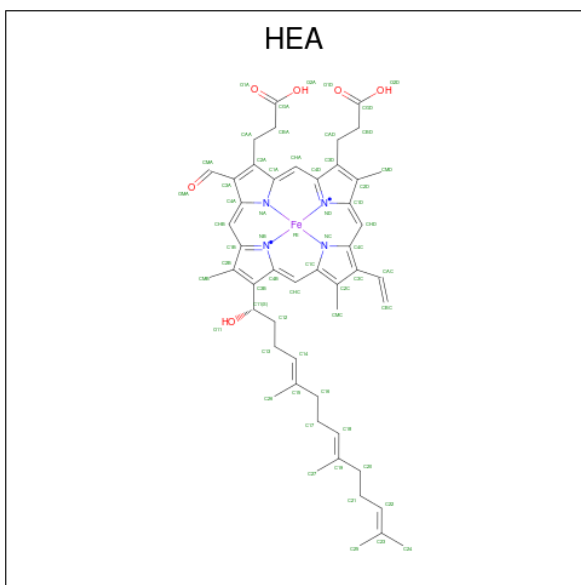
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

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

- Molecule 13 is a protein called Cytochrome c oxidase subunit 8B, mitochondrial.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	43	Total	C	N	O	0	0	0
			336	223	53	60			
13	Z	43	Total	C	N	O	0	0	0
			336	223	53	60			

- 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	C	Fe	N	O	
			81	69	1	4	7	0
14	A	1	Total	C	Fe	N	O	
			60	49	1	4	6	0
14	N	1	Total	C	Fe	N	O	
			81	69	1	4	7	0
14	N	1	Total	C	Fe	N	O	
			60	49	1	4	6	0

- 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

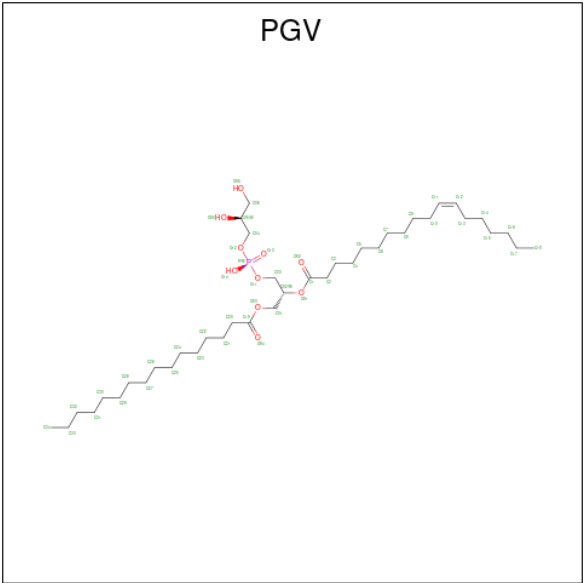
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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	0	0
			1	1		
17	C	1	Total	Na	0	0
			1	1		
17	N	1	Total	Na	0	0
			1	1		
17	P	1	Total	Na	0	0
			1	1		

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



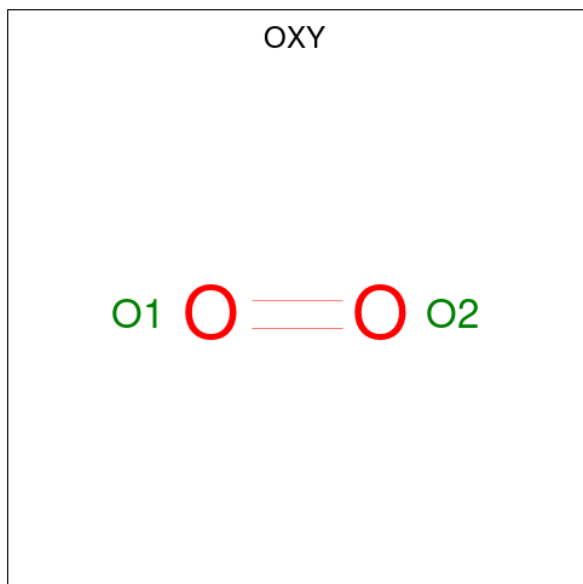
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
18	A	1	Total	C	O		0	0
			33	32	1			
18	A	1	Total	C	O	P	0	0
			51	40	10	1		
18	C	1	Total	C	O	P	0	0
			51	40	10	1		
18	C	1	Total	C	O		0	0
			37	34	3			
18	N	1	Total	C	O	P	0	0
			51	40	10	1		
18	P	1	Total	C	O	P	0	0
			51	40	10	1		
18	P	1	Total	C	O		0	0
			38	36	2			

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	Q	1	Total	C	O	0	0
			37	35	2		

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



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	B	1	Total 4	C 2	O 2	0	0
20	B	1	Total 4	C 2	O 2	0	0
20	B	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	C	1	Total 4	C 2	O 2	0	0
20	D	1	Total 4	C 2	O 2	0	0
20	D	1	Total 4	C 2	O 2	0	0
20	D	1	Total 4	C 2	O 2	0	0
20	D	1	Total 4	C 2	O 2	0	0
20	E	1	Total 4	C 2	O 2	0	0
20	E	1	Total 4	C 2	O 2	0	0
20	E	1	Total 4	C 2	O 2	0	0
20	F	1	Total 4	C 2	O 2	0	0
20	F	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	F	1	Total	C	O	0	0
			4	2	2		
20	F	1	Total	C	O	0	0
			4	2	2		
20	F	1	Total	C	O	0	0
			4	2	2		
20	F	1	Total	C	O	0	0
			4	2	2		
20	G	1	Total	C	O	0	0
			4	2	2		
20	J	1	Total	C	O	0	0
			4	2	2		
20	J	1	Total	C	O	0	0
			4	2	2		
20	L	1	Total	C	O	0	0
			4	2	2		
20	M	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	N	1	Total	C	O	0	0
			4	2	2		
20	O	1	Total	C	O	0	0
			4	2	2		

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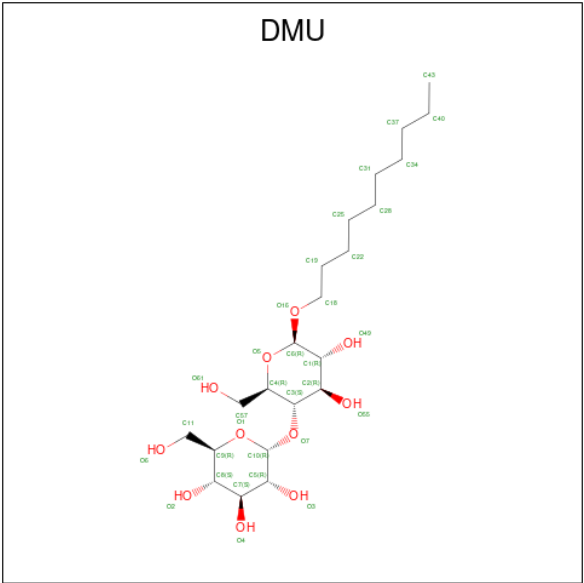
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	O	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	P	1	Total 4	C 2	O 2	0	0
20	Q	1	Total 4	C 2	O 2	0	0
20	Q	1	Total 4	C 2	O 2	0	0
20	R	1	Total 4	C 2	O 2	0	0
20	R	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	S	1	Total 4	C 2	O 2	0	0
20	T	1	Total 4	C 2	O 2	0	0
20	T	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	T	1	Total	C	O	0	0
			4	2	2		
20	W	1	Total	C	O	0	0
			4	2	2		
20	W	1	Total	C	O	0	0
			4	2	2		
20	Y	1	Total	C	O	0	0
			4	2	2		

- Molecule 21 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



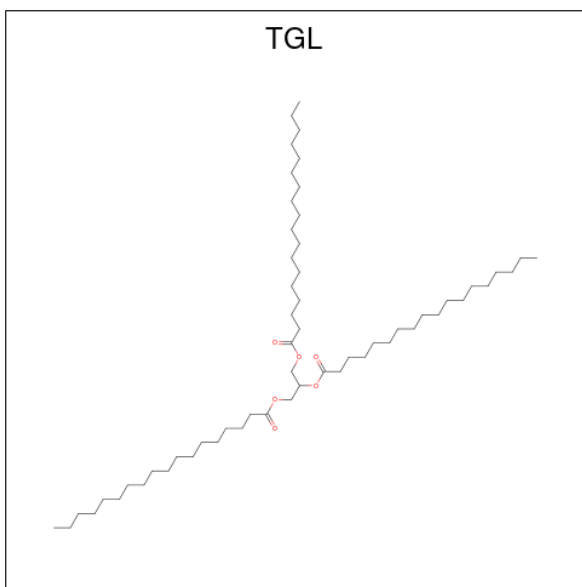
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	A	1	Total	C		0	0
			9	9			
21	A	1	Total	C		0	0
			8	8			
21	C	1	Total	C	O	0	0
			22	16	6		
21	C	1	Total	C	O	0	0
			12	11	1		
21	D	1	Total	C	O	0	0
			11	10	1		
21	D	1	Total	C		0	0
			8	8			
21	J	1	Total	C	O	0	0
			11	10	1		

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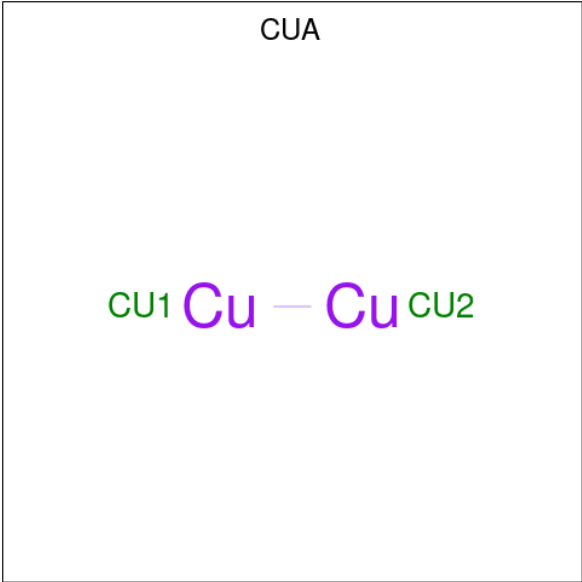
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
21	K	1	Total C 9 9	0	0
21	K	1	Total C 9 9	0	0
21	K	1	Total C 9 9	0	0
21	K	1	Total C 10 10	0	0
21	L	1	Total C O 21 16 5	0	0
21	M	1	Total C O 33 22 11	0	0
21	N	1	Total C 9 9	0	0
21	O	1	Total C O 11 10 1	0	0
21	P	1	Total C O 22 16 6	0	0
21	P	1	Total C O 11 10 1	0	0
21	Q	1	Total C 10 10	0	0
21	W	1	Total C O 11 10 1	0	0
21	X	1	Total C 9 9	0	0
21	X	1	Total C 8 8	0	0
21	X	1	Total C 10 10	0	0
21	Z	1	Total C O 33 22 11	0	0

- Molecule 22 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: C₅₇H₁₁₀O₆).



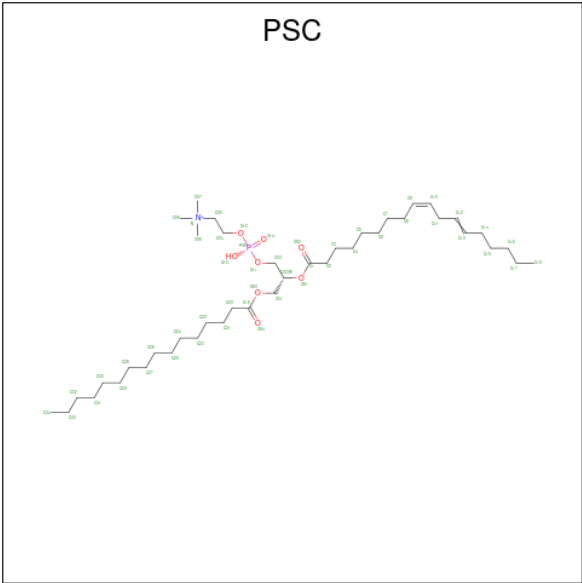
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
22	B	1	Total	C	O	0	0
			63	57	6		
22	D	1	Total	C	O	0	0
			63	57	6		
22	L	1	Total	C	O	0	0
			54	49	5		
22	N	1	Total	C	O	0	0
			63	57	6		
22	N	1	Total	C		0	0
			43	43			
22	N	1	Total	C	O	0	0
			55	53	2		

- Molecule 23 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



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

- Molecule 24 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITO YLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (CCD ID: PSC) (formula: C₄₂H₈₁NO₈P).



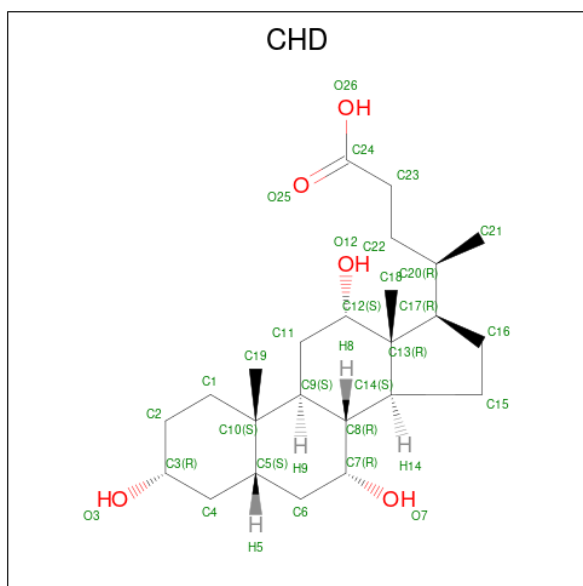
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	B	1	Total	C	O	0	0
			41	37	4		

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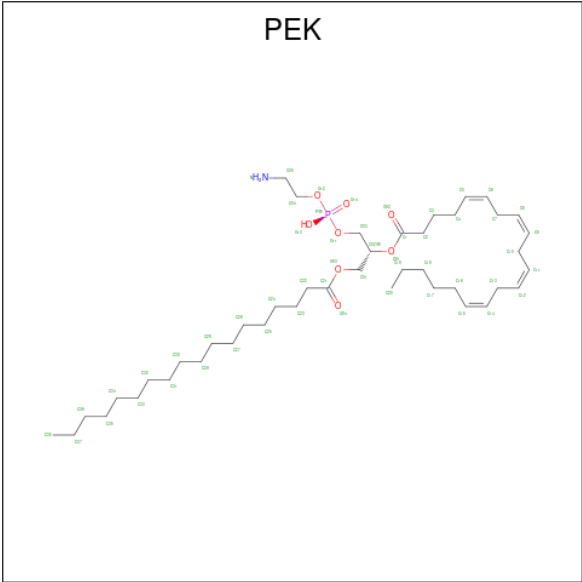
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	O	1	Total	C	O	0	0
			33	32	1		

- Molecule 25 is CHOLIC ACID (CCD ID: CHD) (formula: $C_{24}H_{40}O_5$).



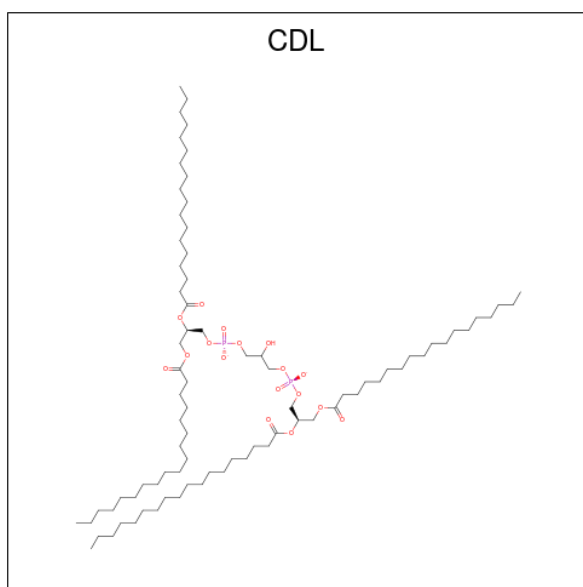
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
25	B	1	Total	C	O	0	0
			29	24	5		
25	C	1	Total	C	O	0	0
			29	24	5		
25	C	1	Total	C	O	0	0
			29	24	5		
25	G	1	Total	C	O	0	0
			29	24	5		
25	L	1	Total	C	O	0	0
			29	24	5		
25	P	1	Total	C	O	0	0
			29	24	5		
25	P	1	Total	C	O	0	0
			29	24	5		

- Molecule 26 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (CCD ID: PEK) (formula: $C_{43}H_{78}NO_8P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	C	1	Total C 18 18	0	0
26	C	1	Total C N O P 53 43 1 8 1	0	0
26	C	1	Total C O 40 38 2	0	0
26	P	1	Total C O 28 27 1	0	0
26	P	1	Total C N O P 53 43 1 8 1	0	0
26	P	1	Total C O 40 38 2	0	0

- Molecule 27 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).

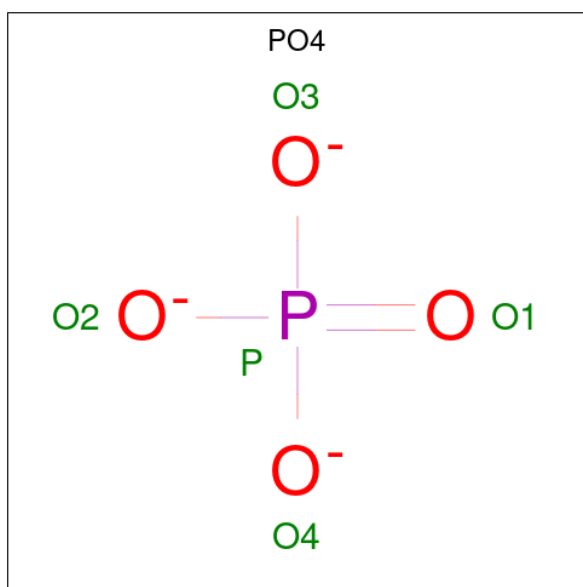


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
27	C	1	Total	C	O	P	0	0
			85	75	9	1		
27	G	1	Total	C	O		0	0
			69	67	2			
27	P	1	Total	C	O		0	0
			77	72	5			
27	T	1	Total	C	O		0	0
			70	66	4			

- 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 PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
29	H	1	Total	O	P	0	0
			5	4	1		
29	U	1	Total	O	P	0	0
			5	4	1		

- Molecule 30 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	A	248	Total	O	0	6
			250	250		
30	B	194	Total	O	0	3
			195	195		
30	C	139	Total	O	0	0
			139	139		
30	D	182	Total	O	0	1
			183	183		
30	E	133	Total	O	0	0
			133	133		
30	F	144	Total	O	0	0
			144	144		
30	G	68	Total	O	0	0
			68	68		
30	H	87	Total	O	0	0
			87	87		
30	I	63	Total	O	0	0
			63	63		
30	J	47	Total	O	0	0
			47	47		

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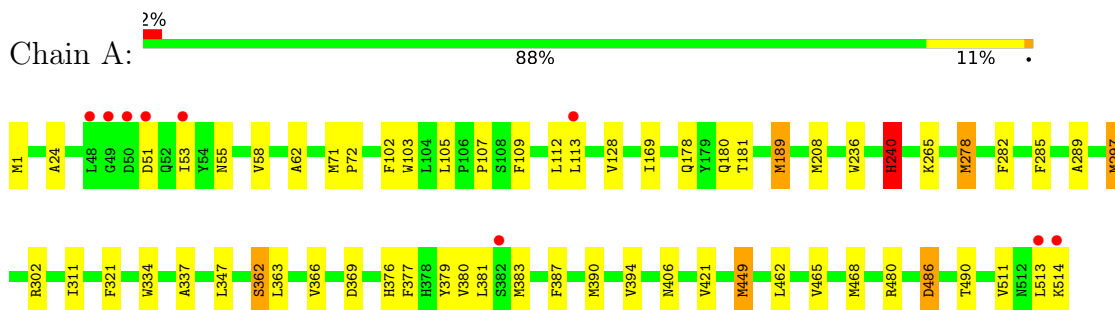
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
30	K	38	Total 38	O 38	0	0
30	L	30	Total 30	O 30	0	0
30	M	35	Total 35	O 35	0	0
30	N	247	Total 247	O 247	0	3
30	O	169	Total 169	O 169	0	1
30	P	145	Total 145	O 145	0	0
30	Q	88	Total 88	O 88	0	0
30	R	106	Total 106	O 106	0	0
30	S	133	Total 133	O 133	0	0
30	T	61	Total 61	O 61	0	0
30	U	78	Total 78	O 78	0	0
30	V	48	Total 48	O 48	0	0
30	W	46	Total 46	O 46	0	0
30	X	28	Total 28	O 28	0	0
30	Y	29	Total 29	O 29	0	0
30	Z	22	Total 22	O 22	0	0

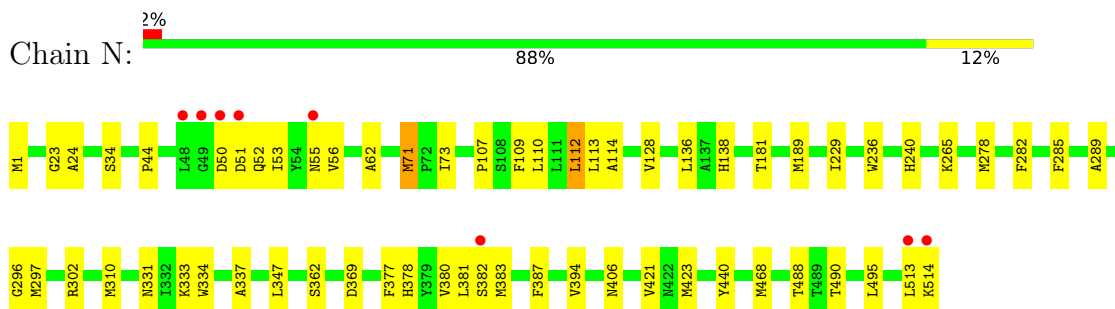
3 Residue-property plots

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.

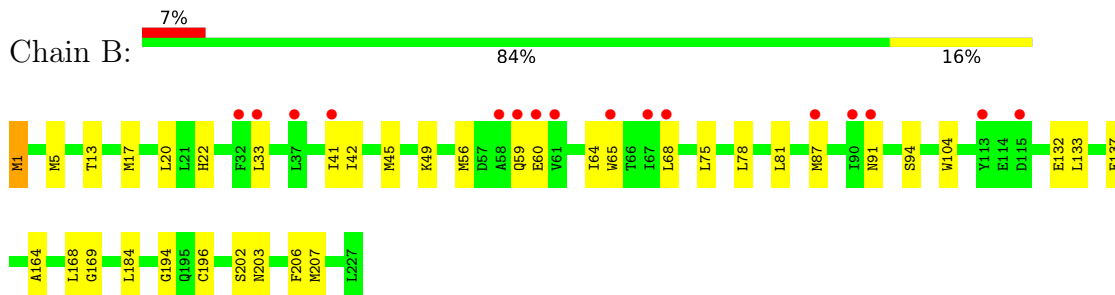
• Molecule 1: Cytochrome c oxidase subunit 1



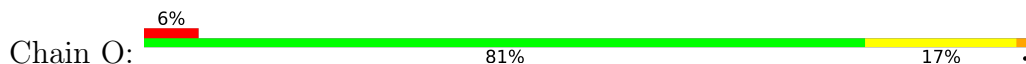
• Molecule 1: Cytochrome c oxidase subunit 1

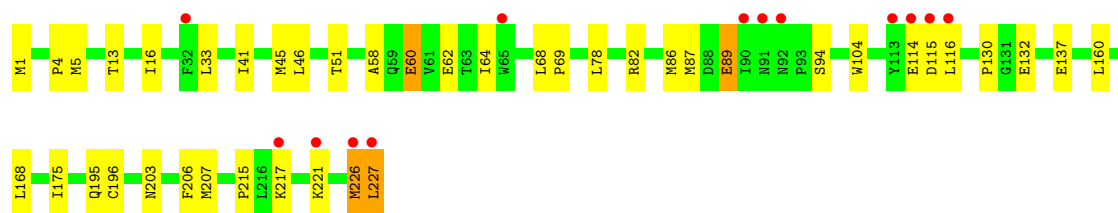


• Molecule 2: Cytochrome c oxidase subunit 2

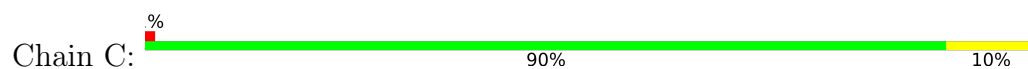


• Molecule 2: Cytochrome c oxidase subunit 2

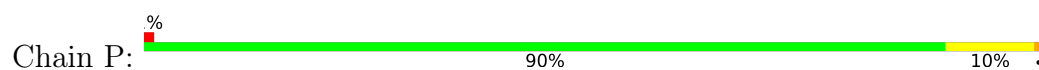




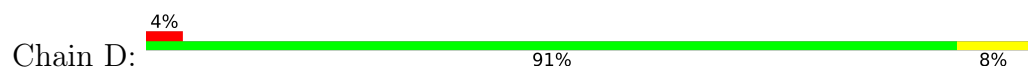
• Molecule 3: Cytochrome c oxidase subunit 3



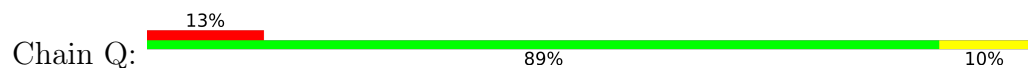
• Molecule 3: Cytochrome c oxidase subunit 3



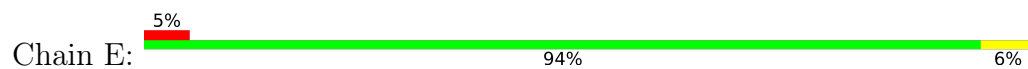
• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



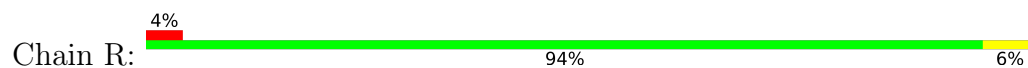
• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



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

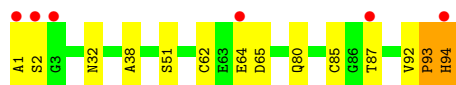
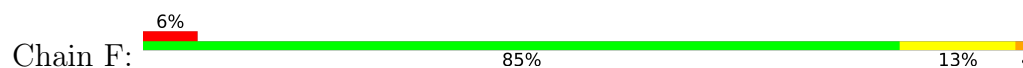


• Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial

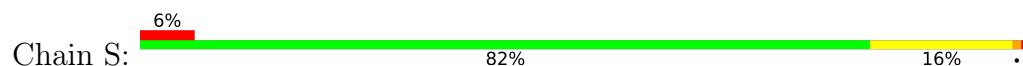




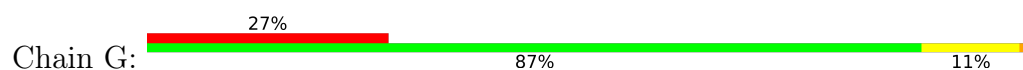
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



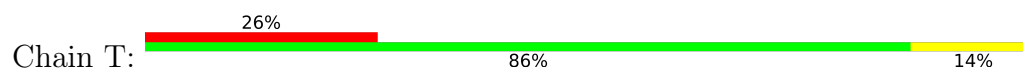
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



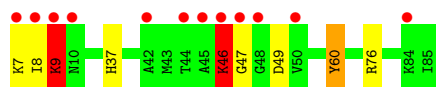
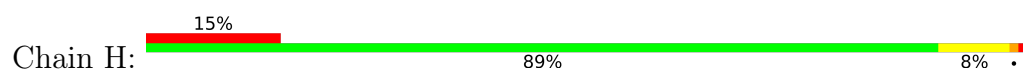
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



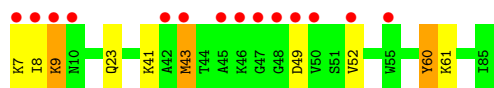
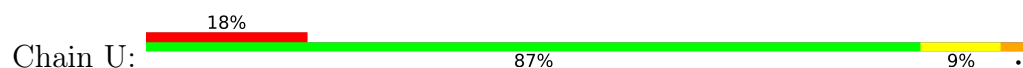
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



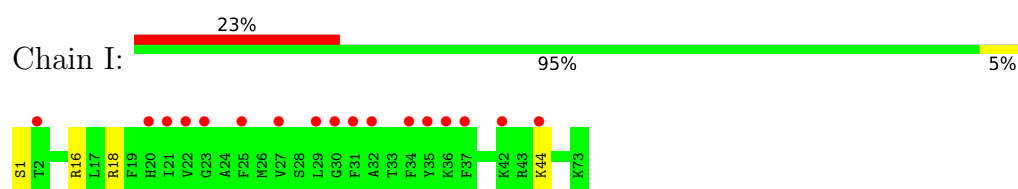
- Molecule 8: Cytochrome c oxidase subunit 6B1



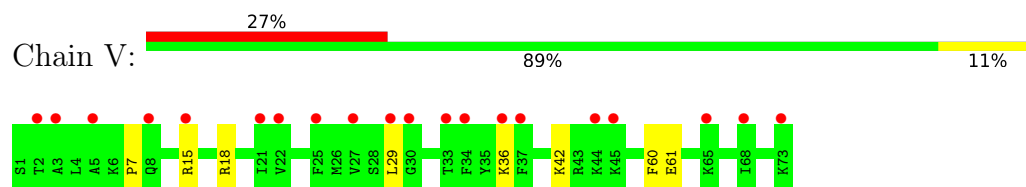
- Molecule 8: Cytochrome c oxidase subunit 6B1



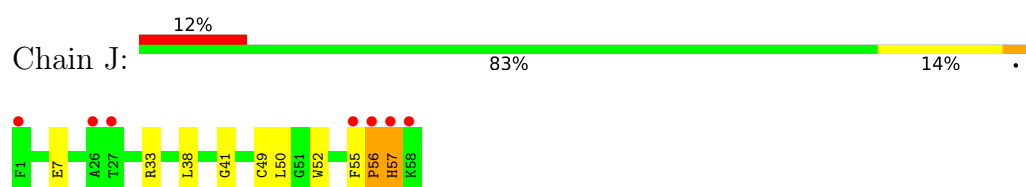
- Molecule 9: Cytochrome c oxidase subunit 6C



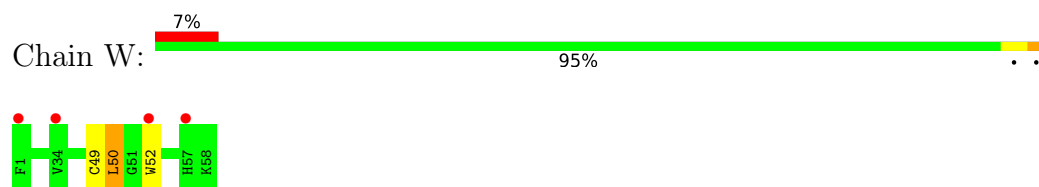
- Molecule 9: Cytochrome c oxidase subunit 6C



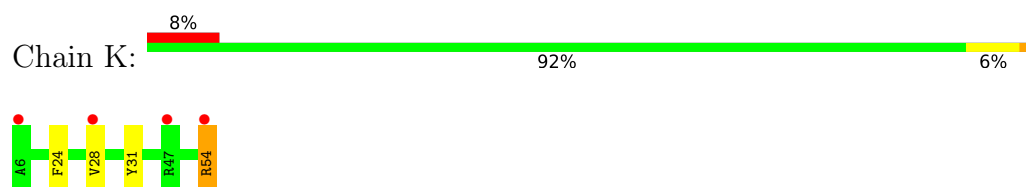
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



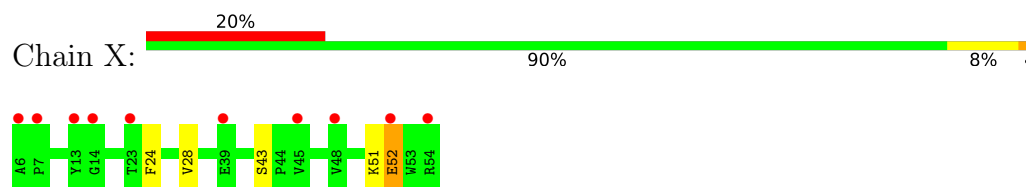
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



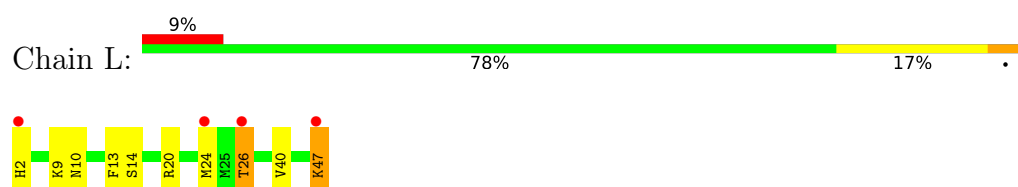
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



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



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



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

Chain Y:  11% 83% 15% .



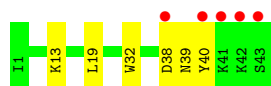
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial

Chain M:  7% 88% 12%



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

Chain Z:  12% 86% 14%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	181.77Å 203.30Å 177.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.70 – 1.74 39.70 – 1.74	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.70-1.74) 99.7 (39.70-1.74)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 1.74Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.156 , 0.184 0.156 , 0.183	Depositor DCC
R_{free} test set	33307 reflections (2.62%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.707	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 68.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.007 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33923	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, TGL, ZN, FME, MG, SAC, CHD, PSC, OXY, PEK, CDL, PGV, PO4, DMU, CUA, HEA, NA, CU

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	1.05	1/4419 (0.0%)	1.02	10/6035 (0.2%)
1	N	0.97	2/4370 (0.0%)	0.97	4/5969 (0.1%)
2	B	0.92	0/1975	1.03	3/2689 (0.1%)
2	O	0.85	0/1937	0.97	2/2637 (0.1%)
3	C	0.92	0/2295	0.86	0/3136
3	P	0.91	0/2263	0.86	0/3092
4	D	0.87	0/1229	0.92	2/1658 (0.1%)
4	Q	0.70	0/1229	0.76	0/1658
5	E	0.84	0/871	0.80	0/1182
5	R	0.70	0/871	0.75	0/1182
6	F	0.87	0/732	0.97	2/993 (0.2%)
6	S	0.89	0/732	0.98	2/993 (0.2%)
7	G	0.86	0/699	0.89	0/950
7	T	0.82	0/699	0.87	0/950
8	H	0.85	0/682	0.94	0/921
8	U	0.76	0/682	0.84	0/921
9	I	0.76	0/605	0.81	0/802
9	V	0.64	0/605	0.78	0/802
10	J	0.75	0/472	0.85	0/636
10	W	0.67	0/472	0.83	0/636
11	K	0.81	0/399	0.84	0/546
11	X	0.70	0/399	0.72	0/546
12	L	0.94	0/393	0.87	0/526
12	Y	0.79	0/393	0.81	0/526
13	M	0.85	0/346	0.83	0/470
13	Z	0.76	0/346	0.80	0/470
All	All	0.89	3/30115 (0.0%)	0.92	25/40926 (0.1%)

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
6	F	0	1
6	S	0	1
8	H	0	1
10	J	0	1
All	All	0	5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	310	MET	SD-CE	-6.42	1.63	1.79
1	A	480	ARG	CD-NE	5.36	1.53	1.46
1	N	278	MET	SD-CE	-5.05	1.67	1.79

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	71	MET	CG-SD-CE	-14.12	69.84	100.90
1	A	278	MET	CG-SD-CE	-11.93	74.65	100.90
1	N	189	MET	CG-SD-CE	-8.32	82.59	100.90
1	A	189	MET	CG-SD-CE	-7.66	84.06	100.90
1	N	240	HIS	CA-CB-CG	-7.46	106.34	113.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	HIS	Sidechain
6	F	93	PRO	Peptide
8	H	9	LYS	Peptide
10	J	56	PRO	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	4183	0	4164	65	0
1	N	4174	0	4155	60	0
2	B	1867	0	1886	27	0
2	O	1853	0	1860	32	0
3	C	2143	0	2059	29	0
3	P	2131	0	2036	27	0
4	D	1195	0	1183	12	0
4	Q	1195	0	1183	15	0
5	E	852	0	845	4	0
5	R	852	0	845	5	0
6	F	716	0	697	11	0
6	S	716	0	697	16	0
7	G	672	0	645	6	0
7	T	672	0	645	10	0
8	H	662	0	623	4	0
8	U	662	0	623	9	0
9	I	601	0	613	2	0
9	V	601	0	613	5	0
10	J	461	0	459	12	0
10	W	461	0	459	3	0
11	K	385	0	366	3	0
11	X	385	0	366	5	0
12	L	380	0	380	12	0
12	Y	380	0	380	5	0
13	M	336	0	352	5	0
13	Z	336	0	352	2	0
14	A	141	0	115	7	0
14	N	141	0	115	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	C	1	0	0	0	0
17	N	1	0	0	0	0
17	P	1	0	0	0	0
18	A	84	0	136	8	0
18	C	88	0	138	2	0
18	N	51	0	76	1	0
18	P	89	0	140	4	0
18	Q	37	0	62	6	0
19	A	2	0	0	0	0
19	N	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	A	44	0	66	4	0
20	B	24	0	36	0	0
20	C	36	0	54	1	0
20	D	16	0	24	0	0
20	E	12	0	18	0	0
20	F	24	0	36	0	0
20	G	4	0	6	0	0
20	J	8	0	12	1	0
20	L	4	0	6	1	0
20	M	4	0	6	0	0
20	N	44	0	66	0	0
20	O	8	0	12	0	0
20	P	28	0	42	2	0
20	Q	8	0	12	1	0
20	R	8	0	12	2	0
20	S	28	0	41	1	0
20	T	12	0	18	0	0
20	W	8	0	12	2	0
20	Y	4	0	6	0	0
21	A	17	0	32	0	0
21	C	34	0	52	7	0
21	D	19	0	36	0	0
21	J	11	0	21	3	0
21	K	37	0	70	2	0
21	L	21	0	30	1	0
21	M	33	0	42	0	0
21	N	9	0	17	1	0
21	O	11	0	21	0	0
21	P	33	0	52	6	0
21	Q	10	0	19	1	0
21	W	11	0	21	0	0
21	X	27	0	51	0	0
21	Z	33	0	42	0	0
22	B	63	0	110	7	0
22	D	63	0	110	14	0
22	L	54	0	87	9	0
22	N	161	0	294	16	0
23	B	2	0	0	0	0
23	O	2	0	0	0	0
24	B	41	0	65	7	0
24	O	33	0	58	4	0
25	B	29	0	39	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	C	58	0	78	1	0
25	G	29	0	39	1	0
25	L	29	0	39	1	0
25	P	58	0	78	3	0
26	C	111	0	168	14	0
26	P	121	0	182	13	0
27	C	85	0	143	12	0
27	G	69	0	126	8	0
27	P	77	0	137	10	0
27	T	70	0	125	19	0
28	F	1	0	0	0	0
28	S	1	0	0	0	0
29	H	5	0	0	0	0
29	U	5	0	0	0	0
30	A	250	0	0	7	0
30	B	195	0	0	3	0
30	C	139	0	0	3	0
30	D	183	0	0	3	0
30	E	133	0	0	3	0
30	F	144	0	0	2	0
30	G	68	0	0	2	0
30	H	87	0	0	0	0
30	I	63	0	0	1	0
30	J	47	0	0	3	0
30	K	38	0	0	0	0
30	L	30	0	0	3	0
30	M	35	0	0	0	0
30	N	247	0	0	3	0
30	O	169	0	0	1	0
30	P	145	0	0	2	0
30	Q	88	0	0	2	0
30	R	106	0	0	0	0
30	S	133	0	0	4	0
30	T	61	0	0	3	0
30	U	78	0	0	3	0
30	V	48	0	0	4	0
30	W	46	0	0	1	0
30	X	28	0	0	1	0
30	Y	29	0	0	0	0
30	Z	22	0	0	1	0
All	All	33923	0	32137	425	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 425 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)
3:P:161[A]:GLN:HE22	26:P:305:PEK:H41	1.27	0.97
1:N:113:LEU:HB2	22:N:607:TGL:H312	1.44	0.95
1:A:486[B]:ASP:OD2	4:D:19:ARG:HD2	1.67	0.93
12:L:20:ARG:HH21	22:L:101:TGL:HC32	1.36	0.88
1:A:113:LEU:HB2	22:L:101:TGL:H302	1.54	0.87

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	547/514 (106%)	531 (97%)	16 (3%)	0	100	100
1	N	540/514 (105%)	529 (98%)	11 (2%)	0	100	100
2	B	239/227 (105%)	232 (97%)	7 (3%)	0	100	100
2	O	234/227 (103%)	227 (97%)	7 (3%)	0	100	100
3	C	269/259 (104%)	264 (98%)	5 (2%)	0	100	100
3	P	265/259 (102%)	259 (98%)	6 (2%)	0	100	100
4	D	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
4	Q	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
5	E	103/105 (98%)	103 (100%)	0	0	100	100
5	R	103/105 (98%)	103 (100%)	0	0	100	100
6	F	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
6	S	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
7	G	82/84 (98%)	70 (85%)	8 (10%)	4 (5%)	1	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	T	82/84 (98%)	69 (84%)	11 (13%)	2 (2%)	4	0
8	H	77/79 (98%)	71 (92%)	3 (4%)	3 (4%)	2	0
8	U	77/79 (98%)	73 (95%)	3 (4%)	1 (1%)	9	1
9	I	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
9	V	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
10	J	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
10	W	56/58 (97%)	56 (100%)	0	0	100	100
11	K	47/49 (96%)	46 (98%)	1 (2%)	0	100	100
11	X	47/49 (96%)	46 (98%)	1 (2%)	0	100	100
12	L	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
12	Y	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
13	M	41/43 (95%)	41 (100%)	0	0	100	100
13	Z	41/43 (95%)	40 (98%)	1 (2%)	0	100	100
All	All	3604/3550 (102%)	3492 (97%)	102 (3%)	10 (0%)	36	23

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	37	LEU
8	H	46	LYS
8	H	47	GLY
7	G	5	LYS
7	T	5	LYS

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	458/426 (108%)	446 (97%)	12 (3%)	40	17
1	N	451/426 (106%)	446 (99%)	5 (1%)	65	50
2	B	224/210 (107%)	213 (95%)	11 (5%)	22	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	O	219/210 (104%)	210 (96%)	9 (4%)	27	6
3	C	236/224 (105%)	234 (99%)	2 (1%)	73	64
3	P	232/224 (104%)	226 (97%)	6 (3%)	40	17
4	D	128/128 (100%)	127 (99%)	1 (1%)	73	64
4	Q	128/128 (100%)	123 (96%)	5 (4%)	28	7
5	E	92/92 (100%)	91 (99%)	1 (1%)	65	50
5	R	92/92 (100%)	92 (100%)	0	100	100
6	F	78/78 (100%)	75 (96%)	3 (4%)	29	8
6	S	78/78 (100%)	75 (96%)	3 (4%)	29	8
7	G	68/68 (100%)	62 (91%)	6 (9%)	9	1
7	T	68/68 (100%)	64 (94%)	4 (6%)	18	3
8	H	71/71 (100%)	66 (93%)	5 (7%)	14	2
8	U	71/71 (100%)	67 (94%)	4 (6%)	19	3
9	I	57/57 (100%)	56 (98%)	1 (2%)	51	30
9	V	57/57 (100%)	54 (95%)	3 (5%)	20	4
10	J	49/49 (100%)	48 (98%)	1 (2%)	48	26
10	W	49/49 (100%)	48 (98%)	1 (2%)	48	26
11	K	39/39 (100%)	38 (97%)	1 (3%)	40	17
11	X	39/39 (100%)	38 (97%)	1 (3%)	40	17
12	L	39/39 (100%)	36 (92%)	3 (8%)	12	1
12	Y	39/39 (100%)	36 (92%)	3 (8%)	12	1
13	M	37/37 (100%)	37 (100%)	0	100	100
13	Z	37/37 (100%)	34 (92%)	3 (8%)	11	1
All	All	3136/3036 (103%)	3042 (97%)	94 (3%)	38	12

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	94	SER
4	Q	58	GLU
2	O	226	MET
3	P	180[B]	GLU
7	T	8	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
6	S	94	HIS
7	T	34	ASN
8	U	32	ASN
7	G	41	HIS
7	G	34	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	FME	N	1	1	8,9,10	0.58	0	8,9,11	1.48	2 (25%)
9	SAC	V	1	9	7,8,9	0.64	0	7,9,11	1.11	0
2	FME	B	1	2	8,9,10	1.18	0	8,9,11	1.91	4 (50%)
9	SAC	I	1	9	7,8,9	0.66	0	7,9,11	0.90	1 (14%)
2	FME	O	1	2	8,9,10	1.08	0	8,9,11	1.24	1 (12%)
1	FME	A	1	1	8,9,10	0.66	0	8,9,11	1.39	2 (25%)

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. '2' 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	-
9	SAC	V	1	9	-	3/7/8/10	-

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

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	1	FME	O-C-CA	-3.23	116.45	124.77
2	B	1	FME	CG-CB-CA	-3.19	103.10	112.87
2	B	1	FME	C-CA-N	-2.41	104.84	109.50
2	B	1	FME	O-C-CA	-2.30	118.84	124.77
1	A	1	FME	O-C-CA	-2.18	119.17	124.77

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	N-CA-CB-CG
1	N	1	FME	O1-CN-N-CA
1	N	1	FME	N-CA-CB-CG
9	V	1	SAC	C2A-C1A-N-CA
9	V	1	SAC	OAC-C1A-N-CA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 161 ligands modelled in this entry, 10 are monoatomic - leaving 151 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$
20	EDO	N	614	-	3,3,3	0.63	0	2,2,2	0.30	0
20	EDO	B	310	-	3,3,3	0.46	0	2,2,2	0.75	0
25	CHD	P	301	-	32,32,32	0.91	1 (3%)	51,51,51	1.54	8 (15%)
20	EDO	E	202	-	3,3,3	0.59	0	2,2,2	0.17	0
20	EDO	N	611	-	3,3,3	0.41	0	2,2,2	0.68	0
20	EDO	F	107	-	3,3,3	0.58	0	2,2,2	0.13	0
20	EDO	A	614	-	3,3,3	0.73	0	2,2,2	0.31	0
14	HEA	A	601[A]	-	67,67,67	1.87	21 (31%)	81,103,103	2.12	26 (32%)
20	EDO	A	616	-	3,3,3	0.15	0	2,2,2	0.31	0
21	DMU	K	104	-	9,9,34	0.36	0	8,8,45	0.53	0
27	CDL	C	308	-	77,82,99	1.41	10 (12%)	76,83,111	1.60	12 (15%)
21	DMU	C	310	-	22,22,34	1.04	1 (4%)	27,27,45	1.59	6 (22%)
22	TGL	L	101	-	49,50,62	1.04	2 (4%)	47,48,65	1.36	5 (10%)
20	EDO	F	103	-	3,3,3	0.81	0	2,2,2	0.53	0
25	CHD	L	102	-	32,32,32	0.75	0	51,51,51	2.80	25 (49%)
24	PSC	O	302	-	30,31,51	0.82	1 (3%)	28,29,59	1.29	2 (7%)
29	PO4	U	101	-	4,4,4	1.22	0	6,6,6	1.08	0
20	EDO	T	102	-	3,3,3	0.49	0	2,2,2	0.35	0
21	DMU	L	104	-	21,21,34	0.72	0	24,25,45	1.66	4 (16%)
20	EDO	N	617	-	3,3,3	0.43	0	2,2,2	0.60	0
23	CUA	O	301	2	0,1,1	-	-	-	-	-
20	EDO	N	621	-	3,3,3	0.21	0	2,2,2	0.97	0
25	CHD	G	102	-	32,32,32	1.16	3 (9%)	51,51,51	1.63	12 (23%)
26	PEK	P	304	-	52,52,52	0.75	2 (3%)	55,57,57	1.11	2 (3%)
20	EDO	C	311	-	3,3,3	1.07	0	2,2,2	0.45	0
20	EDO	Y	101	-	3,3,3	0.35	0	2,2,2	0.27	0
27	CDL	G	101	-	65,65,99	1.41	9 (13%)	62,62,111	1.14	3 (4%)
21	DMU	K	103	-	8,8,34	0.49	0	7,7,45	0.30	0
20	EDO	A	617	-	3,3,3	1.06	0	2,2,2	0.76	0
20	EDO	P	315	-	3,3,3	0.44	0	2,2,2	0.99	0
20	EDO	A	619	-	3,3,3	0.43	0	2,2,2	0.58	0
20	EDO	A	610	-	3,3,3	0.92	0	2,2,2	0.62	0
20	EDO	S	104	-	3,3,3	0.65	0	2,2,2	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	PO4	H	101	-	4,4,4	0.74	0	6,6,6	0.85	0
22	TGL	N	606	-	62,62,62	1.09	3 (4%)	65,65,65	1.18	4 (6%)
20	EDO	P	314	-	3,3,3	0.79	0	2,2,2	0.17	0
25	CHD	B	304	-	32,32,32	0.99	0	51,51,51	1.69	13 (25%)
14	HEA	N	602	1,19	67,67,67	1.85	20 (29%)	81,103,103	1.98	27 (33%)
19	OXY	N	609	14,15	1,1,1	0.14	0	-		
21	DMU	W	103	-	10,10,34	0.31	0	9,9,45	0.89	0
20	EDO	C	313	-	3,3,3	0.67	0	2,2,2	0.46	0
21	DMU	X	101	-	8,8,34	0.40	0	7,7,45	0.42	0
20	EDO	S	106	-	3,3,3	0.63	0	2,2,2	0.88	0
18	PGV	C	307	-	35,35,50	0.95	1 (2%)	34,34,56	1.53	5 (14%)
20	EDO	M	102	-	3,3,3	0.42	0	2,2,2	0.35	0
21	DMU	J	103	-	10,10,34	0.50	0	9,9,45	0.64	0
21	DMU	X	102	-	7,7,34	0.43	0	6,6,45	0.36	0
20	EDO	Q	204	-	3,3,3	0.27	0	2,2,2	0.57	0
14	HEA	N	601[A]	-	67,67,67	1.76	17 (25%)	81,103,103	2.08	26 (32%)
18	PGV	P	306	-	50,50,50	0.81	2 (4%)	53,56,56	1.29	4 (7%)
20	EDO	B	306	-	3,3,3	0.46	0	2,2,2	0.52	0
22	TGL	N	607	-	40,40,62	0.45	0	37,37,65	0.88	1 (2%)
25	CHD	C	309	-	32,32,32	0.82	0	51,51,51	1.33	8 (15%)
20	EDO	T	104	-	3,3,3	0.63	0	2,2,2	1.02	0
20	EDO	P	317	-	3,3,3	0.36	0	2,2,2	0.54	0
20	EDO	A	611	-	3,3,3	0.67	0	2,2,2	0.14	0
20	EDO	N	616	-	3,3,3	0.63	0	2,2,2	0.54	0
20	EDO	C	318	-	3,3,3	0.48	0	2,2,2	0.64	0
20	EDO	S	107	-	3,3,3	0.85	0	2,2,2	0.69	0
27	CDL	P	308	-	73,73,99	1.46	11 (15%)	73,73,111	2.15	9 (12%)
20	EDO	E	203	-	3,3,3	0.45	0	2,2,2	0.62	0
18	PGV	A	608	-	50,50,50	1.10	4 (8%)	53,56,56	1.16	6 (11%)
20	EDO	F	104	-	3,3,3	0.35	0	2,2,2	0.61	0
20	EDO	N	612	-	3,3,3	1.02	0	2,2,2	0.63	0
20	EDO	C	317	-	3,3,3	0.27	0	2,2,2	0.20	0
21	DMU	D	207	-	7,7,34	0.47	0	6,6,45	0.43	0
21	DMU	K	102	-	8,8,34	0.36	0	7,7,45	0.35	0
20	EDO	C	312	-	3,3,3	0.76	0	2,2,2	0.20	0
20	EDO	N	613	-	3,3,3	0.87	0	2,2,2	0.29	0
20	EDO	J	101	-	3,3,3	0.47	0	2,2,2	0.30	0
19	OXY	A	607	14,15	1,1,1	0.12	0	-		
20	EDO	B	305	-	3,3,3	0.66	0	2,2,2	0.23	0
22	TGL	D	201	-	62,62,62	1.18	3 (4%)	65,65,65	1.60	9 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	PEK	C	304	-	52,52,52	0.86	2 (3%)	55,57,57	1.14	2 (3%)
20	EDO	P	313	-	3,3,3	0.41	0	2,2,2	0.28	0
20	EDO	F	106	-	3,3,3	0.54	0	2,2,2	0.63	0
20	EDO	J	102	-	3,3,3	0.32	0	2,2,2	0.64	0
18	PGV	Q	201	-	35,35,50	0.87	1 (2%)	34,34,56	1.39	3 (8%)
20	EDO	N	619	-	3,3,3	0.54	0	2,2,2	0.64	0
20	EDO	B	308	-	3,3,3	0.52	0	2,2,2	0.57	0
20	EDO	D	202	-	3,3,3	0.36	0	2,2,2	0.40	0
20	EDO	A	609	-	3,3,3	0.50	0	2,2,2	0.86	0
21	DMU	C	320	-	11,11,34	0.47	0	10,10,45	0.90	0
20	EDO	G	103	-	3,3,3	0.65	0	2,2,2	0.86	0
20	EDO	A	618	-	3,3,3	0.43	0	2,2,2	0.55	0
20	EDO	N	620	-	3,3,3	0.79	0	2,2,2	0.15	0
20	EDO	B	309	-	3,3,3	0.74	0	2,2,2	0.26	0
20	EDO	O	304	-	3,3,3	0.31	0	2,2,2	0.22	0
20	EDO	F	102	-	3,3,3	0.96	0	2,2,2	0.70	0
20	EDO	S	108	-	3,3,3	0.28	0	2,2,2	1.01	0
20	EDO	R	201	-	3,3,3	0.64	0	2,2,2	0.50	0
25	CHD	C	301	-	32,32,32	1.21	4 (12%)	51,51,51	1.72	14 (27%)
20	EDO	B	307	-	3,3,3	0.32	0	2,2,2	0.85	0
21	DMU	P	318	-	10,10,34	0.33	0	9,9,45	0.47	0
20	EDO	L	103	-	3,3,3	0.53	0	2,2,2	0.66	0
20	EDO	S	103	-	3,3,3	0.57	0	2,2,2	0.08	0
21	DMU	M	101	-	34,34,34	0.52	0	45,45,45	1.22	6 (13%)
21	DMU	D	206	-	10,10,34	0.37	0	9,9,45	0.46	0
20	EDO	C	319	-	3,3,3	0.43	0	2,2,2	0.45	0
20	EDO	A	613	-	3,3,3	0.58	0	2,2,2	0.20	0
18	PGV	N	610	-	50,50,50	1.05	3 (6%)	53,56,56	1.29	6 (11%)
18	PGV	C	306	-	50,50,50	0.86	2 (4%)	53,56,56	1.03	5 (9%)
20	EDO	D	205	-	3,3,3	0.39	0	2,2,2	0.70	0
20	EDO	O	303	-	3,3,3	0.74	0	2,2,2	0.69	0
27	CDL	T	101	-	67,67,99	1.55	11 (16%)	67,67,111	1.64	12 (17%)
20	EDO	F	105	-	3,3,3	0.70	0	2,2,2	0.65	0
21	DMU	K	101	-	8,8,34	0.22	0	7,7,45	0.61	0
26	PEK	C	305	-	38,38,52	0.96	1 (2%)	37,37,57	1.48	4 (10%)
14	HEA	A	602	1,19	67,67,67	1.85	20 (29%)	81,103,103	1.95	27 (33%)
21	DMU	N	622	-	8,8,34	0.25	0	7,7,45	0.66	0
22	TGL	N	608	-	52,52,62	0.74	1 (1%)	50,50,65	0.82	1 (2%)
20	EDO	C	315	-	3,3,3	0.53	0	2,2,2	0.18	0
21	DMU	A	620	-	8,8,34	0.35	0	7,7,45	0.54	0
20	EDO	A	612	-	3,3,3	0.34	0	2,2,2	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	EDO	D	203	-	3,3,3	0.53	0	2,2,2	0.30	0
20	EDO	S	105	-	3,3,3	3.35	1 (33%)	2,2,2	1.89	1 (50%)
20	EDO	Q	203	-	3,3,3	0.37	0	2,2,2	0.16	0
26	PEK	C	303	-	17,17,52	0.48	0	16,16,57	0.96	1 (6%)
21	DMU	X	103	-	9,9,34	0.55	0	8,8,45	0.37	0
20	EDO	P	316	-	3,3,3	0.30	0	2,2,2	1.44	0
18	PGV	A	606	-	30,31,50	0.53	0	28,29,56	0.55	0
20	EDO	N	618	-	3,3,3	0.46	0	2,2,2	0.40	0
20	EDO	A	615	-	3,3,3	0.41	0	2,2,2	0.41	0
20	EDO	W	102	-	3,3,3	0.21	0	2,2,2	0.79	0
21	DMU	O	305	-	10,10,34	0.32	0	9,9,45	0.44	0
20	EDO	D	204	-	3,3,3	0.40	0	2,2,2	0.55	0
21	DMU	P	310	-	22,22,34	1.08	1 (4%)	27,27,45	1.56	4 (14%)
22	TGL	B	301	-	62,62,62	1.08	3 (4%)	65,65,65	1.52	6 (9%)
20	EDO	E	201	-	3,3,3	0.49	0	2,2,2	0.38	0
26	PEK	P	303	-	25,26,52	0.36	0	23,24,57	0.85	1 (4%)
20	EDO	C	316	-	3,3,3	0.52	0	2,2,2	0.91	0
21	DMU	Q	202	-	9,9,34	0.57	0	8,8,45	0.35	0
21	DMU	A	621	-	7,7,34	0.25	0	6,6,45	0.45	0
20	EDO	R	202	-	3,3,3	0.29	0	2,2,2	0.74	0
24	PSC	B	303	-	40,40,51	1.32	3 (7%)	42,42,59	1.87	5 (11%)
26	PEK	P	305	-	38,38,52	0.94	1 (2%)	37,37,57	1.06	4 (10%)
23	CUA	B	302	2	0,1,1	-	-	-	-	-
20	EDO	P	311	-	3,3,3	0.24	0	2,2,2	0.80	0
20	EDO	W	101	-	3,3,3	0.45	0	2,2,2	0.54	0
20	EDO	T	103	-	3,3,3	0.58	0	2,2,2	0.24	0
20	EDO	P	312	-	3,3,3	0.82	0	2,2,2	0.20	0
21	DMU	Z	101	-	34,34,34	0.62	1 (2%)	45,45,45	1.09	3 (6%)
25	CHD	P	309	-	32,32,32	1.07	2 (6%)	51,51,51	1.89	16 (31%)
18	PGV	P	307	-	36,36,50	1.01	1 (2%)	35,35,56	1.34	4 (11%)
20	EDO	C	314	-	3,3,3	0.32	0	2,2,2	0.49	0
20	EDO	N	615	-	3,3,3	0.52	0	2,2,2	0.37	0
20	EDO	S	102	-	3,3,3	0.99	0	2,2,2	0.75	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
20	EDO	N	614	-	-	1/1/1/1	-
20	EDO	B	310	-	-	0/1/1/1	-
25	CHD	P	301	-	-	2/9/74/74	0/4/4/4
20	EDO	E	202	-	-	1/1/1/1	-
20	EDO	N	611	-	-	0/1/1/1	-
20	EDO	F	107	-	-	1/1/1/1	-
20	EDO	A	614	-	-	0/1/1/1	-
14	HEA	A	601[A]	-	-	10/36/76/76	-
20	EDO	A	616	-	-	1/1/1/1	-
21	DMU	K	104	-	-	2/7/7/59	-
27	CDL	C	308	-	-	33/78/80/110	-
21	DMU	C	310	-	-	7/13/33/59	0/1/1/2
22	TGL	L	101	-	-	26/44/44/65	-
20	EDO	F	103	-	-	0/1/1/1	-
25	CHD	L	102	-	-	5/9/74/74	0/4/4/4
24	PSC	O	302	-	-	12/27/27/55	-
20	EDO	T	102	-	-	0/1/1/1	-
21	DMU	L	104	-	-	6/13/29/59	0/1/1/2
20	EDO	N	617	-	-	0/1/1/1	-
20	EDO	N	621	-	-	1/1/1/1	-
25	CHD	G	102	-	-	2/9/74/74	0/4/4/4
26	PEK	P	304	-	-	10/56/56/56	-
20	EDO	C	311	-	-	0/1/1/1	-
20	EDO	Y	101	-	-	0/1/1/1	-
27	CDL	G	101	-	-	17/58/58/110	-
21	DMU	K	103	-	-	4/6/6/59	-
20	EDO	A	617	-	-	0/1/1/1	-
20	EDO	P	315	-	-	0/1/1/1	-
20	EDO	A	619	-	-	1/1/1/1	-
20	EDO	A	610	-	-	0/1/1/1	-
20	EDO	S	104	-	-	0/1/1/1	-
22	TGL	N	606	-	-	33/65/65/65	-
20	EDO	P	314	-	-	0/1/1/1	-
25	CHD	B	304	-	-	2/9/74/74	0/4/4/4
14	HEA	N	602	1,19	-	6/36/76/76	-
21	DMU	W	103	-	-	4/8/8/59	-
20	EDO	C	313	-	-	0/1/1/1	-
21	DMU	X	101	-	-	2/6/6/59	-
20	EDO	S	106	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	PGV	C	307	-	-	8/32/32/55	-
20	EDO	M	102	-	-	1/1/1/1	-
21	DMU	J	103	-	-	1/8/8/59	-
21	DMU	X	102	-	-	1/5/5/59	-
20	EDO	Q	204	-	-	1/1/1/1	-
14	HEA	N	601[A]	-	-	7/36/76/76	-
18	PGV	P	306	-	-	12/55/55/55	-
20	EDO	B	306	-	-	0/1/1/1	-
22	TGL	N	607	-	-	19/34/34/65	-
25	CHD	C	309	-	-	5/9/74/74	0/4/4/4
20	EDO	T	104	-	-	0/1/1/1	-
20	EDO	P	317	-	-	1/1/1/1	-
20	EDO	A	611	-	-	1/1/1/1	-
20	EDO	N	616	-	-	0/1/1/1	-
20	EDO	C	318	-	-	1/1/1/1	-
20	EDO	S	107	-	-	0/1/1/1	-
27	CDL	P	308	-	-	30/70/70/110	-
20	EDO	E	203	-	-	0/1/1/1	-
18	PGV	A	608	-	-	7/55/55/55	-
20	EDO	F	104	-	-	0/1/1/1	-
20	EDO	N	612	-	-	0/1/1/1	-
20	EDO	C	317	-	-	1/1/1/1	-
21	DMU	D	207	-	-	1/5/5/59	-
21	DMU	K	102	-	-	3/6/6/59	-
20	EDO	C	312	-	-	0/1/1/1	-
20	EDO	N	613	-	-	0/1/1/1	-
20	EDO	J	101	-	-	0/1/1/1	-
20	EDO	B	305	-	-	0/1/1/1	-
22	TGL	D	201	-	-	35/65/65/65	-
26	PEK	C	304	-	-	16/56/56/56	-
20	EDO	P	313	-	-	1/1/1/1	-
20	EDO	F	106	-	-	0/1/1/1	-
20	EDO	J	102	-	-	1/1/1/1	-
18	PGV	Q	201	-	-	10/32/32/55	-
20	EDO	N	619	-	-	0/1/1/1	-
20	EDO	B	308	-	-	0/1/1/1	-
20	EDO	D	202	-	-	0/1/1/1	-
20	EDO	A	609	-	-	1/1/1/1	-
21	DMU	C	320	-	-	2/9/9/59	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
20	EDO	G	103	-	-	0/1/1/1	-
20	EDO	A	618	-	-	0/1/1/1	-
20	EDO	N	620	-	-	1/1/1/1	-
20	EDO	B	309	-	-	1/1/1/1	-
20	EDO	O	304	-	-	0/1/1/1	-
20	EDO	F	102	-	-	0/1/1/1	-
20	EDO	S	108	-	-	0/1/1/1	-
20	EDO	R	201	-	-	0/1/1/1	-
25	CHD	C	301	-	-	2/9/74/74	0/4/4/4
20	EDO	B	307	-	-	1/1/1/1	-
21	DMU	P	318	-	-	2/8/8/59	-
20	EDO	L	103	-	-	0/1/1/1	-
20	EDO	S	103	-	-	0/1/1/1	-
21	DMU	M	101	-	-	6/19/59/59	0/2/2/2
21	DMU	D	206	-	-	4/8/8/59	-
20	EDO	C	319	-	-	0/1/1/1	-
20	EDO	A	613	-	-	1/1/1/1	-
18	PGV	N	610	-	-	6/55/55/55	-
18	PGV	C	306	-	-	13/55/55/55	-
20	EDO	D	205	-	-	0/1/1/1	-
20	EDO	O	303	-	-	0/1/1/1	-
27	CDL	T	101	-	-	30/64/64/110	-
20	EDO	F	105	-	-	0/1/1/1	-
21	DMU	K	101	-	-	2/6/6/59	-
26	PEK	C	305	-	-	17/35/35/56	-
14	HEA	A	602	1,19	-	6/36/76/76	-
21	DMU	N	622	-	-	4/6/6/59	-
22	TGL	N	608	-	-	25/47/47/65	-
20	EDO	C	315	-	-	0/1/1/1	-
21	DMU	A	620	-	-	2/6/6/59	-
20	EDO	A	612	-	-	1/1/1/1	-
20	EDO	D	203	-	-	0/1/1/1	-
20	EDO	S	105	-	-	0/1/1/1	-
20	EDO	Q	203	-	-	1/1/1/1	-
26	PEK	C	303	-	-	9/15/15/56	-
21	DMU	X	103	-	-	0/7/7/59	-
20	EDO	P	316	-	-	1/1/1/1	-
18	PGV	A	606	-	-	10/27/27/55	-
20	EDO	N	618	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
20	EDO	A	615	-	-	1/1/1/1	-
20	EDO	W	102	-	-	1/1/1/1	-
21	DMU	O	305	-	-	6/8/8/59	-
20	EDO	D	204	-	-	0/1/1/1	-
21	DMU	P	310	-	-	3/13/33/59	0/1/1/2
22	TGL	B	301	-	-	34/65/65/65	-
20	EDO	E	201	-	-	0/1/1/1	-
26	PEK	P	303	-	-	11/22/22/56	-
20	EDO	C	316	-	-	1/1/1/1	-
21	DMU	Q	202	-	-	3/7/7/59	-
21	DMU	A	621	-	-	2/5/5/59	-
20	EDO	R	202	-	-	0/1/1/1	-
24	PSC	B	303	-	-	16/41/41/55	-
26	PEK	P	305	-	-	15/35/35/56	-
20	EDO	P	311	-	-	1/1/1/1	-
20	EDO	W	101	-	-	1/1/1/1	-
20	EDO	T	103	-	-	1/1/1/1	-
20	EDO	P	312	-	-	0/1/1/1	-
21	DMU	Z	101	-	-	6/19/59/59	0/2/2/2
25	CHD	P	309	-	-	5/9/74/74	0/4/4/4
18	PGV	P	307	-	-	13/33/33/55	-
20	EDO	C	314	-	-	1/1/1/1	-
20	EDO	N	615	-	-	0/1/1/1	-
20	EDO	S	102	-	-	0/1/1/1	-

The worst 5 of 169 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	S	105	EDO	O1-C1	-5.69	1.13	1.42
18	P	307	PGV	O03-C19	5.40	1.49	1.33
22	D	201	TGL	OG2-CB1	5.32	1.49	1.34
27	G	101	CDL	OB8-CB7	5.26	1.48	1.33
27	T	101	CDL	OB8-CB7	5.23	1.48	1.33

The worst 5 of 342 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	P	308	CDL	CB4-OB6-CB5	-13.28	98.63	117.78
22	B	301	TGL	OG2-CB1-CB2	8.51	129.88	111.48
14	N	601[A]	HEA	C13-C12-C11	-7.56	102.32	114.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	T	101	CDL	OB6-CB5-C51	7.52	127.76	111.48
25	L	102	CHD	C11-C12-C13	6.68	118.06	111.26

There are no chirality outliers.

5 of 621 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	602	HEA	C4D-C3D-CAD-CBD
18	A	606	PGV	C1-C2-C3-C4
21	L	104	DMU	O5-C6-O16-C18
22	D	201	TGL	CB2-CB1-OG2-CG2
22	D	201	TGL	OB1-CB1-OG2-CG2

There are no ring outliers.

55 monomers are involved in 199 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	A	601[A]	HEA	3	0
20	A	616	EDO	1	0
21	K	104	DMU	1	0
27	C	308	CDL	12	0
21	C	310	DMU	6	0
22	L	101	TGL	9	0
25	L	102	CHD	1	0
24	O	302	PSC	4	0
21	L	104	DMU	1	0
25	G	102	CHD	1	0
26	P	304	PEK	5	0
27	G	101	CDL	8	0
21	K	103	DMU	1	0
22	N	606	TGL	8	0
14	N	602	HEA	4	0
18	C	307	PGV	1	0
21	J	103	DMU	3	0
14	N	601[A]	HEA	3	0
18	P	306	PGV	1	0
22	N	607	TGL	6	0
25	C	309	CHD	1	0
27	P	308	CDL	10	0
18	A	608	PGV	5	0
22	D	201	TGL	14	0

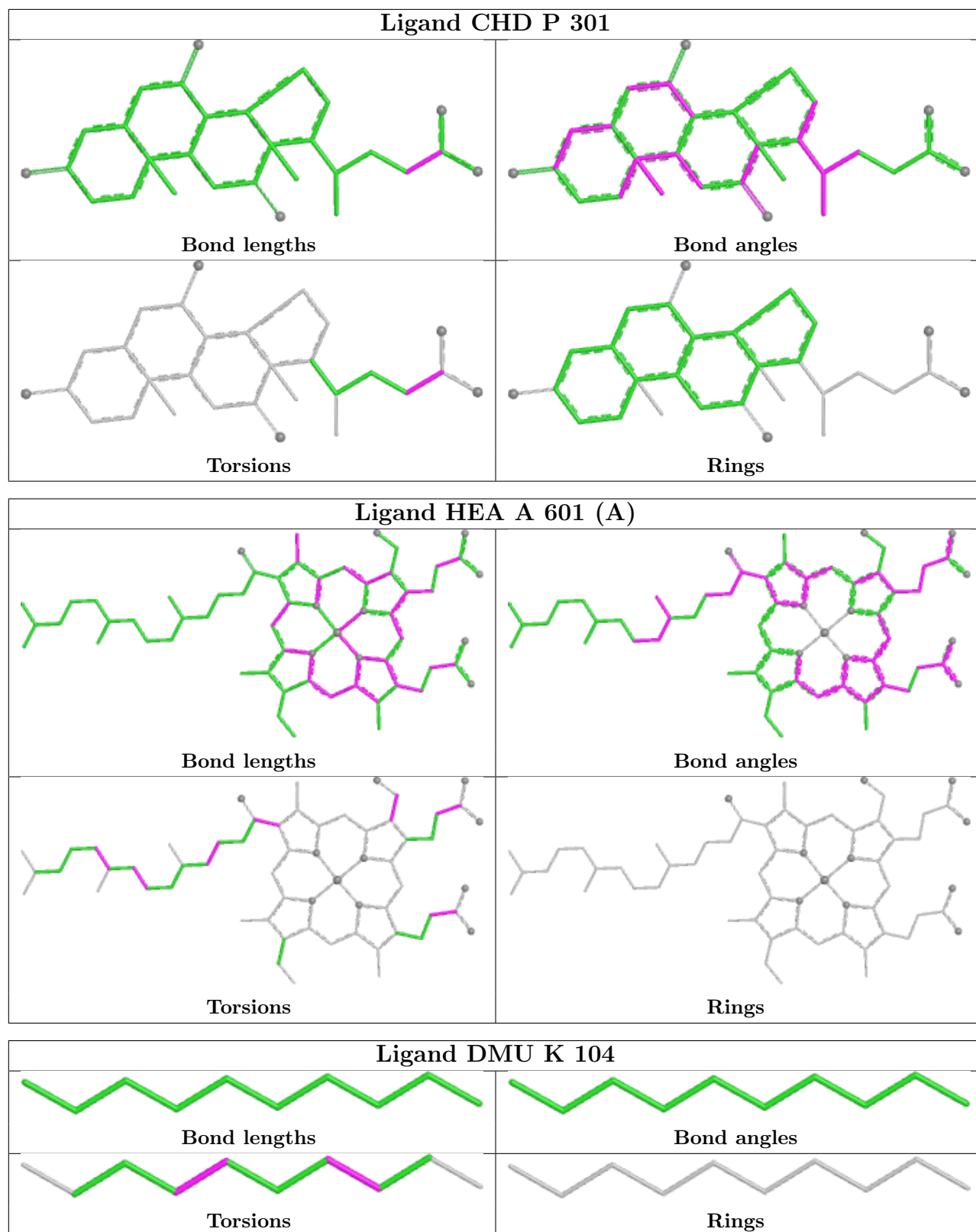
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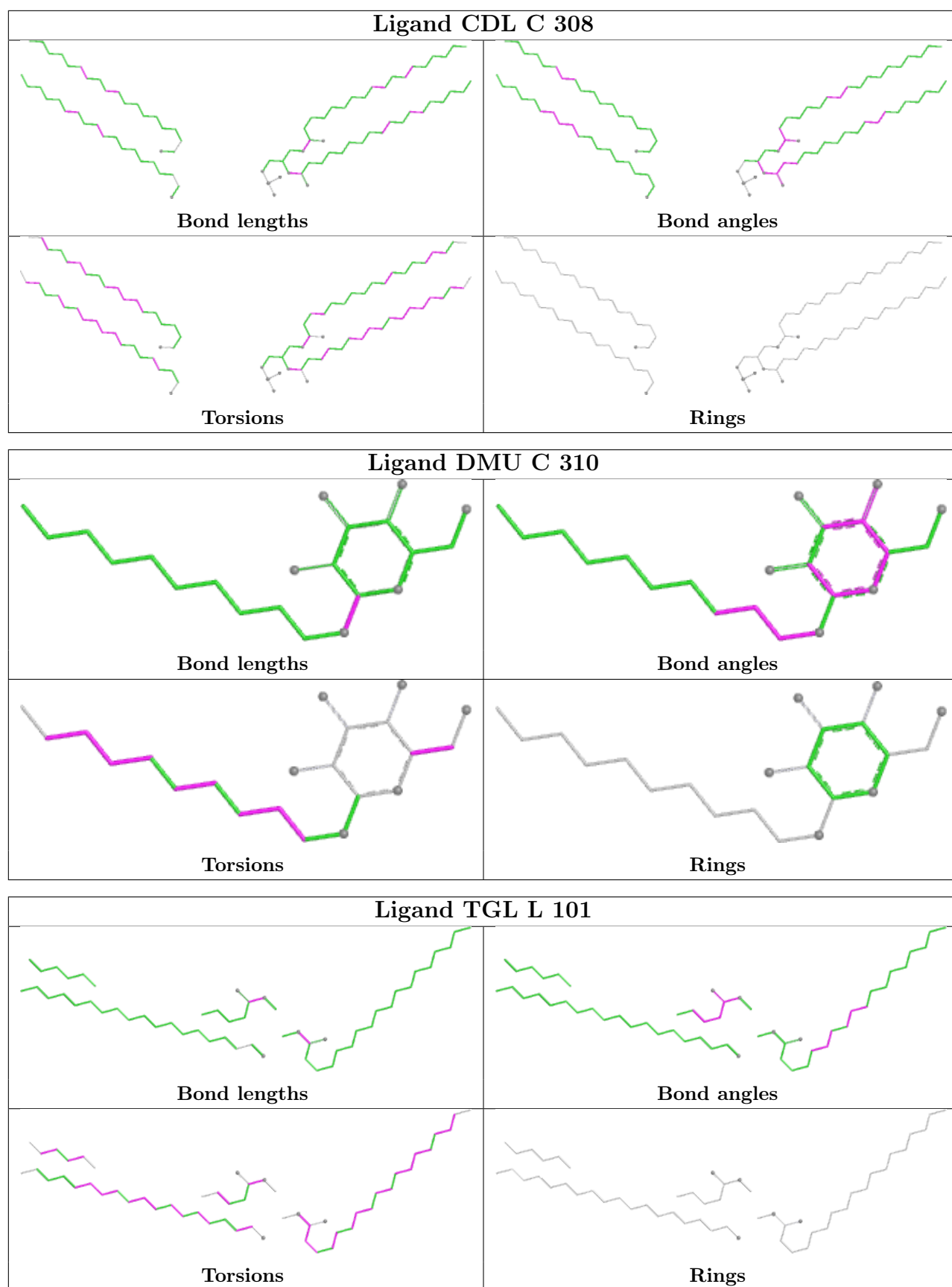
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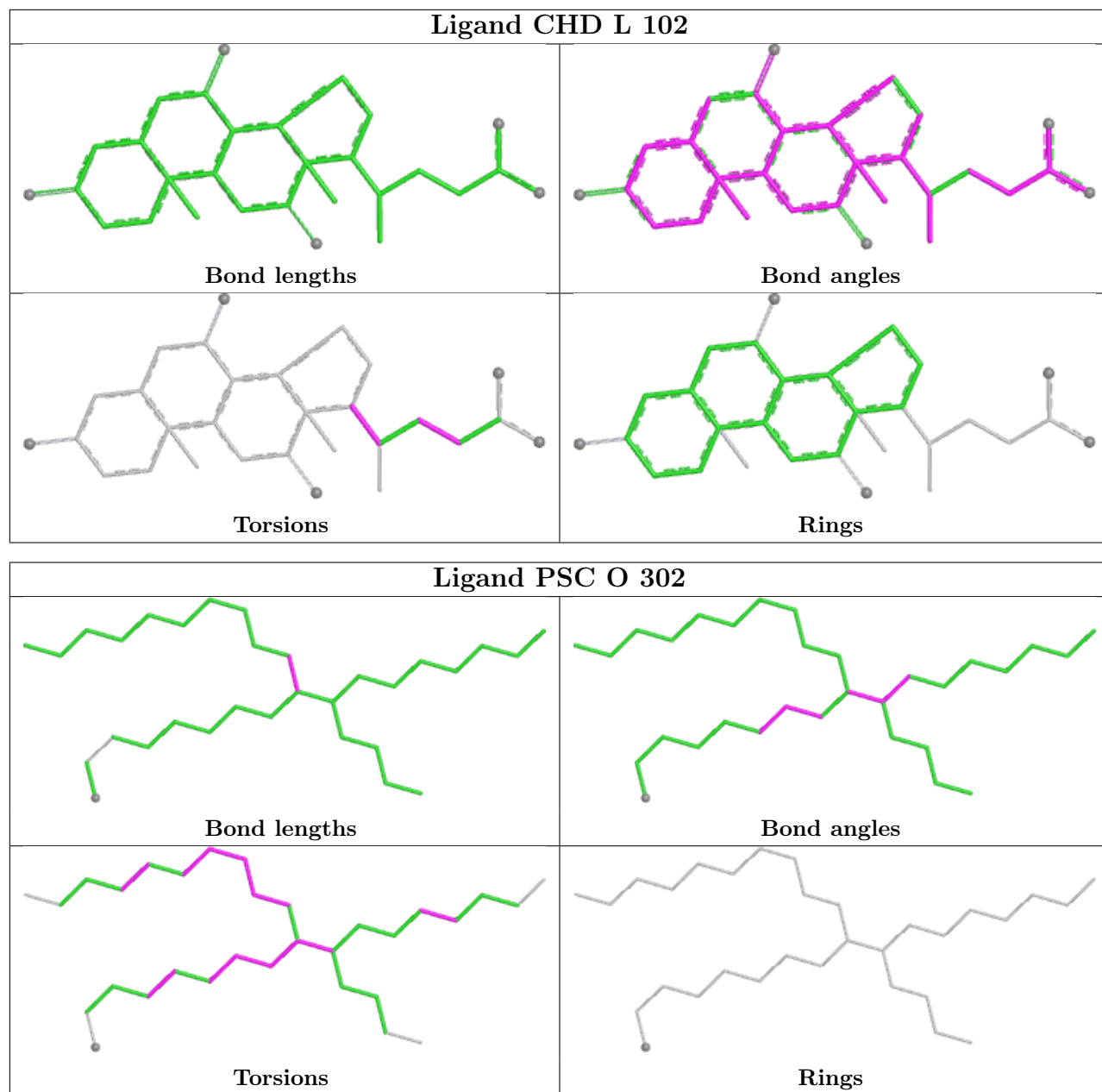
Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	C	304	PEK	9	0
20	J	102	EDO	1	0
18	Q	201	PGV	6	0
20	A	609	EDO	2	0
21	C	320	DMU	1	0
21	P	318	DMU	1	0
20	L	103	EDO	1	0
18	N	610	PGV	1	0
18	C	306	PGV	1	0
27	T	101	CDL	19	0
26	C	305	PEK	5	0
14	A	602	HEA	4	0
21	N	622	DMU	1	0
22	N	608	TGL	2	0
20	S	105	EDO	1	0
20	Q	203	EDO	1	0
20	P	316	EDO	1	0
18	A	606	PGV	3	0
20	A	615	EDO	1	0
20	W	102	EDO	2	0
21	P	310	DMU	5	0
22	B	301	TGL	7	0
26	P	303	PEK	1	0
21	Q	202	DMU	1	0
20	R	202	EDO	2	0
24	B	303	PSC	7	0
26	P	305	PEK	7	0
20	P	311	EDO	1	0
25	P	309	CHD	3	0
18	P	307	PGV	3	0
20	C	314	EDO	1	0

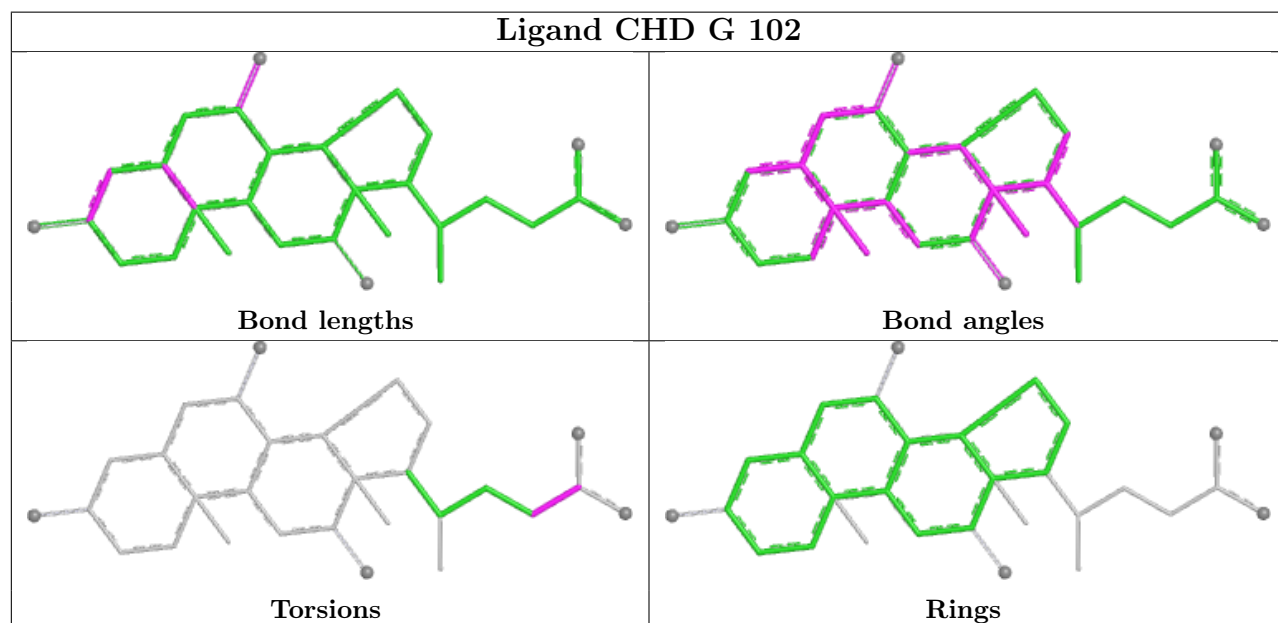
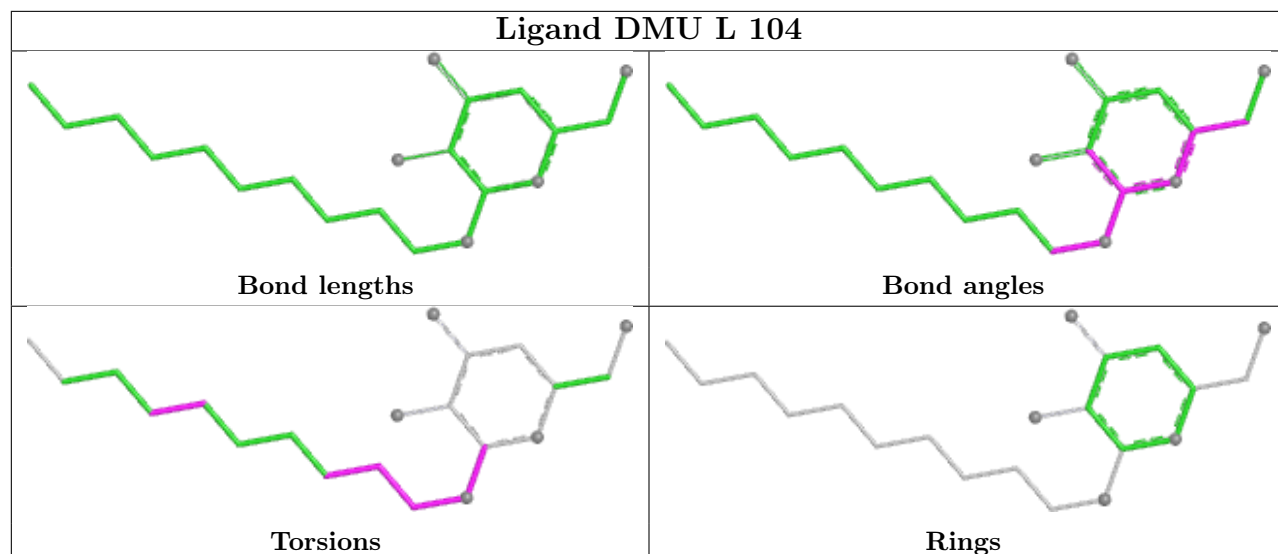
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

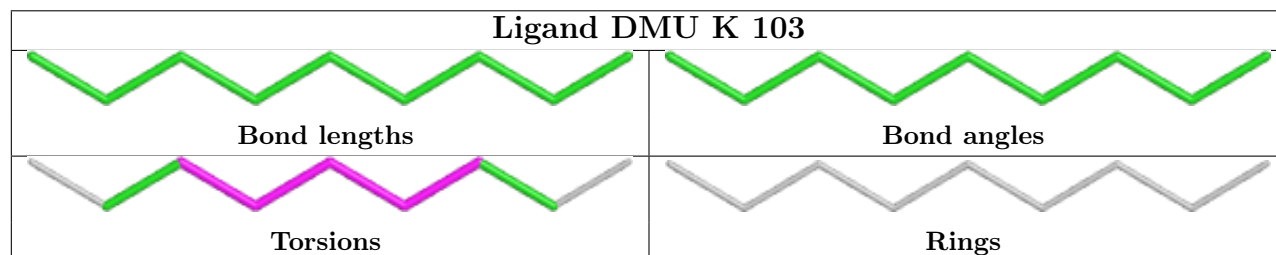
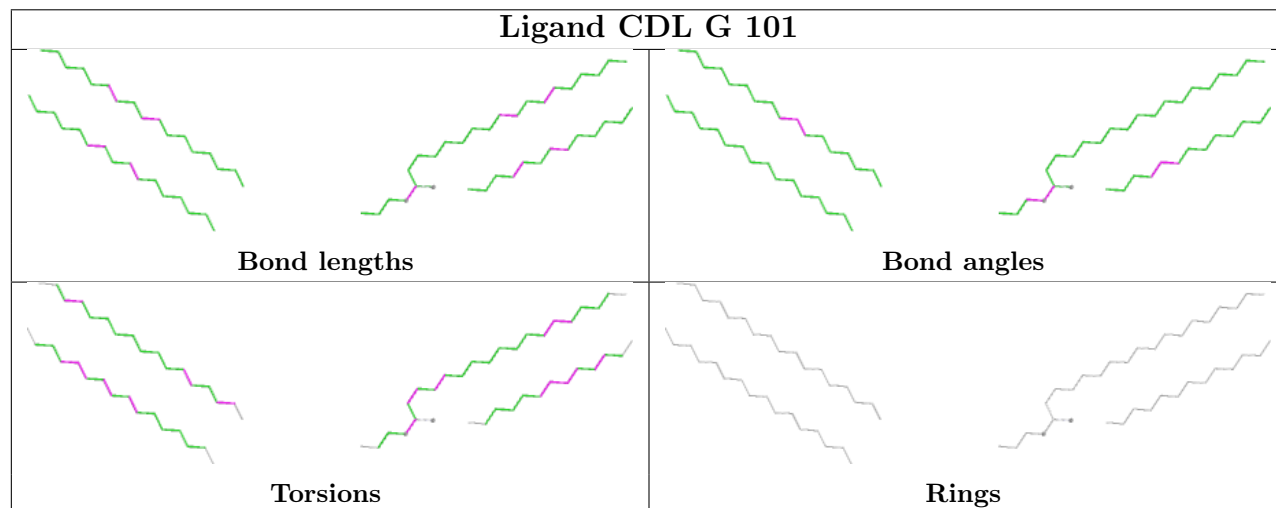
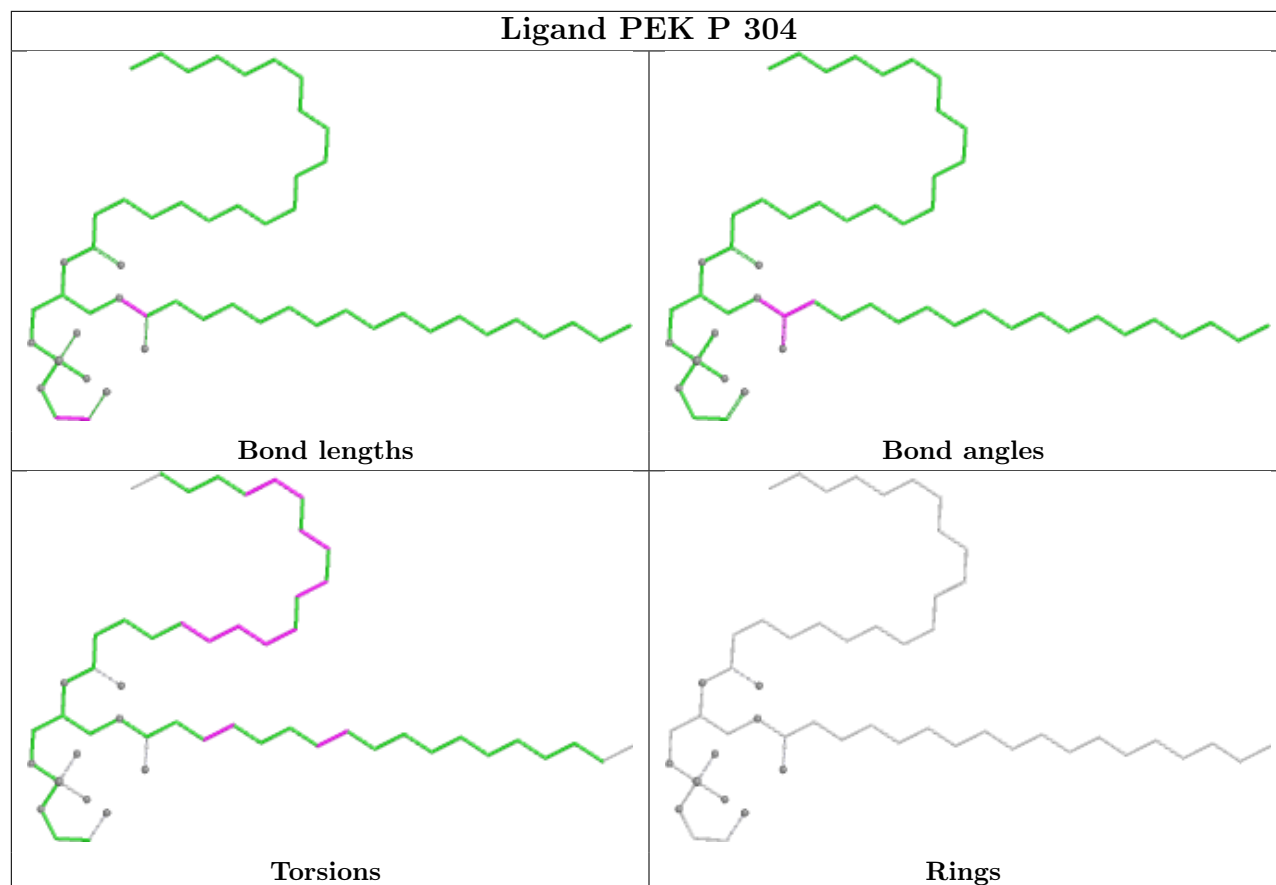
equivalents in the CSD to analyse the geometry.

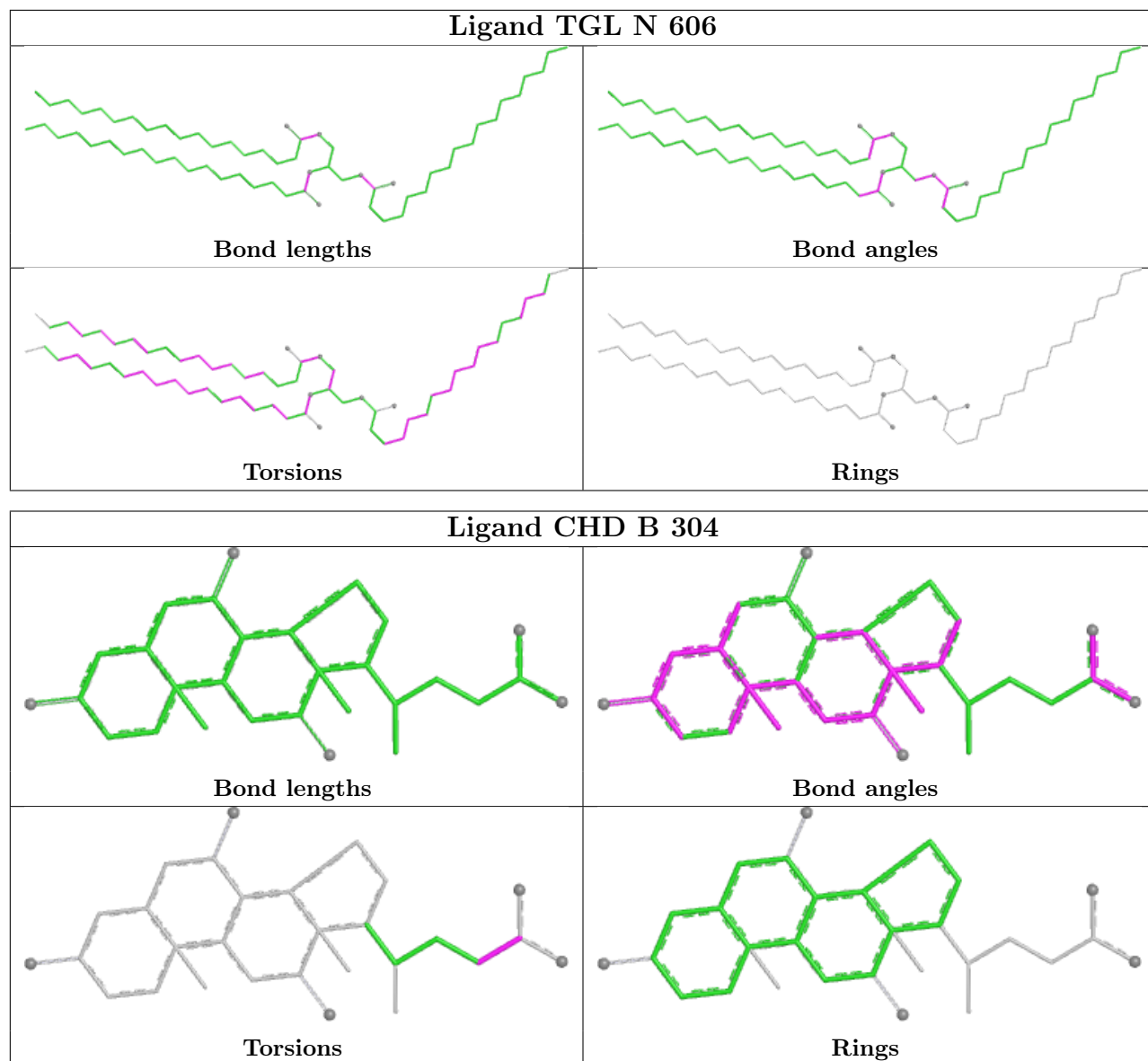


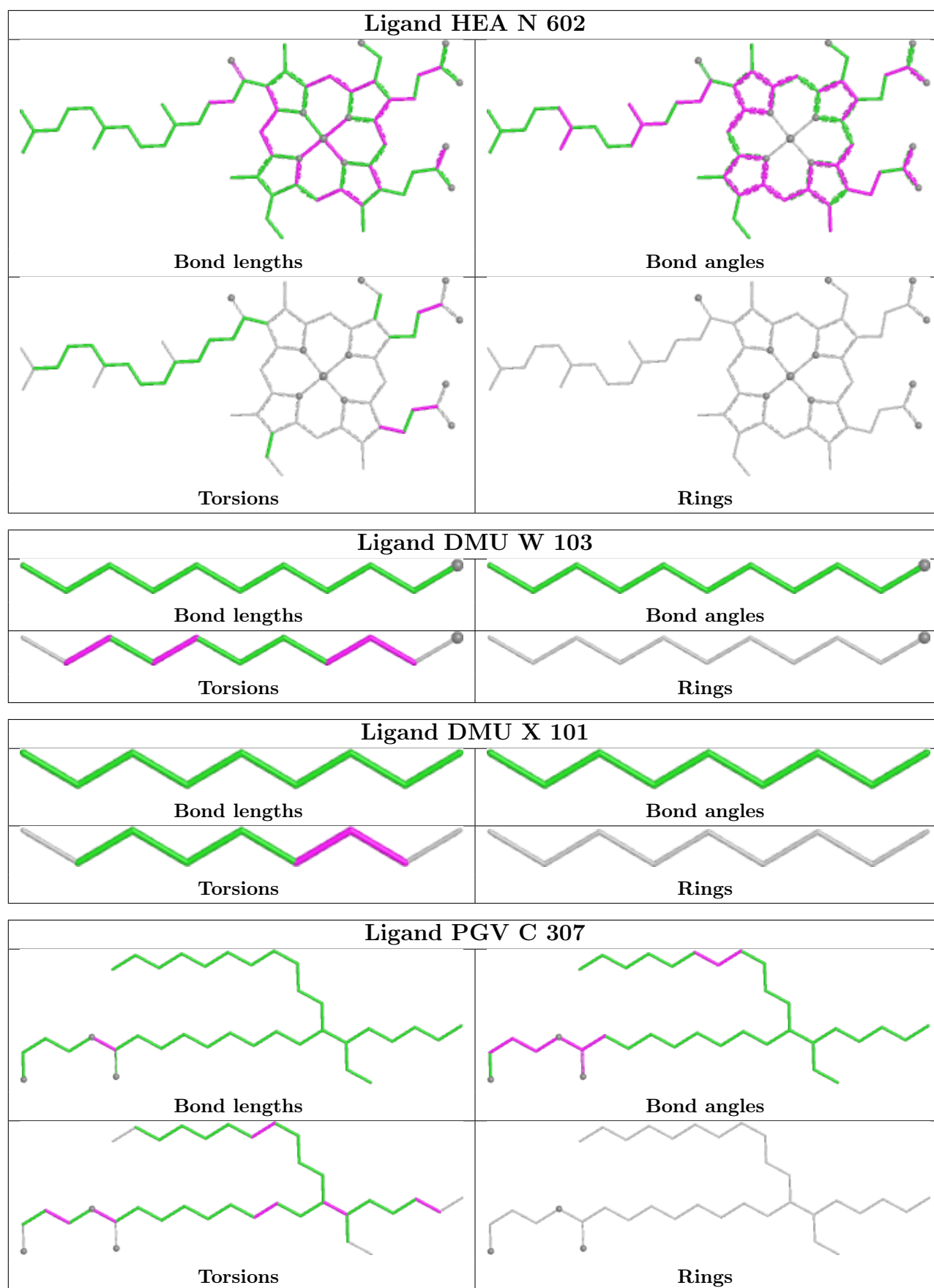


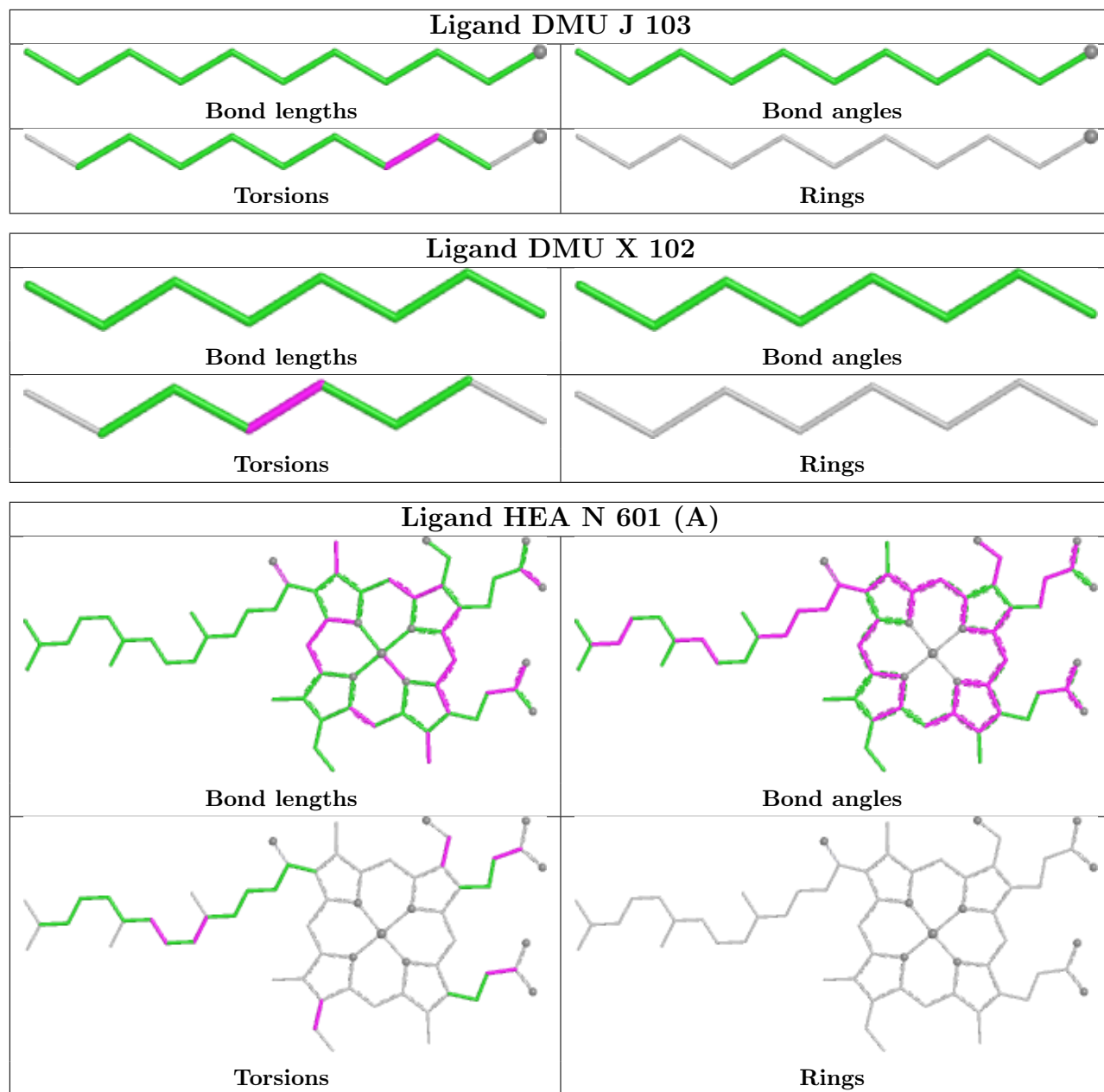


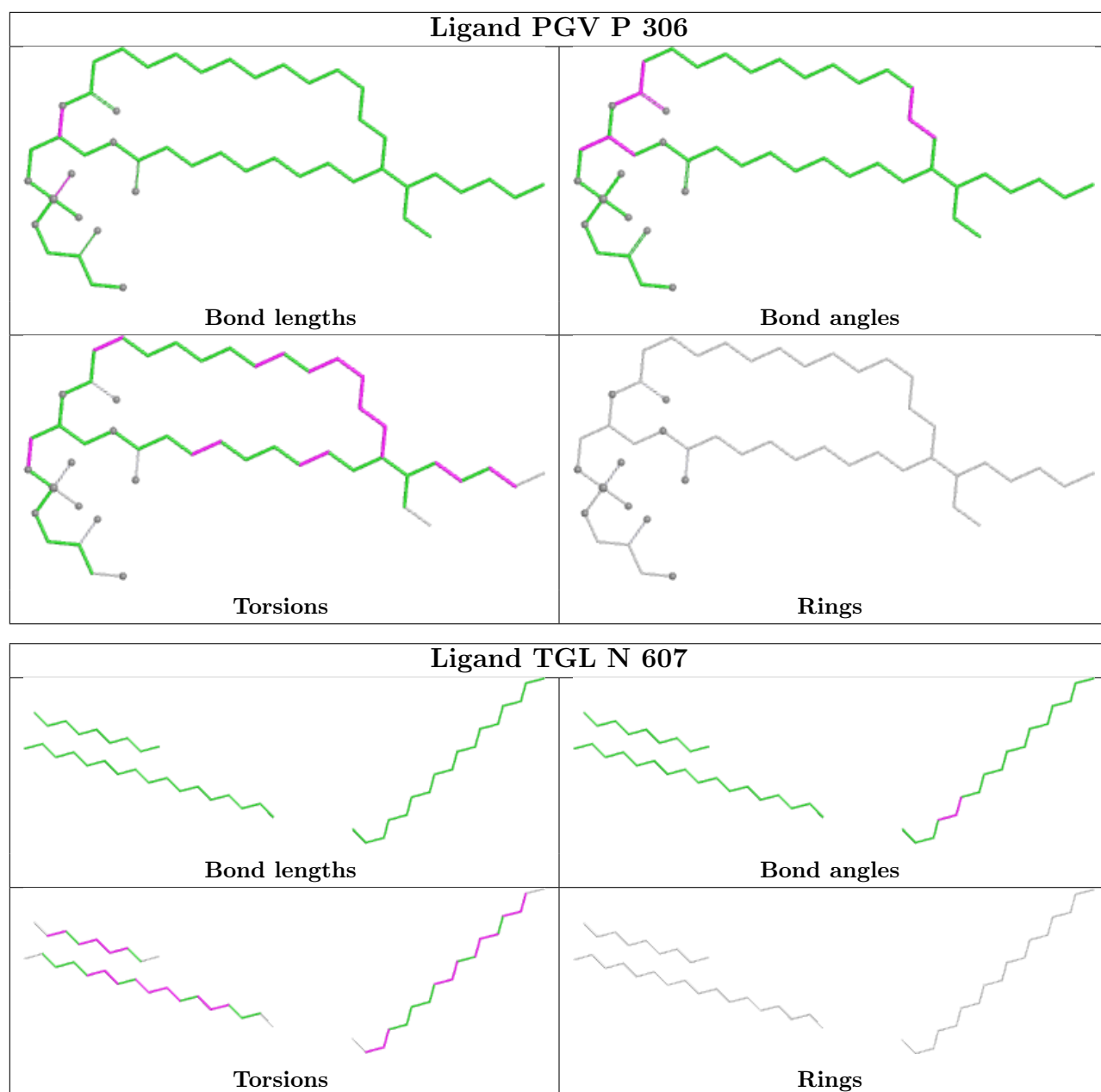


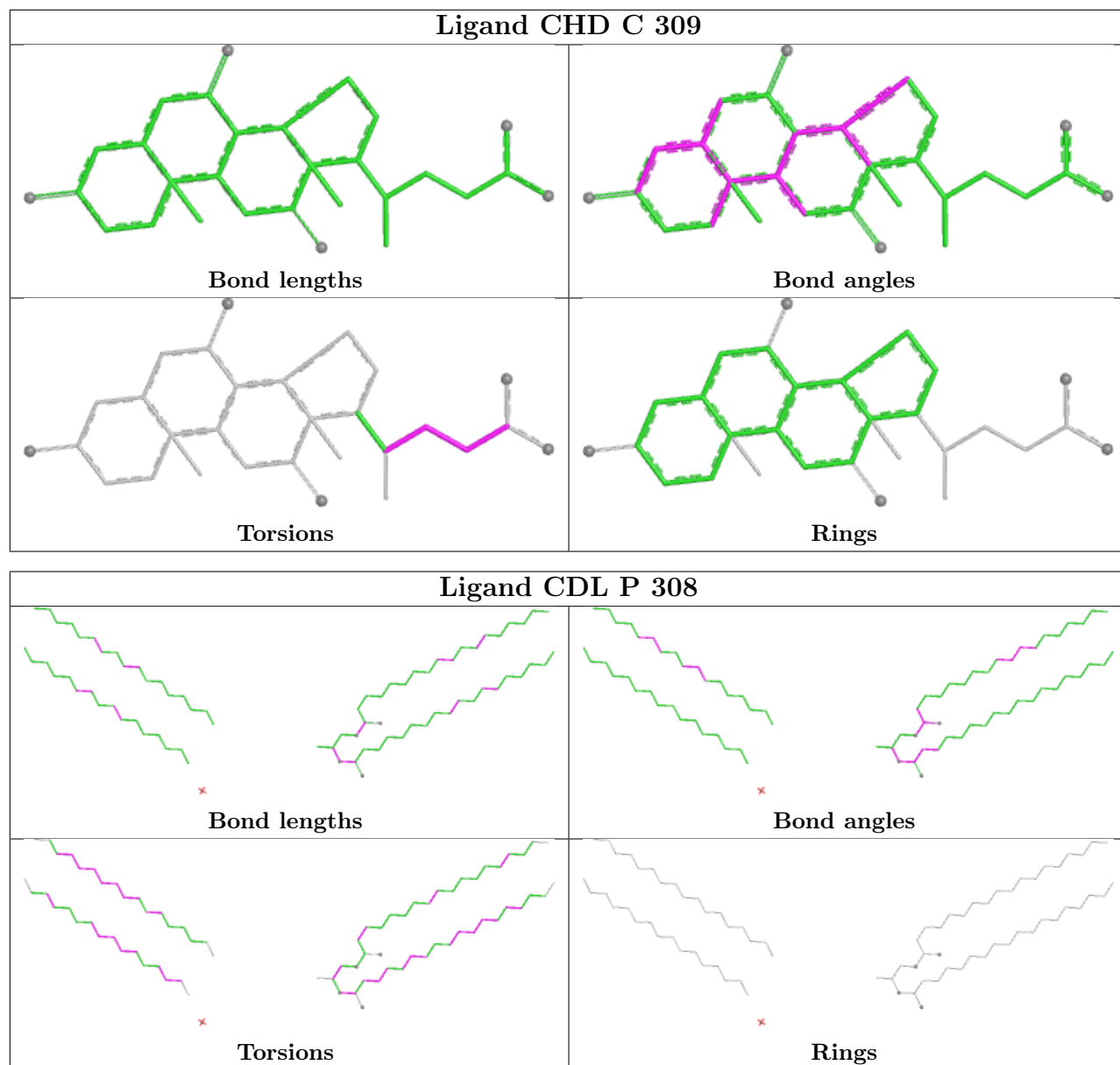


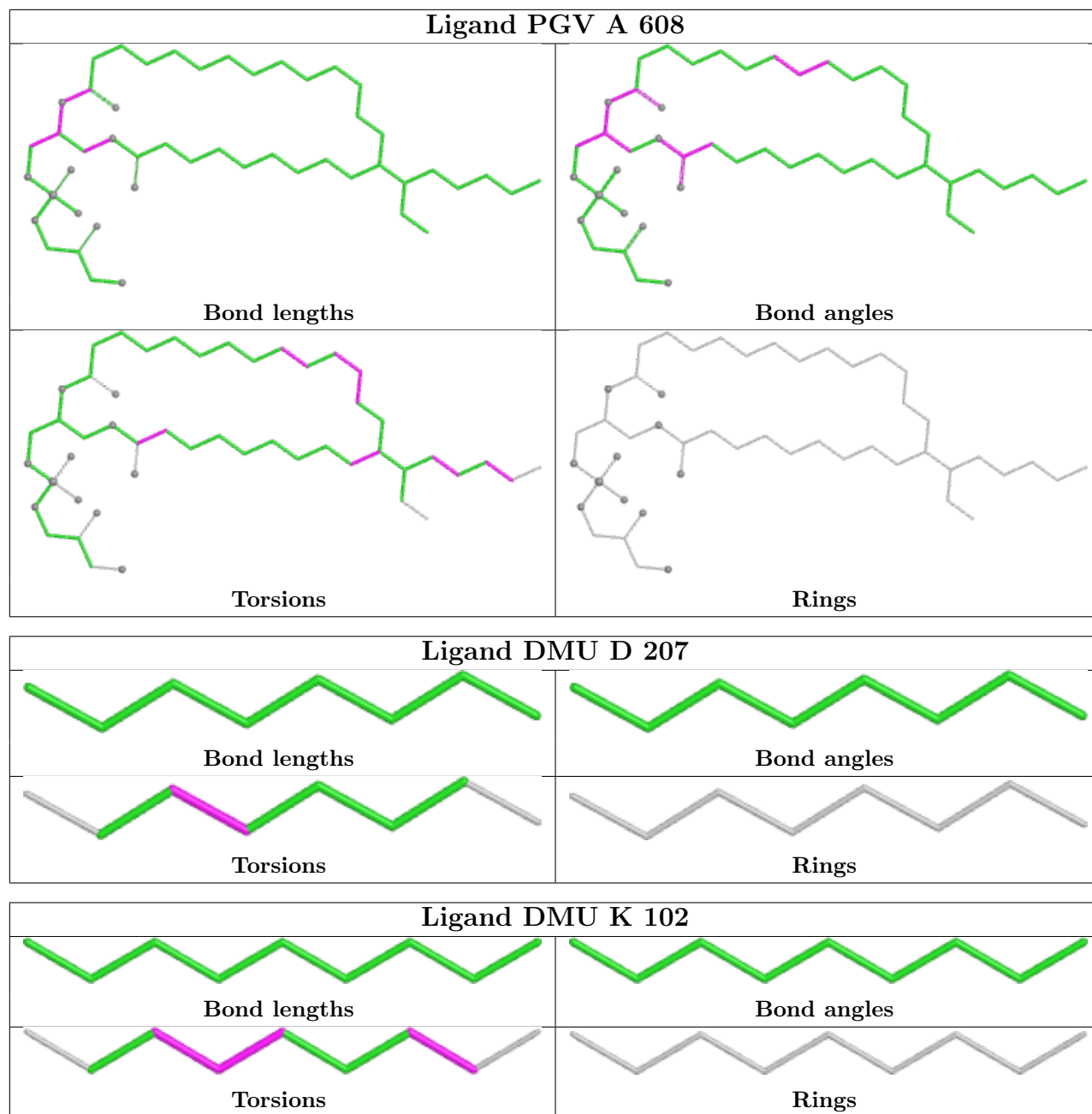


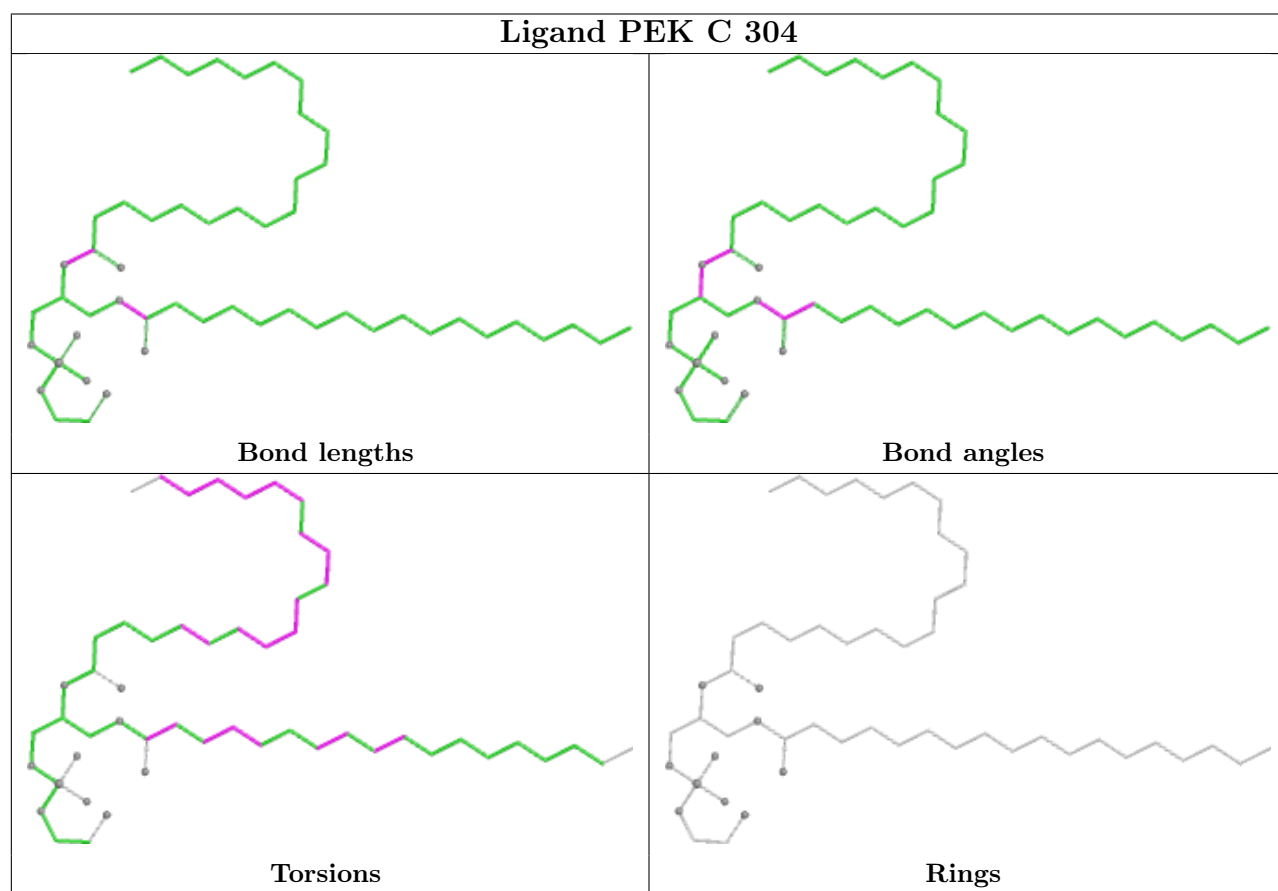
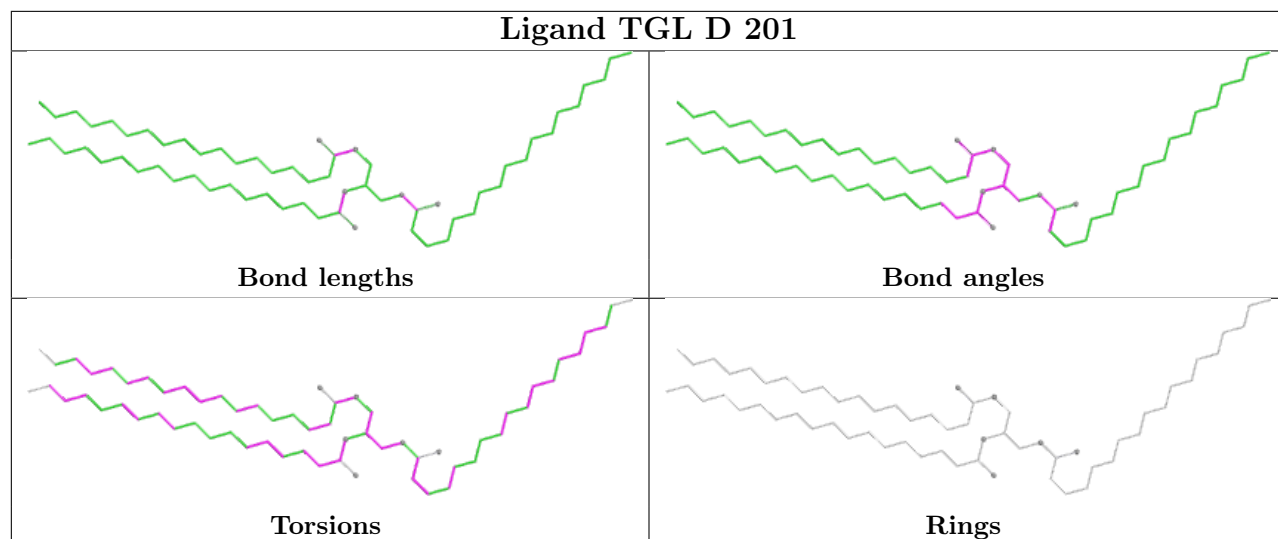


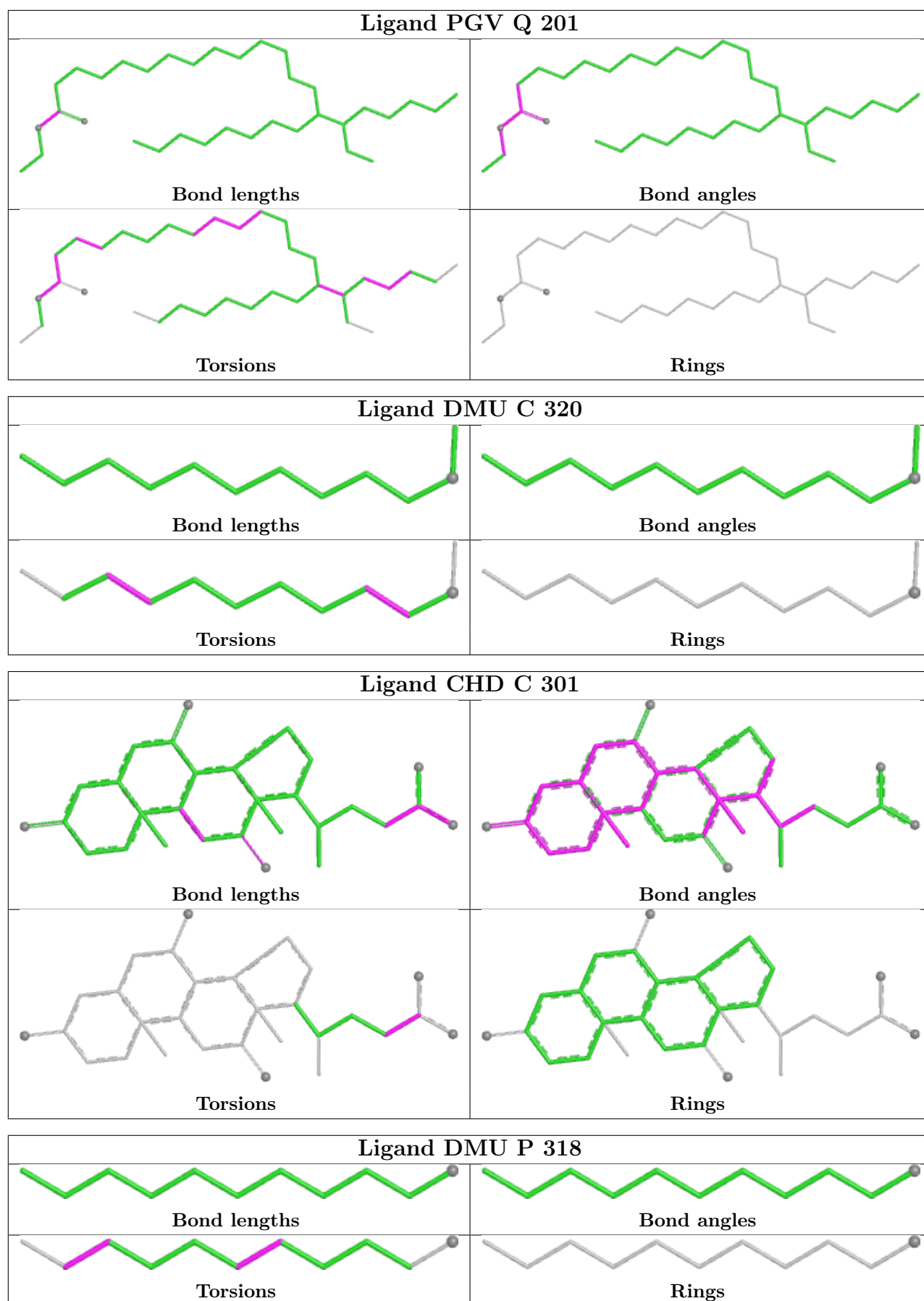


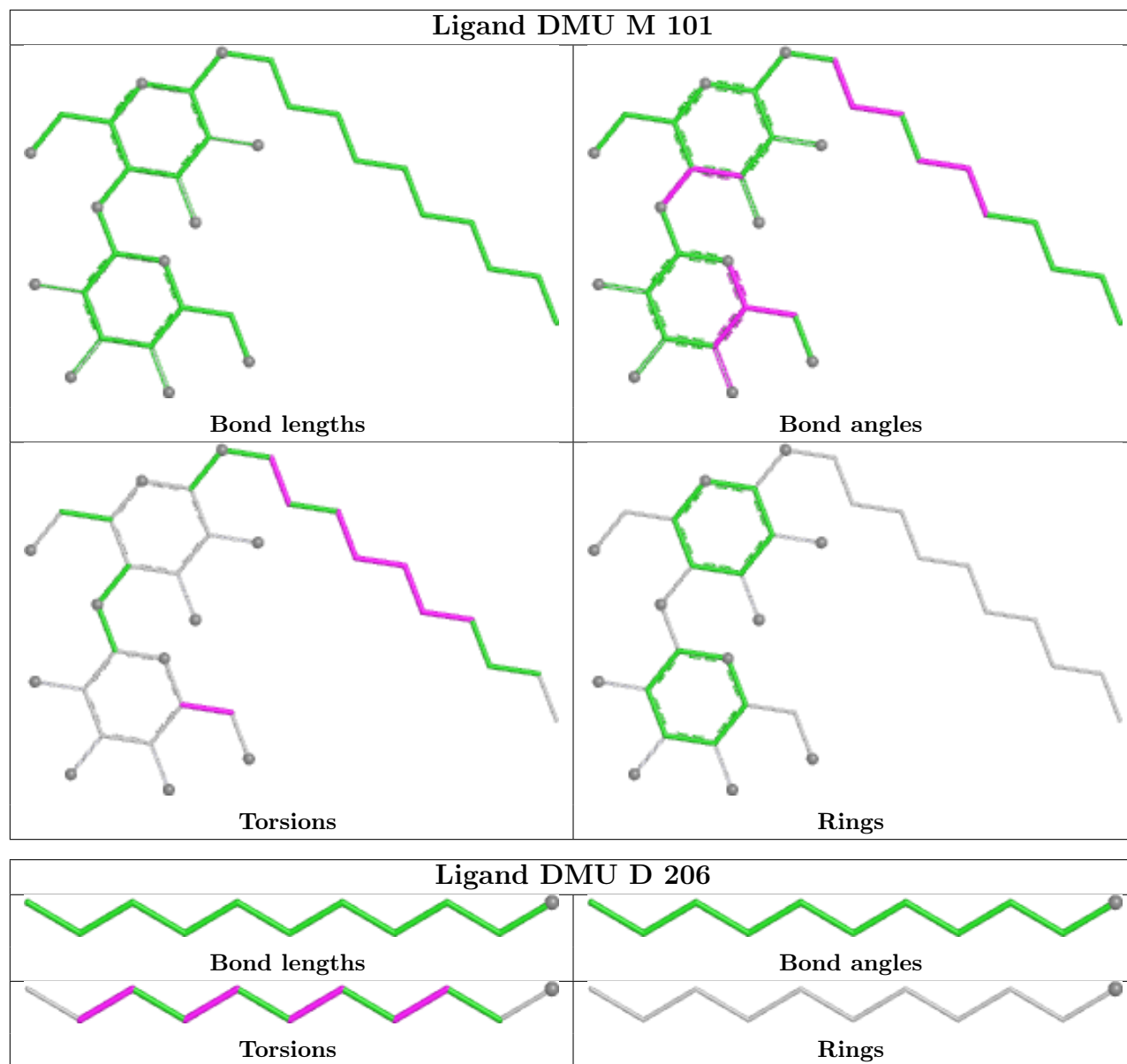


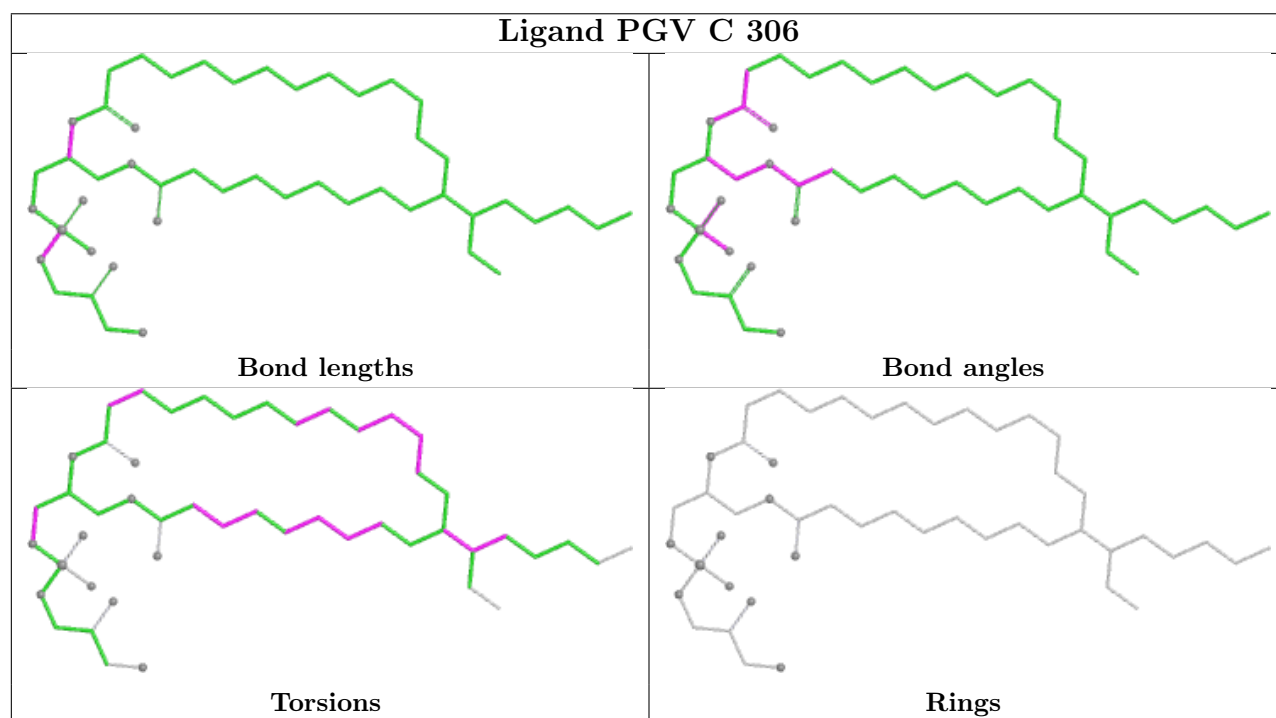
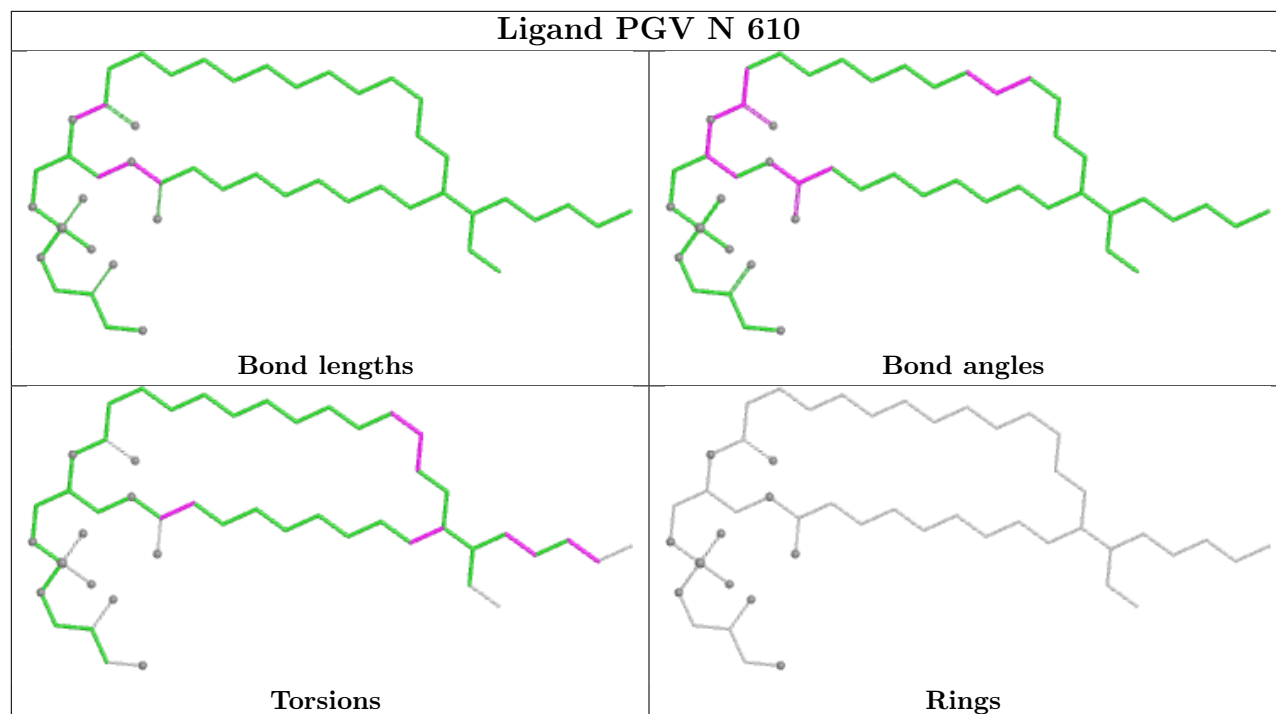


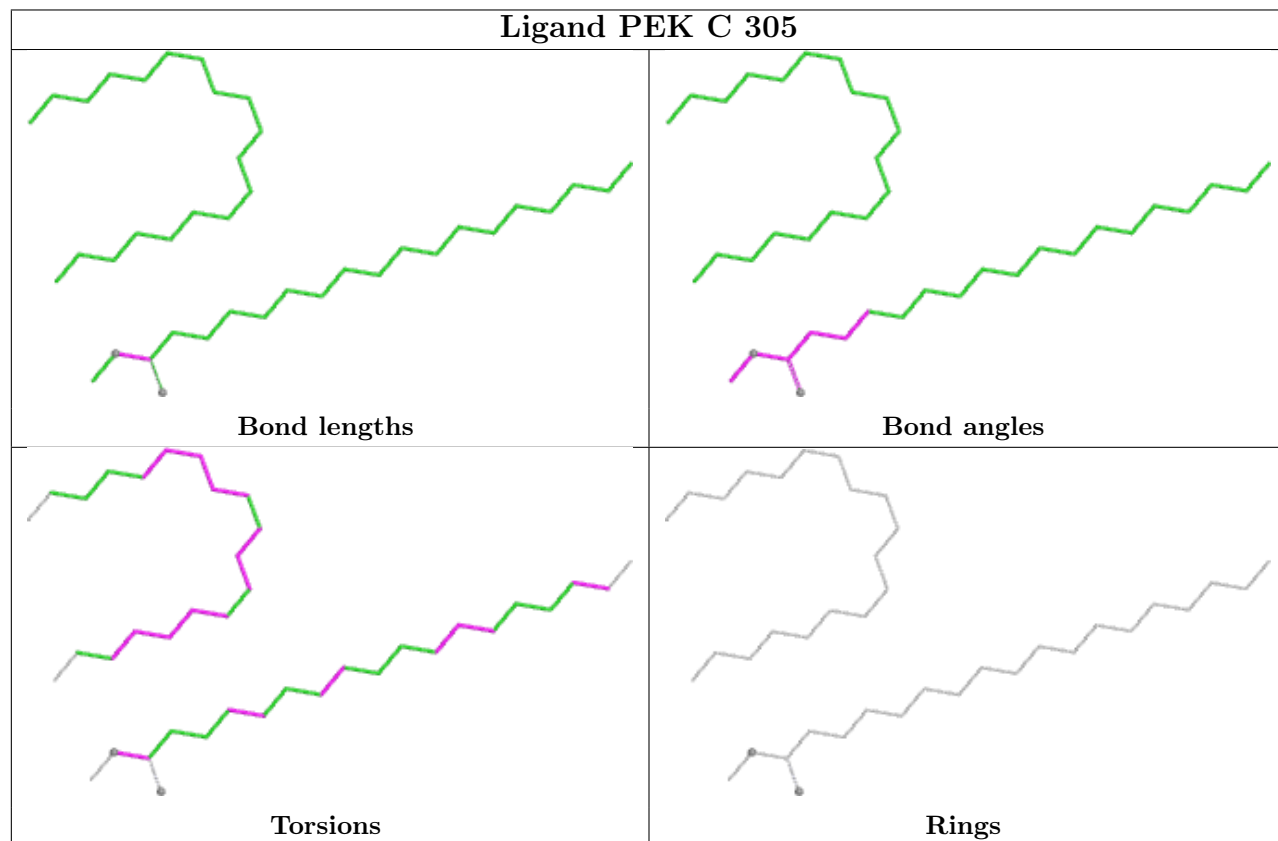
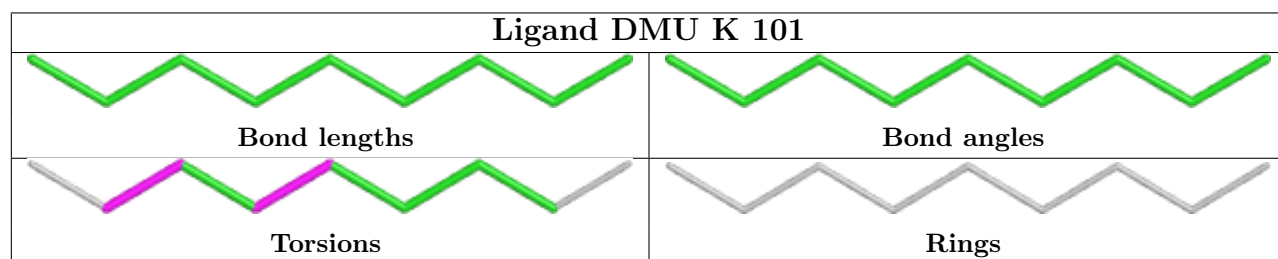
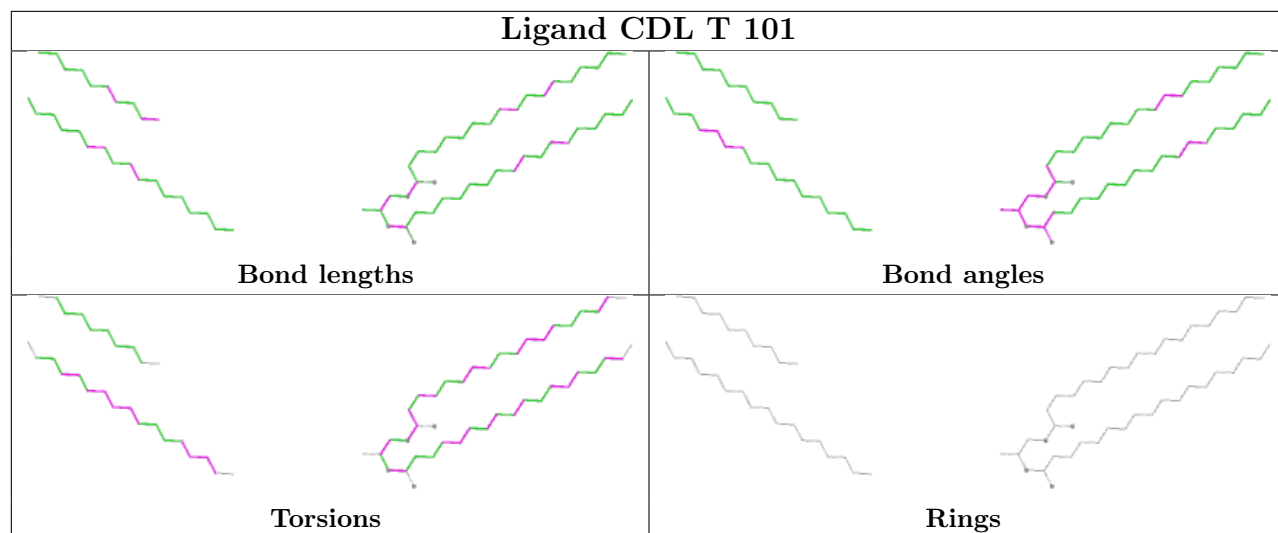


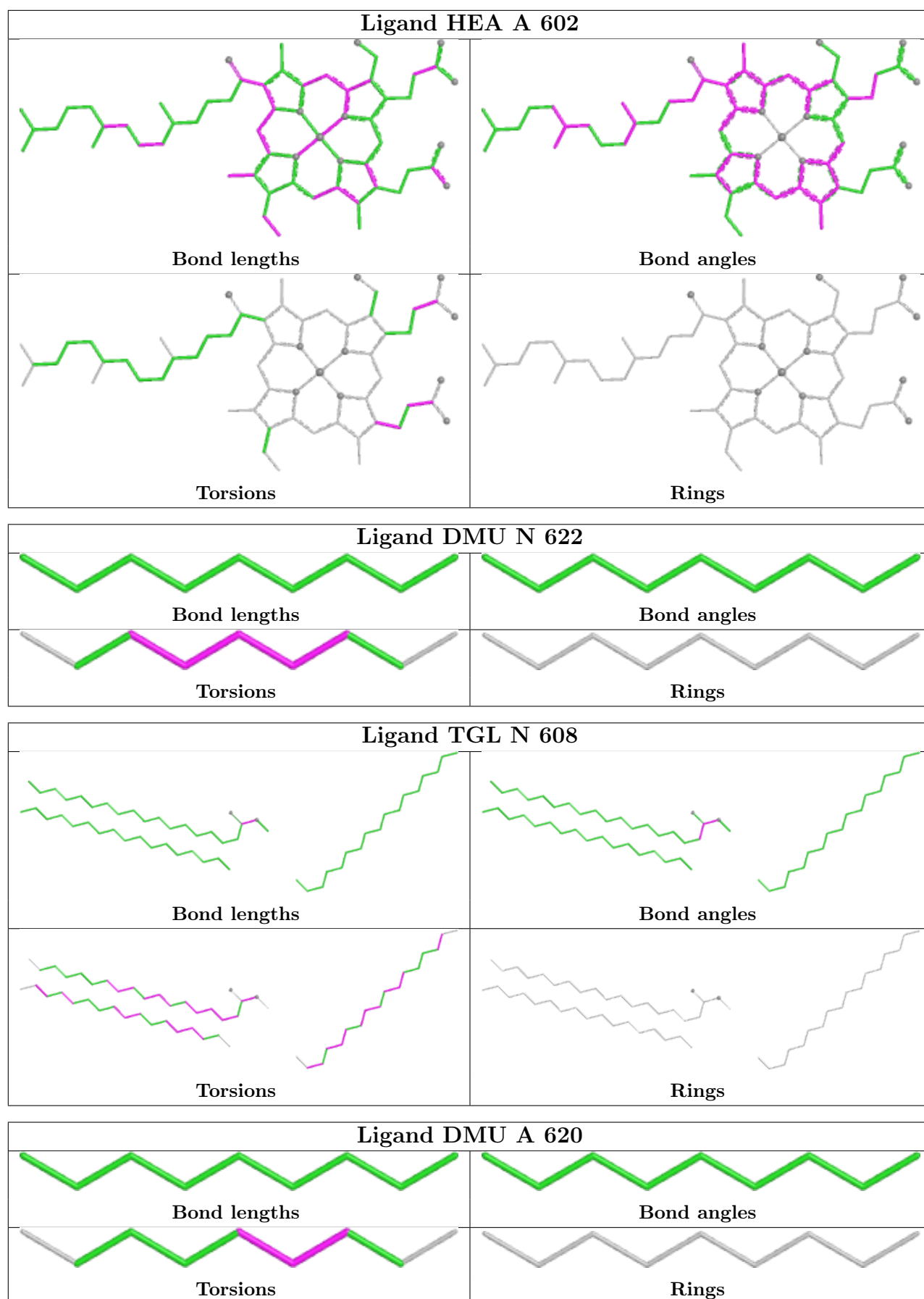


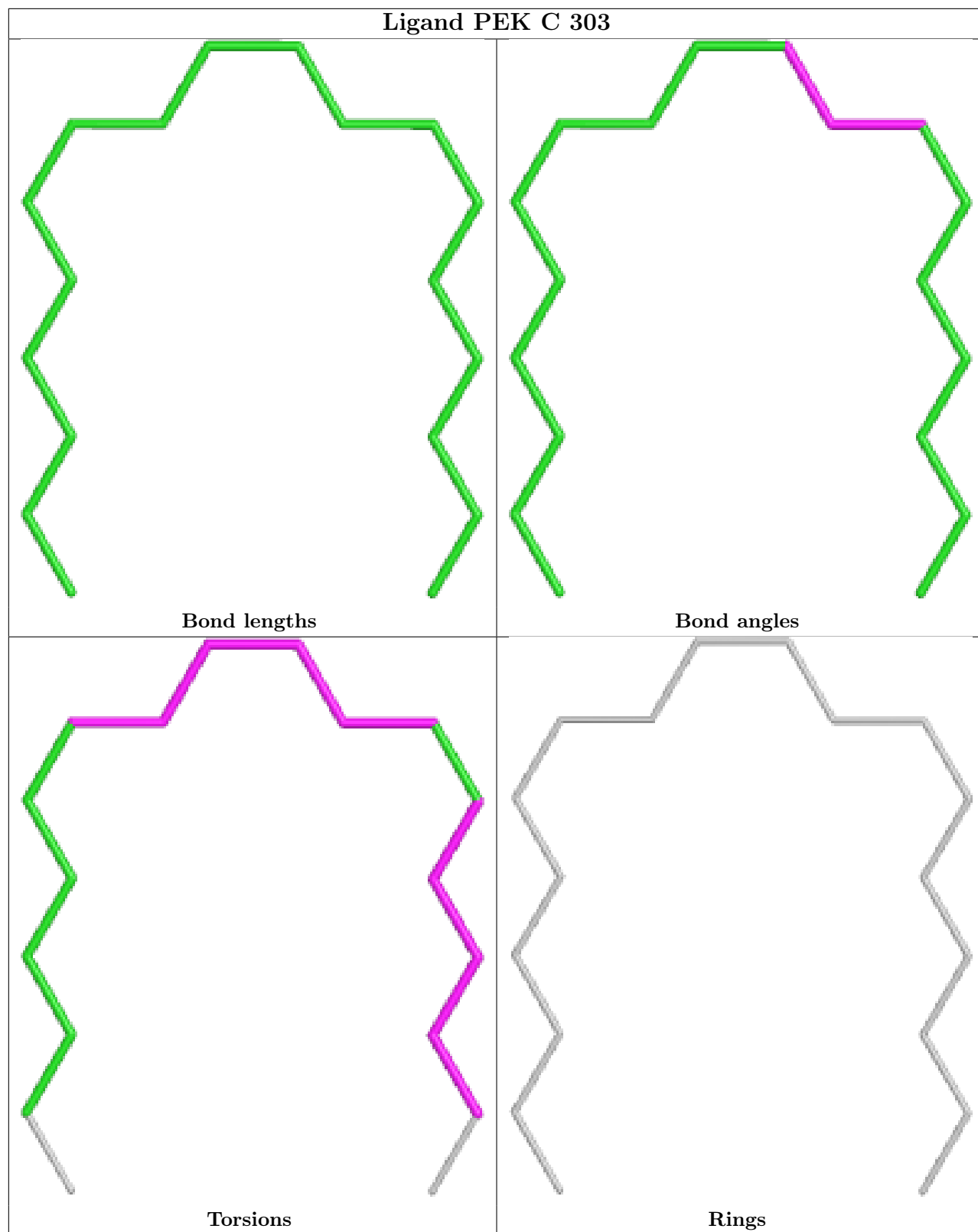


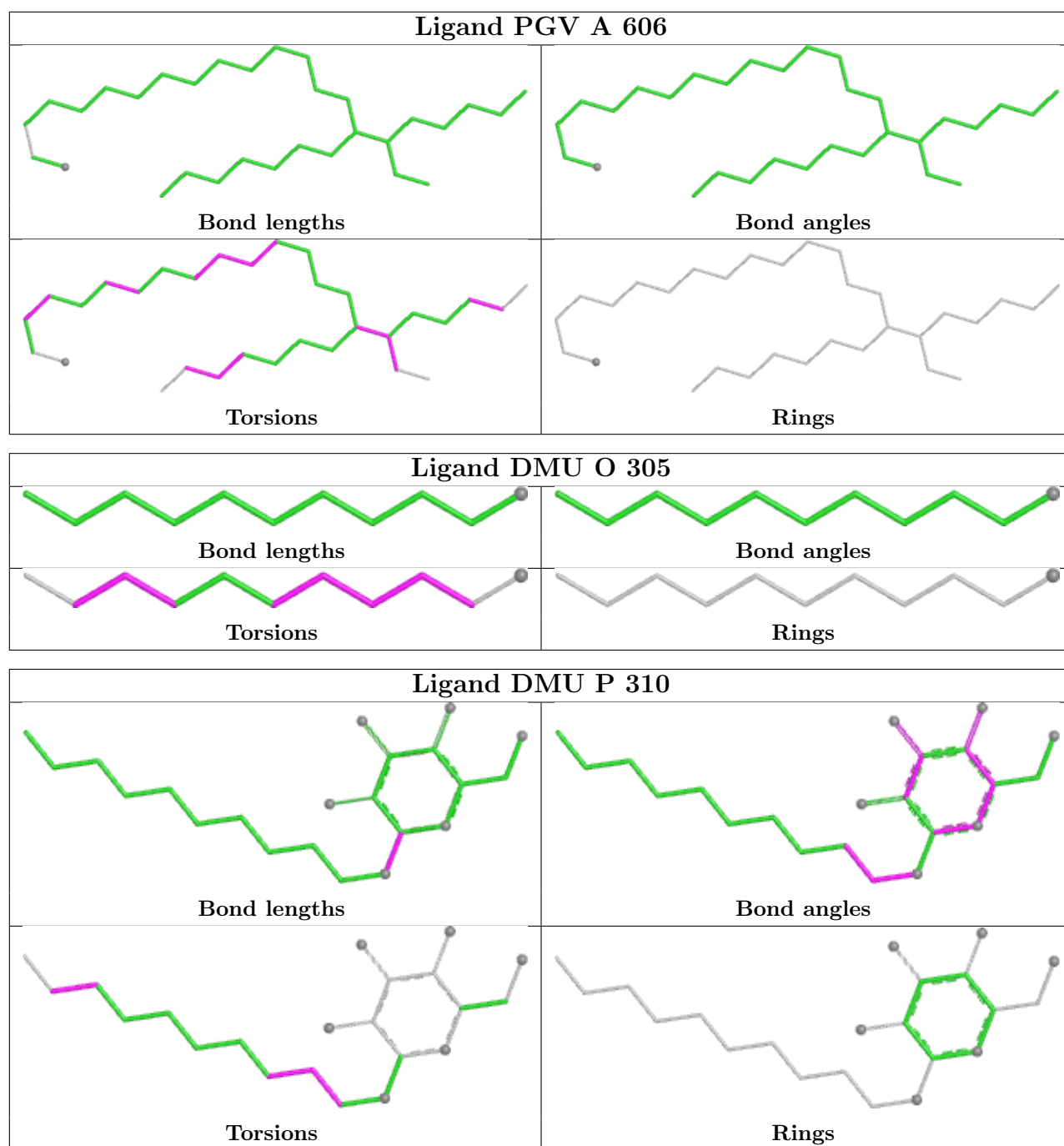


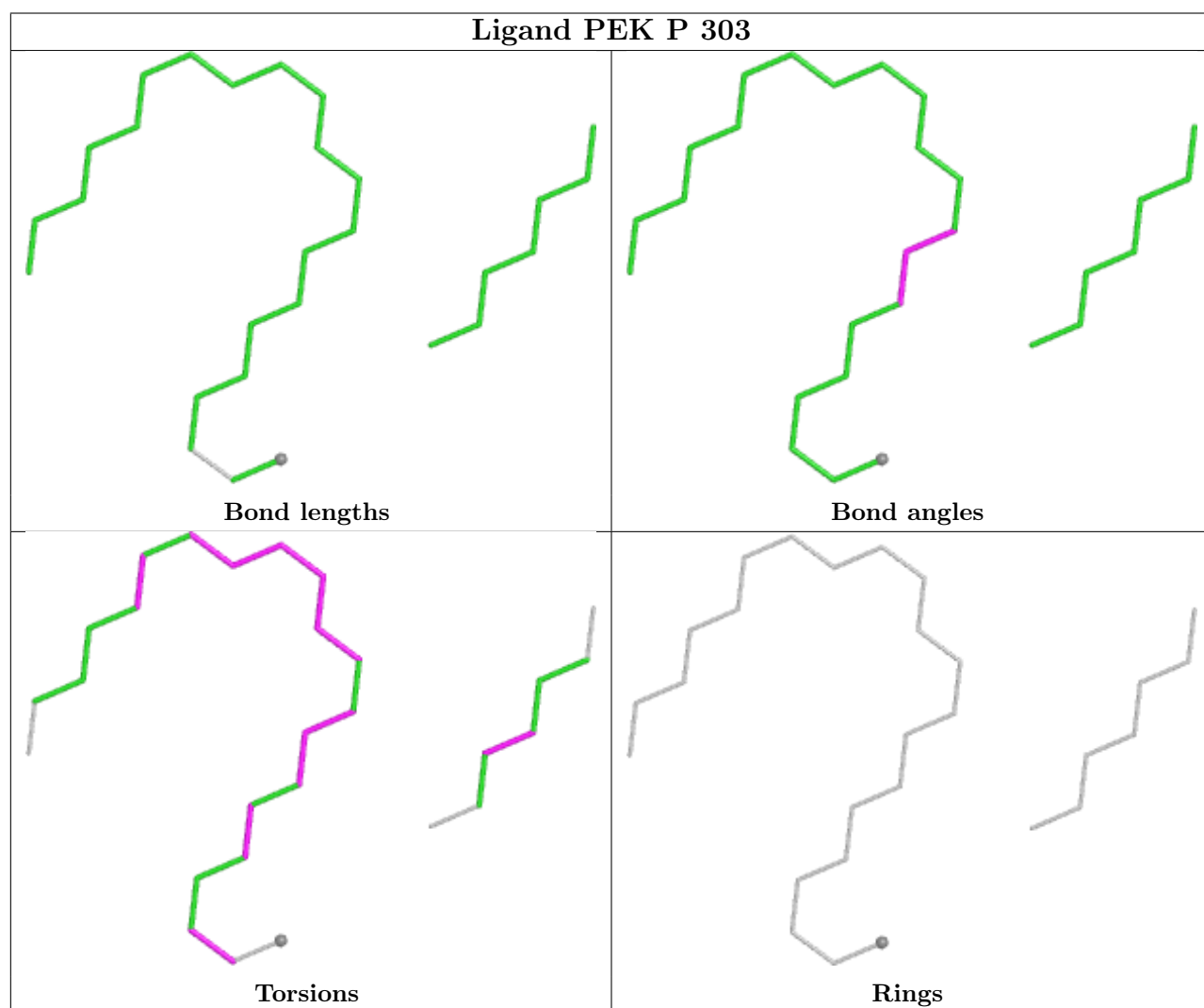
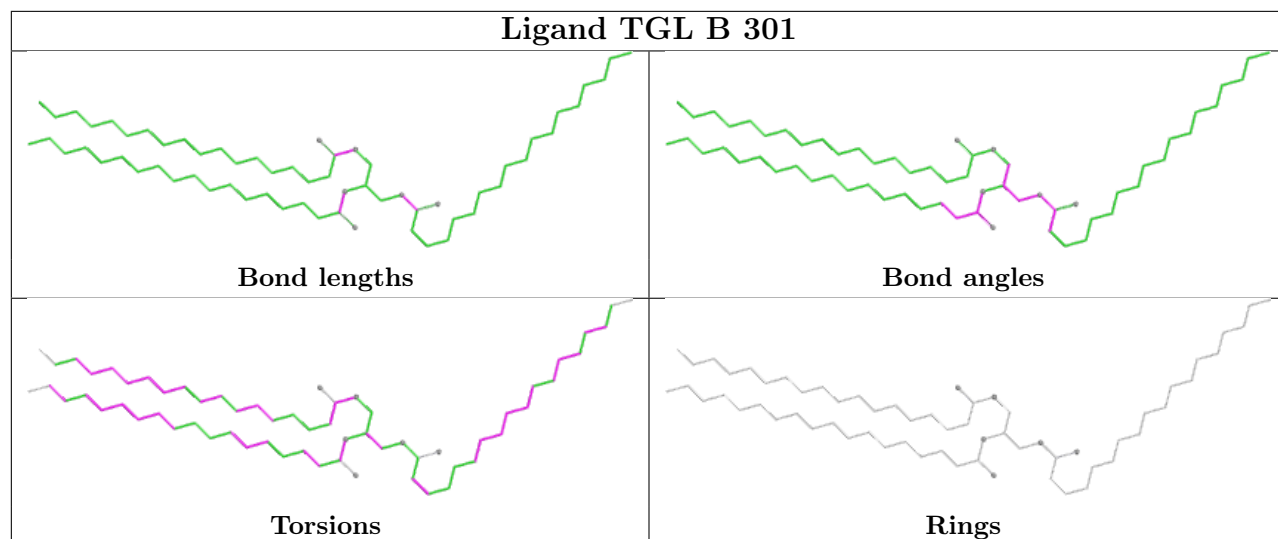


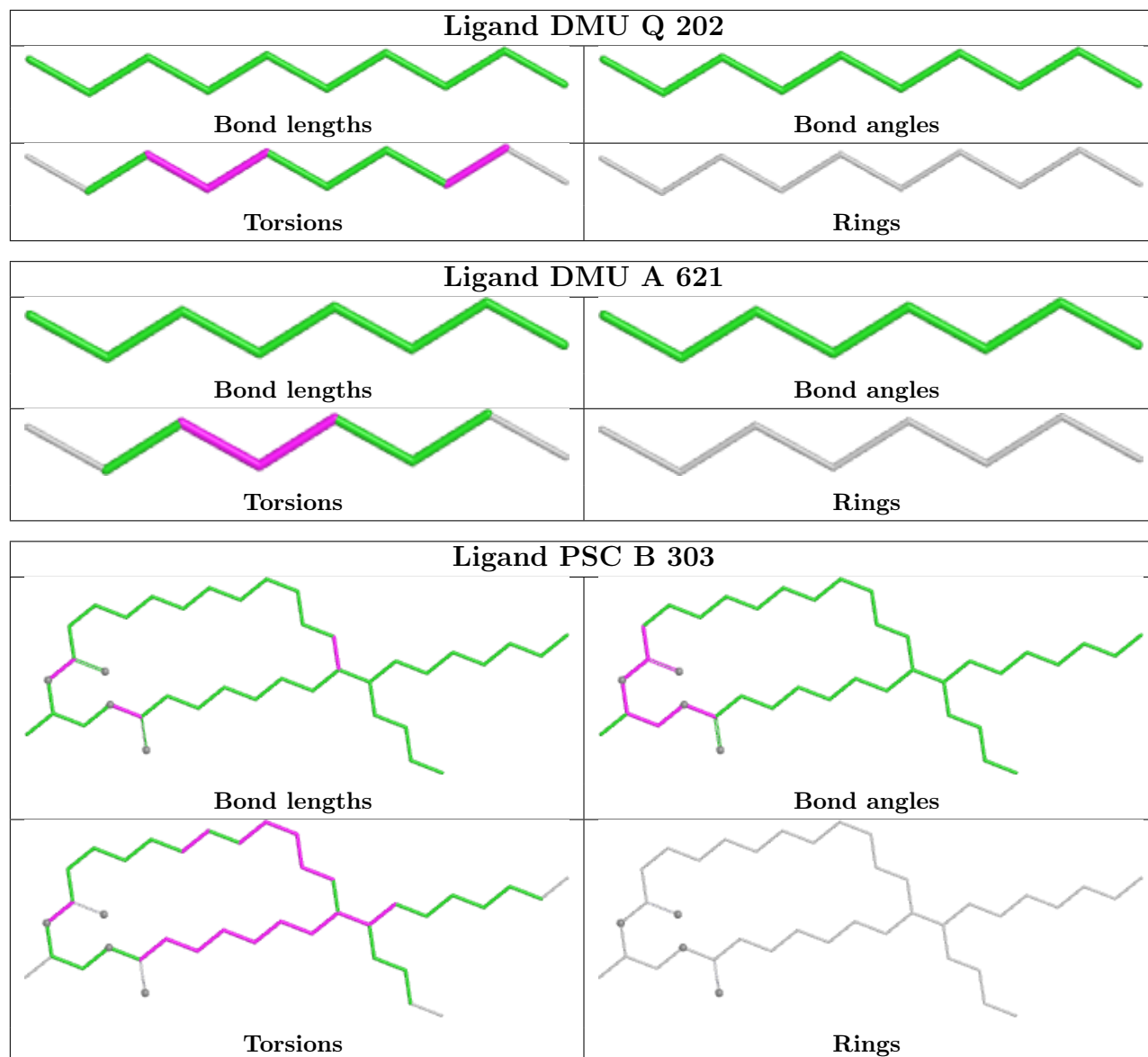


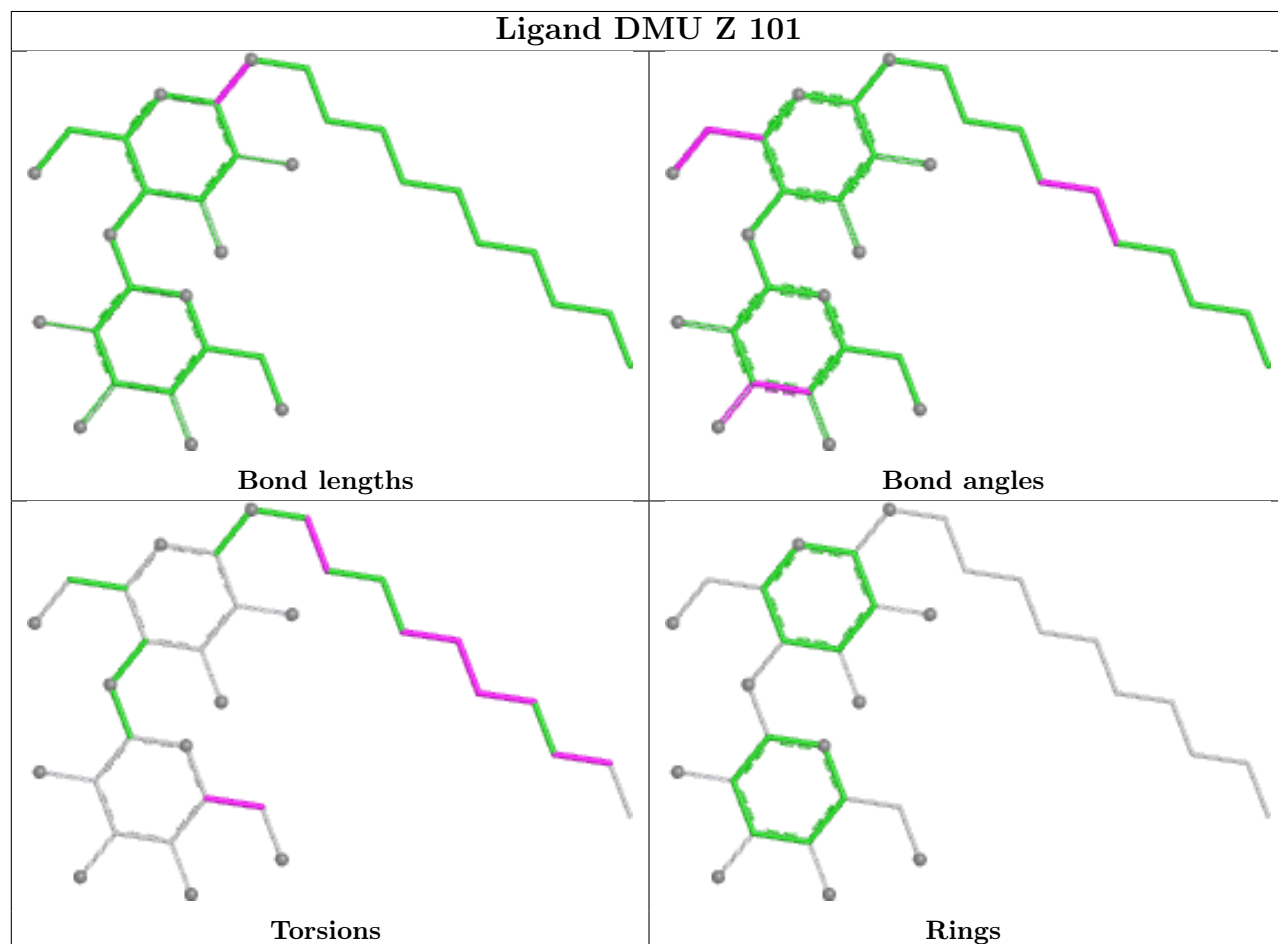
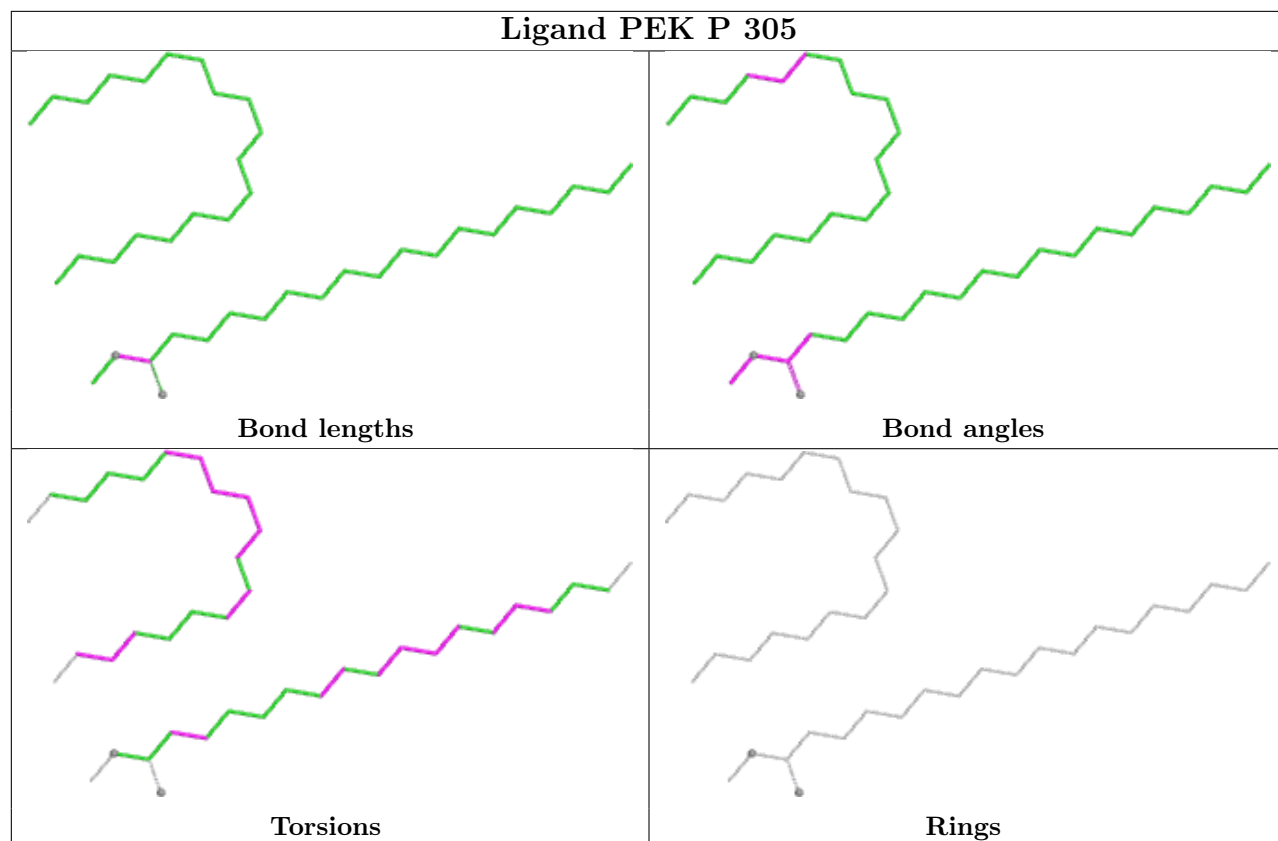


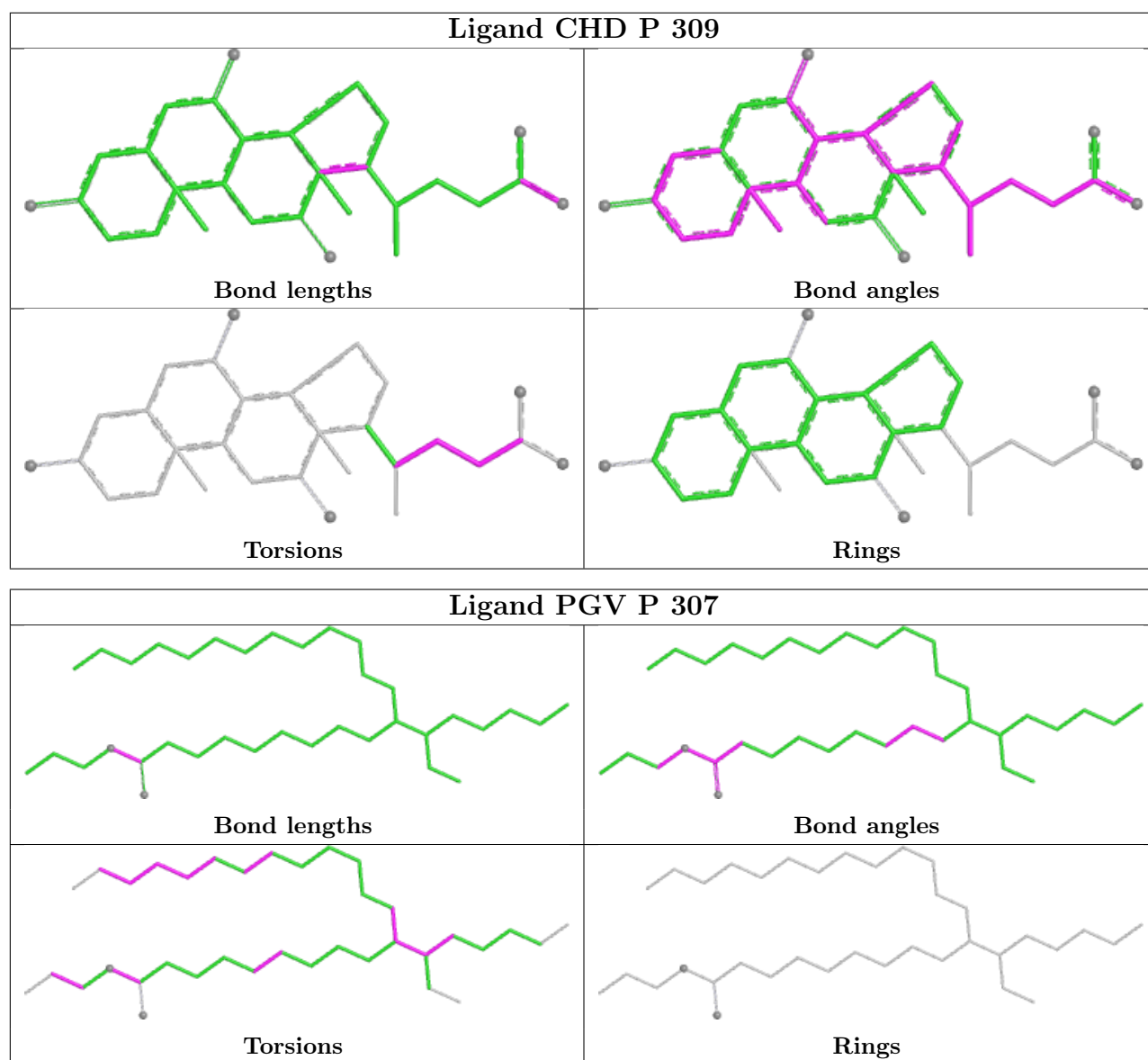












5.7 Other polymers [i](#)

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%)	-0.18	9 (1%) 67 74	11, 24, 32, 89	34 (6%)
1	N	513/514 (99%)	-0.10	8 (1%) 70 77	13, 27, 36, 76	28 (5%)
2	B	226/227 (99%)	0.32	16 (7%) 22 27	21, 32, 56, 112	14 (6%)
2	O	226/227 (99%)	0.37	13 (5%) 29 35	24, 36, 68, 130	9 (3%)
3	C	259/259 (100%)	-0.03	3 (1%) 76 83	18, 27, 40, 91	12 (4%)
3	P	259/259 (100%)	-0.04	3 (1%) 76 83	18, 28, 41, 91	8 (3%)
4	D	144/144 (100%)	0.26	6 (4%) 40 49	26, 34, 62, 94	0
4	Q	144/144 (100%)	0.96	19 (13%) 7 9	32, 48, 89, 218	0
5	E	105/105 (100%)	0.25	5 (4%) 35 43	26, 33, 62, 155	0
5	R	105/105 (100%)	0.38	4 (3%) 44 53	28, 40, 75, 159	0
6	F	94/94 (100%)	0.34	6 (6%) 25 31	23, 35, 61, 166	0
6	S	94/94 (100%)	0.48	6 (6%) 25 31	23, 32, 64, 131	0
7	G	84/84 (100%)	1.73	23 (27%) 1 1	26, 37, 140, 219	0
7	T	84/84 (100%)	1.62	22 (26%) 1 2	25, 39, 146, 232	0
8	H	79/79 (100%)	1.00	12 (15%) 5 7	29, 39, 117, 155	0
8	U	79/79 (100%)	1.04	14 (17%) 4 4	32, 43, 133, 164	0
9	I	72/73 (98%)	1.20	17 (23%) 2 2	28, 46, 78, 102	0
9	V	72/73 (98%)	1.42	20 (27%) 1 1	29, 53, 91, 134	0
10	J	58/58 (100%)	0.76	7 (12%) 8 11	27, 38, 86, 149	0
10	W	58/58 (100%)	0.60	4 (6%) 23 28	28, 40, 79, 154	0
11	K	49/49 (100%)	0.73	4 (8%) 17 23	31, 40, 58, 69	0
11	X	49/49 (100%)	1.23	10 (20%) 3 3	38, 47, 84, 101	0
12	L	46/46 (100%)	0.27	4 (8%) 16 21	26, 30, 53, 113	0
12	Y	46/46 (100%)	0.59	5 (10%) 10 14	29, 36, 71, 131	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	43/43 (100%)	0.31	3 (6%) 22 28	26, 31, 87, 146	0
13	Z	43/43 (100%)	0.83	5 (11%) 9 12	34, 39, 103, 174	0
All	All	3544/3550 (99%)	0.34	248 (6%) 22 28	11, 32, 74, 232	105 (2%)

The worst 5 of 248 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	G	6	GLY	13.4
7	T	6	GLY	12.9
7	T	3	ALA	12.5
1	N	50[A]	ASP	12.3
6	F	1	ALA	10.0

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
9	SAC	V	1	9/10	0.32	0.21	180,189,197,198	0
9	SAC	I	1	9/10	0.68	0.22	99,114,130,131	0
1	FME	N	1	10/11	0.91	0.15	34,43,83,105	0
1	FME	A	1	10/11	0.94	0.09	35,49,83,99	0
2	FME	B	1	10/11	0.96	0.12	27,31,39,120	0
2	FME	O	1	10/11	0.97	0.10	35,36,43,78	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
20	EDO	P	311	4/4	0.71	0.22	55,58,66,107	0
20	EDO	N	621	4/4	0.72	0.22	43,55,64,70	0
21	DMU	A	620	9/33	0.72	0.25	69,78,97,104	0
18	PGV	P	307	38/51	0.74	0.27	41,74,97,111	0
27	CDL	G	101	69/100	0.74	0.27	43,74,103,114	0
20	EDO	C	317	4/4	0.75	0.21	43,69,73,74	0
21	DMU	D	207	8/33	0.76	0.25	59,75,89,97	0
20	EDO	C	319	4/4	0.76	0.16	70,70,71,94	0
21	DMU	K	103	9/33	0.77	0.28	61,87,107,112	0
20	EDO	C	318	4/4	0.77	0.20	57,74,80,83	0
25	CHD	L	102	29/29	0.78	0.24	52,97,132,158	0
21	DMU	X	103	10/33	0.78	0.26	63,81,89,91	0
27	CDL	T	101	70/100	0.78	0.23	46,72,109,137	0
21	DMU	X	101	9/33	0.79	0.21	60,74,88,88	0
22	TGL	B	301	63/63	0.80	0.21	33,71,116,127	0
22	TGL	N	608	55/63	0.80	0.23	49,72,120,127	0
21	DMU	Q	202	10/33	0.80	0.25	58,61,87,98	0
26	PEK	P	303	28/53	0.80	0.22	45,58,92,106	0
18	PGV	C	307	37/51	0.80	0.25	41,72,107,115	0
20	EDO	C	314	4/4	0.80	0.24	57,60,86,89	0
21	DMU	P	310	22/33	0.81	0.18	40,68,94,112	0
22	TGL	D	201	63/63	0.81	0.23	33,67,134,153	0
26	PEK	C	303	18/53	0.81	0.19	44,52,87,92	0
20	EDO	F	107	4/4	0.82	0.23	46,49,61,109	0
26	PEK	P	305	40/53	0.82	0.23	38,75,101,126	0
18	PGV	A	606	33/51	0.82	0.22	32,56,99,123	0
18	PGV	Q	201	37/51	0.82	0.23	43,65,110,121	0
26	PEK	C	305	40/53	0.83	0.21	42,70,103,122	0
21	DMU	K	102	9/33	0.83	0.23	61,71,95,102	0
20	EDO	S	105	4/4	0.83	0.18	60,74,77,87	0
25	CHD	P	309	29/29	0.83	0.18	40,77,135,146	0
21	DMU	K	104	10/33	0.83	0.25	52,65,87,94	0
24	PSC	B	303	41/52	0.84	0.19	46,78,116,162	0
25	CHD	C	309	29/29	0.84	0.15	46,58,110,165	0
20	EDO	J	101	4/4	0.84	0.20	50,51,84,98	0
22	TGL	N	606	63/63	0.84	0.22	45,77,110,145	0
21	DMU	X	102	8/33	0.84	0.17	65,71,83,84	0
27	CDL	P	308	77/100	0.85	0.21	41,75,129,151	0
20	EDO	C	311	4/4	0.86	0.16	33,39,42,42	0
20	EDO	N	620	4/4	0.86	0.22	49,53,55,64	0
21	DMU	C	320	12/33	0.86	0.20	60,63,88,92	0
20	EDO	D	205	4/4	0.86	0.17	56,60,62,71	0
20	EDO	A	619	4/4	0.86	0.14	53,62,70,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
20	EDO	P	312	4/4	0.86	0.15	39,40,47,54	0
20	EDO	P	317	4/4	0.86	0.17	54,59,60,67	0
27	CDL	C	308	85/100	0.86	0.18	42,72,133,153	0
22	TGL	N	607	43/63	0.86	0.23	41,60,99,125	0
21	DMU	L	104	21/33	0.86	0.20	51,77,98,107	0
20	EDO	S	104	4/4	0.86	0.17	55,60,61,83	0
21	DMU	C	310	22/33	0.87	0.16	29,59,107,121	0
20	EDO	D	204	4/4	0.87	0.14	45,49,58,58	0
21	DMU	D	206	11/33	0.87	0.17	46,70,82,83	0
20	EDO	Y	101	4/4	0.87	0.15	46,54,58,61	0
20	EDO	M	102	4/4	0.87	0.14	58,60,82,86	0
24	PSC	O	302	33/52	0.88	0.20	29,62,99,125	0
20	EDO	J	102	4/4	0.88	0.16	53,56,56,70	0
20	EDO	L	103	4/4	0.88	0.21	38,75,81,126	0
20	EDO	Q	204	4/4	0.88	0.15	47,50,53,61	0
20	EDO	A	611	4/4	0.88	0.20	47,55,63,109	0
20	EDO	F	105	4/4	0.88	0.15	33,39,68,69	0
20	EDO	T	102	4/4	0.88	0.20	40,74,80,92	0
22	TGL	L	101	54/63	0.88	0.21	30,56,125,171	0
20	EDO	W	101	4/4	0.88	0.19	49,73,83,132	0
20	EDO	D	203	4/4	0.88	0.19	37,47,73,80	0
21	DMU	O	305	11/33	0.88	0.18	60,66,96,97	0
20	EDO	B	309	4/4	0.88	0.17	31,46,47,64	0
20	EDO	C	315	4/4	0.89	0.16	49,58,68,72	0
21	DMU	W	103	11/33	0.89	0.17	52,63,72,91	0
20	EDO	S	106	4/4	0.89	0.11	37,42,58,59	0
20	EDO	T	103	4/4	0.90	0.15	39,45,60,65	0
20	EDO	A	614	4/4	0.90	0.18	39,40,43,47	0
20	EDO	W	102	4/4	0.90	0.16	50,64,72,81	0
20	EDO	R	202	4/4	0.90	0.14	47,62,63,78	0
20	EDO	A	616	4/4	0.90	0.17	42,49,58,67	0
21	DMU	P	318	11/33	0.90	0.18	45,62,80,85	0
29	PO4	U	101	5/5	0.90	0.12	53,54,120,187	0
20	EDO	B	307	4/4	0.91	0.14	41,50,54,81	0
20	EDO	P	315	4/4	0.91	0.12	28,39,40,52	0
20	EDO	F	106	4/4	0.91	0.18	37,38,45,101	0
29	PO4	H	101	5/5	0.91	0.12	59,71,91,156	0
21	DMU	J	103	11/33	0.91	0.16	49,59,88,96	0
21	DMU	Z	101	33/33	0.92	0.10	37,47,69,80	0
21	DMU	M	101	33/33	0.92	0.10	34,43,60,77	0
21	DMU	N	622	9/33	0.92	0.16	48,68,78,80	0
20	EDO	A	613	4/4	0.92	0.19	43,53,63,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
20	EDO	E	203	4/4	0.92	0.12	44,44,48,70	0
20	EDO	P	313	4/4	0.92	0.11	55,57,62,74	0
21	DMU	K	101	9/33	0.92	0.17	54,62,82,91	0
20	EDO	F	104	4/4	0.92	0.14	39,40,59,88	0
20	EDO	P	316	4/4	0.92	0.11	49,57,59,62	0
20	EDO	S	108	4/4	0.92	0.18	38,50,60,72	0
20	EDO	B	310	4/4	0.92	0.13	41,47,48,52	0
20	EDO	B	305	4/4	0.93	0.13	37,44,49,54	0
17	NA	P	302	1/1	0.93	0.09	39,39,39,39	0
20	EDO	N	614	4/4	0.93	0.20	33,36,50,107	0
20	EDO	N	617	4/4	0.93	0.16	32,42,45,66	0
20	EDO	C	316	4/4	0.93	0.14	29,34,40,52	0
20	EDO	B	308	4/4	0.93	0.18	34,38,47,113	0
20	EDO	A	609	4/4	0.94	0.13	29,33,44,92	0
20	EDO	E	202	4/4	0.94	0.09	36,38,40,45	0
20	EDO	A	617	4/4	0.94	0.10	28,29,31,34	0
20	EDO	N	618	4/4	0.94	0.12	29,45,62,64	0
19	OXY	N	609	2/2	0.94	0.19	16,16,16,25	2
21	DMU	A	621	8/33	0.94	0.12	46,50,67,77	0
20	EDO	C	313	4/4	0.94	0.14	35,56,64,109	0
20	EDO	Q	203	4/4	0.94	0.12	29,47,51,73	0
20	EDO	B	306	4/4	0.95	0.08	25,27,30,33	0
20	EDO	O	304	4/4	0.95	0.09	42,47,54,57	0
20	EDO	N	611	4/4	0.95	0.08	22,27,29,32	0
20	EDO	A	612	4/4	0.95	0.15	28,40,76,100	0
20	EDO	N	615	4/4	0.95	0.10	41,41,42,50	0
26	PEK	P	304	53/53	0.95	0.13	27,44,94,113	0
20	EDO	P	314	4/4	0.95	0.14	35,36,37,44	0
20	EDO	N	616	4/4	0.95	0.11	36,41,42,47	0
19	OXY	A	607	2/2	0.95	0.18	14,14,14,29	2
20	EDO	T	104	4/4	0.95	0.10	29,32,38,43	0
17	NA	C	302	1/1	0.95	0.08	40,40,40,40	0
25	CHD	C	301	29/29	0.95	0.07	25,28,35,38	0
20	EDO	A	615	4/4	0.95	0.17	32,39,39,119	0
20	EDO	N	612	4/4	0.96	0.08	26,27,28,29	0
20	EDO	S	107	4/4	0.96	0.10	28,30,33,33	0
20	EDO	N	613	4/4	0.96	0.08	38,39,42,47	0
18	PGV	P	306	51/51	0.96	0.11	22,30,82,104	0
20	EDO	R	201	4/4	0.96	0.08	41,41,42,44	0
18	PGV	A	608	51/51	0.96	0.11	22,28,70,89	0
20	EDO	S	103	4/4	0.96	0.09	35,37,40,45	0
20	EDO	O	303	4/4	0.96	0.09	30,32,32,33	0

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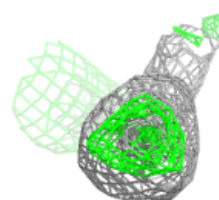
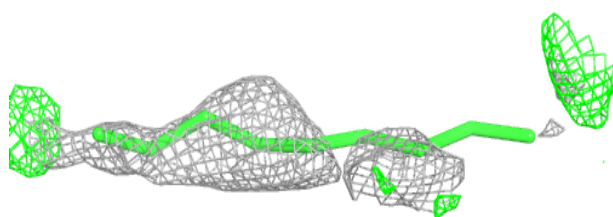
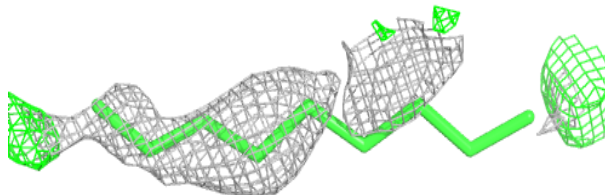
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
18	PGV	N	610	51/51	0.96	0.11	24,31,69,80	0
26	PEK	C	304	53/53	0.96	0.12	25,43,94,114	0
20	EDO	G	103	4/4	0.97	0.07	29,32,37,37	0
20	EDO	A	618	4/4	0.97	0.12	30,37,45,51	0
20	EDO	F	103	4/4	0.97	0.09	31,31,31,33	0
20	EDO	C	312	4/4	0.97	0.07	32,34,35,36	0
18	PGV	C	306	51/51	0.97	0.10	23,29,83,100	0
25	CHD	B	304	29/29	0.97	0.06	23,27,32,43	0
20	EDO	E	201	4/4	0.97	0.09	38,40,43,43	0
20	EDO	S	102	4/4	0.97	0.08	23,24,25,25	0
25	CHD	G	102	29/29	0.97	0.06	22,26,30,39	0
20	EDO	N	619	4/4	0.97	0.09	30,38,39,43	0
25	CHD	P	301	29/29	0.97	0.07	25,29,37,39	0
20	EDO	D	202	4/4	0.97	0.08	33,35,56,63	0
16	MG	A	604	1/1	0.98	0.05	20,20,20,20	0
14	HEA	A	602	60/60	0.98	0.06	19,23,29,36	0
20	EDO	F	102	4/4	0.98	0.05	24,24,24,26	0
20	EDO	A	610	4/4	0.98	0.06	21,23,26,29	0
14	HEA	N	602	60/60	0.98	0.06	20,24,30,35	0
23	CUA	O	301	2/2	0.99	0.03	27,27,27,27	0
14	HEA	N	601[B]	54/60	0.99	0.07	20,25,38,41	12
14	HEA	N	601[C]	51/60	0.99	0.07	20,25,36,42	9
14	HEA	A	601[B]	54/60	0.99	0.07	17,21,31,38	12
15	CU	N	603	1/1	0.99	0.03	24,24,24,24	0
14	HEA	A	601[C]	51/60	0.99	0.07	17,21,28,36	9
16	MG	N	604	1/1	0.99	0.04	23,23,23,23	0
17	NA	A	605	1/1	0.99	0.06	27,27,27,27	0
14	HEA	A	601[A]	60/60	0.99	0.07	15,21,41,52	18
28	ZN	S	101	1/1	0.99	0.03	27,27,27,27	0
17	NA	N	605	1/1	0.99	0.03	31,31,31,31	0
14	HEA	N	601[A]	60/60	0.99	0.07	17,26,42,50	18
15	CU	A	603	1/1	1.00	0.02	22,22,22,22	0
23	CUA	B	302	2/2	1.00	0.02	24,24,24,24	0
28	ZN	F	101	1/1	1.00	0.03	26,26,26,26	0

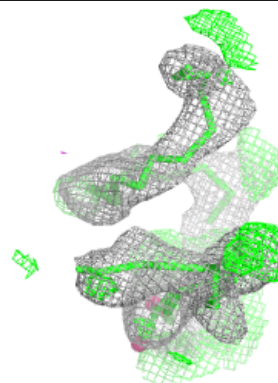
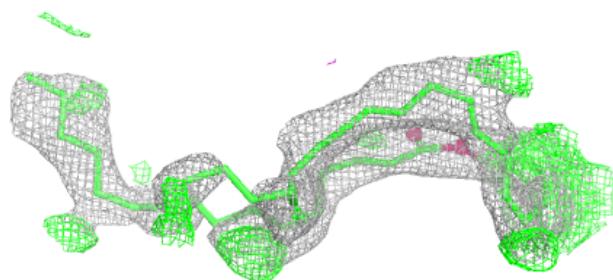
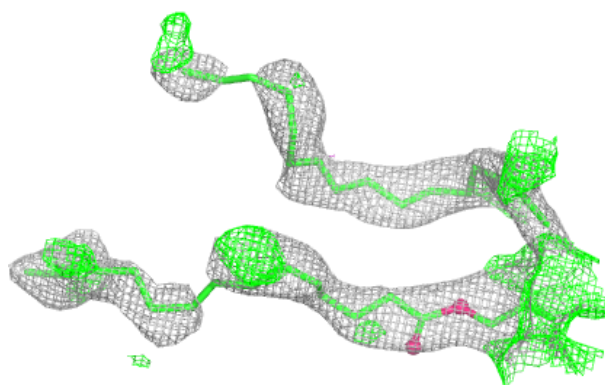
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DMU A 620:

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

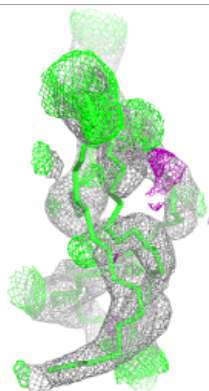
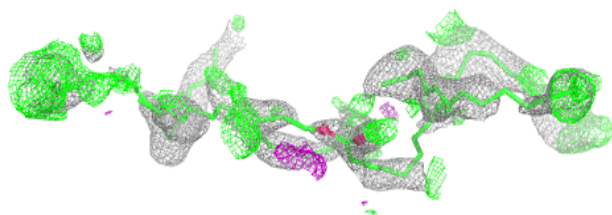
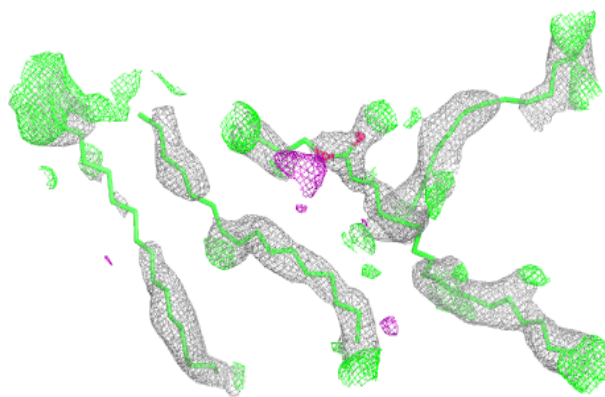
**Electron density around PGV P 307:**

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

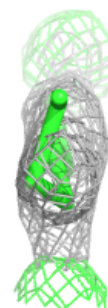
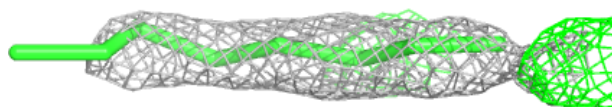
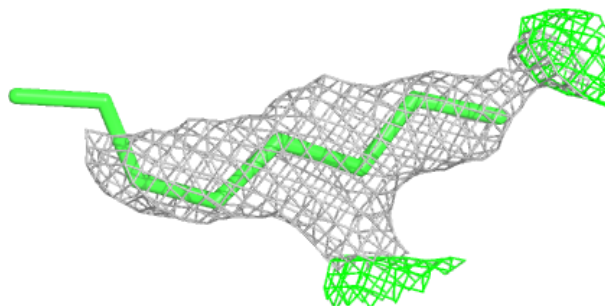


Electron density around CDL G 101:

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

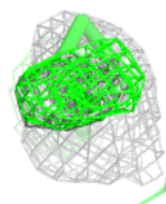
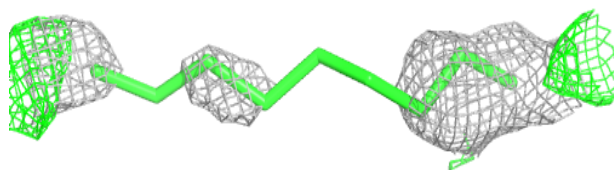
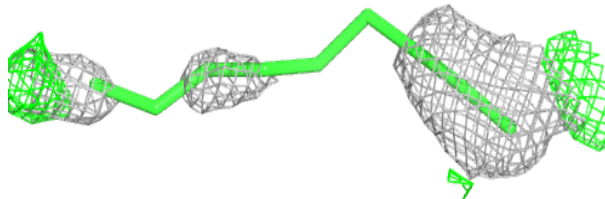
**Electron density around DMU D 207:**

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

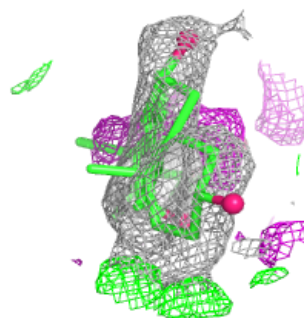
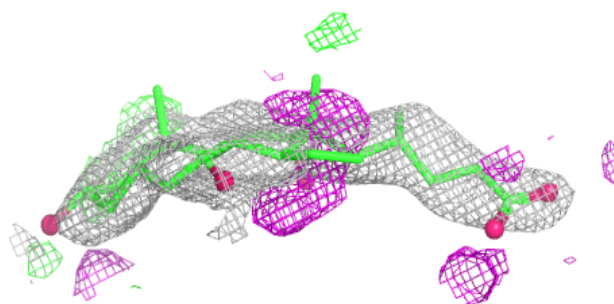
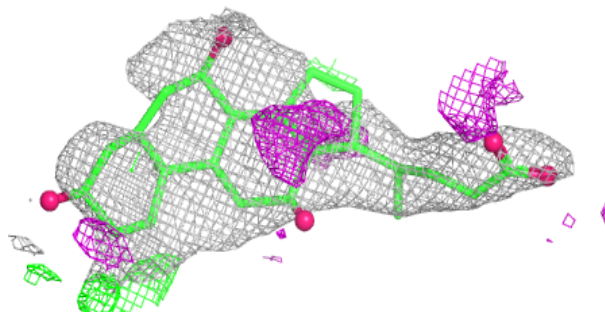


Electron density around DMU K 103:

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

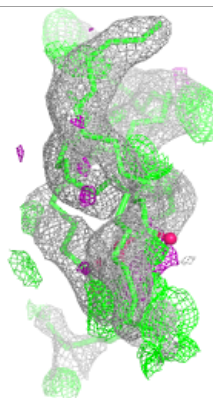
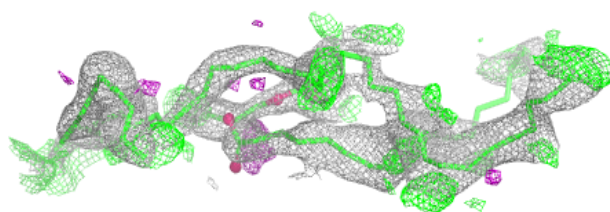
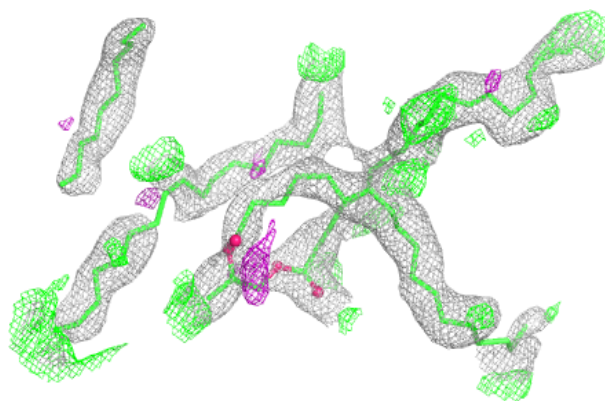
**Electron density around CHD L 102:**

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

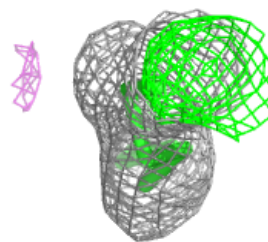
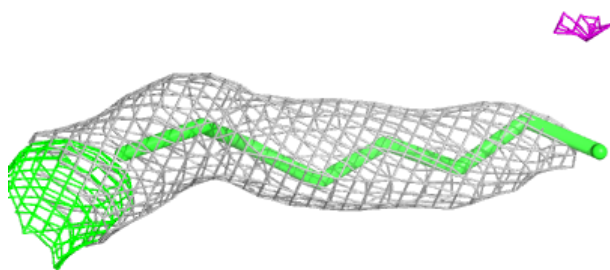
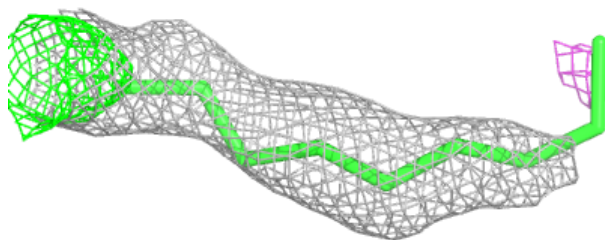


Electron density around CDL T 101:

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

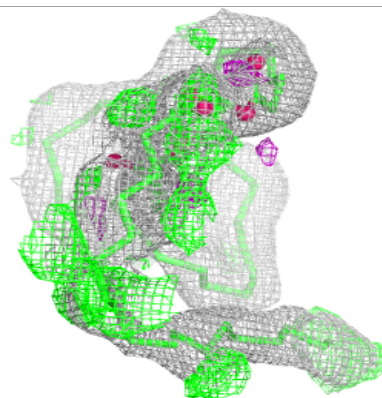
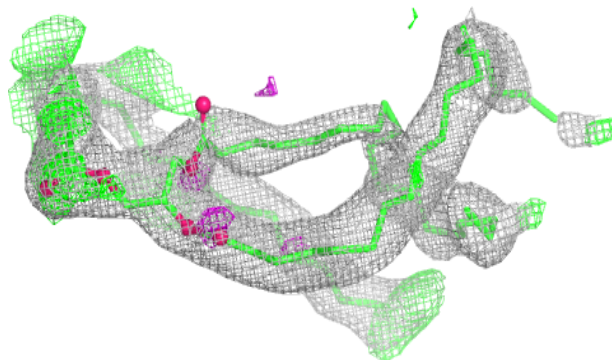
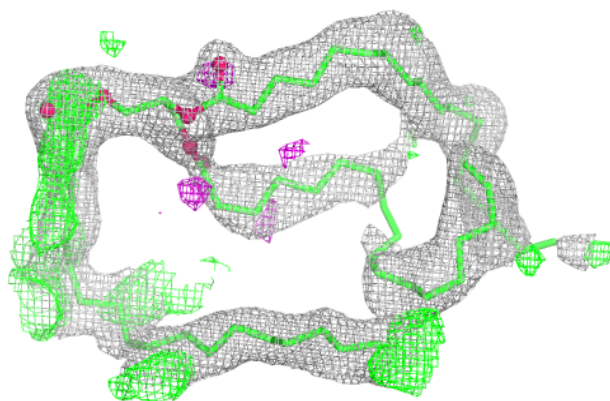
**Electron density around DMU X 101:**

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

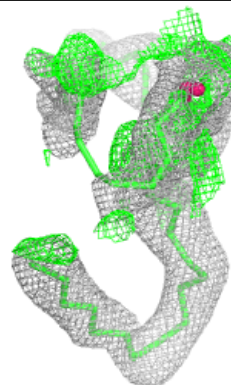
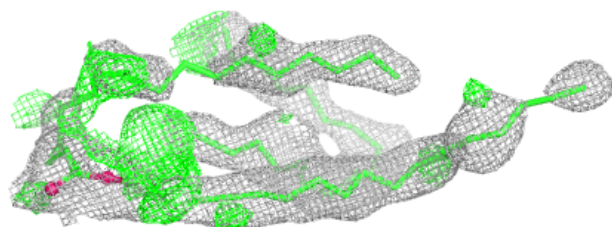
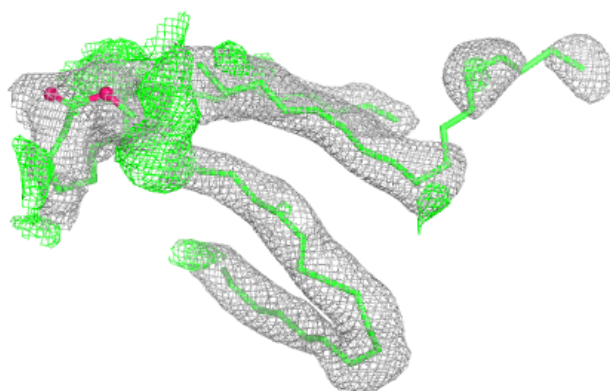


Electron density around TGL B 301:

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

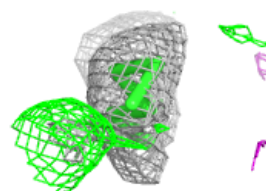
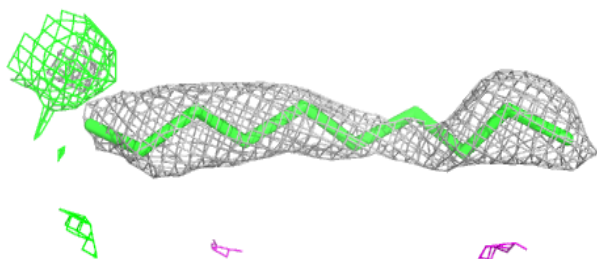
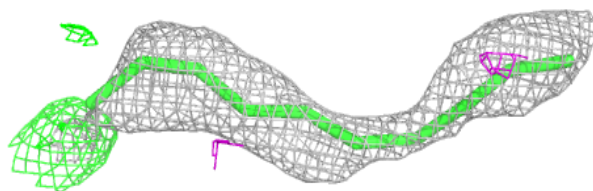
**Electron density around TGL N 608:**

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

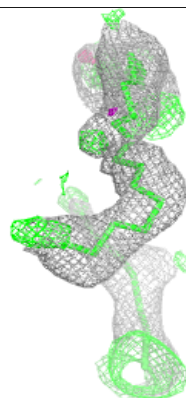
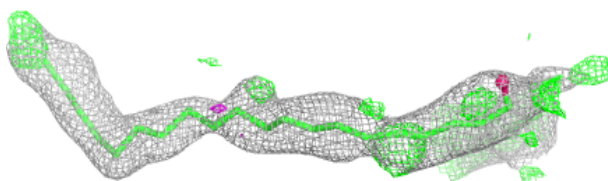
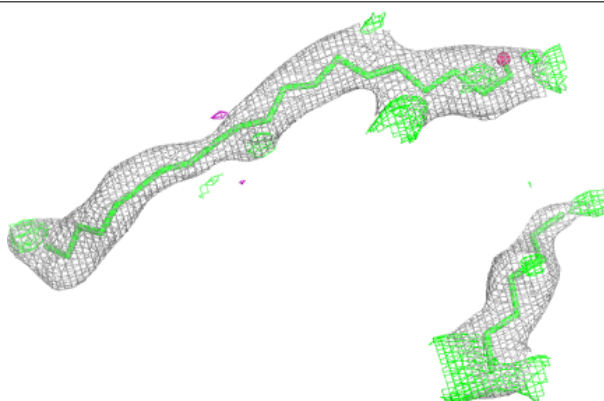


Electron density around DMU Q 202:

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

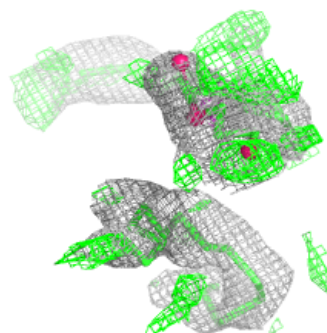
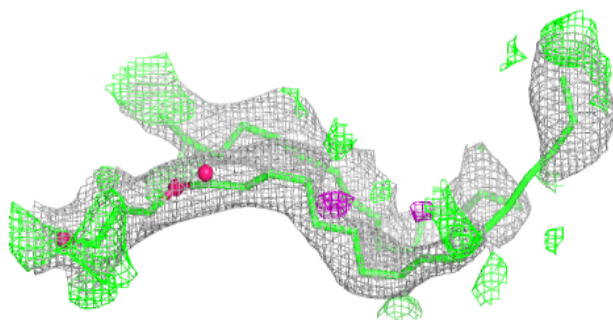
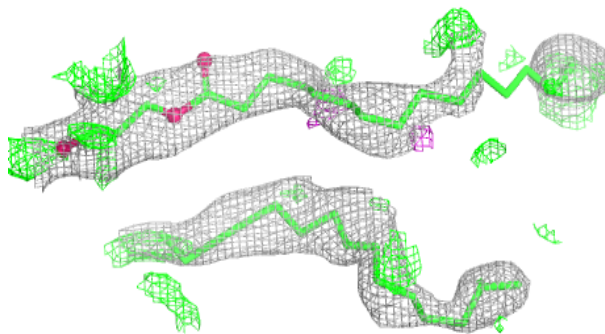
**Electron density around PEK P 303:**

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

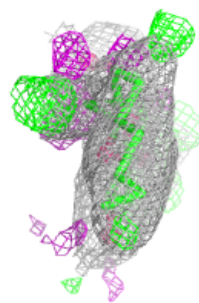
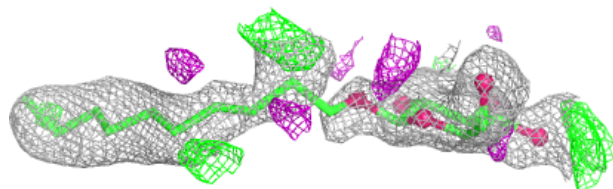
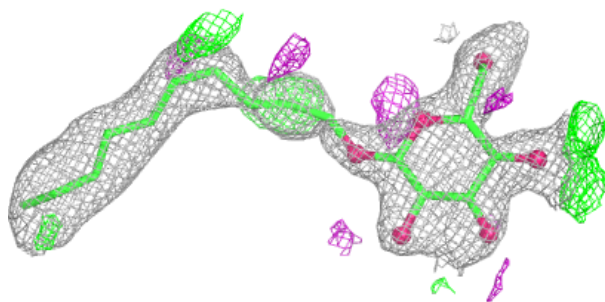


Electron density around PGV C 307:

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

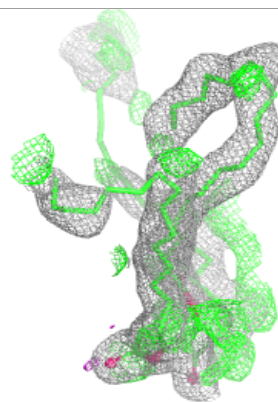
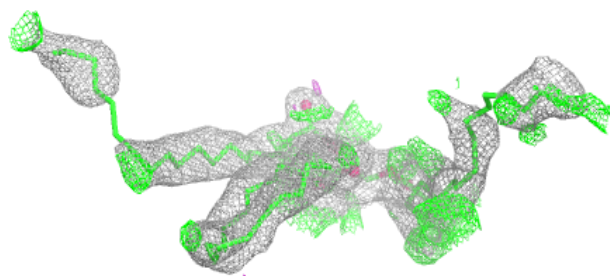
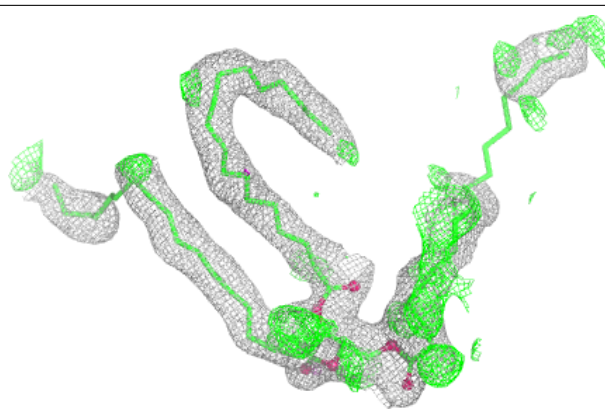
**Electron density around DMU P 310:**

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

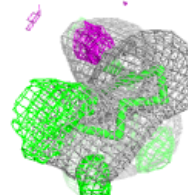
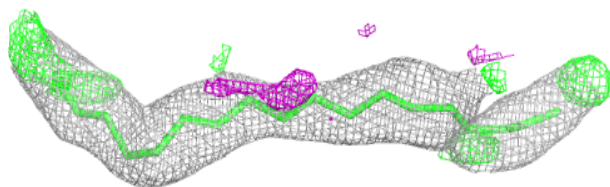
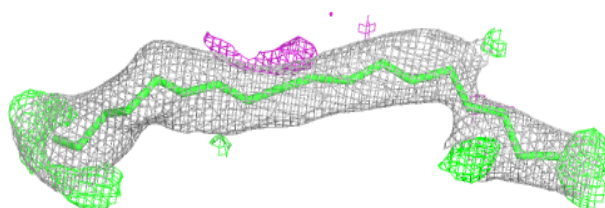


Electron density around TGL D 201:

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

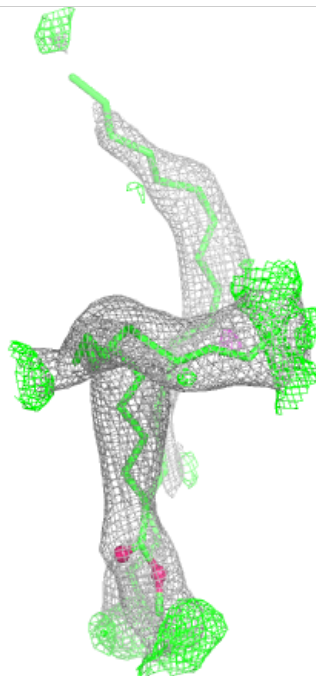
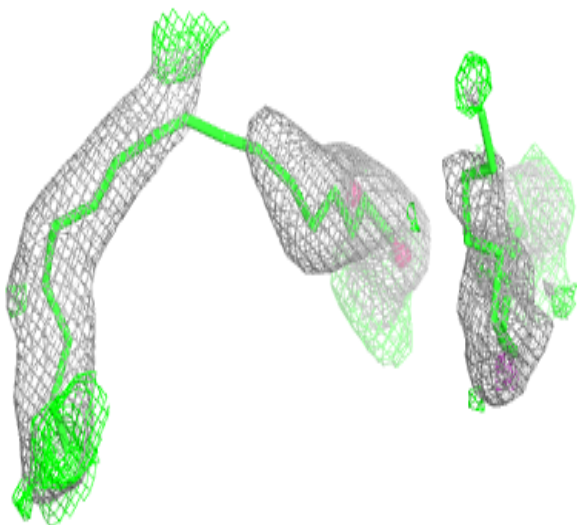
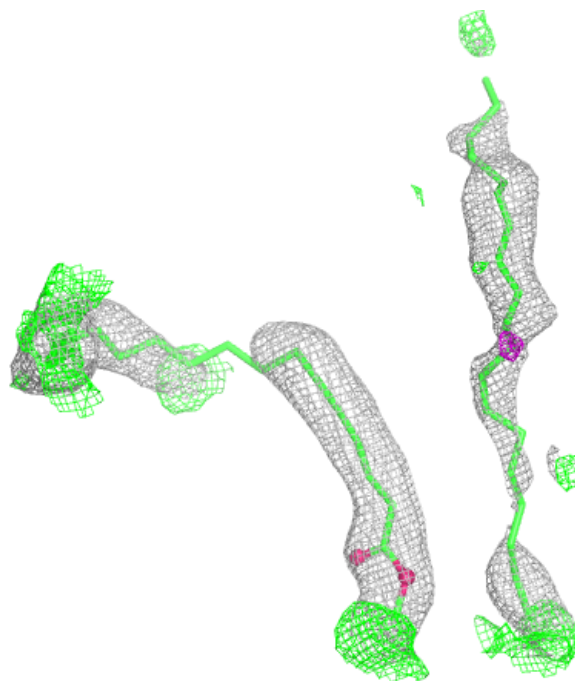
**Electron density around PEK C 303:**

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



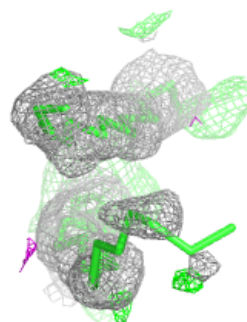
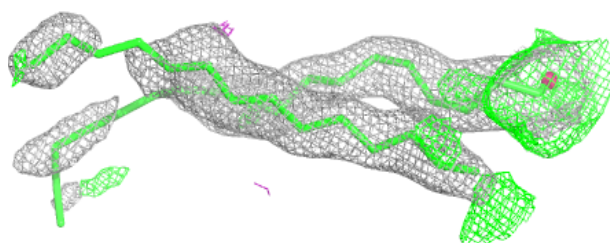
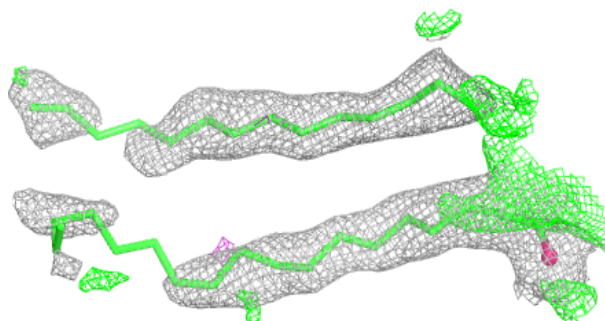
Electron density around PEK P 305:

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

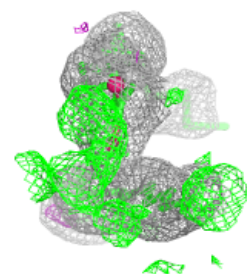
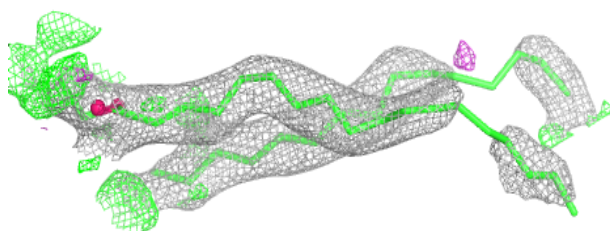
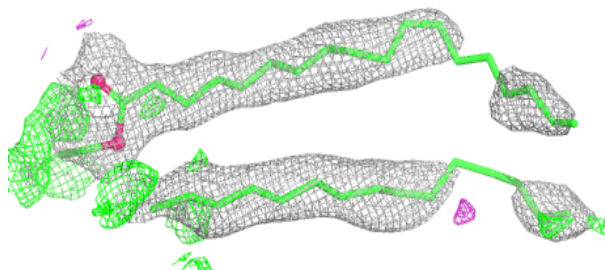


Electron density around PGV A 606:

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

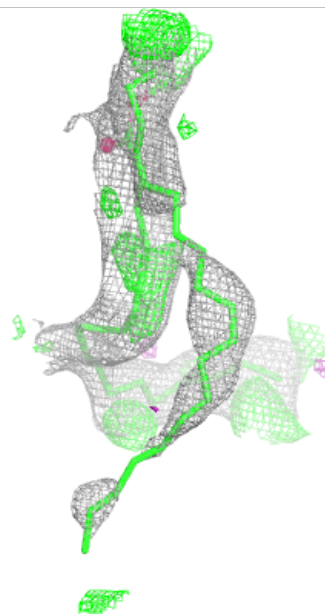
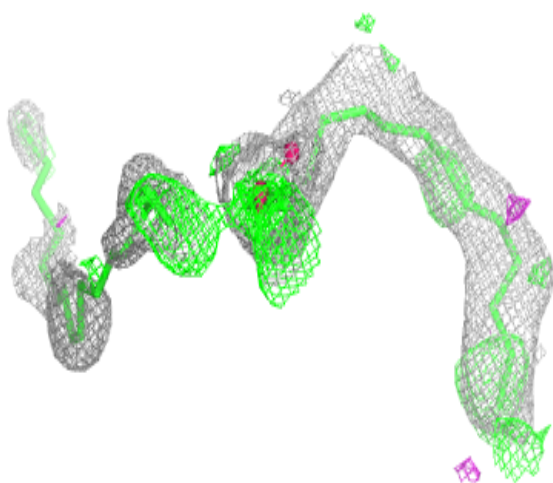
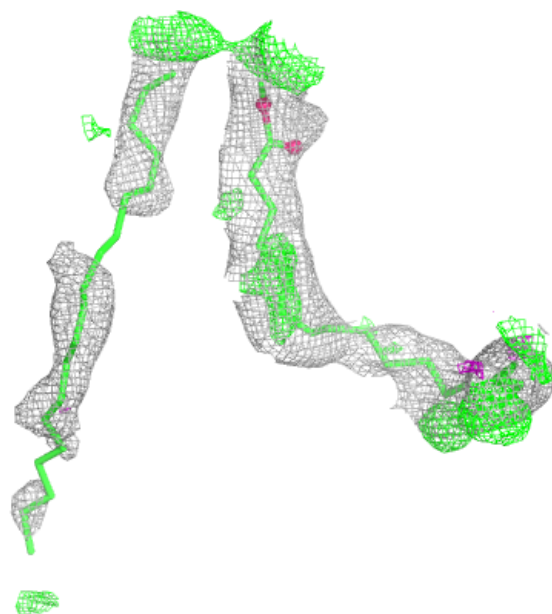
**Electron density around PGV Q 201:**

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



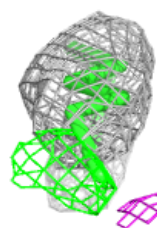
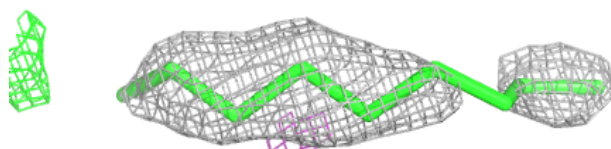
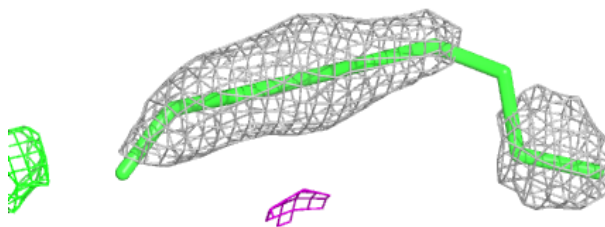
Electron density around PEK C 305:

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

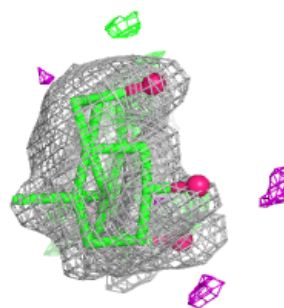
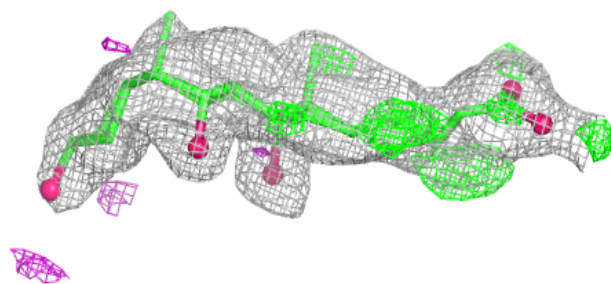
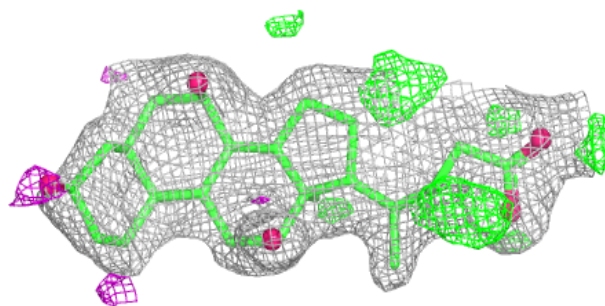


Electron density around DMU K 102:

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

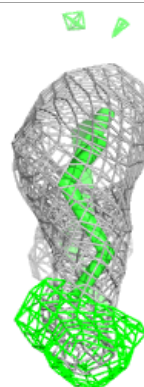
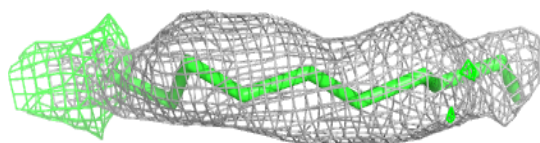
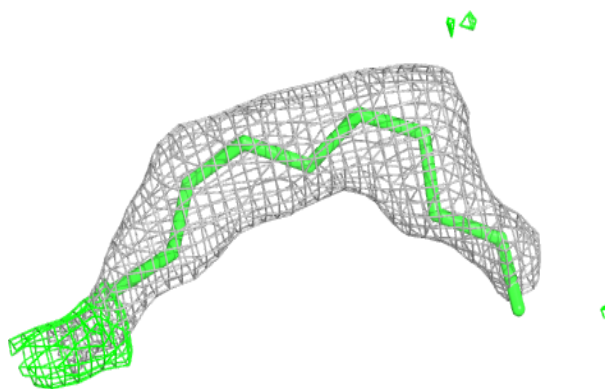
**Electron density around CHD P 309:**

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

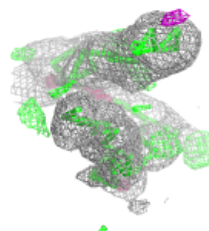
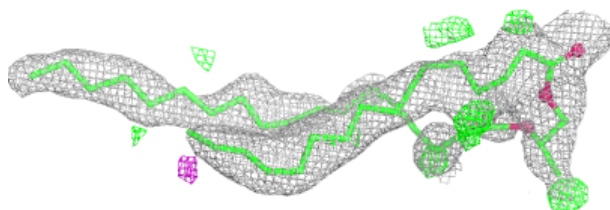
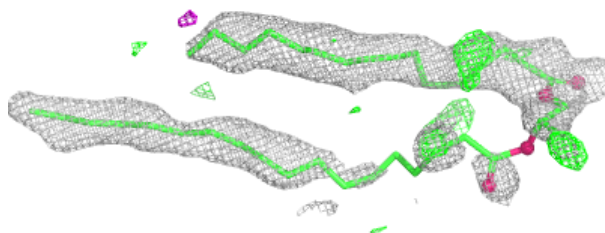


Electron density around DMU K 104:

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

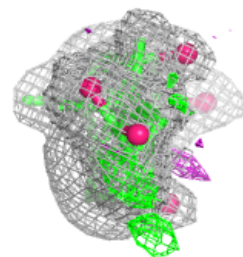
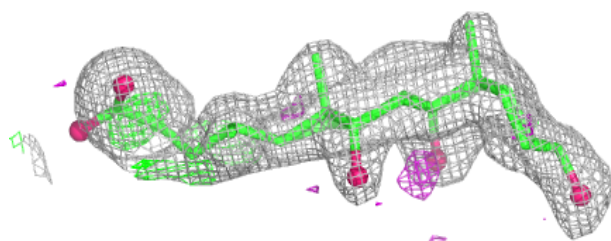
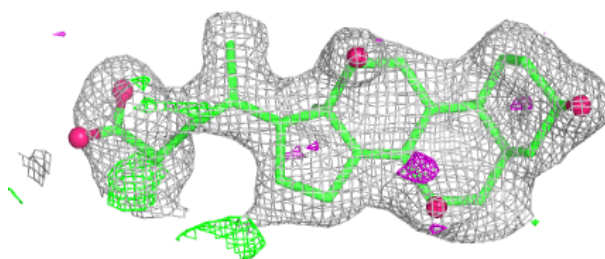
**Electron density around PSC B 303:**

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

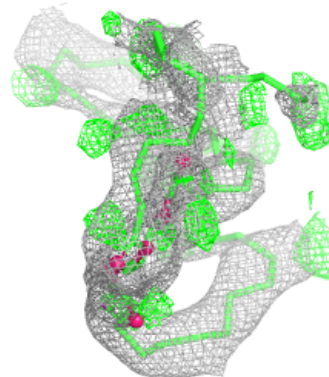
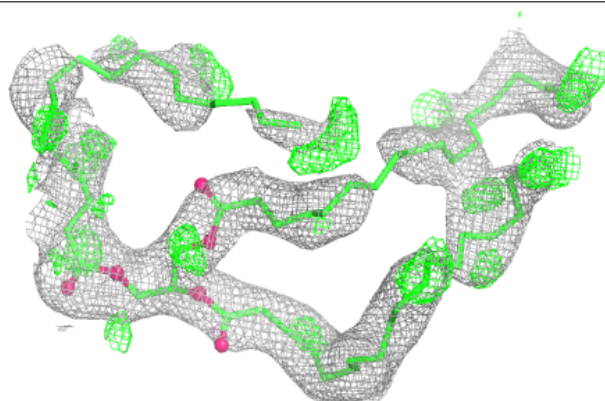


Electron density around CHD C 309:

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

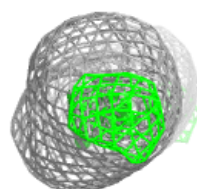
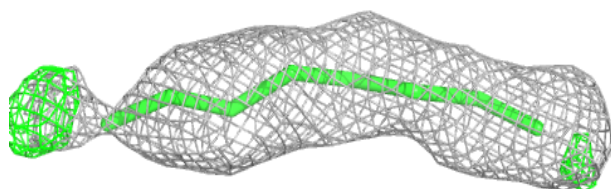
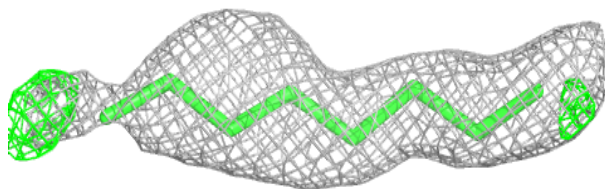
**Electron density around TGL N 606:**

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



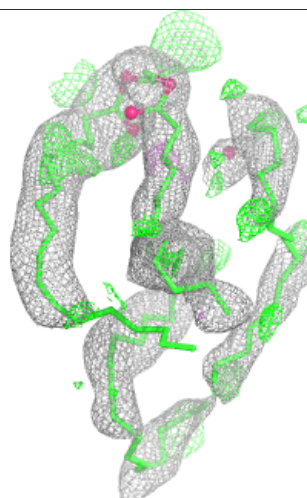
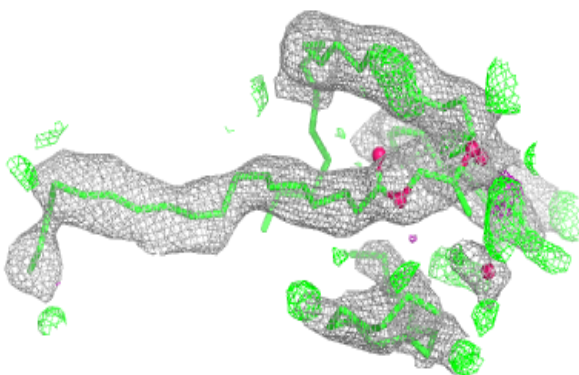
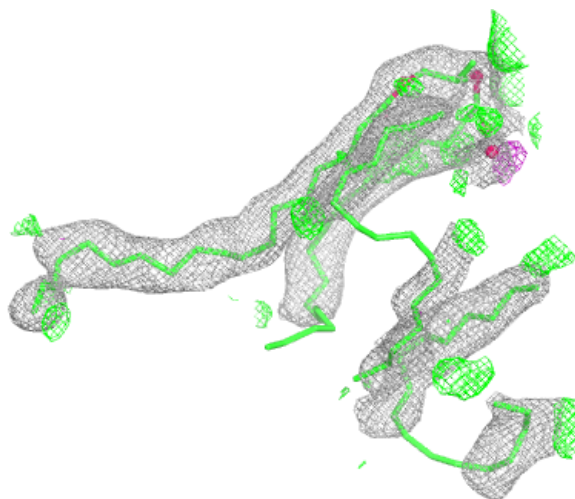
Electron density around DMU X 102:

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



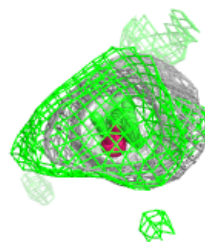
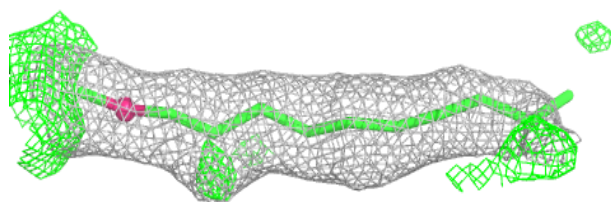
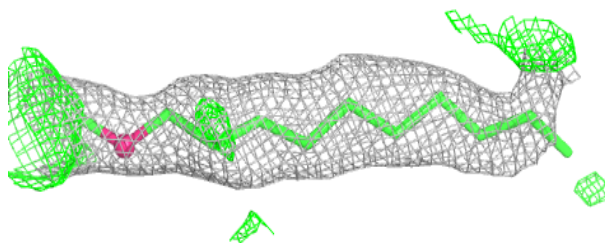
Electron density around CDL P 308:

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



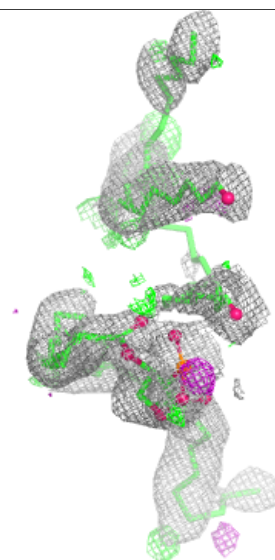
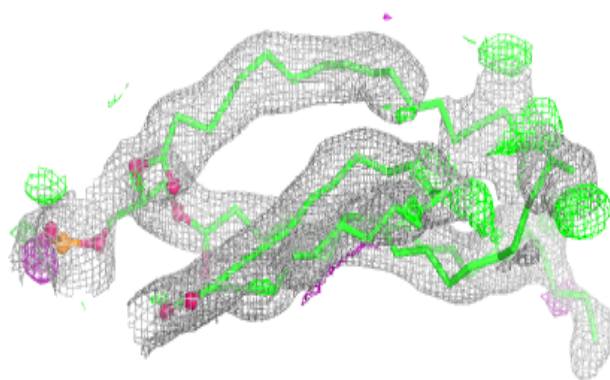
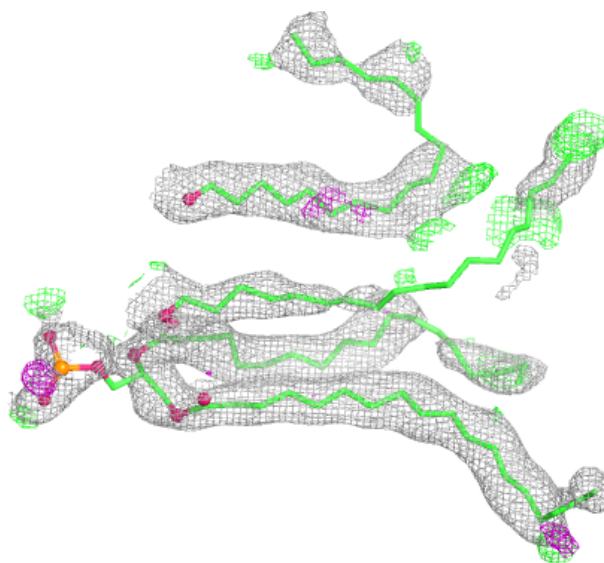
Electron density around DMU C 320:

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



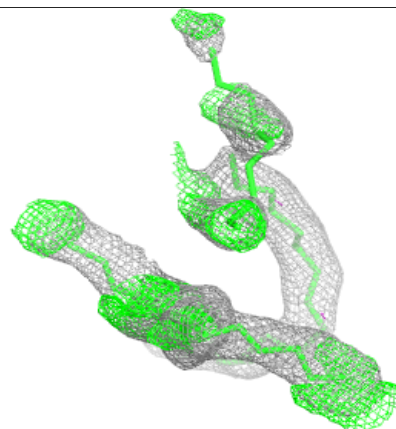
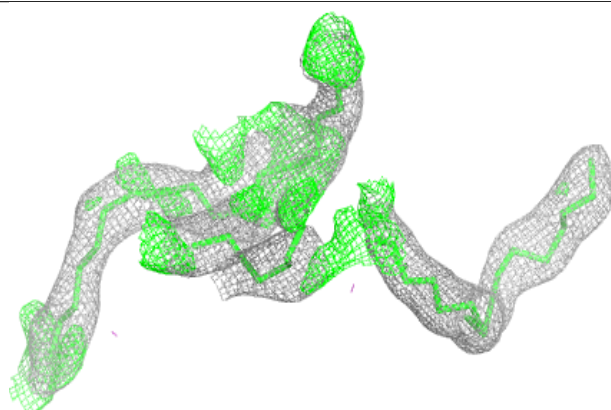
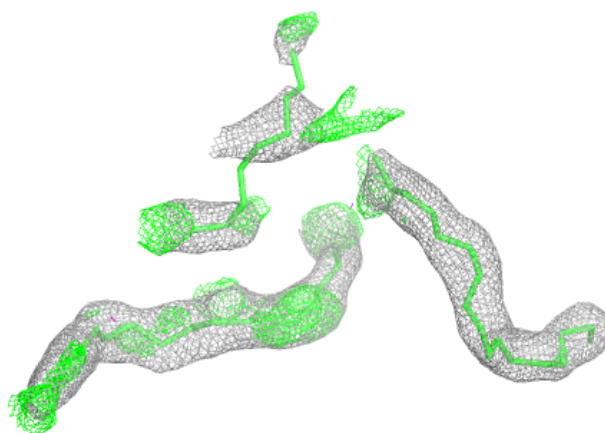
Electron density around CDL C 308:

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

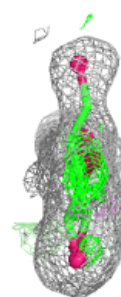
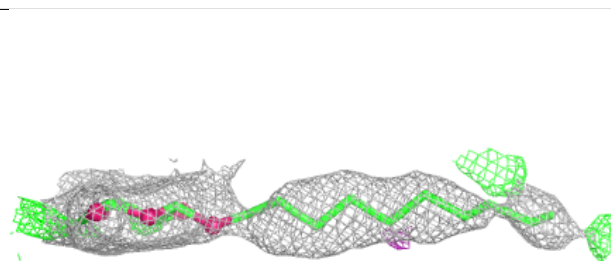
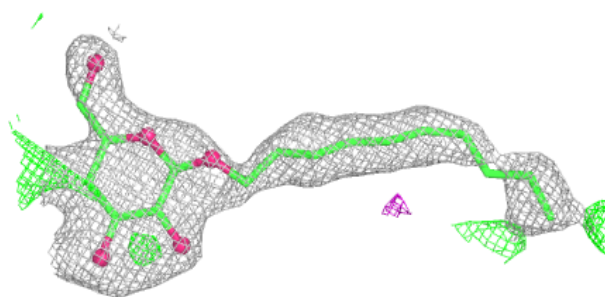


Electron density around TGL N 607:

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

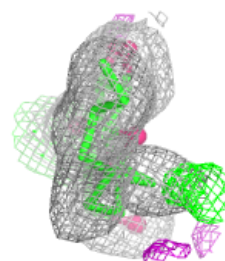
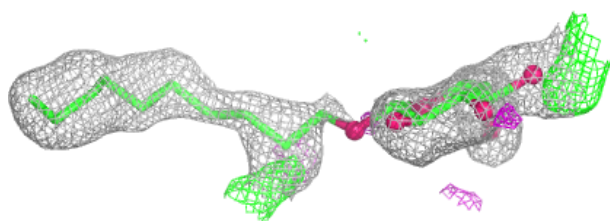
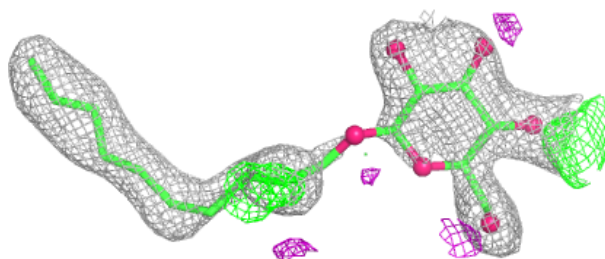
**Electron density around DMU L 104:**

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

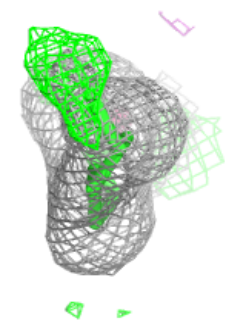
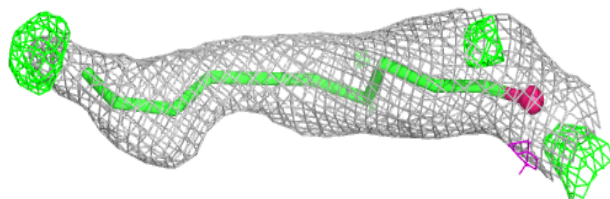
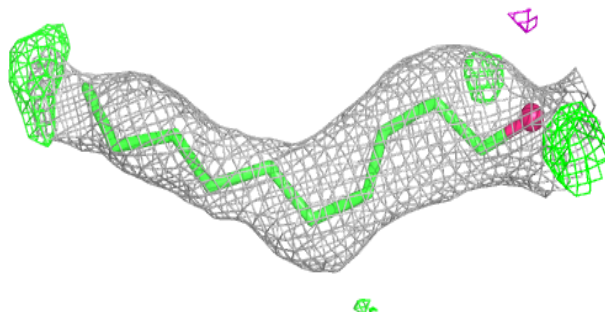


Electron density around DMU C 310:

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

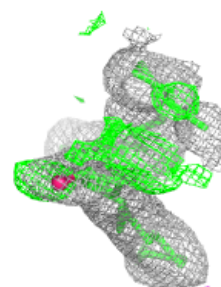
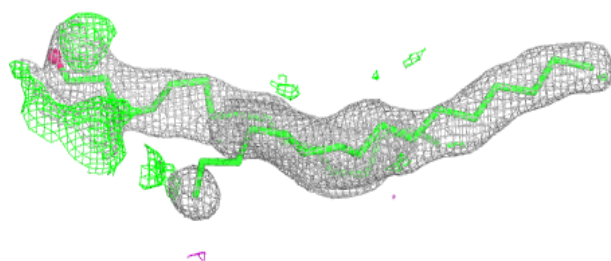
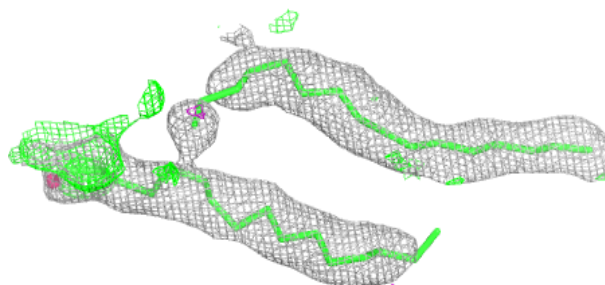
**Electron density around DMU D 206:**

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

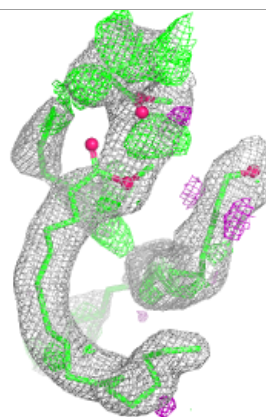
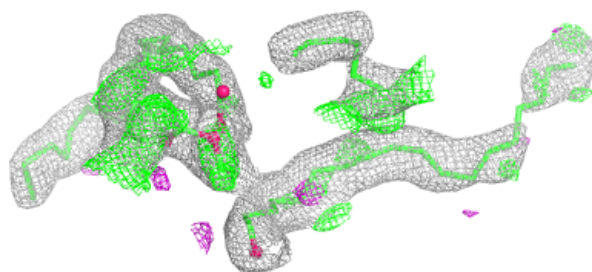
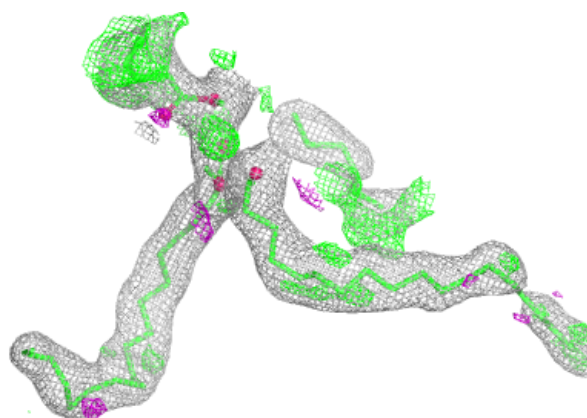


Electron density around PSC O 302:

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

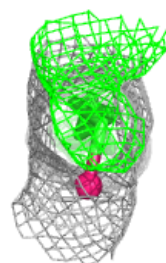
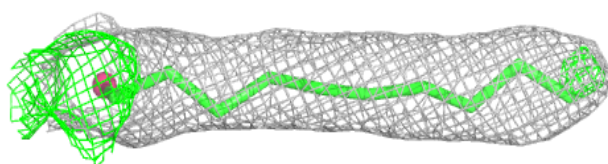
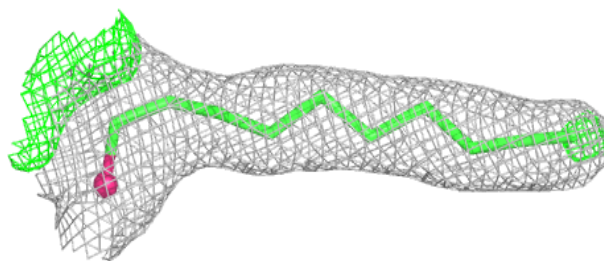
**Electron density around TGL L 101:**

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

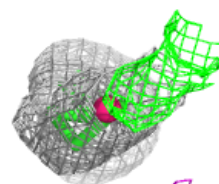
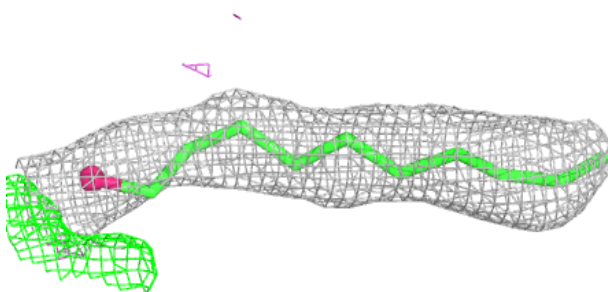
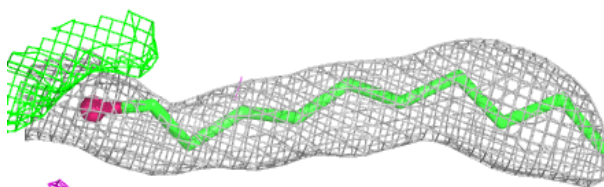


Electron density around DMU O 305:

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

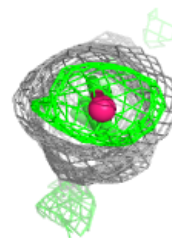
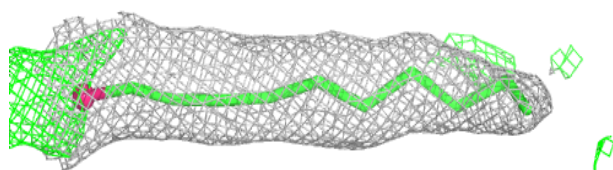
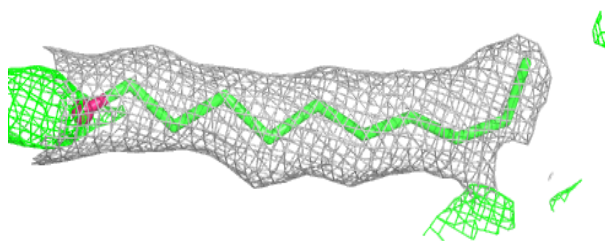
**Electron density around DMU W 103:**

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

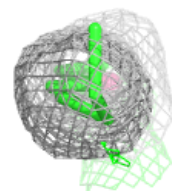
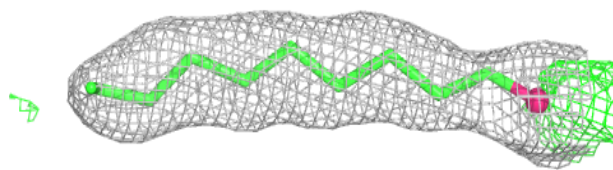
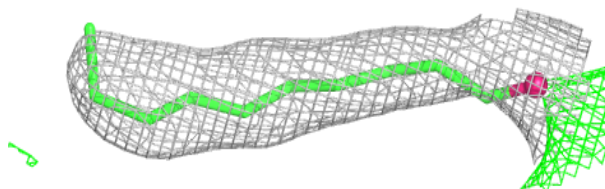


Electron density around DMU P 318:

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

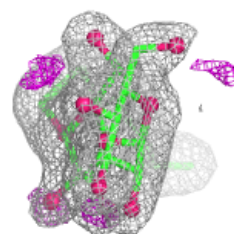
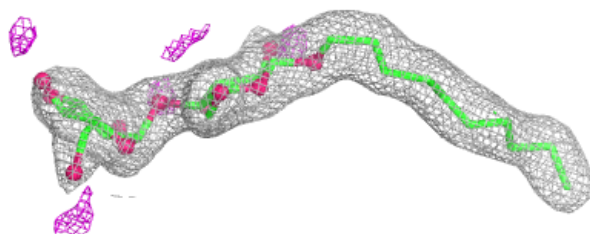
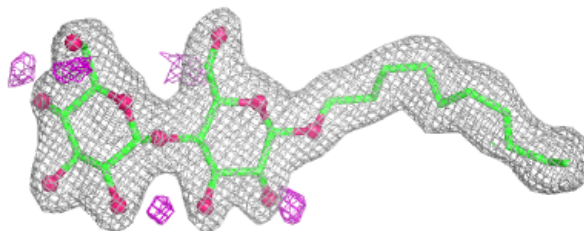
**Electron density around DMU J 103:**

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

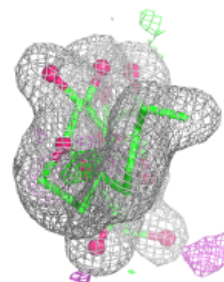
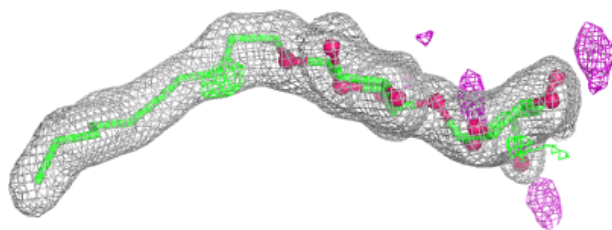
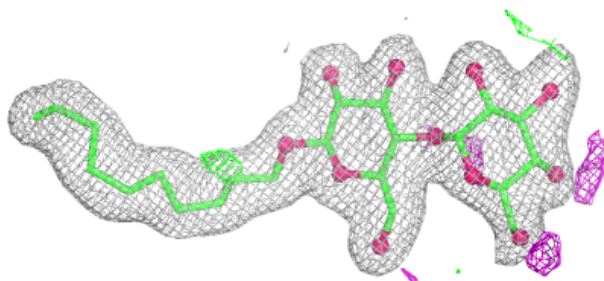


Electron density around DMU Z 101:

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

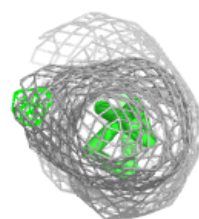
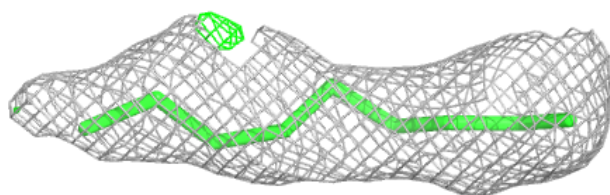
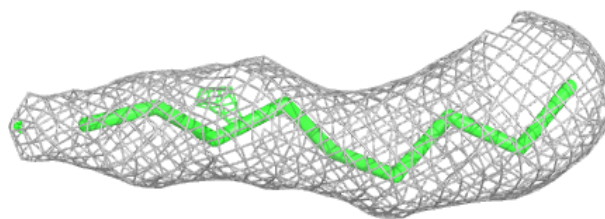
**Electron density around DMU M 101:**

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

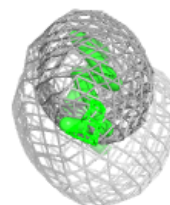
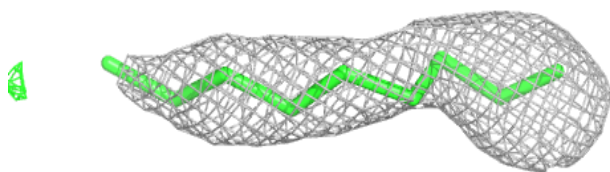
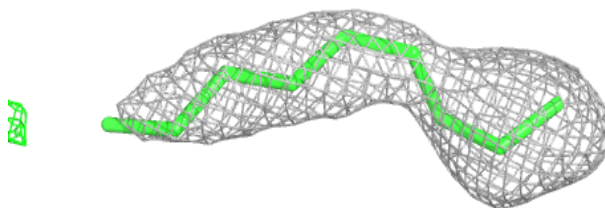


Electron density around DMU N 622:

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

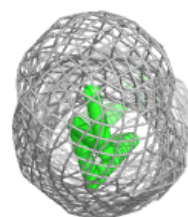
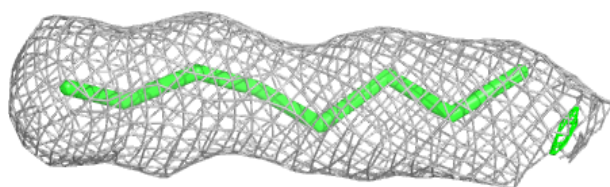
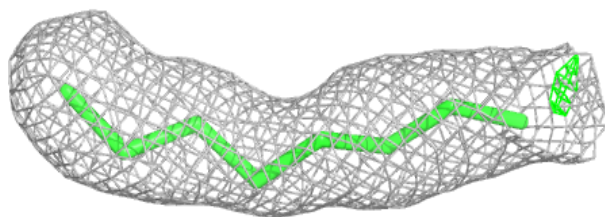
**Electron density around DMU K 101:**

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

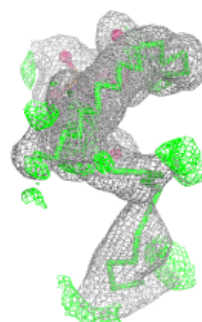
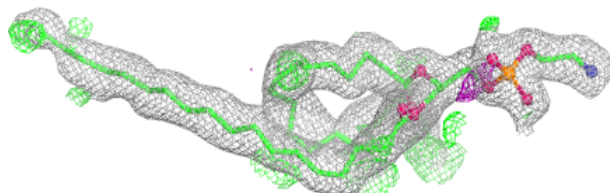
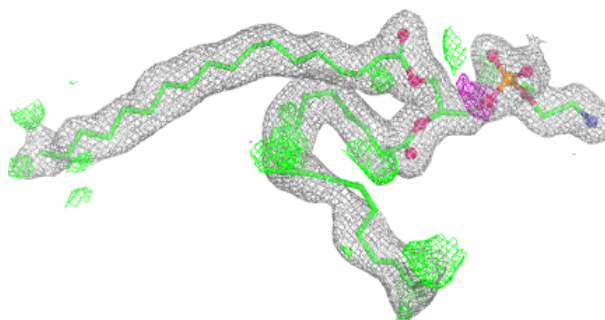


Electron density around DMU A 621:

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

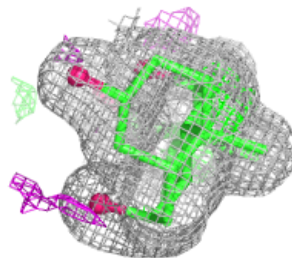
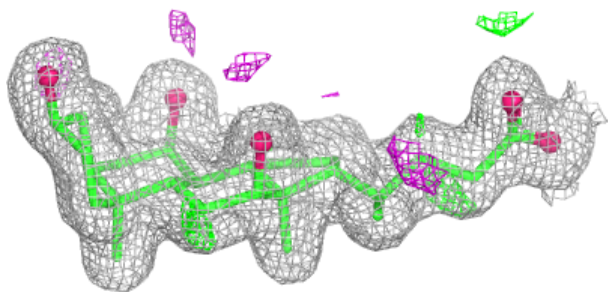
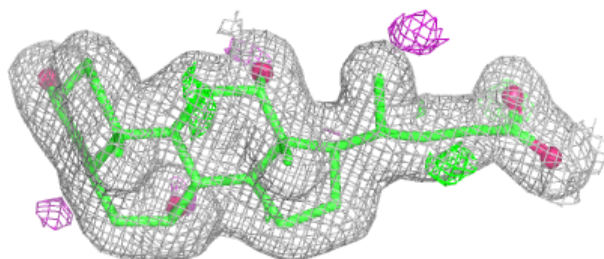
**Electron density around PEK P 304:**

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

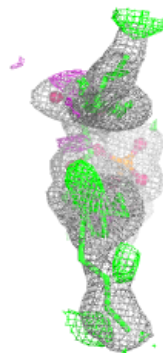
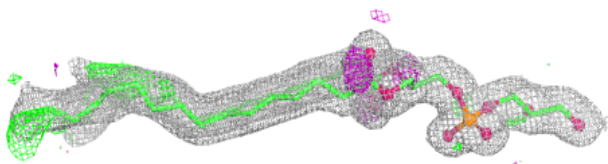
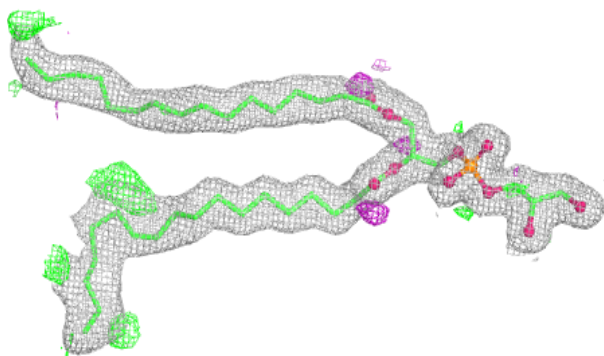


Electron density around CHD C 301:

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

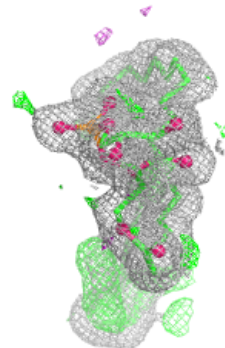
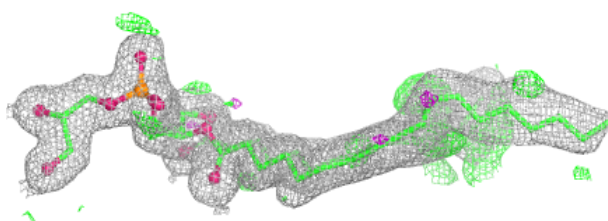
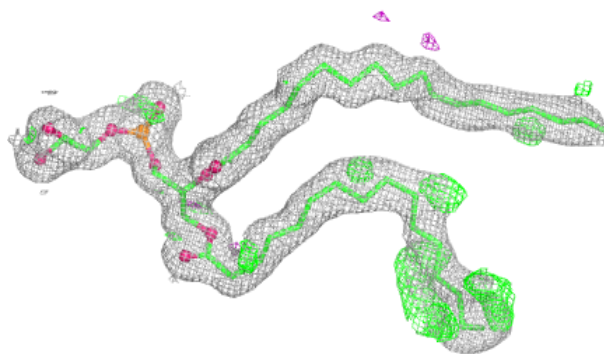
**Electron density around PGV P 306:**

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

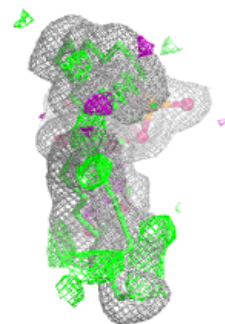
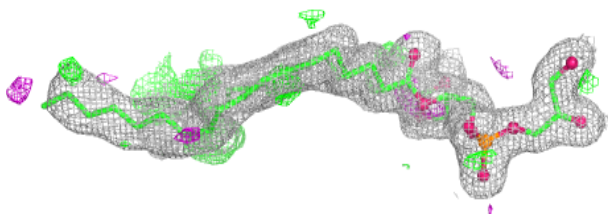
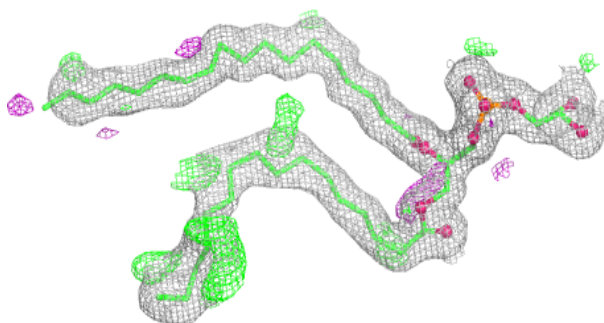


Electron density around PGV A 608:

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

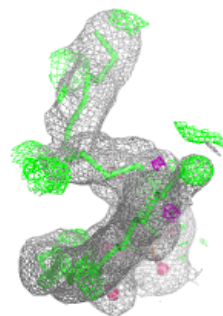
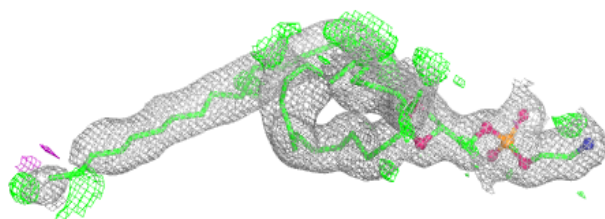
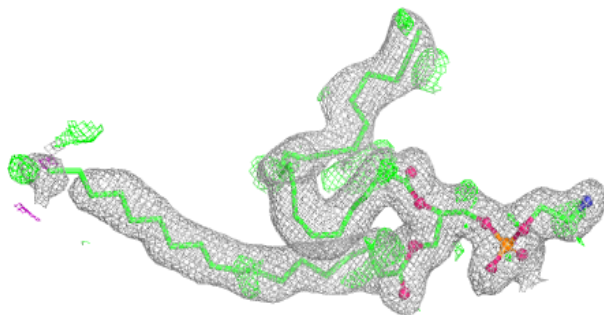
**Electron density around PGV N 610:**

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

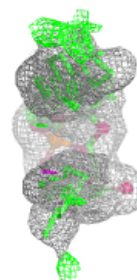
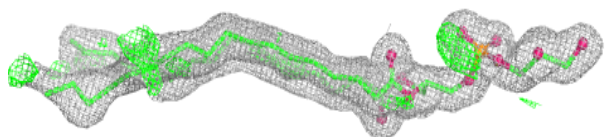
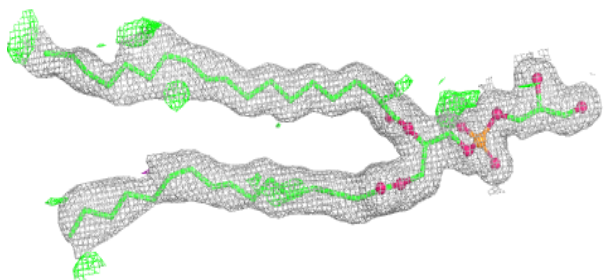


Electron density around PEK C 304:

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

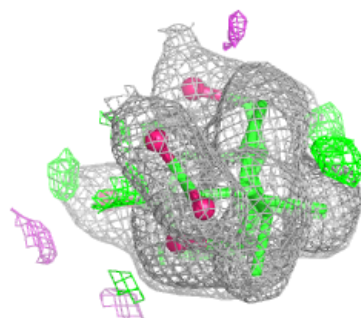
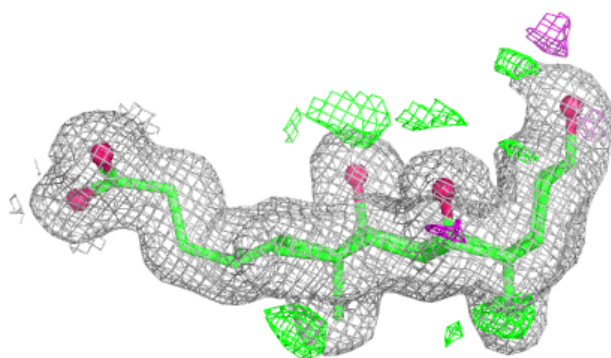
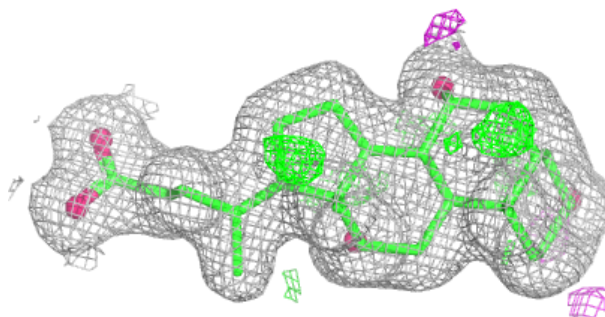
**Electron density around PGV C 306:**

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

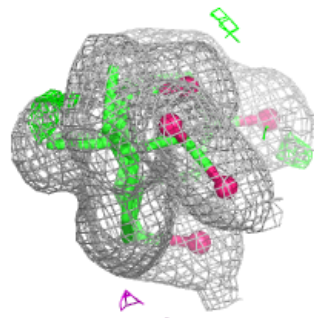
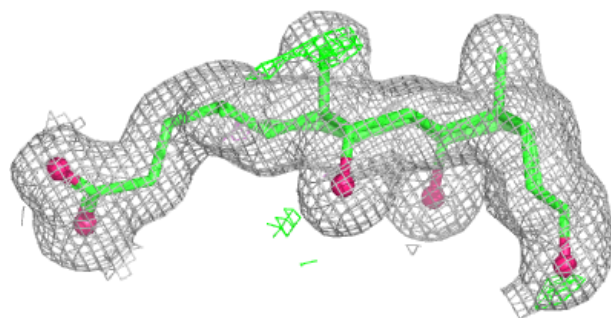
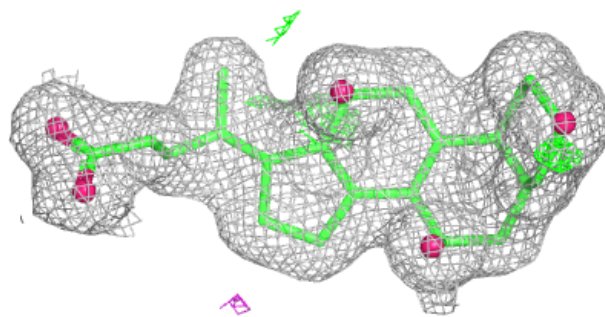


Electron density around CHD B 304:

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

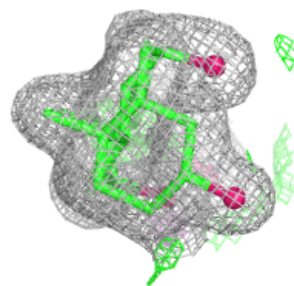
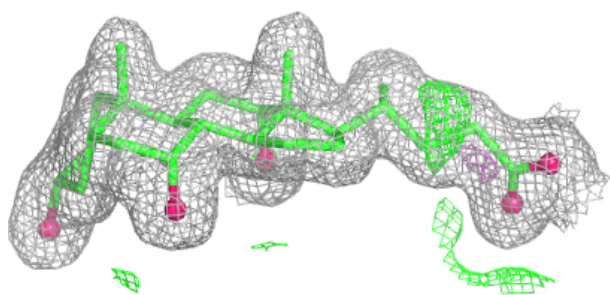
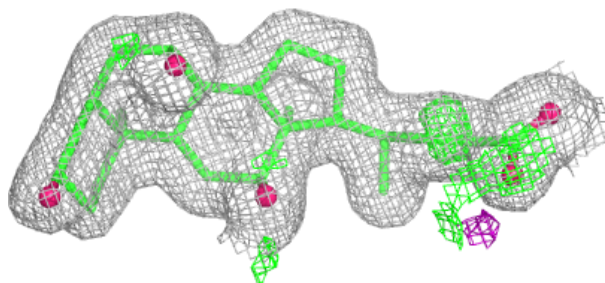
**Electron density around CHD G 102:**

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

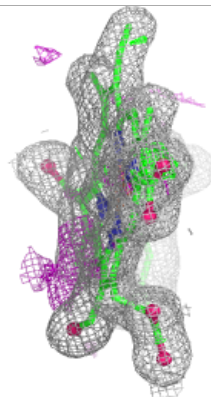
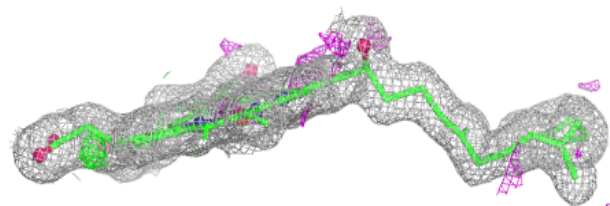
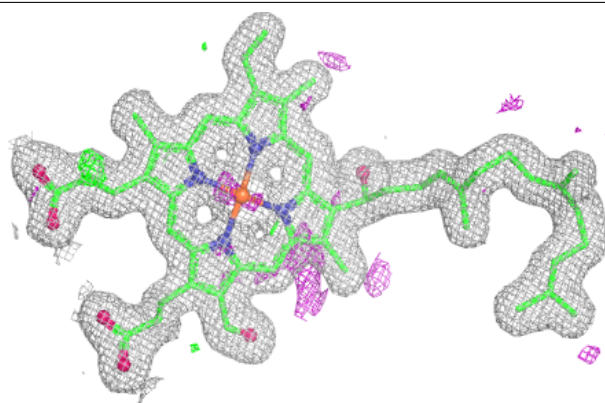


Electron density around CHD P 301:

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

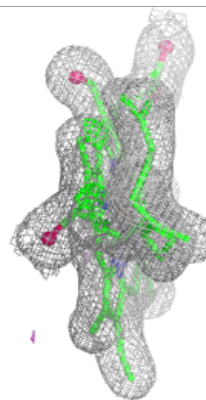
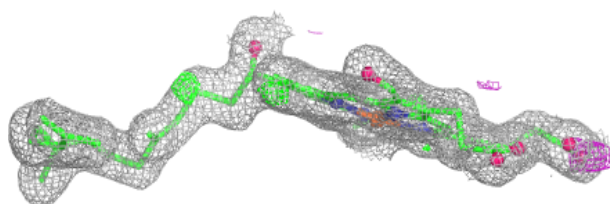
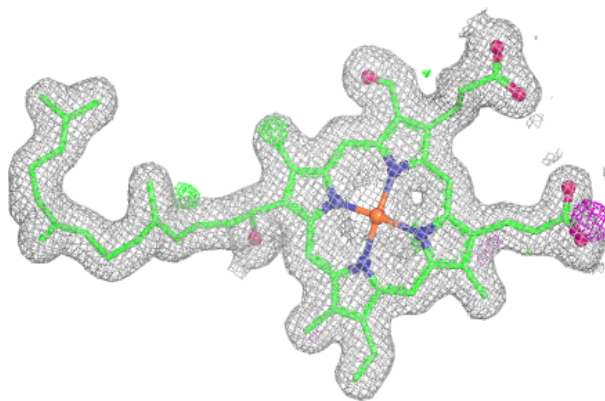
**Electron density around HEA A 602:**

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

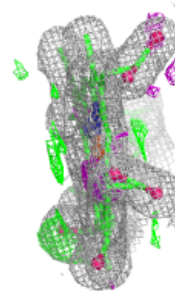
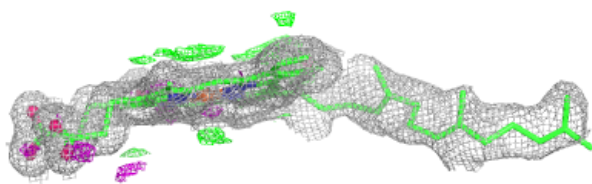
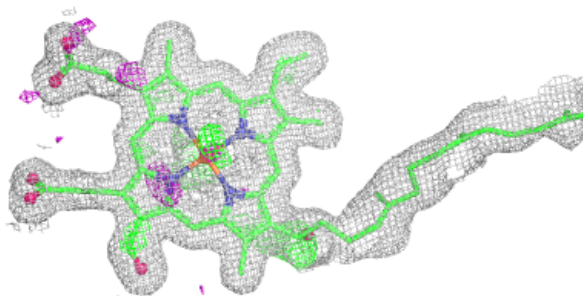


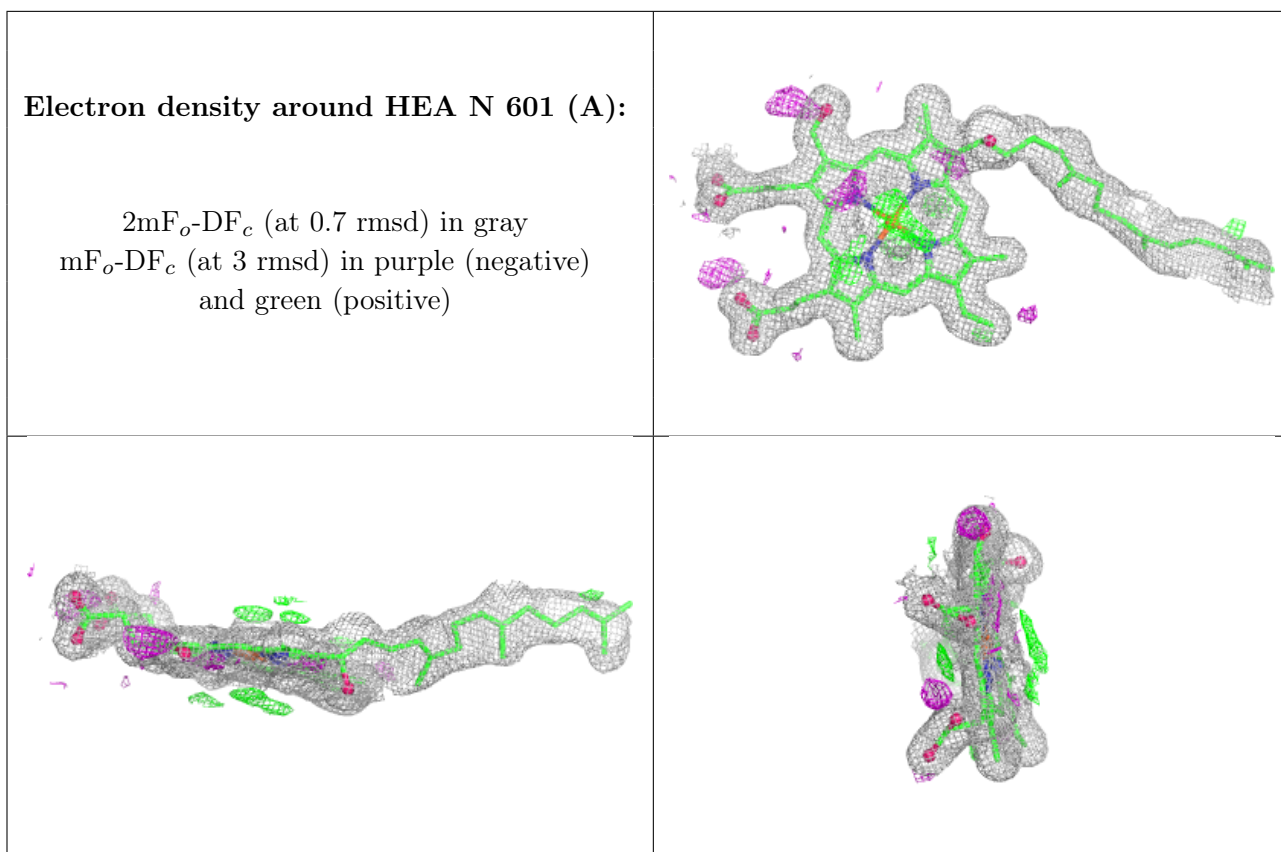
Electron density around HEA N 602:

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

**Electron density around HEA A 601 (A):**

$2mF_o-DF_c$ (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.