



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 07:02 PM UTC

PDB ID : 8H8R / pdb_00008h8r
Title : Bovine Heart Cytochrome c Oxidase in the Calcium-bound Fully Oxidized State
Authors : Muramoto, K.; Shinzawa-Itoh, K.
Deposited on : 2022-10-24
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

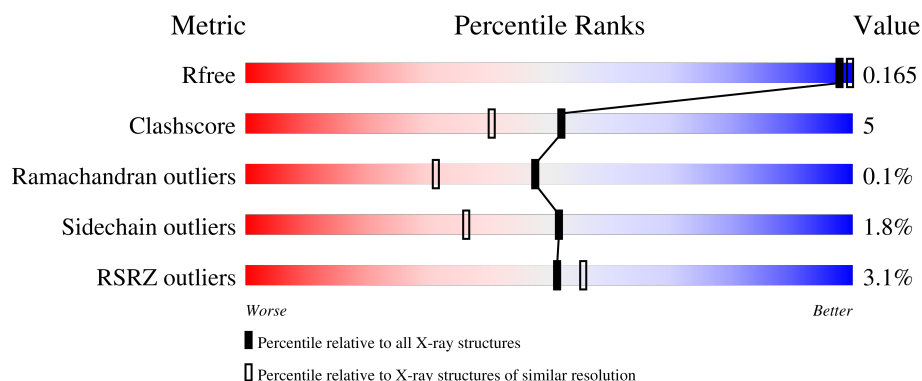
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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.



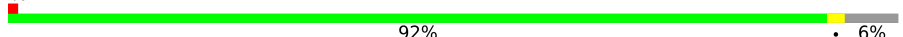
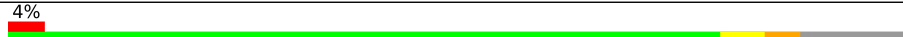
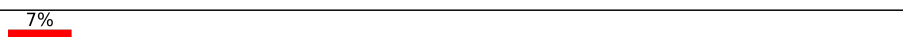
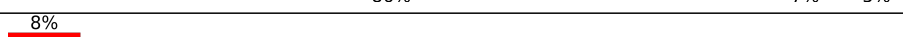
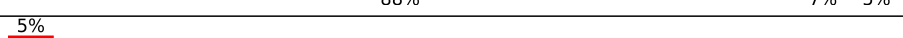
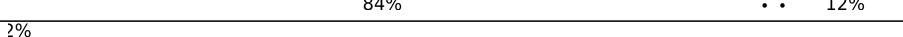
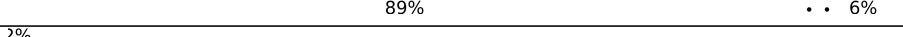
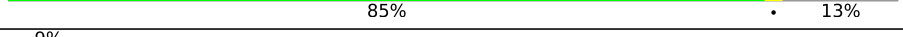
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	90% 9% .
1	N	514	91% 8% .
2	B	227	7% 85% 13% .
2	O	227	4% 87% 12% .
3	C	261	2% 85% 13% .

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Mol	Chain	Length	Quality of chain
3	P	261	
4	D	147	
4	Q	147	
5	E	109	
5	R	109	
6	F	98	
6	S	98	
7	G	85	
7	T	85	
8	H	85	
8	U	85	
9	I	73	
9	V	73	
10	J	59	
10	W	59	
11	K	56	
11	X	56	
12	L	47	
12	Y	47	
13	M	46	
13	Z	46	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
19	LFA	C	308	-	-	-	X
20	DMU	N	611	-	-	-	X

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 33049 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	513	Total	C	N	O	S	0	15	0
			4130	2757	636	696	41			
1	N	513	Total	C	N	O	S	0	15	0
			4130	2757	636	696	41			

- 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	5	0
			1870	1216	288	347	19			
2	O	227	Total	C	N	O	S	0	5	0
			1870	1216	288	347	19			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	258	Total	C	N	O	S	0	9	0
			2171	1449	342	364	16			
3	P	258	Total	C	N	O	S	0	9	0
			2172	1449	343	364	16			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	143	Total	C	N	O	S	0	1	0
			1192	776	195	217	4			
4	Q	137	Total	C	N	O	S	0	1	0
			1148	749	188	207	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	102	Total	C	N	O	S	0	0	0
			825	528	139	156	2			
5	R	102	Total	C	N	O	S	0	0	0
			825	528	139	156	2			

- Molecule 6 is a protein called Cytochrome c oxidase subunit 5B, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	91	Total	C	N	O	S	0	2	0
			709	441	124	138	6			
6	S	91	Total	C	N	O	S	0	2	0
			709	441	124	138	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	72	Total	C	N	O	S	0	1	0
			606	396	114	95	1			
7	T	72	Total	C	N	O	S	0	1	0
			606	396	114	95	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	75	Total	C	N	O	S	0	0	0
			628	395	114	114	5			
8	U	75	Total	C	N	O	S	0	0	0
			628	395	114	114	5			

- Molecule 9 is a protein called Cytochrome c oxidase subunit 6C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	70	Total	C	N	O	S	0	0	0
			575	375	103	93	4			
9	V	70	Total	C	N	O	S	0	0	0
			575	375	103	93	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	56	Total	C	N	O	S	0	0	0
			441	285	73	80	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	56	Total	C	N	O	S	0	0	0
			441	285	73	80	3			

- Molecule 11 is a protein called Cytochrome c oxidase subunit 7B, mitochondrial.

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

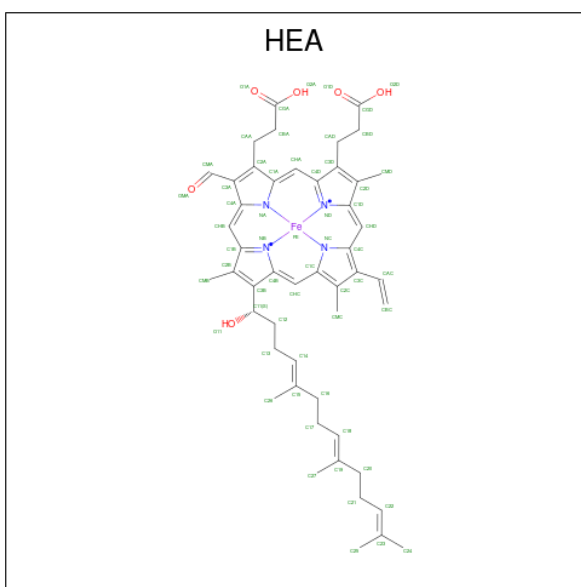
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	44	Total	C	N	O	S	0	0	0
			360	242	59	57	2			
12	Y	44	Total	C	N	O	S	0	0	0
			360	242	59	57	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	40	Total	C	N	O	0	0	0
			311	208	48	55			
13	Z	40	Total	C	N	O	0	0	0
			311	208	48	55			

- 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 69	C 58	Fe 1	N 4	O 6	0	1
14	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
14	N	1	Total 69	C 58	Fe 1	N 4	O 6	0	1
14	N	1	Total 60	C 49	Fe 1	N 4	O 6	0	0

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

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

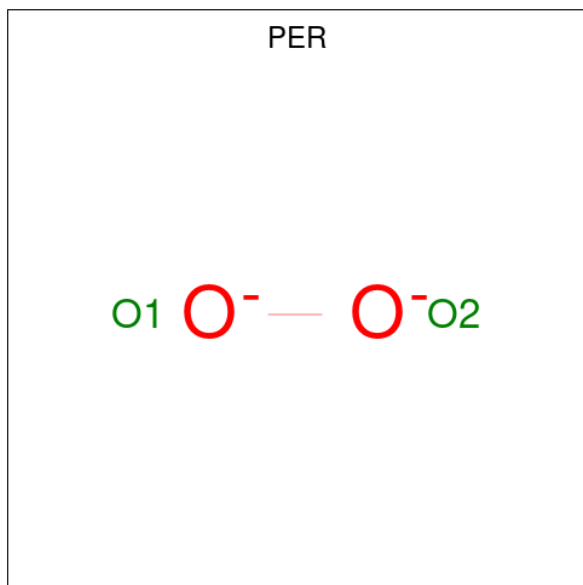
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 17 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

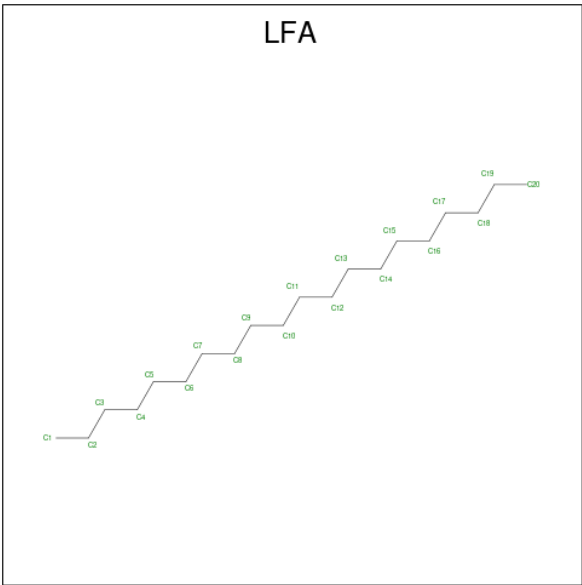
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	1	Total Ca 1 1	0	0
17	N	1	Total Ca 1 1	0	0

- Molecule 18 is PEROXIDE ION (CCD ID: PER) (formula: O₂).



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

- Molecule 19 is EICOSANE (CCD ID: LFA) (formula: C₂₀H₄₂).



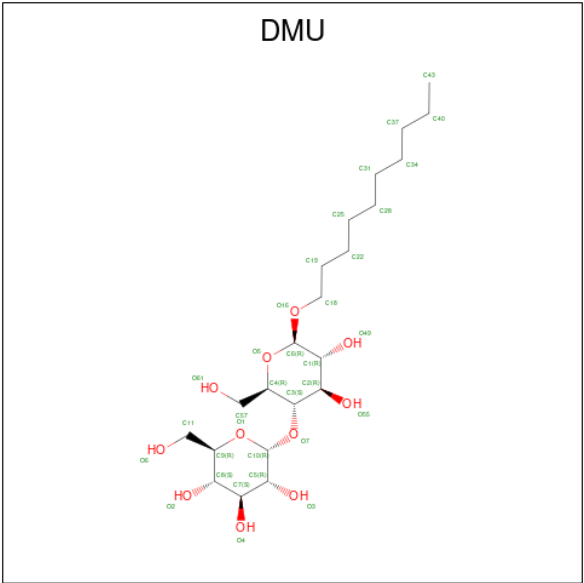
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	1	Total	C	0	0
			14	14		
19	A	1	Total	C	0	0
			14	14		
19	B	1	Total	C	0	0
			17	17		
19	C	1	Total	C	0	0
			11	11		
19	C	1	Total	C	0	0
			6	6		
19	C	1	Total	C	0	0
			18	18		
19	C	1	Total	C	0	0
			11	11		
19	C	1	Total	C	0	0
			14	14		
19	C	1	Total	C	0	0
			11	11		
19	C	1	Total	C	0	0
			15	15		
19	C	1	Total	C	0	0
			13	13		
19	C	1	Total	C	0	0
			15	15		
19	N	1	Total	C	0	0
			17	17		
19	N	1	Total	C	0	0
			14	14		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	N	1	Total C 14 14	0	0
19	O	1	Total C 11 11	0	0
19	P	1	Total C 15 15	0	0
19	P	1	Total C 11 11	0	0
19	P	1	Total C 6 6	0	0
19	P	1	Total C 18 18	0	0
19	P	1	Total C 11 11	0	0
19	P	1	Total C 11 11	0	0
19	P	1	Total C 15 15	0	0
19	P	1	Total C 13 13	0	0
19	T	1	Total C 14 14	0	0
19	T	1	Total C 11 11	0	0

- Molecule 20 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



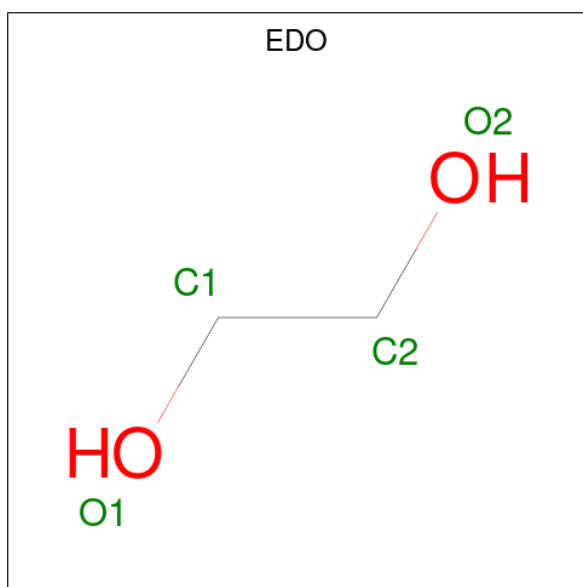
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
20	A	1	Total C 7 7	0	0
20	A	1	Total C O 33 22 11	0	0
20	A	1	Total C O 11 10 1	0	0
20	A	1	Total C O 11 10 1	0	0
20	B	1	Total C O 11 10 1	0	0
20	B	1	Total C O 22 16 6	0	0
20	B	1	Total C O 22 16 6	0	0
20	C	1	Total C O 11 10 1	0	0
20	C	1	Total C O 33 22 11	0	0
20	C	1	Total C 7 7	0	0
20	C	1	Total C O 22 16 6	0	0
20	C	1	Total C O 33 22 11	0	0
20	C	1	Total C O 33 22 11	0	0
20	C	1	Total C O 22 16 6	0	0
20	C	1	Total C O 33 22 11	0	0
20	D	1	Total C O 33 22 11	0	0
20	H	1	Total C O 33 22 11	0	0
20	J	1	Total C O 11 10 1	0	0
20	L	1	Total C O 22 16 6	0	0
20	M	1	Total C O 33 22 11	0	0
20	M	1	Total C 8 8	0	0
20	N	1	Total C O 11 10 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
20	N	1	Total C 7 7	0	0
20	N	1	Total C O 33 22 11	0	0
20	N	1	Total C O 33 22 11	0	0
20	O	1	Total C O 22 16 6	0	0
20	O	1	Total C O 11 10 1	0	0
20	O	1	Total C O 11 10 1	0	0
20	O	1	Total C O 22 16 6	0	0
20	P	1	Total C O 11 10 1	0	0
20	P	1	Total C O 33 22 11	0	0
20	P	1	Total C 7 7	0	0
20	P	1	Total C O 22 16 6	0	0
20	P	1	Total C O 33 22 11	0	0
20	P	1	Total C O 33 22 11	0	0
20	P	1	Total C O 22 16 6	0	0
20	P	1	Total C O 33 22 11	0	0
20	P	1	Total C O 22 16 6	0	0
20	Q	1	Total C O 33 22 11	0	0
20	W	1	Total C O 11 10 1	0	0
20	Y	1	Total C O 22 16 6	0	0
20	Z	1	Total C O 33 22 11	0	0
20	Z	1	Total C 8 8	0	0

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



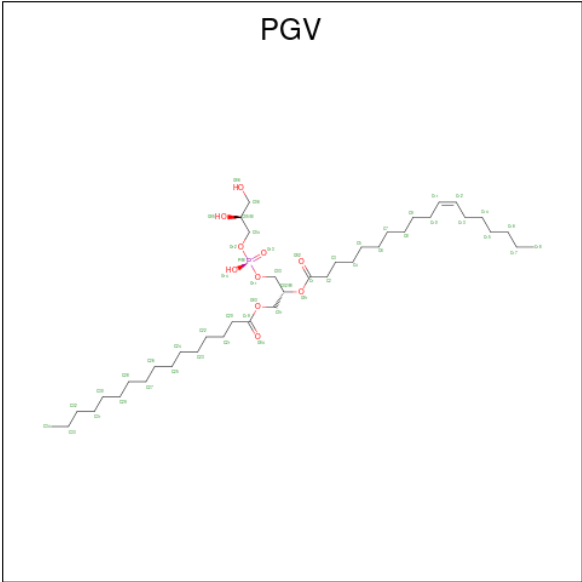
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	A	1	Total	C	O	0	0
			4	2	2		
21	B	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21	C	1	Total	C	O	0	0
			4	2	2		
21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

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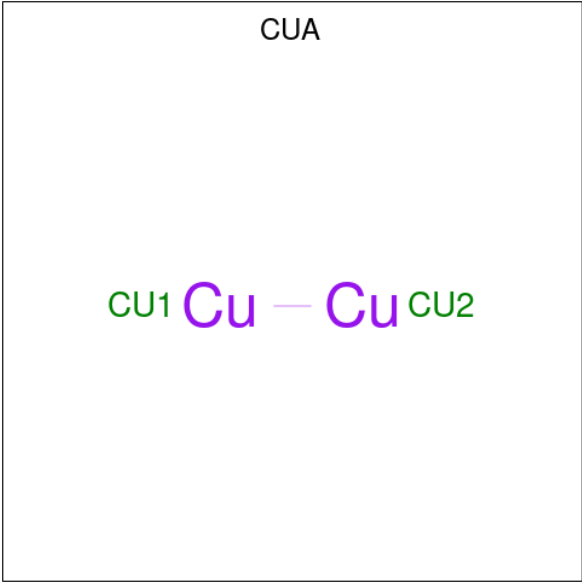
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	N	1	Total	C	O	0	0
			4	2	2		
21	N	1	Total	C	O	0	0
			4	2	2		
21	N	1	Total	C	O	0	0
			4	2	2		
21	N	1	Total	C	O	0	0
			4	2	2		
21	N	1	Total	C	O	0	0
			4	2	2		
21	O	1	Total	C	O	0	0
			4	2	2		
21	P	1	Total	C	O	0	0
			4	2	2		
21	P	1	Total	C	O	0	0
			4	2	2		
21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

- Molecule 22 is (1R)-2-{{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P).



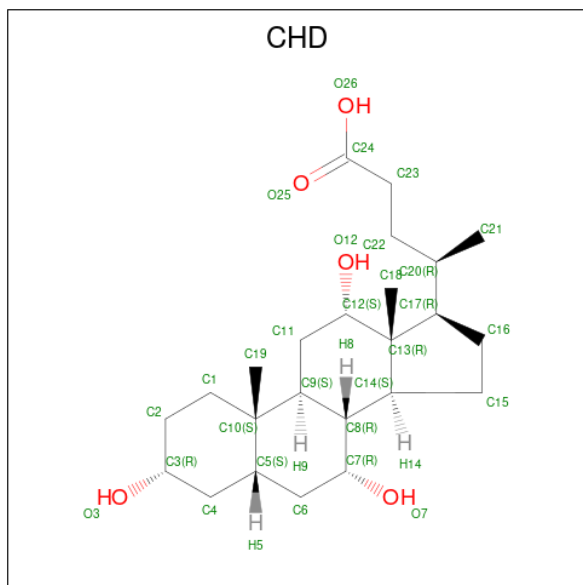
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	A	1	Total	C	O	P	0	0
			51	40	10	1		
22	C	1	Total	C	O	P	0	0
			51	40	10	1		
22	N	1	Total	C	O	P	0	0
			51	40	10	1		
22	P	1	Total	C	O	P	0	0
			51	40	10	1		

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



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

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

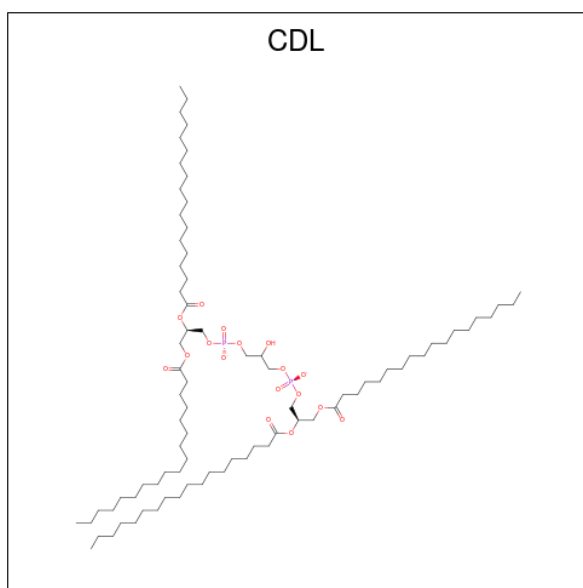


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	B	1	Total C O 29 24 5	0	0
24	C	1	Total C O 29 24 5	0	0
24	C	1	Total C O 29 24 5	0	0
24	O	1	Total C O 29 24 5	0	0
24	P	1	Total C O 29 24 5	0	0
24	P	1	Total C O 29 24 5	0	0

- Molecule 25 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

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

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

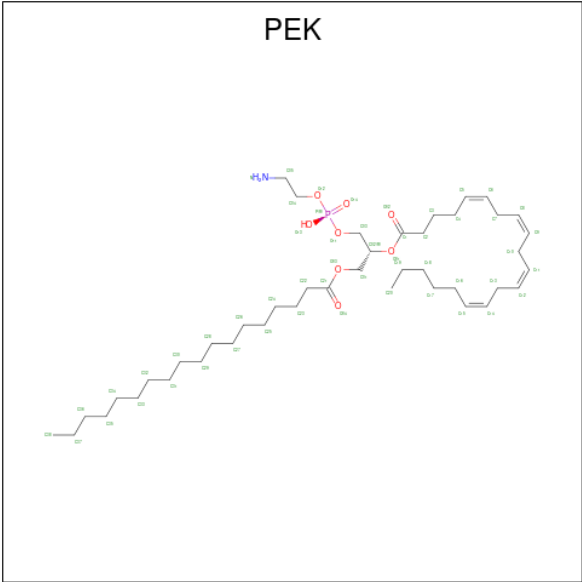


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
26	C	1	Total	C	O	P	0	0
			87	68	17	2		
26	I	1	Total	C	O	P	0	0
			64	45	17	2		
26	L	1	Total	C	O	P	0	0
			94	75	17	2		
26	O	1	Total	C	O	P	0	0
			64	45	17	2		
26	P	1	Total	C	O	P	0	0
			87	68	17	2		
26	Y	1	Total	C	O	P	0	0
			94	75	17	2		

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

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

- Molecule 28 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
28	G	1	Total	C	N	O	P	0	0
			53	43	1	8	1		
28	T	1	Total	C	N	O	P	0	0
			53	43	1	8	1		

- Molecule 29 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	A	239	Total	O	0	11
			250	250		
29	B	175	Total	O	0	2
			177	177		
29	C	102	Total	O	0	1
			103	103		
29	D	135	Total	O	0	9
			144	144		
29	E	109	Total	O	0	7
			116	116		
29	F	104	Total	O	0	7
			111	111		
29	G	42	Total	O	0	1
			43	43		
29	H	61	Total	O	0	0
			61	61		
29	I	41	Total	O	0	0
			41	41		
29	J	20	Total	O	0	0
			20	20		

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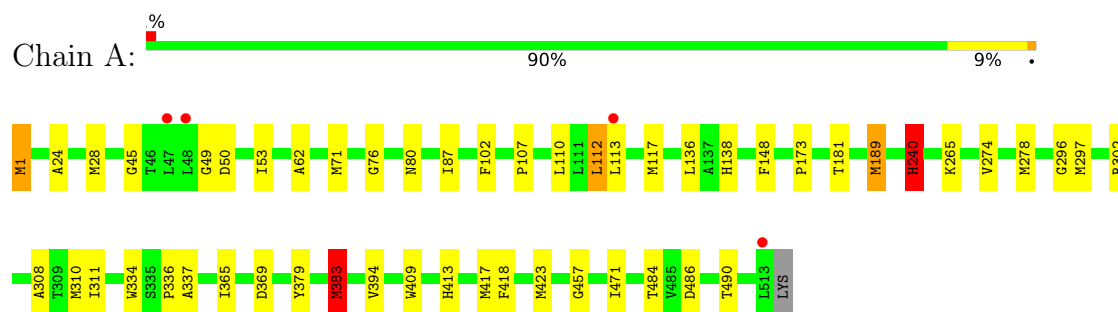
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	K	22	Total 22	O 22	0	0
29	L	25	Total 27	O 27	0	2
29	M	21	Total 21	O 21	0	0
29	N	227	Total 237	O 237	0	10
29	O	148	Total 149	O 149	0	1
29	P	101	Total 102	O 102	0	1
29	Q	81	Total 86	O 86	0	5
29	R	87	Total 94	O 94	0	7
29	S	87	Total 93	O 93	0	6
29	T	37	Total 38	O 38	0	1
29	U	46	Total 46	O 46	0	0
29	V	22	Total 22	O 22	0	0
29	W	15	Total 15	O 15	0	0
29	X	18	Total 18	O 18	0	0
29	Y	25	Total 27	O 27	0	2
29	Z	17	Total 17	O 17	0	0

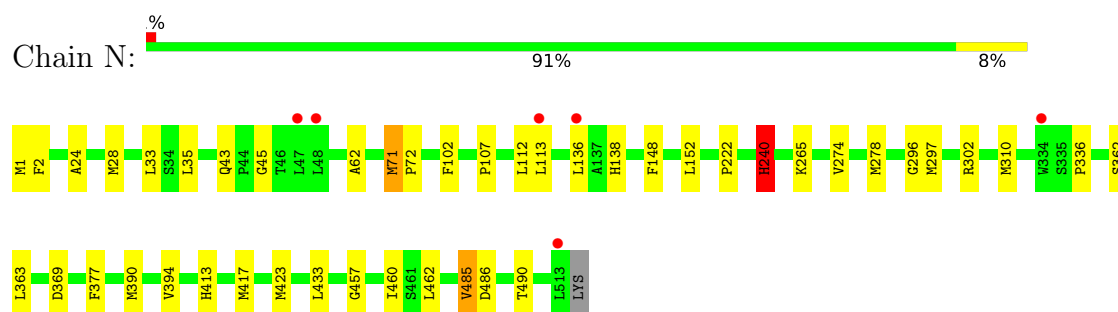
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

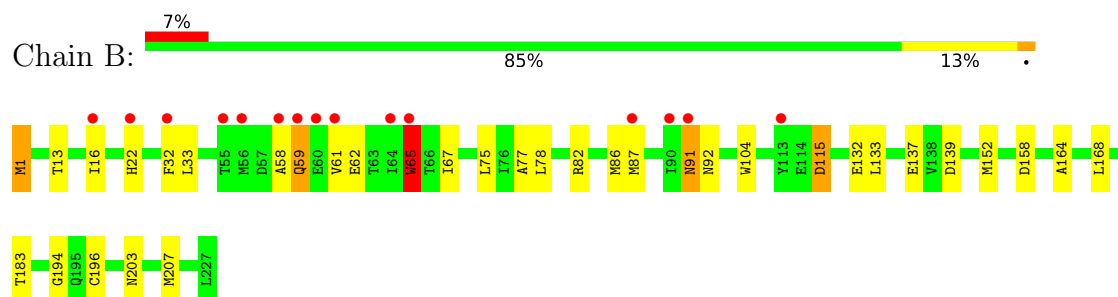
- Molecule 1: Cytochrome c oxidase subunit 1



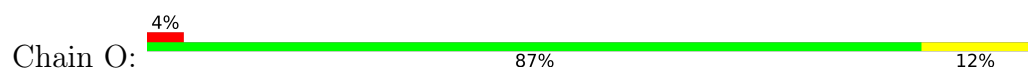
- Molecule 1: Cytochrome c oxidase subunit 1

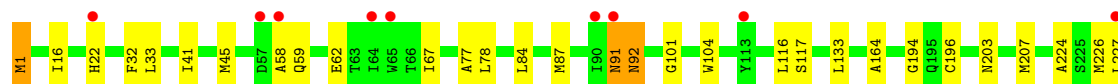


- Molecule 2: Cytochrome c oxidase subunit 2

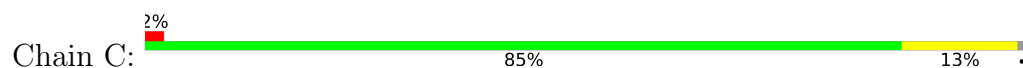


- Molecule 2: Cytochrome c oxidase subunit 2





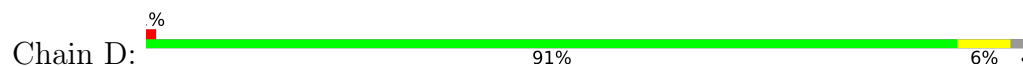
- Molecule 3: Cytochrome c oxidase subunit 3



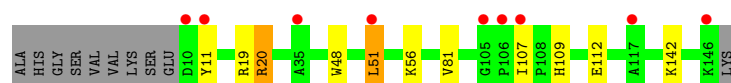
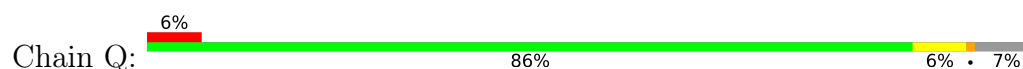
- Molecule 3: Cytochrome c oxidase subunit 3



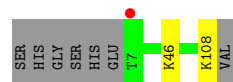
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



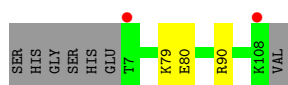
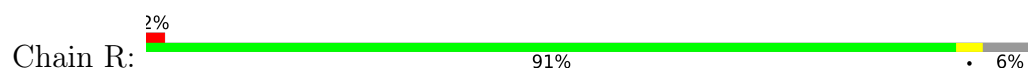
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



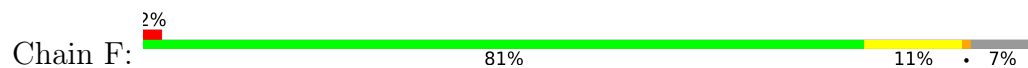
- Molecule 5: Cytochrome c oxidase subunit 5A



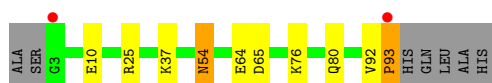
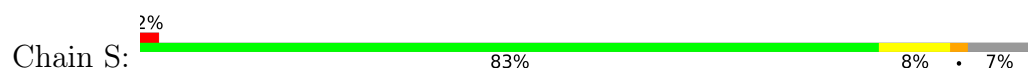
- Molecule 5: Cytochrome c oxidase subunit 5A



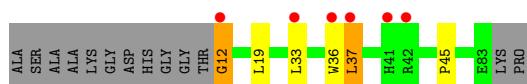
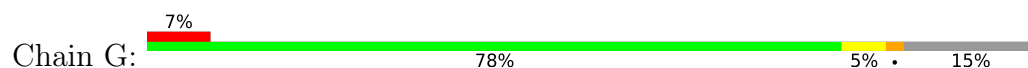
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



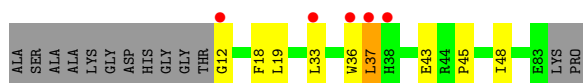
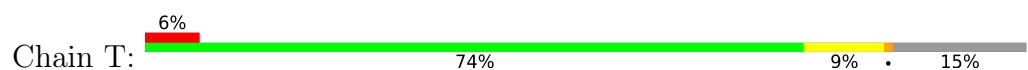
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



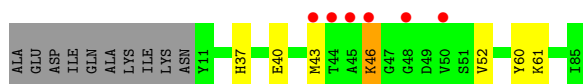
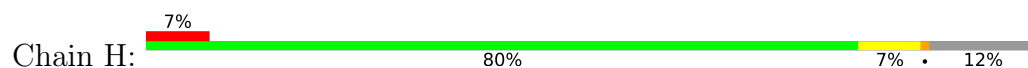
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



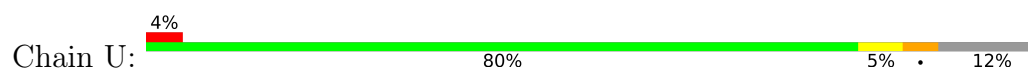
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



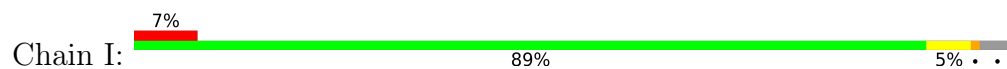
- Molecule 8: Cytochrome c oxidase subunit 6B1



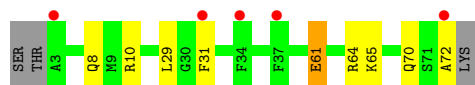
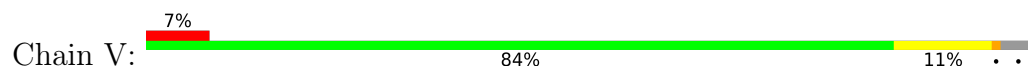
- Molecule 8: Cytochrome c oxidase subunit 6B1



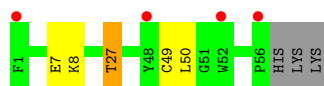
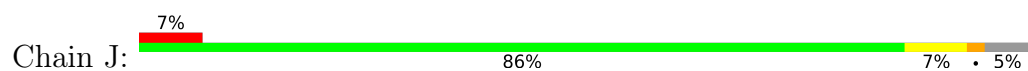
• Molecule 9: Cytochrome c oxidase subunit 6C



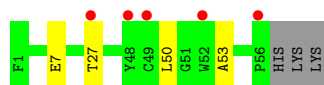
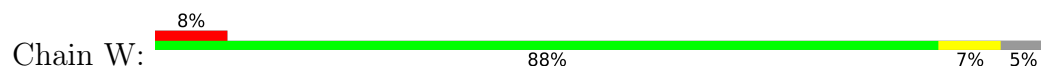
• Molecule 9: Cytochrome c oxidase subunit 6C



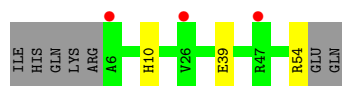
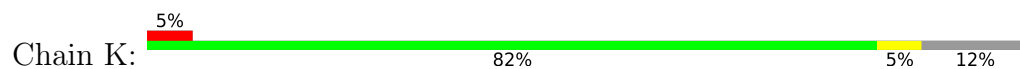
• Molecule 10: Cytochrome c oxidase subunit 7A1



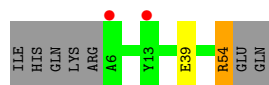
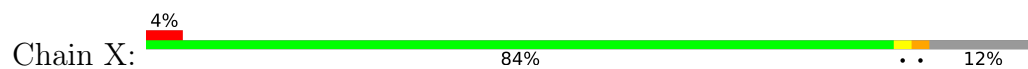
• Molecule 10: Cytochrome c oxidase subunit 7A1



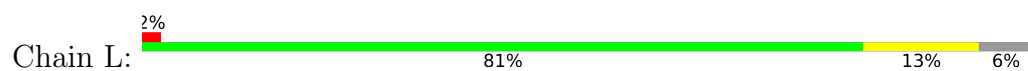
• Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial

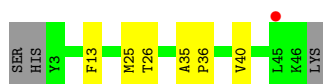


• Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial

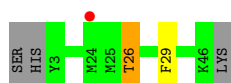
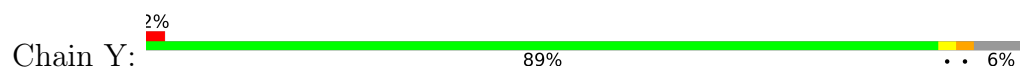


• Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial

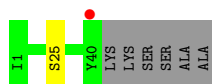
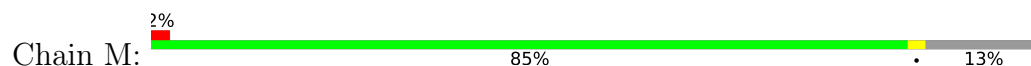




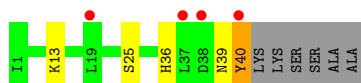
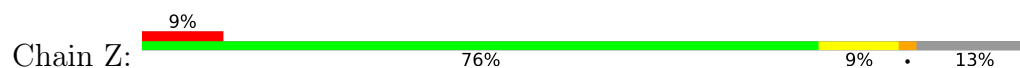
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	182.80Å 205.70Å 177.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.70 40.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.00-1.70) 100.0 (40.00-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.123 , 0.153 0.139 , 0.165	Depositor DCC
R_{free} test set	36325 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 69.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33049	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CUA, FME, PER, UNX, ZN, PGV, LFA, MG, CHD, CU, CDL, CA, DMU, HEA, EDO, PEK

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	1.07	5/4259 (0.1%)	1.21	6/5816 (0.1%)
1	N	1.05	0/4259	1.21	9/5816 (0.2%)
2	B	1.11	1/1908 (0.1%)	1.28	11/2598 (0.4%)
2	O	1.05	1/1908 (0.1%)	1.26	1/2598 (0.0%)
3	C	1.07	3/2258 (0.1%)	1.18	3/3084 (0.1%)
3	P	1.05	1/2258 (0.0%)	1.20	4/3084 (0.1%)
4	D	1.09	1/1226 (0.1%)	1.19	1/1657 (0.1%)
4	Q	1.04	1/1182 (0.1%)	1.34	3/1598 (0.2%)
5	E	1.04	1/843 (0.1%)	1.20	1/1145 (0.1%)
5	R	1.06	1/843 (0.1%)	1.26	0/1145
6	F	1.08	0/724	1.16	0/983
6	S	1.13	1/724 (0.1%)	1.16	2/983 (0.2%)
7	G	1.11	2/633 (0.3%)	1.18	0/864
7	T	1.09	1/633 (0.2%)	1.23	1/864 (0.1%)
8	H	1.01	0/648	1.34	0/877
8	U	1.03	1/648 (0.2%)	1.32	2/877 (0.2%)
9	I	1.15	1/588 (0.2%)	1.41	3/781 (0.4%)
9	V	1.05	0/588	1.40	2/781 (0.3%)
10	J	1.03	0/451	1.30	2/610 (0.3%)
10	W	1.04	0/451	1.31	0/610
11	K	1.16	1/398 (0.3%)	1.27	0/546
11	X	1.13	0/398	1.31	1/546 (0.2%)
12	L	1.03	0/372	1.20	2/500 (0.4%)
12	Y	1.07	0/372	1.26	1/500 (0.2%)
13	M	1.09	0/321	1.10	0/440
13	Z	1.06	0/321	1.34	0/440
All	All	1.07	22/29214 (0.1%)	1.24	55/39743 (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	3
1	N	0	1
6	S	0	1
All	All	0	5

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	383	MET	C-O	8.51	1.35	1.24
4	D	58	GLU	CD-OE1	7.96	1.40	1.25
3	C	243	HIS	CE1-NE2	6.99	1.39	1.32
4	Q	142	LYS	C-O	6.96	1.33	1.23
5	R	80	GLU	CD-OE1	6.88	1.38	1.25
9	I	72	ALA	C-O	6.83	1.37	1.23
1	A	50	ASP	C-O	6.76	1.31	1.23
1	A	49	GLY	C-O	6.62	1.31	1.23
1	A	189	MET	CB-CG	6.51	1.72	1.52
11	K	10	HIS	CE1-NE2	6.31	1.38	1.32
5	E	108	LYS	C-O	5.98	1.35	1.23
8	U	61	LYS	C-O	5.93	1.31	1.24
2	B	152	MET	CB-CG	-5.52	1.35	1.52
3	P	204	HIS	CE1-NE2	5.45	1.38	1.32
2	O	101	GLY	C-O	5.40	1.29	1.23
7	T	48	ILE	N-CA	5.38	1.50	1.45
7	G	37	LEU	C-O	-5.33	1.17	1.24
6	S	93	PRO	C-O	5.25	1.34	1.23
3	C	9	HIS	CE1-NE2	5.17	1.37	1.32
3	C	103	HIS	CE1-NE2	5.14	1.37	1.32
7	G	12	GLY	N-CA	-5.13	1.37	1.45
1	A	413	HIS	CE1-NE2	-5.06	1.27	1.32

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	65	TRP	CA-CB-CG	10.79	134.10	113.60
1	N	240	HIS	CA-CB-CG	-10.66	103.14	113.80
1	A	240	HIS	CA-CB-CG	-10.30	103.50	113.80
4	D	58	GLU	CB-CG-CD	9.77	129.21	112.60
2	B	65	TRP	CB-CA-C	-9.51	93.03	110.63
9	I	72	ALA	CA-C-O	-8.68	106.05	120.80
1	N	43	GLN	CB-CA-C	8.07	121.15	109.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	65	TRP	CB-CG-CD1	-7.94	114.99	126.90
2	O	92	ASN	CB-CA-C	7.50	118.45	110.65
2	B	65	TRP	CB-CG-CD2	7.39	137.15	126.80
6	S	93	PRO	CB-CA-C	7.19	123.77	110.10
2	B	82	ARG	CG-CD-NE	-6.95	96.71	112.00
1	A	71	MET	CG-SD-CE	-6.75	86.06	100.90
2	B	115	ASP	CB-CA-C	6.53	122.22	112.03
9	V	72	ALA	CA-C-O	-6.39	109.93	120.80
5	E	108	LYS	CA-C-O	-6.39	109.94	120.80
1	N	102	PHE	CA-CB-CG	-6.34	107.46	113.80
1	N	377	PHE	CA-CB-CG	6.32	120.11	113.80
1	A	102	PHE	CA-CB-CG	-6.28	107.53	113.80
3	C	122	HIS	CB-CA-C	6.24	117.14	110.65
2	B	158	ASP	CA-CB-CG	6.16	118.76	112.60
3	C	80	ARG	CG-CD-NE	-6.13	98.52	112.00
12	L	25	MET	CA-C-N	6.13	128.81	120.54
12	L	25	MET	C-N-CA	6.13	128.81	120.54
3	P	80	ARG	CG-CD-NE	-6.09	98.59	112.00
11	X	54	ARG	CA-C-O	-6.05	110.51	120.80
3	C	76	GLN	CG-CD-NE2	-6.04	107.34	116.40
3	P	233	PHE	CA-CB-CG	-5.96	107.83	113.80
4	Q	20	ARG	CG-CD-NE	-5.96	98.88	112.00
6	S	93	PRO	N-CA-C	-5.96	97.21	112.10
4	Q	20	ARG	NE-CZ-NH1	5.94	127.44	121.50
2	B	139	ASP	CA-CB-CG	5.84	118.44	112.60
1	N	71	MET	CG-SD-CE	-5.77	88.21	100.90
2	B	65	TRP	N-CA-CB	5.76	119.10	110.22
10	J	7	GLU	CB-CA-C	5.65	120.18	110.79
8	U	61	LYS	CA-C-N	5.54	127.65	120.44
8	U	61	LYS	C-N-CA	5.54	127.65	120.44
2	B	59	GLN	CB-CG-CD	5.52	121.99	112.60
1	N	45	GLY	CA-C-O	-5.48	117.53	122.57
9	V	10	ARG	NE-CZ-NH2	-5.39	114.34	119.20
1	A	486	ASP	CA-CB-CG	5.36	117.96	112.60
9	I	37	PHE	CA-CB-CG	5.36	119.16	113.80
2	B	65	TRP	CA-C-O	-5.31	114.10	120.10
3	P	76	GLN	CG-CD-NE2	-5.29	108.47	116.40
9	I	43	ARG	CG-CD-NE	5.27	123.60	112.00
4	Q	20	ARG	NE-CZ-NH2	-5.23	114.49	119.20
1	A	181	THR	CA-CB-OG1	-5.20	101.80	109.60
1	N	240	HIS	N-CA-CB	5.16	116.51	110.42
12	Y	26	THR	CA-CB-OG1	-5.16	101.86	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	33	LEU	CA-C-N	5.15	127.43	120.38
1	N	33	LEU	C-N-CA	5.15	127.43	120.38
10	J	27	THR	CA-CB-OG1	-5.14	101.89	109.60
1	A	45	GLY	CA-C-O	-5.13	118.47	122.52
3	P	35	PHE	CA-CB-CG	5.08	118.88	113.80
7	T	18	PHE	CA-CB-CG	5.03	118.83	113.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	HIS	Sidechain
1	A	296	GLY	Mainchain
1	A	383	MET	Mainchain
1	N	240	HIS	Sidechain
6	S	92	VAL	Mainchain

5.2 Too-close contacts [i](#)

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	4130	0	4102	48	0
1	N	4130	0	4102	44	0
2	B	1870	0	1870	24	0
2	O	1870	0	1870	28	0
3	C	2171	0	2080	38	0
3	P	2172	0	2081	25	0
4	D	1192	0	1178	7	0
4	Q	1148	0	1131	9	0
5	E	825	0	823	1	0
5	R	825	0	823	1	0
6	F	709	0	691	9	0
6	S	709	0	691	5	0
7	G	606	0	577	4	0
7	T	606	0	577	5	0
8	H	628	0	580	9	0
8	U	628	0	580	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	I	575	0	584	1	0
9	V	575	0	584	4	0
10	J	441	0	439	4	0
10	W	441	0	439	5	0
11	K	384	0	366	1	0
11	X	384	0	366	1	0
12	L	360	0	360	7	0
12	Y	360	0	360	5	0
13	M	311	0	321	2	0
13	Z	311	0	321	4	0
14	A	129	0	88	4	0
14	N	129	0	88	3	0
15	A	1	0	0	0	0
15	N	1	0	0	0	0
16	A	1	0	0	0	0
16	N	1	0	0	0	0
17	A	1	0	0	0	0
17	N	1	0	0	0	0
18	A	2	0	0	1	0
18	N	2	0	0	1	0
19	A	28	0	54	15	0
19	B	17	0	33	3	0
19	C	114	0	203	4	0
19	N	45	0	87	7	0
19	O	11	0	21	4	0
19	P	100	0	174	6	0
19	T	25	0	48	0	0
20	A	62	0	96	2	0
20	B	55	0	83	0	0
20	C	194	0	262	10	0
20	D	33	0	41	4	0
20	H	33	0	26	1	0
20	J	11	0	21	0	0
20	L	22	0	31	2	0
20	M	41	0	57	1	0
20	N	84	0	100	0	0
20	O	66	0	104	0	0
20	P	194	0	262	2	0
20	Q	33	0	41	2	0
20	W	11	0	21	0	0
20	Y	22	0	31	2	0
20	Z	41	0	56	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	A	16	0	24	0	0
21	B	4	0	6	0	0
21	C	12	0	17	0	0
21	E	12	0	18	0	0
21	F	8	0	12	0	0
21	G	4	0	6	0	0
21	N	20	0	30	2	0
21	O	4	0	6	0	0
21	P	12	0	18	1	0
21	R	12	0	18	0	0
21	S	8	0	12	0	0
21	T	4	0	6	0	0
22	A	51	0	76	1	0
22	C	51	0	76	2	0
22	N	51	0	76	1	0
22	P	51	0	76	0	0
23	B	2	0	0	0	0
23	O	2	0	0	0	0
24	B	29	0	39	0	0
24	C	58	0	78	1	0
24	O	29	0	39	1	0
24	P	58	0	78	4	0
25	C	1	0	0	1	0
25	P	1	0	0	1	0
26	C	87	0	124	17	0
26	I	64	0	72	0	0
26	L	94	0	141	3	0
26	O	64	0	72	1	0
26	P	87	0	124	10	0
26	Y	94	0	141	4	0
27	F	1	0	0	0	0
27	S	1	0	0	0	0
28	G	53	0	77	2	0
28	T	53	0	77	4	0
29	A	250	0	0	6	0
29	B	177	0	0	3	0
29	C	103	0	0	4	0
29	D	144	0	0	2	0
29	E	116	0	0	1	0
29	F	111	0	0	1	0
29	G	43	0	0	2	0
29	H	61	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	I	41	0	0	1	0
29	J	20	0	0	0	0
29	K	22	0	0	0	0
29	L	27	0	0	1	0
29	M	21	0	0	0	0
29	N	237	0	0	7	0
29	O	149	0	0	2	0
29	P	102	0	0	5	0
29	Q	86	0	0	3	0
29	R	94	0	0	1	0
29	S	93	0	0	0	0
29	T	38	0	0	2	0
29	U	46	0	0	0	0
29	V	22	0	0	0	0
29	W	15	0	0	0	0
29	X	18	0	0	0	0
29	Y	27	0	0	1	0
29	Z	17	0	0	0	0
All	All	33049	0	31463	315	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 5.

All (315) 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)
8:H:52:VAL:HG12	8:U:46:LYS:HG2	1.23	1.14
18:N:608:PER:O2	18:N:608:PER:O1	1.64	1.14
18:A:606:PER:O2	18:A:606:PER:O1	1.68	1.10
3:P:4:GLN:N	29:P:402:HOH:O	1.88	1.07
19:A:607:LFA:H12	19:A:608:LFA:H11	1.45	0.99
1:A:136[B]:LEU:HD11	29:A:931:HOH:O	1.61	0.98
2:B:16[B]:ILE:HG23	29:B:531:HOH:O	1.64	0.97
3:C:245:VAL:C	3:C:246[B]:ASP:CA	2.39	0.94
2:B:16[A]:ILE:HG21	2:B:87[A]:MET:HE3	1.50	0.93
6:S:76:LYS:HE2	6:S:93:PRO:HG2	1.52	0.91
25:C:302:UNX:UNK	29:C:496:HOH:O	1.52	0.90
3:P:149:HIS:NE2	19:P:312:LFA:H11	1.86	0.89
1:N:297[B]:MET:SD	1:N:302:ARG:HG2	2.13	0.88
24:P:306:CHD:H162	24:P:306:CHD:H231	1.57	0.86
1:A:297[B]:MET:SD	1:A:302:ARG:HG2	2.17	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:303:UNX:UNK	29:P:497:HOH:O	1.57	0.84
3:C:67:PHE:CE2	26:C:304:CDL:O1	2.32	0.81
1:N:274:VAL:HG12	1:N:278[A]:MET:HE2	1.62	0.80
7:G:19:LEU:HD23	19:N:610:LFA:H61	1.65	0.78
4:Q:20:ARG:HG2	29:Q:348:HOH:O	1.84	0.78
3:C:33[A]:MET:HE3	3:C:39:SER:OG	1.85	0.77
3:P:67:PHE:CE2	26:P:305:CDL:O1	2.36	0.77
8:H:52:VAL:HG12	8:U:46:LYS:CG	2.09	0.76
1:A:278[B]:MET:SD	19:A:607:LFA:H51	2.26	0.76
2:O:84:LEU:HA	2:O:87[A]:MET:HE2	1.68	0.75
1:A:53:ILE:HD11	12:L:40:VAL:HG13	1.70	0.74
8:H:52:VAL:CG1	8:U:46:LYS:HG2	2.10	0.74
1:N:297[B]:MET:SD	1:N:302:ARG:CG	2.75	0.74
2:O:59:GLN:HE22	19:O:302:LFA:H32	1.53	0.74
1:A:278[A]:MET:CE	19:A:608:LFA:H51	2.18	0.73
3:C:33[B]:MET:CA	3:C:33[B]:MET:HE2	2.10	0.73
2:B:13:THR:OG1	29:B:402:HOH:O	2.08	0.72
1:A:112:LEU:C	1:A:112:LEU:HD23	2.13	0.72
2:B:16[A]:ILE:CG2	2:B:87[A]:MET:HE3	2.20	0.72
4:Q:112:GLU:OE2	29:Q:301:HOH:O	2.07	0.72
24:P:306:CHD:H162	24:P:306:CHD:C23	2.19	0.70
1:A:278[A]:MET:HE1	19:A:608:LFA:C5	2.21	0.69
28:T:101:PEK:H32	28:T:101:PEK:H71	1.75	0.69
1:A:112:LEU:HG	29:A:919:HOH:O	1.92	0.69
1:A:297[B]:MET:SD	1:A:302:ARG:CG	2.81	0.69
12:L:26:THR:HG21	20:L:102:DMU:H26	1.74	0.68
26:L:101:CDL:O1	29:L:222[B]:HOH:O	1.85	0.68
3:P:258:TRP:CE2	19:P:308:LFA:H32	2.27	0.68
1:N:423[B]:MET:HE2	1:N:457:GLY:HA2	1.76	0.68
20:A:610:DMU:O6	29:A:706:HOH:O	2.12	0.66
3:C:149:HIS:NE2	19:C:312:LFA:H11	2.10	0.66
3:C:180[A]:GLU:OE2	29:C:404:HOH:O	2.13	0.66
1:A:113[B]:LEU:HD11	1:A:117[B]:MET:SD	2.36	0.66
8:H:43:MET:HE1	8:U:52:VAL:HG11	1.78	0.66
24:C:305:CHD:H162	24:C:305:CHD:H231	1.77	0.65
3:C:33[B]:MET:HE1	20:C:324:DMU:H12	1.76	0.65
1:N:136[B]:LEU:HD11	29:N:3025:HOH:O	1.96	0.65
3:P:4:GLN:CA	29:P:402:HOH:O	2.32	0.65
26:C:304:CDL:H752	10:J:27:THR:HG21	1.79	0.65
7:G:12:GLY:HA3	29:G:235:HOH:O	1.97	0.65
9:V:61:GLU:OE1	9:V:64:ARG:NH2	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:U:43:MET:O	8:U:48:GLY:N	2.30	0.64
1:N:485:VAL:HG13	21:N:617:EDO:H21	1.80	0.64
3:C:33[A]:MET:CE	3:C:42:LEU:H	2.10	0.64
4:Q:48:TRP:HA	4:Q:51:LEU:HD22	1.80	0.63
26:Y:101:CDL:O1	29:Y:216[B]:HOH:O	2.16	0.63
2:O:116:LEU:CD1	2:O:226:MET:HG2	2.28	0.63
1:N:278[A]:MET:HE1	19:N:610:LFA:H51	1.80	0.62
3:C:51[B]:MET:HE2	26:C:304:CDL:H861	1.82	0.62
6:F:37:LYS:HG2	29:F:297:HOH:O	1.99	0.62
1:A:365:ILE:HD11	29:A:715:HOH:O	2.00	0.62
3:P:33[B]:MET:HE3	3:P:42:LEU:HD12	1.82	0.61
26:P:305:CDL:HB61	26:P:305:CDL:HB22	1.82	0.61
1:A:278[A]:MET:HE1	19:A:608:LFA:H52	1.82	0.61
9:V:61:GLU:OE1	9:V:64:ARG:NE	2.30	0.60
3:C:33[A]:MET:HE2	3:C:42:LEU:H	1.65	0.60
1:N:112:LEU:HD23	1:N:112:LEU:C	2.27	0.60
3:P:33[B]:MET:CE	3:P:42:LEU:HD12	2.32	0.60
22:N:618:PGV:H183	28:T:101:PEK:H331	1.84	0.60
1:A:278[A]:MET:HE1	19:A:608:LFA:H51	1.83	0.59
1:N:486:ASP:OD2	4:Q:19:ARG:NE	2.35	0.59
2:O:116:LEU:HD13	2:O:226:MET:HG2	1.82	0.59
26:C:304:CDL:OA3	26:C:304:CDL:H1	2.03	0.59
3:C:33[B]:MET:CE	20:C:324:DMU:H12	2.31	0.59
26:C:304:CDL:HB61	26:C:304:CDL:HB21	1.84	0.59
12:Y:26:THR:HG23	13:Z:25:SER:CB	2.33	0.59
1:A:278[A]:MET:SD	19:A:608:LFA:H51	2.43	0.59
26:P:305:CDL:H121	26:P:305:CDL:HA62	1.85	0.58
2:O:59:GLN:HE22	19:O:302:LFA:C3	2.16	0.58
1:A:297[B]:MET:HG2	1:A:302:ARG:HG3	1.84	0.58
1:N:417[B]:MET:CE	29:N:2932:HOH:O	2.49	0.58
2:O:92:ASN:ND2	29:O:403:HOH:O	2.36	0.58
1:A:297[B]:MET:CG	1:A:302:ARG:HG3	2.34	0.58
26:C:304:CDL:HB21	26:C:304:CDL:HB32	1.86	0.58
1:N:423[B]:MET:HE2	1:N:460:ILE:HD12	1.85	0.58
1:A:274:VAL:HG12	1:A:278[A]:MET:HE2	1.85	0.57
3:C:33[A]:MET:HE1	3:C:41:THR:HB	1.85	0.57
6:F:64:GLU:O	6:F:65:ASP:HB2	2.05	0.57
3:C:59:ARG:HB2	26:C:304:CDL:OA9	2.04	0.57
12:L:13:PHE:HB3	26:L:101:CDL:H512	1.87	0.57
3:C:258:TRP:CE2	19:C:307:LFA:H32	2.40	0.57
20:C:324:DMU:H20	10:J:50:LEU:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:278[B]:MET:SD	19:N:609:LFA:H51	2.45	0.56
7:G:19:LEU:CD2	19:N:610:LFA:H61	2.35	0.56
1:N:297[B]:MET:HG2	1:N:302:ARG:HG3	1.88	0.56
3:P:205:GLY:HA3	28:T:101:PEK:H182	1.86	0.56
1:N:297[B]:MET:CG	1:N:302:ARG:HG3	2.36	0.56
4:Q:48:TRP:O	4:Q:51:LEU:HB2	2.04	0.56
12:Y:26:THR:HG23	13:Z:25:SER:HB3	1.87	0.56
26:P:305:CDL:C75	10:W:27:THR:HG21	2.35	0.56
3:P:156:ARG:HE	24:P:306:CHD:C24	2.19	0.56
1:A:334:TRP:CE3	20:A:609:DMU:H19	2.41	0.56
4:D:17[A]:VAL:HG12	29:D:302:HOH:O	2.06	0.55
4:Q:107:ILE:HD13	11:X:39:GLU:HB2	1.86	0.55
6:S:76:LYS:CE	6:S:93:PRO:HG2	2.33	0.55
2:B:67:ILE:HD11	19:B:306:LFA:H42	1.89	0.54
3:C:54[A]:MET:HE1	22:C:303:PGV:H141	1.89	0.54
1:A:110:LEU:HD21	20:C:324:DMU:H24	1.89	0.54
1:N:278[B]:MET:HE1	19:N:609:LFA:H52	1.90	0.54
4:D:42:GLU:OE2	29:D:301:HOH:O	2.18	0.54
2:O:58:ALA:O	2:O:62:GLU:HG3	2.08	0.54
3:P:133:ASN:ND2	29:P:404:HOH:O	2.34	0.54
4:Q:81:VAL:HG11	20:Q:201:DMU:H11	1.90	0.54
1:A:278[A]:MET:CE	19:A:608:LFA:C5	2.84	0.54
1:N:107:PRO:HB3	3:P:25:LEU:HB2	1.90	0.54
1:N:296:GLY:HA2	8:U:23:GLN:OE1	2.08	0.54
29:P:453[B]:HOH:O	10:W:27:THR:HG22	2.09	0.53
2:B:16[A]:ILE:HG21	2:B:87[A]:MET:CE	2.32	0.53
1:N:2:PHE:CE2	26:Y:101:CDL:H712	2.44	0.53
3:P:224:LYS:HE3	26:P:305:CDL:HB31	1.88	0.53
19:C:313:LFA:H21	19:C:314:LFA:H71	1.89	0.53
4:D:107:ILE:HD13	11:K:39:GLU:HB2	1.90	0.53
1:N:28:MET:HE3	12:Y:29:PHE:CD1	2.43	0.53
3:C:180[B]:GLU:HG2	29:C:428:HOH:O	2.08	0.53
20:C:324:DMU:H11	10:J:49:CYS:HB3	1.91	0.53
2:O:1:FME:HE1	2:O:133:LEU:HD22	1.91	0.53
1:A:189:MET:HE3	19:A:607:LFA:H31	1.91	0.53
28:T:101:PEK:H32	28:T:101:PEK:C7	2.36	0.53
3:C:33[B]:MET:HE1	20:C:324:DMU:C25	2.39	0.52
6:S:54:ASN:HD22	6:S:54:ASN:C	2.17	0.52
6:F:87[A]:THR:HG22	6:F:89:TYR:CE1	2.44	0.52
1:A:24:ALA:HB2	14:A:601[B]:HEA:H253	1.92	0.52
1:N:423[B]:MET:CE	1:N:460:ILE:HD12	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:ASN:OD1	2:B:183:THR:HG21	2.10	0.52
26:C:304:CDL:HB21	26:C:304:CDL:CB3	2.40	0.51
26:P:305:CDL:H752	10:W:27:THR:HG21	1.91	0.51
20:P:324:DMU:H10	10:W:53:ALA:HB2	1.92	0.51
1:A:1:FME:HE2	1:A:1:FME:HA	1.91	0.51
2:B:91:ASN:HD22	2:B:92:ASN:N	2.08	0.51
4:D:82:VAL:HG12	4:D:86:MET:HE2	1.92	0.51
3:C:37:PHE:CE2	20:C:324:DMU:H13	2.45	0.51
19:N:601:LFA:H42	2:O:67:ILE:HD11	1.91	0.51
26:P:305:CDL:HB61	26:P:305:CDL:CB2	2.41	0.51
7:T:45:PRO:HD2	29:T:218:HOH:O	2.10	0.51
3:P:258:TRP:CZ2	19:P:308:LFA:H32	2.46	0.51
1:A:484:THR:HG22	29:A:864:HOH:O	2.09	0.51
3:C:33[B]:MET:HE2	3:C:33[B]:MET:N	2.26	0.51
2:O:16[B]:ILE:HG23	29:O:517:HOH:O	2.10	0.51
1:A:107:PRO:HB3	3:C:25:LEU:HB2	1.92	0.50
12:L:26:THR:CG2	20:L:102:DMU:H26	2.41	0.50
2:B:1:FME:HE1	2:B:133:LEU:HD22	1.92	0.50
12:Y:26:THR:CG2	20:Y:102:DMU:H26	2.41	0.50
2:B:58:ALA:O	2:B:62:GLU:HG3	2.11	0.50
1:N:417[B]:MET:HE2	29:N:2932:HOH:O	2.11	0.50
1:N:35:LEU:HD11	1:N:462:LEU:HB2	1.93	0.50
26:P:305:CDL:HB32	26:P:305:CDL:HB21	1.94	0.49
6:F:41:GLY:HA3	6:F:87[B]:THR:CG2	2.42	0.49
1:N:297[B]:MET:SD	1:N:302:ARG:HG3	2.50	0.49
2:B:61:VAL:HG22	2:B:65:TRP:CZ3	2.47	0.49
2:O:22[B]:HIS:O	2:O:22[B]:HIS:CG	2.65	0.49
26:C:304:CDL:H121	26:C:304:CDL:CA6	2.43	0.49
6:F:41:GLY:HA3	6:F:87[B]:THR:HG22	1.94	0.49
1:N:113[A]:LEU:HD12	26:Y:101:CDL:C87	2.42	0.49
2:O:224:ALA:O	2:O:227:LEU:HD12	2.12	0.49
22:A:616:PGV:H183	28:G:101:PEK:H322	1.94	0.49
29:N:2884:HOH:O	19:P:310:LFA:H51	2.11	0.49
5:E:46:LYS:NZ	29:E:305:HOH:O	2.46	0.48
2:O:59:GLN:NE2	19:O:302:LFA:C3	2.76	0.48
3:P:50:ASN:ND2	3:P:54[A]:MET:HE2	2.28	0.48
3:P:116:TRP:HA	3:P:117:PRO:C	2.39	0.48
19:A:607:LFA:C1	19:A:608:LFA:H11	2.32	0.48
1:N:112:LEU:HG	29:N:3010:HOH:O	2.13	0.48
1:N:240:HIS:C	1:N:240:HIS:CD2	2.91	0.48
1:A:336:PRO:HB2	1:A:394[B]:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:24:ALA:HB2	14:N:603[B]:HEA:H253	1.95	0.48
20:Q:201:DMU:O55	20:Q:201:DMU:H36	2.14	0.48
14:N:604:HEA:HBC1	14:N:604:HEA:HMC3	1.95	0.47
3:C:210:ILE:HD13	22:C:303:PGV:H312	1.95	0.47
1:N:310:MET:HE1	2:O:77:ALA:HB2	1.96	0.47
2:B:67:ILE:CD1	19:B:306:LFA:H61	2.44	0.47
1:N:278[B]:MET:SD	19:N:609:LFA:C5	3.02	0.47
1:A:240:HIS:C	1:A:240:HIS:CD2	2.92	0.47
1:N:362[B]:SER:O	2:O:87[B]:MET:HE1	2.15	0.47
26:P:305:CDL:H751	10:W:27:THR:HG21	1.96	0.47
24:P:306:CHD:C23	24:P:306:CHD:C16	2.92	0.47
8:U:46:LYS:HG3	8:U:48:GLY:N	2.30	0.47
1:A:110:LEU:CD2	20:C:324:DMU:H24	2.44	0.47
2:B:32[B]:PHE:CD2	9:I:31:PHE:CZ	3.03	0.47
3:C:226:HIS:HE1	26:C:304:CDL:H111	1.79	0.47
1:N:423[B]:MET:HE3	1:N:457:GLY:N	2.29	0.47
3:P:33[A]:MET:HG2	3:P:39:SER:O	2.14	0.47
20:D:201:DMU:H36	20:D:201:DMU:O55	2.15	0.46
1:A:28:MET:HE2	14:A:601[A]:HEA:H271	1.98	0.46
4:D:98:TRP:CE2	20:M:101:DMU:H11	2.50	0.46
3:P:177:GLN:OE1	3:P:177:GLN:HA	2.16	0.46
3:C:205:GLY:HA3	28:G:101:PEK:H192	1.98	0.46
3:C:104:SER:OG	29:C:405:HOH:O	2.20	0.46
1:N:362[A]:SER:HA	2:O:87[A]:MET:HE1	1.98	0.46
2:B:16[A]:ILE:HD11	2:B:86:MET:HG2	1.97	0.46
2:B:22[B]:HIS:HD2	29:B:447:HOH:O	1.97	0.46
2:B:196:CYS:HB2	2:B:207:MET:HG3	1.96	0.46
8:H:43:MET:CE	8:U:52:VAL:HG11	2.44	0.46
24:O:301:CHD:H212	24:O:301:CHD:H12	1.96	0.46
2:B:16[A]:ILE:HG21	2:B:87[A]:MET:HG2	1.97	0.46
2:B:104:TRP:CG	2:B:203:ASN:HB2	2.51	0.46
12:L:26:THR:HG23	13:M:25:SER:CB	2.46	0.46
4:Q:109:HIS:HD2	29:Q:347:HOH:O	1.98	0.46
1:A:278[B]:MET:HE3	19:A:608:LFA:H122	1.97	0.45
2:B:1:FME:HE1	2:B:133:LEU:CD2	2.46	0.45
3:P:106:LEU:HD22	19:P:311:LFA:H21	1.98	0.45
2:O:32[B]:PHE:CD2	9:V:31:PHE:CZ	3.04	0.45
4:Q:51:LEU:HB3	4:Q:56:LYS:HG3	1.97	0.45
19:A:608:LFA:C6	7:T:19:LEU:HD23	2.47	0.45
2:O:116:LEU:HD12	2:O:117:SER:N	2.31	0.45
6:F:53:THR:HG23	6:F:55:LYS:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:50:ASN:ND2	3:C:54[A]:MET:HE2	2.31	0.45
4:D:81:VAL:HG11	20:D:201:DMU:H11	1.99	0.45
26:C:304:CDL:CA5	26:C:304:CDL:OB4	2.65	0.45
9:V:61:GLU:OE1	9:V:64:ARG:CZ	2.65	0.45
1:A:53:ILE:HG22	29:A:819:HOH:O	2.16	0.44
3:C:67:PHE:HE2	26:C:304:CDL:O1	1.93	0.44
3:C:131:LEU:CD2	20:C:323:DMU:H18	2.47	0.44
3:P:33[B]:MET:HB2	3:P:33[B]:MET:HE2	1.53	0.44
3:C:47:LEU:O	3:C:51[A]:MET:HG2	2.17	0.44
1:N:390:MET:HE2	1:N:413:HIS:HE1	1.82	0.44
3:P:224:LYS:CE	26:P:305:CDL:HB31	2.48	0.44
1:A:418:PHE:CD1	20:D:201:DMU:H24	2.51	0.44
2:B:132:GLU:HB3	2:B:137:GLU:HG3	1.99	0.44
3:C:55:TYR:OH	26:C:304:CDL:HA61	2.18	0.44
2:O:22[B]:HIS:O	2:O:22[B]:HIS:ND1	2.50	0.44
13:Z:36:HIS:HD2	13:Z:39:ASN:ND2	2.16	0.44
3:P:146:TRP:CD2	3:P:162:ALA:HB2	2.53	0.44
26:L:101:CDL:OB9	26:L:101:CDL:H122	2.17	0.44
3:C:208:VAL:HG22	3:C:245:VAL:CG1	2.48	0.43
8:U:46:LYS:HE2	8:U:46:LYS:O	2.18	0.43
1:A:297[B]:MET:SD	1:A:302:ARG:HG3	2.58	0.43
8:H:46:LYS:HE2	8:H:46:LYS:O	2.18	0.43
1:A:87:ILE:O	1:A:173:PRO:HD3	2.18	0.43
1:A:423[B]:MET:HE2	1:A:457:GLY:N	2.34	0.43
6:S:10:GLU:OE2	6:S:25:ARG:NH1	2.43	0.43
1:A:409:TRP:HB3	1:A:471:ILE:HG12	2.00	0.43
1:A:278[B]:MET:HE1	19:A:607:LFA:C5	2.48	0.43
3:C:39:SER:HB2	20:C:318:DMU:O55	2.18	0.43
1:N:265:LYS:HB2	1:N:490:THR:HG21	2.01	0.43
29:N:2884:HOH:O	19:P:310:LFA:C3	2.66	0.43
1:N:222:PRO:HB2	21:P:321:EDO:H22	2.01	0.43
8:H:37:HIS:HD2	8:H:40:GLU:OE2	2.02	0.43
2:O:164:ALA:O	2:O:194:GLY:HA3	2.19	0.43
6:F:64:GLU:O	6:F:65:ASP:CB	2.67	0.42
2:O:104:TRP:CG	2:O:203:ASN:HB2	2.54	0.42
1:A:76:GLY:O	1:A:80:ASN:HB2	2.20	0.42
3:C:177:GLN:HA	3:C:177:GLN:OE1	2.19	0.42
26:C:304:CDL:H121	26:C:304:CDL:HA62	2.01	0.42
1:A:337:ALA:HB2	1:A:394[A]:VAL:HG23	2.01	0.42
1:A:334:TRP:HB2	20:D:201:DMU:C57	2.49	0.42
2:B:164:ALA:O	2:B:194:GLY:HA3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:T:12:GLY:HA3	29:T:228:HOH:O	2.18	0.42
1:A:310:MET:HE1	2:B:77:ALA:HB2	2.01	0.42
3:P:77:LYS:NZ	3:P:81:TYR:OH	2.52	0.42
19:A:608:LFA:H92	19:A:608:LFA:H121	1.82	0.42
2:B:13:THR:HB	2:B:168:LEU:HD23	2.01	0.42
26:C:304:CDL:H121	26:C:304:CDL:OA8	2.20	0.42
2:O:91:ASN:C	2:O:91:ASN:HD22	2.27	0.42
3:C:33[B]:MET:HG3	3:C:37:PHE:HB2	2.00	0.42
4:D:127:LYS:HD2	29:I:239:HOH:O	2.19	0.42
1:N:148:PHE:HB3	3:P:28:THR:HB	2.01	0.42
2:O:196:CYS:HB2	2:O:207:MET:HG3	2.01	0.42
1:A:379:TYR:O	1:A:383:MET:HB2	2.20	0.42
26:C:304:CDL:H531	26:C:304:CDL:HB4	2.00	0.42
8:H:46:LYS:HD3	8:U:52:VAL:HG22	2.01	0.42
2:O:1:FME:HE1	2:O:133:LEU:CD2	2.50	0.42
26:C:304:CDL:HB22	10:J:8:LYS:HE3	2.02	0.41
1:N:71:MET:HB2	1:N:72:PRO:HD3	2.01	0.41
1:N:136[B]:LEU:CD1	29:N:3025:HOH:O	2.61	0.41
1:N:433:LEU:HD11	26:O:304:CDL:OA7	2.20	0.41
8:H:52:VAL:HG21	8:U:43:MET:HE1	2.01	0.41
1:N:336:PRO:HB2	1:N:394[B]:VAL:HG11	2.02	0.41
12:Y:26:THR:HG21	20:Y:102:DMU:H26	2.01	0.41
1:A:265:LYS:HB2	1:A:490:THR:HG21	2.02	0.41
3:C:103:HIS:HA	20:H:101:DMU:H11	2.01	0.41
2:O:16[A]:ILE:HG21	2:O:87[A]:MET:HG2	2.02	0.41
13:Z:40:TYR:CD1	13:Z:40:TYR:N	2.88	0.41
7:G:45:PRO:HD2	29:G:220:HOH:O	2.19	0.41
1:A:308:ALA:O	1:A:311[B]:ILE:HG12	2.21	0.41
6:F:54:ASN:ND2	6:F:76:LYS:HD2	2.35	0.41
12:L:35:ALA:HB3	12:L:36:PRO:HD3	2.02	0.41
3:P:33[B]:MET:CE	20:P:324:DMU:H12	2.50	0.41
2:B:67:ILE:HD11	19:B:306:LFA:H61	2.01	0.41
3:C:33[A]:MET:CE	3:C:41:THR:HB	2.48	0.41
6:F:21[B]:MET:HE2	6:F:21[B]:MET:HB2	1.87	0.41
12:L:26:THR:HG23	13:M:25:SER:HB3	2.03	0.41
1:N:485:VAL:CG1	21:N:617:EDO:H21	2.48	0.41
3:C:116:TRP:HA	3:C:117:PRO:C	2.45	0.41
6:S:64:GLU:O	6:S:65:ASP:HB2	2.20	0.41
1:A:148:PHE:HB3	3:C:28:THR:HB	2.03	0.40
3:C:258:TRP:NE1	19:C:307:LFA:H12	2.36	0.40
2:O:59:GLN:NE2	19:O:302:LFA:H31	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:608:LFA:H61	7:T:19:LEU:HD23	2.04	0.40
2:O:41:ILE:O	2:O:45:MET:HG2	2.21	0.40
5:R:90:ARG:NH1	29:R:308:HOH:O	2.49	0.40
1:N:113[A]:LEU:HD12	26:Y:101:CDL:H871	2.03	0.40
14:N:603[A]:HEA:H271	14:N:603[A]:HEA:H212	1.85	0.40
2:O:116:LEU:HD13	2:O:226:MET:CG	2.51	0.40
7:T:37:LEU:HD12	7:T:37:LEU:HA	1.82	0.40
14:A:601[A]:HEA:H271	14:A:601[A]:HEA:H212	1.90	0.40
1:A:28:MET:HE2	14:A:601[A]:HEA:C27	2.52	0.40
1:N:152:LEU:CD2	3:P:24:ALA:HB1	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	526/514 (102%)	512 (97%)	14 (3%)	0	100	100
1	N	526/514 (102%)	514 (98%)	12 (2%)	0	100	100
2	B	230/227 (101%)	224 (97%)	6 (3%)	0	100	100
2	O	230/227 (101%)	225 (98%)	5 (2%)	0	100	100
3	C	265/261 (102%)	261 (98%)	4 (2%)	0	100	100
3	P	265/261 (102%)	261 (98%)	4 (2%)	0	100	100
4	D	142/147 (97%)	139 (98%)	3 (2%)	0	100	100
4	Q	136/147 (92%)	132 (97%)	3 (2%)	1 (1%)	18	7
5	E	100/109 (92%)	100 (100%)	0	0	100	100
5	R	100/109 (92%)	100 (100%)	0	0	100	100
6	F	91/98 (93%)	90 (99%)	1 (1%)	0	100	100
6	S	91/98 (93%)	90 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	71/85 (84%)	67 (94%)	4 (6%)	0	100	100
7	T	71/85 (84%)	68 (96%)	3 (4%)	0	100	100
8	H	73/85 (86%)	70 (96%)	3 (4%)	0	100	100
8	U	73/85 (86%)	71 (97%)	1 (1%)	1 (1%)	9	2
9	I	68/73 (93%)	67 (98%)	1 (2%)	0	100	100
9	V	68/73 (93%)	67 (98%)	1 (2%)	0	100	100
10	J	54/59 (92%)	54 (100%)	0	0	100	100
10	W	54/59 (92%)	54 (100%)	0	0	100	100
11	K	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
11	X	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
12	L	42/47 (89%)	41 (98%)	1 (2%)	0	100	100
12	Y	42/47 (89%)	41 (98%)	1 (2%)	0	100	100
13	M	38/46 (83%)	38 (100%)	0	0	100	100
13	Z	38/46 (83%)	37 (97%)	1 (3%)	0	100	100
All	All	3488/3614 (96%)	3415 (98%)	71 (2%)	2 (0%)	48	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	U	48	GLY
4	Q	11	TYR

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	440/426 (103%)	437 (99%)	3 (1%)	76	69
1	N	440/426 (103%)	436 (99%)	4 (1%)	70	62
2	B	215/210 (102%)	208 (97%)	7 (3%)	33	17
2	O	215/210 (102%)	212 (99%)	3 (1%)	59	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	232/226 (103%)	230 (99%)	2 (1%)	70	62
3	P	232/226 (103%)	230 (99%)	2 (1%)	70	62
4	D	128/129 (99%)	128 (100%)	0	100	100
4	Q	122/129 (95%)	121 (99%)	1 (1%)	73	65
5	E	89/95 (94%)	89 (100%)	0	100	100
5	R	89/95 (94%)	88 (99%)	1 (1%)	65	54
6	F	78/81 (96%)	75 (96%)	3 (4%)	29	13
6	S	78/81 (96%)	75 (96%)	3 (4%)	29	13
7	G	63/69 (91%)	60 (95%)	3 (5%)	23	8
7	T	63/69 (91%)	59 (94%)	4 (6%)	16	5
8	H	67/75 (89%)	64 (96%)	3 (4%)	24	9
8	U	67/75 (89%)	64 (96%)	3 (4%)	24	9
9	I	55/58 (95%)	53 (96%)	2 (4%)	31	14
9	V	55/58 (95%)	50 (91%)	5 (9%)	9	2
10	J	47/50 (94%)	47 (100%)	0	100	100
10	W	47/50 (94%)	45 (96%)	2 (4%)	26	10
11	K	39/46 (85%)	38 (97%)	1 (3%)	40	23
11	X	39/46 (85%)	38 (97%)	1 (3%)	40	23
12	L	37/40 (92%)	37 (100%)	0	100	100
12	Y	37/40 (92%)	37 (100%)	0	100	100
13	M	34/38 (90%)	34 (100%)	0	100	100
13	Z	34/38 (90%)	32 (94%)	2 (6%)	18	5
All	All	3042/3086 (99%)	2987 (98%)	55 (2%)	51	36

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	LEU
1	A	138	HIS
1	A	369	ASP
2	B	33	LEU
2	B	59	GLN
2	B	65	TRP
2	B	75	LEU

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Mol	Chain	Res	Type
2	B	78	LEU
2	B	91	ASN
2	B	115	ASP
3	C	159	MET
3	C	230	ASN
6	F	80	GLN
6	F	87[A]	THR
6	F	87[B]	THR
7	G	33	LEU
7	G	36	TRP
7	G	37	LEU
8	H	46	LYS
8	H	60	TYR
8	H	61	LYS
9	I	36	LYS
9	I	43	ARG
11	K	54	ARG
1	N	138	HIS
1	N	363	LEU
1	N	369	ASP
1	N	485	VAL
2	O	33	LEU
2	O	78	LEU
2	O	91	ASN
3	P	159	MET
3	P	230	ASN
4	Q	51	LEU
5	R	79	LYS
6	S	37	LYS
6	S	54	ASN
6	S	80	GLN
7	T	33	LEU
7	T	36	TRP
7	T	37	LEU
7	T	43	GLU
8	U	46	LYS
8	U	60	TYR
8	U	61	LYS
9	V	8	GLN
9	V	29	LEU
9	V	61	GLU
9	V	65	LYS

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Mol	Chain	Res	Type
9	V	70	GLN
10	W	7	GLU
10	W	50	LEU
11	X	54	ARG
13	Z	13	LYS
13	Z	40	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	ASN
1	A	422	ASN
2	B	52	HIS
2	B	140	ASN
2	B	203	ASN
3	C	38	ASN
3	C	50	ASN
3	C	56	GLN
4	D	29	HIS
4	D	109	HIS
4	D	119	GLN
5	E	94	ASN
6	F	54	ASN
8	H	22	ASN
8	H	37	HIS
10	J	29	ASN
11	K	35	GLN
13	M	39	ASN
1	N	170	ASN
1	N	422	ASN
1	N	503	HIS
2	O	59	GLN
3	P	50	ASN
4	Q	32	ASN
4	Q	76	ASN
4	Q	101	HIS
4	Q	109	HIS
4	Q	119	GLN
5	R	94	ASN
6	S	54	ASN
8	U	22	ASN
8	U	28	ASN

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Mol	Chain	Res	Type
8	U	32	ASN
10	W	29	ASN
13	Z	36	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	0.49	0	8,9,11	0.95	1 (12%)
2	FME	B	1	2	8,9,10	1.14	1 (12%)	8,9,11	1.36	1 (12%)
1	FME	A	1	1	8,9,10	0.45	0	8,9,11	1.03	1 (12%)
2	FME	O	1	2	8,9,10	0.61	0	8,9,11	0.98	1 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	FME	N	1	1	-	3/7/9/11	-
2	FME	B	1	2	-	0/7/9/11	-
1	FME	A	1	1	-	2/7/9/11	-
2	FME	O	1	2	-	0/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	FME	CG-SD	-2.83	1.66	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	FME	CG-CB-CA	-2.59	104.95	112.87
1	N	1	FME	O-C-CA	-2.27	118.92	124.77
2	O	1	FME	O-C-CA	-2.19	119.14	124.77
1	A	1	FME	O-C-CA	-2.02	119.58	124.77

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	N-CA-CB-CG
1	N	1	FME	N-CA-CB-CG
1	N	1	FME	C-CA-CB-CG
1	A	1	FME	C-CA-CB-CG
1	N	1	FME	CA-CB-CG-SD

There are no ring outliers.

3 monomers are involved in 5 short contacts:

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 135 ligands modelled in this entry, 8 are monoatomic and 2 are unknown - leaving 125 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	DMU	B	307	-	22,22,34	0.50	0	27,27,45	1.25	2 (7%)
19	LFA	N	601	-	16,16,19	0.33	0	15,15,18	0.21	0
22	PGV	P	304	-	50,50,50	0.78	1 (2%)	53,56,56	0.94	3 (5%)
26	CDL	P	305	-	86,86,99	0.50	0	92,98,111	0.84	5 (5%)
21	EDO	C	322	-	3,3,3	0.82	0	2,2,2	0.70	0
14	HEA	N	603[A]	-	67,67,67	1.77	20 (29%)	81,103,103	2.35	28 (34%)
21	EDO	A	614	-	3,3,3	0.30	0	2,2,2	0.10	0
21	EDO	R	201	-	3,3,3	0.17	0	2,2,2	0.18	0
19	LFA	P	313	-	14,14,19	0.32	0	13,13,18	0.22	0
19	LFA	P	309	-	5,5,19	0.17	0	4,4,18	0.08	0
20	DMU	Z	101	-	34,34,34	0.99	3 (8%)	45,45,45	0.98	3 (6%)
21	EDO	A	612	-	3,3,3	0.06	0	2,2,2	0.06	0
21	EDO	A	613	-	3,3,3	0.38	0	2,2,2	0.12	0
21	EDO	R	203	-	3,3,3	0.25	0	2,2,2	0.51	0
28	PEK	G	101	-	52,52,52	0.58	1 (1%)	55,57,57	0.61	0
20	DMU	C	317	-	22,22,34	0.57	0	27,27,45	1.26	4 (14%)
19	LFA	C	312	-	10,10,19	0.25	0	9,9,18	0.18	0
19	LFA	N	610	-	13,13,19	0.62	0	12,12,18	0.39	0
20	DMU	A	617	-	10,10,34	0.24	0	9,9,45	0.56	0
14	HEA	A	601[B]	-	67,67,67	1.80	15 (22%)	81,103,103	2.41	28 (34%)
19	LFA	P	301	-	14,14,19	0.27	0	13,13,18	0.17	0
20	DMU	C	315	-	34,34,34	0.98	1 (2%)	45,45,45	1.65	10 (22%)
23	CUA	O	305	2	0,1,1	-	-	-	-	-
19	LFA	C	311	-	13,13,19	0.24	0	12,12,18	0.13	0
18	PER	N	608	15,14	1,1,1	1.54	0	-	-	-
21	EDO	N	615	-	3,3,3	0.46	0	2,2,2	0.33	0
21	EDO	N	613	-	3,3,3	0.17	0	2,2,2	0.18	0
24	CHD	B	305	-	32,32,32	0.67	0	51,51,51	0.90	1 (1%)
21	EDO	P	320	-	3,3,3	0.19	0	2,2,2	0.12	0
20	DMU	N	619	19	34,34,34	0.82	1 (2%)	45,45,45	1.32	6 (13%)
20	DMU	P	315	-	34,34,34	0.81	2 (5%)	45,45,45	1.35	4 (8%)
20	DMU	Q	201	-	34,34,34	1.29	6 (17%)	45,45,45	1.49	4 (8%)
20	DMU	B	303	-	22,22,34	0.90	1 (4%)	27,27,45	0.87	1 (3%)
19	LFA	O	302	-	10,10,19	0.23	0	9,9,18	0.16	0
21	EDO	P	321	-	3,3,3	0.19	0	2,2,2	0.15	0
22	PGV	A	616	-	50,50,50	0.70	0	53,56,56	1.21	4 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	DMU	A	615	-	10,10,34	0.30	0	9,9,45	0.52	0
21	EDO	A	611	-	3,3,3	0.32	0	2,2,2	0.52	0
20	DMU	A	609	-	6,6,34	0.65	0	5,5,45	0.31	0
21	EDO	S	102	-	3,3,3	0.39	0	2,2,2	0.35	0
14	HEA	A	602	1,18	67,67,67	1.72	18 (26%)	81,103,103	2.25	27 (33%)
20	DMU	D	201	-	34,34,34	1.46	8 (23%)	45,45,45	1.54	5 (11%)
23	CUA	B	301	2	0,1,1	-	-	-	-	-
20	DMU	M	102	-	7,7,34	0.27	0	6,6,45	0.56	0
21	EDO	C	320	-	3,3,3	0.06	0	2,2,2	0.08	0
20	DMU	A	610	-	34,34,34	1.25	6 (17%)	45,45,45	1.19	5 (11%)
24	CHD	C	301	-	32,32,32	0.87	1 (3%)	51,51,51	0.72	0
14	HEA	A	601[A]	-	67,67,67	1.79	15 (22%)	81,103,103	2.42	26 (32%)
19	LFA	C	313	-	14,14,19	0.31	0	13,13,18	0.41	0
20	DMU	C	316	-	6,6,34	0.28	0	5,5,45	0.49	0
20	DMU	P	318	-	34,34,34	0.92	3 (8%)	45,45,45	1.17	4 (8%)
20	DMU	J	101	-	10,10,34	0.20	0	9,9,45	0.58	0
26	CDL	O	304	-	63,63,99	0.41	0	69,75,111	0.71	1 (1%)
21	EDO	S	103	-	3,3,3	0.14	0	2,2,2	0.09	0
19	LFA	C	310	-	10,10,19	0.12	0	9,9,18	0.11	0
20	DMU	P	323	-	22,22,34	0.76	0	27,27,45	1.48	1 (3%)
19	LFA	A	607	-	13,13,19	0.41	0	12,12,18	0.26	0
19	LFA	P	311	-	10,10,19	0.15	0	9,9,18	0.11	0
21	EDO	N	614	-	3,3,3	0.19	0	2,2,2	0.37	0
22	PGV	N	618	-	50,50,50	0.78	1 (2%)	53,56,56	1.23	3 (5%)
24	CHD	O	301	-	32,32,32	0.73	0	51,51,51	0.77	0
19	LFA	A	608	-	13,13,19	0.74	1 (7%)	12,12,18	0.55	0
21	EDO	E	202	-	3,3,3	0.17	0	2,2,2	0.10	0
19	LFA	P	308	-	10,10,19	0.27	0	9,9,18	0.28	0
21	EDO	F	103	-	3,3,3	0.20	0	2,2,2	0.28	0
20	DMU	W	101	-	10,10,34	0.29	0	9,9,45	0.56	0
20	DMU	P	319	-	34,34,34	0.78	2 (5%)	45,45,45	1.21	3 (6%)
20	DMU	P	317	-	22,22,34	0.93	1 (4%)	27,27,45	1.32	2 (7%)
26	CDL	Y	101	-	93,93,99	0.35	0	99,105,111	0.44	1 (1%)
20	DMU	Y	102	-	22,22,34	0.56	0	27,27,45	1.00	1 (3%)
21	EDO	G	102	-	3,3,3	0.27	0	2,2,2	0.17	0
20	DMU	H	101	19	34,34,34	0.90	2 (5%)	45,45,45	1.11	4 (8%)
20	DMU	O	307	-	10,10,34	0.53	0	9,9,45	0.44	0
21	EDO	T	104	-	3,3,3	0.18	0	2,2,2	0.16	0
21	EDO	E	203	-	3,3,3	0.42	0	2,2,2	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	DMU	N	612	-	34,34,34	1.32	4 (11%)	45,45,45	1.00	3 (6%)
20	DMU	M	101	-	34,34,34	0.86	1 (2%)	45,45,45	1.13	3 (6%)
24	CHD	P	306	-	32,32,32	0.81	1 (3%)	51,51,51	1.30	5 (9%)
21	EDO	P	322	-	3,3,3	0.39	0	2,2,2	0.76	0
19	LFA	C	309	20	17,17,19	0.25	0	16,16,18	0.19	0
20	DMU	N	602	-	10,10,34	0.28	0	9,9,45	0.52	0
21	EDO	E	201	-	3,3,3	0.07	0	2,2,2	0.16	0
21	EDO	N	616	-	3,3,3	0.21	0	2,2,2	0.05	0
21	EDO	O	309	-	3,3,3	0.45	0	2,2,2	0.22	0
19	LFA	C	308	-	5,5,19	0.19	0	4,4,18	0.05	0
20	DMU	C	324	-	34,34,34	0.85	1 (2%)	45,45,45	1.17	4 (8%)
19	LFA	C	307	-	10,10,19	0.16	0	9,9,18	0.19	0
20	DMU	C	323	-	22,22,34	0.66	1 (4%)	27,27,45	1.03	1 (3%)
22	PGV	C	303	-	50,50,50	0.79	2 (4%)	53,56,56	1.08	3 (5%)
20	DMU	B	302	-	10,10,34	0.21	0	9,9,45	0.58	0
26	CDL	L	101	-	93,93,99	0.44	0	99,105,111	0.63	2 (2%)
20	DMU	C	306	-	10,10,34	0.43	0	9,9,45	0.58	0
20	DMU	O	306	-	10,10,34	0.13	0	9,9,45	0.63	0
20	DMU	C	319	-	34,34,34	0.83	1 (2%)	45,45,45	1.30	5 (11%)
26	CDL	C	304	-	86,86,99	0.56	0	92,98,111	1.12	8 (8%)
19	LFA	C	325	-	14,14,19	0.14	0	13,13,18	0.10	0
19	LFA	P	310	20	17,17,19	0.20	0	16,16,18	0.17	0
19	LFA	P	312	-	10,10,19	0.20	0	9,9,18	0.32	0
20	DMU	P	307	-	10,10,34	0.33	0	9,9,45	0.56	0
24	CHD	P	302	-	32,32,32	0.77	2 (6%)	51,51,51	0.85	0
19	LFA	N	609	-	13,13,19	0.36	0	12,12,18	0.41	0
20	DMU	P	316	-	6,6,34	0.30	0	5,5,45	0.49	0
26	CDL	I	101	-	63,63,99	0.47	0	69,75,111	1.04	4 (5%)
19	LFA	T	102	-	13,13,19	0.23	0	12,12,18	0.15	0
14	HEA	N	603[B]	-	67,67,67	1.78	20 (29%)	81,103,103	2.29	27 (33%)
20	DMU	O	303	-	22,22,34	0.74	0	27,27,45	1.46	3 (11%)
19	LFA	T	103	-	10,10,19	0.27	0	9,9,18	0.13	0
20	DMU	O	308	-	22,22,34	0.69	0	27,27,45	1.07	2 (7%)
21	EDO	C	321	-	3,3,3	0.30	0	2,2,2	0.35	0
19	LFA	C	314	-	12,12,19	0.31	0	11,11,18	0.27	0
21	EDO	B	304	-	3,3,3	0.40	0	2,2,2	0.14	0
21	EDO	R	202	-	3,3,3	0.20	0	2,2,2	0.28	0
19	LFA	B	306	-	16,16,19	0.39	0	15,15,18	0.18	0
21	EDO	N	617	-	3,3,3	0.38	0	2,2,2	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	PEK	T	101	-	52,52,52	0.62	2 (3%)	55,57,57	0.99	3 (5%)
18	PER	A	606	15,14	1,1,1	1.85	0	-		
20	DMU	C	318	-	34,34,34	0.88	2 (5%)	45,45,45	1.26	2 (4%)
19	LFA	P	314	-	12,12,19	0.34	0	11,11,18	0.25	0
24	CHD	C	305	-	32,32,32	0.70	1 (3%)	51,51,51	1.57	9 (17%)
21	EDO	F	102	-	3,3,3	0.19	0	2,2,2	0.09	0
20	DMU	Z	102	-	7,7,34	0.28	0	6,6,45	0.45	0
14	HEA	N	604	1,18	67,67,67	1.77	16 (23%)	81,103,103	2.30	28 (34%)
20	DMU	N	611	-	6,6,34	0.37	0	5,5,45	0.37	0
20	DMU	L	102	-	22,22,34	0.73	1 (4%)	27,27,45	1.20	4 (14%)
20	DMU	P	324	-	34,34,34	0.69	0	45,45,45	1.55	4 (8%)

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	DMU	B	307	-	-	9/13/33/59	0/1/1/2
19	LFA	N	601	-	-	10/14/14/17	-
22	PGV	P	304	-	-	11/55/55/55	-
26	CDL	P	305	-	-	45/97/97/110	-
21	EDO	C	322	-	-	0/1/1/1	-
14	HEA	N	603[A]	-	-	7/36/76/76	-
21	EDO	A	614	-	-	1/1/1/1	-
21	EDO	R	201	-	-	1/1/1/1	-
19	LFA	P	313	-	-	5/12/12/17	-
19	LFA	P	309	-	-	1/3/3/17	-
20	DMU	Z	101	-	-	6/19/59/59	0/2/2/2
21	EDO	A	612	-	-	1/1/1/1	-
21	EDO	A	613	-	-	0/1/1/1	-
21	EDO	R	203	-	-	1/1/1/1	-
28	PEK	G	101	-	-	15/56/56/56	-
20	DMU	C	317	-	-	8/13/33/59	0/1/1/2
19	LFA	C	312	-	-	4/8/8/17	-
19	LFA	N	610	-	-	7/11/11/17	-
20	DMU	A	617	-	-	6/8/8/59	-
14	HEA	A	601[B]	-	-	2/36/76/76	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	LFA	P	301	-	-	7/12/12/17	-
20	DMU	C	315	-	-	12/19/59/59	0/2/2/2
19	LFA	C	311	-	-	5/11/11/17	-
21	EDO	N	615	-	-	0/1/1/1	-
21	EDO	N	613	-	-	0/1/1/1	-
24	CHD	B	305	-	-	2/9/74/74	0/4/4/4
21	EDO	P	320	-	-	1/1/1/1	-
20	DMU	N	619	19	-	5/19/59/59	0/2/2/2
20	DMU	P	315	-	-	6/19/59/59	0/2/2/2
20	DMU	Q	201	-	-	8/19/59/59	0/2/2/2
20	DMU	B	303	-	-	7/13/33/59	0/1/1/2
19	LFA	O	302	-	-	3/8/8/17	-
21	EDO	P	321	-	-	1/1/1/1	-
22	PGV	A	616	-	-	10/55/55/55	-
20	DMU	A	615	-	-	6/8/8/59	-
21	EDO	A	611	-	-	0/1/1/1	-
20	DMU	A	609	-	-	3/4/4/59	-
21	EDO	S	102	-	-	0/1/1/1	-
14	HEA	A	602	1,18	-	4/36/76/76	-
20	DMU	D	201	-	-	7/19/59/59	0/2/2/2
20	DMU	M	102	-	-	5/5/5/59	-
21	EDO	C	320	-	-	0/1/1/1	-
20	DMU	A	610	-	-	7/19/59/59	0/2/2/2
24	CHD	C	301	-	-	2/9/74/74	0/4/4/4
14	HEA	A	601[A]	-	-	6/36/76/76	-
19	LFA	C	313	-	-	3/12/12/17	-
20	DMU	C	316	-	-	3/4/4/59	-
20	DMU	P	318	-	-	15/19/59/59	0/2/2/2
20	DMU	J	101	-	-	6/8/8/59	-
26	CDL	O	304	-	-	40/74/74/110	-
21	EDO	S	103	-	-	0/1/1/1	-
19	LFA	C	310	-	-	8/8/8/17	-
20	DMU	P	323	-	-	6/13/33/59	0/1/1/2
19	LFA	A	607	-	-	3/11/11/17	-
19	LFA	P	311	-	-	5/8/8/17	-
21	EDO	N	614	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PGV	N	618	-	-	8/55/55/55	-
24	CHD	O	301	-	-	2/9/74/74	0/4/4/4
19	LFA	A	608	-	-	5/11/11/17	-
21	EDO	E	202	-	-	0/1/1/1	-
19	LFA	P	308	-	-	4/8/8/17	-
21	EDO	F	103	-	-	1/1/1/1	-
20	DMU	W	101	-	-	5/8/8/59	-
20	DMU	P	319	-	-	8/19/59/59	0/2/2/2
20	DMU	P	317	-	-	8/13/33/59	0/1/1/2
26	CDL	Y	101	-	-	52/104/104/110	-
20	DMU	Y	102	-	-	9/13/33/59	0/1/1/2
21	EDO	G	102	-	-	0/1/1/1	-
20	DMU	H	101	19	-	5/19/59/59	0/2/2/2
20	DMU	O	307	-	-	5/8/8/59	-
21	EDO	T	104	-	-	0/1/1/1	-
21	EDO	E	203	-	-	1/1/1/1	-
20	DMU	N	612	-	-	5/19/59/59	0/2/2/2
20	DMU	M	101	-	-	3/19/59/59	0/2/2/2
24	CHD	P	306	-	-	9/9/74/74	0/4/4/4
21	EDO	P	322	-	-	0/1/1/1	-
19	LFA	C	309	20	-	9/15/15/17	-
20	DMU	N	602	-	-	4/8/8/59	-
21	EDO	E	201	-	-	0/1/1/1	-
21	EDO	N	616	-	-	0/1/1/1	-
21	EDO	O	309	-	-	0/1/1/1	-
19	LFA	C	308	-	-	1/3/3/17	-
20	DMU	C	324	-	-	5/19/59/59	0/2/2/2
19	LFA	C	307	-	-	7/8/8/17	-
20	DMU	C	323	-	-	10/13/33/59	0/1/1/2
22	PGV	C	303	-	-	14/55/55/55	-
20	DMU	B	302	-	-	5/8/8/59	-
26	CDL	L	101	-	-	54/104/104/110	-
20	DMU	C	306	-	-	3/8/8/59	-
20	DMU	O	306	-	-	5/8/8/59	-
20	DMU	C	319	-	-	10/19/59/59	0/2/2/2
26	CDL	C	304	-	-	40/97/97/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	LFA	C	325	-	-	8/12/12/17	-
19	LFA	P	310	20	-	6/15/15/17	-
19	LFA	P	312	-	-	5/8/8/17	-
20	DMU	P	307	-	-	2/8/8/59	-
24	CHD	P	302	-	-	2/9/74/74	0/4/4/4
19	LFA	N	609	-	-	4/11/11/17	-
20	DMU	P	316	-	-	3/4/4/59	-
26	CDL	I	101	-	-	43/74/74/110	-
19	LFA	T	102	-	-	6/11/11/17	-
14	HEA	N	603[B]	-	-	3/36/76/76	-
20	DMU	O	303	-	-	7/13/33/59	0/1/1/2
19	LFA	T	103	-	-	3/8/8/17	-
20	DMU	O	308	-	-	4/13/33/59	0/1/1/2
21	EDO	C	321	-	-	0/1/1/1	-
19	LFA	C	314	-	-	5/10/10/17	-
21	EDO	B	304	-	-	0/1/1/1	-
21	EDO	R	202	-	-	0/1/1/1	-
19	LFA	B	306	-	-	11/14/14/17	-
21	EDO	N	617	-	-	0/1/1/1	-
28	PEK	T	101	-	-	19/56/56/56	-
20	DMU	C	318	-	-	13/19/59/59	0/2/2/2
19	LFA	P	314	-	-	3/10/10/17	-
24	CHD	C	305	-	-	8/9/74/74	0/4/4/4
21	EDO	F	102	-	-	0/1/1/1	-
20	DMU	Z	102	-	-	2/5/5/59	-
14	HEA	N	604	1,18	-	4/36/76/76	-
20	DMU	N	611	-	-	2/4/4/59	-
20	DMU	L	102	-	-	11/13/33/59	0/1/1/2
20	DMU	P	324	-	-	7/19/59/59	0/2/2/2

All (164) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	603[A]	HEA	C1D-ND	-5.06	1.31	1.40
14	N	603[B]	HEA	C1D-ND	-5.06	1.31	1.40
20	N	612	DMU	O16-C6	-4.88	1.32	1.40
14	N	603[A]	HEA	C3B-C2B	4.54	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	603[B]	HEA	C3B-C2B	4.54	1.45	1.34
14	N	604	HEA	C3B-C2B	4.38	1.44	1.34
14	A	601[A]	HEA	C1D-ND	-4.30	1.32	1.40
14	A	601[B]	HEA	C1D-ND	-4.30	1.32	1.40
14	A	601[A]	HEA	C16-C17	-4.28	1.39	1.53
14	A	601[B]	HEA	C16-C17	-4.28	1.39	1.53
14	N	604	HEA	C3D-C2D	4.04	1.45	1.36
14	A	601[A]	HEA	C3B-C2B	4.03	1.43	1.34
14	A	601[B]	HEA	C3B-C2B	4.03	1.43	1.34
14	A	602	HEA	CHD-C1D	3.98	1.46	1.38
14	N	604	HEA	C1D-ND	-3.85	1.33	1.40
14	N	604	HEA	CHB-C4A	3.83	1.45	1.38
14	A	601[A]	HEA	C3D-C2D	3.82	1.45	1.36
14	A	601[B]	HEA	C3D-C2D	3.82	1.45	1.36
20	P	317	DMU	O16-C6	3.80	1.46	1.40
14	A	601[A]	HEA	C1B-NB	-3.75	1.31	1.38
14	A	601[B]	HEA	C1B-NB	-3.75	1.31	1.38
14	N	604	HEA	C3A-C2A	3.67	1.45	1.37
14	A	601[A]	HEA	CHD-C1D	3.67	1.45	1.38
14	A	601[B]	HEA	CHD-C1D	3.67	1.45	1.38
14	A	602	HEA	C4C-NC	-3.66	1.32	1.39
14	N	603[A]	HEA	CHD-C1D	3.61	1.45	1.38
14	N	603[B]	HEA	CHD-C1D	3.61	1.45	1.38
20	Q	201	DMU	O3-C5	-3.56	1.34	1.43
14	A	602	HEA	C3B-C2B	3.43	1.42	1.34
14	N	604	HEA	CHD-C1D	3.42	1.45	1.38
20	D	201	DMU	O61-C57	3.40	1.56	1.42
14	A	602	HEA	FE-NC	3.29	2.06	1.95
14	N	604	HEA	C1C-NC	-3.28	1.33	1.39
14	N	603[A]	HEA	C3D-C2D	3.27	1.43	1.36
14	N	603[B]	HEA	C3D-C2D	3.27	1.43	1.36
14	A	601[A]	HEA	C3A-C2A	3.24	1.44	1.37
14	A	601[B]	HEA	C3A-C2A	3.24	1.44	1.37
14	N	603[A]	HEA	C1B-NB	-3.22	1.32	1.38
14	N	603[B]	HEA	C1B-NB	-3.22	1.32	1.38
20	Q	201	DMU	C10-C5	-3.17	1.43	1.52
20	C	315	DMU	C7-C5	-3.16	1.44	1.52
14	N	603[A]	HEA	C11-C3B	-3.15	1.47	1.51
14	N	603[B]	HEA	C11-C3B	-3.15	1.47	1.51
14	A	601[A]	HEA	C11-C3B	-3.10	1.47	1.51
14	A	601[B]	HEA	C11-C3B	-3.10	1.47	1.51
20	A	610	DMU	O3-C5	-2.99	1.35	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	602	HEA	C1C-NC	-2.99	1.34	1.39
14	N	603[A]	HEA	CHA-C1A	2.96	1.44	1.38
14	N	603[B]	HEA	CHA-C1A	2.96	1.44	1.38
14	A	602	HEA	CHA-C1A	2.96	1.44	1.38
20	Z	101	DMU	O3-C5	-2.96	1.35	1.43
14	N	603[A]	HEA	C3A-C2A	2.93	1.43	1.37
14	N	603[B]	HEA	C3A-C2A	2.93	1.43	1.37
28	G	101	PEK	C23-C22	-2.91	1.41	1.52
14	N	604	HEA	FE-ND	2.91	2.03	1.94
20	D	201	DMU	O5-C6	-2.90	1.34	1.41
14	N	603[A]	HEA	CHC-C4B	2.86	1.44	1.38
14	N	603[B]	HEA	CHC-C4B	2.86	1.44	1.38
14	A	602	HEA	CHB-C4A	2.84	1.43	1.38
14	A	602	HEA	CHC-C4B	2.83	1.44	1.38
20	N	612	DMU	C10-C5	-2.79	1.44	1.52
14	N	603[A]	HEA	C16-C17	-2.79	1.44	1.53
14	N	603[B]	HEA	C16-C17	-2.79	1.44	1.53
14	N	604	HEA	C4C-NC	-2.76	1.34	1.39
14	A	601[A]	HEA	CHC-C4B	2.75	1.44	1.38
14	A	601[B]	HEA	CHC-C4B	2.75	1.44	1.38
20	C	318	DMU	O5-C6	-2.73	1.34	1.41
14	A	602	HEA	C1B-NB	-2.72	1.33	1.38
20	D	201	DMU	O3-C5	-2.72	1.36	1.43
22	P	304	PGV	O03-C19	2.71	1.41	1.33
14	A	602	HEA	C3D-C2D	2.71	1.42	1.36
14	N	604	HEA	C3C-C4C	2.70	1.50	1.42
14	A	602	HEA	C1D-ND	-2.67	1.35	1.40
22	C	303	PGV	O01-C1	2.66	1.41	1.34
14	A	601[A]	HEA	C4C-NC	-2.64	1.34	1.39
14	A	601[B]	HEA	C4C-NC	-2.64	1.34	1.39
20	P	319	DMU	C10-C5	-2.60	1.44	1.52
24	C	301	CHD	O26-C24	-2.60	1.22	1.30
20	N	619	DMU	C6-C1	-2.60	1.44	1.52
14	A	602	HEA	C4D-ND	-2.59	1.33	1.38
28	T	101	PEK	C2-C1	2.57	1.58	1.50
22	N	618	PGV	O03-C19	2.56	1.40	1.33
14	A	602	HEA	C3A-C4A	2.51	1.50	1.46
20	N	612	DMU	C7-C5	-2.50	1.45	1.52
20	P	318	DMU	O5-C6	-2.48	1.35	1.41
24	C	305	CHD	O26-C24	-2.48	1.22	1.30
20	A	610	DMU	C10-C5	-2.47	1.45	1.52
14	N	604	HEA	C1A-C2A	2.42	1.49	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	603[A]	HEA	C12-C11	-2.41	1.48	1.53
14	N	603[B]	HEA	C12-C11	-2.41	1.48	1.53
20	A	610	DMU	O7-C10	2.41	1.48	1.41
20	Q	201	DMU	O5-C6	-2.38	1.35	1.41
20	C	319	DMU	O55-C2	-2.37	1.37	1.43
20	N	612	DMU	O3-C5	-2.36	1.37	1.43
14	N	604	HEA	FE-NC	2.36	2.02	1.95
14	A	602	HEA	C3A-C2A	2.35	1.42	1.37
22	C	303	PGV	O03-C19	2.35	1.40	1.33
14	N	604	HEA	CHC-C4B	2.33	1.43	1.38
14	A	601[A]	HEA	CHB-C1B	2.33	1.44	1.39
14	A	601[B]	HEA	CHB-C1B	2.33	1.44	1.39
14	A	602	HEA	C1C-C2C	2.30	1.48	1.43
14	N	603[A]	HEA	FE-ND	2.30	2.02	1.94
14	N	603[B]	HEA	FE-ND	2.30	2.02	1.94
20	C	318	DMU	C7-C5	-2.30	1.46	1.52
28	T	101	PEK	C23-C22	-2.28	1.43	1.52
20	P	319	DMU	C7-C5	-2.28	1.46	1.52
20	P	318	DMU	C7-C5	-2.27	1.46	1.52
24	P	306	CHD	O26-C24	-2.26	1.23	1.30
20	M	101	DMU	O3-C5	-2.24	1.37	1.43
24	P	302	CHD	O26-C24	-2.23	1.23	1.30
14	A	602	HEA	FE-NB	2.22	2.01	1.94
20	P	315	DMU	C7-C5	-2.22	1.46	1.52
14	N	604	HEA	FE-NB	2.22	2.01	1.94
14	A	602	HEA	FE-ND	2.22	2.01	1.94
20	D	201	DMU	O5-C4	-2.21	1.39	1.44
14	N	604	HEA	CHB-C1B	2.20	1.44	1.39
20	A	610	DMU	O55-C2	2.19	1.48	1.43
20	P	318	DMU	O3-C5	2.19	1.48	1.43
14	A	601[A]	HEA	CBD-CGD	2.19	1.55	1.50
14	A	601[B]	HEA	CBD-CGD	2.19	1.55	1.50
20	B	303	DMU	O16-C6	2.18	1.43	1.40
14	N	603[A]	HEA	FE-NA	2.18	2.02	1.95
14	N	603[B]	HEA	FE-NA	2.18	2.02	1.95
14	A	602	HEA	C4B-NB	-2.17	1.36	1.40
20	C	324	DMU	C7-C5	-2.17	1.46	1.52
20	A	610	DMU	O16-C6	-2.16	1.36	1.40
14	N	603[A]	HEA	CBA-CGA	2.16	1.55	1.50
14	N	603[B]	HEA	CBA-CGA	2.16	1.55	1.50
20	D	201	DMU	O49-C1	-2.16	1.37	1.43
20	A	610	DMU	O4-C7	-2.15	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	L	102	DMU	O16-C6	2.14	1.43	1.40
20	H	101	DMU	O16-C6	-2.14	1.36	1.40
20	Z	101	DMU	O16-C6	-2.13	1.36	1.40
20	D	201	DMU	O1-C10	2.13	1.47	1.41
20	P	315	DMU	O3-C5	-2.12	1.37	1.43
14	N	603[A]	HEA	C4B-NB	-2.10	1.36	1.40
14	N	603[B]	HEA	C4B-NB	-2.10	1.36	1.40
14	N	603[A]	HEA	C26-C15	-2.10	1.45	1.50
14	N	603[B]	HEA	C26-C15	-2.10	1.45	1.50
20	Q	201	DMU	C7-C5	-2.09	1.46	1.52
14	N	603[A]	HEA	FE-NB	2.09	2.01	1.94
14	N	603[B]	HEA	FE-NB	2.09	2.01	1.94
14	N	603[A]	HEA	CHB-C4A	2.08	1.42	1.38
14	N	603[B]	HEA	CHB-C4A	2.08	1.42	1.38
19	A	608	LFA	C10-C9	-2.08	1.41	1.51
20	D	201	DMU	O55-C2	2.07	1.48	1.43
14	A	601[A]	HEA	O1D-CGD	2.06	1.28	1.22
14	A	601[B]	HEA	O1D-CGD	2.06	1.28	1.22
20	Q	201	DMU	O16-C6	-2.05	1.36	1.40
14	N	604	HEA	C4B-NB	-2.05	1.36	1.40
20	D	201	DMU	C3-C4	2.05	1.58	1.52
14	N	603[A]	HEA	C1A-C2A	2.04	1.48	1.45
14	N	603[B]	HEA	C1A-C2A	2.04	1.48	1.45
24	P	302	CHD	C22-C23	-2.04	1.46	1.52
20	Q	201	DMU	O49-C1	-2.03	1.37	1.43
20	C	323	DMU	C6-C1	-2.02	1.46	1.52
20	H	101	DMU	O5-C6	-2.02	1.36	1.41
14	A	601[A]	HEA	FE-NA	2.02	2.01	1.95
14	A	601[B]	HEA	FE-NA	2.02	2.01	1.95
14	A	601[A]	HEA	FE-NC	2.01	2.01	1.95
14	A	601[B]	HEA	FE-NC	2.01	2.01	1.95
14	N	603[A]	HEA	O1A-CGA	2.01	1.28	1.22
14	N	603[B]	HEA	O1A-CGA	2.01	1.28	1.22
20	Z	101	DMU	C10-C5	-2.00	1.46	1.52

All (306) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601[A]	HEA	C3D-C4D-ND	8.05	118.13	110.35
14	A	601[B]	HEA	C3D-C4D-ND	8.05	118.13	110.35
14	N	603[A]	HEA	C3D-C4D-ND	7.34	117.44	110.35
14	N	603[B]	HEA	C3D-C4D-ND	7.34	117.44	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601[A]	HEA	C3C-C4C-NC	6.96	115.66	109.80
14	A	601[B]	HEA	C3C-C4C-NC	6.96	115.66	109.80
14	A	602	HEA	C2B-C1B-NB	6.84	117.81	109.90
20	D	201	DMU	O16-C6-C1	6.05	117.47	108.27
20	P	323	DMU	O16-C6-C1	6.02	117.42	108.27
14	A	601[A]	HEA	C2B-C1B-NB	5.91	116.74	109.90
14	A	601[B]	HEA	C2B-C1B-NB	5.91	116.74	109.90
14	N	604	HEA	C2D-C1D-ND	5.85	116.57	109.84
20	Q	201	DMU	O16-C6-C1	5.84	117.14	108.27
14	N	603[A]	HEA	C3C-C4C-NC	5.82	114.70	109.80
14	N	603[B]	HEA	C3C-C4C-NC	5.82	114.70	109.80
14	N	603[A]	HEA	C2D-C1D-ND	5.65	116.33	109.84
14	N	603[B]	HEA	C2D-C1D-ND	5.65	116.33	109.84
20	P	315	DMU	O16-C6-C1	5.64	116.83	108.27
14	N	603[A]	HEA	C2B-C1B-NB	5.63	116.42	109.90
14	N	603[B]	HEA	C2B-C1B-NB	5.63	116.42	109.90
14	N	604	HEA	C3D-C4D-ND	5.62	115.78	110.35
24	C	305	CHD	C17-C13-C12	-5.36	112.84	117.67
20	C	315	DMU	O16-C6-C1	5.34	116.39	108.27
20	P	324	DMU	O16-C6-C1	5.29	116.31	108.27
14	N	604	HEA	C3B-C4B-NB	5.20	115.82	109.84
14	N	604	HEA	C2B-C1B-NB	5.15	115.85	109.90
14	A	602	HEA	C3B-C4B-NB	5.09	115.69	109.84
14	N	604	HEA	C3C-C4C-NC	5.00	114.01	109.80
24	C	305	CHD	C16-C17-C20	4.98	119.72	112.18
14	A	601[A]	HEA	C27-C19-C20	4.93	123.79	115.23
14	A	602	HEA	C3D-C4D-ND	4.93	115.12	110.35
20	C	324	DMU	O16-C6-C1	4.91	115.73	108.27
14	N	604	HEA	C3A-C2A-C1A	-4.90	102.41	107.05
22	N	618	PGV	O03-C19-O04	-4.87	111.43	123.63
20	P	324	DMU	C10-C5-C7	4.85	120.22	110.01
20	P	319	DMU	O16-C6-C1	4.81	115.58	108.27
14	A	601[A]	HEA	CHA-C4D-C3D	-4.78	117.81	124.77
14	A	601[B]	HEA	CHA-C4D-C3D	-4.78	117.81	124.77
14	A	601[A]	HEA	C2D-C1D-ND	4.73	115.28	109.84
14	A	601[B]	HEA	C2D-C1D-ND	4.73	115.28	109.84
14	N	603[A]	HEA	C27-C19-C20	4.62	123.25	115.23
14	A	601[A]	HEA	C13-C12-C11	-4.62	107.02	114.39
14	A	601[B]	HEA	C13-C12-C11	-4.62	107.02	114.39
14	A	601[A]	HEA	CHB-C1B-C2B	-4.58	117.79	125.03
14	A	601[B]	HEA	CHB-C1B-C2B	-4.58	117.79	125.03
14	A	601[A]	HEA	C3B-C4B-NB	4.57	115.10	109.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601[B]	HEA	C3B-C4B-NB	4.57	115.10	109.84
20	P	317	DMU	O5-C6-C1	4.56	119.73	110.37
26	I	101	CDL	CA4-OA6-CA5	4.54	128.66	117.80
26	C	304	CDL	OA5-PA1-OA3	4.53	126.89	108.94
22	A	616	PGV	O03-C19-O04	-4.52	112.33	123.63
20	C	318	DMU	O16-C6-C1	4.47	115.07	108.27
14	N	603[A]	HEA	CHB-C1B-C2B	-4.46	117.99	125.03
14	N	603[B]	HEA	CHB-C1B-C2B	-4.46	117.99	125.03
14	A	602	HEA	C13-C12-C11	-4.44	107.29	114.39
14	N	604	HEA	C1D-C2D-C3D	-4.39	102.36	106.98
20	O	303	DMU	O5-C6-C1	4.38	119.36	110.37
14	A	602	HEA	C2D-C1D-ND	4.35	114.84	109.84
14	N	603[A]	HEA	C3B-C4B-NB	4.27	114.75	109.84
14	N	603[B]	HEA	C3B-C4B-NB	4.27	114.75	109.84
26	C	304	CDL	OA4-PA1-OA5	-4.27	88.21	107.57
14	A	601[A]	HEA	C4D-C3D-C2D	-4.25	100.70	106.89
14	A	601[B]	HEA	C4D-C3D-C2D	-4.25	100.70	106.89
14	A	602	HEA	CHB-C1B-C2B	-4.17	118.44	125.03
28	T	101	PEK	O01-C1-O02	-4.14	114.03	123.70
20	C	317	DMU	O5-C6-C1	4.07	118.73	110.37
20	B	307	DMU	O16-C6-C1	4.04	114.41	108.27
20	C	318	DMU	C10-C5-C7	3.95	118.32	110.01
14	N	603[A]	HEA	C4D-C3D-C2D	-3.94	101.16	106.89
14	N	603[B]	HEA	C4D-C3D-C2D	-3.94	101.16	106.89
14	A	602	HEA	CMD-C2D-C1D	3.93	131.18	125.03
20	M	101	DMU	O16-C6-C1	3.92	114.23	108.27
22	N	618	PGV	O03-C19-C20	3.92	123.78	111.83
20	N	619	DMU	C10-C5-C7	3.91	118.24	110.01
14	A	602	HEA	C4B-NB-C1B	-3.91	100.58	105.21
24	P	306	CHD	C22-C23-C24	-3.89	102.12	112.49
14	N	603[A]	HEA	C3A-C2A-C1A	-3.89	103.37	107.05
14	N	603[B]	HEA	C3A-C2A-C1A	-3.89	103.37	107.05
20	P	318	DMU	O16-C6-C1	3.81	114.06	108.27
14	A	601[A]	HEA	C4C-C3C-C2C	-3.80	102.58	107.30
14	A	601[B]	HEA	C4C-C3C-C2C	-3.80	102.58	107.30
20	O	303	DMU	O16-C6-C1	3.80	114.04	108.27
14	N	604	HEA	CHB-C1B-C2B	-3.79	119.05	125.03
26	C	304	CDL	OA6-CA5-C11	-3.77	103.33	111.48
14	A	602	HEA	CHA-C4D-C3D	-3.76	119.28	124.77
22	C	303	PGV	O03-C19-O04	-3.76	114.21	123.63
14	A	602	HEA	C1B-C2B-C3B	-3.73	102.48	106.80
14	A	602	HEA	CMB-C2B-C1B	3.68	130.79	125.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	604	HEA	C1B-C2B-C3B	-3.68	102.54	106.80
20	C	319	DMU	C10-C5-C7	3.66	117.72	110.01
14	A	601[B]	HEA	C27-C19-C20	3.65	121.57	115.23
14	A	602	HEA	C3C-C4C-NC	3.65	112.88	109.80
14	A	602	HEA	C27-C19-C20	3.64	121.55	115.23
14	N	604	HEA	C2C-C1C-NC	3.58	115.88	110.14
20	P	318	DMU	C10-C5-C7	3.57	117.51	110.01
22	A	616	PGV	O03-C19-C20	3.55	122.67	111.83
26	I	101	CDL	OA6-CA4-CA3	3.50	120.90	108.34
20	C	319	DMU	O16-C6-C1	3.49	113.58	108.27
20	C	323	DMU	O16-C6-C1	3.49	113.58	108.27
14	A	602	HEA	C3C-C2C-C1C	-3.46	103.08	107.17
14	N	604	HEA	CAD-C3D-C4D	3.45	130.72	124.70
20	C	315	DMU	C6-O5-C4	3.45	120.47	113.72
14	N	604	HEA	CMD-C2D-C1D	3.41	130.36	125.03
24	P	306	CHD	C16-C17-C20	3.40	117.32	112.18
14	N	603[A]	HEA	C1D-C2D-C3D	-3.40	103.41	106.98
14	N	603[B]	HEA	C1D-C2D-C3D	-3.40	103.41	106.98
20	H	101	DMU	C10-C5-C7	3.38	117.12	110.01
28	T	101	PEK	O02-C1-C2	3.34	136.86	123.78
14	N	603[A]	HEA	C3C-C2C-C1C	-3.34	103.23	107.17
14	N	603[B]	HEA	C3C-C2C-C1C	-3.34	103.23	107.17
14	N	603[A]	HEA	C2C-C1C-NC	3.32	115.47	110.14
14	N	603[B]	HEA	C2C-C1C-NC	3.32	115.47	110.14
20	L	102	DMU	O5-C6-O16	3.31	117.87	110.04
26	P	305	CDL	OA5-PA1-OA3	3.31	122.06	108.94
14	N	603[A]	HEA	C1D-ND-C4D	-3.30	101.30	105.21
14	N	603[B]	HEA	C1D-ND-C4D	-3.30	101.30	105.21
14	A	601[A]	HEA	C1D-ND-C4D	-3.28	101.33	105.21
14	A	601[B]	HEA	C1D-ND-C4D	-3.28	101.33	105.21
26	C	304	CDL	OB5-PB2-OB3	3.27	121.90	108.94
24	C	305	CHD	C14-C13-C12	3.24	110.38	107.42
20	N	619	DMU	O16-C6-C1	3.23	113.17	108.27
26	I	101	CDL	OA8-CA6-CA4	3.22	117.69	108.40
14	N	603[A]	HEA	C20-C19-C18	-3.22	113.93	121.17
24	P	306	CHD	C17-C13-C12	-3.21	114.78	117.67
24	C	305	CHD	C17-C13-C14	-3.20	96.90	100.11
26	O	304	CDL	OA6-CA5-C11	3.20	118.41	111.48
24	C	305	CHD	C22-C23-C24	-3.17	104.04	112.49
14	A	601[A]	HEA	C1B-C2B-C3B	-3.16	103.14	106.80
14	A	601[B]	HEA	C1B-C2B-C3B	-3.16	103.14	106.80
20	O	303	DMU	C6-C1-C2	3.13	116.61	110.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	Q	201	DMU	C2-C3-C4	-3.12	104.03	110.93
14	N	604	HEA	C4C-C3C-C2C	-3.11	103.43	107.30
22	P	304	PGV	C27-C26-C25	-3.10	98.67	114.37
20	C	315	DMU	C10-O1-C9	3.05	119.68	113.72
20	B	307	DMU	O5-C6-C1	3.05	116.63	110.37
14	N	604	HEA	C2A-C1A-NA	3.04	113.26	110.32
20	M	101	DMU	C18-O16-C6	-3.04	108.48	113.68
20	Z	101	DMU	O16-C6-C1	3.02	112.86	108.27
14	N	604	HEA	CAD-CBD-CGD	-3.02	105.66	113.67
14	N	603[A]	HEA	CHA-C4D-C3D	-3.02	120.38	124.77
14	N	603[B]	HEA	CHA-C4D-C3D	-3.02	120.38	124.77
20	C	315	DMU	O1-C9-C8	3.01	115.13	109.70
14	A	601[A]	HEA	CAD-C3D-C4D	3.01	129.94	124.70
14	A	601[B]	HEA	CAD-C3D-C4D	3.01	129.94	124.70
20	P	324	DMU	C10-O1-C9	-3.00	107.86	113.72
22	A	616	PGV	C25-C24-C23	3.00	129.54	114.37
26	L	101	CDL	OB4-PB2-OB2	3.00	121.17	107.57
14	N	603[A]	HEA	C13-C12-C11	-3.00	109.61	114.39
14	N	603[B]	HEA	C13-C12-C11	-3.00	109.61	114.39
14	N	603[A]	HEA	C4B-C3B-C2B	-2.98	102.44	107.44
14	N	603[B]	HEA	C4B-C3B-C2B	-2.98	102.44	107.44
14	N	604	HEA	C3C-C2C-C1C	-2.94	103.71	107.17
14	A	602	HEA	C1D-C2D-C3D	-2.93	103.90	106.98
14	N	603[A]	HEA	C1B-C2B-C3B	-2.91	103.42	106.80
14	N	603[B]	HEA	C1B-C2B-C3B	-2.91	103.42	106.80
14	N	604	HEA	CHA-C4D-C3D	-2.91	120.53	124.77
24	P	306	CHD	C23-C22-C20	-2.90	109.05	114.46
20	D	201	DMU	C57-C4-C3	2.89	121.51	113.38
14	A	601[A]	HEA	C3A-C2A-C1A	-2.89	104.31	107.05
14	A	601[B]	HEA	C3A-C2A-C1A	-2.89	104.31	107.05
26	P	305	CDL	OB5-PB2-OB3	2.88	120.35	108.94
20	C	315	DMU	O5-C6-C1	2.88	116.29	110.37
20	P	315	DMU	C10-C5-C7	2.87	116.05	110.01
14	N	604	HEA	C13-C12-C11	-2.86	109.83	114.39
14	N	603[A]	HEA	C2A-C1A-NA	2.85	113.07	110.32
14	N	603[B]	HEA	C2A-C1A-NA	2.85	113.07	110.32
14	A	601[A]	HEA	O11-C11-C12	2.85	116.70	109.14
14	A	601[B]	HEA	O11-C11-C12	2.85	116.70	109.14
14	A	601[A]	HEA	C20-C19-C18	-2.82	114.84	121.17
20	C	315	DMU	C18-O16-C6	-2.82	108.87	113.68
20	N	619	DMU	O5-C6-O16	2.80	116.65	110.04
14	A	601[A]	HEA	C4B-NB-C1B	-2.78	101.91	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601[B]	HEA	C4B-NB-C1B	-2.78	101.91	105.21
20	Y	102	DMU	O5-C6-O16	2.78	116.62	110.04
20	M	101	DMU	O3-C5-C7	2.78	116.93	110.38
26	I	101	CDL	OA6-CA4-CA6	2.77	118.29	108.34
14	N	604	HEA	C4D-C3D-C2D	-2.75	102.88	106.89
14	N	603[A]	HEA	CAD-C3D-C4D	2.75	129.49	124.70
14	N	603[B]	HEA	CAD-C3D-C4D	2.75	129.49	124.70
14	A	602	HEA	C3A-C2A-C1A	-2.75	104.44	107.05
20	C	315	DMU	O3-C5-C10	2.73	116.57	110.08
20	D	201	DMU	C2-C3-C4	-2.71	104.92	110.93
20	N	619	DMU	C10-O7-C3	-2.69	111.60	117.98
26	C	304	CDL	OA4-PA1-OA3	2.69	124.97	112.44
20	Z	101	DMU	O3-C5-C7	2.69	116.71	110.38
20	Q	201	DMU	C6-O5-C4	-2.69	108.48	113.72
14	N	604	HEA	C4B-NB-C1B	-2.68	102.03	105.21
20	A	610	DMU	C10-C5-C7	2.67	115.63	110.01
20	C	315	DMU	O5-C6-O16	-2.67	103.74	110.04
14	A	602	HEA	CAD-CBD-CGD	-2.65	106.63	113.67
14	N	604	HEA	CMB-C2B-C1B	2.65	129.17	125.03
20	A	610	DMU	C10-O7-C3	-2.63	111.74	117.98
26	L	101	CDL	OB5-PB2-OB3	-2.61	98.60	108.94
14	A	601[A]	HEA	C4B-C3B-C2B	-2.58	103.10	107.44
14	A	601[B]	HEA	C4B-C3B-C2B	-2.58	103.10	107.44
14	A	602	HEA	C4D-C3D-C2D	-2.57	103.15	106.89
20	D	201	DMU	C10-C5-C7	2.57	115.41	110.01
20	O	308	DMU	O5-C6-C1	2.57	115.64	110.37
20	C	319	DMU	O3-C5-C10	2.55	116.15	110.08
20	H	101	DMU	O3-C5-C10	2.53	116.11	110.08
26	P	305	CDL	OA6-CA5-OA7	-2.53	117.79	123.70
24	C	305	CHD	C6-C7-C8	2.50	114.23	111.50
20	N	612	DMU	C10-O1-C9	2.49	118.59	113.72
20	A	610	DMU	O3-C5-C7	2.49	116.24	110.38
14	N	604	HEA	CHB-C4A-NA	-2.48	121.75	124.45
20	P	315	DMU	C18-O16-C6	-2.47	109.46	113.68
20	B	303	DMU	O5-C6-C1	2.47	115.44	110.37
14	N	603[B]	HEA	C21-C20-C19	-2.46	105.04	113.19
22	C	303	PGV	C23-C22-C21	2.45	126.74	114.37
14	N	603[A]	HEA	CHC-C1C-C2C	-2.45	120.32	127.43
14	N	603[B]	HEA	CHC-C1C-C2C	-2.45	120.32	127.43
14	A	601[A]	HEA	CHD-C1D-C2D	-2.44	120.02	126.95
14	A	601[B]	HEA	CHD-C1D-C2D	-2.44	120.02	126.95
14	N	603[A]	HEA	C4C-NC-C1C	-2.42	101.87	105.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	603[B]	HEA	C4C-NC-C1C	-2.42	101.87	105.82
14	N	603[A]	HEA	CHD-C1D-C2D	-2.41	120.10	126.95
14	N	603[B]	HEA	CHD-C1D-C2D	-2.41	120.10	126.95
14	A	602	HEA	C4B-C3B-C2B	-2.41	103.39	107.44
14	A	601[A]	HEA	C1D-C2D-C3D	-2.40	104.45	106.98
14	A	601[B]	HEA	C1D-C2D-C3D	-2.40	104.45	106.98
14	A	602	HEA	O1D-CGD-CBD	-2.39	115.50	123.09
14	N	604	HEA	C1D-ND-C4D	-2.39	102.38	105.21
26	C	304	CDL	OB6-CB5-C51	2.38	116.63	111.48
14	A	602	HEA	O1A-CGA-CBA	-2.38	115.54	123.09
20	C	317	DMU	C18-O16-C6	-2.38	109.62	113.68
20	O	308	DMU	C57-C4-C3	-2.36	107.23	113.02
20	C	319	DMU	O3-C5-C7	2.35	115.92	110.38
20	L	102	DMU	C3-C2-C1	-2.34	106.72	110.83
26	P	305	CDL	OA4-PA1-OA5	-2.34	96.97	107.57
20	N	612	DMU	O5-C6-C1	2.34	115.17	110.37
22	C	303	PGV	O14-P-O13	2.33	123.30	112.44
26	C	304	CDL	OA7-CA5-C11	2.33	132.88	123.78
14	N	604	HEA	CHC-C1C-C2C	-2.33	120.67	127.43
20	C	315	DMU	C7-C8-C9	2.29	114.39	110.23
14	N	603[A]	HEA	CHB-C4A-NA	-2.28	121.97	124.45
14	N	603[B]	HEA	CHB-C4A-NA	-2.28	121.97	124.45
14	N	603[A]	HEA	C25-C23-C24	2.28	119.84	114.59
14	A	601[A]	HEA	CHC-C1C-C2C	-2.28	120.81	127.43
14	A	601[B]	HEA	CHC-C1C-C2C	-2.28	120.81	127.43
14	A	602	HEA	OMA-CMA-C3A	-2.27	120.49	125.62
14	A	602	HEA	C20-C19-C18	-2.26	116.09	121.17
26	P	305	CDL	OA4-PA1-OA3	2.26	122.96	112.44
20	N	619	DMU	C57-C4-C3	-2.26	107.02	113.38
20	P	324	DMU	O7-C10-O1	-2.25	104.77	110.69
20	C	317	DMU	C2-C3-C4	-2.25	106.15	110.23
20	C	315	DMU	C10-C5-C7	2.25	114.74	110.01
20	A	610	DMU	O16-C6-C1	2.25	111.68	108.27
20	L	102	DMU	O5-C6-C1	2.23	114.95	110.37
20	P	319	DMU	O3-C5-C7	2.23	115.62	110.38
14	N	603[A]	HEA	O11-C11-C3B	-2.23	107.18	111.26
14	N	603[B]	HEA	O11-C11-C3B	-2.23	107.18	111.26
20	P	317	DMU	C18-O16-C6	-2.22	109.89	113.68
20	A	610	DMU	O5-C6-O16	2.21	115.27	110.04
22	P	304	PGV	C22-C21-C20	-2.21	105.01	113.13
20	N	619	DMU	O3-C5-C10	2.21	115.34	110.08
14	N	604	HEA	C4B-C3B-C2B	-2.20	103.74	107.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	601[B]	HEA	C21-C22-C23	-2.20	120.31	127.64
14	N	604	HEA	C20-C19-C18	-2.19	116.26	121.17
14	A	601[B]	HEA	C20-C19-C18	-2.18	116.27	121.17
14	A	602	HEA	CHC-C1C-C2C	-2.18	121.11	127.43
14	N	604	HEA	CHD-C1D-ND	-2.17	121.68	124.37
14	N	603[A]	HEA	C4C-C3C-C2C	-2.17	104.60	107.30
14	N	603[B]	HEA	C4C-C3C-C2C	-2.17	104.60	107.30
20	P	319	DMU	C10-C5-C7	2.16	114.56	110.01
20	Z	101	DMU	O5-C6-C1	2.16	114.81	110.37
24	C	305	CHD	C15-C14-C8	2.16	121.32	118.36
20	P	318	DMU	C1-C2-C3	2.15	114.55	109.68
24	C	305	CHD	C18-C13-C17	2.15	114.57	111.20
26	C	304	CDL	OB2-PB2-OB3	-2.14	100.44	108.94
14	A	602	HEA	C2C-C1C-NC	2.14	113.57	110.14
22	P	304	PGV	O03-C19-O04	-2.13	118.29	123.63
14	A	601[A]	HEA	CHC-C4B-NB	-2.13	121.73	124.37
14	A	601[B]	HEA	CHC-C4B-NB	-2.13	121.73	124.37
20	C	319	DMU	O5-C6-C1	2.12	114.73	110.37
14	N	604	HEA	C4A-CHB-C1B	-2.11	121.53	126.02
22	A	616	PGV	O01-C1-O02	-2.11	118.76	123.70
14	N	603[A]	HEA	CHA-C4D-ND	-2.10	122.16	124.42
14	N	603[B]	HEA	CHA-C4D-ND	-2.10	122.16	124.42
22	N	618	PGV	O01-C1-O02	-2.10	118.80	123.70
20	N	612	DMU	O1-C9-C11	2.09	111.62	106.44
14	A	602	HEA	C1D-ND-C4D	-2.08	102.74	105.21
24	B	305	CHD	C17-C13-C14	2.08	102.20	100.11
14	A	601[A]	HEA	O11-C11-C3B	-2.07	107.45	111.26
14	A	601[B]	HEA	O11-C11-C3B	-2.07	107.45	111.26
14	A	601[A]	HEA	CMD-C2D-C1D	2.07	128.27	125.03
14	A	601[B]	HEA	CMD-C2D-C1D	2.07	128.27	125.03
20	L	102	DMU	C57-C4-C3	-2.07	107.95	113.02
20	C	317	DMU	C6-C1-C2	2.06	114.35	110.01
20	C	324	DMU	O5-C6-C1	2.05	114.59	110.37
20	C	324	DMU	C10-C5-C7	2.05	114.33	110.01
20	C	324	DMU	C10-O7-C3	-2.05	113.12	117.98
20	H	101	DMU	C10-O1-C9	2.05	117.72	113.72
20	D	201	DMU	O5-C4-C3	-2.04	105.50	109.72
28	T	101	PEK	C2-C3-C4	2.04	117.81	113.35
24	C	305	CHD	O12-C12-C13	-2.04	107.58	111.02
14	A	601[A]	HEA	C2C-C1C-NC	2.04	113.41	110.14
14	A	601[B]	HEA	C2C-C1C-NC	2.04	113.41	110.14
20	P	315	DMU	O7-C3-C2	2.03	112.39	107.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	603[B]	HEA	C25-C23-C24	2.03	119.26	114.59
24	P	306	CHD	C18-C13-C14	2.03	114.38	111.20
14	A	601[B]	HEA	C21-C20-C19	-2.02	106.50	113.19
14	A	602	HEA	O11-C11-C3B	-2.02	107.56	111.26
20	Q	201	DMU	C10-C5-C7	2.01	114.25	110.01
20	H	101	DMU	O16-C6-C1	2.01	111.33	108.27
26	Y	101	CDL	OA6-CA5-C11	2.01	115.83	111.48
20	P	318	DMU	O3-C5-C10	2.00	114.84	110.08

There are no chirality outliers.

All (815) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	N	603[A]	HEA	C27-C19-C20-C21
20	C	318	DMU	C19-C18-O16-C6
20	C	323	DMU	C19-C18-O16-C6
20	L	102	DMU	C19-C18-O16-C6
20	O	303	DMU	C19-C18-O16-C6
20	O	308	DMU	C19-C18-O16-C6
20	Q	201	DMU	C19-C18-O16-C6
20	Y	102	DMU	O5-C6-O16-C18
20	Y	102	DMU	C19-C18-O16-C6
24	C	305	CHD	C13-C17-C20-C21
24	C	305	CHD	C16-C17-C20-C22
26	C	304	CDL	O1-C1-CB2-OB2
26	C	304	CDL	C1-CA2-OA2-PA1
26	C	304	CDL	CA3-OA5-PA1-OA2
26	C	304	CDL	OB7-CB5-OB6-CB4
26	C	304	CDL	C51-CB5-OB6-CB4
26	I	101	CDL	CA2-C1-CB2-OB2
26	I	101	CDL	C1-CA2-OA2-PA1
26	I	101	CDL	CA3-OA5-PA1-OA2
26	I	101	CDL	CA3-OA5-PA1-OA3
26	I	101	CDL	CA3-OA5-PA1-OA4
26	I	101	CDL	CB2-OB2-PB2-OB3
26	I	101	CDL	CB2-OB2-PB2-OB4
26	I	101	CDL	CB2-OB2-PB2-OB5
26	I	101	CDL	CB3-OB5-PB2-OB2
26	I	101	CDL	CB3-OB5-PB2-OB3
26	I	101	CDL	CB3-OB5-PB2-OB4
26	I	101	CDL	C51-CB5-OB6-CB4
26	L	101	CDL	CB2-C1-CA2-OA2

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Mol	Chain	Res	Type	Atoms
26	L	101	CDL	CA2-OA2-PA1-OA3
26	L	101	CDL	CA2-OA2-PA1-OA4
26	L	101	CDL	CA2-OA2-PA1-OA5
26	L	101	CDL	CA3-OA5-PA1-OA3
26	L	101	CDL	CB2-OB2-PB2-OB5
26	L	101	CDL	OB6-CB4-CB6-OB8
26	L	101	CDL	OB7-CB5-OB6-CB4
26	L	101	CDL	C51-CB5-OB6-CB4
26	O	304	CDL	CA2-OA2-PA1-OA3
26	O	304	CDL	C11-CA5-OA6-CA4
26	O	304	CDL	CB2-OB2-PB2-OB3
26	O	304	CDL	CB2-OB2-PB2-OB5
26	O	304	CDL	CB3-OB5-PB2-OB2
26	P	305	CDL	O1-C1-CB2-OB2
26	P	305	CDL	C1-CA2-OA2-PA1
26	P	305	CDL	CA2-OA2-PA1-OA3
26	P	305	CDL	CA2-OA2-PA1-OA5
26	P	305	CDL	CA3-OA5-PA1-OA2
26	P	305	CDL	C11-CA5-OA6-CA4
26	P	305	CDL	CB3-OB5-PB2-OB4
26	P	305	CDL	OB7-CB5-OB6-CB4
26	Y	101	CDL	CA2-OA2-PA1-OA3
26	Y	101	CDL	CA3-OA5-PA1-OA2
26	Y	101	CDL	CA3-OA5-PA1-OA3
26	Y	101	CDL	CA3-OA5-PA1-OA4
26	Y	101	CDL	C11-CA5-OA6-CA4
26	Y	101	CDL	CB2-OB2-PB2-OB4
26	Y	101	CDL	CB2-OB2-PB2-OB5
26	Y	101	CDL	C51-CB5-OB6-CB4
28	G	101	PEK	C11-C12-C13-C14
28	T	101	PEK	C11-C12-C13-C14
28	T	101	PEK	C12-C13-C14-C15
24	C	305	CHD	C16-C17-C20-C21
24	C	305	CHD	C13-C17-C20-C22
20	L	102	DMU	C3-C4-C57-O61
26	C	304	CDL	OA7-CA5-OA6-CA4
26	I	101	CDL	OA7-CA5-OA6-CA4
26	I	101	CDL	OB7-CB5-OB6-CB4
26	O	304	CDL	OA7-CA5-OA6-CA4
26	P	305	CDL	OA7-CA5-OA6-CA4
26	Y	101	CDL	OA7-CA5-OA6-CA4
26	Y	101	CDL	OB7-CB5-OB6-CB4

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Mol	Chain	Res	Type	Atoms
26	O	304	CDL	C31-CA7-OA8-CA6
26	C	304	CDL	C11-CA5-OA6-CA4
26	L	101	CDL	C11-CA5-OA6-CA4
26	P	305	CDL	C51-CB5-OB6-CB4
24	P	306	CHD	C16-C17-C20-C21
24	P	306	CHD	C13-C17-C20-C22
14	A	601[A]	HEA	C27-C19-C20-C21
14	A	601[A]	HEA	C18-C19-C20-C21
14	N	603[A]	HEA	C18-C19-C20-C21
26	C	304	CDL	C71-CB7-OB8-CB6
20	D	201	DMU	O6-C11-C9-O1
20	L	102	DMU	O5-C4-C57-O61
26	O	304	CDL	OA9-CA7-OA8-CA6
26	L	101	CDL	OA7-CA5-OA6-CA4
24	P	306	CHD	C13-C17-C20-C21
22	A	616	PGV	C26-C27-C28-C29
26	I	101	CDL	O1-C1-CB2-OB2
26	L	101	CDL	O1-C1-CA2-OA2
26	P	305	CDL	C31-CA7-OA8-CA6
20	C	318	DMU	O5-C4-C57-O61
20	C	323	DMU	O5-C4-C57-O61
20	O	303	DMU	O5-C4-C57-O61
20	A	610	DMU	O6-C11-C9-O1
20	C	319	DMU	O5-C4-C57-O61
20	C	319	DMU	O6-C11-C9-O1
20	P	319	DMU	O6-C11-C9-O1
20	N	612	DMU	O6-C11-C9-C8
26	O	304	CDL	C51-CB5-OB6-CB4
20	N	612	DMU	O6-C11-C9-O1
20	P	324	DMU	O6-C11-C9-O1
20	A	610	DMU	O6-C11-C9-C8
20	C	315	DMU	O6-C11-C9-O1
20	N	619	DMU	O5-C4-C57-O61
14	A	601[A]	HEA	C15-C16-C17-C18
14	N	603[A]	HEA	C15-C16-C17-C18
20	P	324	DMU	O6-C11-C9-C8
26	C	304	CDL	CA4-CA3-OA5-PA1
20	C	319	DMU	C3-C4-C57-O61
20	C	319	DMU	O6-C11-C9-C8
20	D	201	DMU	O6-C11-C9-C8
26	L	101	CDL	C72-C73-C74-C75
26	C	304	CDL	OB9-CB7-OB8-CB6

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Mol	Chain	Res	Type	Atoms
20	B	303	DMU	O5-C6-O16-C18
20	Q	201	DMU	O5-C6-O16-C18
19	N	610	LFA	C9-C10-C11-C12
19	P	310	LFA	C11-C10-C9-C8
20	O	303	DMU	C3-C4-C57-O61
26	C	304	CDL	C31-CA7-OA8-CA6
22	A	616	PGV	C23-C24-C25-C26
22	C	303	PGV	C28-C29-C30-C31
20	P	315	DMU	C31-C34-C37-C40
20	B	307	DMU	C3-C4-C57-O61
20	C	318	DMU	C3-C4-C57-O61
19	P	301	LFA	C10-C11-C12-C13
26	L	101	CDL	C31-CA7-OA8-CA6
26	Y	101	CDL	C31-CA7-OA8-CA6
19	A	608	LFA	C9-C10-C11-C12
19	P	301	LFA	C2-C3-C4-C5
20	B	303	DMU	C1-C6-O16-C18
20	P	323	DMU	C1-C6-O16-C18
20	P	319	DMU	C2-C3-O7-C10
26	I	101	CDL	O1-C1-CA2-OA2
26	Y	101	CDL	O1-C1-CA2-OA2
26	L	101	CDL	OA9-CA7-OA8-CA6
20	C	323	DMU	C3-C4-C57-O61
19	C	309	LFA	C12-C13-C14-C15
26	P	305	CDL	OA9-CA7-OA8-CA6
20	P	318	DMU	O5-C4-C57-O61
20	C	324	DMU	O6-C11-C9-C8
26	O	304	CDL	OB7-CB5-OB6-CB4
24	P	306	CHD	C21-C20-C22-C23
20	P	319	DMU	O6-C11-C9-C8
19	C	325	LFA	C9-C10-C11-C12
20	C	318	DMU	O6-C11-C9-O1
24	P	306	CHD	C16-C17-C20-C22
20	C	319	DMU	O16-C18-C19-C22
20	C	317	DMU	O16-C18-C19-C22
20	Y	102	DMU	O16-C18-C19-C22
26	L	101	CDL	CA5-C11-C12-C13
26	O	304	CDL	CA7-C31-C32-C33
26	C	304	CDL	OA9-CA7-OA8-CA6
26	O	304	CDL	C1-CA2-OA2-PA1
20	B	307	DMU	O5-C4-C57-O61
20	N	619	DMU	C3-C4-C57-O61

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Mol	Chain	Res	Type	Atoms
26	C	304	CDL	CB5-C51-C52-C53
26	P	305	CDL	CB7-C71-C72-C73
20	N	612	DMU	O5-C6-O16-C18
20	P	319	DMU	C4-C3-O7-C10
26	Y	101	CDL	OA9-CA7-OA8-CA6
26	C	304	CDL	CA7-C31-C32-C33
20	L	102	DMU	O16-C18-C19-C22
20	A	610	DMU	C3-C4-C57-O61
20	B	303	DMU	O16-C18-C19-C22
20	Z	101	DMU	O16-C18-C19-C22
20	C	324	DMU	O6-C11-C9-O1
26	I	101	CDL	CA5-C11-C12-C13
26	Y	101	CDL	CB2-C1-CA2-OA2
19	P	310	LFA	C12-C13-C14-C15
20	C	318	DMU	O16-C18-C19-C22
20	P	318	DMU	O1-C10-O7-C3
20	O	308	DMU	O16-C18-C19-C22
26	I	101	CDL	C11-CA5-OA6-CA4
20	C	318	DMU	C1-C6-O16-C18
20	C	319	DMU	C1-C6-O16-C18
20	L	102	DMU	C1-C6-O16-C18
20	N	619	DMU	C1-C6-O16-C18
20	P	318	DMU	C1-C6-O16-C18
20	Y	102	DMU	C1-C6-O16-C18
28	T	101	PEK	C7-C8-C9-C10
20	A	610	DMU	O5-C4-C57-O61
26	C	304	CDL	O1-C1-CA2-OA2
26	P	305	CDL	O1-C1-CA2-OA2
20	C	315	DMU	O6-C11-C9-C8
20	C	323	DMU	O16-C18-C19-C22
19	C	309	LFA	C11-C10-C9-C8
20	P	323	DMU	O5-C6-O16-C18
20	Y	102	DMU	C18-C19-C22-C25
26	P	305	CDL	C82-C83-C84-C85
20	A	617	DMU	C18-C19-C22-C25
19	T	102	LFA	C10-C11-C12-C13
19	T	103	LFA	C3-C4-C5-C6
20	P	318	DMU	C25-C28-C31-C34
26	C	304	CDL	C35-C36-C37-C38
26	L	101	CDL	C58-C59-C60-C61
26	O	304	CDL	C31-C32-C33-C34
26	Y	101	CDL	C79-C80-C81-C82

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Mol	Chain	Res	Type	Atoms
26	C	304	CDL	C11-C12-C13-C14
26	C	304	CDL	C72-C73-C74-C75
26	L	101	CDL	C12-C13-C14-C15
20	D	201	DMU	C19-C18-O16-C6
20	A	615	DMU	C18-C19-C22-C25
26	O	304	CDL	C17-C18-C19-C20
20	C	315	DMU	C19-C22-C25-C28
20	W	101	DMU	C25-C28-C31-C34
22	C	303	PGV	C7-C8-C9-C10
26	C	304	CDL	CB7-C71-C72-C73
20	P	317	DMU	C18-C19-C22-C25
19	C	309	LFA	C3-C4-C5-C6
19	N	601	LFA	C5-C6-C7-C8
20	C	317	DMU	C31-C34-C37-C40
20	M	101	DMU	C19-C22-C25-C28
20	O	306	DMU	C19-C22-C25-C28
19	B	306	LFA	C13-C14-C15-C16
26	C	304	CDL	C75-C76-C77-C78
26	Y	101	CDL	C19-C20-C21-C22
20	C	318	DMU	C31-C34-C37-C40
20	B	302	DMU	C18-C19-C22-C25
20	Z	101	DMU	C22-C25-C28-C31
19	P	311	LFA	C6-C7-C8-C9
20	N	602	DMU	C25-C28-C31-C34
19	N	601	LFA	C13-C14-C15-C16
19	P	308	LFA	C3-C4-C5-C6
19	P	310	LFA	C4-C5-C6-C7
20	M	102	DMU	C25-C28-C31-C34
20	P	318	DMU	C22-C25-C28-C31
26	P	305	CDL	C35-C36-C37-C38
20	H	101	DMU	C3-C4-C57-O61
26	I	101	CDL	C31-C32-C33-C34
19	A	607	LFA	C6-C7-C8-C9
22	C	303	PGV	C13-C14-C15-C16
20	P	323	DMU	C18-C19-C22-C25
19	B	306	LFA	C11-C12-C13-C14
19	P	301	LFA	C4-C5-C6-C7
20	A	617	DMU	C19-C22-C25-C28
22	C	303	PGV	C22-C23-C24-C25
26	Y	101	CDL	CA5-C11-C12-C13
28	T	101	PEK	C1-C2-C3-C4
19	N	609	LFA	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
20	A	610	DMU	C31-C34-C37-C40
20	N	612	DMU	C31-C34-C37-C40
19	B	306	LFA	C10-C11-C12-C13
20	Z	101	DMU	C25-C28-C31-C34
19	C	307	LFA	C5-C6-C7-C8
22	C	303	PGV	C25-C26-C27-C28
24	P	306	CHD	C17-C20-C22-C23
20	B	307	DMU	C18-C19-C22-C25
26	P	305	CDL	CB5-C51-C52-C53
20	A	615	DMU	C19-C22-C25-C28
26	P	305	CDL	C74-C75-C76-C77
19	C	307	LFA	C4-C5-C6-C7
22	C	303	PGV	C14-C15-C16-C17
19	P	312	LFA	C1-C2-C3-C4
20	M	101	DMU	C22-C25-C28-C31
22	P	304	PGV	C7-C8-C9-C10
26	C	304	CDL	C22-C23-C24-C25
26	C	304	CDL	C71-C72-C73-C74
28	T	101	PEK	C26-C27-C28-C29
26	O	304	CDL	C76-C77-C78-C79
20	C	316	DMU	C31-C34-C37-C40
26	L	101	CDL	C59-C60-C61-C62
20	C	318	DMU	O5-C6-O16-C18
26	L	101	CDL	C37-C38-C39-C40
20	P	319	DMU	C22-C25-C28-C31
19	C	312	LFA	C1-C2-C3-C4
26	L	101	CDL	C74-C75-C76-C77
26	O	304	CDL	C12-C13-C14-C15
26	O	304	CDL	C78-C79-C80-C81
26	P	305	CDL	C13-C14-C15-C16
20	P	317	DMU	C31-C34-C37-C40
20	N	602	DMU	C28-C31-C34-C37
26	L	101	CDL	C51-C52-C53-C54
19	T	102	LFA	C3-C4-C5-C6
20	C	315	DMU	C28-C31-C34-C37
20	J	101	DMU	C18-C19-C22-C25
20	A	615	DMU	C25-C28-C31-C34
20	J	101	DMU	C31-C34-C37-C40
19	P	301	LFA	C6-C7-C8-C9
20	C	319	DMU	C25-C28-C31-C34
19	C	325	LFA	C4-C5-C6-C7
22	C	303	PGV	C30-C31-C32-C33

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Mol	Chain	Res	Type	Atoms
26	L	101	CDL	C17-C18-C19-C20
20	H	101	DMU	C19-C22-C25-C28
24	C	305	CHD	C21-C20-C22-C23
26	O	304	CDL	C73-C74-C75-C76
20	O	303	DMU	C34-C37-C40-C43
19	C	310	LFA	C7-C8-C9-C10
20	P	317	DMU	C28-C31-C34-C37
26	Y	101	CDL	C13-C14-C15-C16
26	O	304	CDL	CA5-C11-C12-C13
28	G	101	PEK	C15-C16-C17-C18
19	P	311	LFA	C2-C3-C4-C5
20	C	323	DMU	C19-C22-C25-C28
26	O	304	CDL	C74-C75-C76-C77
28	G	101	PEK	C28-C29-C30-C31
19	A	608	LFA	C11-C10-C9-C8
20	D	201	DMU	C4-C3-O7-C10
20	P	316	DMU	C28-C31-C34-C37
28	T	101	PEK	C14-C15-C16-C17
19	A	608	LFA	C2-C3-C4-C5
20	C	317	DMU	C19-C22-C25-C28
26	P	305	CDL	C71-C72-C73-C74
20	P	318	DMU	O6-C11-C9-O1
19	C	325	LFA	C7-C8-C9-C10
20	P	307	DMU	C31-C34-C37-C40
20	W	101	DMU	O16-C18-C19-C22
20	O	306	DMU	C22-C25-C28-C31
26	Y	101	CDL	C31-C32-C33-C34
20	P	323	DMU	O16-C18-C19-C22
19	C	309	LFA	C5-C6-C7-C8
20	C	317	DMU	C28-C31-C34-C37
26	L	101	CDL	C38-C39-C40-C41
19	C	325	LFA	C10-C11-C12-C13
19	C	311	LFA	C11-C10-C9-C8
26	I	101	CDL	C31-CA7-OA8-CA6
20	P	318	DMU	O5-C6-O16-C18
22	N	618	PGV	C26-C27-C28-C29
22	N	618	PGV	C29-C30-C31-C32
26	Y	101	CDL	C14-C15-C16-C17
19	C	311	LFA	C4-C5-C6-C7
22	P	304	PGV	C12-C13-C14-C15
20	L	102	DMU	C22-C25-C28-C31
19	P	313	LFA	C5-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
22	C	303	PGV	C24-C25-C26-C27
26	L	101	CDL	C34-C35-C36-C37
20	B	302	DMU	O16-C18-C19-C22
20	P	307	DMU	O16-C18-C19-C22
20	P	318	DMU	C3-C4-C57-O61
26	Y	101	CDL	C51-C52-C53-C54
19	T	103	LFA	C6-C7-C8-C9
20	A	609	DMU	C28-C31-C34-C37
20	C	315	DMU	O5-C4-C57-O61
20	P	315	DMU	O6-C11-C9-O1
26	Y	101	CDL	C80-C81-C82-C83
26	O	304	CDL	C77-C78-C79-C80
26	C	304	CDL	C23-C24-C25-C26
26	Y	101	CDL	C72-C73-C74-C75
26	Y	101	CDL	C63-C64-C65-C66
19	N	610	LFA	C5-C6-C7-C8
20	C	319	DMU	C31-C34-C37-C40
26	I	101	CDL	C76-C77-C78-C79
26	C	304	CDL	CB3-CB4-CB6-OB8
26	I	101	CDL	CA3-CA4-CA6-OA8
26	P	305	CDL	CA3-CA4-CA6-OA8
28	G	101	PEK	C34-C35-C36-C37
22	N	618	PGV	C11-C10-C9-C8
28	T	101	PEK	C2-C3-C4-C5
28	T	101	PEK	C15-C16-C17-C18
19	B	306	LFA	C12-C13-C14-C15
19	P	313	LFA	C2-C3-C4-C5
20	L	102	DMU	C31-C34-C37-C40
20	Y	102	DMU	O5-C4-C57-O61
20	P	318	DMU	C28-C31-C34-C37
21	P	320	EDO	O1-C1-C2-O2
20	Q	201	DMU	C4-C3-O7-C10
26	P	305	CDL	C75-C76-C77-C78
19	N	601	LFA	C11-C12-C13-C14
26	I	101	CDL	C15-C16-C17-C18
22	A	616	PGV	C29-C30-C31-C32
19	P	310	LFA	C3-C4-C5-C6
20	P	318	DMU	C19-C22-C25-C28
20	P	319	DMU	C31-C34-C37-C40
19	P	314	LFA	C5-C6-C7-C8
20	C	323	DMU	C28-C31-C34-C37
19	N	601	LFA	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
19	A	607	LFA	C2-C3-C4-C5
19	C	309	LFA	C13-C14-C15-C16
19	C	312	LFA	C5-C6-C7-C8
19	O	302	LFA	C5-C6-C7-C8
19	N	601	LFA	C4-C5-C6-C7
22	A	616	PGV	C14-C15-C16-C17
26	I	101	CDL	C19-C20-C21-C22
19	C	309	LFA	C14-C15-C16-C17
26	C	304	CDL	C74-C75-C76-C77
26	I	101	CDL	C71-C72-C73-C74
26	I	101	CDL	C16-C17-C18-C19
26	P	305	CDL	CA7-C31-C32-C33
28	T	101	PEK	C4-C5-C6-C7
20	C	318	DMU	C2-C3-O7-C10
20	C	318	DMU	C19-C22-C25-C28
26	I	101	CDL	C71-CB7-OB8-CB6
26	C	304	CDL	C59-C60-C61-C62
20	W	101	DMU	C31-C34-C37-C40
20	Z	101	DMU	C34-C37-C40-C43
26	Y	101	CDL	C59-C60-C61-C62
20	C	318	DMU	C34-C37-C40-C43
26	Y	101	CDL	C64-C65-C66-C67
26	Y	101	CDL	C84-C85-C86-C87
28	G	101	PEK	C17-C18-C19-C20
19	C	310	LFA	C3-C4-C5-C6
19	P	314	LFA	C6-C7-C8-C9
20	J	101	DMU	C25-C28-C31-C34
28	T	101	PEK	C32-C33-C34-C35
20	C	318	DMU	C4-C3-O7-C10
20	A	617	DMU	C28-C31-C34-C37
20	P	315	DMU	C19-C22-C25-C28
20	C	316	DMU	C28-C31-C34-C37
20	O	306	DMU	C25-C28-C31-C34
26	I	101	CDL	OA6-CA4-CA6-OA8
26	O	304	CDL	OA6-CA4-CA6-OA8
19	N	601	LFA	C14-C15-C16-C17
20	N	611	DMU	C34-C37-C40-C43
20	Z	102	DMU	C34-C37-C40-C43
19	C	309	LFA	C2-C3-C4-C5
20	C	316	DMU	C34-C37-C40-C43
20	W	101	DMU	C34-C37-C40-C43
20	A	617	DMU	C25-C28-C31-C34

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Mol	Chain	Res	Type	Atoms
20	C	319	DMU	C19-C22-C25-C28
28	G	101	PEK	C16-C17-C18-C19
19	P	301	LFA	C1-C2-C3-C4
26	I	101	CDL	C12-C13-C14-C15
26	I	101	CDL	C17-C18-C19-C20
26	P	305	CDL	C71-CB7-OB8-CB6
20	D	201	DMU	C2-C3-O7-C10
19	C	310	LFA	C11-C10-C9-C8
26	Y	101	CDL	C76-C77-C78-C79
19	C	307	LFA	C6-C7-C8-C9
19	P	310	LFA	C5-C6-C7-C8
19	P	314	LFA	C10-C11-C12-C13
28	T	101	PEK	C10-C11-C12-C13
20	C	324	DMU	O16-C18-C19-C22
26	L	101	CDL	C75-C76-C77-C78
20	A	615	DMU	C28-C31-C34-C37
20	B	307	DMU	C19-C18-O16-C6
20	A	615	DMU	O16-C18-C19-C22
20	J	101	DMU	O16-C18-C19-C22
26	L	101	CDL	C76-C77-C78-C79
20	N	602	DMU	C19-C22-C25-C28
22	P	304	PGV	C14-C15-C16-C17
26	C	304	CDL	C33-C34-C35-C36
20	B	303	DMU	C34-C37-C40-C43
22	P	304	PGV	C30-C31-C32-C33
26	P	305	CDL	C57-C58-C59-C60
19	B	306	LFA	C9-C10-C11-C12
19	P	311	LFA	C7-C8-C9-C10
20	Z	102	DMU	C31-C34-C37-C40
20	O	303	DMU	C1-C6-O16-C18
20	Y	102	DMU	C31-C34-C37-C40
22	A	616	PGV	C28-C29-C30-C31
26	P	305	CDL	C19-C20-C21-C22
19	N	610	LFA	C3-C4-C5-C6
19	P	312	LFA	C3-C4-C5-C6
26	C	304	CDL	C51-C52-C53-C54
19	C	310	LFA	C1-C2-C3-C4
19	P	311	LFA	C11-C10-C9-C8
20	M	102	DMU	C22-C25-C28-C31
26	O	304	CDL	C32-C33-C34-C35
20	J	101	DMU	C34-C37-C40-C43
26	I	101	CDL	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
20	N	602	DMU	C34-C37-C40-C43
28	T	101	PEK	C17-C18-C19-C20
26	L	101	CDL	C15-C16-C17-C18
26	P	305	CDL	C21-C22-C23-C24
20	L	102	DMU	C34-C37-C40-C43
26	I	101	CDL	C18-C19-C20-C21
22	A	616	PGV	C11-C10-C9-C8
26	Y	101	CDL	C73-C74-C75-C76
26	L	101	CDL	CB3-CB4-CB6-OB8
26	P	305	CDL	CB3-CB4-CB6-OB8
20	N	611	DMU	C31-C34-C37-C40
22	A	616	PGV	C30-C31-C32-C33
20	P	323	DMU	O5-C4-C57-O61
19	C	310	LFA	C2-C3-C4-C5
20	L	102	DMU	C25-C28-C31-C34
22	N	618	PGV	C30-C31-C32-C33
28	G	101	PEK	C26-C27-C28-C29
19	B	306	LFA	C4-C5-C6-C7
20	O	303	DMU	C22-C25-C28-C31
26	O	304	CDL	C15-C16-C17-C18
19	B	306	LFA	C3-C4-C5-C6
19	N	601	LFA	C12-C13-C14-C15
19	P	301	LFA	C11-C12-C13-C14
19	T	102	LFA	C4-C5-C6-C7
26	L	101	CDL	C84-C85-C86-C87
19	C	313	LFA	C4-C5-C6-C7
20	O	307	DMU	C19-C22-C25-C28
20	Y	102	DMU	C22-C25-C28-C31
26	Y	101	CDL	OB6-CB4-CB6-OB8
19	C	312	LFA	C11-C10-C9-C8
20	B	302	DMU	C19-C22-C25-C28
28	G	101	PEK	C9-C10-C11-C12
28	G	101	PEK	C12-C13-C14-C15
28	T	101	PEK	C11-C10-C9-C8
19	C	309	LFA	C11-C12-C13-C14
26	L	101	CDL	C21-C22-C23-C24
20	Y	102	DMU	C34-C37-C40-C43
20	Q	201	DMU	C28-C31-C34-C37
26	Y	101	CDL	C61-C62-C63-C64
19	N	609	LFA	C7-C8-C9-C10
20	B	302	DMU	C25-C28-C31-C34
20	P	316	DMU	C25-C28-C31-C34

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Mol	Chain	Res	Type	Atoms
19	P	310	LFA	C13-C14-C15-C16
26	L	101	CDL	C14-C15-C16-C17
26	P	305	CDL	C53-C54-C55-C56
20	P	324	DMU	C25-C28-C31-C34
19	C	308	LFA	C3-C4-C5-C6
20	N	619	DMU	C18-C19-C22-C25
20	A	609	DMU	C34-C37-C40-C43
19	C	310	LFA	C4-C5-C6-C7
26	O	304	CDL	C18-C19-C20-C21
20	B	307	DMU	O16-C18-C19-C22
20	P	324	DMU	O16-C18-C19-C22
26	Y	101	CDL	C71-CB7-OB8-CB6
26	O	304	CDL	C72-C73-C74-C75
28	G	101	PEK	C29-C30-C31-C32
20	H	101	DMU	O5-C4-C57-O61
20	C	324	DMU	C18-C19-C22-C25
26	I	101	CDL	OB9-CB7-OB8-CB6
19	C	307	LFA	C11-C10-C9-C8
20	A	617	DMU	O16-C18-C19-C22
26	Y	101	CDL	OA5-CA3-CA4-CA6
20	Z	101	DMU	O6-C11-C9-C8
19	T	103	LFA	C7-C8-C9-C10
26	Y	101	CDL	C37-C38-C39-C40
20	Q	201	DMU	C2-C3-O7-C10
19	C	311	LFA	C10-C11-C12-C13
22	P	304	PGV	C24-C25-C26-C27
26	O	304	CDL	C71-CB7-OB8-CB6
19	A	608	LFA	C5-C6-C7-C8
26	I	101	CDL	OA9-CA7-OA8-CA6
26	Y	101	CDL	OB9-CB7-OB8-CB6
20	N	612	DMU	O16-C18-C19-C22
26	L	101	CDL	C53-C54-C55-C56
26	P	305	CDL	OB9-CB7-OB8-CB6
22	A	616	PGV	C31-C32-C33-C34
20	P	323	DMU	C22-C25-C28-C31
19	N	610	LFA	C6-C7-C8-C9
26	P	305	CDL	C54-C55-C56-C57
20	C	306	DMU	C18-C19-C22-C25
20	C	315	DMU	C18-C19-C22-C25
20	C	318	DMU	O6-C11-C9-C8
19	P	308	LFA	C2-C3-C4-C5
19	P	313	LFA	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
20	O	306	DMU	C31-C34-C37-C40
20	P	317	DMU	C22-C25-C28-C31
26	P	305	CDL	OB6-CB4-CB6-OB8
20	A	617	DMU	C34-C37-C40-C43
20	O	307	DMU	C18-C19-C22-C25
22	C	303	PGV	C21-C22-C23-C24
26	L	101	CDL	C13-C14-C15-C16
19	C	307	LFA	C3-C4-C5-C6
20	C	315	DMU	C31-C34-C37-C40
28	G	101	PEK	C27-C28-C29-C30
20	P	318	DMU	C31-C34-C37-C40
26	C	304	CDL	C18-C19-C20-C21
26	I	101	CDL	C77-C78-C79-C80
26	Y	101	CDL	C22-C23-C24-C25
19	B	306	LFA	C6-C7-C8-C9
19	N	610	LFA	C1-C2-C3-C4
19	P	308	LFA	C11-C10-C9-C8
26	L	101	CDL	C18-C19-C20-C21
26	L	101	CDL	C22-C23-C24-C25
20	B	303	DMU	C31-C34-C37-C40
19	N	609	LFA	C11-C12-C13-C14
26	C	304	CDL	C12-C11-CA5-OA6
20	O	307	DMU	C28-C31-C34-C37
26	O	304	CDL	C20-C21-C22-C23
24	P	306	CHD	C20-C22-C23-C24
26	I	101	CDL	C73-C74-C75-C76
26	Y	101	CDL	C56-C57-C58-C59
20	C	315	DMU	C25-C28-C31-C34
20	O	303	DMU	C18-C19-C22-C25
20	P	319	DMU	C28-C31-C34-C37
26	L	101	CDL	O1-C1-CB2-OB2
22	P	304	PGV	C11-C12-C13-C14
26	O	304	CDL	OB9-CB7-OB8-CB6
22	P	304	PGV	C02-C03-O11-P
20	C	317	DMU	C25-C28-C31-C34
26	Y	101	CDL	OA5-CA3-CA4-OA6
26	L	101	CDL	C36-C37-C38-C39
19	C	314	LFA	C6-C7-C8-C9
22	N	618	PGV	C14-C15-C16-C17
26	P	305	CDL	OA6-CA4-CA6-OA8
28	G	101	PEK	C4-C5-C6-C7
20	C	323	DMU	C34-C37-C40-C43

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Mol	Chain	Res	Type	Atoms
26	O	304	CDL	CA3-CA4-CA6-OA8
24	C	305	CHD	C17-C20-C22-C23
20	P	324	DMU	C3-C4-C57-O61
19	C	309	LFA	C1-C2-C3-C4
20	P	324	DMU	C4-C3-O7-C10
19	N	609	LFA	C2-C3-C4-C5
26	C	304	CDL	CA2-OA2-PA1-OA5
26	C	304	CDL	CA3-OA5-PA1-OA3
26	I	101	CDL	CA2-OA2-PA1-OA3
26	L	101	CDL	CA3-OA5-PA1-OA2
26	L	101	CDL	CA3-OA5-PA1-OA4
26	L	101	CDL	CB2-OB2-PB2-OB3
26	O	304	CDL	CB2-OB2-PB2-OB4
26	O	304	CDL	CB3-OB5-PB2-OB3
26	O	304	CDL	CB3-OB5-PB2-OB4
26	P	305	CDL	CA2-OA2-PA1-OA4
26	P	305	CDL	CA3-OA5-PA1-OA3
22	C	303	PGV	C02-C03-O11-P
26	P	305	CDL	CA4-CA3-OA5-PA1
26	Y	101	CDL	C1-CA2-OA2-PA1
26	Y	101	CDL	C20-C21-C22-C23
20	O	307	DMU	O16-C18-C19-C22
20	Z	101	DMU	O6-C11-C9-O1
20	P	318	DMU	C2-C3-O7-C10
20	P	324	DMU	C2-C3-O7-C10
19	C	314	LFA	C1-C2-C3-C4
28	T	101	PEK	C30-C31-C32-C33
19	C	307	LFA	C7-C8-C9-C10
19	C	311	LFA	C5-C6-C7-C8
20	M	102	DMU	C31-C34-C37-C40
20	C	315	DMU	C4-C3-O7-C10
26	Y	101	CDL	C21-C22-C23-C24
20	B	307	DMU	O5-C6-O16-C18
26	P	305	CDL	C72-C73-C74-C75
20	P	319	DMU	C1-C6-O16-C18
20	C	323	DMU	C22-C25-C28-C31
20	C	306	DMU	C31-C34-C37-C40
20	C	315	DMU	C34-C37-C40-C43
19	C	325	LFA	C6-C7-C8-C9
19	P	313	LFA	C9-C10-C11-C12
22	P	304	PGV	C28-C29-C30-C31
26	Y	101	CDL	C53-C54-C55-C56

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Mol	Chain	Res	Type	Atoms
26	C	304	CDL	C20-C21-C22-C23
14	A	601[A]	HEA	C19-C20-C21-C22
20	Q	201	DMU	C34-C37-C40-C43
20	O	308	DMU	C34-C37-C40-C43
22	N	618	PGV	C31-C32-C33-C34
20	C	315	DMU	C2-C3-O7-C10
20	P	318	DMU	C4-C3-O7-C10
21	N	614	EDO	O1-C1-C2-O2
20	P	317	DMU	C25-C28-C31-C34
26	L	101	CDL	C71-C72-C73-C74
26	Y	101	CDL	C33-C34-C35-C36
19	P	312	LFA	C11-C10-C9-C8
20	H	101	DMU	C28-C31-C34-C37
19	N	610	LFA	C2-C3-C4-C5
19	O	302	LFA	C2-C3-C4-C5
20	B	303	DMU	C19-C18-O16-C6
20	C	317	DMU	C19-C18-O16-C6
20	P	317	DMU	C19-C18-O16-C6
26	C	304	CDL	C36-C37-C38-C39
19	T	102	LFA	C2-C3-C4-C5
20	H	101	DMU	C18-C19-C22-C25
20	B	303	DMU	C18-C19-C22-C25
22	P	304	PGV	C11-C10-C9-C8
20	C	306	DMU	C28-C31-C34-C37
20	B	307	DMU	C25-C28-C31-C34
19	C	312	LFA	C4-C5-C6-C7
19	N	601	LFA	C2-C3-C4-C5
26	L	101	CDL	C31-C32-C33-C34
28	G	101	PEK	C25-C26-C27-C28
20	C	323	DMU	C18-C19-C22-C25
26	L	101	CDL	C16-C17-C18-C19
19	P	308	LFA	C7-C8-C9-C10
26	P	305	CDL	C73-C74-C75-C76
20	C	317	DMU	C22-C25-C28-C31
26	O	304	CDL	C11-C12-C13-C14
28	T	101	PEK	O02-C1-O01-C02
20	Q	201	DMU	O5-C4-C57-O61
19	C	311	LFA	C6-C7-C8-C9
26	I	101	CDL	CB2-C1-CA2-OA2
26	L	101	CDL	C19-C20-C21-C22
20	L	102	DMU	C19-C22-C25-C28
28	G	101	PEK	C13-C14-C15-C16

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Mol	Chain	Res	Type	Atoms
26	I	101	CDL	C75-C76-C77-C78
26	P	305	CDL	C33-C34-C35-C36
26	I	101	CDL	CA3-CA4-OA6-CA5
24	O	301	CHD	C22-C23-C24-O25
21	P	321	EDO	O1-C1-C2-O2
21	R	203	EDO	O1-C1-C2-O2
26	Y	101	CDL	C52-C53-C54-C55
24	C	305	CHD	C22-C23-C24-O26
26	L	101	CDL	C78-C79-C80-C81
26	P	305	CDL	C12-C11-CA5-OA6
26	C	304	CDL	C57-C58-C59-C60
24	C	305	CHD	C22-C23-C24-O25
26	O	304	CDL	CB4-CB3-OB5-PB2
19	C	325	LFA	C12-C13-C14-C15
19	C	310	LFA	C6-C7-C8-C9
26	Y	101	CDL	C57-C58-C59-C60
14	A	602	HEA	CAD-CBD-CGD-O2D
24	O	301	CHD	C22-C23-C24-O26
26	C	304	CDL	C79-C80-C81-C82
26	C	304	CDL	OB6-CB4-CB6-OB8
24	B	305	CHD	C22-C23-C24-O25
19	P	311	LFA	C3-C4-C5-C6
26	L	101	CDL	CA2-C1-CB2-OB2
20	P	316	DMU	C31-C34-C37-C40
14	A	602	HEA	CAD-CBD-CGD-O1D
20	B	307	DMU	C34-C37-C40-C43
20	P	317	DMU	O5-C4-C57-O61
19	B	306	LFA	C1-C2-C3-C4
19	C	314	LFA	C10-C11-C12-C13
24	P	302	CHD	C22-C23-C24-O26
20	A	609	DMU	C31-C34-C37-C40
22	C	303	PGV	C29-C30-C31-C32
22	N	618	PGV	C15-C16-C17-C18
14	A	601[A]	HEA	CAD-CBD-CGD-O1D
14	A	601[B]	HEA	CAD-CBD-CGD-O1D
26	I	101	CDL	C74-C75-C76-C77
26	Y	101	CDL	CB3-CB4-CB6-OB8
24	C	301	CHD	C22-C23-C24-O26
14	N	604	HEA	CAA-CBA-CGA-O2A
20	P	318	DMU	C34-C37-C40-C43
20	J	101	DMU	C19-C22-C25-C28
19	N	601	LFA	C11-C10-C9-C8

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Mol	Chain	Res	Type	Atoms
14	A	602	HEA	CAA-CBA-CGA-O1A
22	A	616	PGV	C15-C16-C17-C18
20	O	307	DMU	C22-C25-C28-C31
22	A	616	PGV	O03-C19-C20-C21
14	A	602	HEA	CAA-CBA-CGA-O2A
19	A	608	LFA	C6-C7-C8-C9
19	B	306	LFA	C11-C10-C9-C8
19	P	312	LFA	C4-C5-C6-C7
26	O	304	CDL	OB5-CB3-CB4-CB6
14	N	604	HEA	CAD-CBD-CGD-O2D
24	P	306	CHD	C22-C23-C24-O25
24	P	306	CHD	C22-C23-C24-O26
19	B	306	LFA	C14-C15-C16-C17
22	P	304	PGV	C27-C28-C29-C30
14	N	604	HEA	CAA-CBA-CGA-O1A
14	N	604	HEA	CAD-CBD-CGD-O1D
19	C	325	LFA	C11-C12-C13-C14
26	L	101	CDL	C56-C57-C58-C59
20	Q	201	DMU	C31-C34-C37-C40
19	P	312	LFA	C2-C3-C4-C5
20	A	610	DMU	C4-C3-O7-C10
19	P	313	LFA	C11-C10-C9-C8
22	N	618	PGV	O03-C19-C20-C21
28	T	101	PEK	C35-C36-C37-C38
24	B	305	CHD	C22-C23-C24-O26
19	C	313	LFA	C9-C10-C11-C12
20	B	307	DMU	C31-C34-C37-C40
24	C	301	CHD	C22-C23-C24-O25
24	P	302	CHD	C22-C23-C24-O25
20	C	323	DMU	C1-C6-O16-C18
26	L	101	CDL	C80-C81-C82-C83
14	N	603[A]	HEA	CAD-CBD-CGD-O1D
14	N	603[B]	HEA	CAD-CBD-CGD-O1D
22	C	303	PGV	C05-C04-O12-P
19	N	601	LFA	C7-C8-C9-C10
26	P	305	CDL	CA2-C1-CB2-OB2
19	C	313	LFA	C1-C2-C3-C4
20	B	302	DMU	C31-C34-C37-C40
20	P	315	DMU	C4-C3-O7-C10
26	I	101	CDL	C79-C80-C81-C82
22	C	303	PGV	C1-C2-C3-C4
26	P	305	CDL	C17-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
20	P	318	DMU	O16-C18-C19-C22
19	T	102	LFA	C5-C6-C7-C8
21	F	103	EDO	O1-C1-C2-O2
21	R	201	EDO	O1-C1-C2-O2
20	P	315	DMU	C28-C31-C34-C37
20	M	101	DMU	C25-C28-C31-C34
26	O	304	CDL	C32-C31-CA7-OA8
14	N	603[A]	HEA	C2C-C3C-CAC-CBC
14	N	603[B]	HEA	C2C-C3C-CAC-CBC
28	T	101	PEK	C2-C1-O01-C02
26	I	101	CDL	CB4-CB3-OB5-PB2
19	P	301	LFA	C12-C13-C14-C15
20	D	201	DMU	C19-C22-C25-C28
26	O	304	CDL	C72-C71-CB7-OB8
20	A	610	DMU	C2-C3-O7-C10
26	P	305	CDL	C55-C56-C57-C58
20	D	201	DMU	O16-C18-C19-C22
26	Y	101	CDL	C32-C33-C34-C35
19	C	310	LFA	C5-C6-C7-C8
14	N	603[A]	HEA	CAD-CBD-CGD-O2D
14	N	603[B]	HEA	CAD-CBD-CGD-O2D
19	P	309	LFA	C2-C3-C4-C5
26	P	305	CDL	C52-C53-C54-C55
26	L	101	CDL	C64-C65-C66-C67
26	C	304	CDL	C52-C51-CB5-OB6
26	Y	101	CDL	C72-C71-CB7-OB8
20	P	317	DMU	C19-C22-C25-C28
19	N	610	LFA	C11-C10-C9-C8
20	M	102	DMU	C28-C31-C34-C37
20	C	315	DMU	O1-C10-O7-C3
14	N	603[A]	HEA	C19-C20-C21-C22
20	L	102	DMU	O5-C6-O16-C18
14	A	601[A]	HEA	CAD-CBD-CGD-O2D
14	A	601[B]	HEA	CAD-CBD-CGD-O2D
26	L	101	CDL	C60-C61-C62-C63
19	A	607	LFA	C7-C8-C9-C10
20	A	615	DMU	C22-C25-C28-C31
21	A	612	EDO	O1-C1-C2-O2
21	A	614	EDO	O1-C1-C2-O2
21	E	203	EDO	O1-C1-C2-O2
19	C	307	LFA	C2-C3-C4-C5
26	P	305	CDL	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
20	N	619	DMU	C19-C22-C25-C28
19	C	314	LFA	C2-C3-C4-C5
26	Y	101	CDL	C77-C78-C79-C80
26	L	101	CDL	C72-C71-CB7-OB8
22	P	304	PGV	C1-C2-C3-C4
28	T	101	PEK	C25-C26-C27-C28
20	W	101	DMU	C18-C19-C22-C25
28	G	101	PEK	C32-C33-C34-C35
22	C	303	PGV	C9-C10-C11-C12
19	C	314	LFA	C3-C4-C5-C6
20	O	306	DMU	C18-C19-C22-C25
20	O	308	DMU	C18-C19-C22-C25
19	O	302	LFA	C1-C2-C3-C4
26	O	304	CDL	C32-C31-CA7-OA9
26	O	304	CDL	C72-C71-CB7-OB9
26	Y	101	CDL	C72-C71-CB7-OB9
26	L	101	CDL	C77-C78-C79-C80
26	Y	101	CDL	C34-C35-C36-C37
26	C	304	CDL	C52-C51-CB5-OB7
19	T	102	LFA	C1-C2-C3-C4
26	C	304	CDL	C12-C11-CA5-OA7
20	M	102	DMU	C34-C37-C40-C43
20	C	324	DMU	C22-C25-C28-C31
20	C	317	DMU	C3-C4-C57-O61
20	C	319	DMU	O5-C6-O16-C18
26	L	101	CDL	C72-C71-CB7-OB9
26	Y	101	CDL	C38-C39-C40-C41
28	T	101	PEK	O01-C1-C2-C3
20	P	315	DMU	O1-C10-O7-C3
19	C	325	LFA	C1-C2-C3-C4

There are no ring outliers.

49 monomers are involved in 126 short contacts:

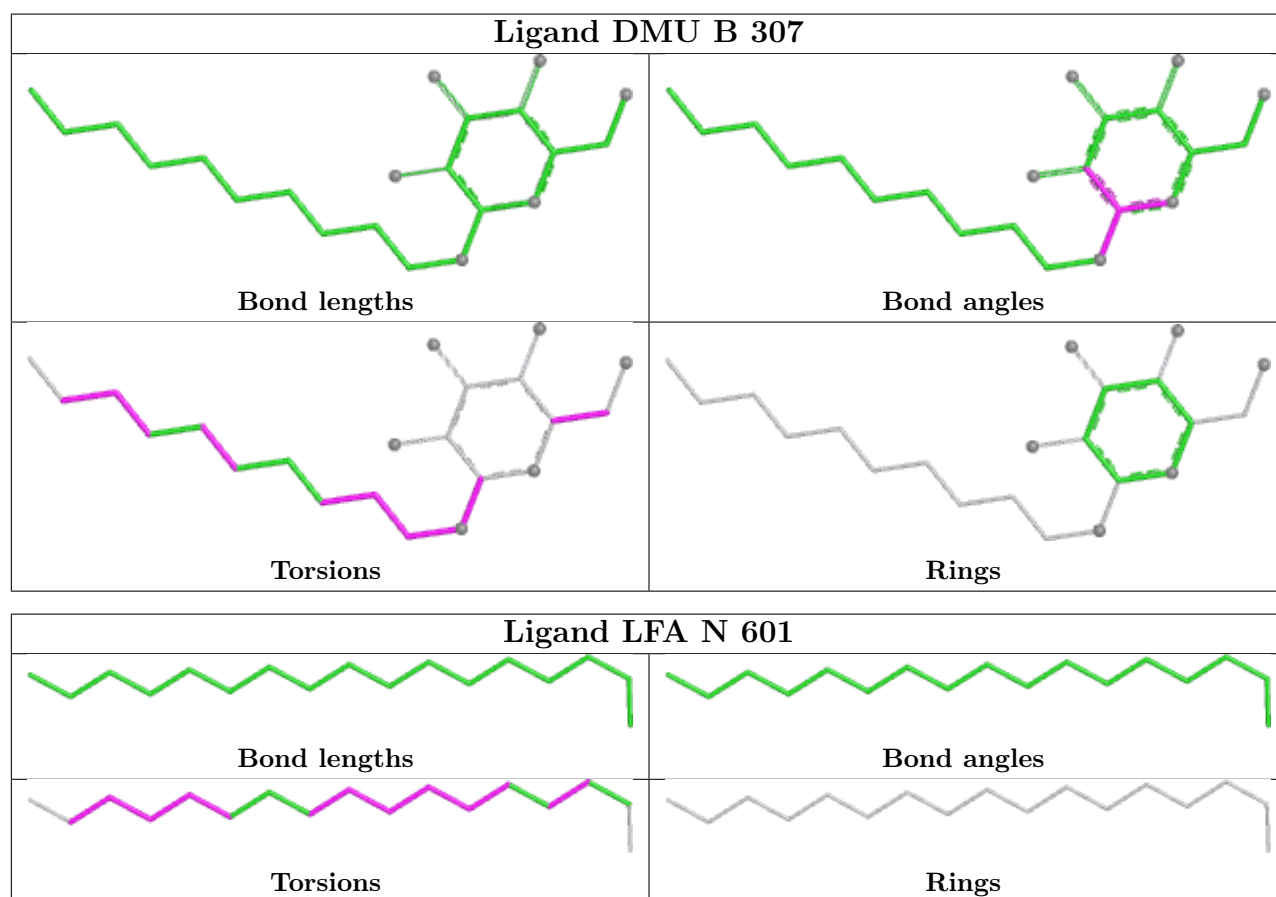
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	N	601	LFA	1	0
26	P	305	CDL	10	0
14	N	603[A]	HEA	1	0
28	G	101	PEK	2	0
19	C	312	LFA	1	0
19	N	610	LFA	3	0
14	A	601[B]	HEA	1	0

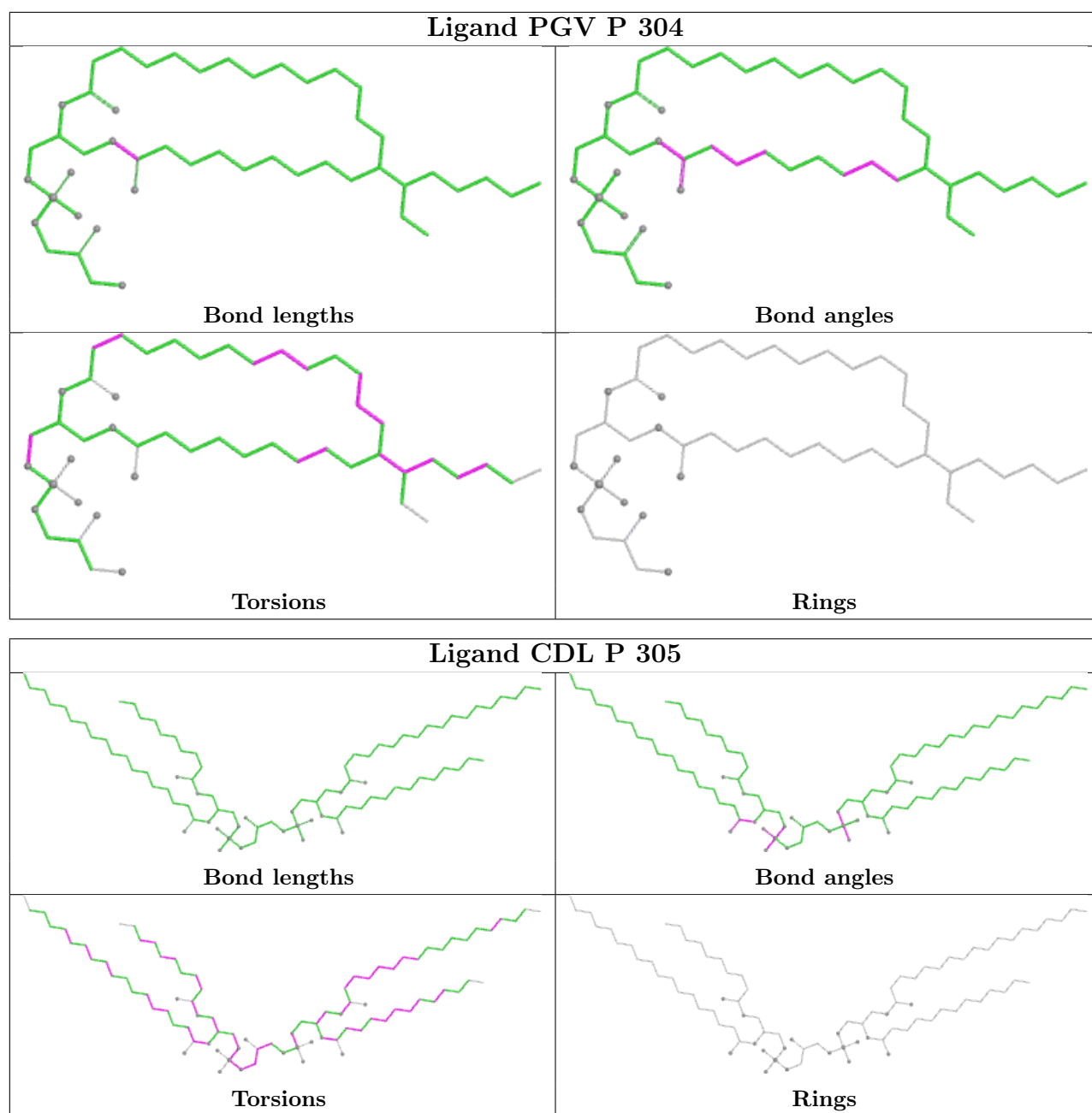
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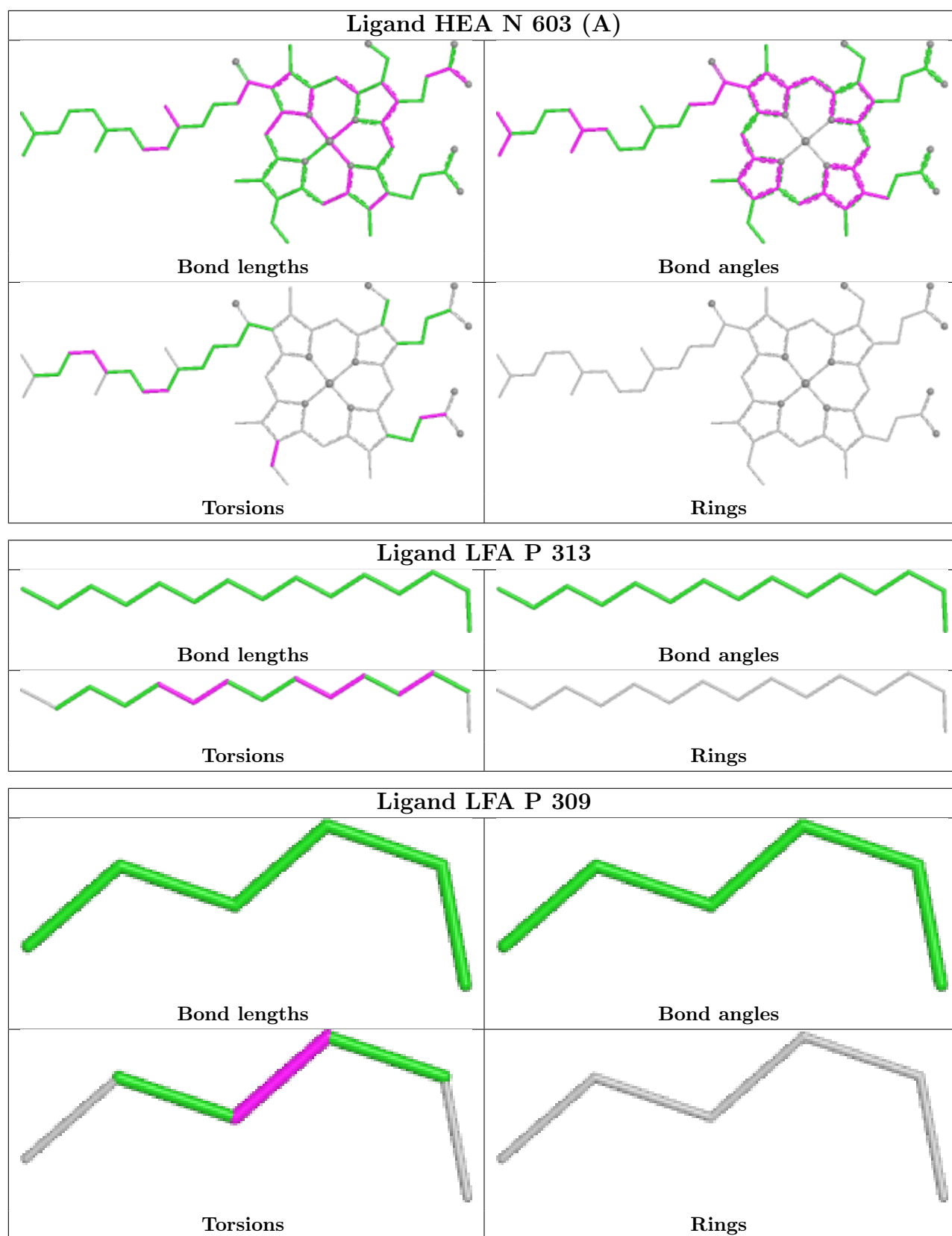
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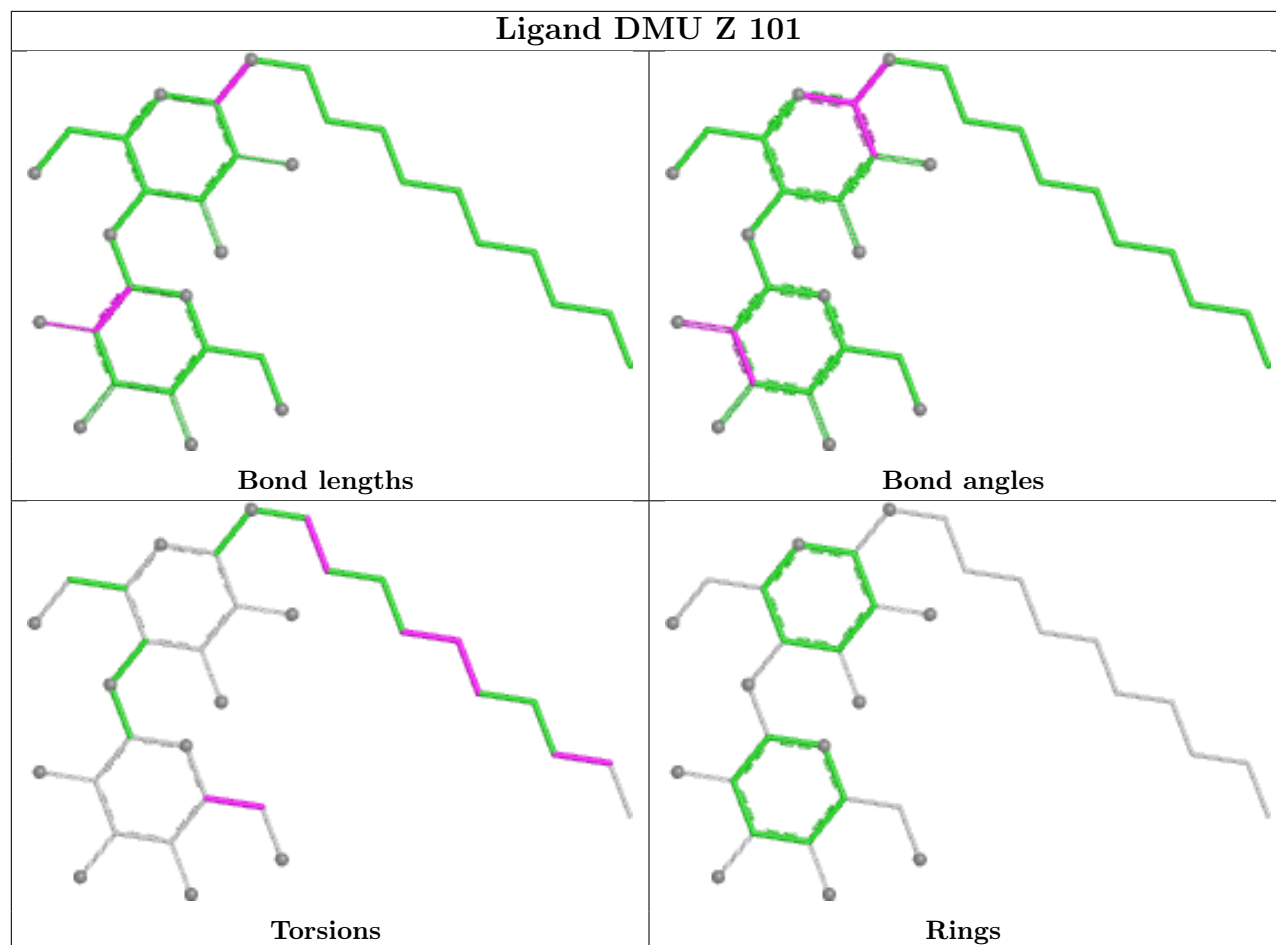
Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	N	608	PER	1	0
20	Q	201	DMU	2	0
19	O	302	LFA	4	0
21	P	321	EDO	1	0
22	A	616	PGV	1	0
20	A	609	DMU	1	0
20	D	201	DMU	4	0
20	A	610	DMU	1	0
14	A	601[A]	HEA	3	0
19	C	313	LFA	1	0
26	O	304	CDL	1	0
19	A	607	LFA	5	0
19	P	311	LFA	1	0
22	N	618	PGV	1	0
24	O	301	CHD	1	0
19	A	608	LFA	12	0
19	P	308	LFA	2	0
26	Y	101	CDL	4	0
20	Y	102	DMU	2	0
20	H	101	DMU	1	0
20	M	101	DMU	1	0
24	P	306	CHD	4	0
20	C	324	DMU	8	0
19	C	307	LFA	2	0
20	C	323	DMU	1	0
22	C	303	PGV	2	0
26	L	101	CDL	3	0
26	C	304	CDL	17	0
19	P	310	LFA	2	0
19	P	312	LFA	1	0
19	N	609	LFA	3	0
14	N	603[B]	HEA	1	0
19	C	314	LFA	1	0
19	B	306	LFA	3	0
21	N	617	EDO	2	0
28	T	101	PEK	4	0
18	A	606	PER	1	0
20	C	318	DMU	1	0
24	C	305	CHD	1	0
14	N	604	HEA	1	0
20	L	102	DMU	2	0
20	P	324	DMU	2	0

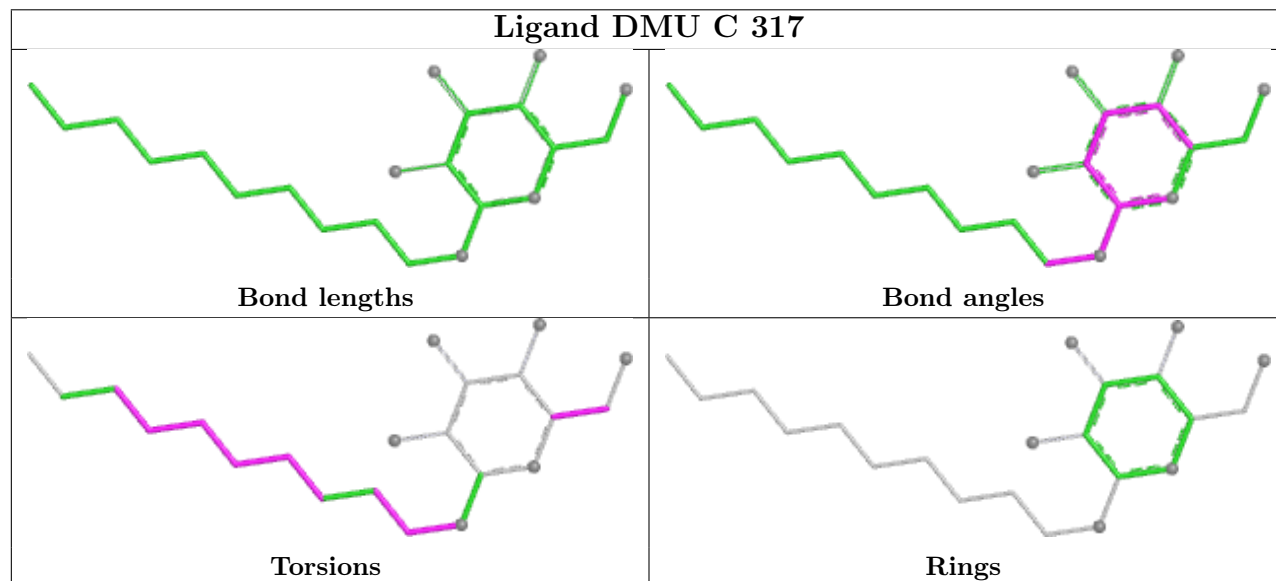
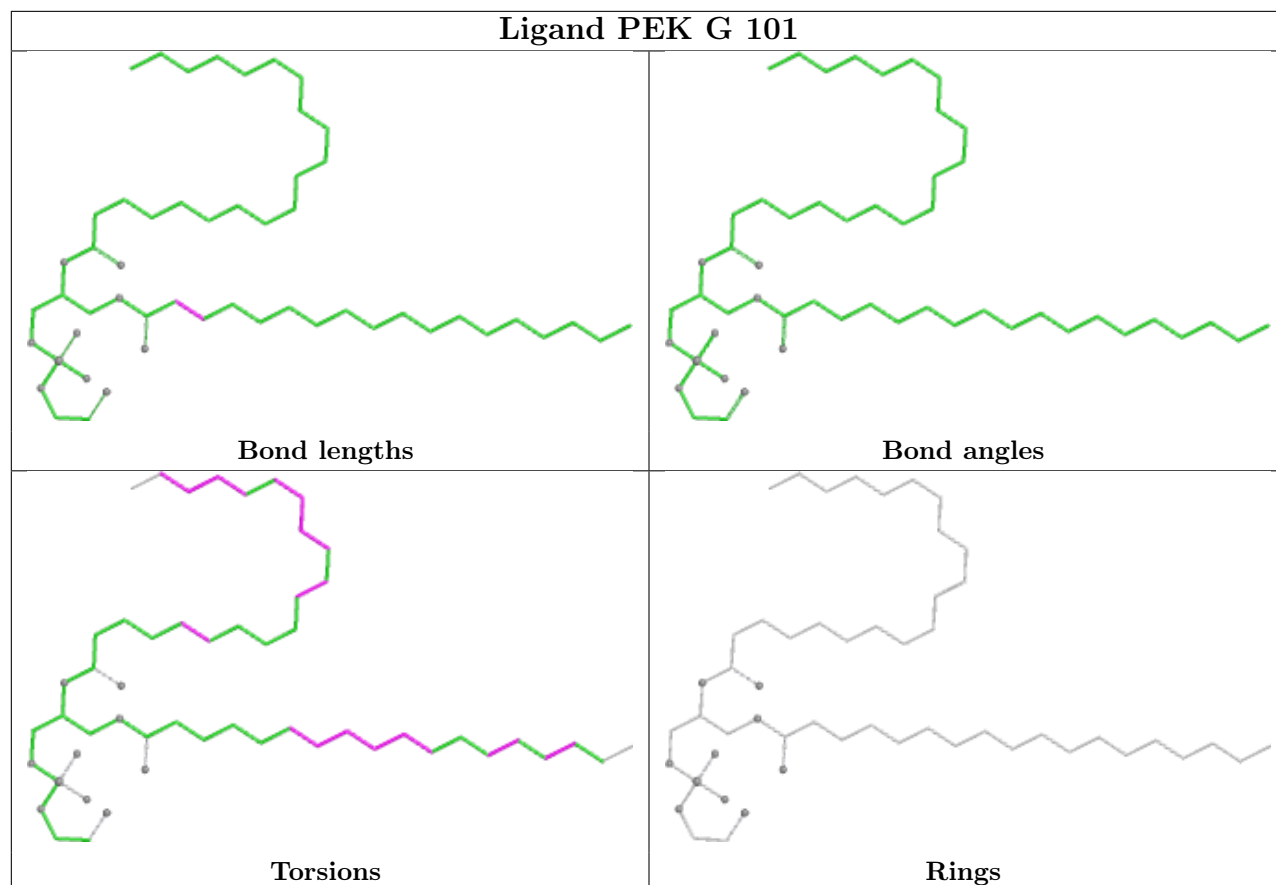
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

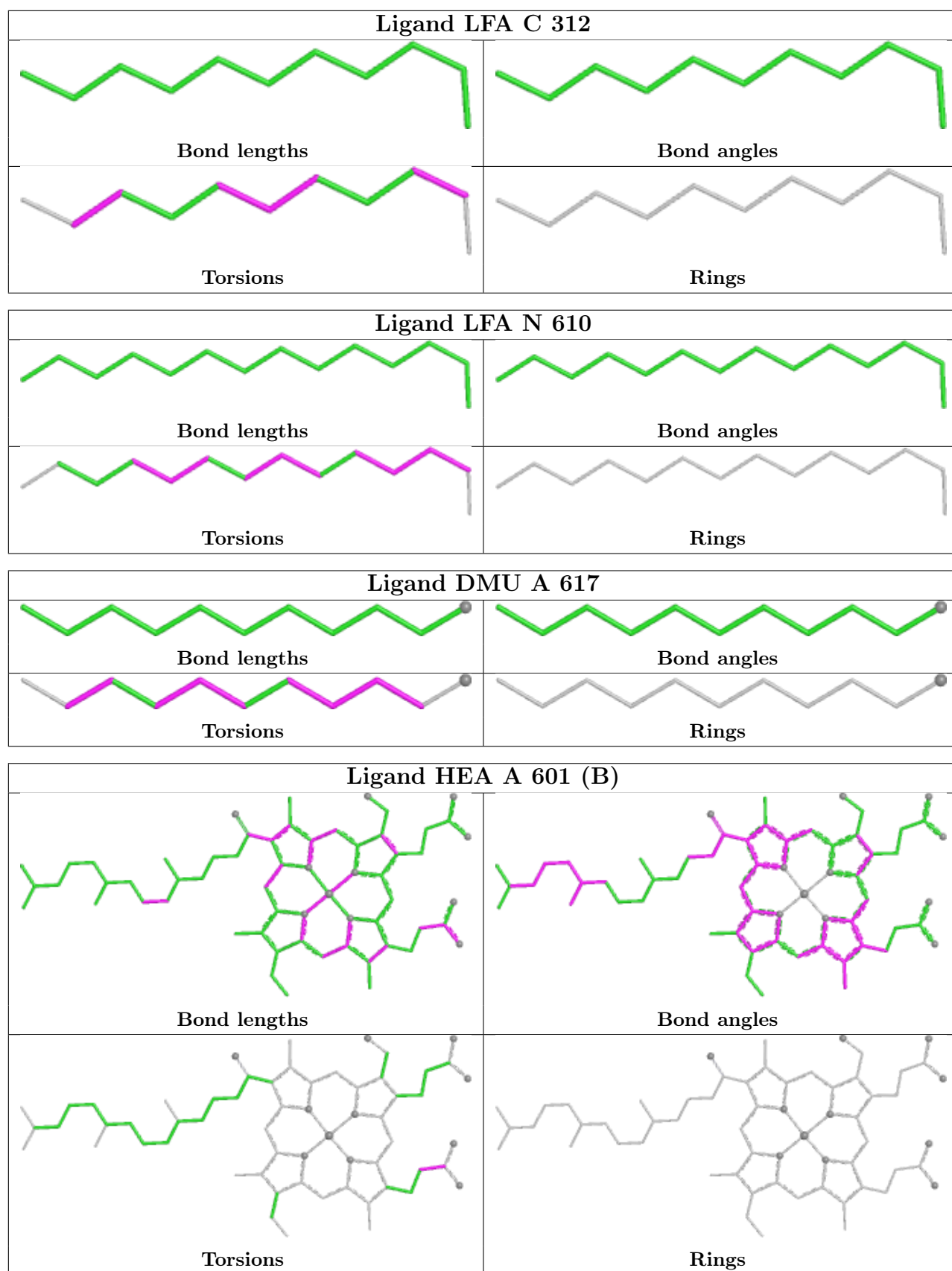


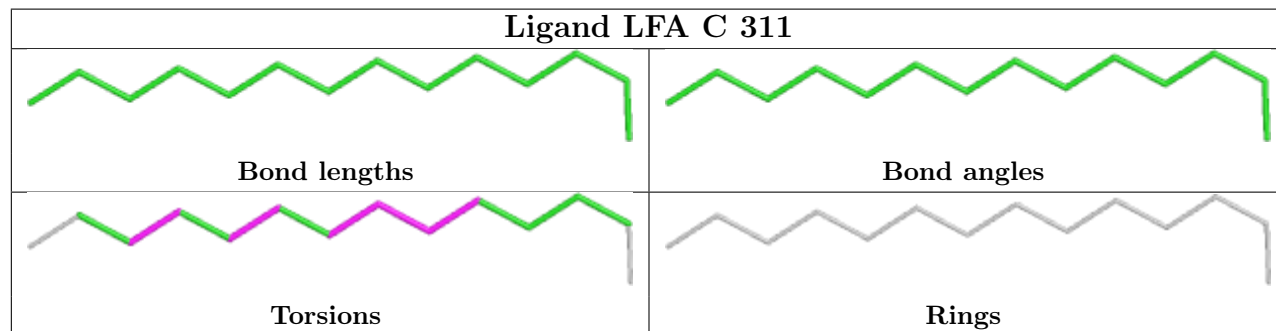
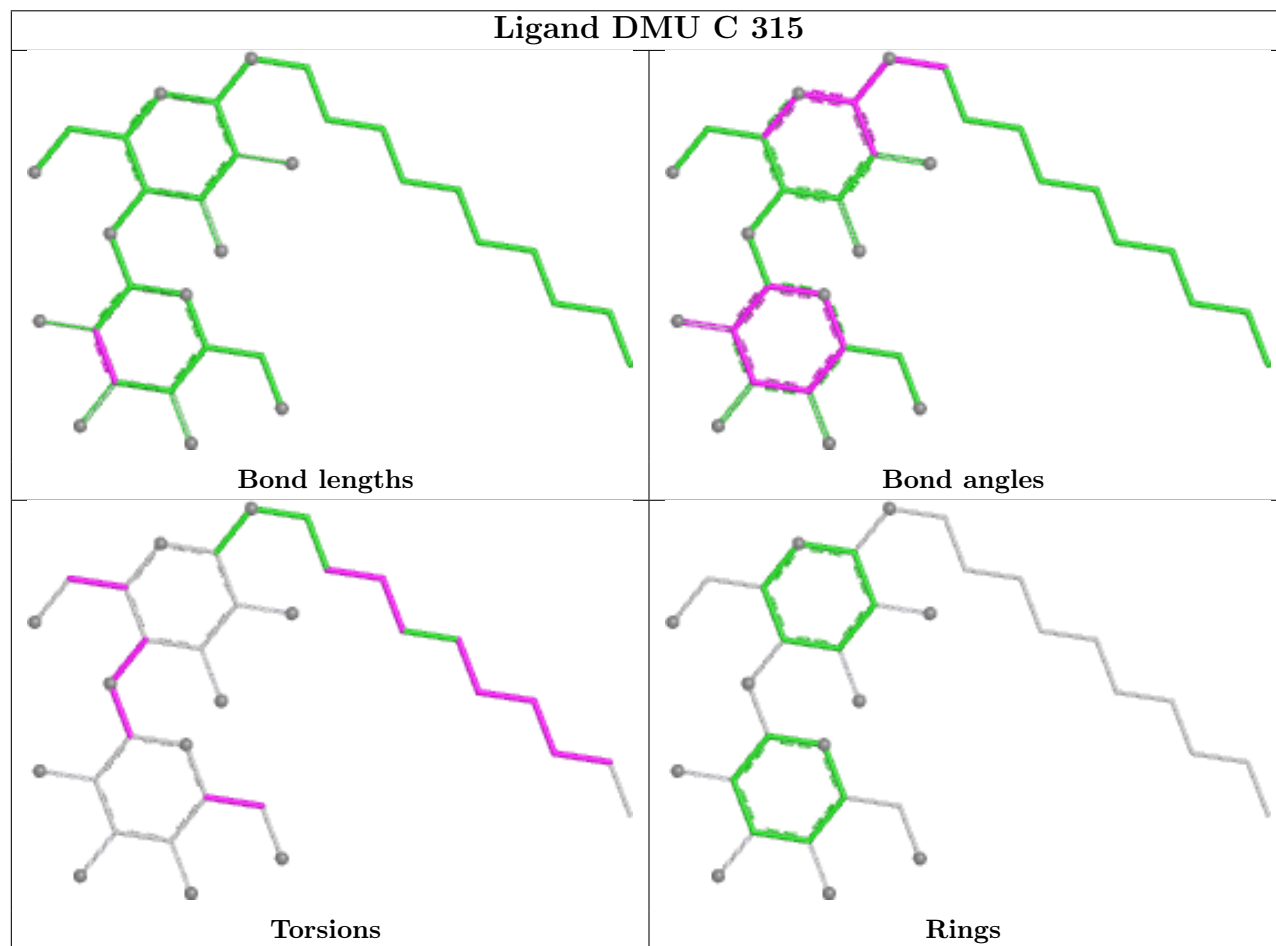
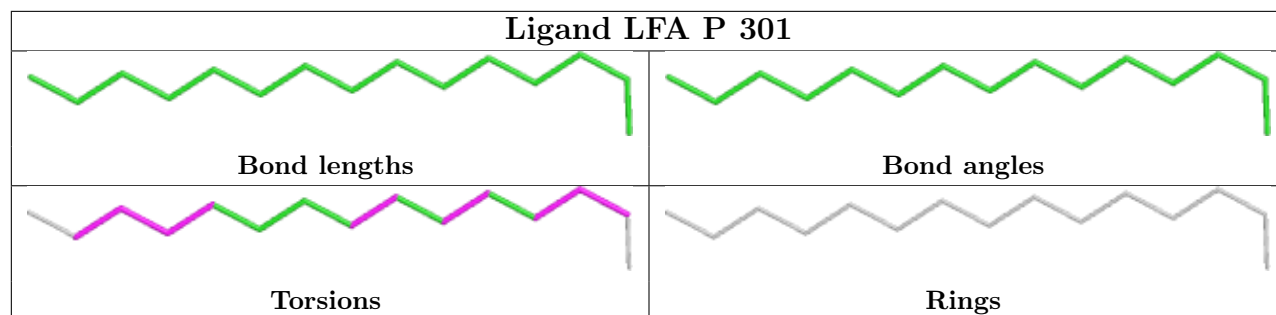


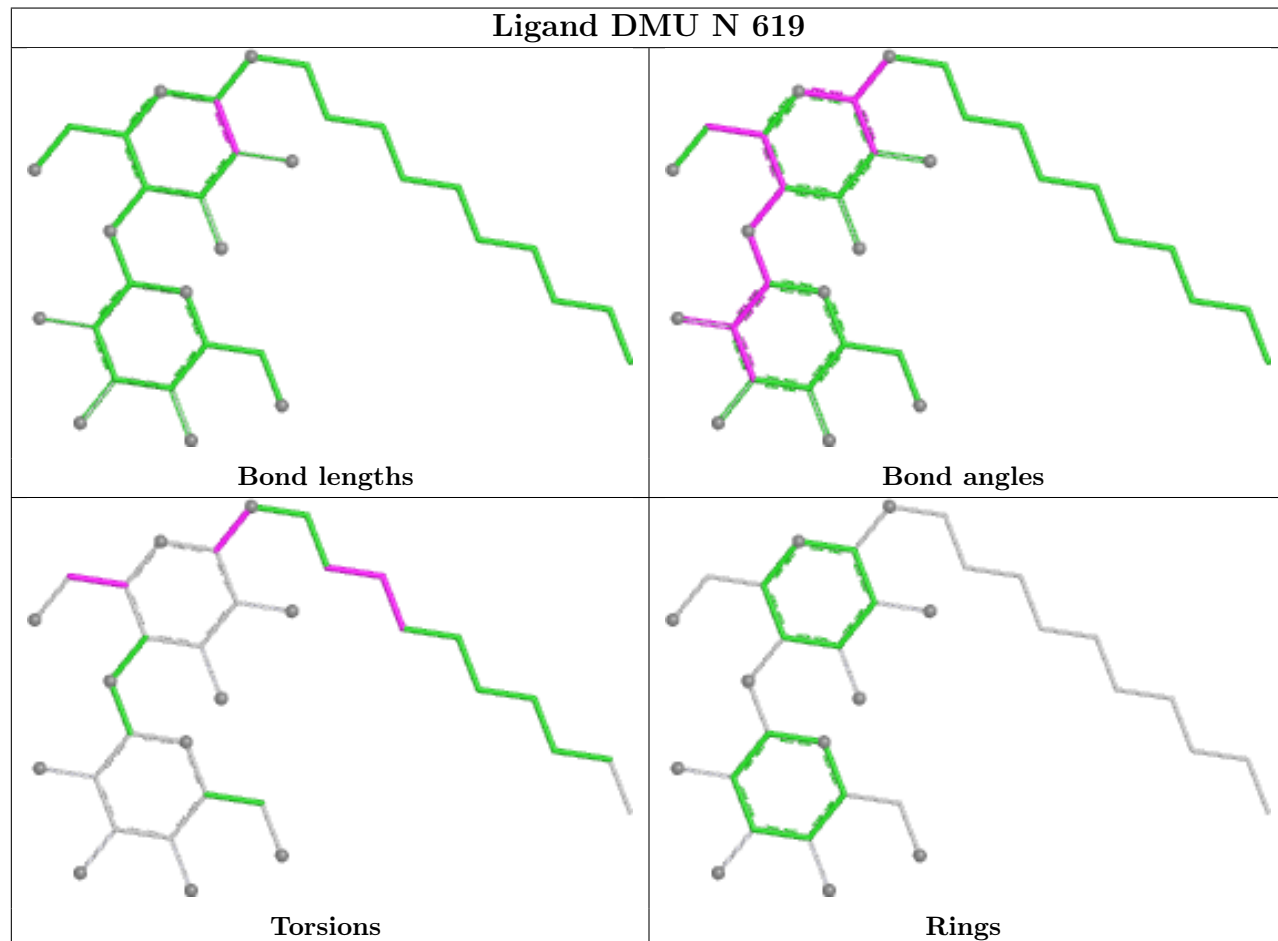
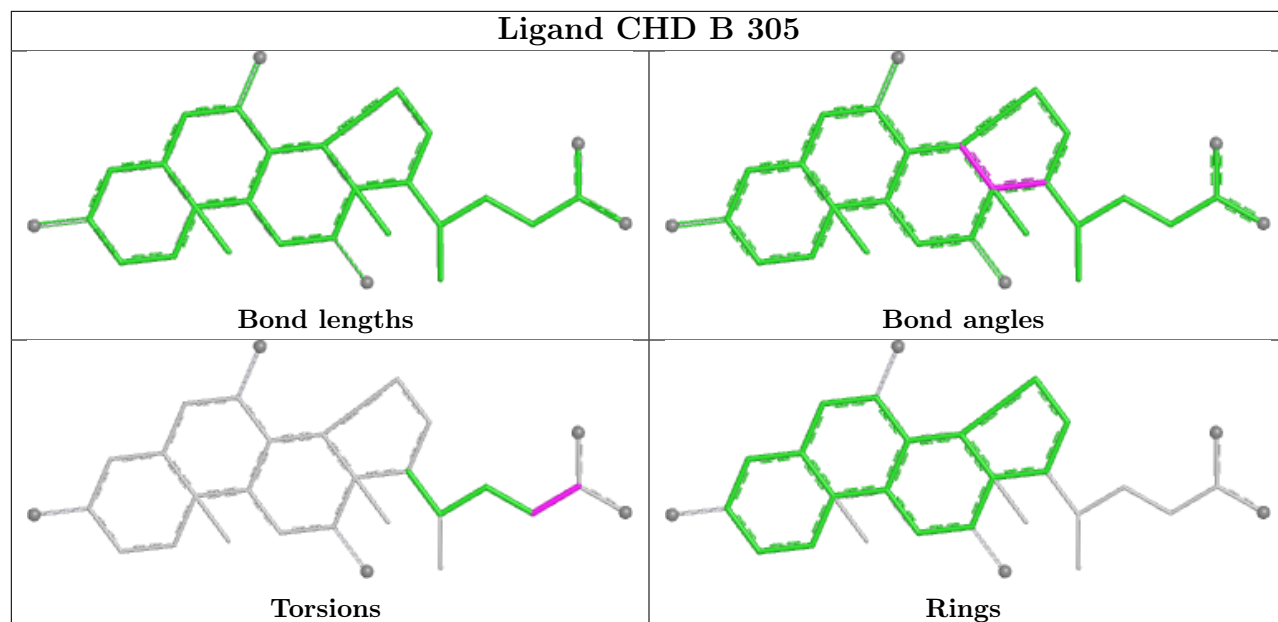


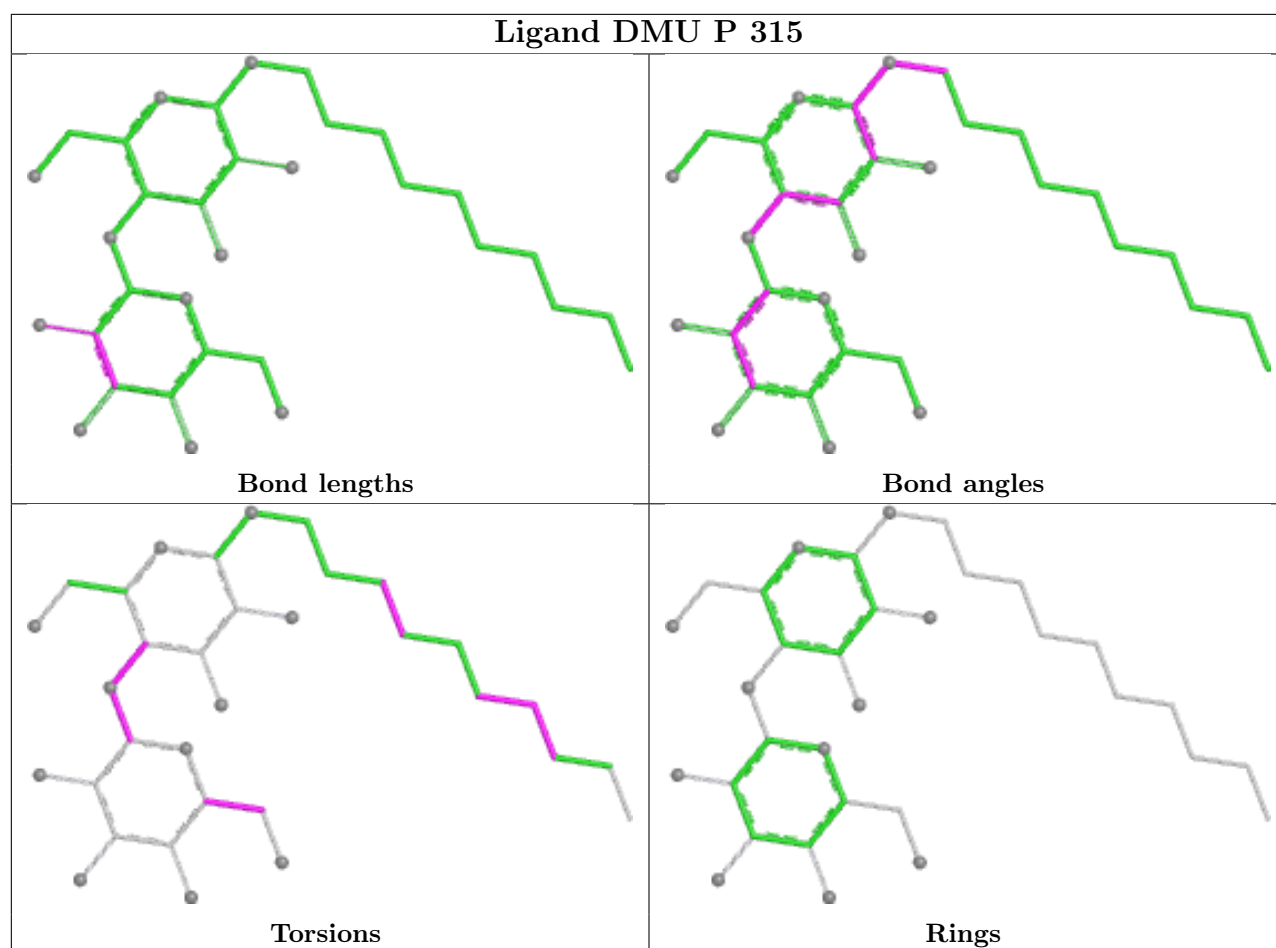


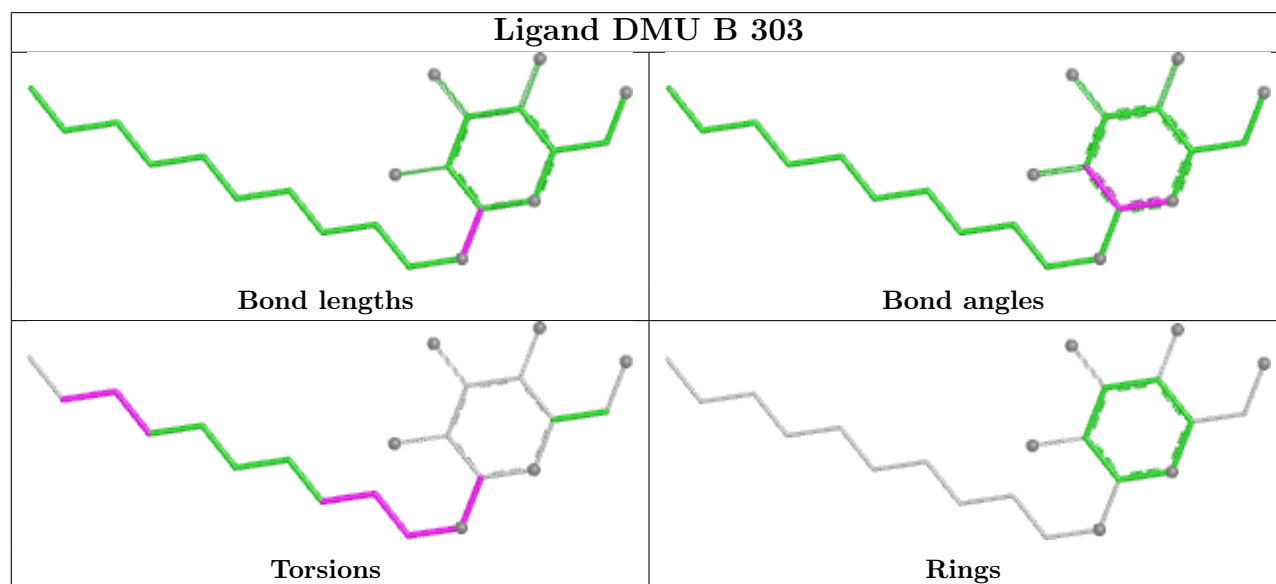
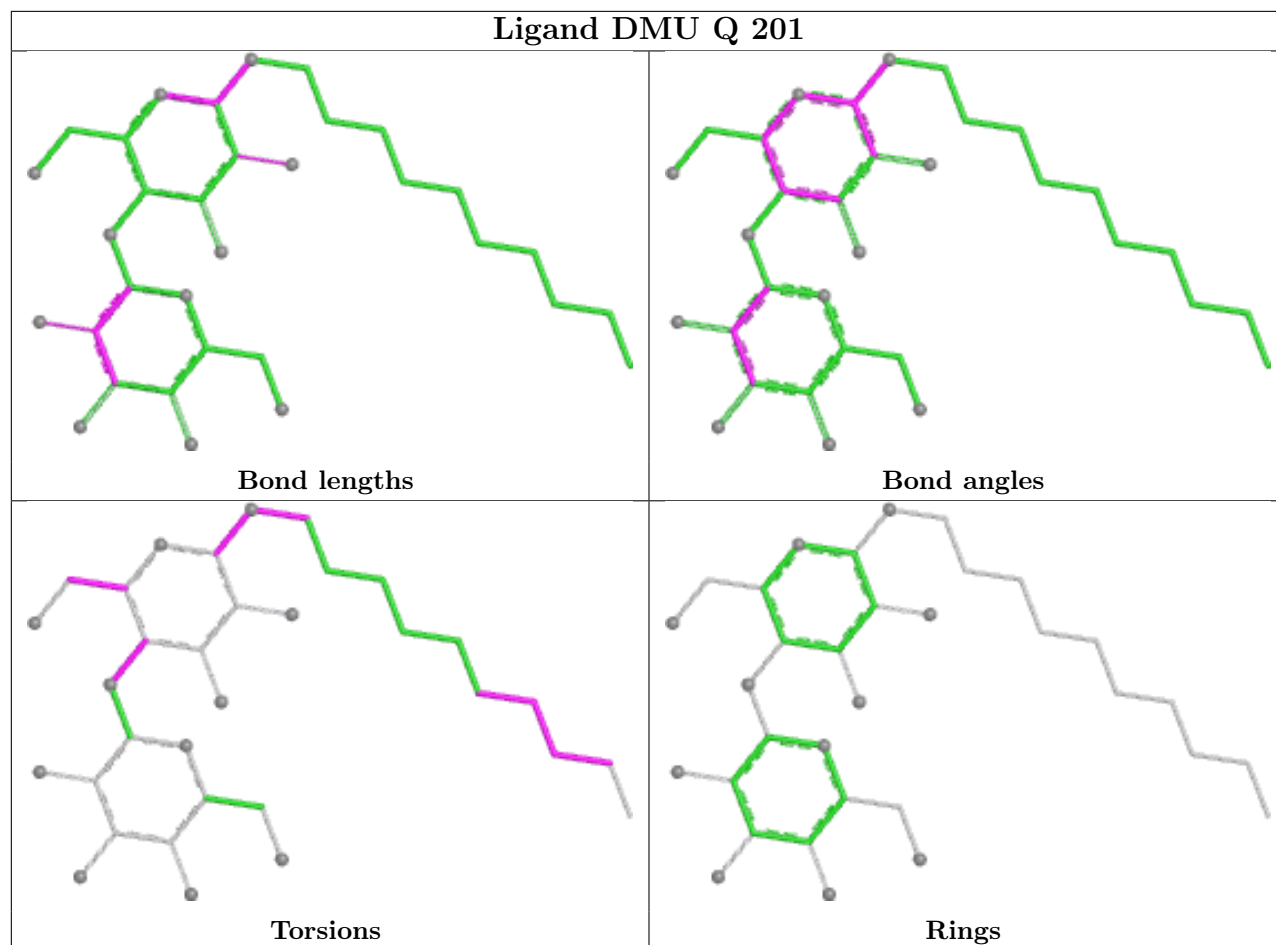


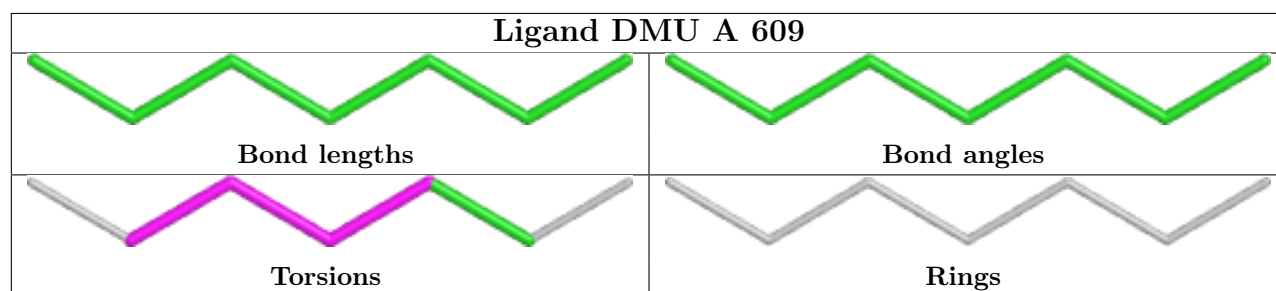
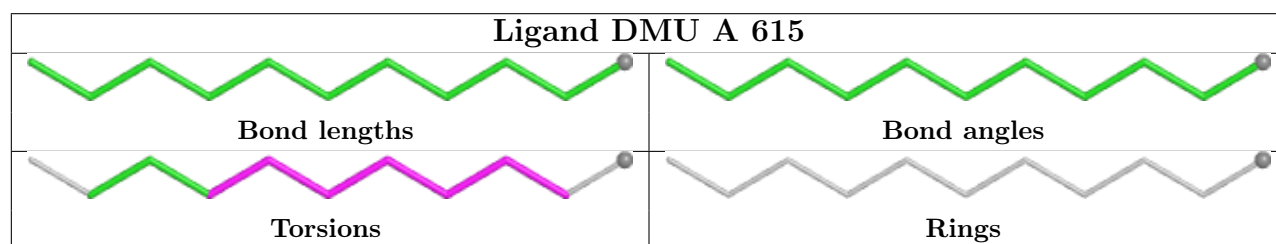
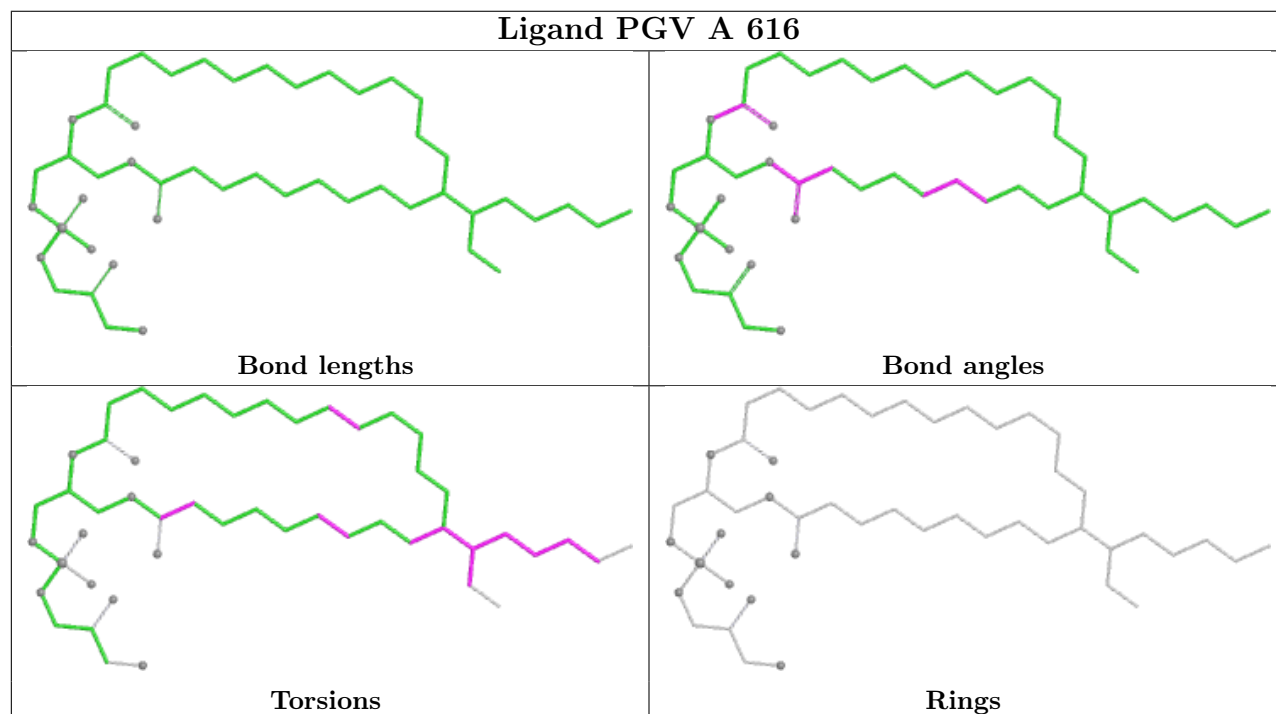
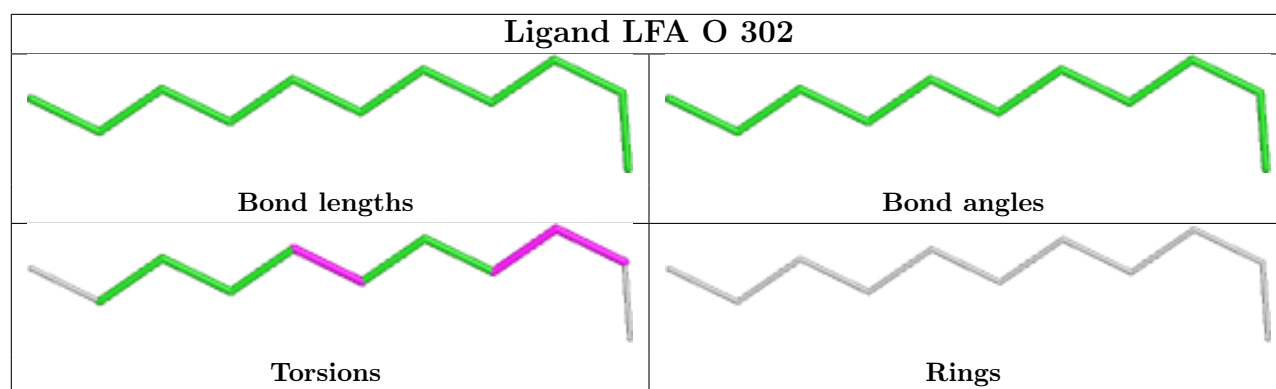


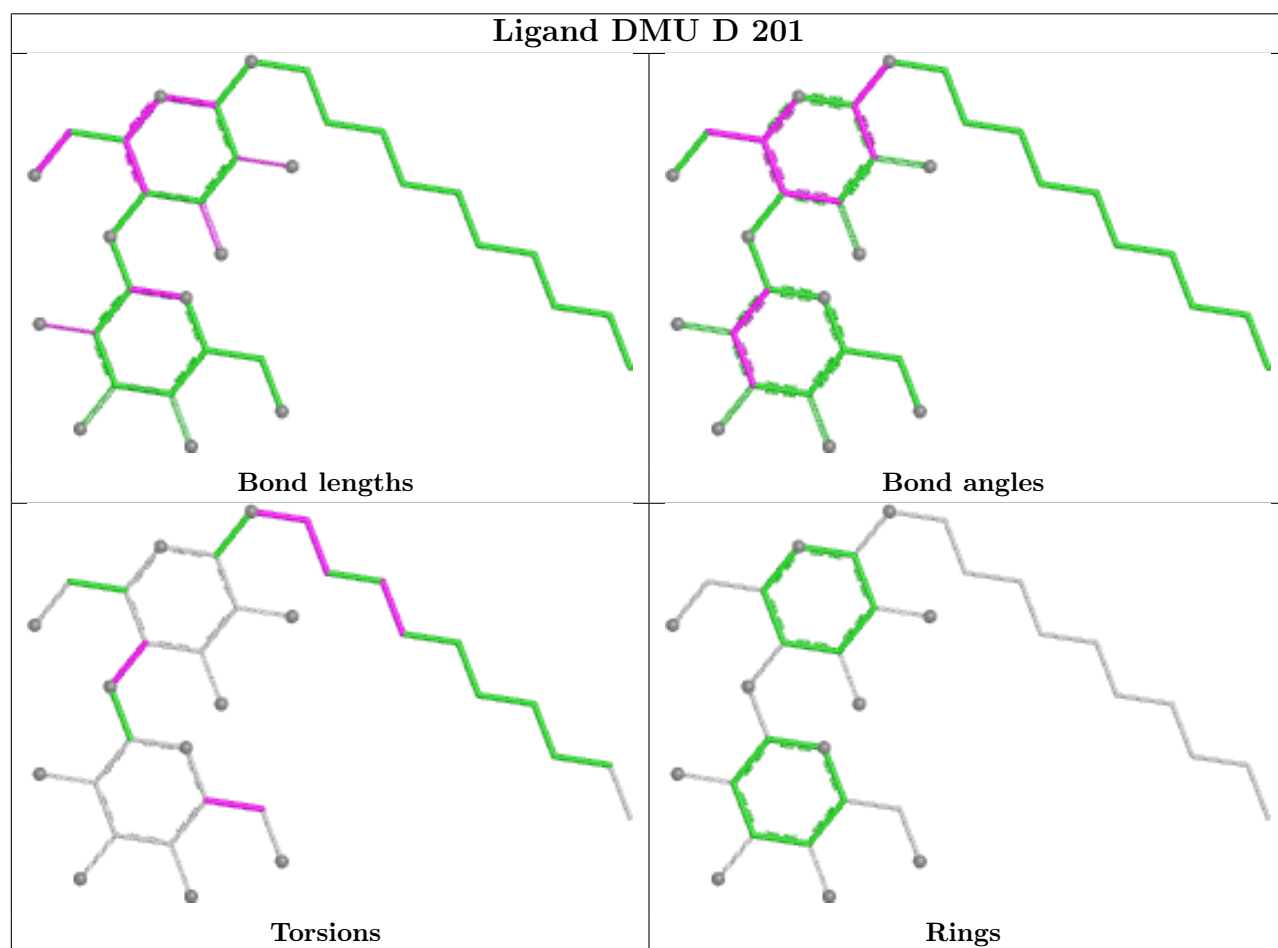
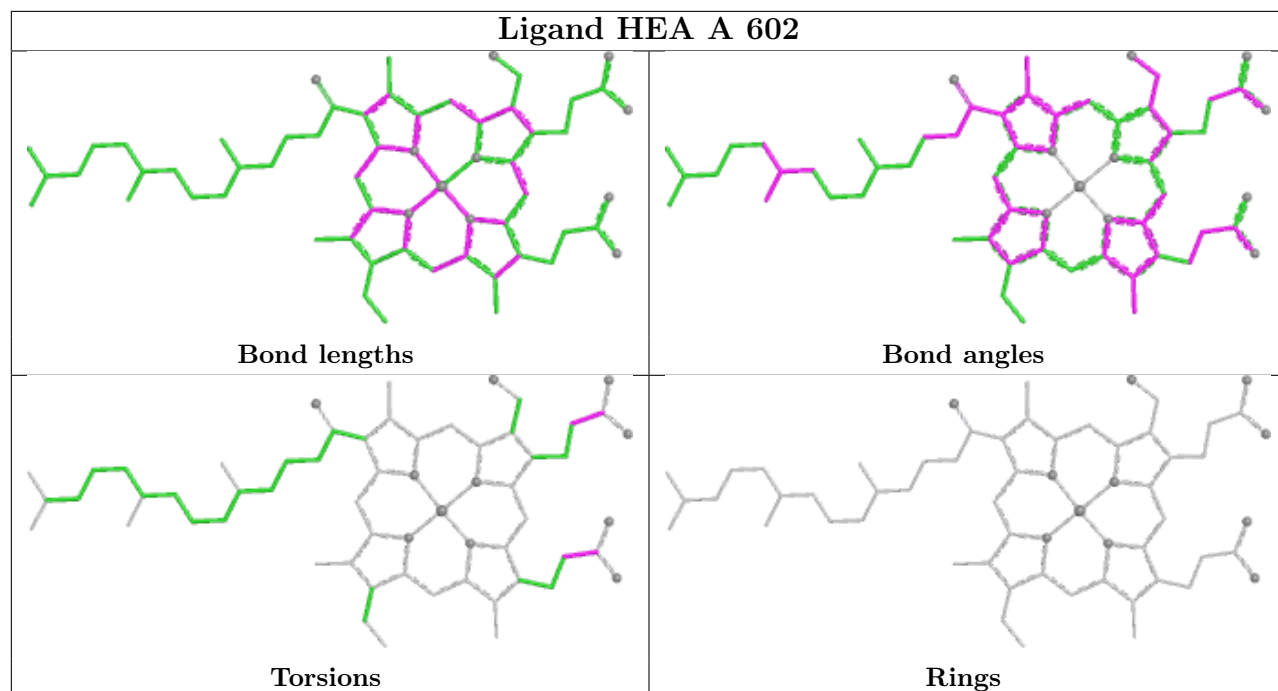


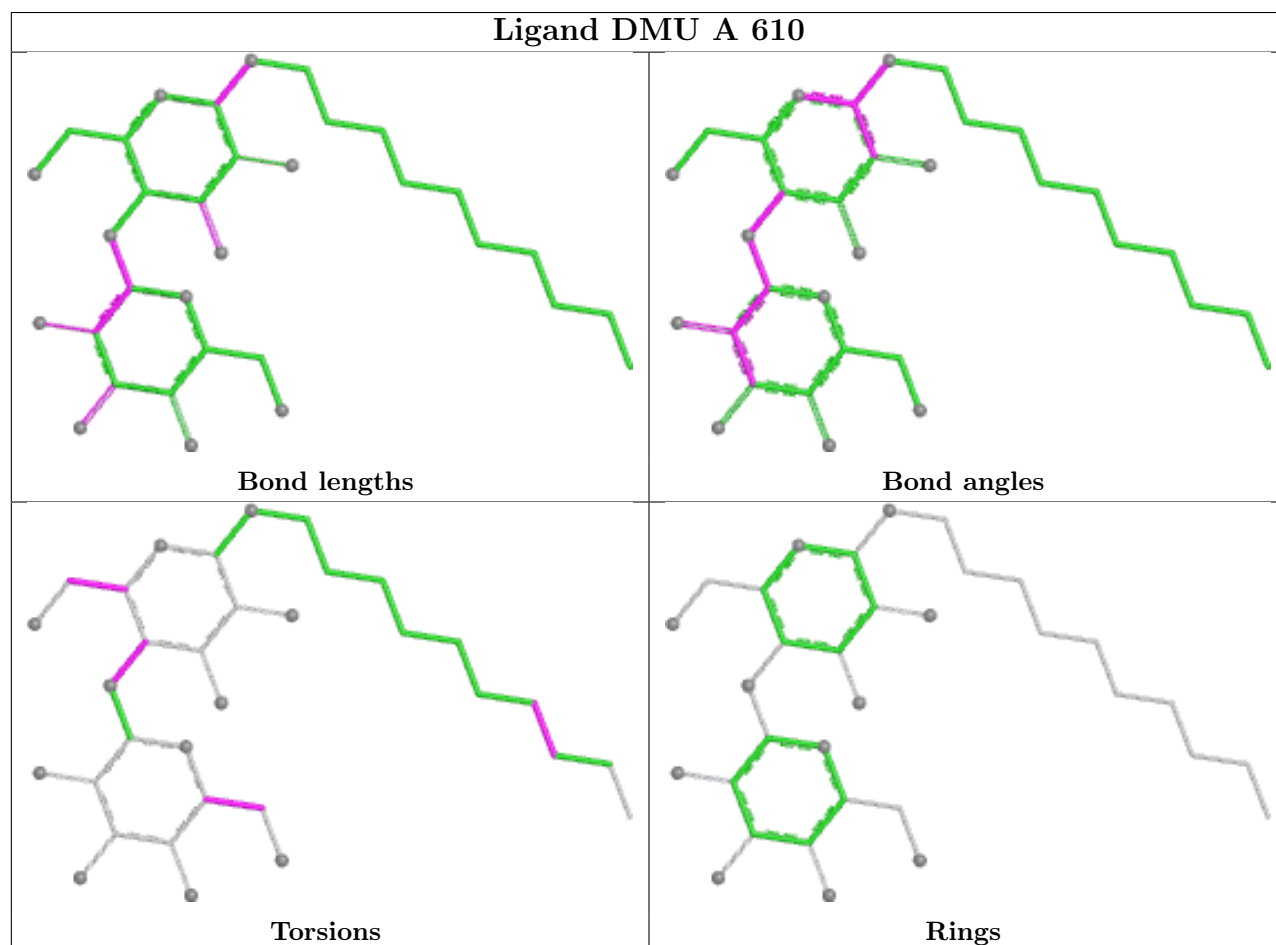
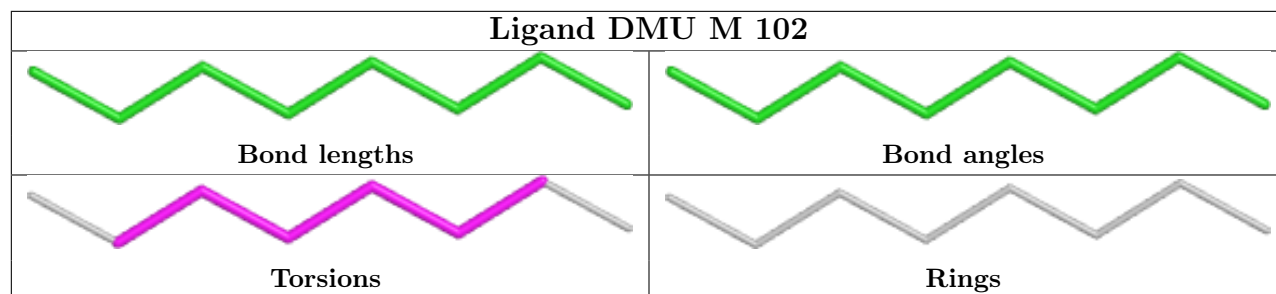


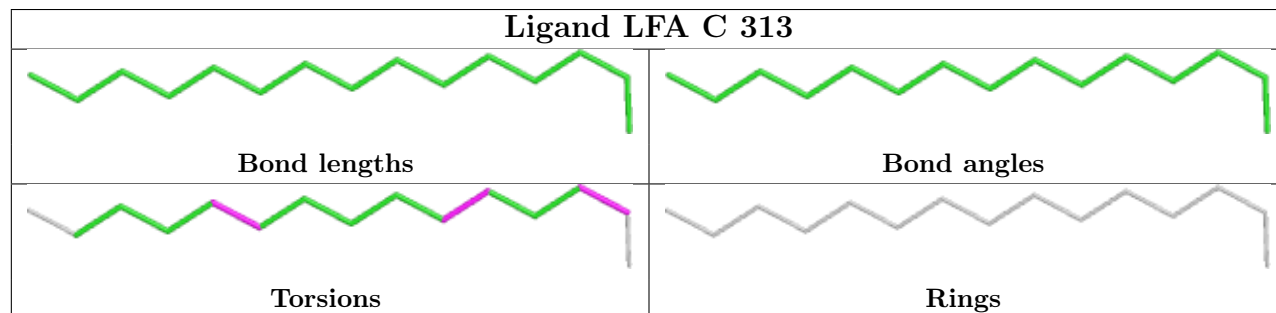
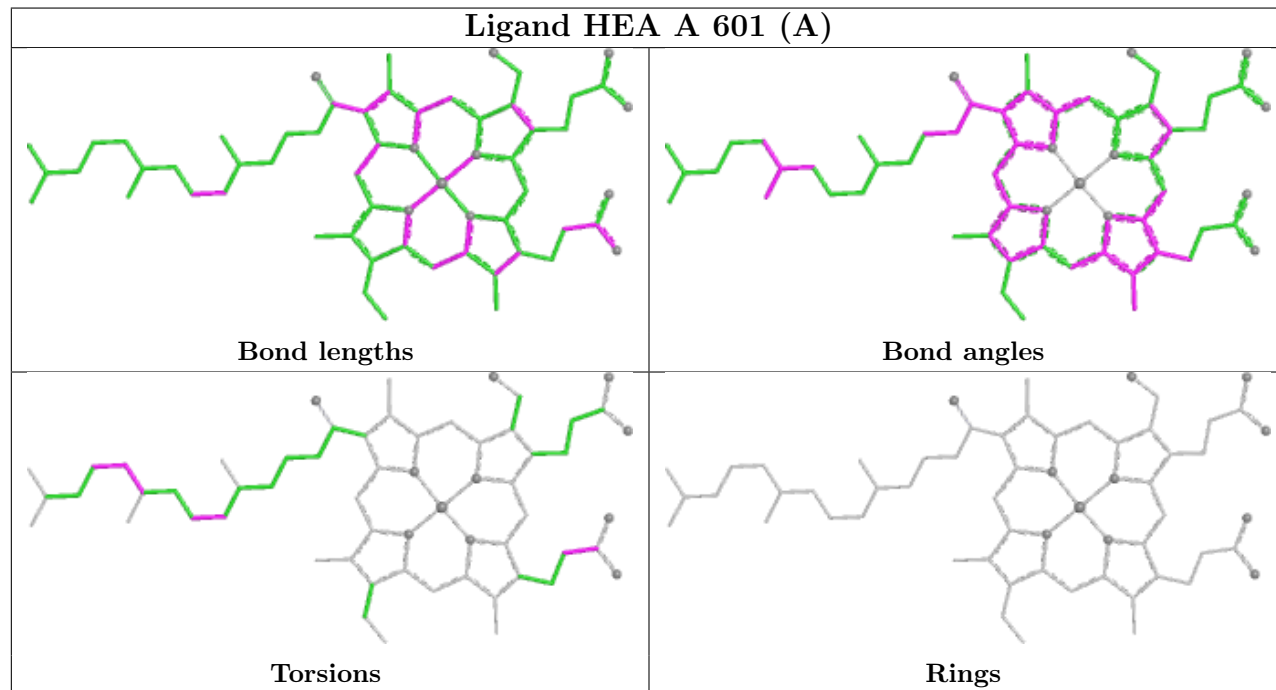
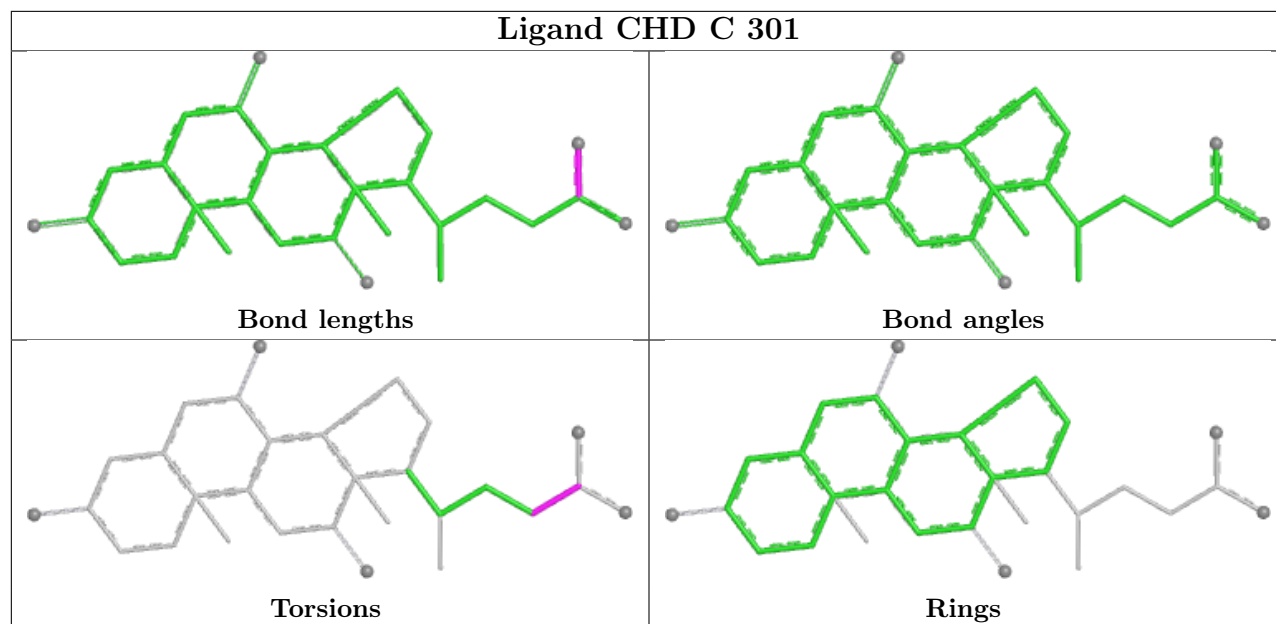


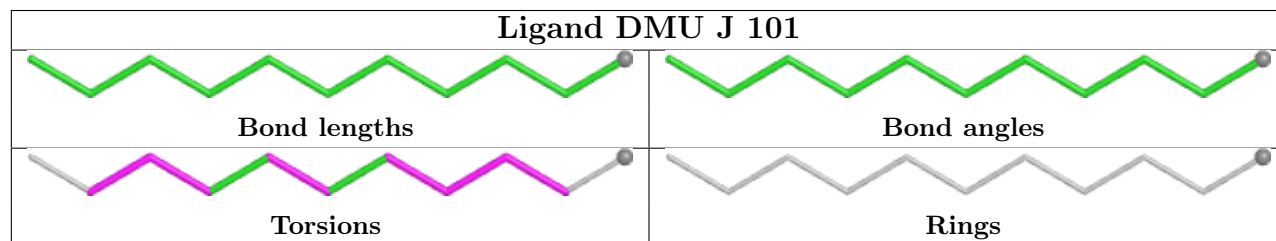
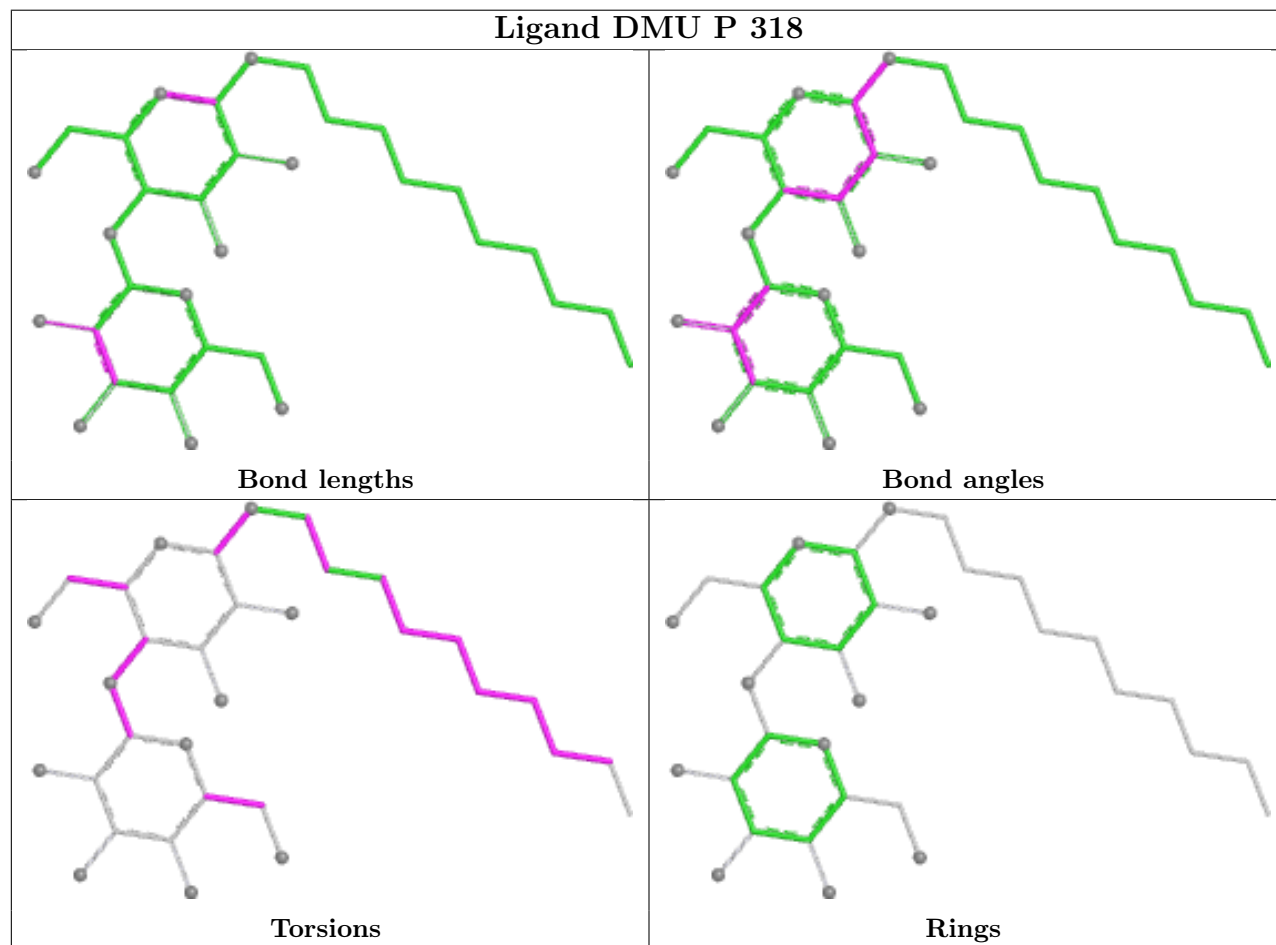
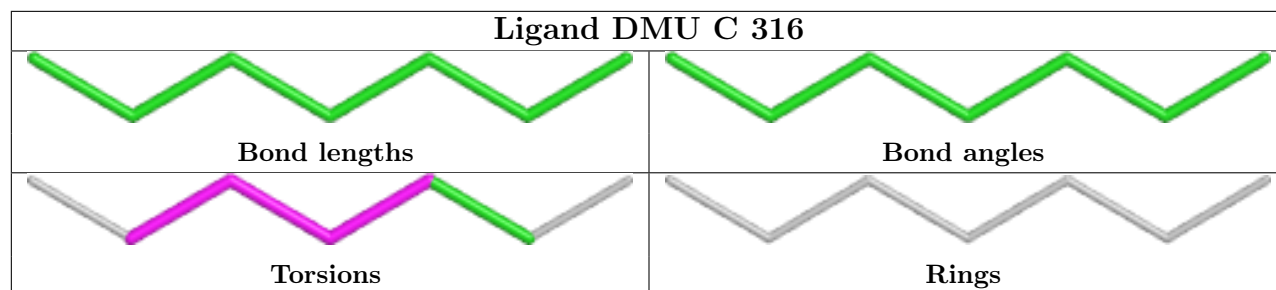


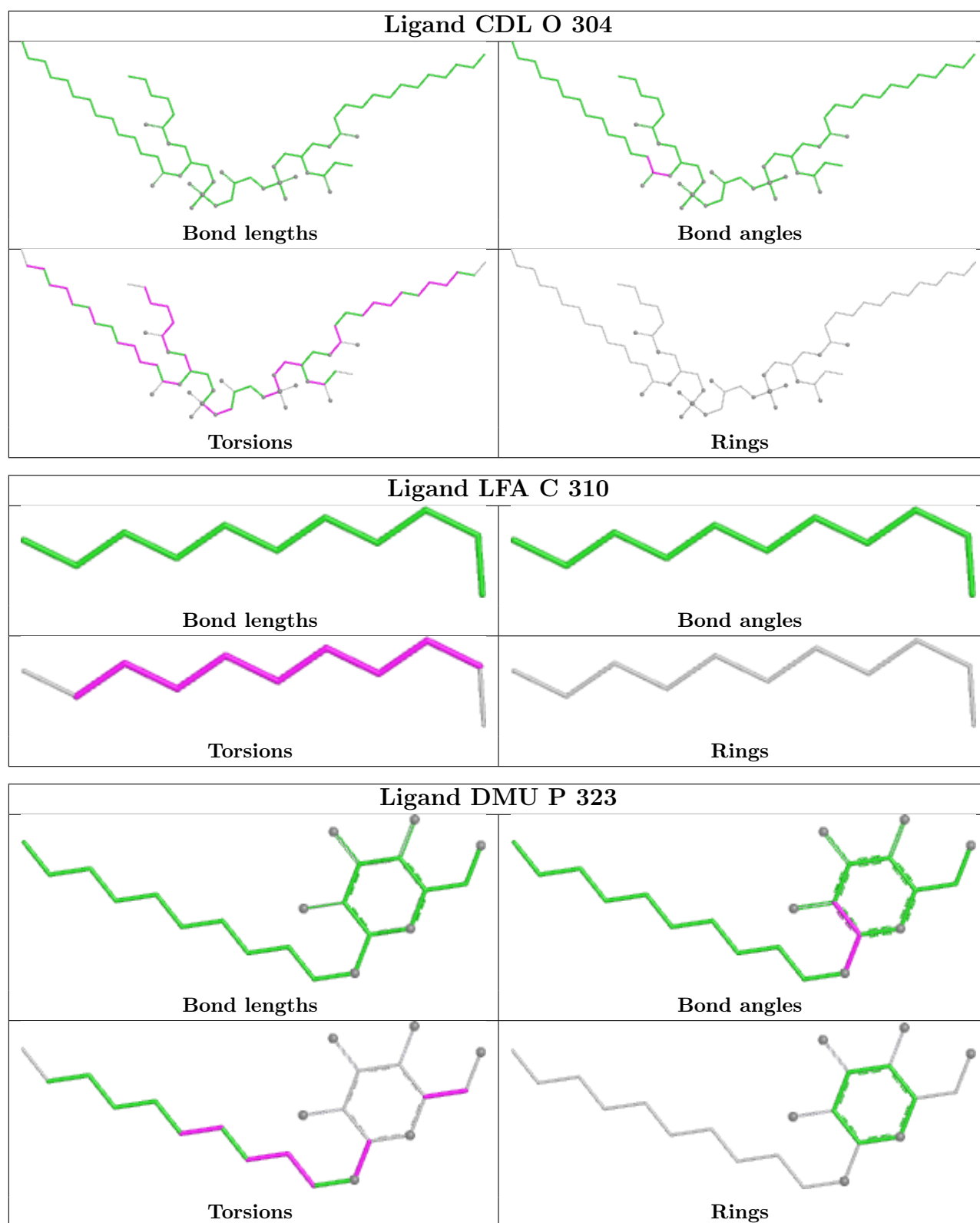


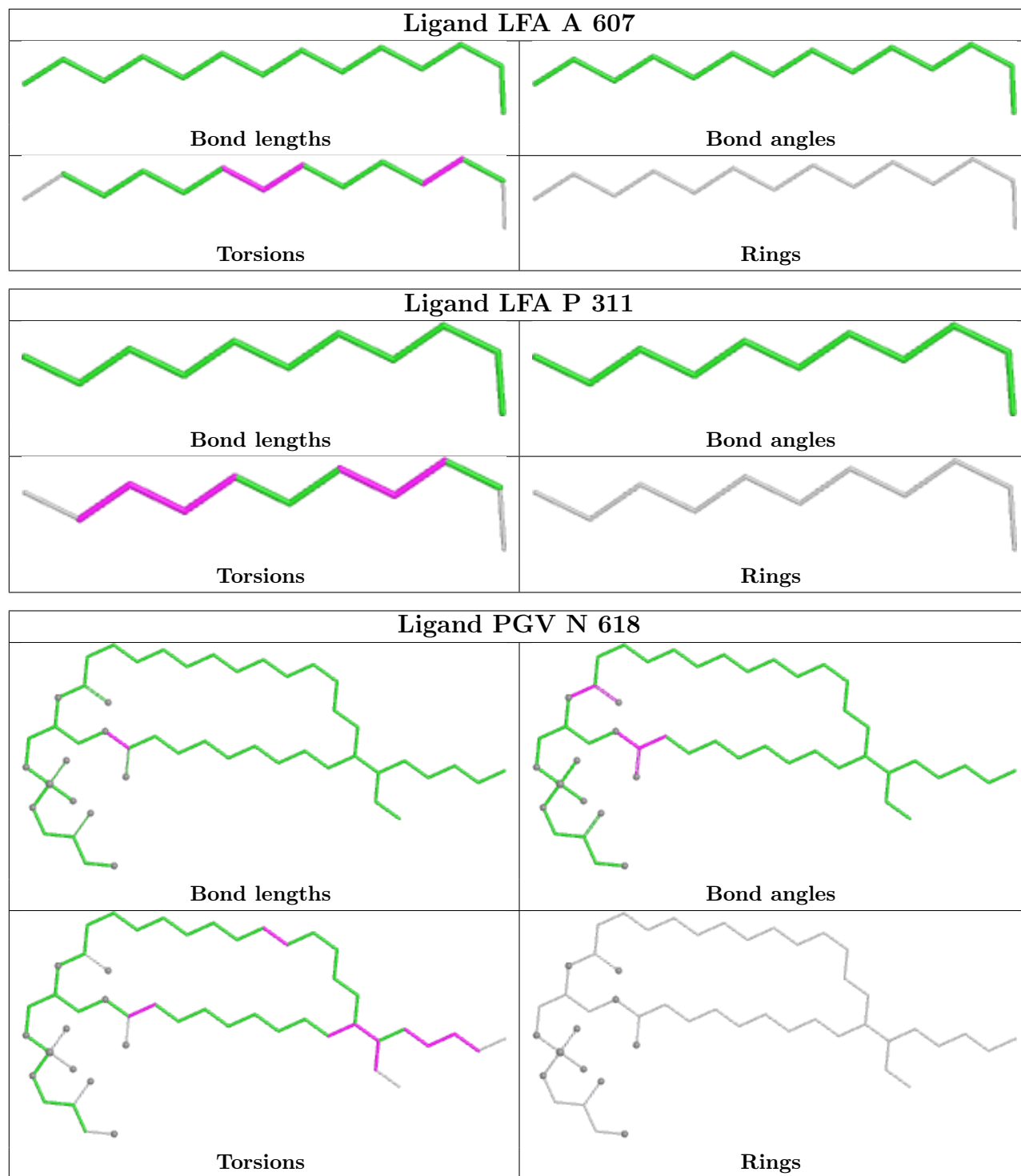


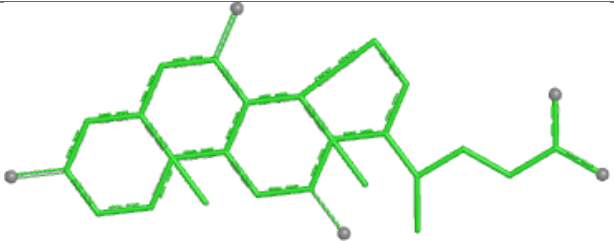
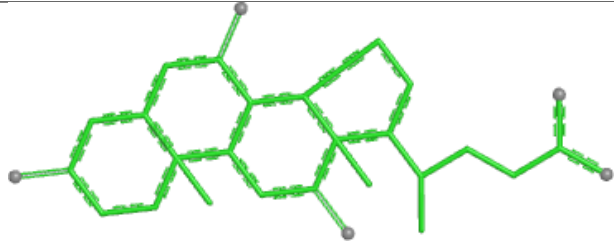
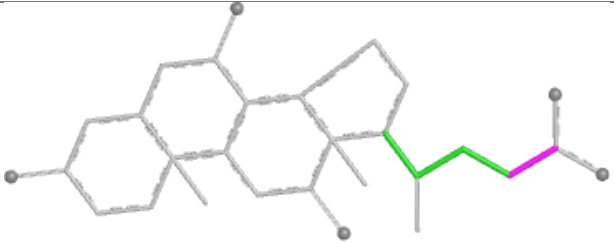
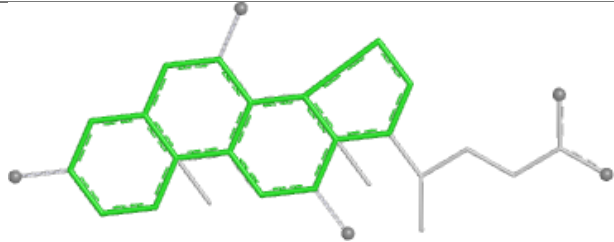




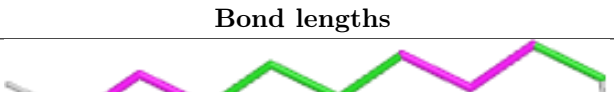
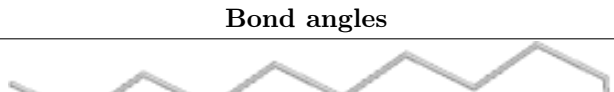




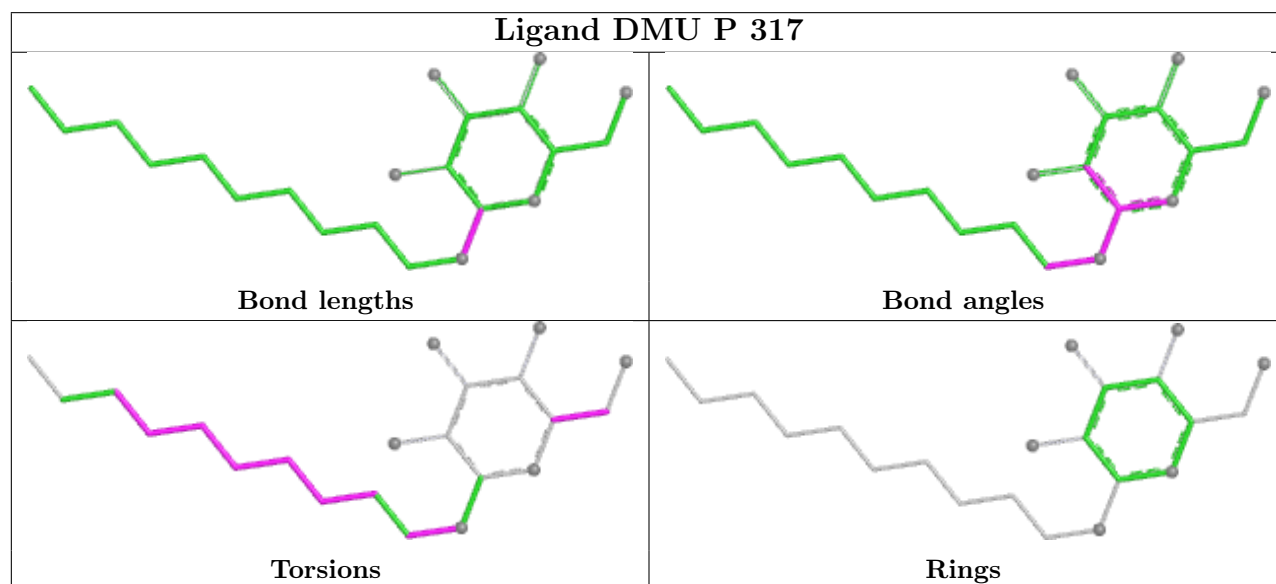
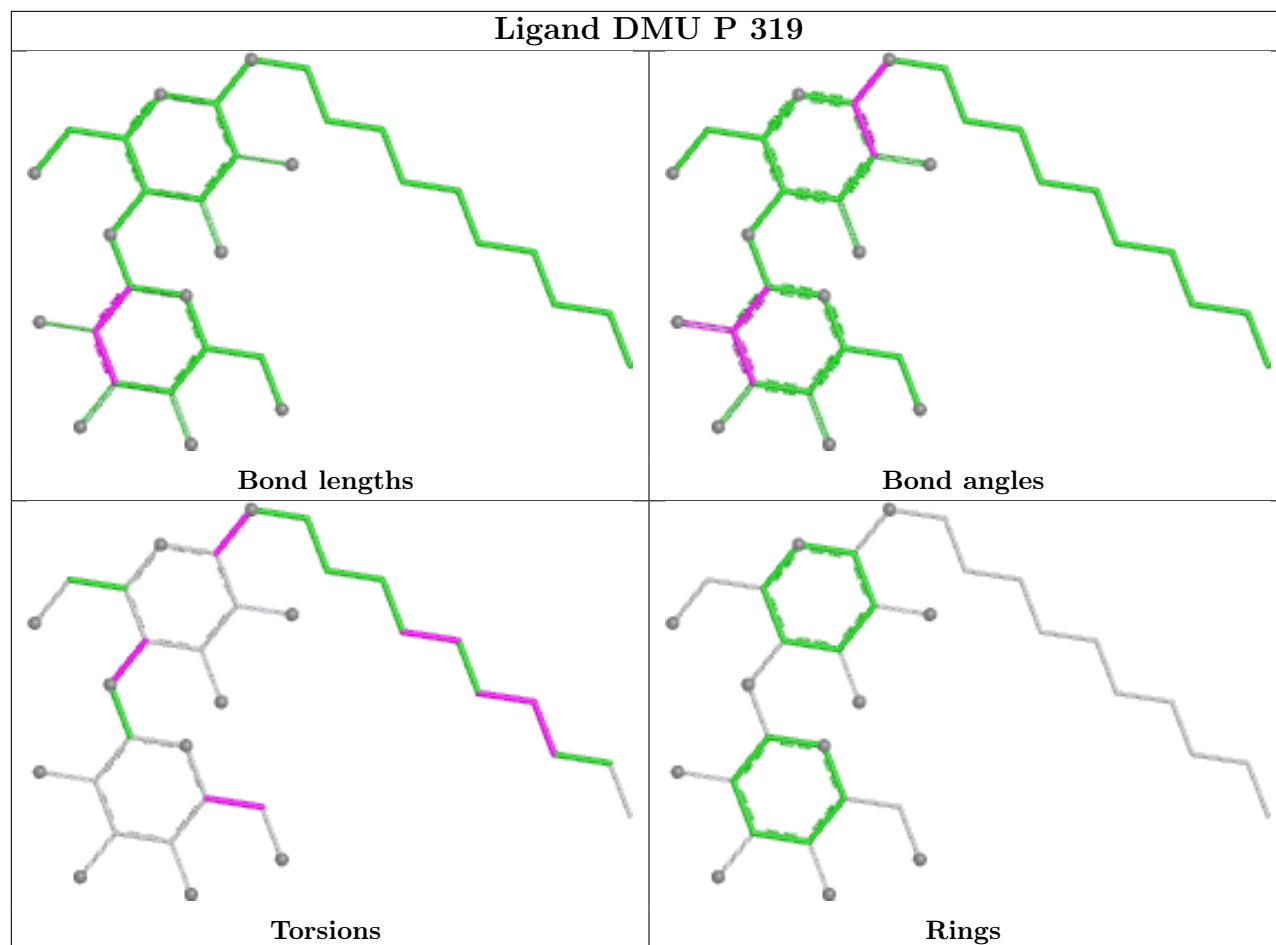


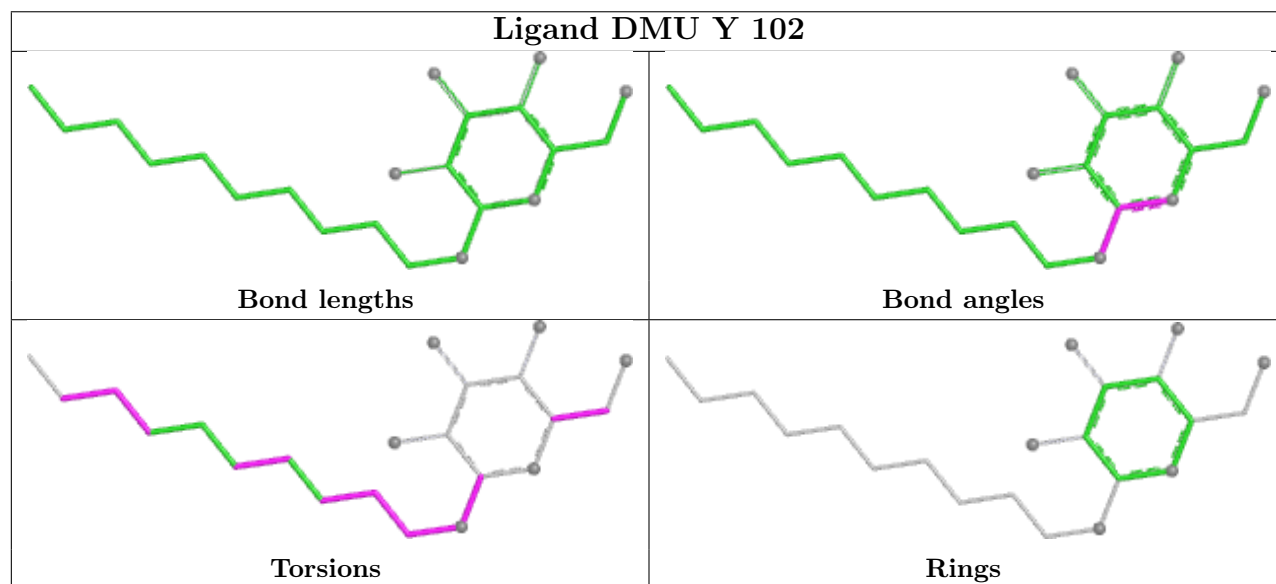
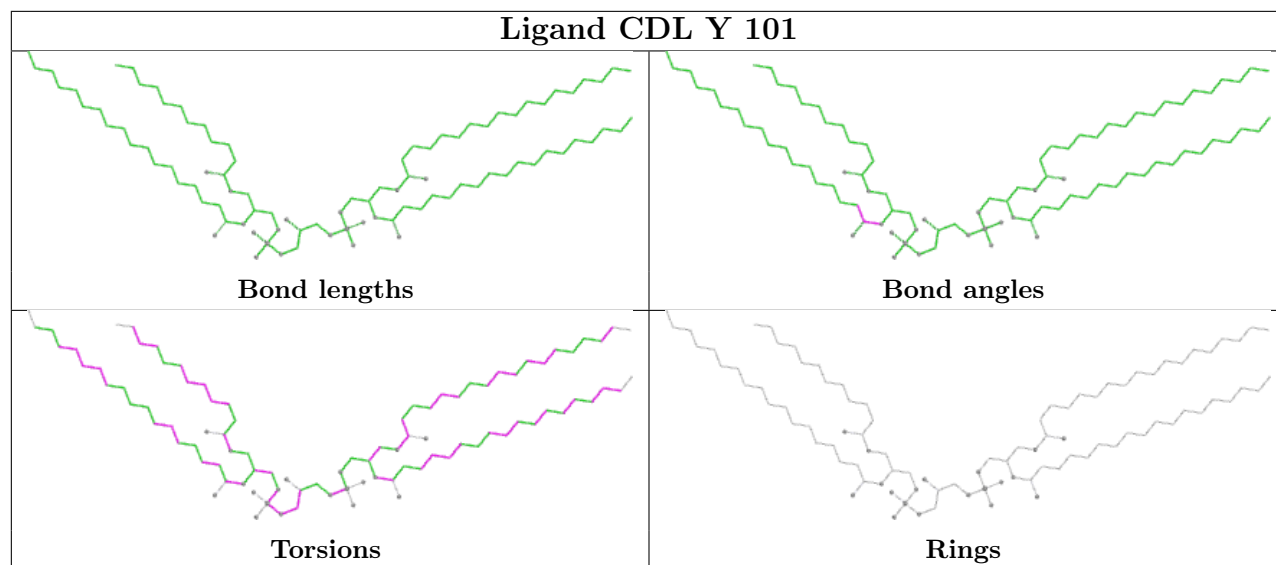
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Bond lengths	Bond angles
	
Torsions	Rings

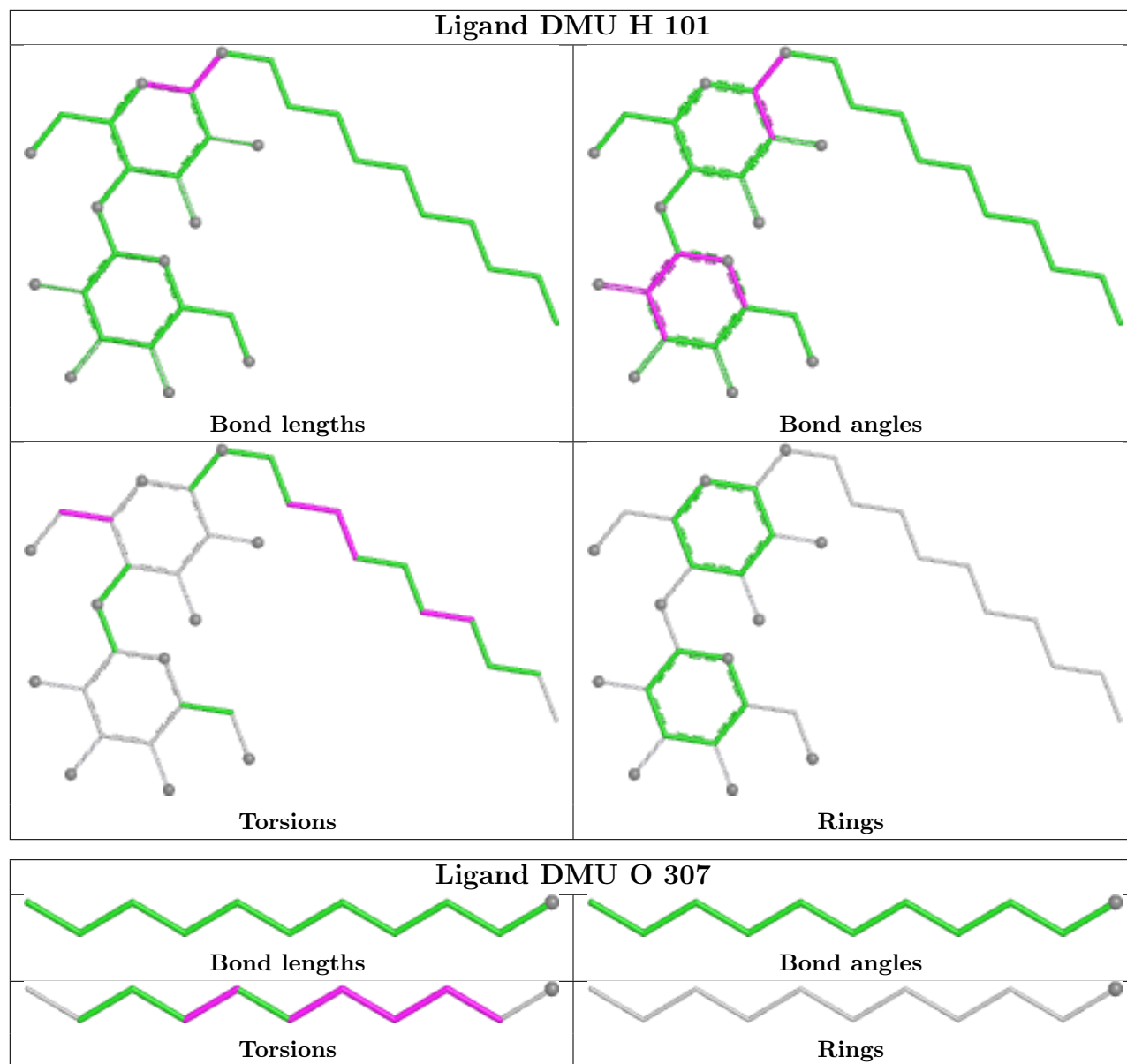
Ligand LFA A 608	
	
Bond lengths	Bond angles
	
Torsions	Rings

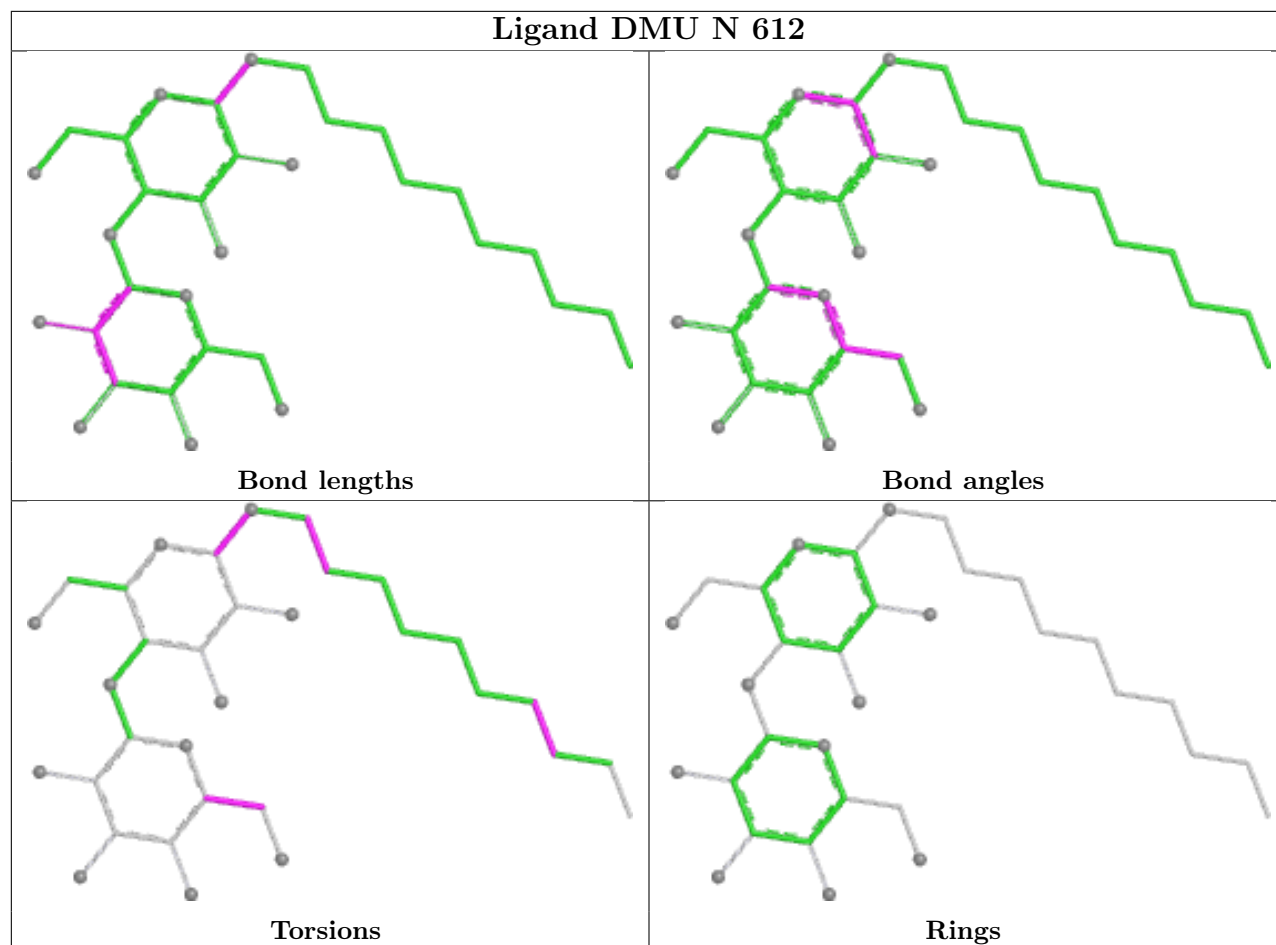
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Bond lengths	Bond angles
	
Torsions	Rings

Ligand DMU W 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

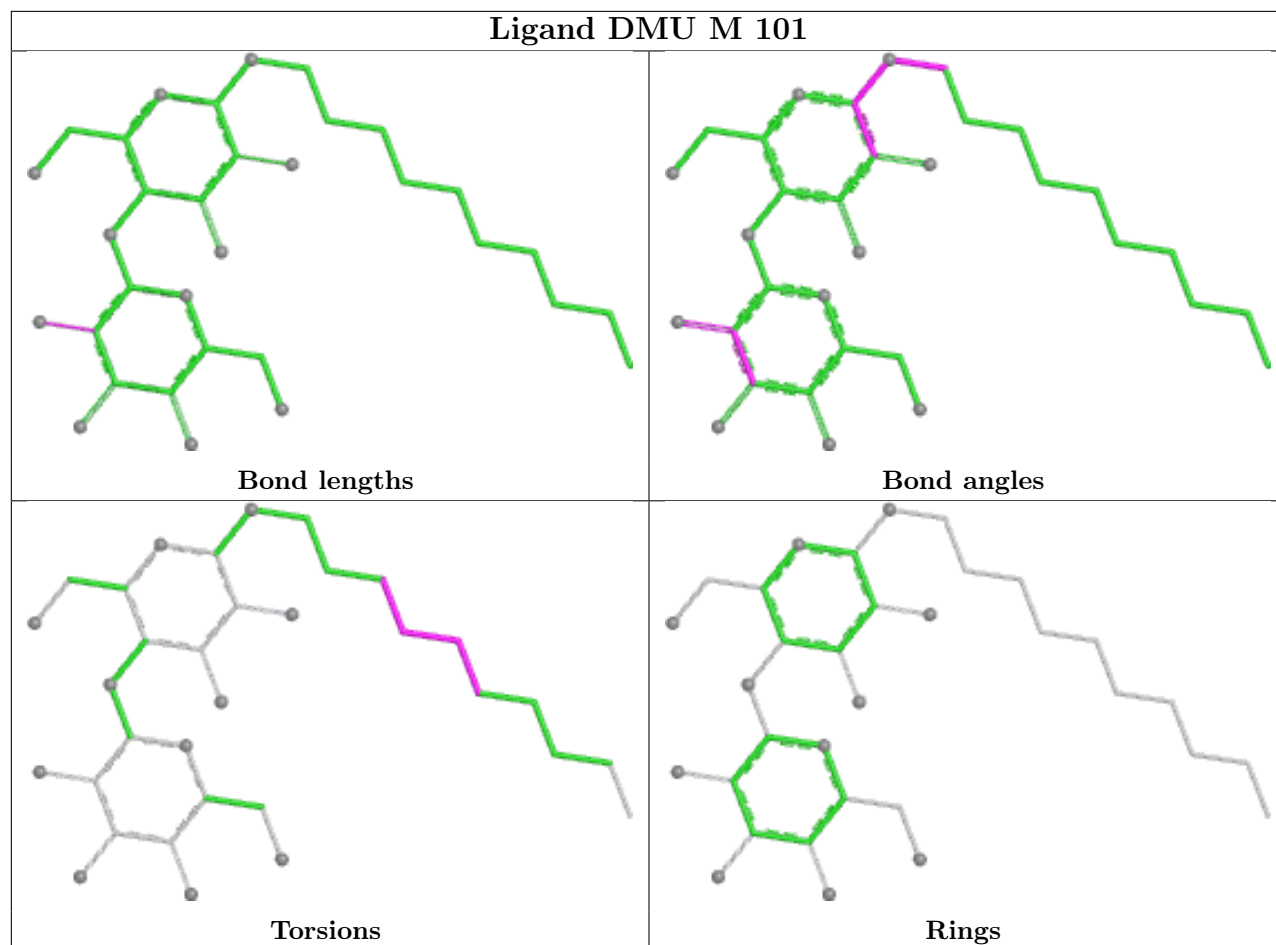




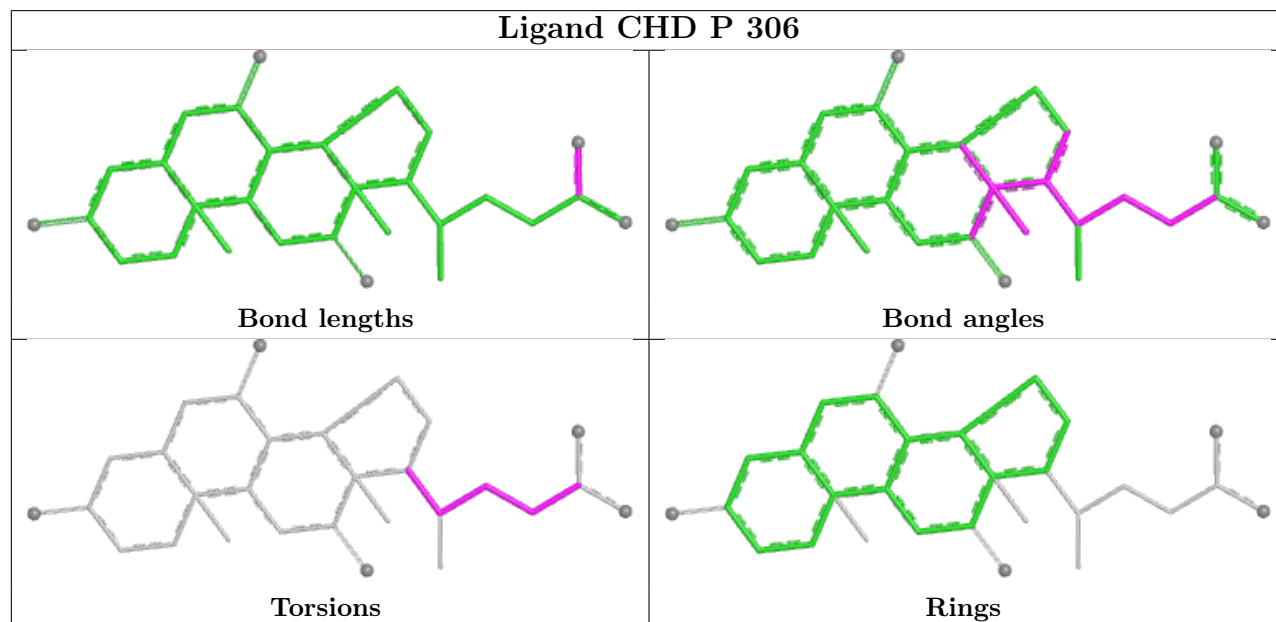


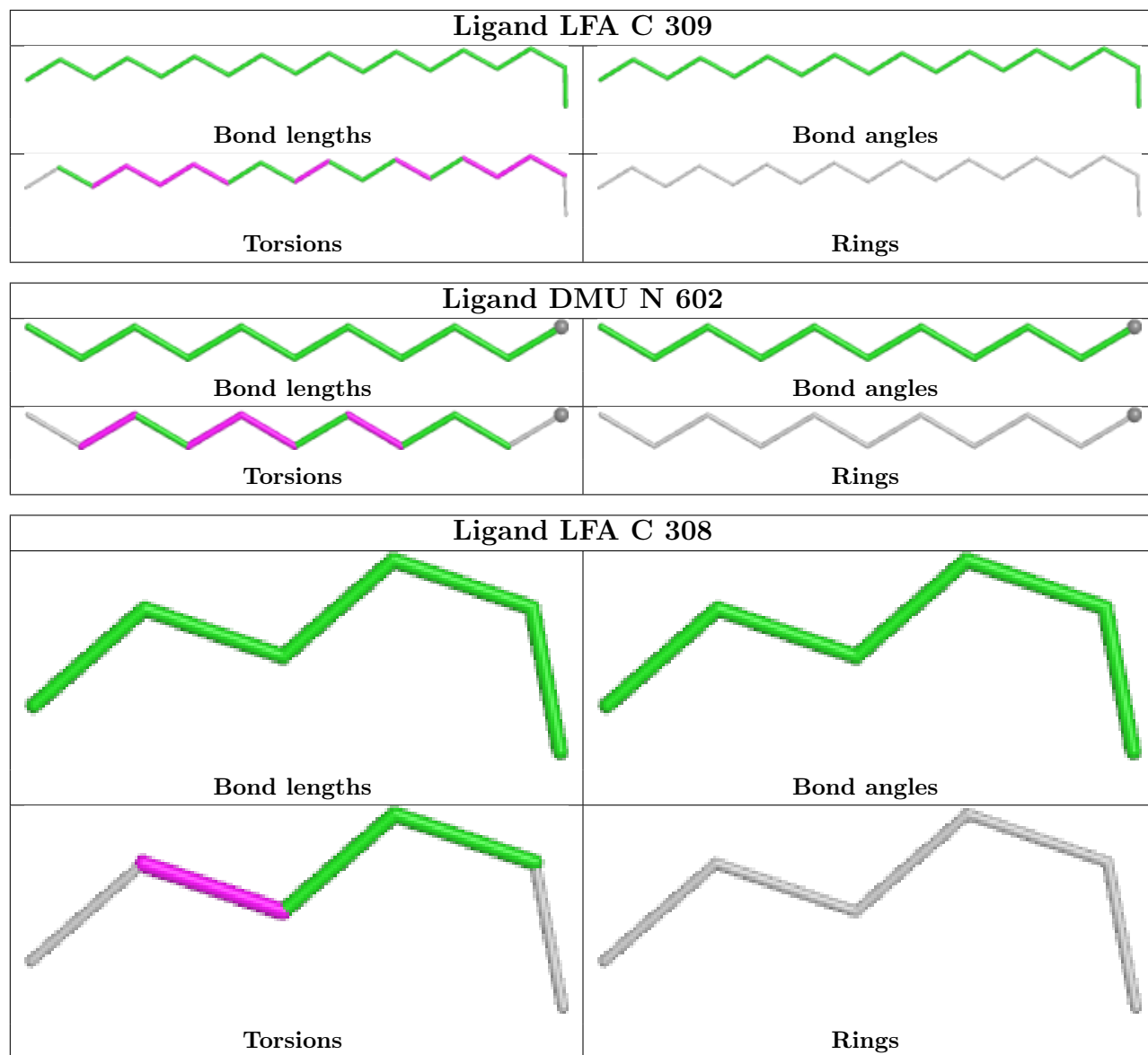


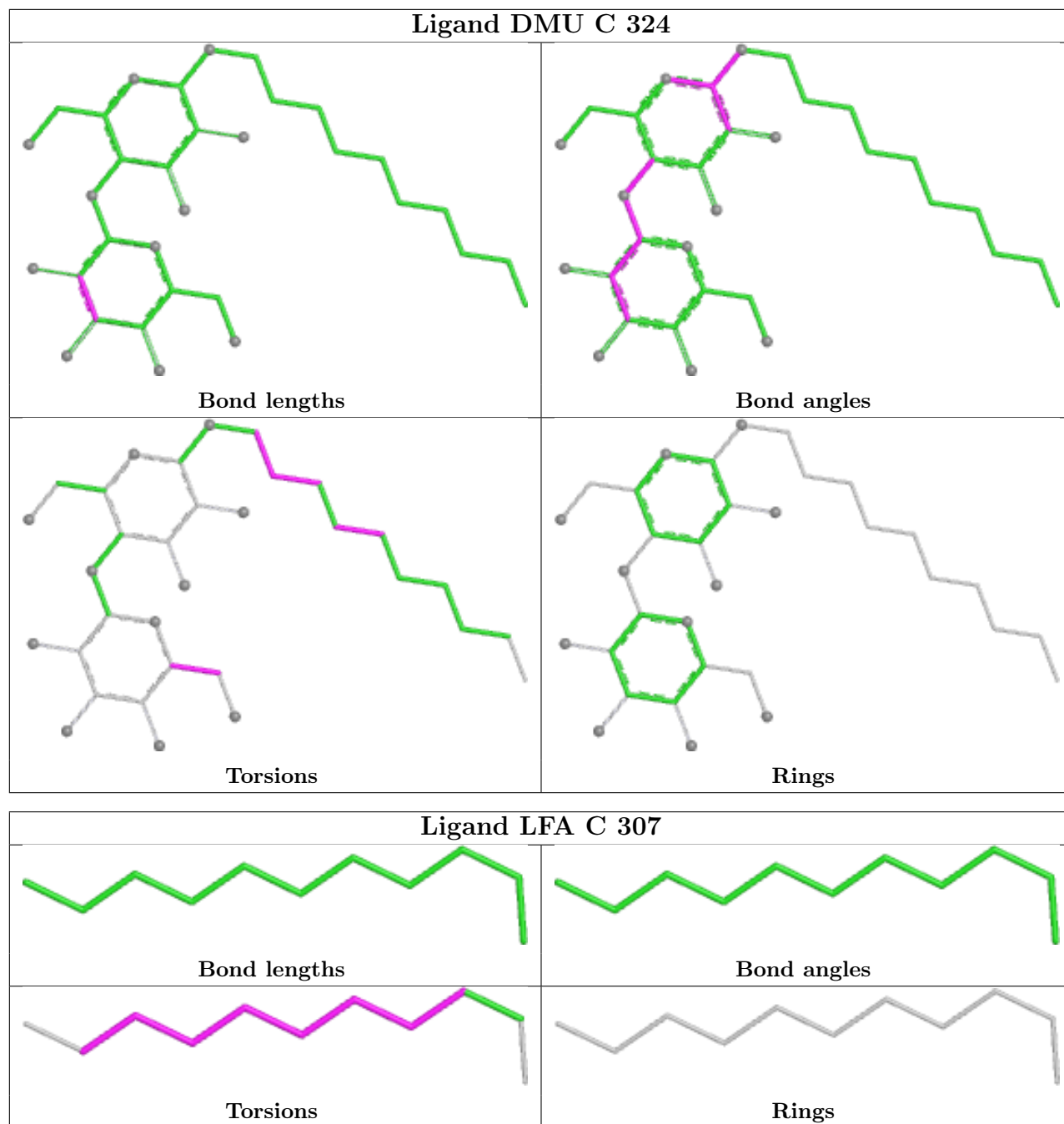
Ligand DMU M 101

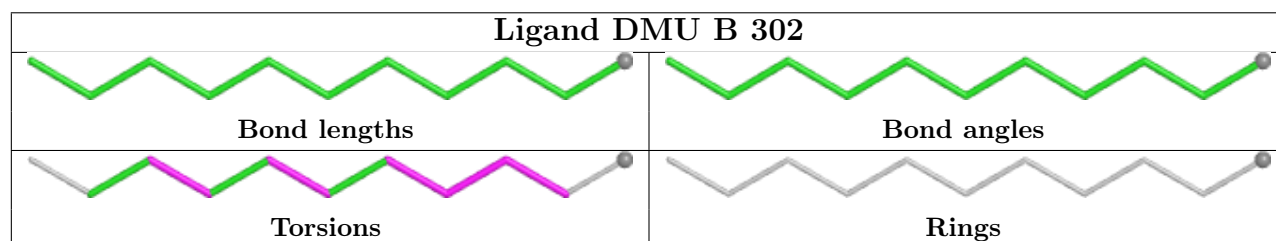
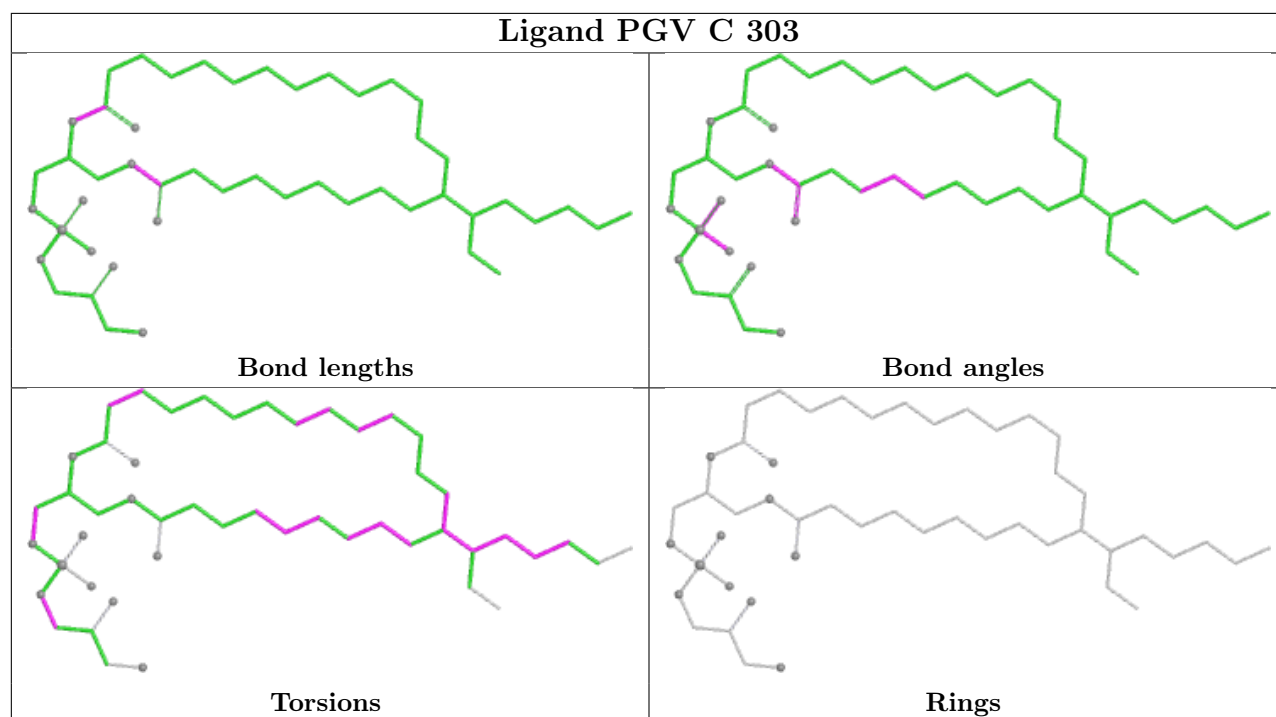
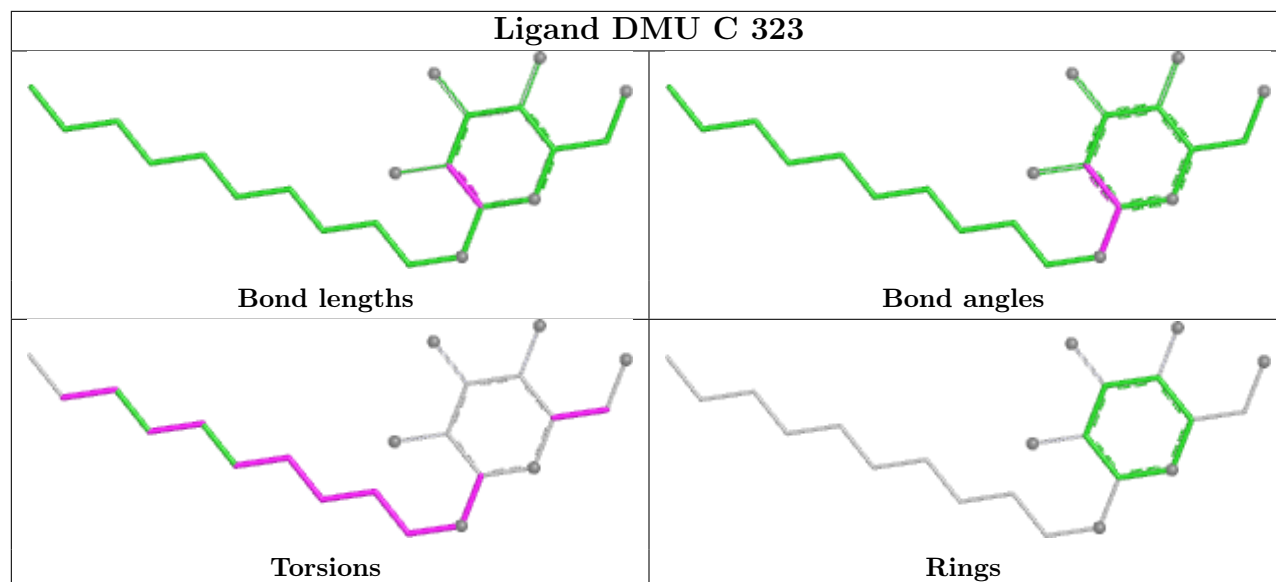


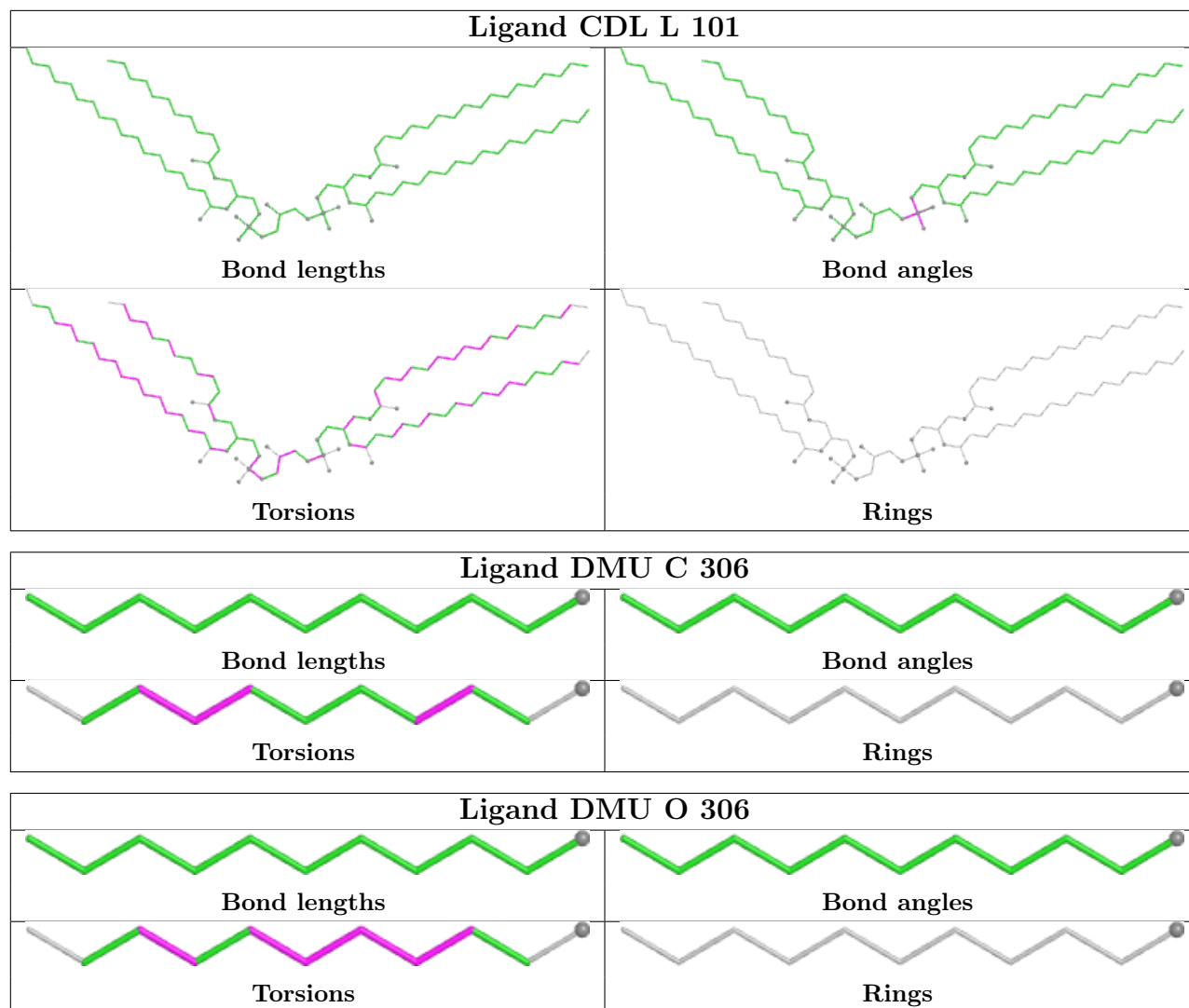
Ligand CHD P 306

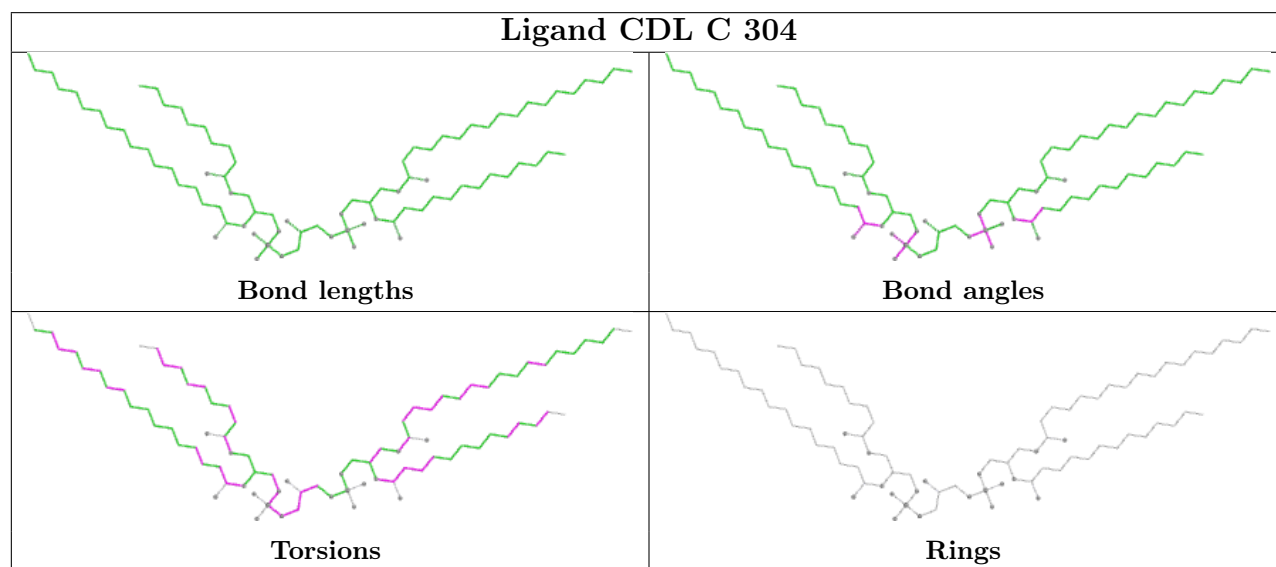
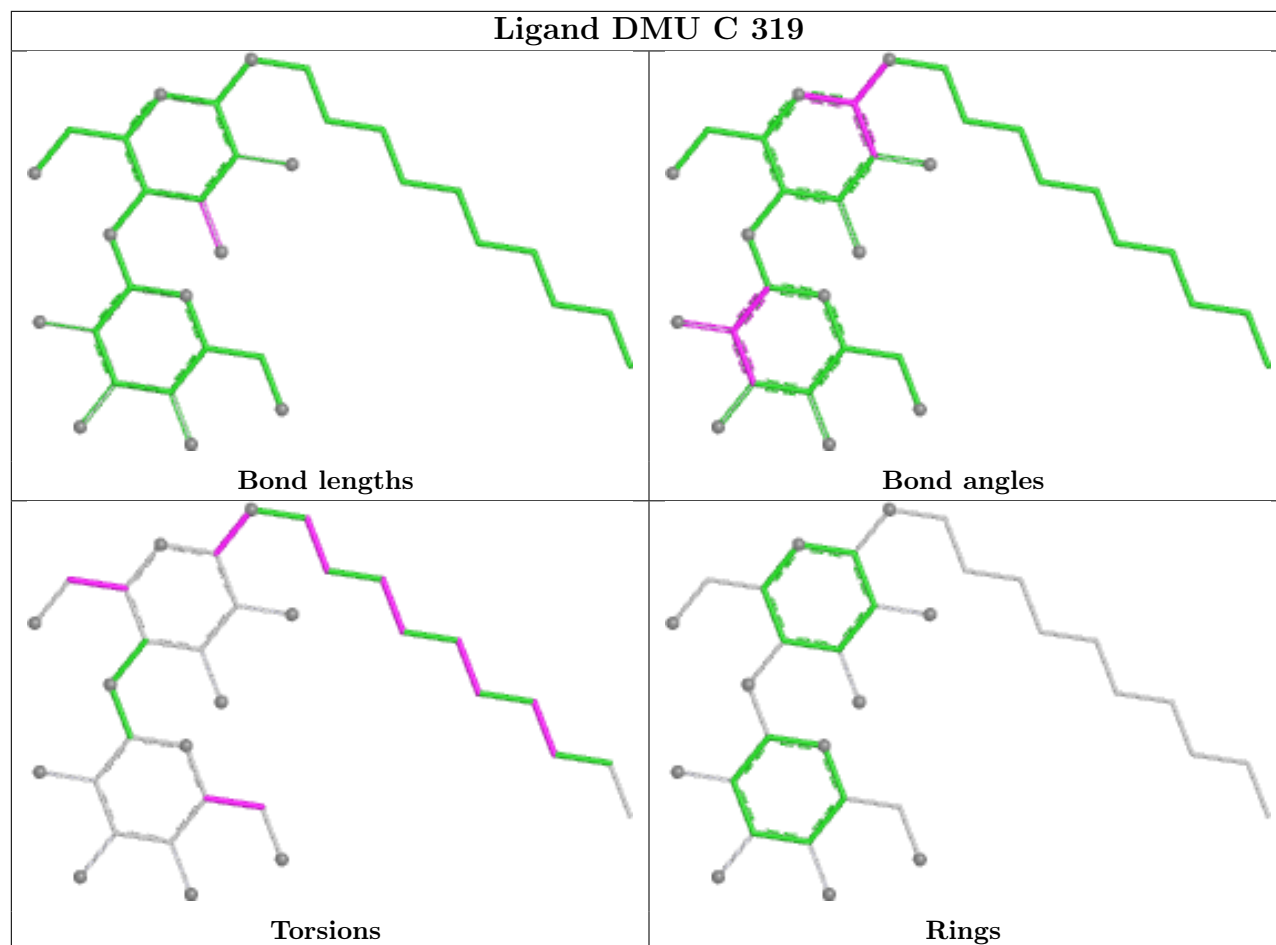


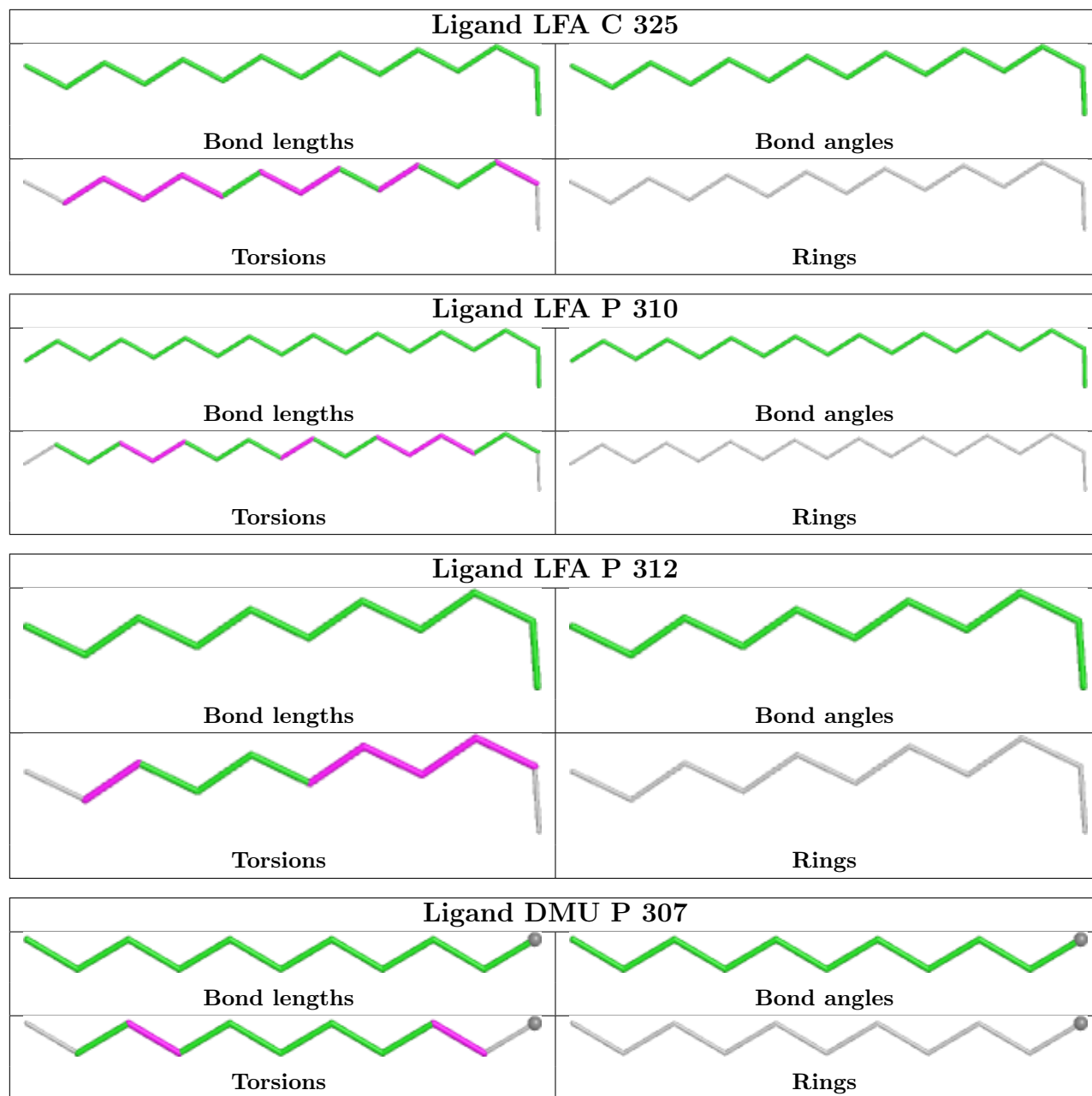


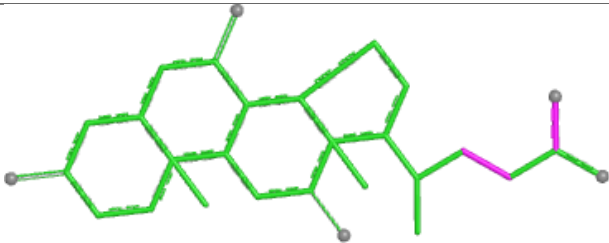
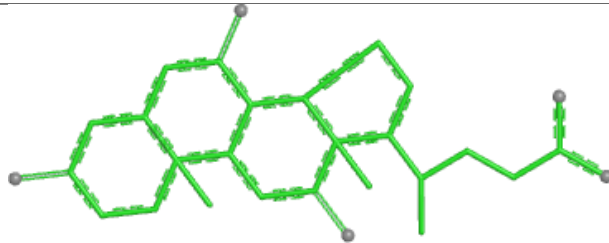
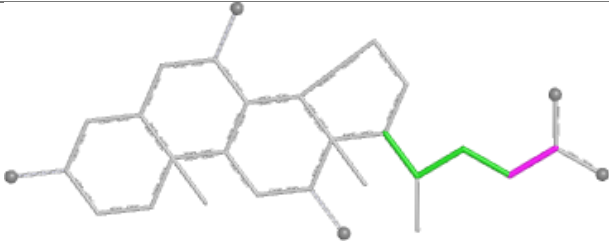
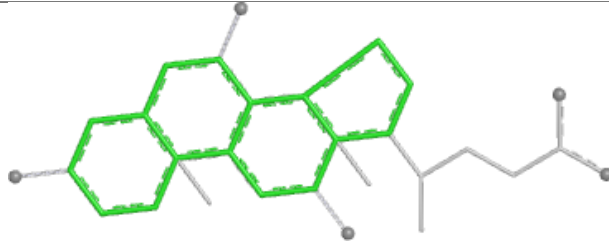


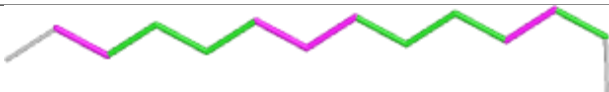




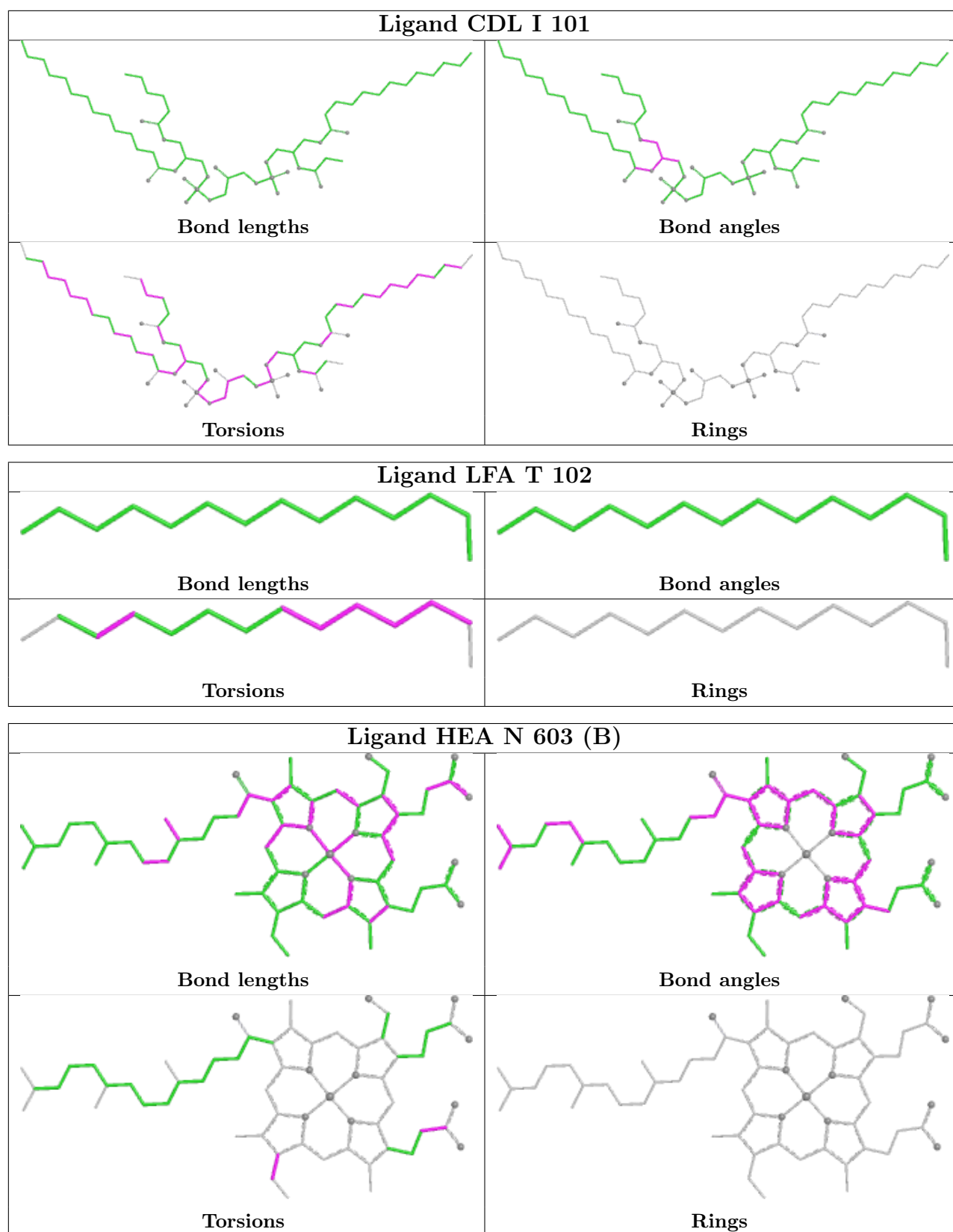


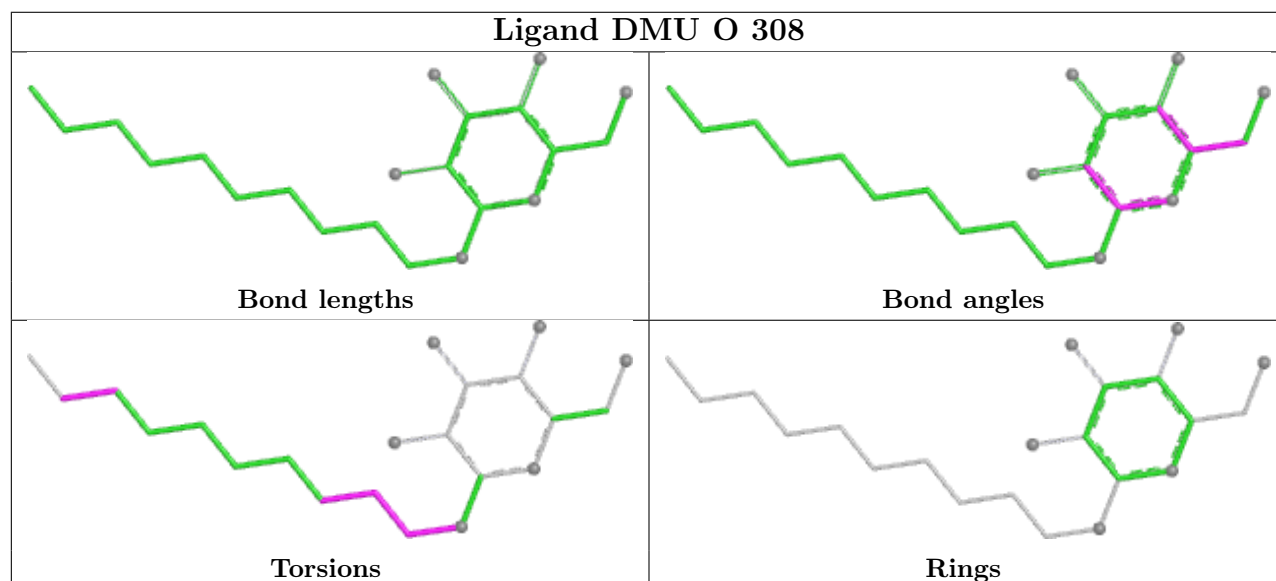
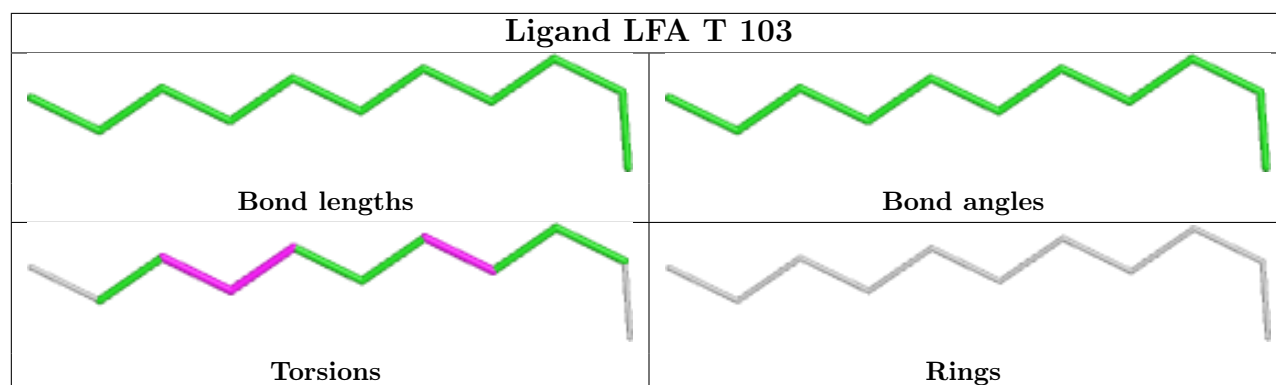
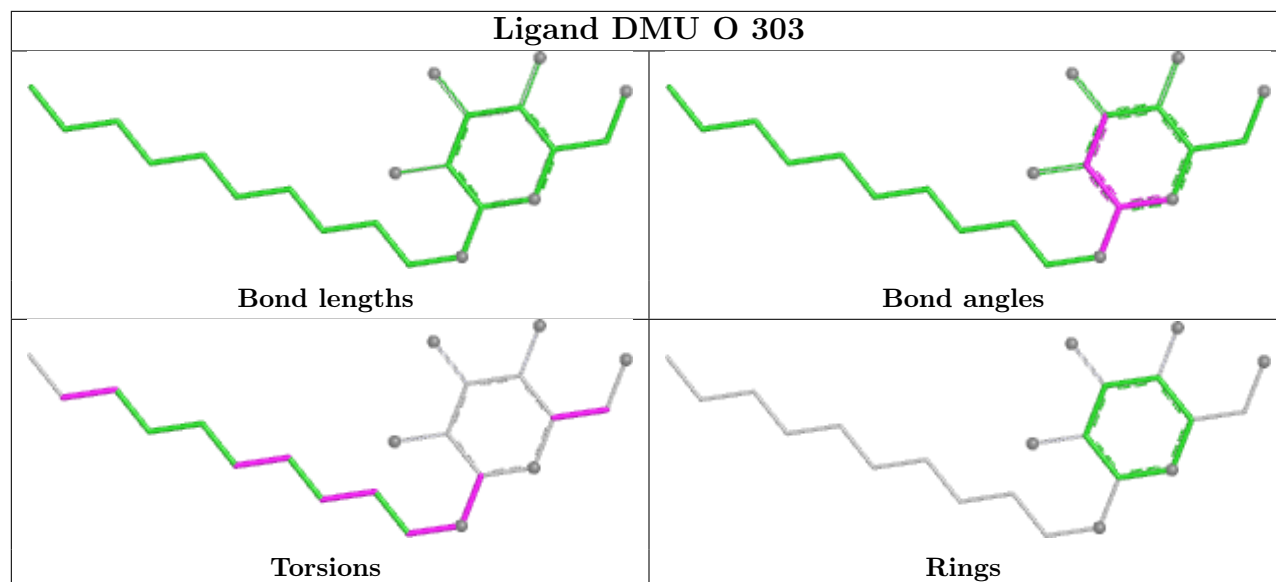


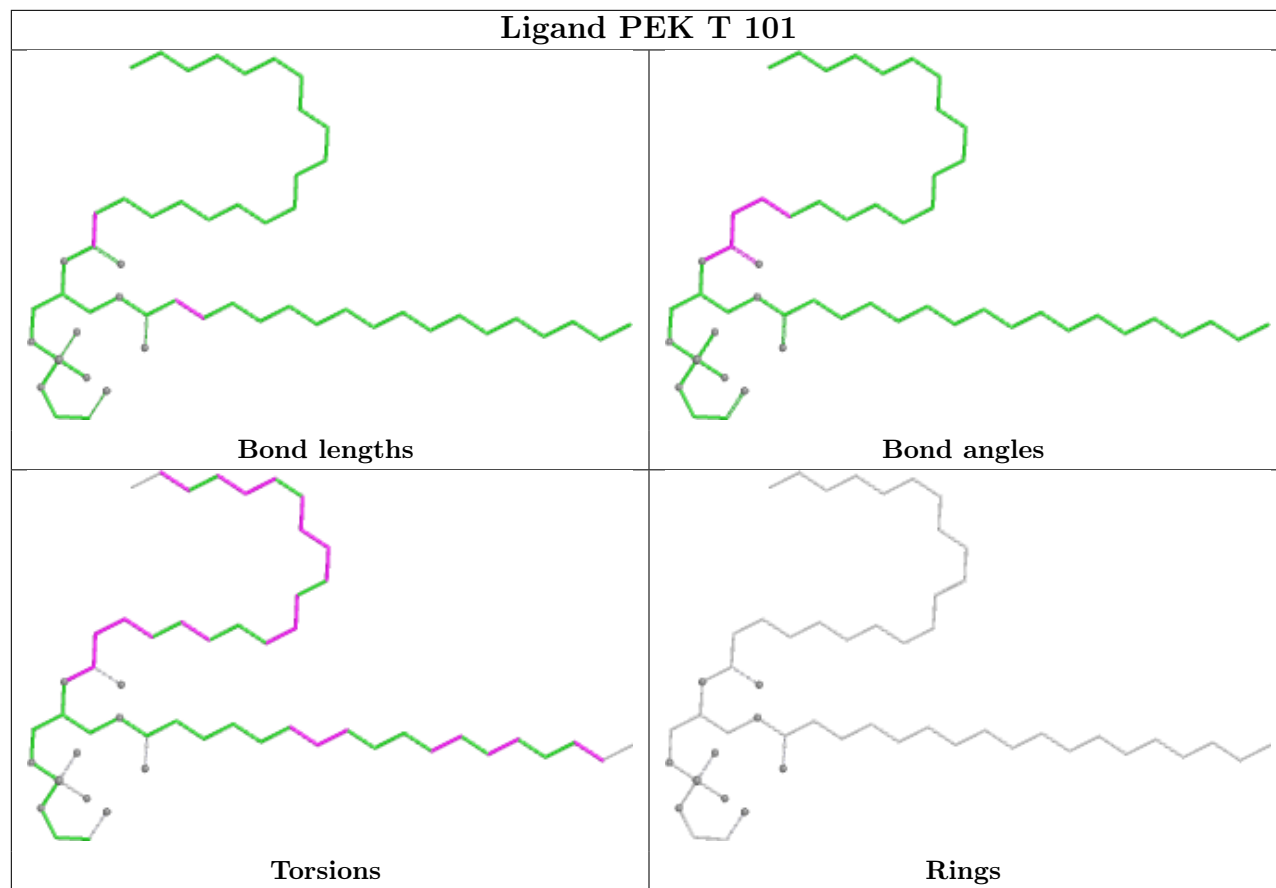
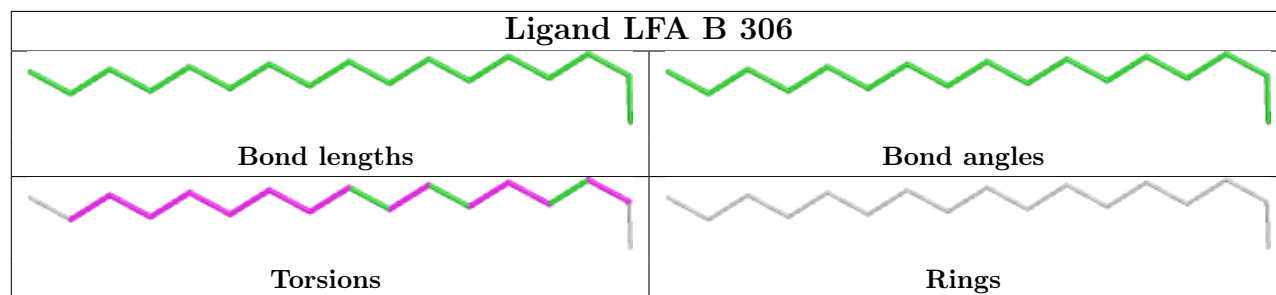
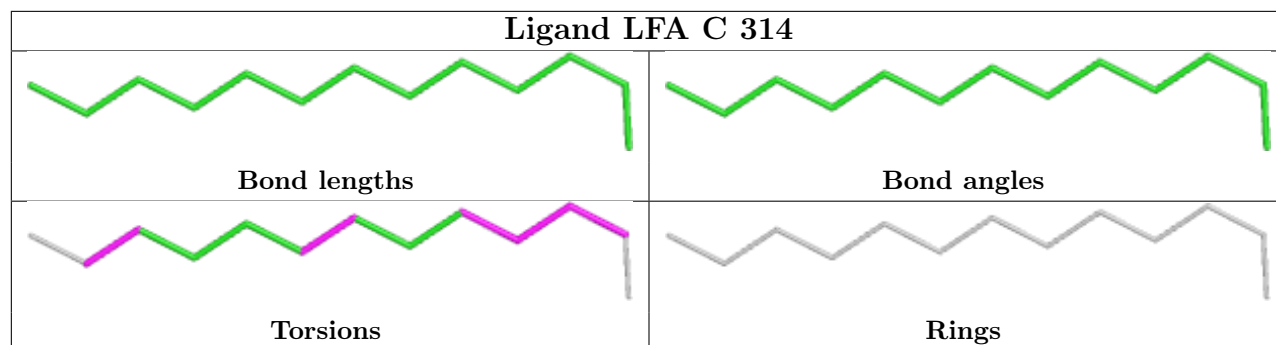
Ligand CHD P 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

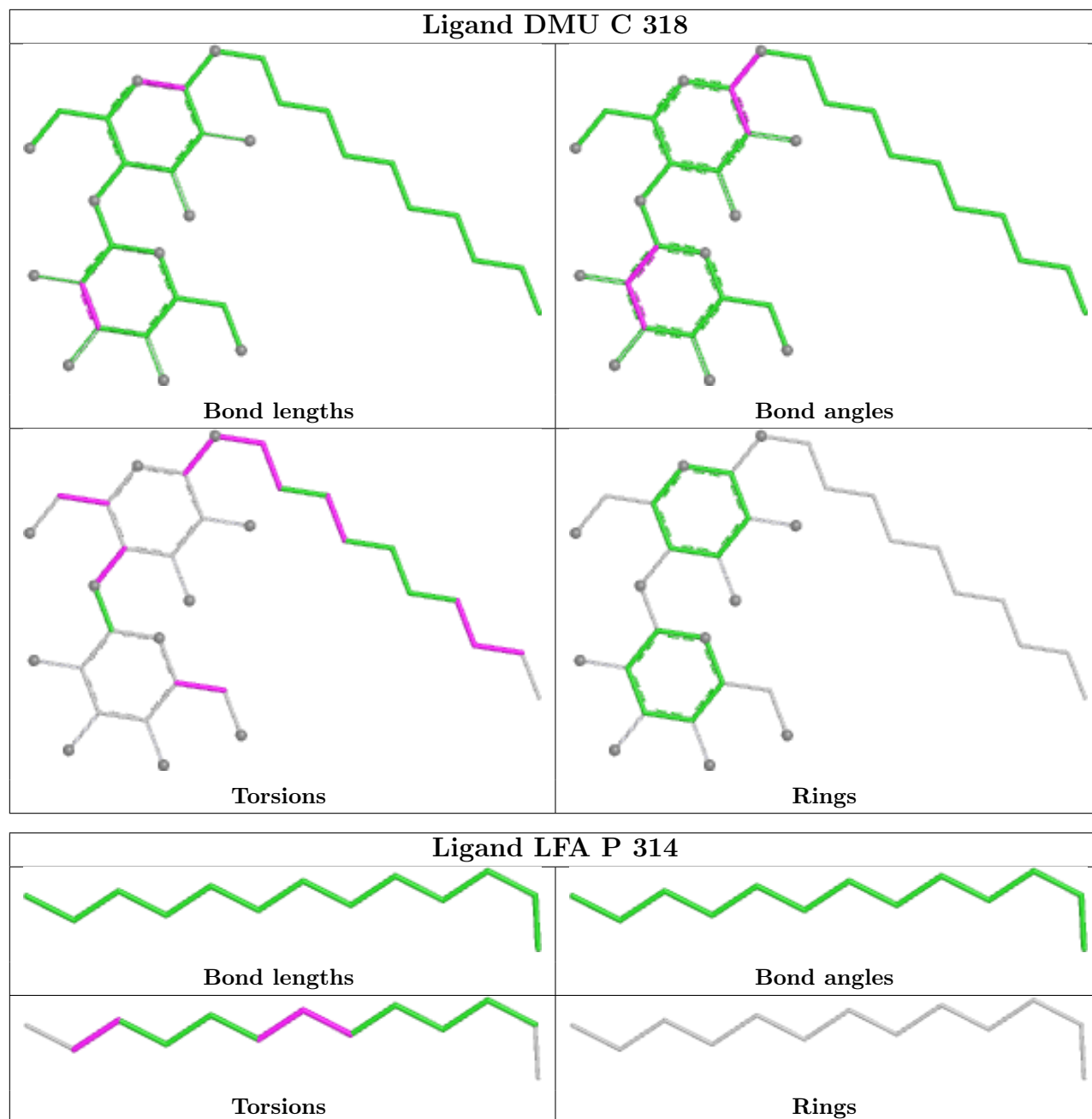
Ligand LFA N 609	
	
Bond lengths	Bond angles
	
Torsions	Rings

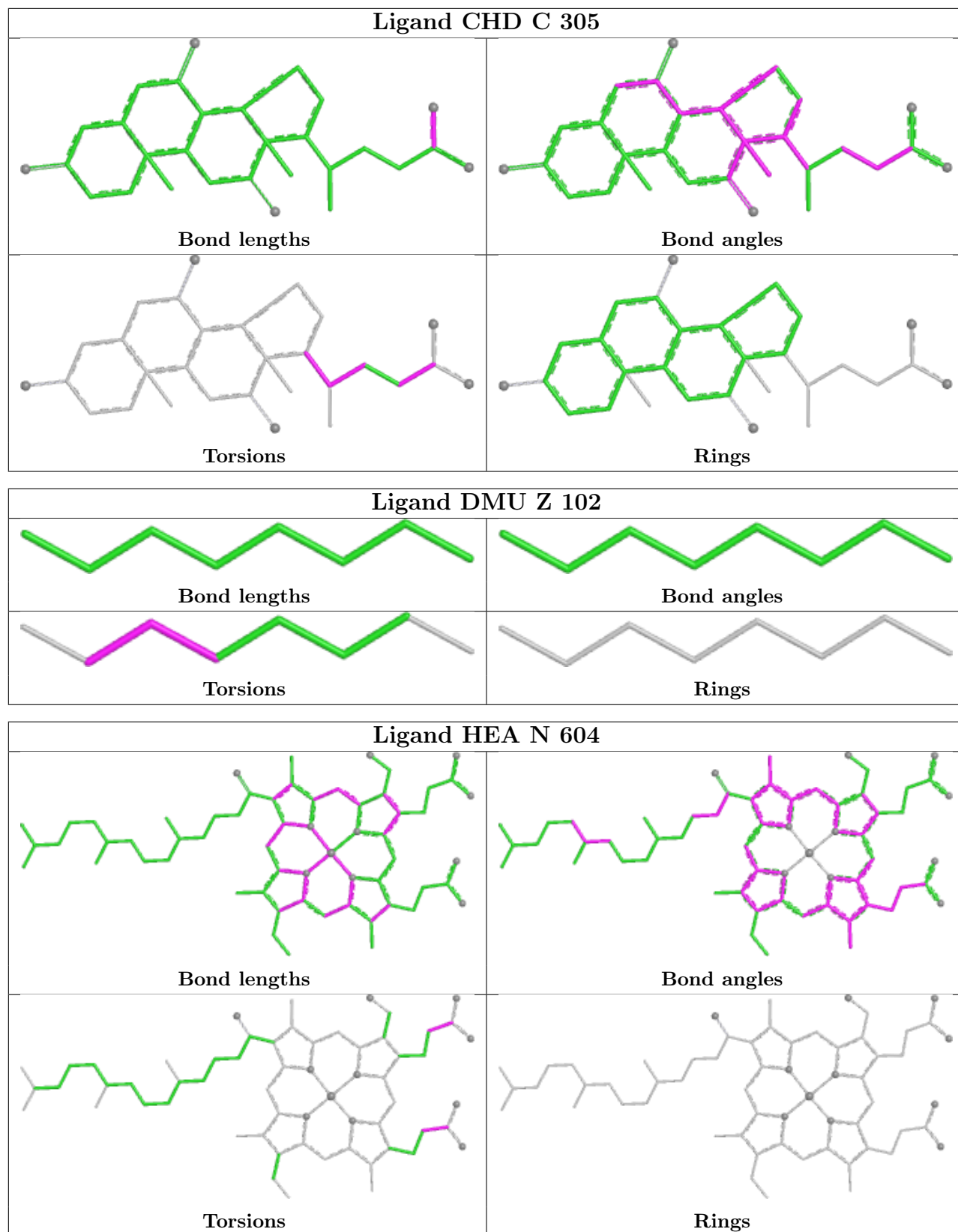
Ligand DMU P 316	
	
Bond lengths	Bond angles
	
Torsions	Rings

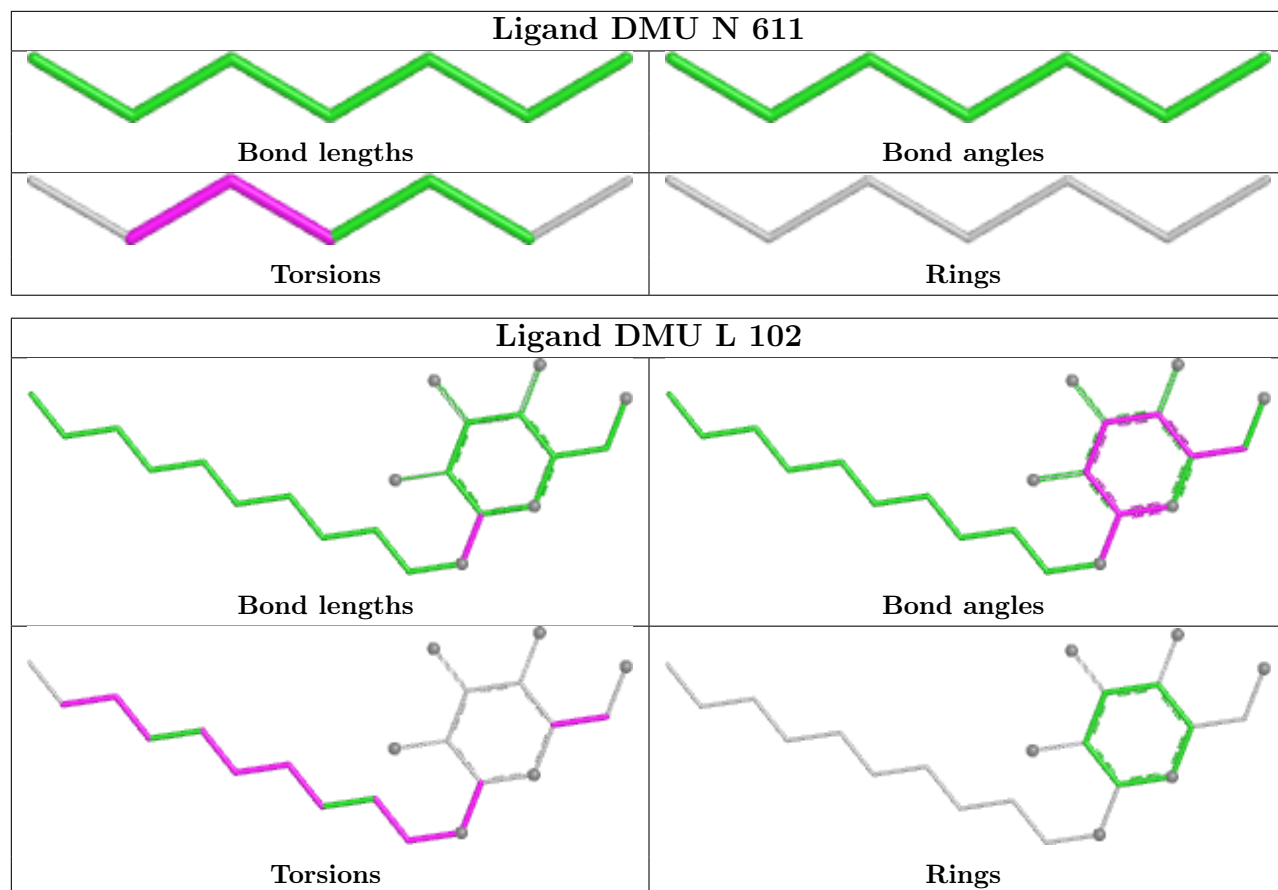


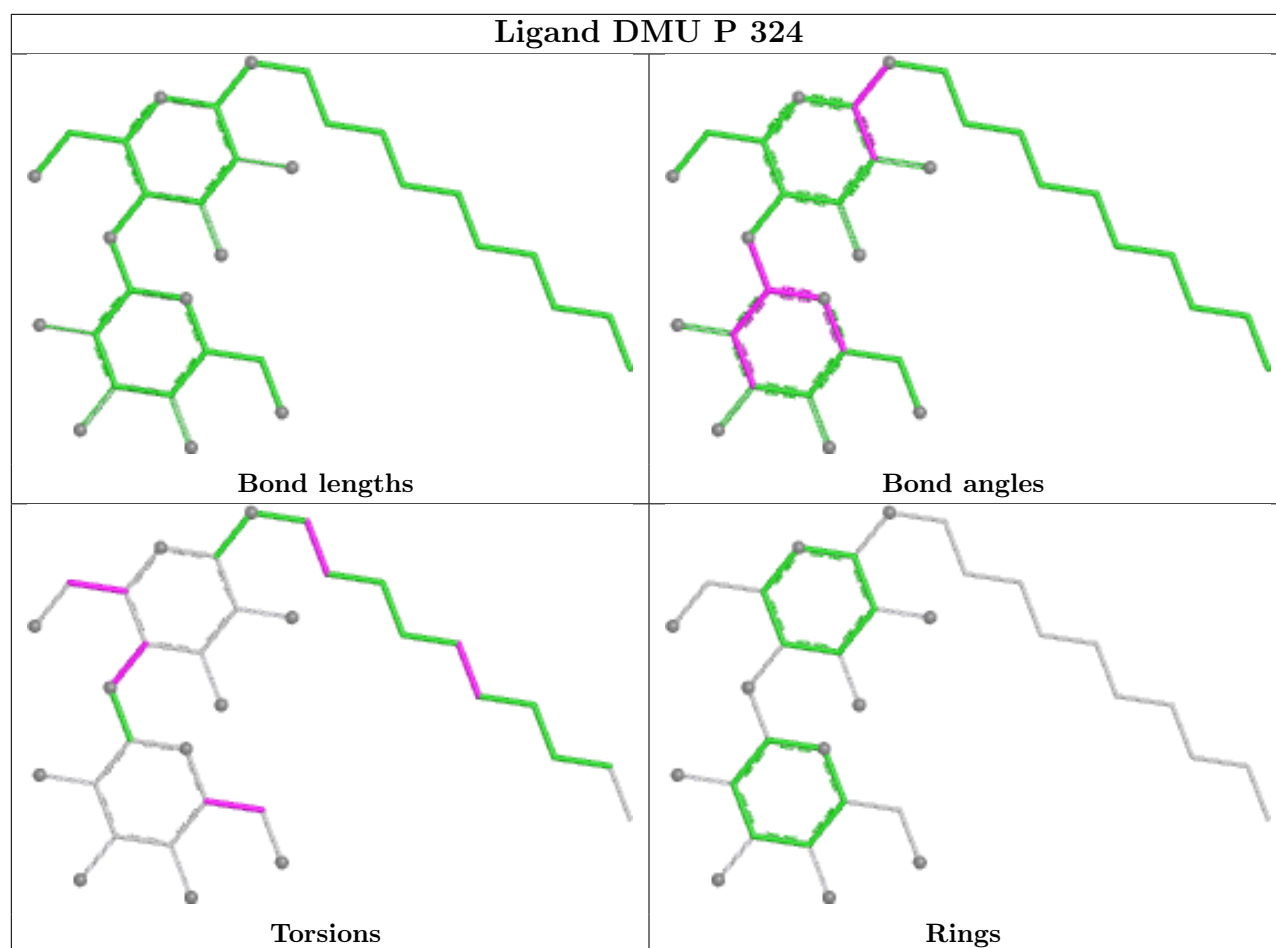












5.7 Other polymers [i](#)

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	512/514 (99%)	-0.27	4 (0%)	82 85	15, 31, 39, 57	15 (2%)
1	N	512/514 (99%)	-0.04	6 (1%)	76 80	17, 36, 47, 66	15 (2%)
2	B	226/227 (99%)	0.14	15 (6%)	24 26	19, 37, 57, 81	5 (2%)
2	O	226/227 (99%)	0.32	9 (3%)	42 46	23, 47, 74, 84	5 (2%)
3	C	258/261 (98%)	-0.10	4 (1%)	70 75	16, 35, 47, 62	9 (3%)
3	P	258/261 (98%)	0.01	1 (0%)	88 90	16, 37, 49, 76	9 (3%)
4	D	143/147 (97%)	0.06	2 (1%)	73 77	19, 40, 56, 70	1 (0%)
4	Q	137/147 (93%)	0.59	9 (6%)	24 26	24, 59, 85, 104	1 (0%)
5	E	102/109 (93%)	-0.11	1 (0%)	79 82	33, 39, 56, 74	0
5	R	102/109 (93%)	0.12	2 (1%)	65 69	37, 48, 64, 82	0
6	F	91/98 (92%)	0.18	2 (2%)	62 66	20, 42, 65, 79	2 (2%)
6	S	91/98 (92%)	0.32	2 (2%)	62 66	19, 41, 66, 79	2 (2%)
7	G	72/85 (84%)	0.41	6 (8%)	17 18	20, 41, 96, 108	1 (1%)
7	T	72/85 (84%)	0.47	5 (6%)	23 25	22, 46, 94, 105	1 (1%)
8	H	75/85 (88%)	0.42	6 (8%)	18 19	34, 45, 89, 110	0
8	U	75/85 (88%)	0.49	3 (4%)	42 46	42, 50, 89, 114	0
9	I	70/73 (95%)	0.45	5 (7%)	22 24	36, 48, 72, 91	0
9	V	70/73 (95%)	0.72	5 (7%)	22 24	37, 61, 79, 101	0
10	J	56/59 (94%)	0.35	4 (7%)	22 24	36, 45, 66, 78	0
10	W	56/59 (94%)	0.61	5 (8%)	15 16	40, 51, 75, 83	0
11	K	49/56 (87%)	0.43	3 (6%)	27 29	38, 45, 60, 76	0
11	X	49/56 (87%)	0.82	2 (4%)	41 45	50, 60, 76, 100	0
12	L	44/47 (93%)	0.05	1 (2%)	61 65	32, 37, 50, 60	0
12	Y	44/47 (93%)	0.43	1 (2%)	61 65	41, 49, 65, 71	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	40/46 (86%)	0.27	1 (2%) 58 62	34, 38, 74, 89	0
13	Z	40/46 (86%)	0.90	4 (10%) 12 13	47, 54, 94, 101	0
All	All	3470/3614 (96%)	0.13	108 (3%) 51 55	15, 39, 68, 114	66 (1%)

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	S	93	PRO	7.1
7	T	36	TRP	6.6
2	B	59	GLN	5.5
6	F	3	GLY	5.5
2	O	113	TYR	5.5
6	S	3	GLY	5.3
1	N	48	LEU	5.1
1	N	113[A]	LEU	5.1
7	G	36	TRP	4.9
8	H	45	ALA	4.6
9	V	37	PHE	4.3
2	B	65	TRP	4.2
3	P	37	PHE	4.2
10	W	52	TRP	4.2
11	X	6	ALA	4.1
9	V	3	ALA	3.9
1	A	113[A]	LEU	3.9
7	T	38	HIS	3.7
10	W	27	THR	3.6
11	K	6	ALA	3.5
1	N	136[A]	LEU	3.5
12	Y	24	MET	3.5
13	M	40	TYR	3.5
9	I	37	PHE	3.4
2	B	61	VAL	3.4
4	D	4	SER	3.4
7	G	37	LEU	3.3
2	O	22[A]	HIS	3.3
9	V	72	ALA	3.2
13	Z	40	TYR	3.2
8	H	46	LYS	3.2
8	U	45	ALA	3.2
1	A	48	LEU	3.1
10	J	52	TRP	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	60	GLU	3.1
1	A	47	LEU	3.1
7	T	37	LEU	3.0
9	I	3	ALA	3.0
2	O	90	ILE	3.0
4	Q	51	LEU	3.0
3	C	38	ASN	3.0
4	Q	35	ALA	2.9
9	I	25	PHE	2.9
10	J	48	TYR	2.9
4	Q	106	PRO	2.9
4	D	5	VAL	2.8
9	I	26	MET	2.8
5	R	7	THR	2.8
8	H	48	GLY	2.8
2	O	91	ASN	2.7
2	O	227	LEU	2.7
10	W	49	CYS	2.7
7	G	33	LEU	2.7
13	Z	19	LEU	2.7
5	E	7	THR	2.6
8	H	44	THR	2.6
1	N	47	LEU	2.6
7	G	41	HIS	2.6
10	W	56	PRO	2.6
2	B	55	THR	2.6
9	V	34	PHE	2.6
4	Q	10	ASP	2.6
4	Q	11	TYR	2.6
5	R	108	LYS	2.6
7	T	33	LEU	2.5
1	A	513	LEU	2.5
2	B	90	ILE	2.5
3	C	258	TRP	2.4
4	Q	105	GLY	2.4
2	O	58	ALA	2.4
2	B	58	ALA	2.4
2	B	113	TYR	2.4
2	B	16[A]	ILE	2.4
4	Q	117	ALA	2.4
8	U	47	GLY	2.3
1	N	513	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
3	C	51[A]	MET	2.3
2	B	22[A]	HIS	2.3
4	Q	107	ILE	2.3
9	I	36	LYS	2.3
10	W	48	TYR	2.2
7	G	12	GLY	2.2
7	T	12	GLY	2.2
2	B	64	ILE	2.2
13	Z	38	ASP	2.2
2	O	65	TRP	2.2
13	Z	37	LEU	2.2
11	K	47	ARG	2.2
4	Q	146	LYS	2.2
6	F	93	PRO	2.1
9	V	31	PHE	2.1
10	J	56	PRO	2.1
11	X	13	TYR	2.1
2	B	91	ASN	2.1
2	B	32[A]	PHE	2.1
10	J	1	PHE	2.1
8	H	50	VAL	2.1
12	L	45	LEU	2.1
1	N	334	TRP	2.1
2	O	64	ILE	2.1
2	B	87[A]	MET	2.0
8	H	43	MET	2.0
2	O	57	ASP	2.0
7	G	42	ARG	2.0
8	U	52	VAL	2.0
11	K	26	VAL	2.0
2	B	56	MET	2.0
3	C	37	PHE	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	FME	A	1	10/11	0.91	0.14	42,50,91,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	FME	N	1	10/11	0.95	0.16	48,54,98,107	0
2	FME	B	1	10/11	0.97	0.09	32,35,45,85	0
2	FME	O	1	10/11	0.98	0.07	40,49,57,73	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
20	DMU	C	317	22/33	0.68	0.33	42,65,78,85	22
19	LFA	P	311	11/20	0.72	0.39	59,67,76,82	11
20	DMU	P	317	22/33	0.72	0.32	50,66,82,91	22
20	DMU	N	611	7/33	0.78	0.44	72,76,81,93	7
20	DMU	C	318	33/33	0.78	0.35	46,55,68,81	33
20	DMU	P	319	33/33	0.78	0.28	55,74,82,94	33
19	LFA	C	308	6/20	0.79	0.45	49,51,55,59	6
20	DMU	A	609	7/33	0.81	0.39	61,69,77,86	7
19	LFA	C	325	15/20	0.81	0.40	57,66,74,75	15
19	LFA	C	310	11/20	0.81	0.32	59,70,85,90	11
21	EDO	P	322	4/4	0.81	0.27	32,36,40,42	4
20	DMU	M	102	8/33	0.82	0.26	48,51,58,60	8
20	DMU	P	318	33/33	0.82	0.34	52,62,77,100	33
19	LFA	P	312	11/20	0.82	0.33	47,59,70,74	11
21	EDO	C	322	4/4	0.82	0.31	36,36,37,38	4
20	DMU	P	315	33/33	0.82	0.27	45,54,67,71	33
19	LFA	C	312	11/20	0.83	0.33	53,59,73,76	11
20	DMU	C	324	33/33	0.83	0.22	39,54,72,82	33
20	DMU	P	324	33/33	0.83	0.23	50,63,84,91	33
20	DMU	P	316	7/33	0.83	0.32	62,66,71,72	7
21	EDO	E	201	4/4	0.83	0.32	39,41,48,51	4
19	LFA	O	302	11/20	0.83	0.30	49,56,73,80	11
19	LFA	C	311	14/20	0.84	0.33	40,62,72,75	14
19	LFA	C	313	15/20	0.84	0.29	44,52,70,73	15
21	EDO	C	320	4/4	0.84	0.32	53,57,58,71	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
20	DMU	C	319	33/33	0.84	0.24	43,71,86,87	33
19	LFA	P	310	18/20	0.84	0.28	43,52,62,69	18
20	DMU	C	315	33/33	0.84	0.26	43,56,69,70	33
20	DMU	O	306	11/33	0.85	0.29	44,47,72,75	11
19	LFA	P	308	11/20	0.85	0.31	36,52,58,59	11
20	DMU	B	307	22/33	0.85	0.26	61,71,81,85	22
19	LFA	P	309	6/20	0.85	0.34	45,51,54,55	6
19	LFA	N	601	17/20	0.85	0.28	41,60,75,78	17
19	LFA	N	610	14/20	0.85	0.27	42,51,71,72	14
19	LFA	C	307	11/20	0.85	0.32	41,52,64,70	11
19	LFA	P	313	15/20	0.85	0.24	48,53,63,66	15
19	LFA	P	314	13/20	0.85	0.29	46,63,74,76	13
19	LFA	T	102	14/20	0.85	0.36	42,70,86,87	14
20	DMU	O	303	22/33	0.85	0.27	51,76,86,88	22
19	LFA	A	607	14/20	0.86	0.28	36,51,76,78	14
20	DMU	A	615	11/33	0.86	0.28	54,63,68,71	11
26	CDL	C	304	87/100	0.86	0.20	46,81,122,135	0
26	CDL	O	304	64/100	0.86	0.17	62,91,140,180	0
19	LFA	C	314	13/20	0.87	0.25	56,59,77,86	13
21	EDO	A	612	4/4	0.87	0.25	35,41,50,53	4
20	DMU	C	323	22/33	0.87	0.28	50,62,70,83	22
20	DMU	C	316	7/33	0.87	0.29	47,51,63,69	7
19	LFA	P	301	15/20	0.87	0.28	51,57,62,64	15
19	LFA	T	103	11/20	0.87	0.29	55,59,73,75	11
20	DMU	N	612	33/33	0.87	0.23	40,55,75,86	33
26	CDL	I	101	64/100	0.87	0.17	54,87,129,158	0
20	DMU	N	619	33/33	0.87	0.23	35,49,63,66	33
26	CDL	P	305	87/100	0.87	0.19	50,86,130,152	0
26	CDL	Y	101	94/100	0.87	0.17	57,95,141,156	0
20	DMU	P	323	22/33	0.88	0.22	46,60,70,77	22
20	DMU	H	101	33/33	0.88	0.20	31,45,59,68	33
20	DMU	Q	201	33/33	0.88	0.21	39,57,69,89	33
20	DMU	W	101	11/33	0.88	0.36	68,74,76,78	11
20	DMU	Y	102	22/33	0.88	0.33	55,63,76,86	22
21	EDO	A	611	4/4	0.88	0.17	27,29,29,33	4
19	LFA	A	608	14/20	0.88	0.27	37,50,62,63	14
20	DMU	A	617	11/33	0.88	0.32	47,60,69,72	11
25	UNX	P	303	1/1	0.89	0.24	55,55,55,55	0
19	LFA	B	306	17/20	0.89	0.28	43,59,87,90	17
20	DMU	A	610	33/33	0.89	0.19	31,42,53,63	33
20	DMU	N	602	11/33	0.89	0.31	52,67,72,75	11
21	EDO	N	614	4/4	0.89	0.20	39,40,50,50	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
19	LFA	N	609	14/20	0.89	0.24	40,50,68,71	14
20	DMU	B	302	11/33	0.90	0.24	47,58,64,68	11
24	CHD	P	306	29/29	0.90	0.12	54,60,72,86	0
19	LFA	C	309	18/20	0.90	0.18	37,45,54,56	18
20	DMU	J	101	11/33	0.90	0.35	63,68,71,82	11
20	DMU	O	308	22/33	0.90	0.18	46,52,59,63	22
21	EDO	F	102	4/4	0.90	0.19	23,24,31,31	4
20	DMU	L	102	22/33	0.90	0.30	49,59,67,70	22
21	EDO	N	617	4/4	0.90	0.18	31,39,39,43	4
24	CHD	C	305	29/29	0.91	0.12	50,58,77,111	0
21	EDO	N	613	4/4	0.91	0.17	31,37,37,39	4
21	EDO	P	320	4/4	0.91	0.26	53,60,63,73	4
20	DMU	C	306	11/33	0.91	0.27	59,63,70,72	11
20	DMU	B	303	22/33	0.92	0.19	50,61,72,75	22
21	EDO	G	102	4/4	0.92	0.17	30,34,35,38	4
26	CDL	L	101	94/100	0.92	0.15	44,85,129,155	0
20	DMU	Z	101	33/33	0.92	0.12	56,67,90,94	0
20	DMU	Z	102	8/33	0.92	0.23	51,57,61,62	8
20	DMU	D	201	33/33	0.92	0.15	28,44,51,78	33
21	EDO	O	309	4/4	0.93	0.16	36,37,39,40	4
21	EDO	E	202	4/4	0.93	0.24	35,35,37,39	4
20	DMU	P	307	11/33	0.93	0.25	52,53,61,63	11
20	DMU	O	307	11/33	0.93	0.24	47,55,65,70	11
21	EDO	A	614	4/4	0.94	0.12	37,39,40,44	4
21	EDO	N	615	4/4	0.94	0.21	31,32,32,33	4
21	EDO	S	102	4/4	0.94	0.11	25,25,31,31	4
21	EDO	E	203	4/4	0.95	0.21	34,35,41,42	4
21	EDO	C	321	4/4	0.95	0.16	37,37,39,40	4
24	CHD	C	301	29/29	0.95	0.07	32,35,40,43	0
21	EDO	N	616	4/4	0.95	0.15	37,39,42,45	4
28	PEK	T	101	53/53	0.95	0.13	38,62,110,159	0
24	CHD	P	302	29/29	0.96	0.07	32,37,41,45	0
21	EDO	A	613	4/4	0.96	0.18	27,28,28,29	4
21	EDO	T	104	4/4	0.96	0.10	36,37,39,40	4
20	DMU	M	101	33/33	0.96	0.08	41,52,78,83	0
21	EDO	R	202	4/4	0.96	0.15	38,39,41,41	4
21	EDO	R	201	4/4	0.97	0.26	63,63,64,70	4
21	EDO	P	321	4/4	0.97	0.12	42,42,45,45	4
22	PGV	N	618	51/51	0.97	0.09	33,46,79,92	0
28	PEK	G	101	53/53	0.97	0.11	33,56,90,112	0
24	CHD	B	305	29/29	0.97	0.07	30,36,41,50	0
21	EDO	R	203	4/4	0.98	0.16	44,49,51,58	4

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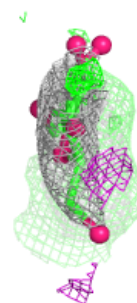
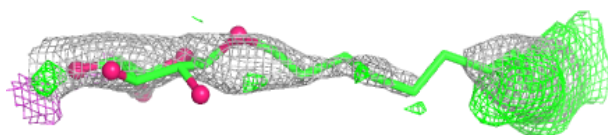
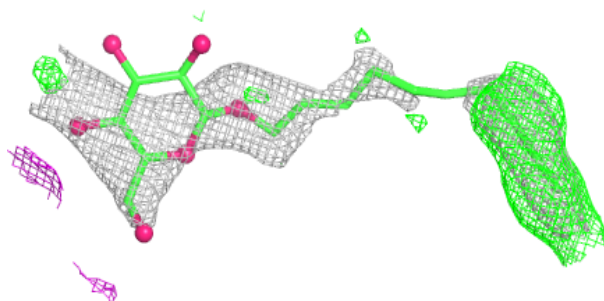
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	PGV	P	304	51/51	0.98	0.09	34,43,102,119	0
21	EDO	B	304	4/4	0.98	0.08	25,26,27,30	4
21	EDO	S	103	4/4	0.98	0.13	32,36,37,37	4
21	EDO	F	103	4/4	0.98	0.08	32,34,37,38	4
24	CHD	O	301	29/29	0.98	0.06	32,36,39,47	0
22	PGV	A	616	51/51	0.98	0.08	29,41,80,92	0
22	PGV	C	303	51/51	0.98	0.09	32,41,90,108	0
25	UNX	C	302	1/1	0.98	0.19	56,56,56,56	0
14	HEA	A	601[A]	60/60	0.99	0.05	25,28,41,47	9
14	HEA	A	601[B]	60/60	0.99	0.05	25,28,45,51	9
14	HEA	A	602	60/60	0.99	0.05	24,27,36,41	0
14	HEA	N	603[A]	60/60	0.99	0.05	31,35,46,52	9
14	HEA	N	603[B]	60/60	0.99	0.05	31,35,49,53	9
14	HEA	N	604	60/60	0.99	0.06	28,32,40,43	0
16	MG	A	604	1/1	0.99	0.02	30,30,30,30	0
18	PER	A	606	2/2	0.99	0.05	29,29,29,34	0
18	PER	N	608	2/2	0.99	0.07	33,33,33,40	0
15	CU	N	605	1/1	1.00	0.01	32,32,32,32	0
15	CU	A	603	1/1	1.00	0.02	28,28,28,28	0
16	MG	N	606	1/1	1.00	0.02	37,37,37,37	0
23	CUA	B	301	2/2	1.00	0.02	29,29,29,30	0
23	CUA	O	305	2/2	1.00	0.02	39,39,39,40	0
27	ZN	F	101	1/1	1.00	0.01	36,36,36,36	0
27	ZN	S	101	1/1	1.00	0.03	37,37,37,37	0
17	CA	A	605	1/1	1.00	0.02	33,33,33,33	0
17	CA	N	607	1/1	1.00	0.02	45,45,45,45	0

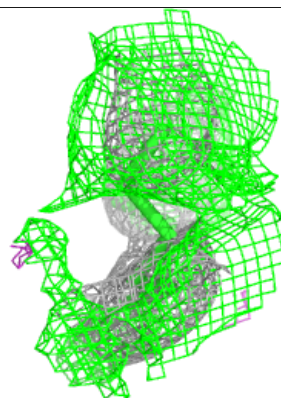
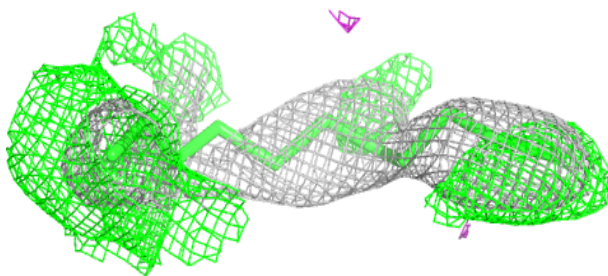
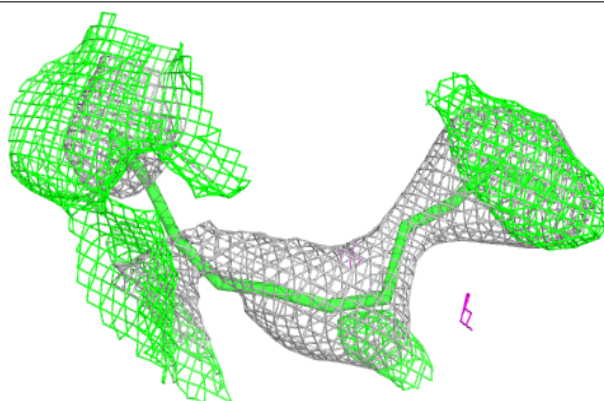
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DMU C 317:

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

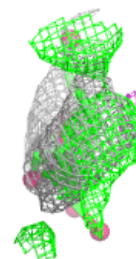
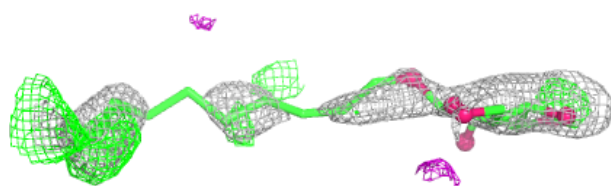
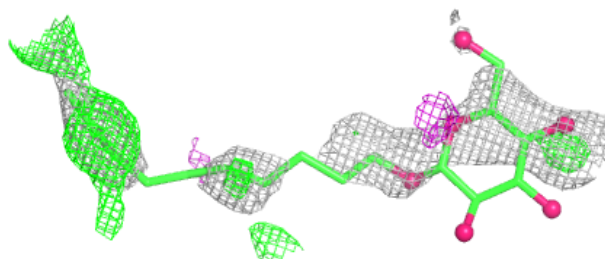
**Electron density around LFA P 311:**

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

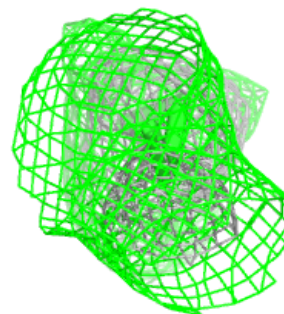
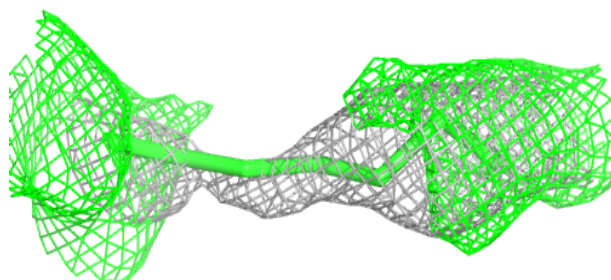
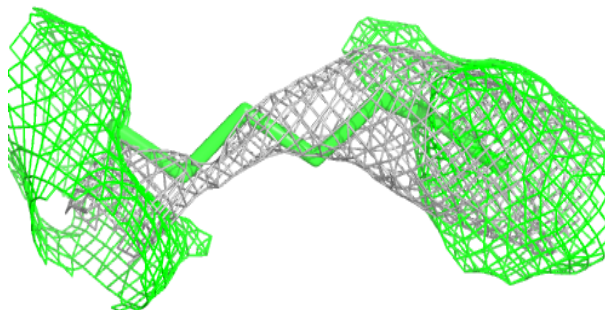


Electron density around DMU P 317:

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

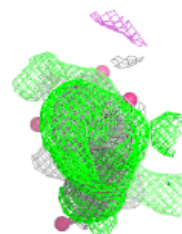
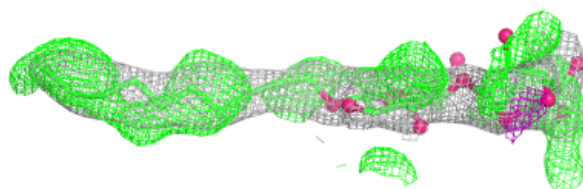
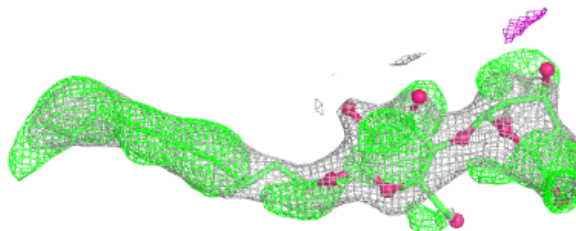
**Electron density around DMU N 611:**

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

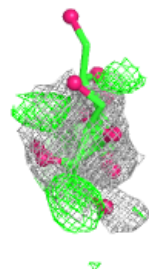
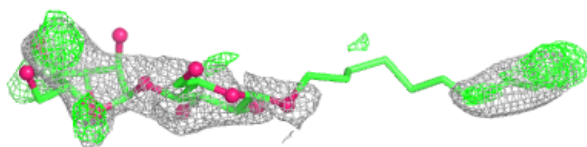
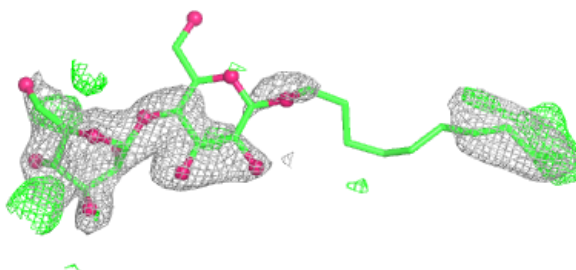


Electron density around DMU C 318:

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

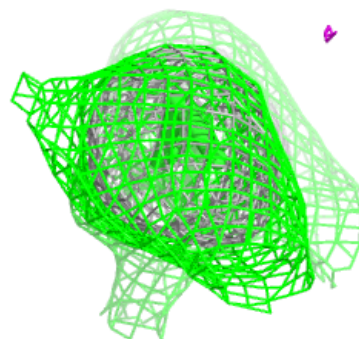
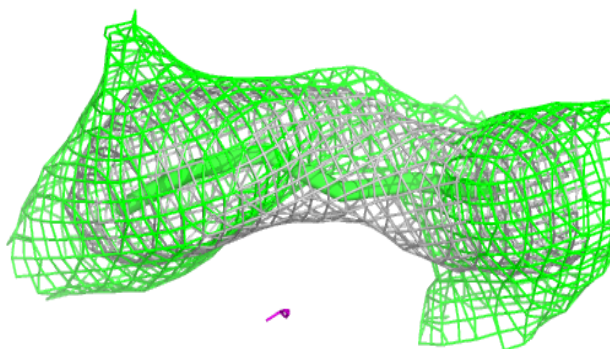
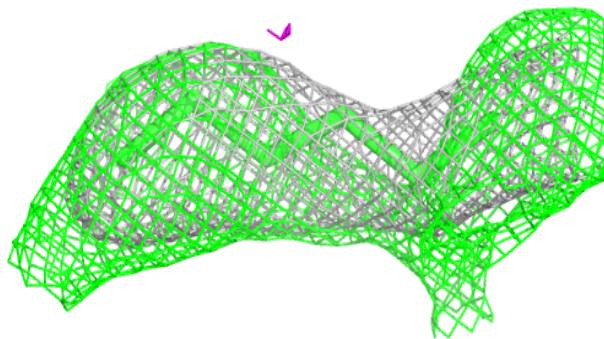
**Electron density around DMU P 319:**

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

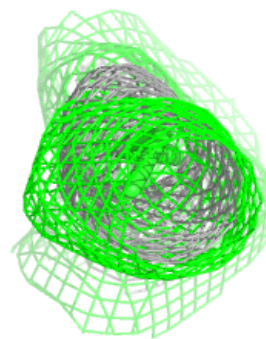
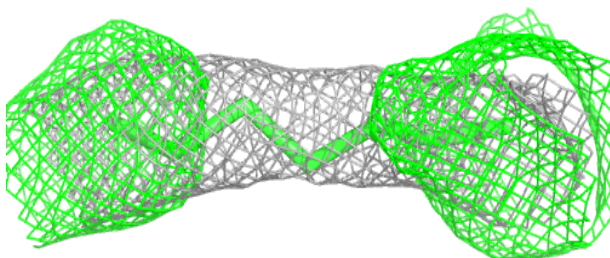
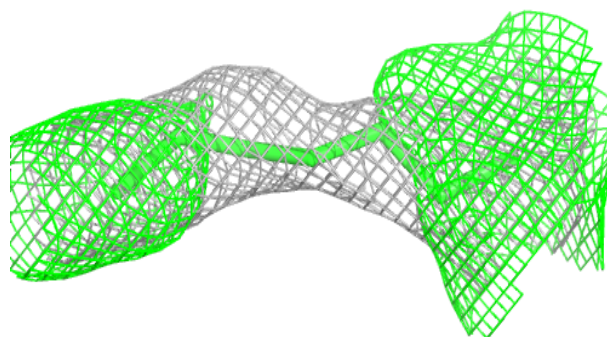


Electron density around LFA C 308:

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

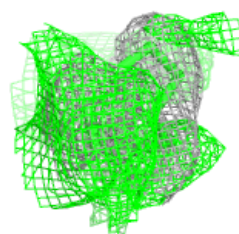
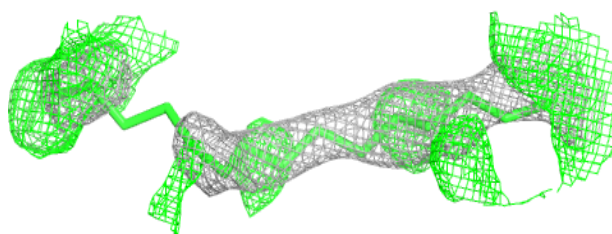
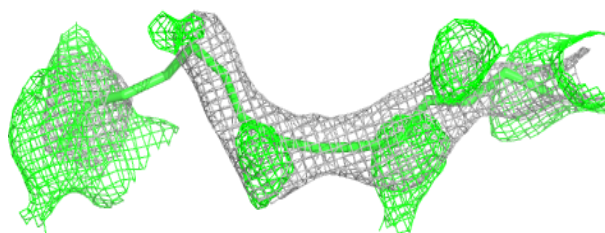
**Electron density around DMU A 609:**

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

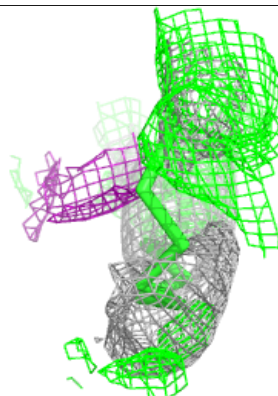
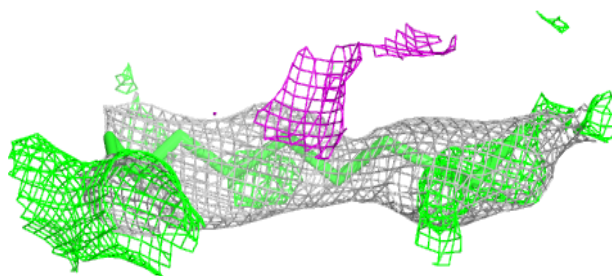
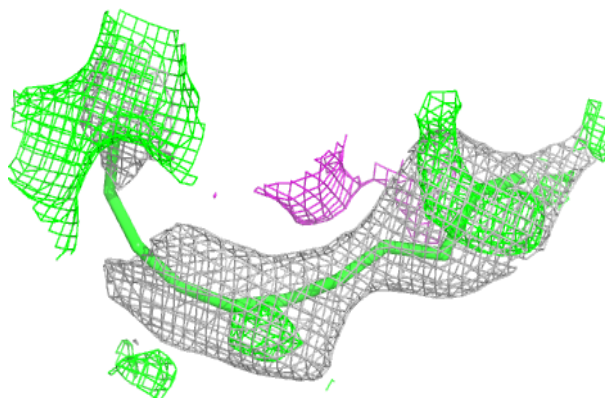


Electron density around LFA C 325:

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

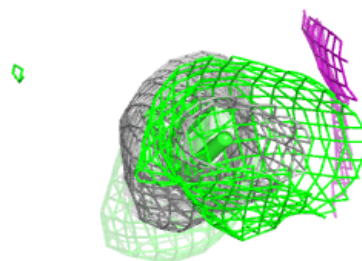
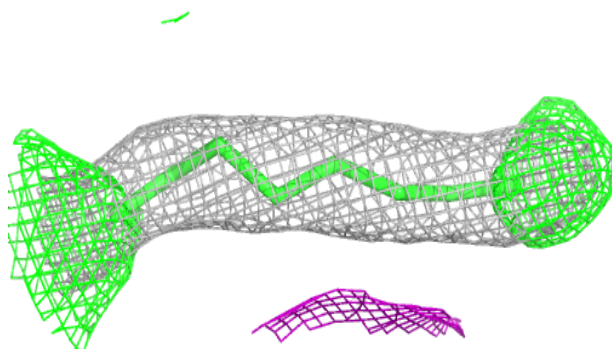
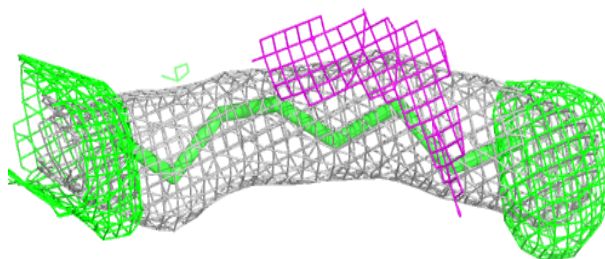
**Electron density around LFA C 310:**

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

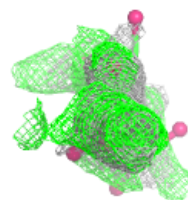
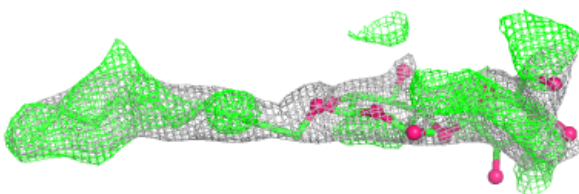
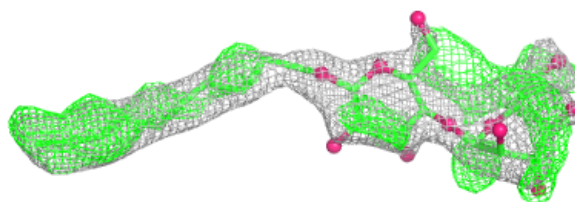


Electron density around DMU M 102:

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

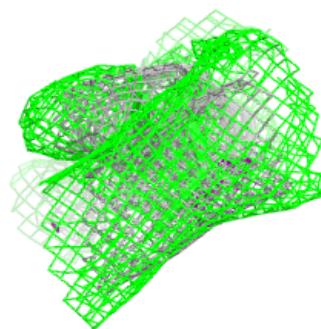
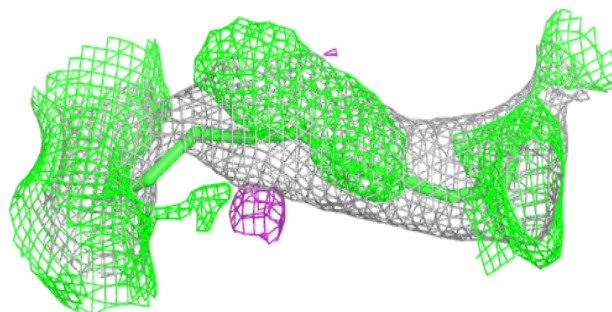
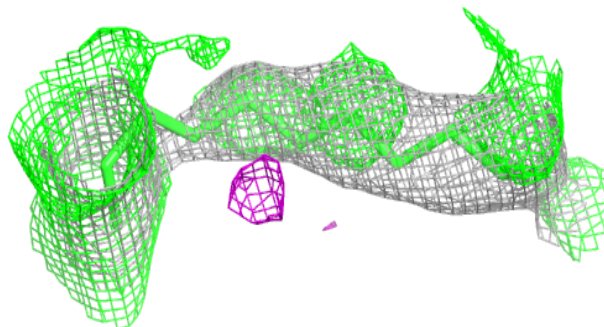
**Electron density around DMU P 318:**

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

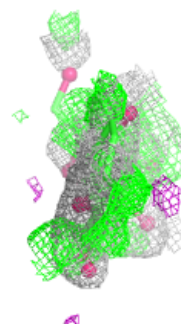
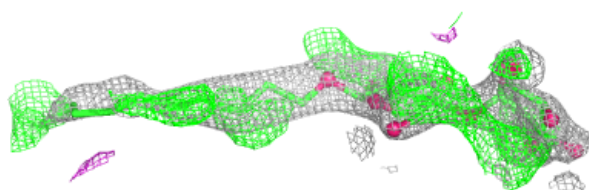
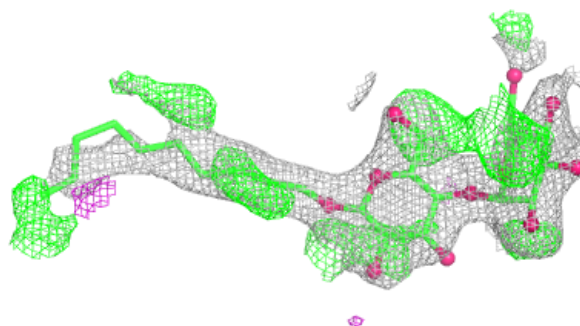


Electron density around LFA P 312:

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

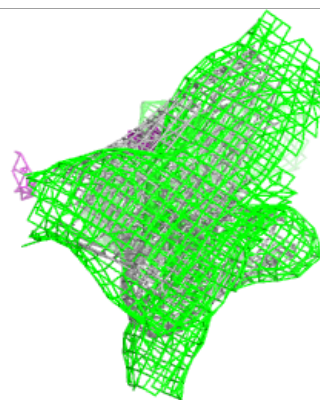
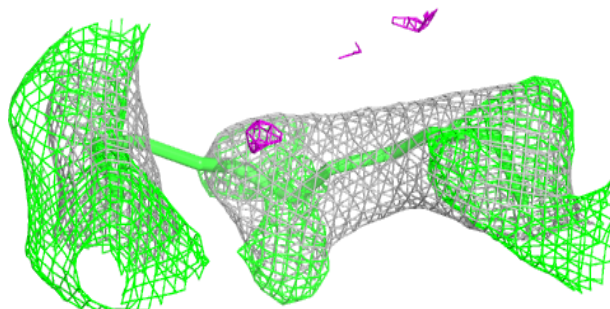
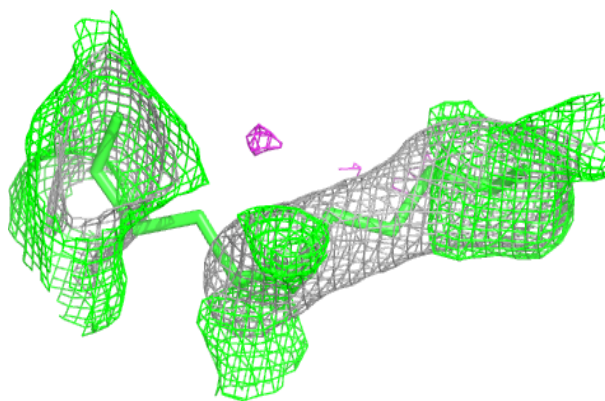
**Electron density around DMU P 315:**

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

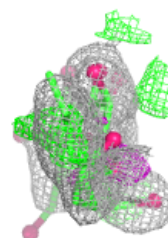
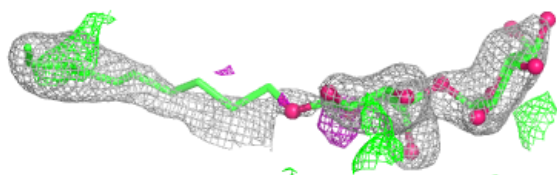
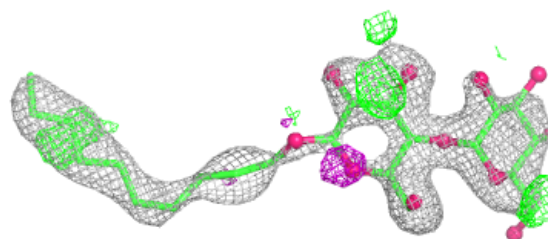


Electron density around LFA C 312:

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

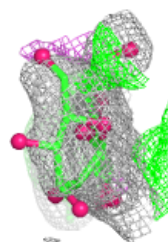
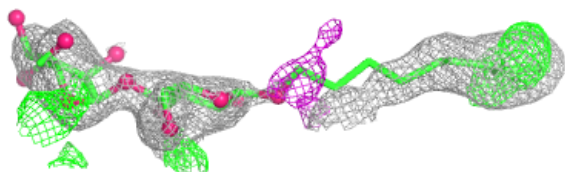
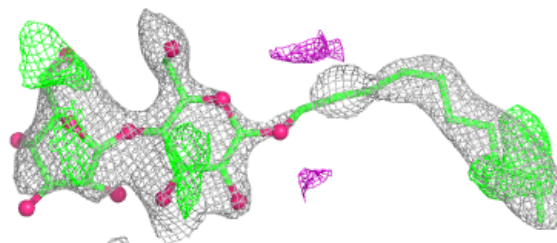
**Electron density around DMU C 324:**

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

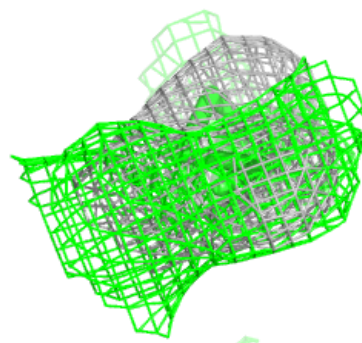
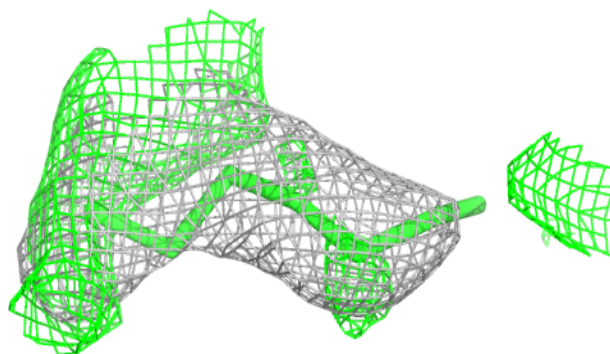
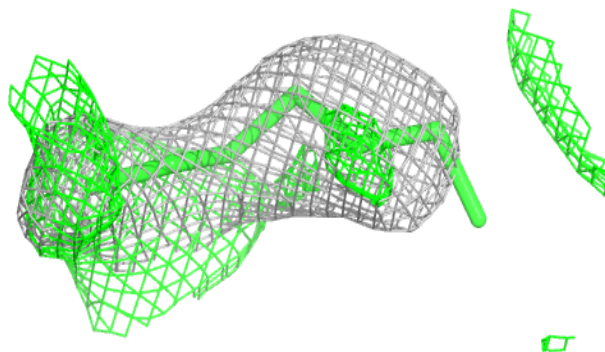


Electron density around DMU P 324:

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

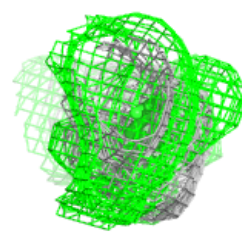
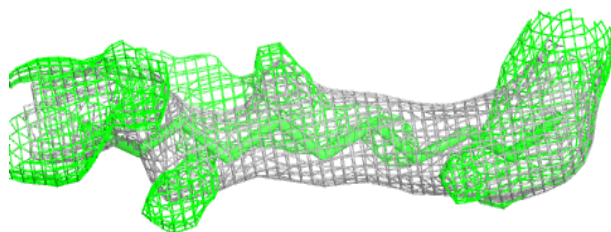
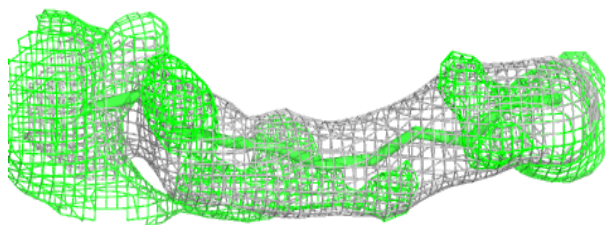
**Electron density around DMU P 316:**

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

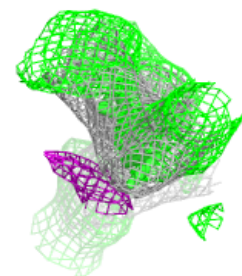
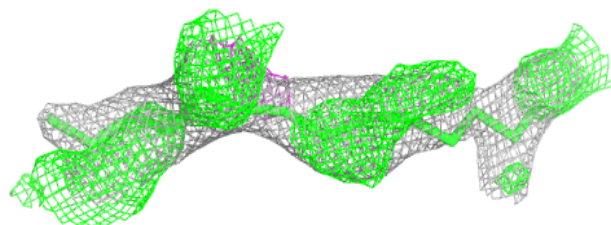
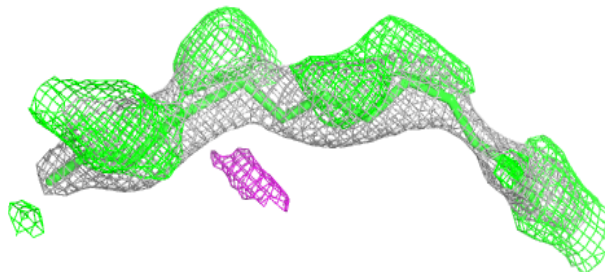


Electron density around LFA O 302:

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

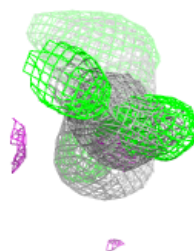
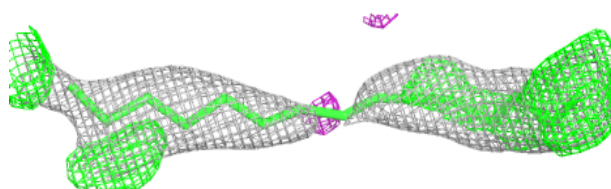
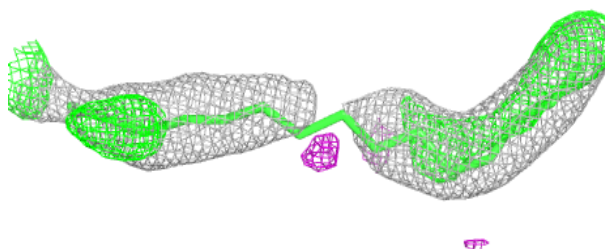
**Electron density around LFA C 311:**

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

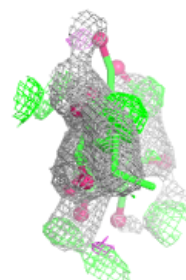
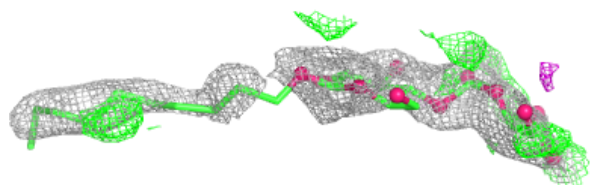
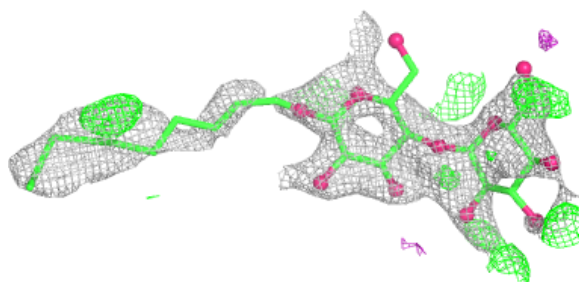


Electron density around LFA C 313:

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

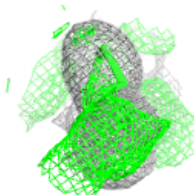
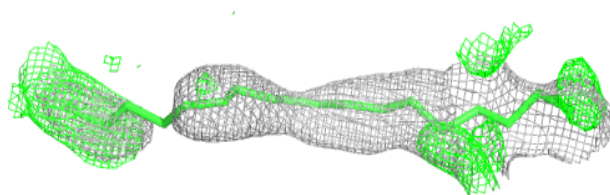
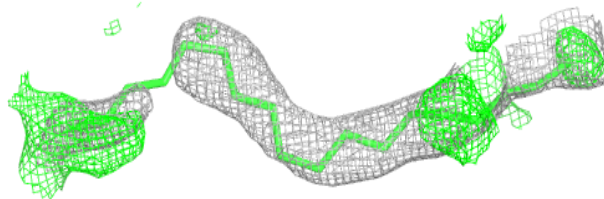
**Electron density around DMU C 319:**

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

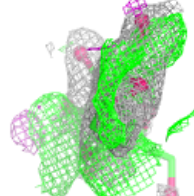
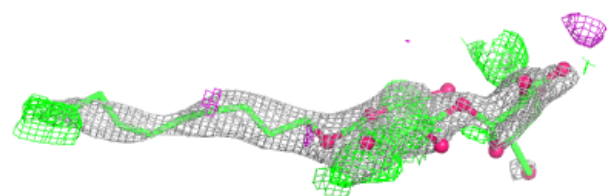
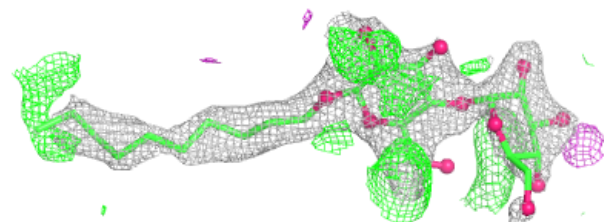


Electron density around LFA P 310:

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

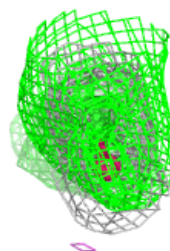
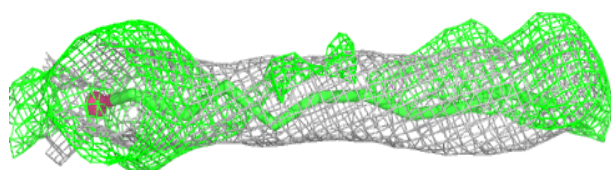
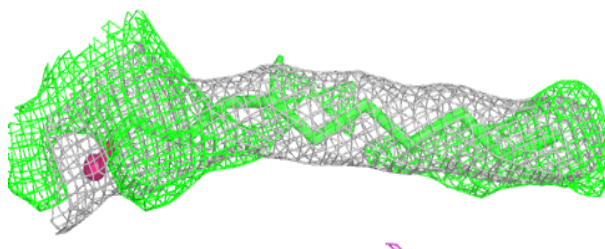
**Electron density around DMU C 315:**

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

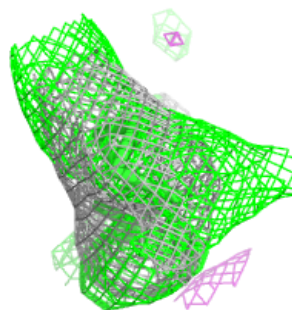
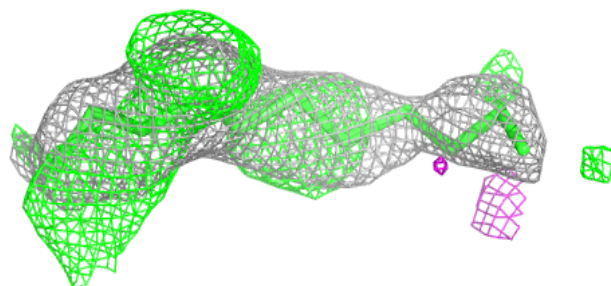
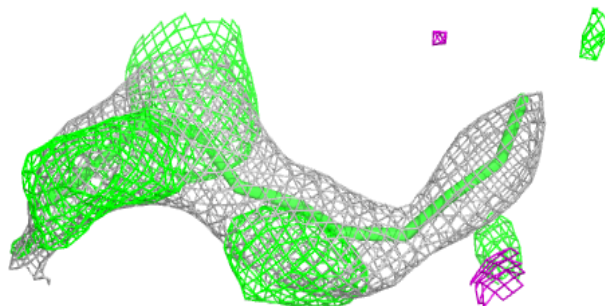


Electron density around DMU O 306:

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

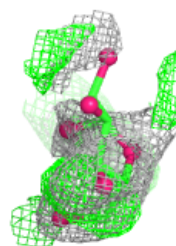
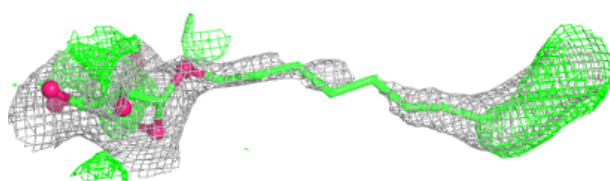
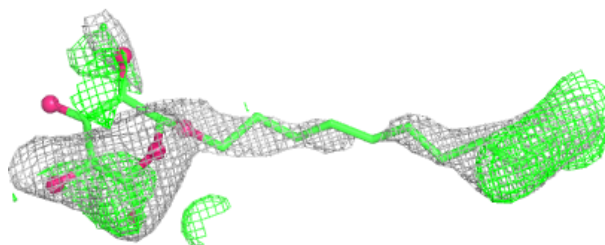
**Electron density around LFA P 308:**

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

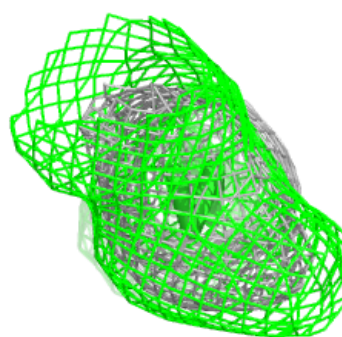
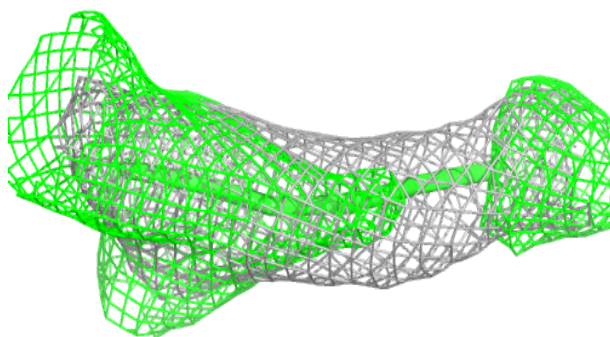
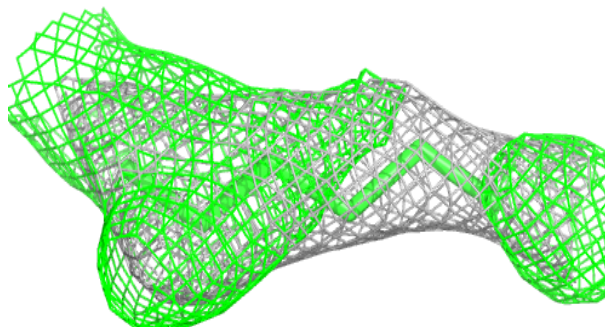


Electron density around DMU B 307:

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

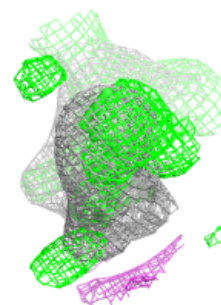
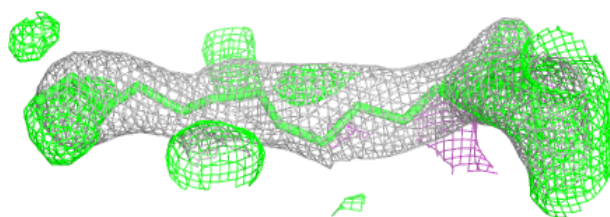
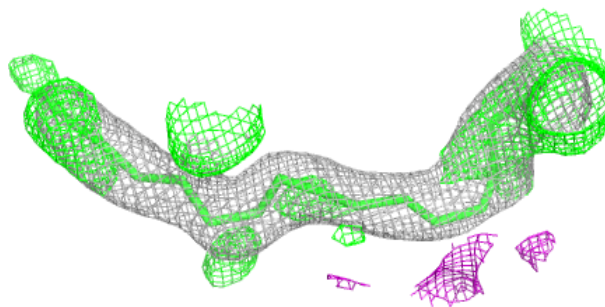
**Electron density around LFA P 309:**

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

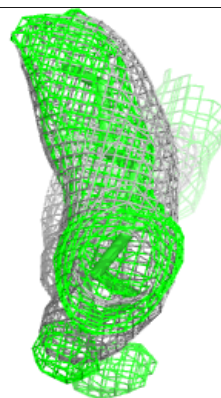
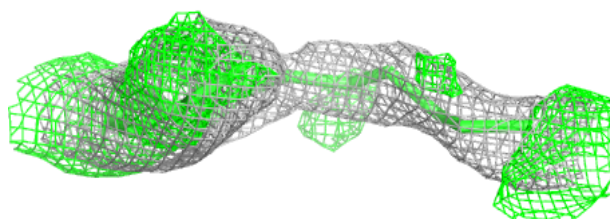
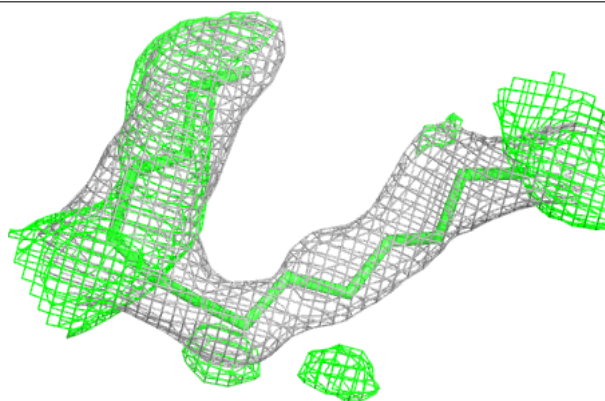


Electron density around LFA N 601:

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

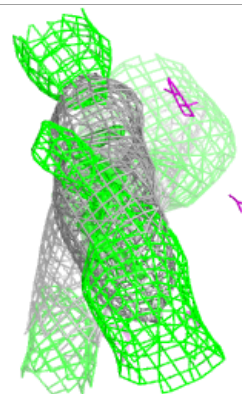
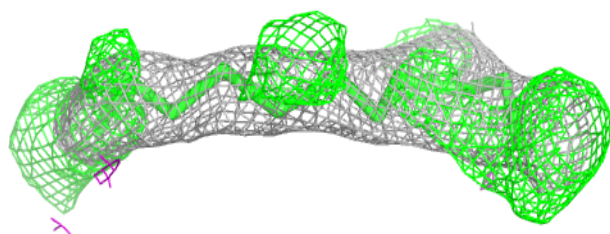
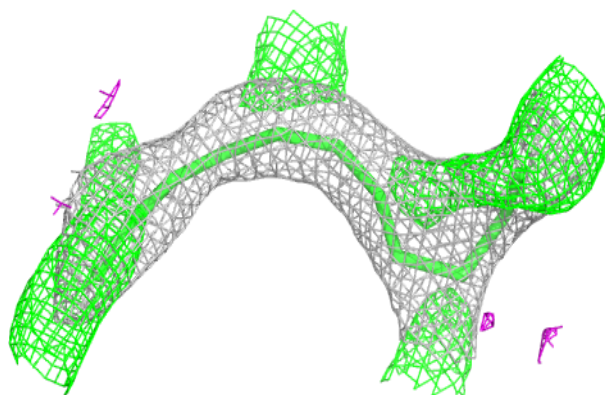
**Electron density around LFA N 610:**

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

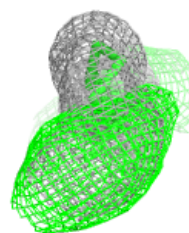
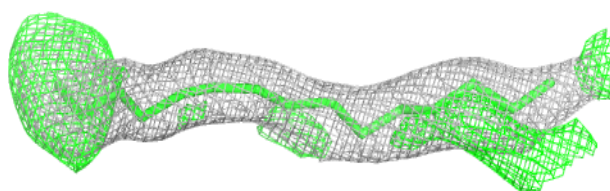
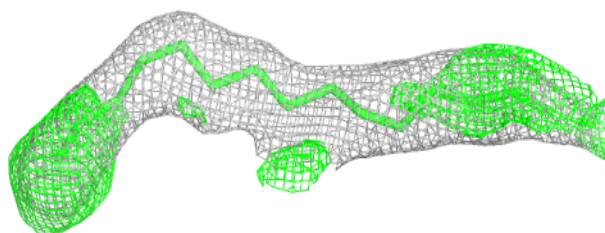


Electron density around LFA C 307:

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

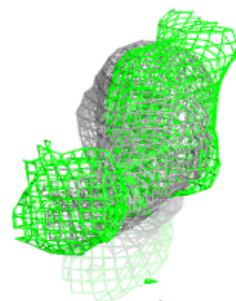
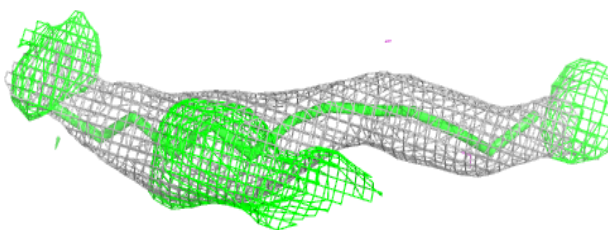
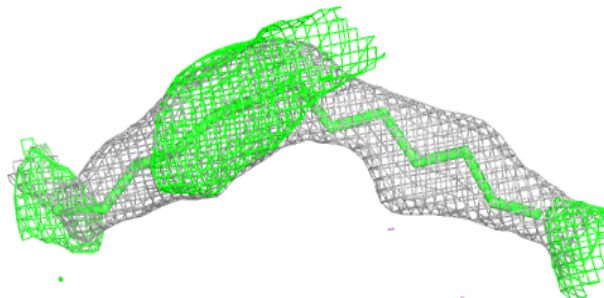
**Electron density around LFA P 313:**

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

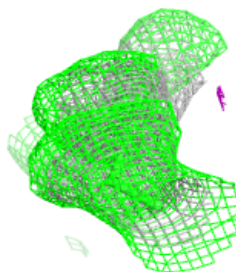
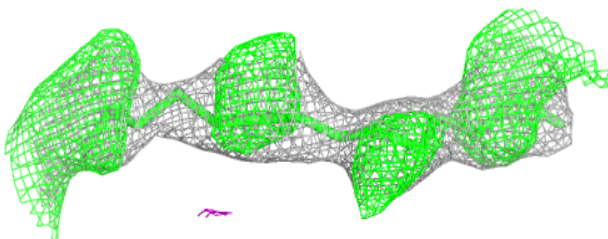
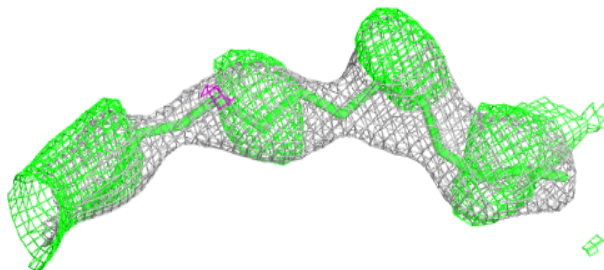


Electron density around LFA P 314:

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

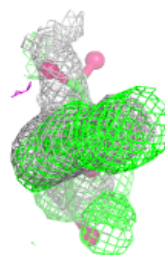
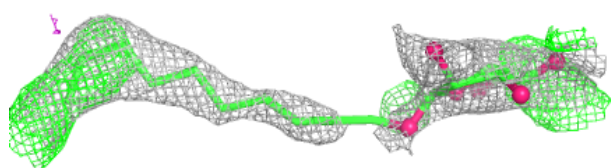
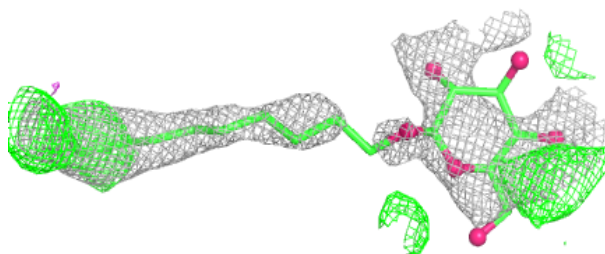
**Electron density around LFA T 102:**

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

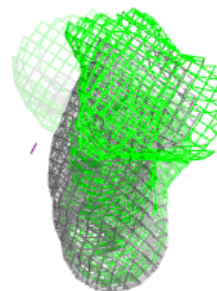
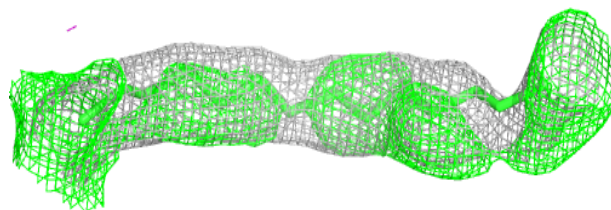
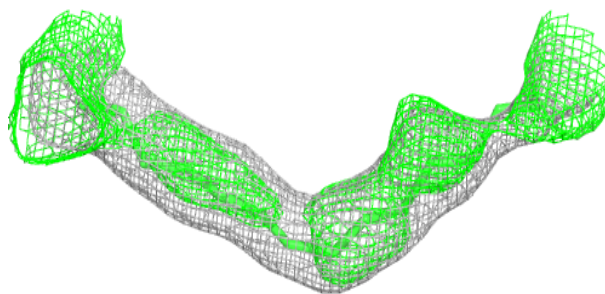


Electron density around DMU O 303:

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

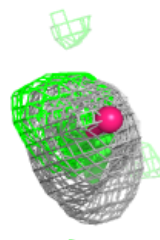
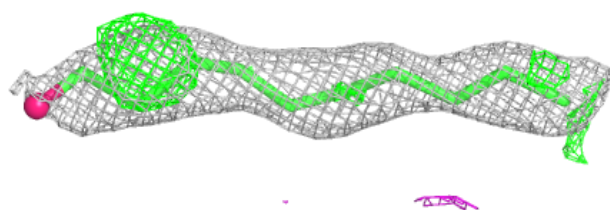
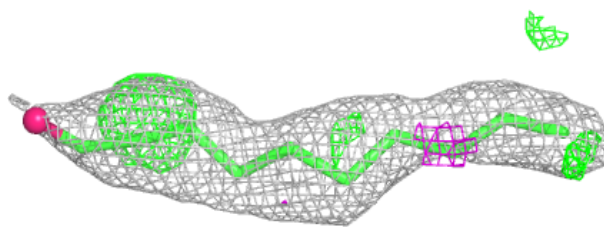
**Electron density around LFA A 607:**

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

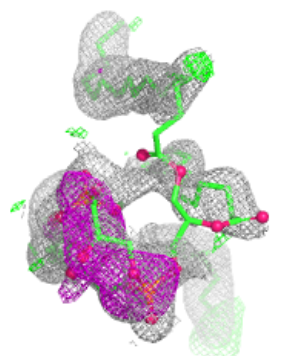
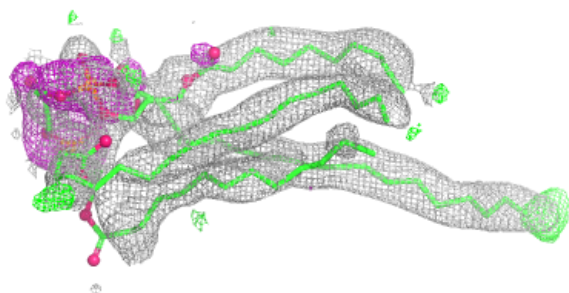
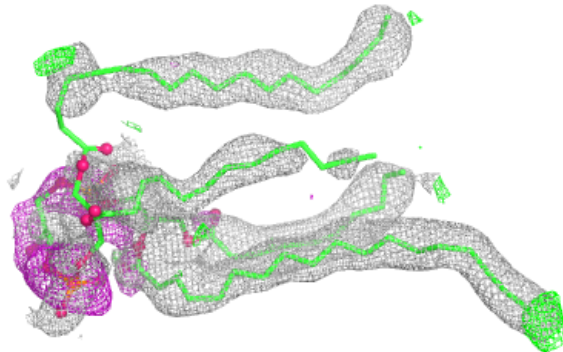


Electron density around DMU A 615:

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

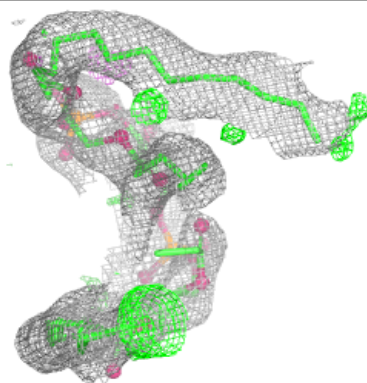
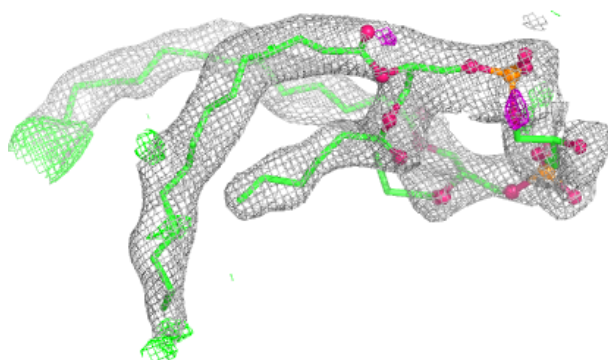
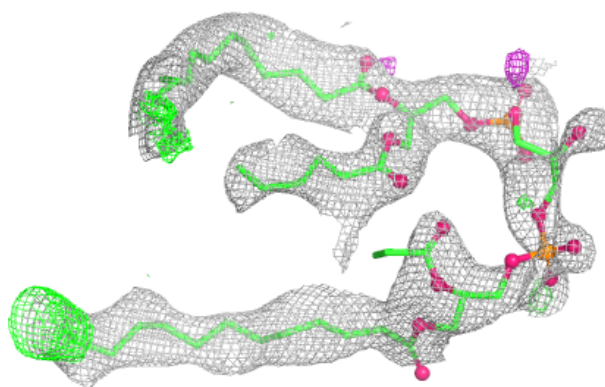
**Electron density around CDL C 304:**

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

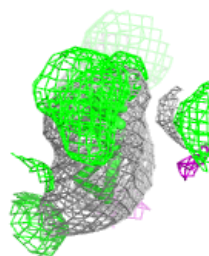
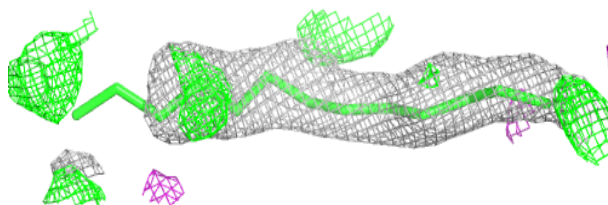
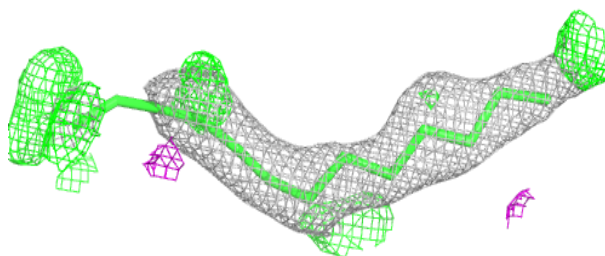


Electron density around CDL O 304:

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

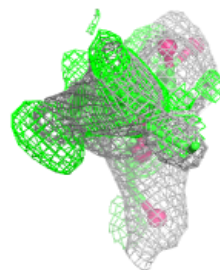
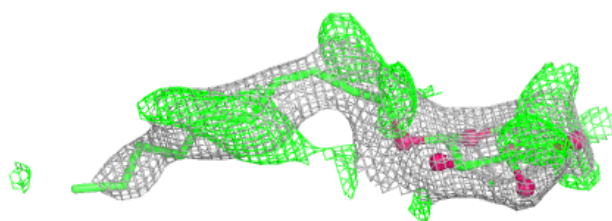
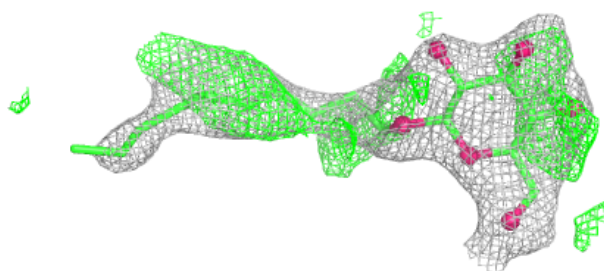
**Electron density around LFA C 314:**

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

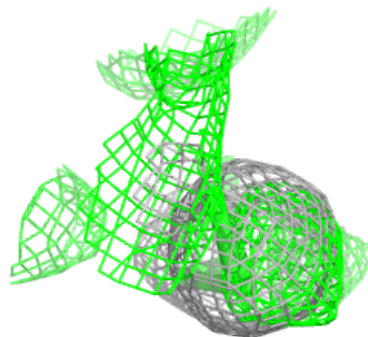
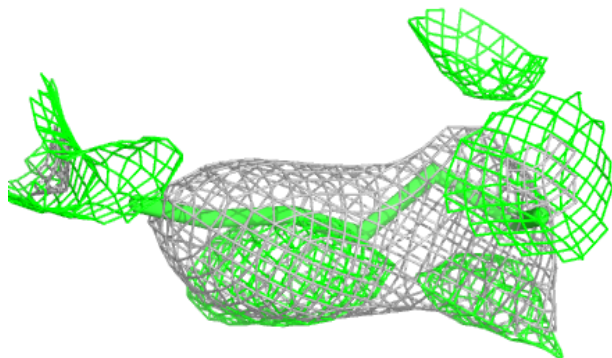
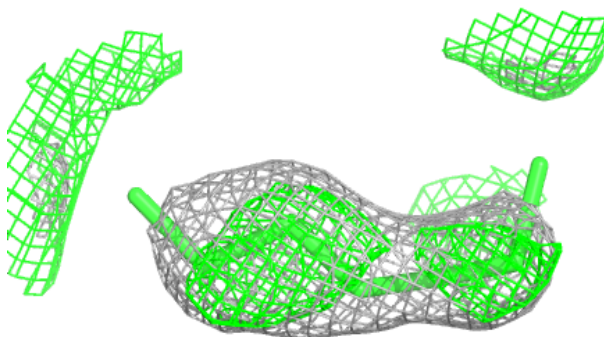


Electron density around DMU C 323:

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

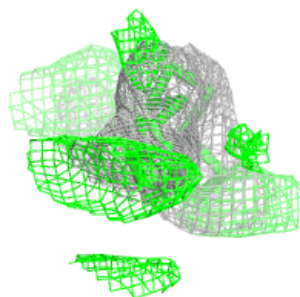
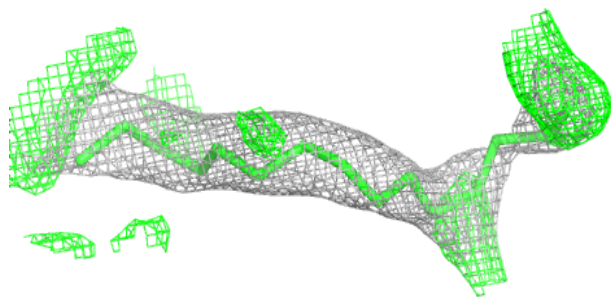
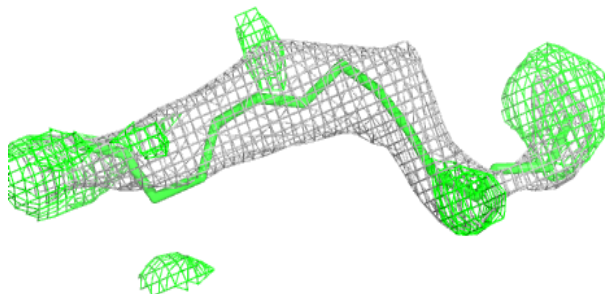
**Electron density around DMU C 316:**

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

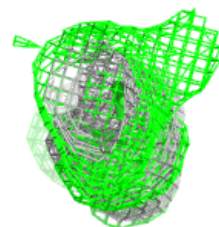
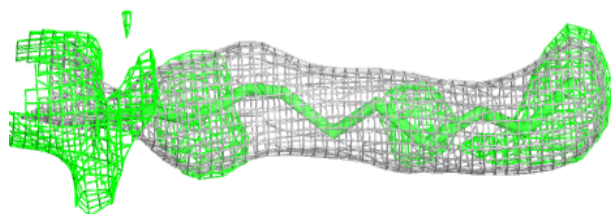
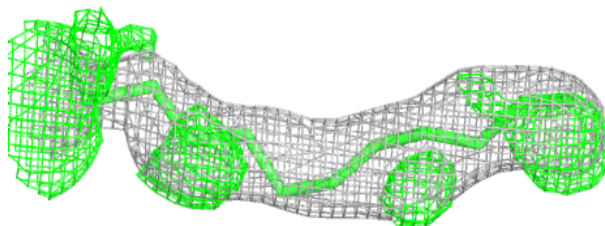


Electron density around LFA P 301:

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

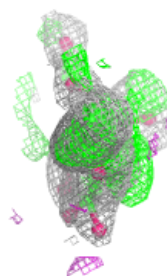
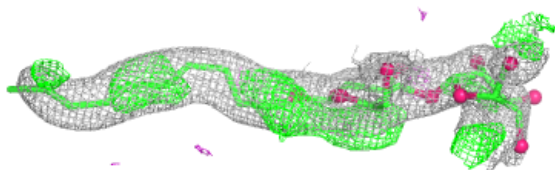
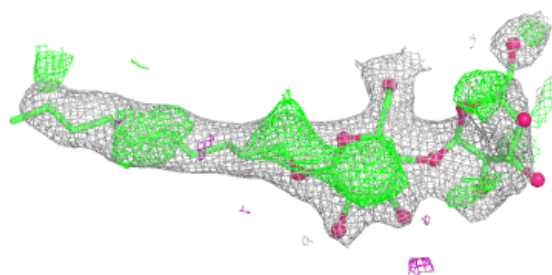
**Electron density around LFA T 103:**

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

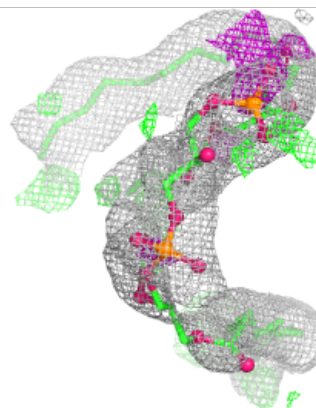
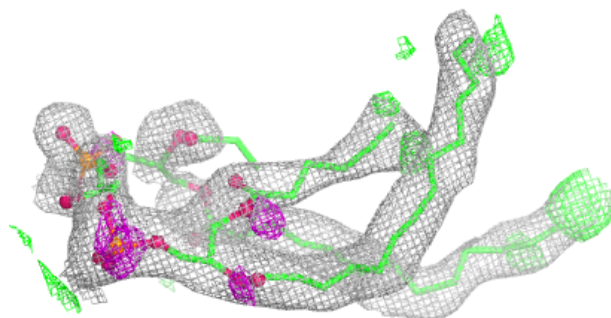
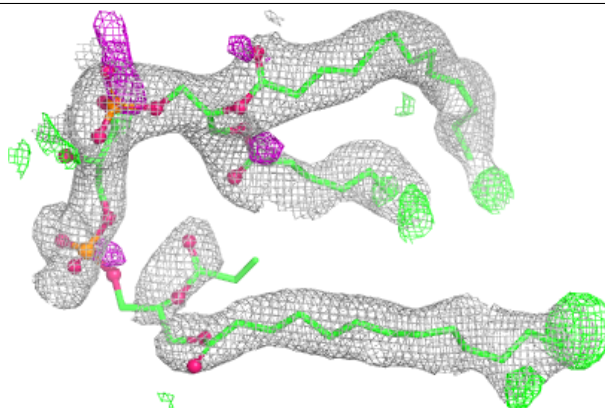


Electron density around DMU N 612:

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

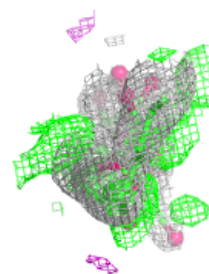
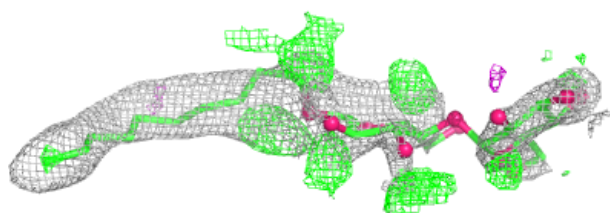
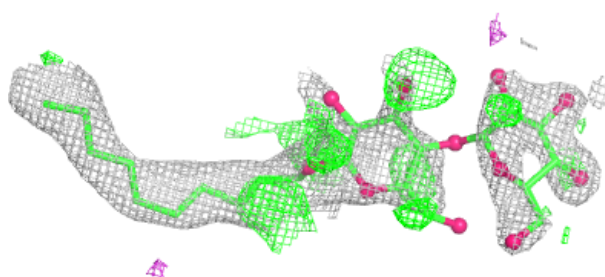
**Electron density around CDL I 101:**

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

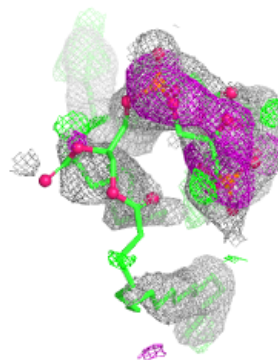
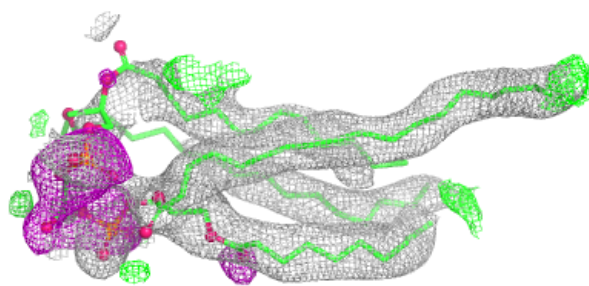
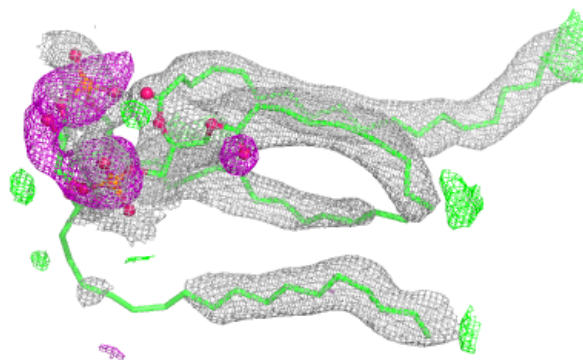


Electron density around DMU N 619:

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

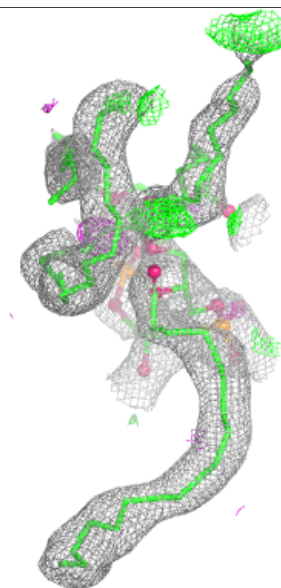
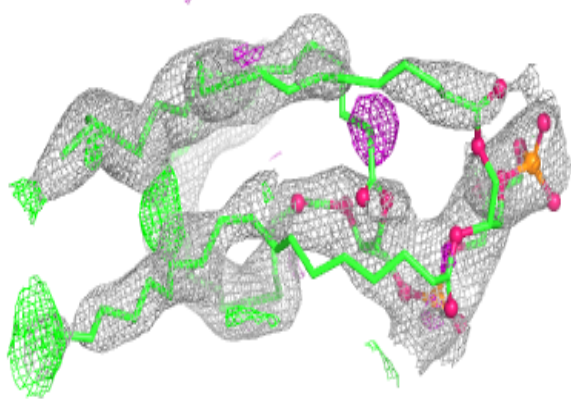
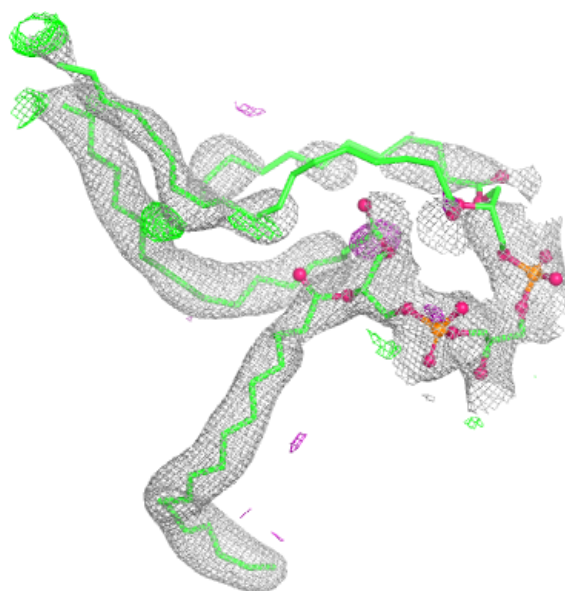
**Electron density around CDL P 305:**

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



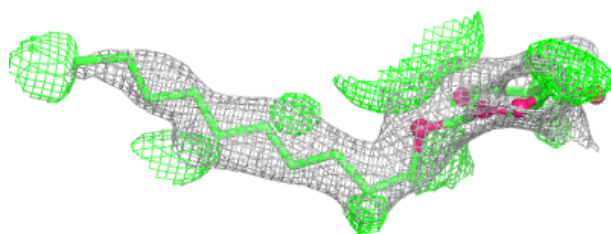
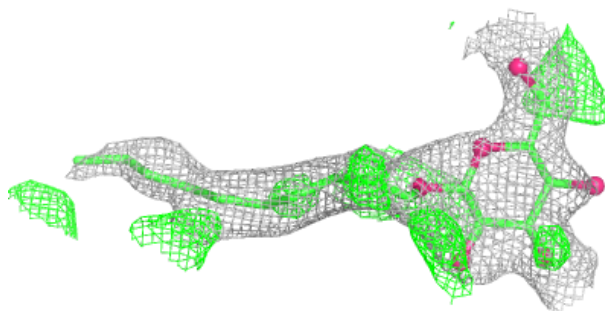
Electron density around CDL Y 101:

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

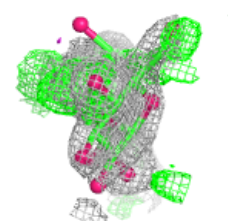
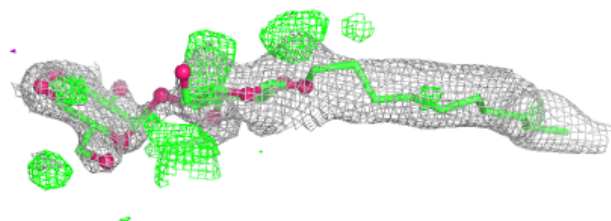
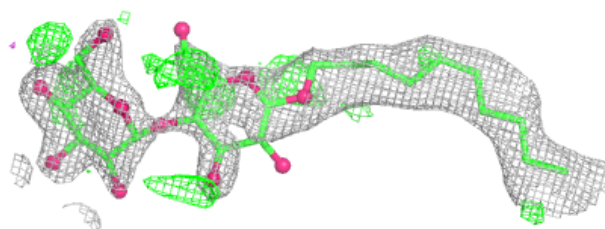


Electron density around DMU P 323:

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

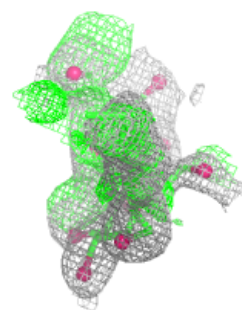
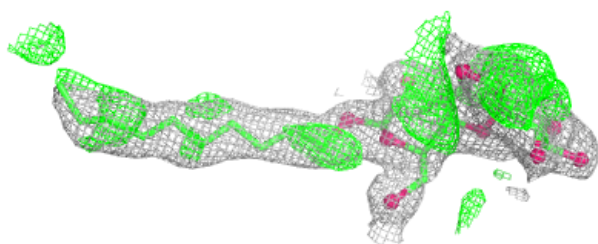
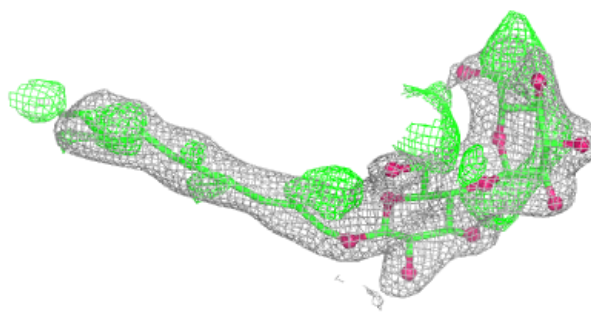
**Electron density around DMU H 101:**

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

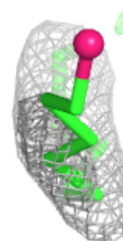
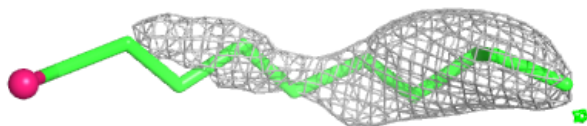
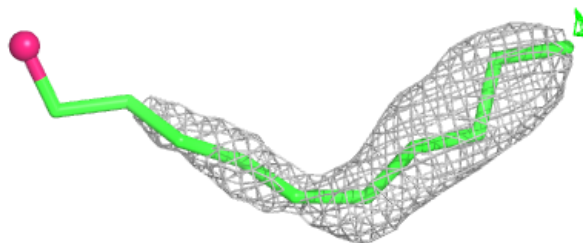


Electron density around DMU Q 201:

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

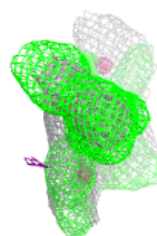
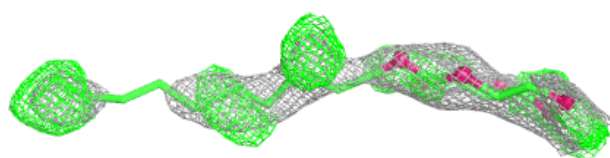
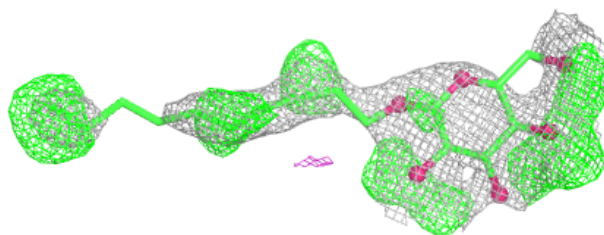
**Electron density around DMU W 101:**

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

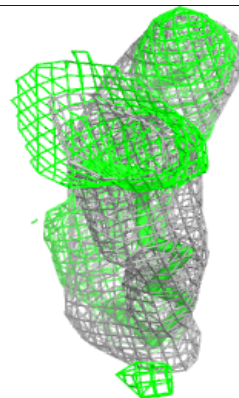
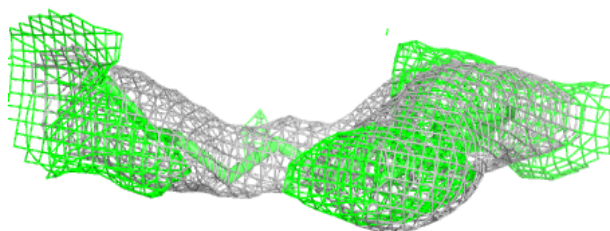
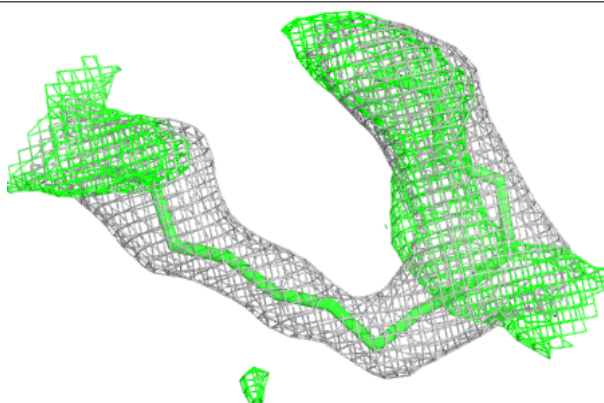


Electron density around DMU Y 102:

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

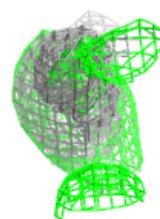
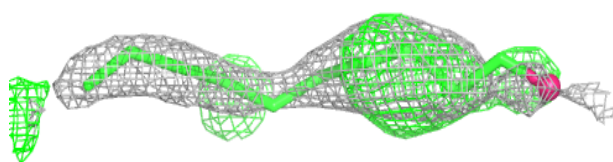
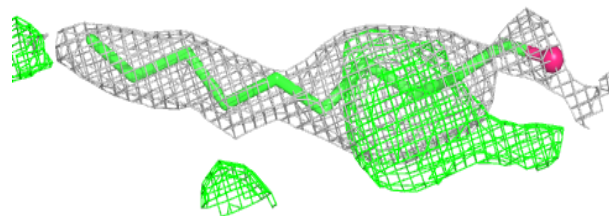
**Electron density around LFA A 608:**

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

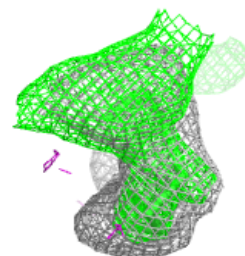
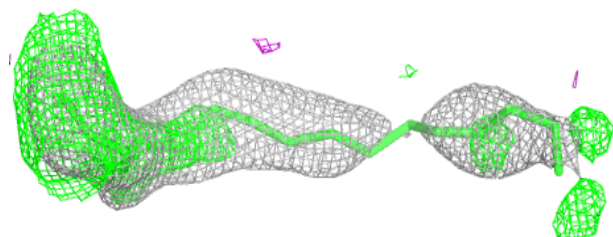
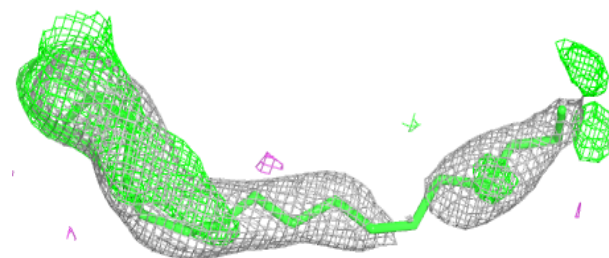


Electron density around DMU A 617:

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

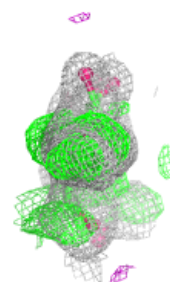
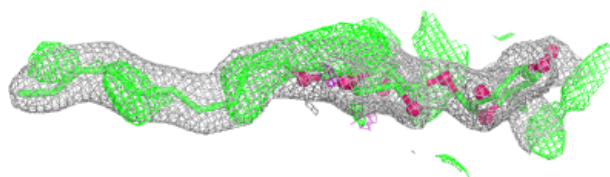
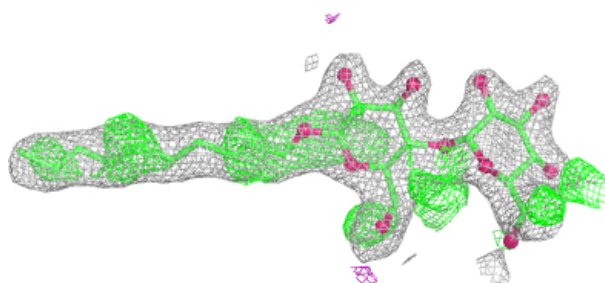
**Electron density around LFA B 306:**

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

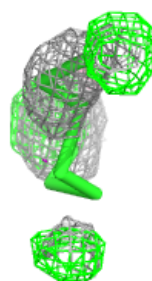
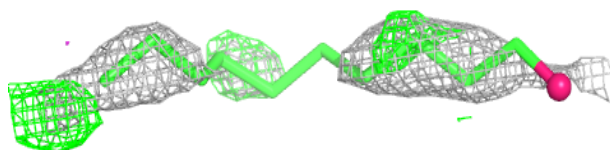
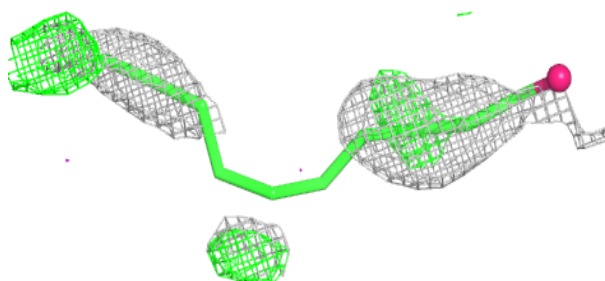


Electron density around DMU A 610:

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

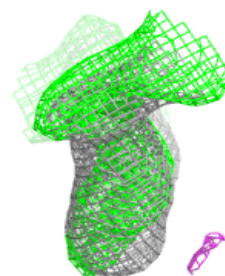
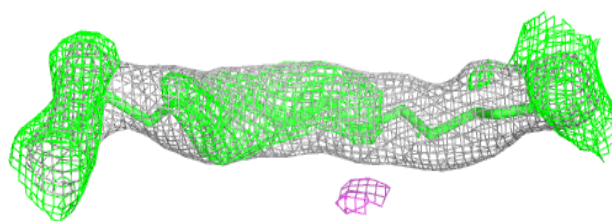
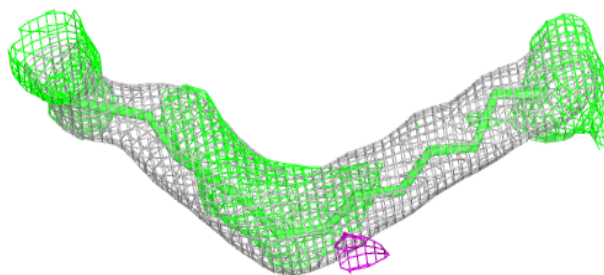
**Electron density around DMU N 602:**

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

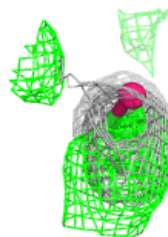
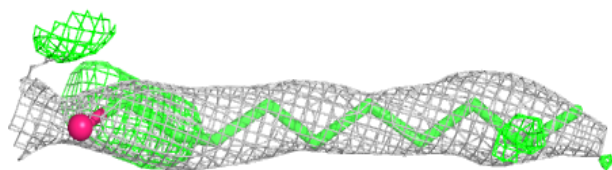
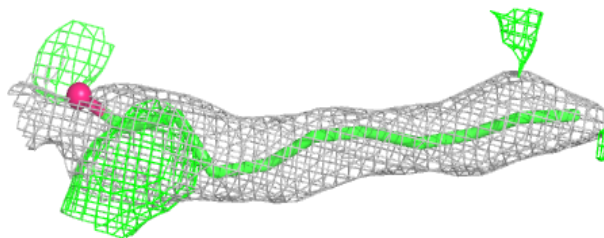


Electron density around LFA N 609:

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

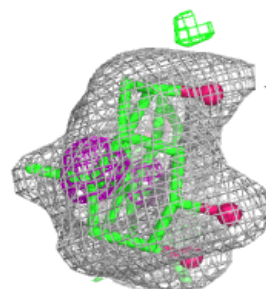
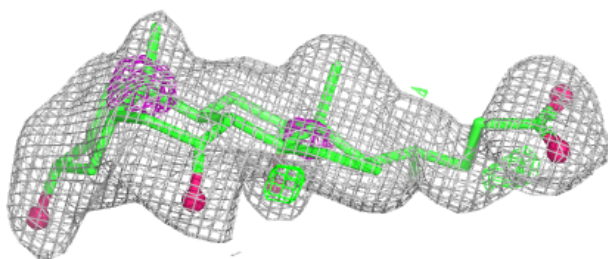
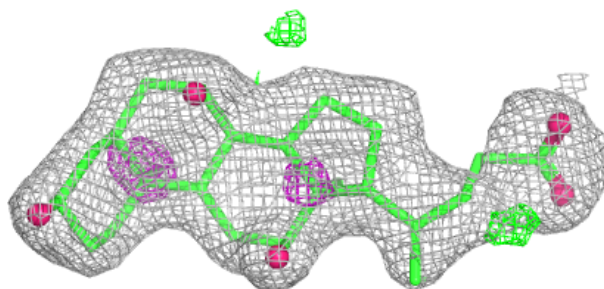
**Electron density around DMU B 302:**

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

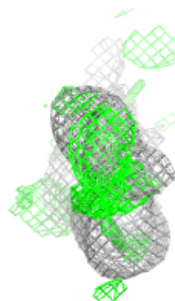
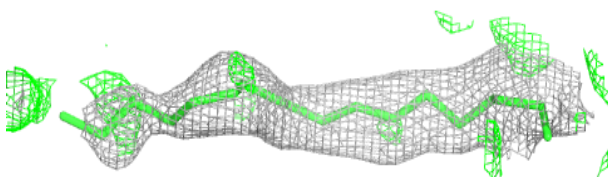
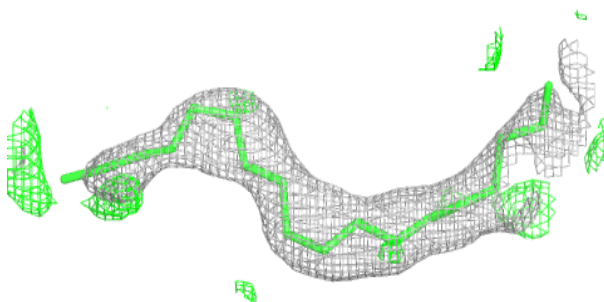


Electron density around CHD P 306:

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

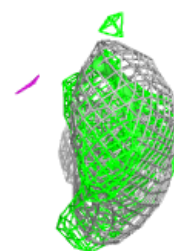
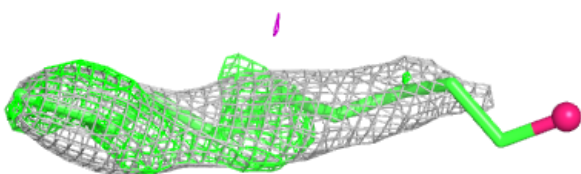
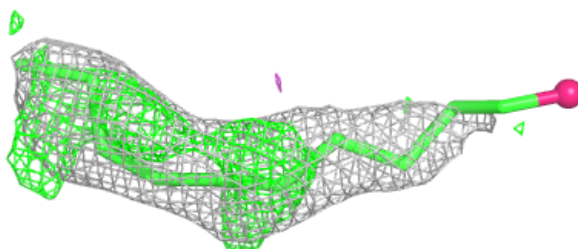
**Electron density around LFA C 309:**

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

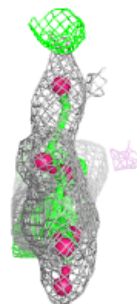
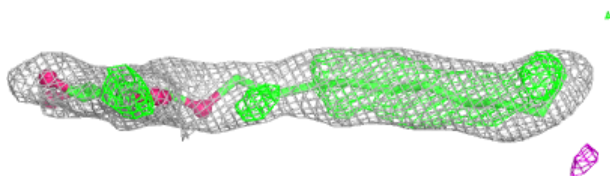
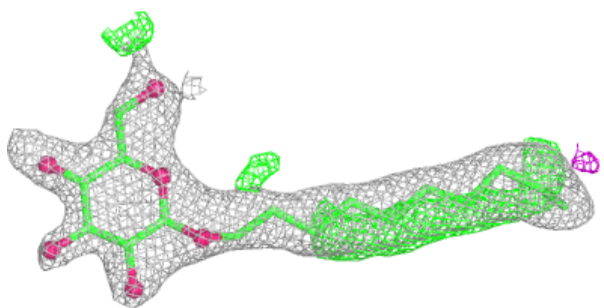


Electron density around DMU J 101:

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

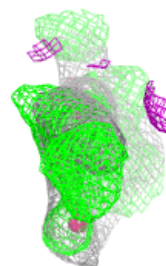
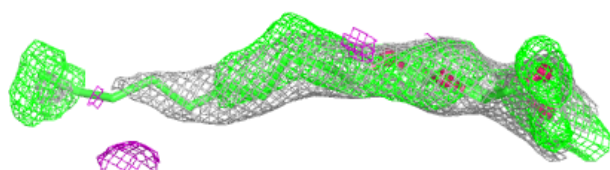
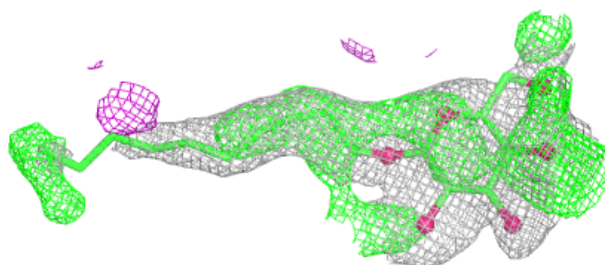
**Electron density around DMU O 308:**

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

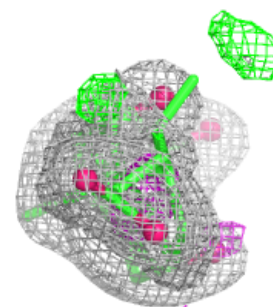
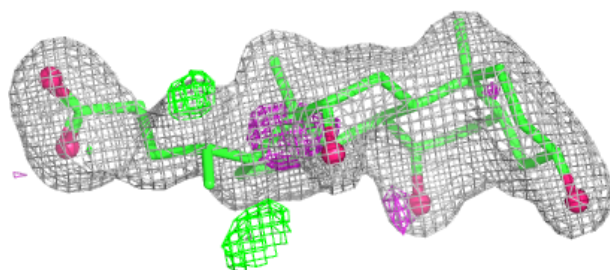
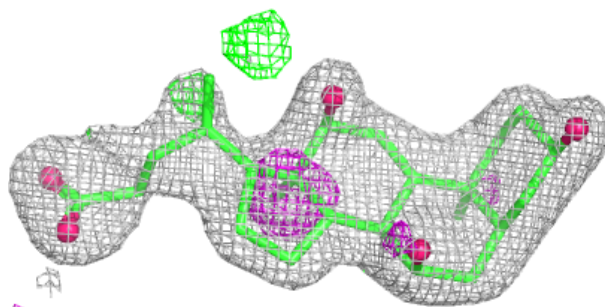


Electron density around DMU L 102:

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

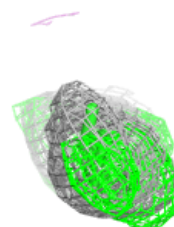
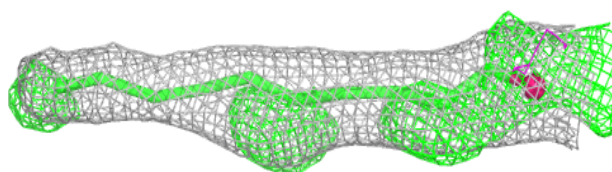
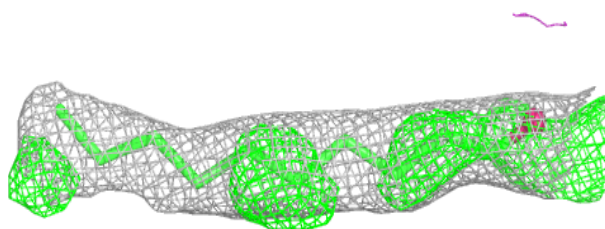
**Electron density around CHD C 305:**

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

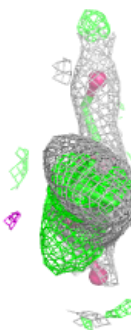
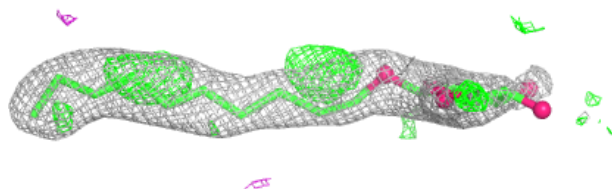
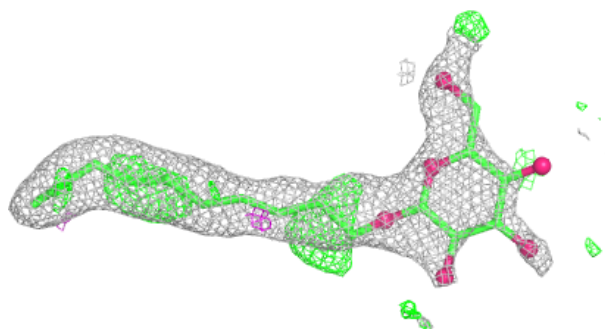


Electron density around DMU C 306:

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

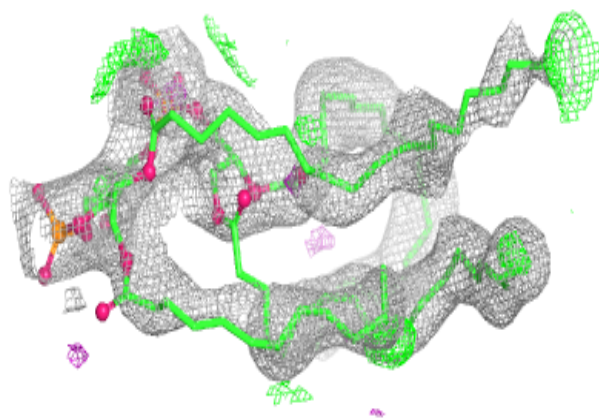
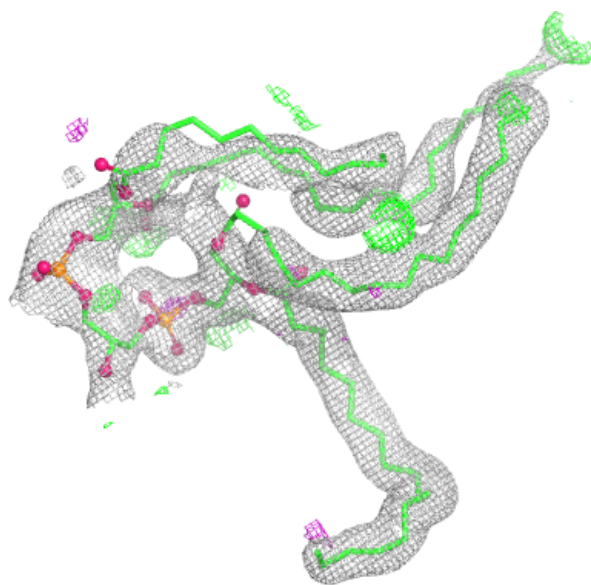
**Electron density around DMU B 303:**

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



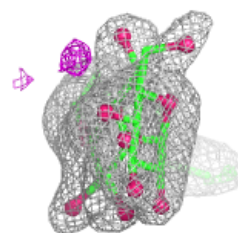
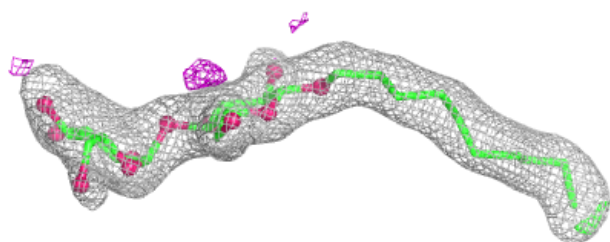
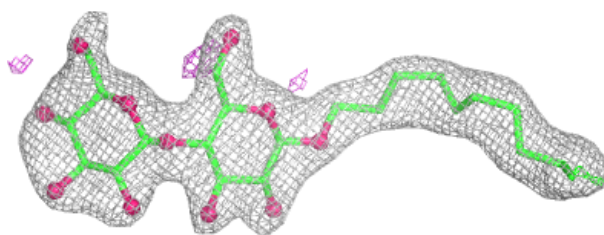
Electron density around CDL L 101:

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

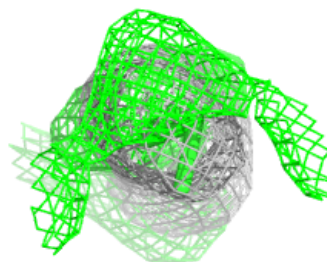
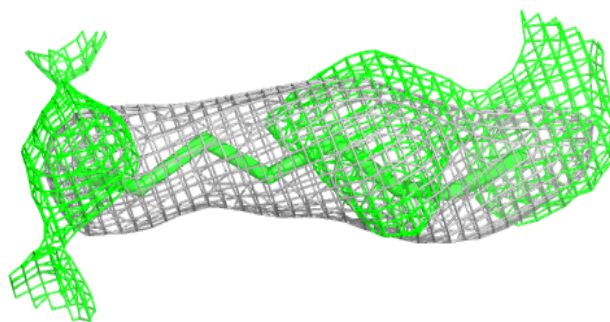
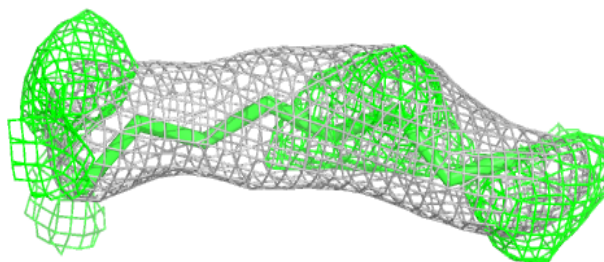


Electron density around DMU Z 101:

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

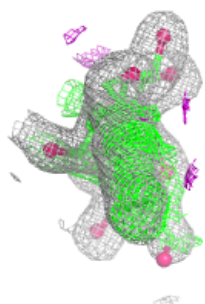
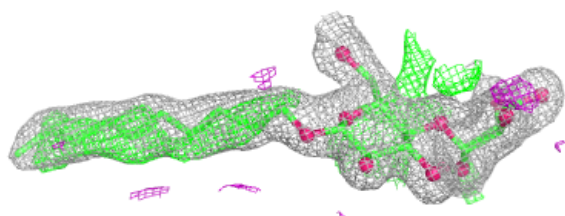
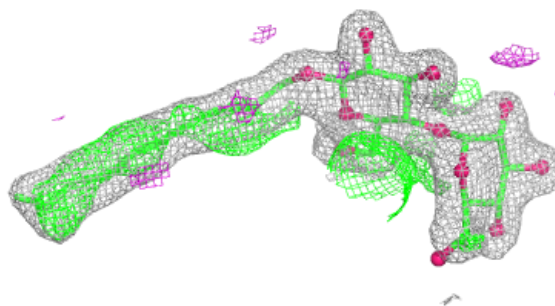
**Electron density around DMU Z 102:**

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

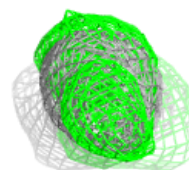
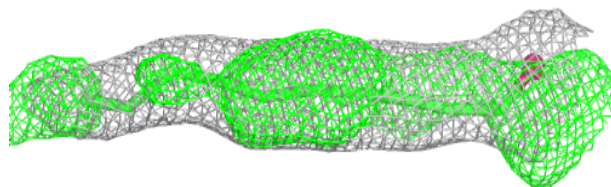
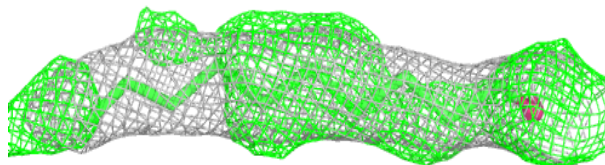


Electron density around DMU D 201:

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

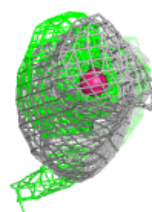
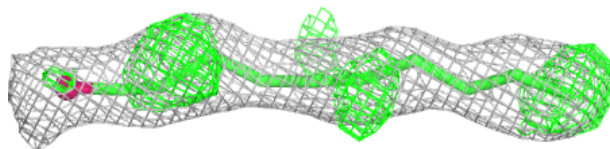
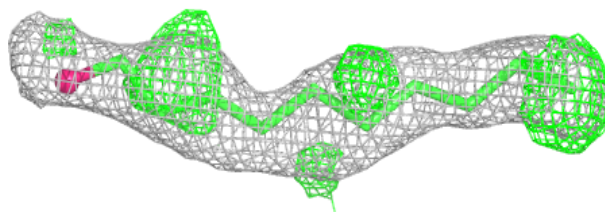
**Electron density around DMU P 307:**

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

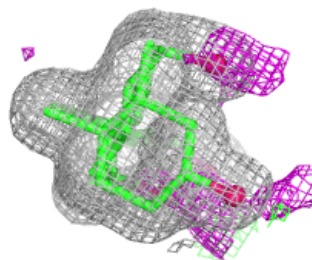
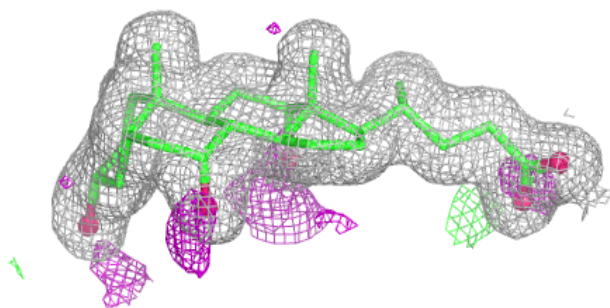
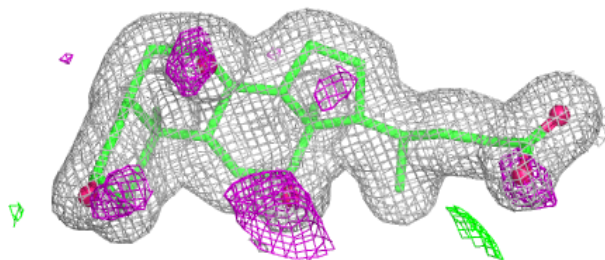


Electron density around DMU O 307:

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

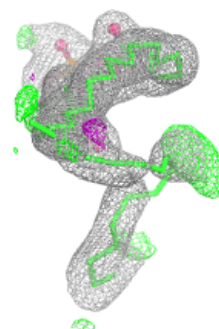
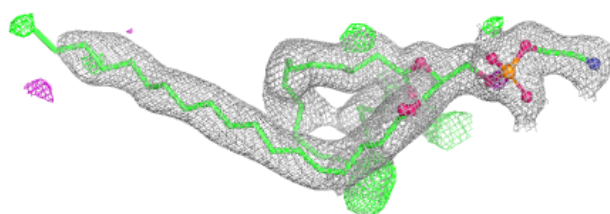
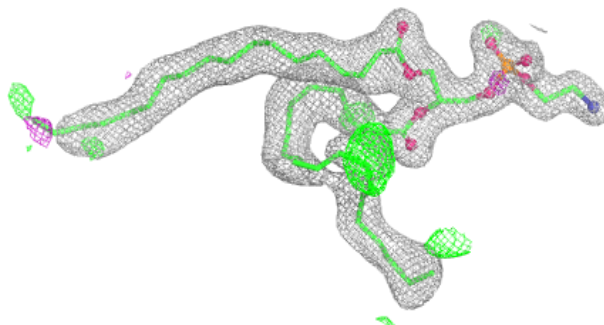
**Electron density around CHD C 301:**

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

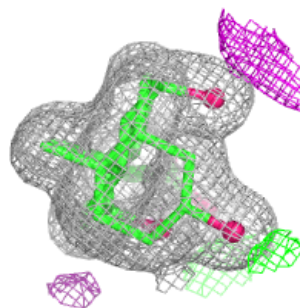
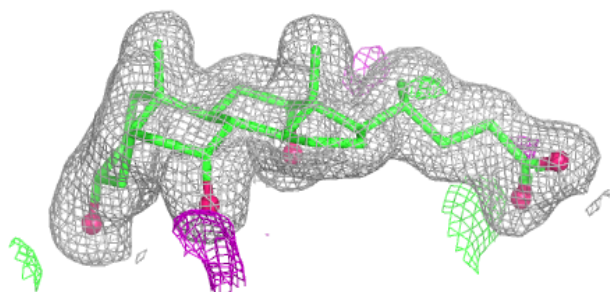
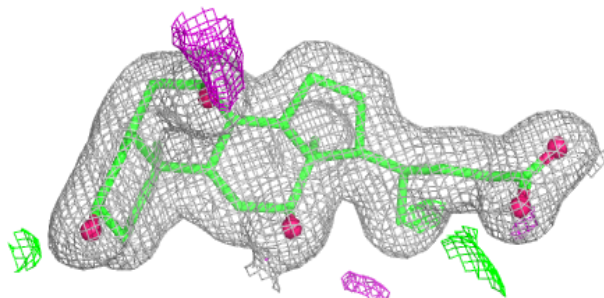


Electron density around PEK T 101:

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

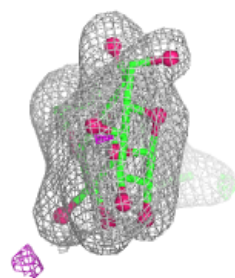
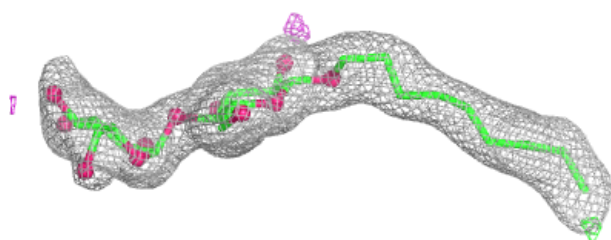
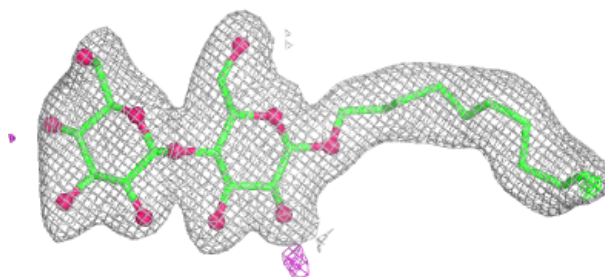
**Electron density around CHD P 302:**

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

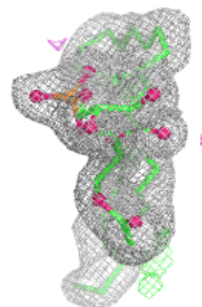
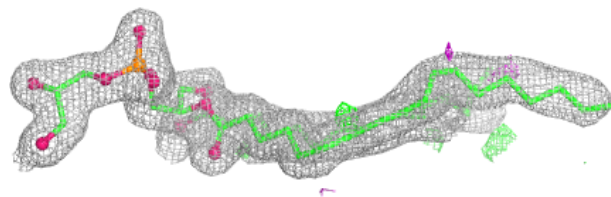
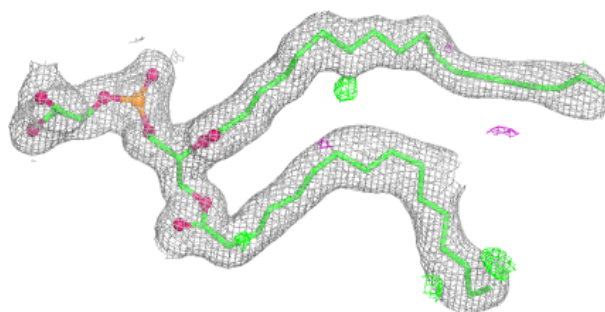


Electron density around DMU M 101:

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

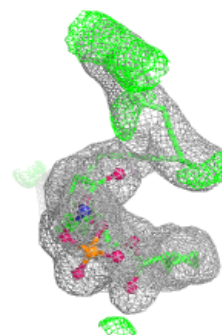
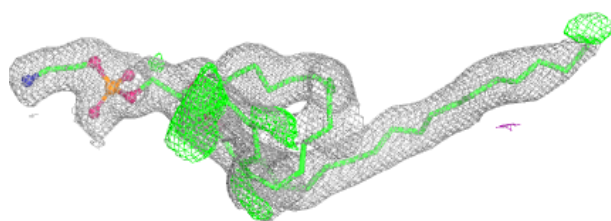
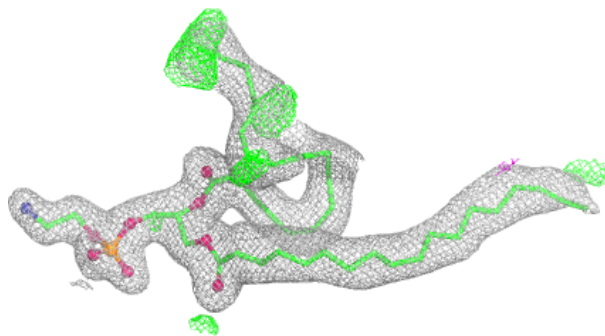
**Electron density around PGV N 618:**

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

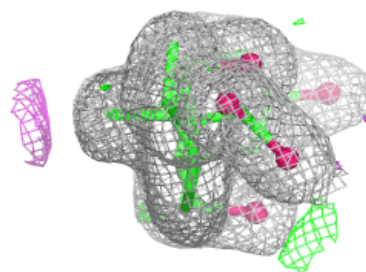
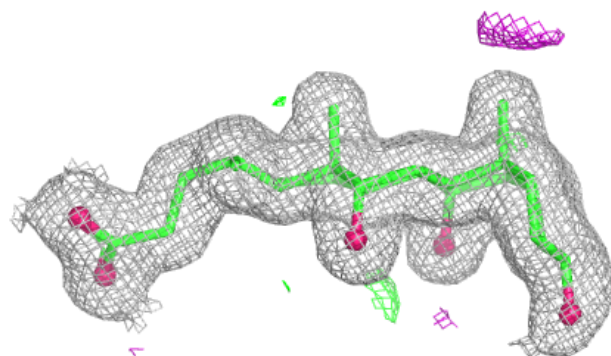
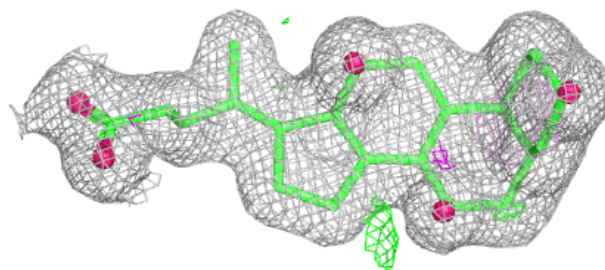


Electron density around PEK G 101:

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

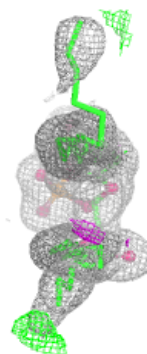
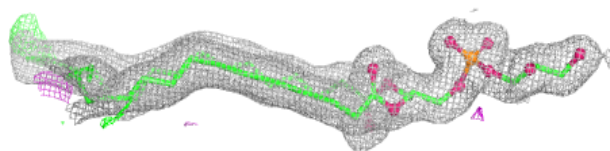
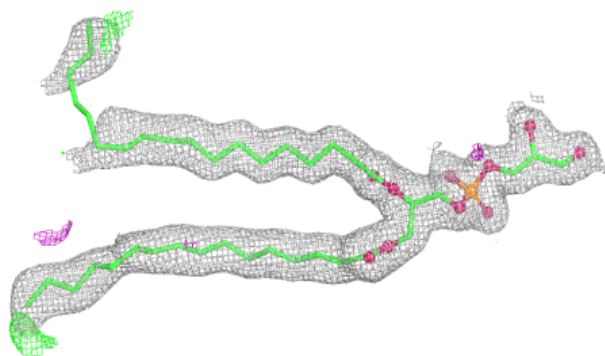
**Electron density around CHD B 305:**

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

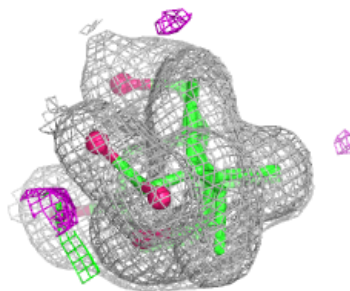
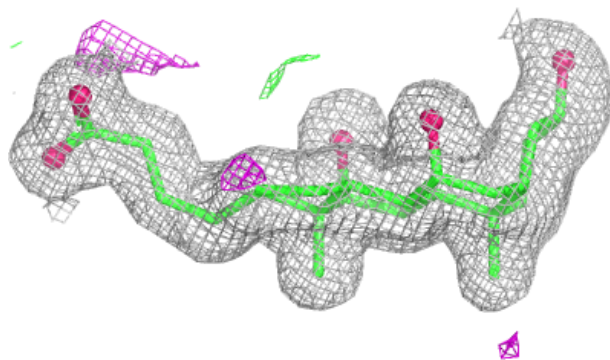
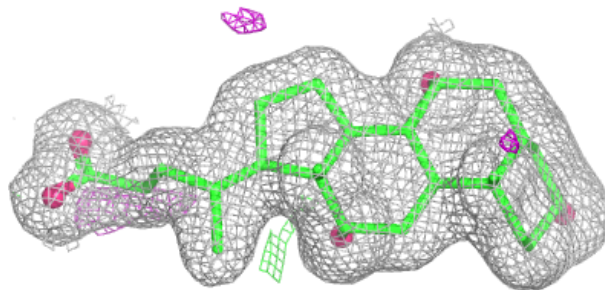


Electron density around PGV P 304:

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

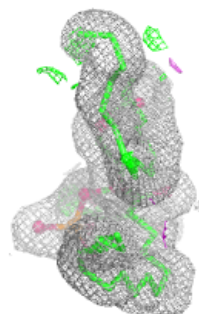
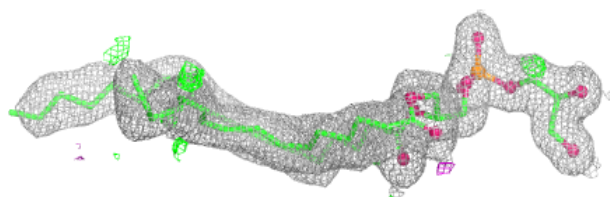
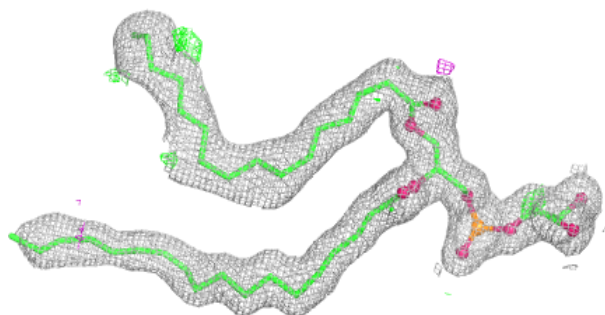
**Electron density around CHD O 301:**

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

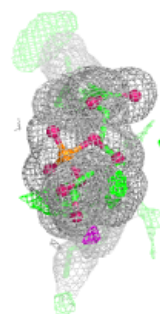
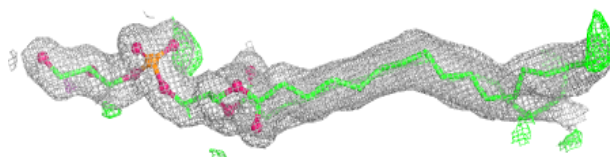
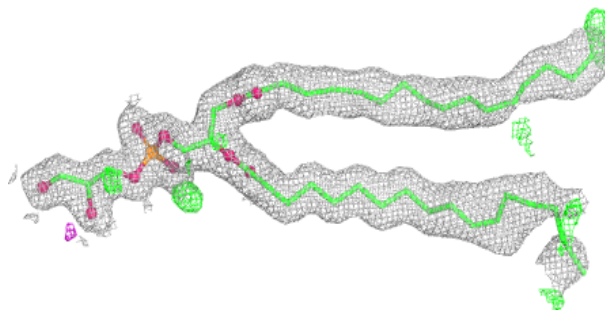


Electron density around PGV A 616:

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

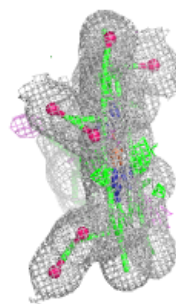
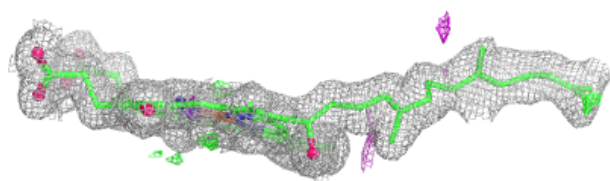
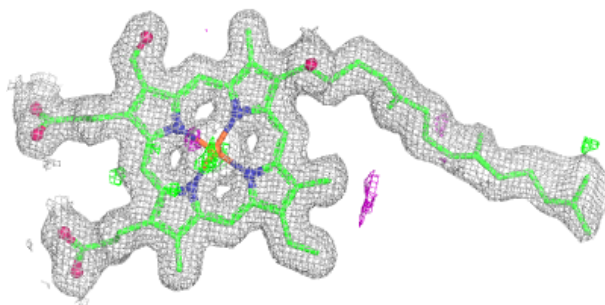
**Electron density around PGV C 303:**

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

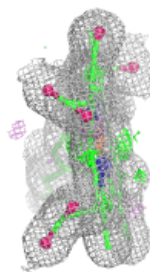
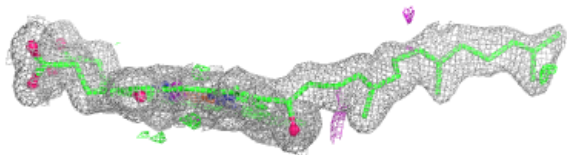
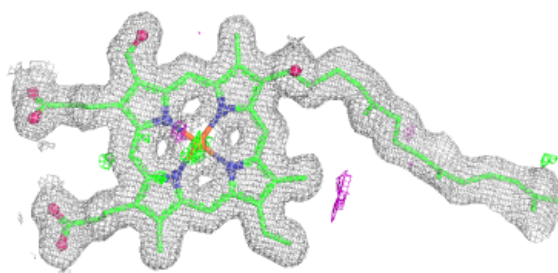


Electron density around HEA A 601 (A):

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

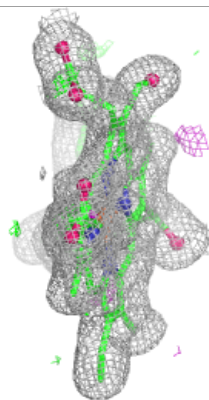
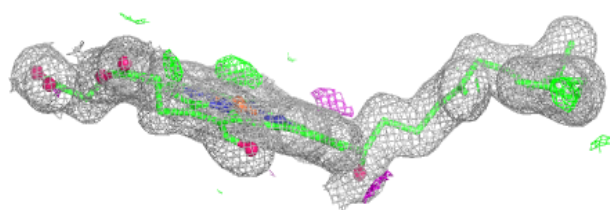
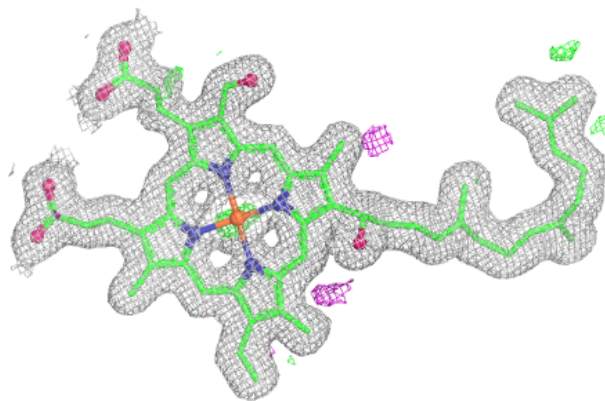
**Electron density around HEA A 601 (B):**

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

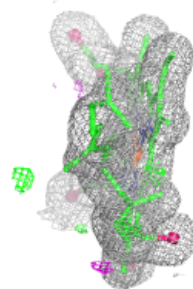
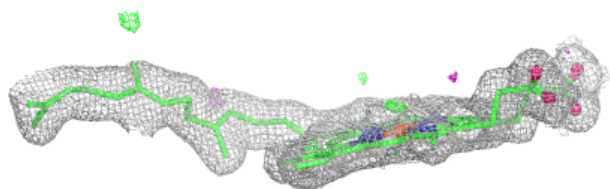
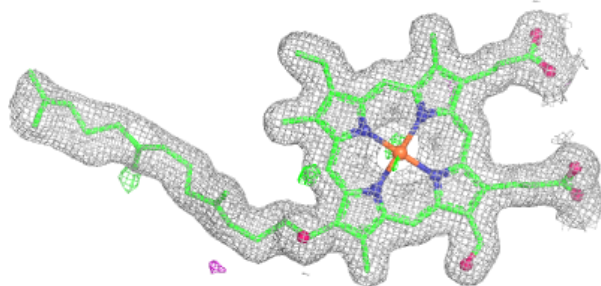


Electron density around HEA A 602:

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

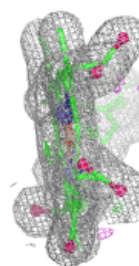
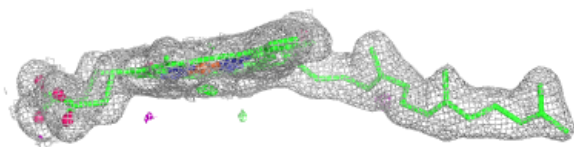
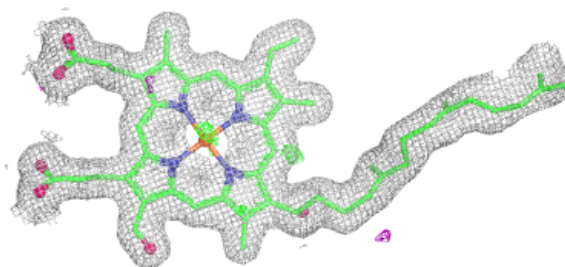
**Electron density around HEA N 603 (A):**

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

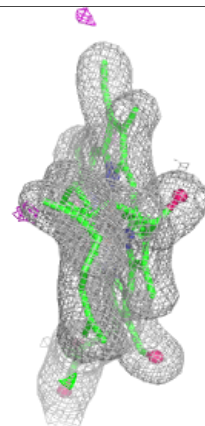
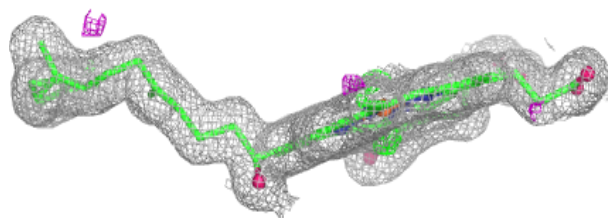
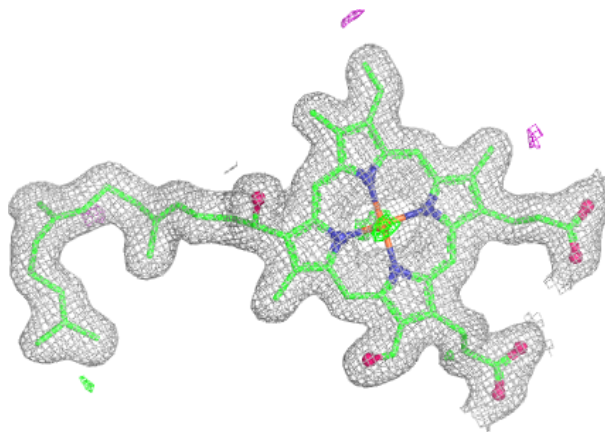


Electron density around HEA N 603 (B):

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

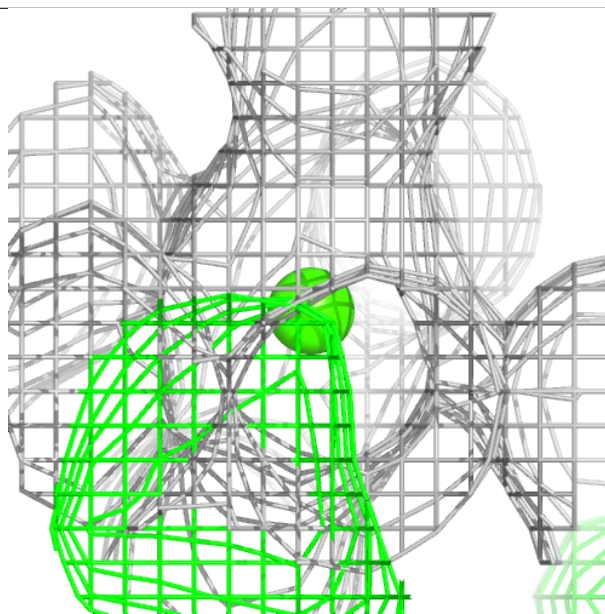
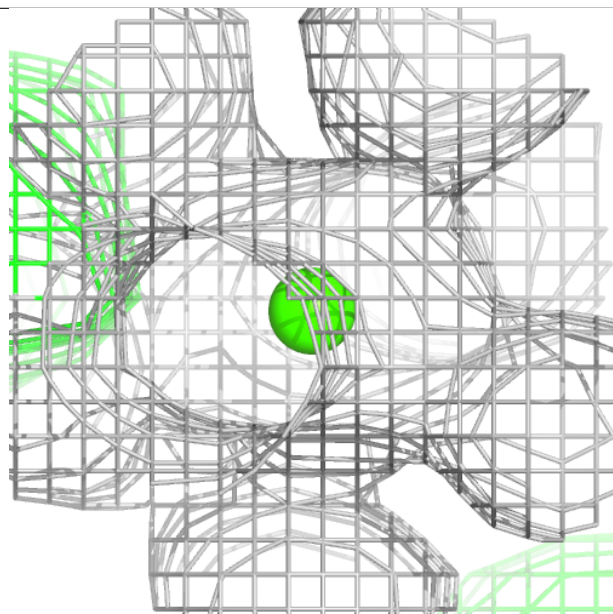
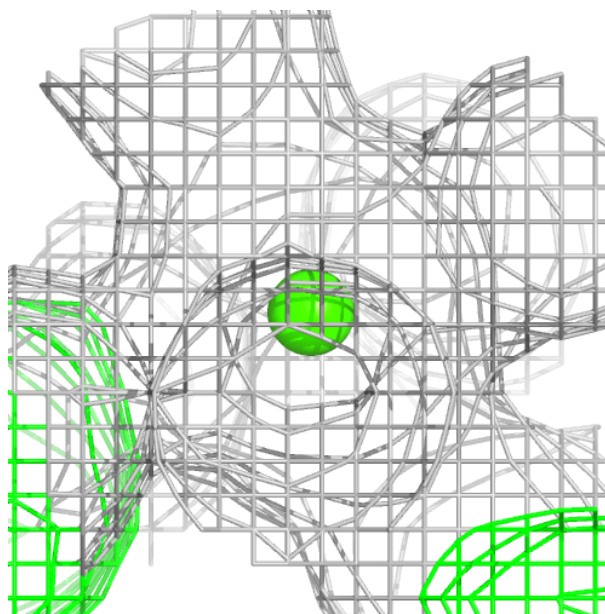
**Electron density around HEA N 604:**

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



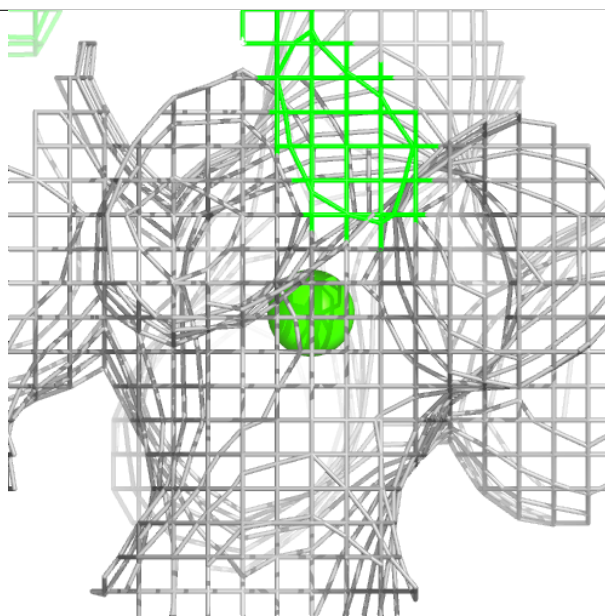
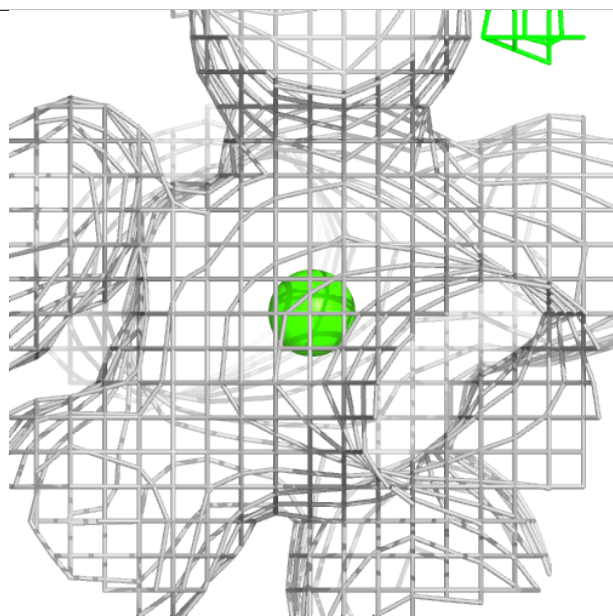
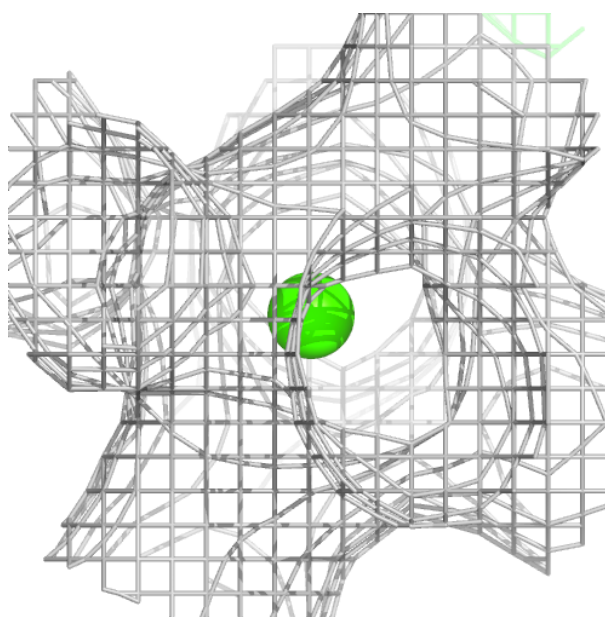
Electron density around CA A 605:

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



Electron density around CA 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.