



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:07 AM UTC

PDB ID : 5B1B / pdb_00005b1b
Title : Bovine heart cytochrome c oxidase in the fully reduced state at 1.6 angstrom resolution
Authors : Yano, N.; Muramoto, K.; Shimada, A.; Takemura, S.; Baba, J.; Fujisawa, H.; Mochizuki, M.; Shinzawa-Itoh, K.; Yamashita, E.; Tsukihara, T.; Yoshikawa, S.
Deposited on : 2015-12-01
Resolution : 1.60 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>.

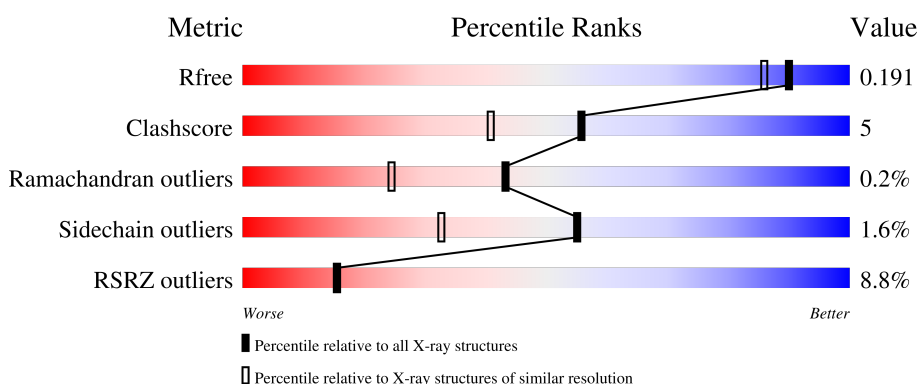
The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtrriage (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

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X-RAY DIFFRACTION

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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	89% 11%
2	B	227	87% 12%
2	O	227	86% 14%
3	C	259	93% 7%

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

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
21	EDO	C	311	-	-	-	X
21	EDO	S	103	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	DMU	D	203	-	-	-	X
24	DMU	K	104	-	-	-	X
24	DMU	X	103	-	-	-	X
28	PO4	U	101	-	-	-	X

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 34425 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	20	0
			4107	2743	633	689	42			
1	N	514	Total	C	N	O	S	0	21	0
			4107	2742	633	689	43			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	227	Total	C	N	O	S	0	6	0
			1844	1198	283	344	19			
2	O	227	Total	C	N	O	S	0	4	0
			1841	1196	284	343	18			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	259	Total	C	N	O	S	0	8	0
			2126	1420	337	356	13			
3	P	259	Total	C	N	O	S	0	8	0
			2129	1423	336	355	15			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	144	Total	C	N	O	S	0	6	0
			1214	792	200	218	4			
4	Q	144	Total	C	N	O	S	0	1	0
			1196	778	196	218	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	105	Total	C	N	O	S	0	1	0
			858	547	147	162	2			
5	R	105	Total	C	N	O	S	0	0	0
			852	544	144	162	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	4	0
			758	470	136	147	5			
6	S	98	Total	C	N	O	S	0	1	0
			750	465	134	146	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	84	Total	C	N	O	S	0	1	0
			677	437	129	110	1			
7	T	84	Total	C	N	O	S	0	3	0
			687	445	130	111	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			
8	U	79	Total	C	N	O	S	0	0	0
			662	417	121	119	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	73	Total	C	N	O	S	0	0	0
			601	390	107	100	4			
9	V	73	Total	C	N	O	S	0	1	0
			602	391	107	100	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	W	58	Total	C	N	O	S	0	0	0
			460	297	78	82	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	49	Total	C	N	O	S	0	1	0
			386	252	65	67	2			
11	X	49	Total	C	N	O	S	0	1	0
			386	252	65	67	2			

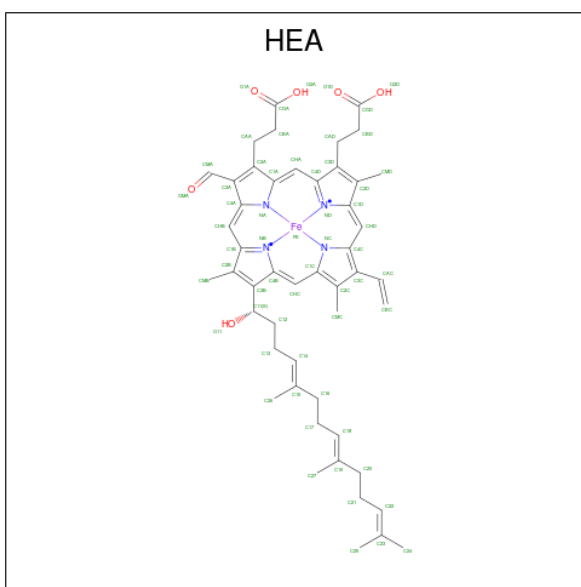
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	43	Total	C	N	O	0	0	0
			335	223	53	59			
13	Z	43	Total	C	N	O	0	0	0
			335	223	53	59			

- Molecule 14 is HEME-A (CCD ID: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	A	1	Total 70	C 58	Fe 1	N 4	O 7	0	1
14	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
14	N	1	Total 70	C 58	Fe 1	N 4	O 7	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		

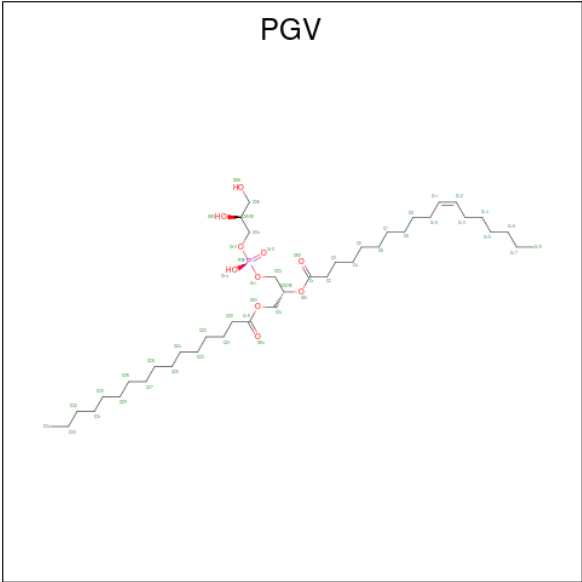
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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 SODIUM ION (CCD ID: NA) (formula: Na).

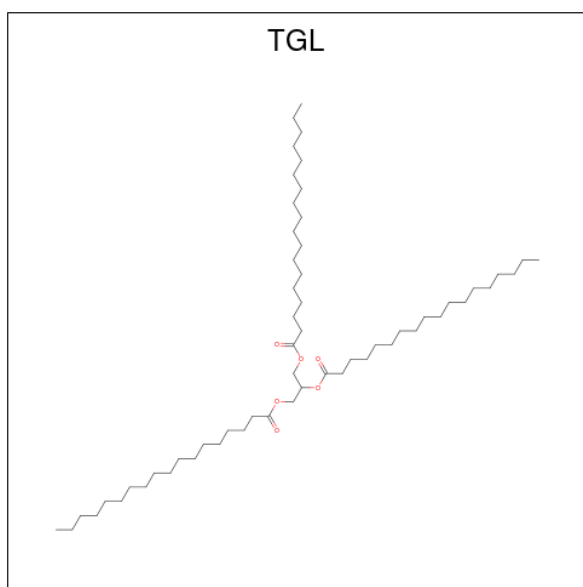
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Na	0	0
			1	1		
17	N	1	Total	Na	0	0
			1	1		

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



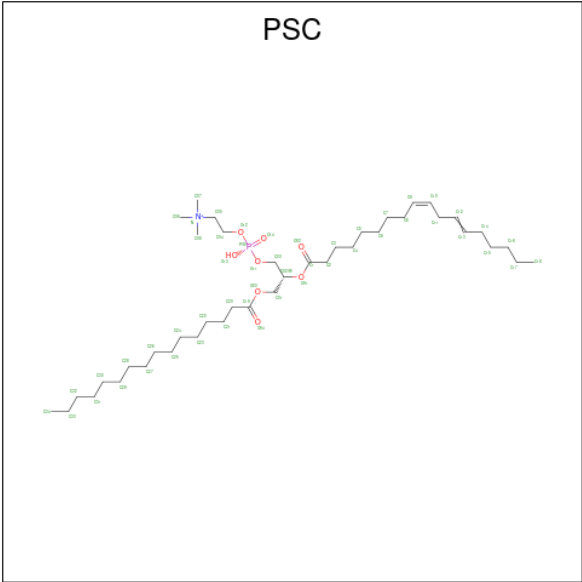
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
18	A	1	Total	C	O	P	0	0
			51	40	10	1		
18	A	1	Total	C	O		0	0
			37	34	3			
18	C	1	Total	C	O	P	0	0
			51	40	10	1		
18	C	1	Total	C	O		0	0
			36	34	2			
18	N	1	Total	C	O		0	0
			40	36	4			
18	N	1	Total	C	O	P	0	0
			51	40	10	1		
18	P	1	Total	C	O		0	0
			41	37	4			
18	P	1	Total	C	O	P	0	0
			50	39	10	1		

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



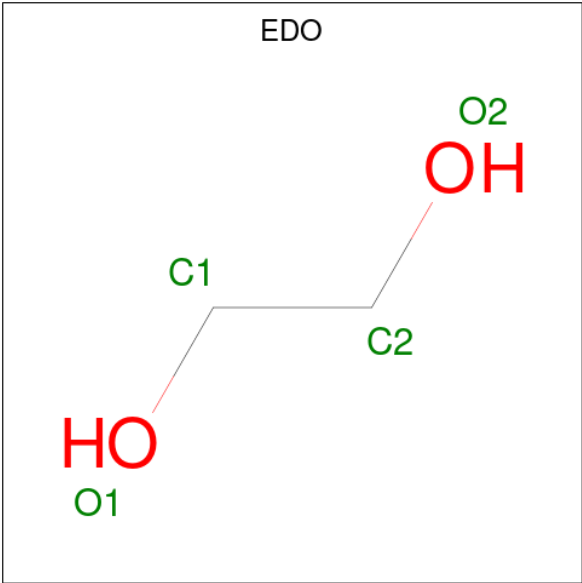
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	A	1	Total	C	O	0	0
			62	57	5		
19	D	1	Total	C	O	0	0
			63	57	6		
19	L	1	Total	C	O	0	0
			59	53	6		
19	N	1	Total	C	O	0	0
			57	54	3		
19	O	1	Total	C	O	0	0
			58	52	6		
19	Q	1	Total	C	O	0	0
			63	57	6		

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



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	A	1	Total	C	0	0
			25	25		
20	O	1	Total	C	0	0
			24	24		

- 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		

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

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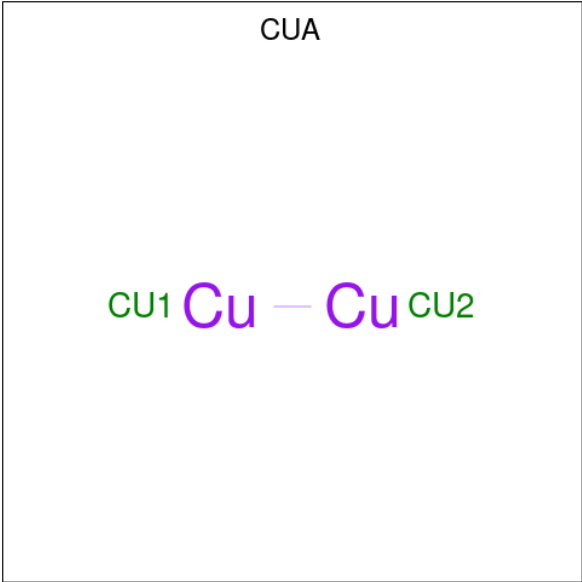
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	F	1	Total 4	C 2	O 2	0	0
21	F	1	Total 4	C 2	O 2	0	0
21	F	1	Total 4	C 2	O 2	0	0
21	G	1	Total 4	C 2	O 2	0	0
21	J	1	Total 4	C 2	O 2	0	0
21	J	1	Total 4	C 2	O 2	0	0
21	N	1	Total 4	C 2	O 2	0	0
21	N	1	Total 4	C 2	O 2	0	0
21	N	1	Total 4	C 2	O 2	0	0
21	N	1	Total 4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

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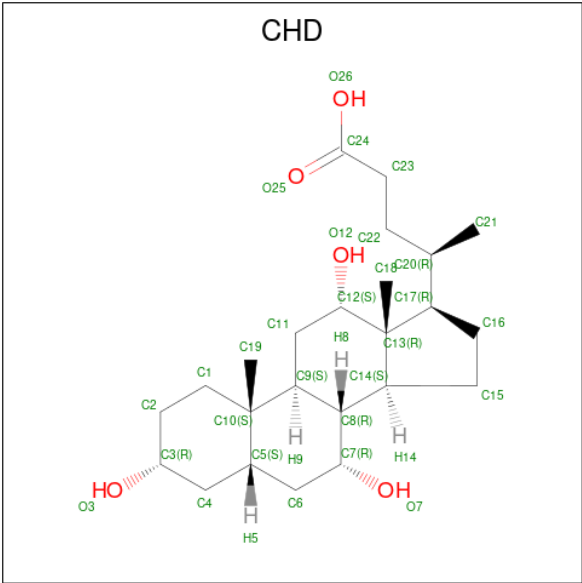
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	O	1	Total	C	O	0	0
			4	2	2		
21	P	1	Total	C	O	0	0
			4	2	2		
21	P	1	Total	C	O	0	0
			4	2	2		
21	P	1	Total	C	O	0	0
			4	2	2		
21	Q	1	Total	C	O	0	0
			4	2	2		
21	Q	1	Total	C	O	0	0
			4	2	2		
21	Q	1	Total	C	O	0	0
			4	2	2		
21	R	1	Total	C	O	0	0
			4	2	2		
21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

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



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

- Molecule 23 is CHOLIC ACID (CCD ID: CHD) (formula: C₂₄H₄₀O₅).



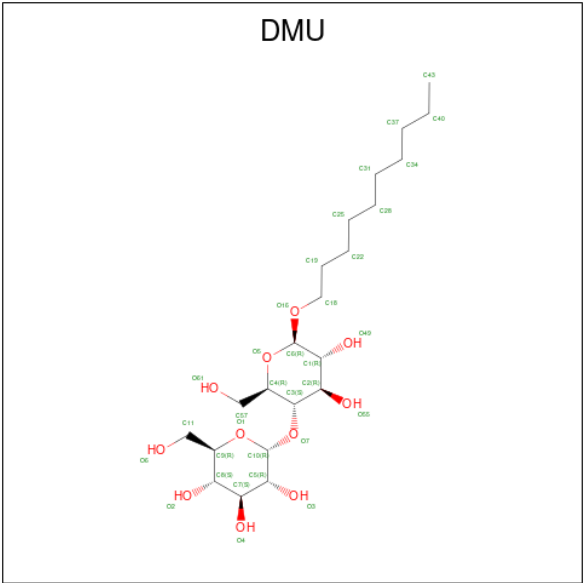
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
23	B	1	Total	C	O	0	0
			29	24	5		
23	C	1	Total	C	O	0	0
			29	24	5		

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

- Molecule 24 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



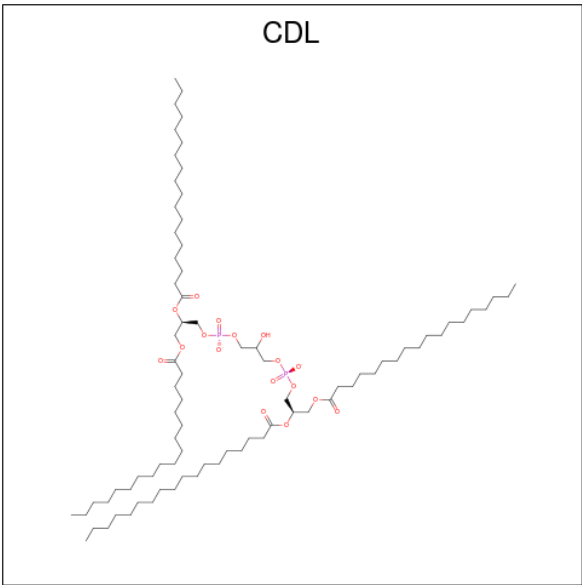
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	C	1	Total	C		0	0
			9	9			
24	C	1	Total	C	O	0	0
			12	11	1		
24	D	1	Total	C	O	0	0
			12	11	1		
24	D	1	Total	C		0	0
			9	9			
24	J	1	Total	C	O	0	0
			12	10	2		
24	K	1	Total	C	O	0	0
			10	9	1		
24	K	1	Total	C		0	0
			9	9			

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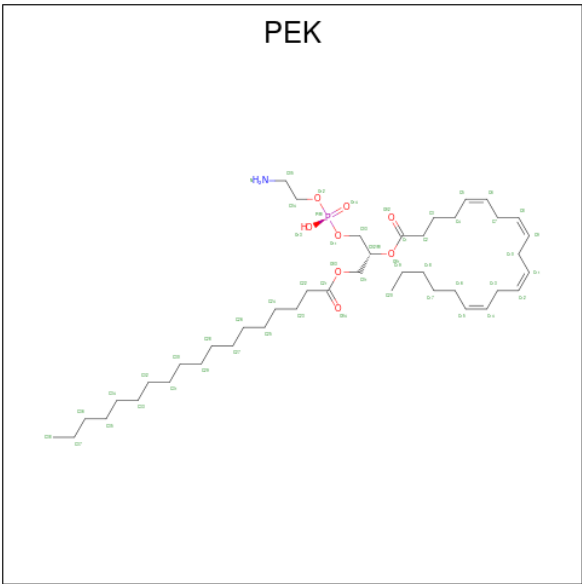
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	K	1	Total C O 33 22 11	0	0
24	K	1	Total C 10 10	0	0
24	K	1	Total C 9 9	0	0
24	K	1	Total C 9 9	0	0
24	L	1	Total C O 21 16 5	0	0
24	M	1	Total C O 33 22 11	0	0
24	O	1	Total C 10 10	0	0
24	P	1	Total C O 33 22 11	0	0
24	P	1	Total C O 11 10 1	0	0
24	W	1	Total C 9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

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
25	C	1	Total	C	O	0	0
			56	52	4		
25	G	1	Total	C	O	0	0
			64	63	1		
25	P	1	Total	C	O	0	0
			69	65	4		
25	T	1	Total	C	O	0	0
			79	73	6		

- Molecule 26 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (CCD ID: PEK) (formula: C₄₃H₇₈NO₈P).

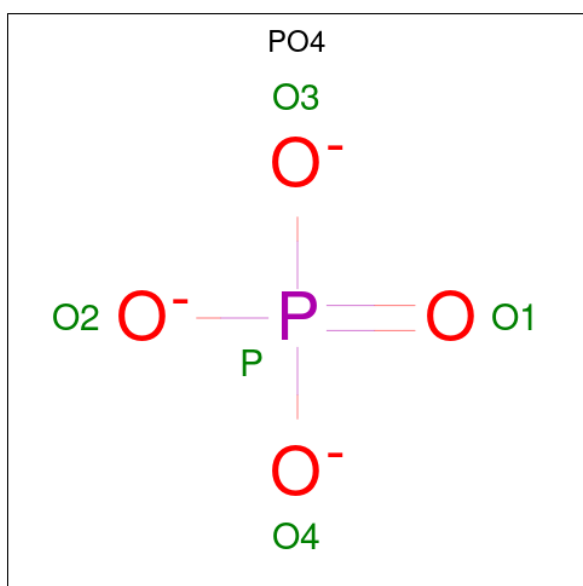


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	C	1	Total C 37 37	0	0
26	C	1	Total C 26 26	0	0
26	G	1	Total C N O P 53 43 1 8 1	0	0
26	P	1	Total C 20 20	0	0
26	P	1	Total C N O P 53 43 1 8 1	0	0
26	P	1	Total C O 39 37 2	0	0

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

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

- Molecule 28 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 29 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
29	A	266	Total O 266 266	0	1
29	B	232	Total O 233 233	0	1
29	C	161	Total O 161 161	0	0
29	D	232	Total O 232 232	0	0
29	E	171	Total O 171 171	0	0
29	F	187	Total O 187 187	0	1
29	G	101	Total O 101 101	0	0
29	H	121	Total O 121 121	0	0
29	I	75	Total O 75 75	0	0
29	J	63	Total O 63 63	0	0
29	K	55	Total O 55 55	0	0
29	L	53	Total O 53 53	0	0
29	M	48	Total O 48 48	0	0
29	N	265	Total O 265 265	0	0
29	O	203	Total O 204 204	0	1
29	P	180	Total O 180 180	0	1
29	Q	133	Total O 133 133	0	0
29	R	148	Total O 148 148	0	0
29	S	174	Total O 174 174	0	0
29	T	84	Total O 84 84	0	0
29	U	103	Total O 103 103	0	0

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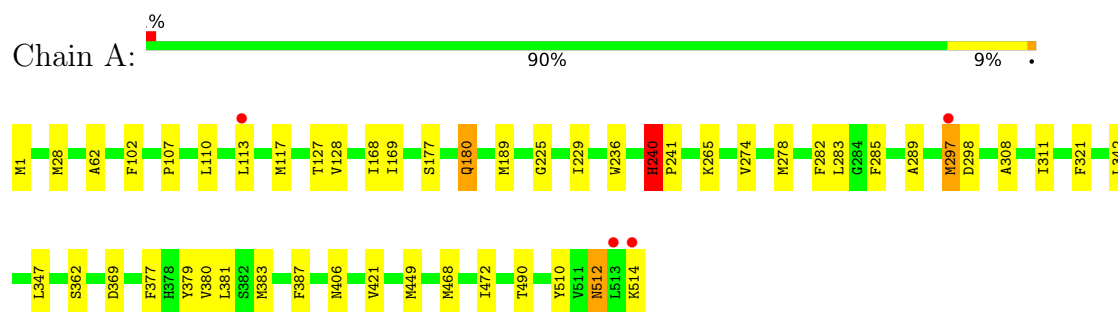
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	V	69	Total 69	O 69	0	0
29	W	66	Total 66	O 66	0	0
29	X	48	Total 48	O 48	0	0
29	Y	35	Total 35	O 35	0	0
29	Z	30	Total 30	O 30	0	0

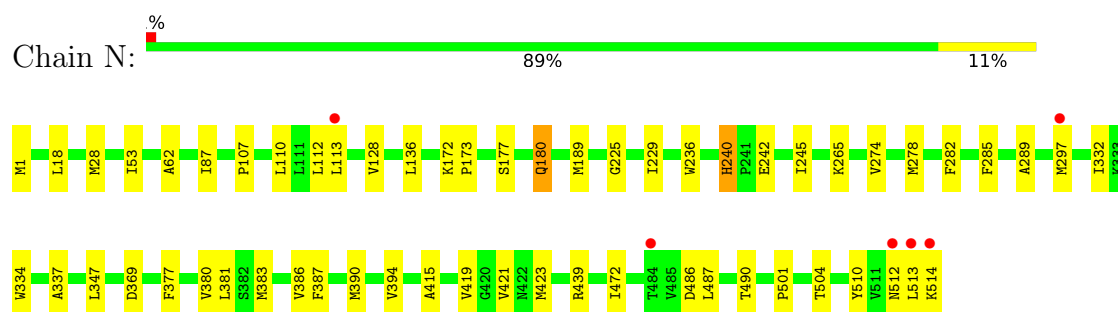
3 Residue-property plots [i](#)

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

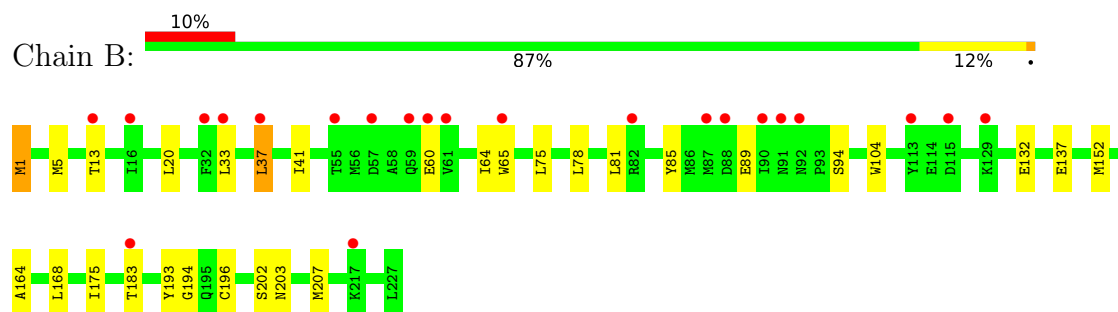
- Molecule 1: Cytochrome c oxidase subunit 1



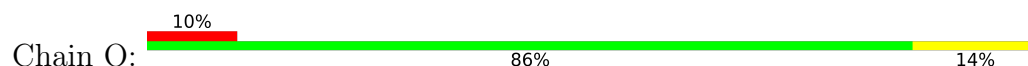
- Molecule 1: Cytochrome c oxidase subunit 1

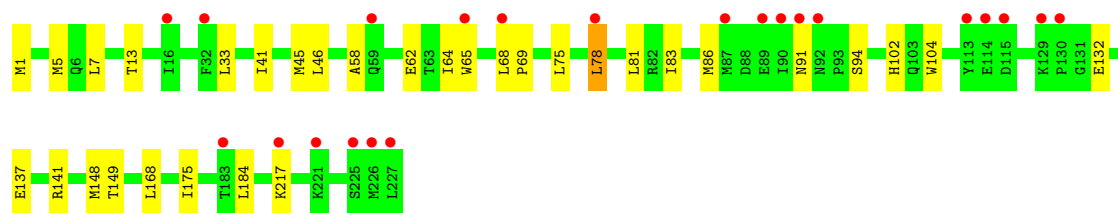


- Molecule 2: Cytochrome c oxidase subunit 2

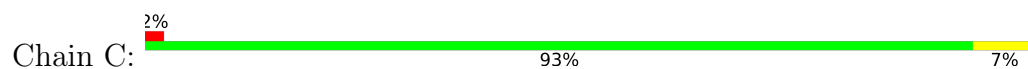


- Molecule 2: Cytochrome c oxidase subunit 2

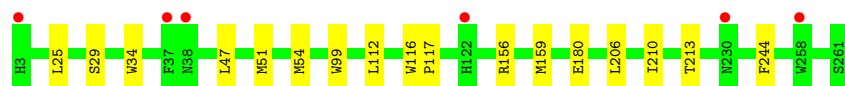




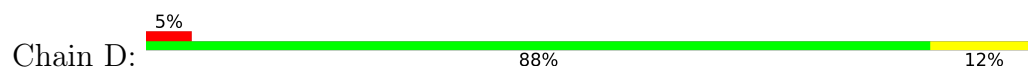
• Molecule 3: Cytochrome c oxidase subunit 3



• Molecule 3: Cytochrome c oxidase subunit 3



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



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

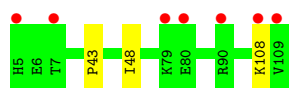


• Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial

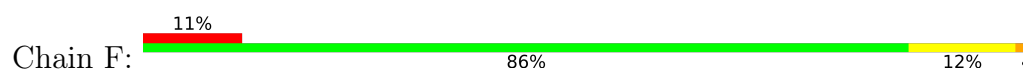


• Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial

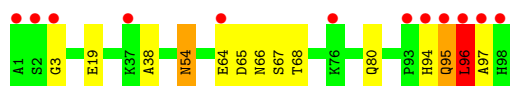
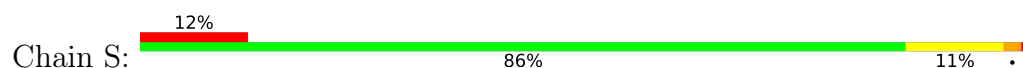




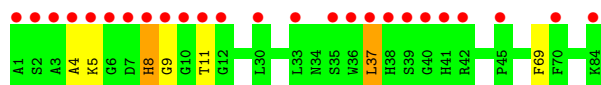
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



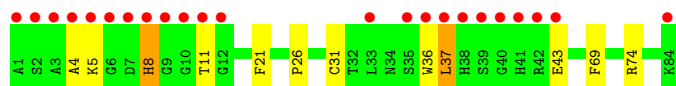
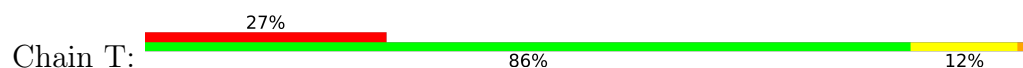
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



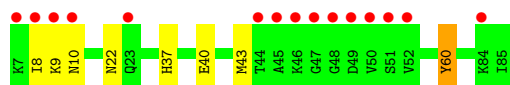
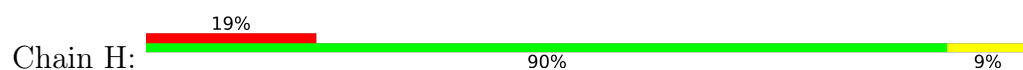
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



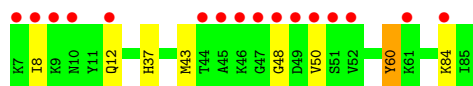
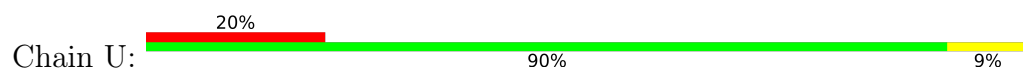
- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial



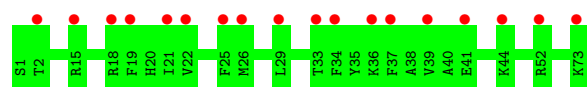
- Molecule 8: Cytochrome c oxidase subunit 6B1



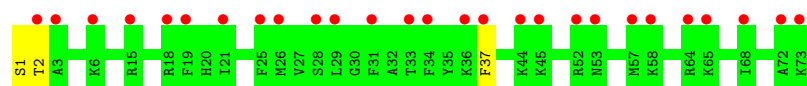
- Molecule 8: Cytochrome c oxidase subunit 6B1



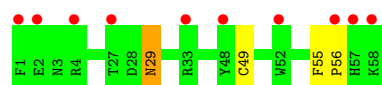
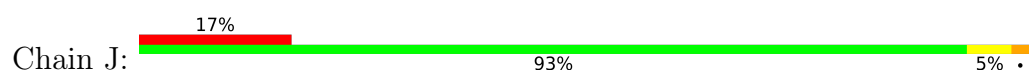
- Molecule 9: Cytochrome c oxidase subunit 6C



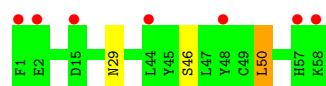
- Molecule 9: Cytochrome c oxidase subunit 6C



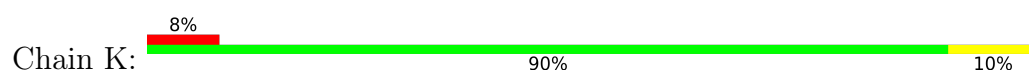
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



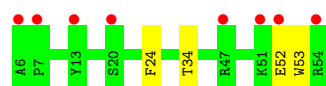
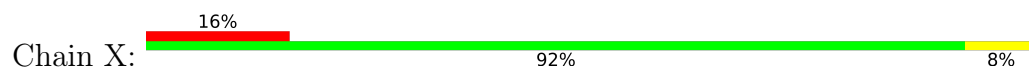
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



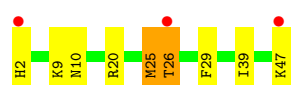
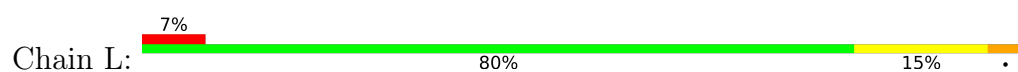
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



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

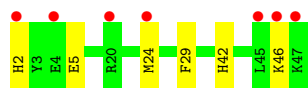


- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



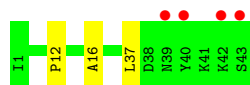
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial

Chain Y:  15% 87% 13%



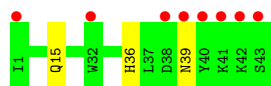
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial

Chain M:  9% 93% 7%



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

Chain Z:  19% 93% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	181.61Å 204.14Å 177.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.90 – 1.60 39.90 – 1.60	Depositor EDS
% Data completeness (in resolution range)	97.5 (39.90-1.60) 97.5 (39.90-1.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 1.40Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.168 , 0.191 0.169 , 0.191	Depositor DCC
R_{free} test set	61730 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.588	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.001 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	34425	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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: ZN, HEA, DMU, TGL, PSC, CDL, PGV, SAC, PO4, PEK, FME, EDO, NA, CHD, CU, MG, CUA

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	1.08	1/4306 (0.0%)	1.02	2/5877 (0.0%)
1	N	0.98	1/4321 (0.0%)	0.96	2/5896 (0.0%)
2	B	0.95	1/1912 (0.1%)	1.02	3/2603 (0.1%)
2	O	0.81	0/1900	0.91	4/2588 (0.2%)
3	C	0.92	1/2261 (0.0%)	0.88	0/3090
3	P	0.91	0/2260	0.87	0/3088
4	D	0.83	1/1284 (0.1%)	0.94	3/1730 (0.2%)
4	Q	0.60	0/1237	0.65	0/1668
5	E	0.76	0/882	0.77	0/1196
5	R	0.65	0/871	0.66	0/1182
6	F	0.83	0/797	0.96	0/1082
6	S	0.78	0/772	0.85	0/1048
7	G	0.79	0/710	0.79	0/966
7	T	0.68	0/732	0.76	0/997
8	H	0.76	0/682	0.89	0/921
8	U	0.71	0/682	0.79	0/921
9	I	0.66	0/605	0.69	0/802
9	V	0.58	0/613	0.67	0/812
10	J	0.63	0/471	0.70	0/636
10	W	0.60	0/471	0.67	0/636
11	K	0.75	0/405	0.78	0/556
11	X	0.55	0/405	0.59	0/556
12	L	0.96	1/393 (0.3%)	0.93	2/526 (0.4%)
12	Y	0.73	0/393	0.73	0/526
13	M	0.82	0/345	0.80	0/470
13	Z	0.67	0/345	0.69	0/470
All	All	0.87	6/30055 (0.0%)	0.89	16/40843 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	N	0	1
All	All	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	20	ARG	CZ-NH1	7.20	1.42	1.32
1	A	512	ASN	CB-CG	-5.41	1.38	1.52
12	L	26	THR	CA-CB	5.36	1.61	1.53
1	N	439	ARG	CD-NE	5.35	1.53	1.46
3	C	76	GLN	CD-OE1	5.24	1.33	1.23
2	B	152	MET	CB-CG	-5.03	1.37	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	20	ARG	NE-CZ-NH1	11.79	133.29	121.50
4	D	20	ARG	NE-CZ-NH2	-11.08	109.23	119.20
1	N	189	MET	CG-SD-CE	-8.76	81.63	100.90
1	N	240	HIS	CA-CB-CG	-8.15	105.65	113.80
1	A	240	HIS	CA-CB-CG	-7.94	105.86	113.80
4	D	20	ARG	CD-NE-CZ	6.11	132.96	124.40
2	O	64	ILE	CA-C-N	-5.62	112.89	122.56
2	O	64	ILE	C-N-CA	-5.62	112.89	122.56
2	B	64	ILE	CA-C-N	-5.61	112.91	122.56
2	B	64	ILE	C-N-CA	-5.61	112.91	122.56
2	O	65	TRP	CA-CB-CG	5.51	124.07	113.60
12	L	25	MET	CA-C-N	5.36	127.41	120.44
12	L	25	MET	C-N-CA	5.36	127.41	120.44
2	B	202	SER	CB-CA-C	-5.15	102.24	110.79
1	A	102	PHE	CA-CB-CG	-5.11	108.69	113.80
2	O	141	ARG	NE-CZ-NH1	-5.01	116.49	121.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	HIS	Sidechain
1	N	240	HIS	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4107	0	4099	47	0
1	N	4107	0	4086	51	0
2	B	1844	0	1850	19	0
2	O	1841	0	1841	19	0
3	C	2126	0	2026	19	0
3	P	2129	0	2043	15	0
4	D	1214	0	1203	14	0
4	Q	1196	0	1180	9	0
5	E	858	0	854	0	0
5	R	852	0	845	1	0
6	F	758	0	736	10	0
6	S	750	0	731	10	0
7	G	677	0	650	7	0
7	T	687	0	657	13	0
8	H	662	0	623	8	0
8	U	662	0	623	6	0
9	I	601	0	613	0	0
9	V	602	0	610	1	0
10	J	460	0	459	5	0
10	W	460	0	459	3	0
11	K	386	0	371	4	0
11	X	386	0	371	3	0
12	L	380	0	380	9	0
12	Y	380	0	380	5	0
13	M	335	0	352	3	0
13	Z	335	0	352	2	0
14	A	130	0	90	3	0
14	N	130	0	90	5	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	88	0	140	6	0
18	C	87	0	136	6	0
18	N	91	0	142	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	P	91	0	138	3	0
19	A	62	0	110	1	0
19	D	63	0	110	5	0
19	L	59	0	99	6	0
19	N	57	0	103	6	0
19	O	58	0	96	1	0
19	Q	63	0	110	7	0
20	A	25	0	41	3	0
20	O	24	0	40	0	0
21	A	40	0	59	5	0
21	B	16	0	24	2	0
21	C	20	0	30	0	0
21	E	8	0	12	0	0
21	F	20	0	30	3	0
21	G	4	0	6	0	0
21	J	8	0	12	0	0
21	N	52	0	78	5	0
21	O	12	0	18	1	0
21	P	12	0	18	0	0
21	Q	12	0	18	0	0
21	R	4	0	6	0	0
21	S	20	0	30	4	0
21	T	8	0	12	0	0
21	W	8	0	12	0	0
21	Y	4	0	6	0	0
22	B	2	0	0	0	0
22	O	2	0	0	0	0
23	B	29	0	39	0	0
23	C	29	0	39	0	0
23	G	29	0	39	1	0
23	J	29	0	39	1	0
23	P	58	0	78	1	0
24	C	21	0	38	2	0
24	D	21	0	38	1	0
24	J	12	0	21	0	0
24	K	80	0	127	2	0
24	L	21	0	30	4	0
24	M	33	0	42	0	0
24	O	10	0	19	0	0
24	P	44	0	63	4	0
24	W	9	0	17	0	0
24	X	73	0	116	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	Z	33	0	42	1	0
25	C	56	0	89	7	0
25	G	64	0	122	9	0
25	P	69	0	121	2	0
25	T	79	0	139	12	0
26	C	63	0	103	3	0
26	G	53	0	77	5	0
26	P	112	0	170	11	0
27	F	1	0	0	0	0
27	S	1	0	0	0	0
28	H	5	0	0	0	0
28	U	5	0	0	0	0
29	A	266	0	0	3	0
29	B	233	0	0	1	0
29	C	161	0	0	0	0
29	D	232	0	0	1	0
29	E	171	0	0	0	0
29	F	187	0	0	4	0
29	G	101	0	0	0	0
29	H	121	0	0	2	0
29	I	75	0	0	1	0
29	J	63	0	0	0	0
29	K	55	0	0	0	0
29	L	53	0	0	2	0
29	M	48	0	0	0	0
29	N	265	0	0	4	0
29	O	204	0	0	1	0
29	P	180	0	0	2	0
29	Q	133	0	0	1	0
29	R	148	0	0	0	0
29	S	174	0	0	3	0
29	T	84	0	0	1	0
29	U	103	0	0	2	0
29	V	69	0	0	0	0
29	W	66	0	0	0	0
29	X	48	0	0	0	0
29	Y	35	0	0	1	0
29	Z	30	0	0	0	0
All	All	34425	0	31818	297	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 (297) 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)
6:S:68:THR:H	21:S:103:EDO:H12	1.43	0.82
1:A:282:PHE:HA	7:T:4:ALA:HB3	1.68	0.76
3:C:213:THR:HG23	25:C:303:CDL:H771	1.68	0.74
25:T:101:CDL:H541	25:T:101:CDL:H231	1.72	0.71
7:G:9:GLY:HA3	29:N:707:HOH:O	1.91	0.70
4:Q:100:LYS:NZ	29:Q:301:HOH:O	2.23	0.68
7:G:4:ALA:HB3	1:N:282:PHE:HA	1.77	0.67
1:A:169:ILE:HG12	1:A:189[B]:MET:HE1	1.77	0.66
7:G:69:PHE:HB3	26:G:101:PEK:H011	1.78	0.66
20:A:609:PSC:H322	2:B:41:ILE:HD13	1.78	0.66
7:G:37:LEU:HD23	25:G:102:CDL:H391	1.76	0.66
26:C:307:PEK:H282	7:T:8:HIS:HE2	1.62	0.65
1:A:308:ALA:O	1:A:311[B]:ILE:HG12	1.97	0.64
21:O:307:EDO:H12	29:P:459:HOH:O	1.97	0.64
25:T:101:CDL:H181	25:T:101:CDL:H511	1.79	0.63
24:C:301:DMU:H11	10:J:49:CYS:HB3	1.79	0.63
6:F:30:PRO:O	6:F:96:LEU:HD11	1.98	0.63
6:F:51:SER:O	6:F:94:HIS:N	2.29	0.63
26:C:305:PEK:H383	25:G:102:CDL:H273	1.79	0.63
21:A:615:EDO:H11	21:A:616:EDO:H22	1.81	0.62
25:G:102:CDL:H771	25:G:102:CDL:H581	1.82	0.62
1:N:347:LEU:HD13	1:N:383[B]:MET:HB3	1.81	0.61
3:P:99:TRP:CD1	18:P:302:PGV:H211	2.35	0.61
7:T:31:CYS:SG	25:T:101:CDL:H551	2.40	0.61
11:K:20:SER:HA	24:K:103:DMU:H1	1.83	0.61
25:G:102:CDL:H142	25:G:102:CDL:H412	1.83	0.60
10:J:55:PHE:HE1	24:L:102:DMU:H29	1.67	0.60
2:B:203:ASN:HD22	21:B:304:EDO:H22	1.66	0.59
1:N:337:ALA:HB2	1:N:394[A]:VAL:HG23	1.85	0.59
1:A:468:MET:HG3	29:A:928:HOH:O	2.02	0.59
6:F:54[B]:ASN:ND2	29:F:202:HOH:O	2.36	0.59
4:D:82:VAL:HG12	4:D:86[B]:MET:HE2	1.85	0.59
1:A:347:LEU:HD13	1:A:383[B]:MET:HB3	1.84	0.58
2:O:83:ILE:HA	2:O:86:MET:HG2	1.84	0.58
1:N:289:ALA:HB1	1:N:297[C]:MET:HE1	1.84	0.58
1:N:377:PHE:HA	1:N:380[B]:VAL:HG22	1.85	0.58
1:A:406:ASN:HD21	18:A:607:PGV:H21	1.68	0.58
3:C:206:LEU:HD13	26:G:101:PEK:H12	1.86	0.58
7:T:8:HIS:ND1	7:T:8:HIS:N	2.51	0.57
24:L:102:DMU:H6	29:L:210:HOH:O	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113[B]:LEU:HD23	12:L:39:ILE:HD11	1.88	0.56
3:C:59:ARG:HB2	25:C:303:CDL:H521	1.88	0.56
1:A:117[A]:MET:HE1	24:L:102:DMU:H10	1.87	0.56
18:A:607:PGV:H231	13:M:12:PRO:HG3	1.88	0.55
26:P:308:PEK:H011	7:T:69:PHE:HB3	1.87	0.55
1:A:377:PHE:HA	1:A:380[B]:VAL:HG22	1.87	0.55
3:P:210:ILE:HG12	18:P:304:PGV:H132	1.87	0.55
6:S:66:ASN:HA	21:S:103:EDO:H21	1.88	0.55
7:G:8:HIS:ND1	7:G:8:HIS:N	2.53	0.55
6:S:3:GLY:HA3	29:S:201:HOH:O	2.06	0.55
21:A:615:EDO:C1	21:A:616:EDO:H22	2.37	0.55
18:N:606:PGV:H242	18:N:606:PGV:H41	1.88	0.55
1:A:383[B]:MET:HG2	1:A:421:VAL:HG21	1.87	0.55
23:G:103:CHD:H212	23:G:103:CHD:H12	1.89	0.54
18:A:606:PGV:H12	3:C:24:ALA:HB2	1.89	0.54
3:C:52:LEU:HD23	25:C:303:CDL:H362	1.90	0.54
12:L:9:LYS:NZ	29:L:201:HOH:O	2.41	0.54
21:N:612:EDO:HO2	21:S:103:EDO:HO1	1.55	0.54
10:J:55:PHE:CE1	24:L:102:DMU:H29	2.42	0.54
1:N:514:LYS:HA	6:S:38:ALA:HB3	1.90	0.53
1:A:472:ILE:HG21	19:L:101:TGL:HA92	1.89	0.53
18:A:607:PGV:H302	13:M:16:ALA:HA	1.88	0.53
4:D:19[B]:ARG:NH2	4:D:21:ASP:OD1	2.42	0.53
7:G:4:ALA:HB2	1:N:285:PHE:CD2	2.43	0.53
1:N:28:MET:HE3	12:Y:29:PHE:CD1	2.44	0.53
1:A:285:PHE:CD2	7:T:4:ALA:HB2	2.44	0.52
1:A:362:SER:HB3	2:B:20:LEU:HD21	1.92	0.52
3:P:244:PHE:HA	26:P:301:PEK:H101	1.90	0.52
2:O:7:LEU:HD11	19:O:301:TGL:H162	1.91	0.52
26:P:308:PEK:H262	24:P:310:DMU:H13	1.91	0.52
2:O:13:THR:HB	2:O:168:LEU:HD23	1.92	0.52
21:N:617:EDO:H22	29:N:820:HOH:O	2.10	0.52
29:P:402:HOH:O	7:T:74:ARG:NH2	2.42	0.51
6:F:34:LEU:O	21:F:105:EDO:O2	2.25	0.51
4:Q:118:LYS:HB3	11:X:53:TRP:HB3	1.92	0.51
2:B:132:GLU:HB3	2:B:137:GLU:HG3	1.92	0.51
4:D:78:TRP:N	19:D:201:TGL:HB22	2.26	0.51
25:G:102:CDL:H401	2:O:81:LEU:HD12	1.92	0.51
3:C:134:THR:HG21	25:G:102:CDL:H611	1.93	0.51
3:C:210:ILE:HD13	18:C:302:PGV:H302	1.92	0.51
1:N:487:LEU:H	21:N:611:EDO:H12	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:34:TRP:HZ3	26:P:308:PEK:H261	1.75	0.51
12:L:20:ARG:HH22	19:L:101:TGL:HC42	1.76	0.51
18:A:607:PGV:H312	18:A:607:PGV:H151	1.93	0.51
2:B:203:ASN:ND2	21:B:304:EDO:H22	2.25	0.51
1:N:332:ILE:H	21:N:621:EDO:H12	1.76	0.50
25:G:102:CDL:H412	25:G:102:CDL:H161	1.93	0.50
1:N:229:ILE:HD11	2:O:175:ILE:HD13	1.93	0.50
4:Q:78:TRP:HA	19:Q:201:TGL:HB22	1.94	0.50
4:D:127:LYS:HD2	29:I:140:HOH:O	2.12	0.49
2:B:81:LEU:HD12	25:T:101:CDL:H371	1.94	0.49
26:G:101:PEK:H8	26:G:101:PEK:H302	1.94	0.49
8:U:43:MET:HE3	8:U:48:GLY:HA3	1.93	0.49
1:A:379:TYR:CZ	1:A:383[B]:MET:HE1	2.47	0.49
20:A:609:PSC:C33	20:A:609:PSC:H142	2.43	0.49
1:N:107:PRO:HB3	3:P:25:LEU:HB2	1.94	0.49
11:X:24:PHE:HE1	24:X:105:DMU:H16	1.77	0.49
1:A:342:LEU:HB2	19:D:201:TGL:H202	1.94	0.49
21:A:610:EDO:H11	12:L:10:ASN:HD22	1.77	0.49
18:A:606:PGV:H12	3:C:24:ALA:CB	2.43	0.49
6:F:13:ALA:CB	6:F:21[B]:MET:HE1	2.43	0.49
2:O:132:GLU:HB3	2:O:137:GLU:HG3	1.95	0.49
6:F:85:CYS:SG	6:F:87:THR:HG23	2.53	0.49
2:B:183:THR:HG22	29:B:596:HOH:O	2.12	0.48
3:P:206:LEU:HB2	26:P:308:PEK:H12	1.95	0.48
1:A:110:LEU:HD12	1:A:113[B]:LEU:HD12	1.95	0.48
1:A:510:TYR:OH	1:A:512:ASN:ND2	2.43	0.48
25:T:101:CDL:H382	25:T:101:CDL:H131	1.95	0.48
1:N:177:SER:H	1:N:180:GLN:NE2	2.12	0.48
1:N:390:MET:O	1:N:394[A]:VAL:HG22	2.13	0.48
1:A:283:LEU:HD22	1:A:311[B]:ILE:HD11	1.94	0.48
12:L:29:PHE:HZ	19:L:101:TGL:HA91	1.77	0.48
1:N:510:TYR:OH	1:N:512:ASN:ND2	2.43	0.48
6:S:54:ASN:HD22	6:S:54:ASN:C	2.22	0.47
12:L:20:ARG:HH21	19:L:101:TGL:HC61	1.79	0.47
1:A:107:PRO:HB3	3:C:25:LEU:HB2	1.94	0.47
1:A:177:SER:H	1:A:180:GLN:NE2	2.13	0.47
2:O:102:HIS:O	2:O:104:TRP:HA	2.15	0.47
12:Y:42:HIS:NE2	12:Y:46:LYS:HD2	2.30	0.47
1:N:274:VAL:HG12	1:N:278[A]:MET:HE2	1.96	0.47
1:A:265:LYS:HB2	1:A:490:THR:HG21	1.97	0.47
3:P:29:SER:HB2	24:P:303:DMU:H19	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:265:LYS:HB2	1:N:490:THR:HG21	1.97	0.46
26:P:309:PEK:H281	7:T:26:PRO:HG3	1.97	0.46
3:C:210:ILE:HG12	18:C:302:PGV:H132	1.97	0.46
19:N:608:TGL:HC72	12:Y:24:MET:HE1	1.97	0.46
1:A:225:GLY:HA3	3:C:112:LEU:HD21	1.98	0.46
1:A:321:PHE:CD2	2:B:65:TRP:HB2	2.50	0.46
1:A:236:TRP:HH2	14:A:602:HEA:HBD1	1.79	0.46
4:D:4:SER:N	29:D:305:HOH:O	2.49	0.46
26:G:101:PEK:H71	26:G:101:PEK:H42	1.67	0.46
1:A:449[A]:MET:SD	2:B:5:MET:HG2	2.56	0.46
2:B:37:LEU:HD22	2:B:37:LEU:HA	1.78	0.46
3:C:99:TRP:CE3	18:C:306:PGV:H271	2.50	0.46
8:H:40:GLU:OE2	29:H:201:HOH:O	2.21	0.46
1:A:240:HIS:C	1:A:240:HIS:CD2	2.93	0.46
8:H:43:MET:HE1	8:U:43:MET:HE1	1.98	0.46
4:Q:98:TRP:CE3	24:Z:101:DMU:H12	2.51	0.46
1:A:169:ILE:HG12	1:A:189[B]:MET:CE	2.44	0.46
2:B:13:THR:HB	2:B:168:LEU:HD23	1.98	0.46
1:N:236:TRP:CH2	14:N:602:HEA:HBD1	2.51	0.46
3:P:34:TRP:CZ3	26:P:308:PEK:H261	2.51	0.46
2:B:196:CYS:HB2	2:B:207:MET:HG3	1.96	0.46
10:J:29:ASN:HD22	10:J:29:ASN:H	1.61	0.46
6:S:96:LEU:HB3	6:S:97:ALA:H	1.42	0.46
1:N:472:ILE:HG21	19:N:608:TGL:HA82	1.97	0.45
26:P:309:PEK:H241	7:T:21:PHE:CD1	2.51	0.45
1:N:87:ILE:O	1:N:173:PRO:HD3	2.16	0.45
1:A:289:ALA:HB1	1:A:297[A]:MET:HE1	1.99	0.45
4:D:82:VAL:HG21	24:D:203:DMU:H14	1.98	0.45
1:N:377:PHE:CD2	14:N:602:HEA:HAD1	2.52	0.45
1:N:112:LEU:HD23	1:N:112:LEU:C	2.42	0.45
1:A:168:ILE:HB	1:A:189[B]:MET:HE2	1.99	0.45
1:N:347:LEU:CD1	1:N:383[B]:MET:HB3	2.47	0.45
7:T:37:LEU:HD23	25:T:101:CDL:H361	1.99	0.45
6:F:95:GLN:NE2	29:F:205:HOH:O	2.50	0.45
18:N:606:PGV:H222	13:Z:15:GLN:HE22	1.81	0.45
1:A:274:VAL:HG12	1:A:278:MET:HE2	1.98	0.45
2:B:104:TRP:CG	2:B:203:ASN:HB2	2.52	0.45
3:P:47:LEU:O	3:P:51[B]:MET:HG3	2.17	0.45
11:X:34:THR:HA	24:X:103:DMU:H11	1.99	0.45
1:A:298[A]:ASP:OD1	8:H:22:ASN:HB3	2.16	0.44
1:N:289:ALA:HB1	1:N:297[A]:MET:HE1	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:P:308:PEK:H221	26:P:308:PEK:H251	1.65	0.44
3:C:210:ILE:HG23	18:C:302:PGV:H91	1.98	0.44
3:C:244:PHE:HA	26:C:307:PEK:H101	1.99	0.44
4:D:132:GLN:O	4:D:137[B]:LYS:NZ	2.50	0.44
2:O:168:LEU:HD13	2:O:184:LEU:HG	2.00	0.44
1:A:311[B]:ILE:HG22	25:T:101:CDL:H441	1.99	0.44
26:P:308:PEK:H291	26:P:308:PEK:H8	1.99	0.44
25:P:305:CDL:H382	25:P:305:CDL:H351	1.70	0.44
1:N:486:ASP:OD2	4:Q:19:ARG:HD2	2.18	0.44
10:W:29:ASN:HD22	10:W:29:ASN:H	1.65	0.44
6:S:19:GLU:HG2	29:S:301:HOH:O	2.18	0.44
26:P:309:PEK:H383	25:T:101:CDL:H272	2.00	0.44
7:T:31:CYS:SG	25:T:101:CDL:H532	2.58	0.44
1:A:347:LEU:HD22	1:A:383[B]:MET:SD	2.58	0.44
4:Q:78:TRP:CA	19:Q:201:TGL:HB22	2.48	0.44
6:S:64:GLU:O	6:S:65:ASP:HB2	2.17	0.44
8:U:60:TYR:CD1	8:U:60:TYR:C	2.96	0.44
1:A:381[A]:LEU:HB2	14:A:602:HEA:CAC	2.47	0.44
4:D:33:LEU:O	4:D:38:LYS:NZ	2.51	0.44
19:D:201:TGL:OA1	19:D:201:TGL:HC52	2.18	0.43
1:N:419:VAL:HG21	19:Q:201:TGL:H301	2.00	0.43
6:S:67:SER:H	21:S:103:EDO:C2	2.31	0.43
7:T:43:GLU:H	7:T:43:GLU:CD	2.26	0.43
1:N:513:LEU:HA	1:N:513:LEU:HD23	1.67	0.43
24:K:103:DMU:H2	24:K:103:DMU:H36	1.78	0.43
1:N:136[B]:LEU:HD11	29:T:267:HOH:O	2.19	0.43
2:O:41:ILE:O	2:O:45:MET:HG2	2.19	0.43
19:Q:201:TGL:H221	19:Q:201:TGL:HA81	2.01	0.43
1:A:514:LYS:HA	6:F:38:ALA:HB3	1.99	0.43
3:C:51[A]:MET:SD	25:C:303:CDL:H611	2.58	0.43
12:L:9:LYS:HA	12:L:9:LYS:HD2	1.76	0.43
1:N:172:LYS:NZ	29:N:707:HOH:O	2.51	0.43
25:T:101:CDL:H762	25:T:101:CDL:H561	2.00	0.43
20:A:609:PSC:H242	20:A:609:PSC:H82	2.01	0.43
3:C:54[A]:MET:HE1	18:C:302:PGV:H141	2.00	0.43
2:O:68:LEU:HB3	2:O:69:PRO:HD3	2.01	0.43
3:P:47:LEU:O	3:P:51[A]:MET:HG2	2.18	0.43
2:O:58:ALA:O	2:O:62:GLU:HG3	2.19	0.43
3:P:213:THR:HG23	25:P:305:CDL:C77	2.49	0.43
2:B:85:TYR:O	2:B:89:GLU:HG3	2.19	0.43
4:D:81:VAL:HG11	19:D:201:TGL:HB62	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:131[A]:ILE:HG22	4:D:132:GLN:HG3	1.99	0.43
19:Q:201:TGL:HA52	19:Q:201:TGL:HB72	2.01	0.43
8:U:12:GLN:HE21	8:U:12:GLN:HB3	1.59	0.43
1:A:285:PHE:CE2	7:T:4:ALA:HB2	2.54	0.42
2:B:164:ALA:O	2:B:194:GLY:HA3	2.18	0.42
8:H:37:HIS:HD2	8:H:40:GLU:OE2	2.02	0.42
8:U:37:HIS:HE1	29:U:218:HOH:O	2.02	0.42
21:A:614:EDO:H21	29:A:921:HOH:O	2.19	0.42
8:H:9:LYS:HB3	8:H:10:ASN:H	1.67	0.42
3:P:116:TRP:HA	3:P:117:PRO:C	2.44	0.42
3:C:175:LEU:HD21	25:C:303:CDL:H873	2.01	0.42
4:D:89:ILE:HD13	19:D:201:TGL:H312	2.01	0.42
23:J:101:CHD:H183	23:J:101:CHD:H221	2.00	0.42
25:G:102:CDL:H761	1:N:282:PHE:HZ	1.85	0.42
2:O:91:ASN:HB3	2:O:149:THR:HG21	2.02	0.42
3:P:156:ARG:HE	23:P:306:CHD:C24	2.33	0.42
13:Z:36:HIS:HB3	13:Z:39:ASN:HD21	1.85	0.42
1:A:383[B]:MET:HA	1:A:387:PHE:CD1	2.54	0.42
19:A:608:TGL:H282	19:A:608:TGL:H251	1.83	0.42
1:N:383[B]:MET:HE2	1:N:421:VAL:HB	2.02	0.42
1:N:415:ALA:HB1	19:Q:201:TGL:H132	2.01	0.42
12:Y:2:HIS:N	29:Y:201:HOH:O	2.53	0.42
1:A:229:ILE:HD11	2:B:175:ILE:HD13	2.01	0.42
2:B:104:TRP:CD2	2:B:203:ASN:HB2	2.55	0.42
1:N:334:TRP:CH2	2:O:46:LEU:HD13	2.54	0.42
1:N:381[A]:LEU:HB2	14:N:602:HEA:CAC	2.50	0.42
2:B:1:FME:O1	2:B:193:TYR:HB2	2.19	0.42
26:G:101:PEK:H8	26:G:101:PEK:C30	2.50	0.42
18:C:306:PGV:H241	18:C:306:PGV:H272	1.84	0.41
4:D:86[B]:MET:HE1	11:K:22:ALA:HB2	2.02	0.41
1:N:110:LEU:HD13	19:N:608:TGL:H311	2.00	0.41
1:A:311[B]:ILE:CD1	25:T:101:CDL:H221	2.49	0.41
25:C:303:CDL:H131	25:C:303:CDL:H162	1.88	0.41
6:F:80[A]:GLN:HE21	21:F:103:EDO:H21	1.85	0.41
1:N:377:PHE:HA	1:N:380[A]:VAL:HG12	2.01	0.41
24:P:303:DMU:H21	10:W:50:LEU:HG	2.02	0.41
7:G:4:ALA:HB2	1:N:285:PHE:CE2	2.54	0.41
25:G:102:CDL:H382	2:O:78:LEU:HD12	2.03	0.41
1:N:236:TRP:HH2	14:N:602:HEA:HBD1	1.84	0.41
5:R:43:PRO:HB2	5:R:48:ILE:HD11	2.03	0.41
1:N:334:TRP:CZ2	2:O:46:LEU:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:423[A]:MET:HE1	24:X:102:DMU:H24	2.03	0.41
1:N:501:PRO:HB3	12:Y:5:GLU:OE2	2.20	0.41
3:C:33:MET:HB2	24:C:301:DMU:C19	2.50	0.41
6:S:95:GLN:NE2	29:S:204:HOH:O	2.53	0.41
4:D:17[B]:VAL:HG22	4:D:19[B]:ARG:HG3	2.03	0.41
1:N:18:LEU:CD2	19:N:608:TGL:HB21	2.50	0.41
2:O:5:MET:HE2	2:O:5:MET:HB3	1.87	0.41
25:C:303:CDL:H762	25:C:303:CDL:H732	1.88	0.41
6:F:80[A]:GLN:NE2	29:F:207:HOH:O	2.54	0.41
2:O:94:SER:OG	2:O:148:MET:HE2	2.21	0.41
4:Q:132:GLN:O	4:Q:137:LYS:NZ	2.54	0.41
1:A:113[A]:LEU:HD12	19:L:101:TGL:H131	2.02	0.41
1:A:177:SER:H	1:A:180:GLN:HE21	1.66	0.41
1:N:225:GLY:HA3	3:P:112:LEU:HD21	2.03	0.41
1:N:386[B]:VAL:HG21	14:N:601[B]:HEA:H261	2.02	0.41
4:Q:20:ARG:H	4:Q:20:ARG:HG2	1.57	0.41
9:V:1:SAC:H2A1	9:V:2:THR:H	1.86	0.41
2:B:5:MET:HE2	2:B:5:MET:HB3	1.84	0.41
21:F:105:EDO:H22	29:F:239:HOH:O	2.21	0.41
8:H:9:LYS:HD3	8:H:9:LYS:HA	1.77	0.41
11:K:7:PRO:O	11:K:12:LYS:NZ	2.53	0.41
8:U:50:VAL:HG23	29:U:249:HOH:O	2.20	0.41
1:A:377:PHE:HA	1:A:380[A]:VAL:HG12	2.03	0.40
8:H:37:HIS:HE1	29:H:213:HOH:O	2.04	0.40
1:N:53:ILE:HG12	29:N:889:HOH:O	2.20	0.40
8:H:60:TYR:CD1	8:H:60:TYR:C	2.99	0.40
1:A:28:MET:HE3	12:L:29:PHE:CD1	2.57	0.40
1:A:240:HIS:O	1:A:241:PRO:C	2.63	0.40
21:A:615:EDO:H22	29:A:939:HOH:O	2.20	0.40
3:C:50:ASN:ND2	3:C:54[A]:MET:HE2	2.36	0.40
4:D:121:LYS:HD3	11:K:52:GLU:HA	2.03	0.40
10:J:55:PHE:HA	10:J:56:PRO:HD3	1.96	0.40
12:L:25:MET:HG2	19:L:101:TGL:HA41	2.04	0.40
13:M:37:LEU:HD23	13:M:37:LEU:HA	1.95	0.40
1:N:113[A]:LEU:HD12	19:N:608:TGL:H132	2.03	0.40
3:P:54:MET:HE1	18:P:304:PGV:H142	2.03	0.40
19:Q:201:TGL:HA32	19:Q:201:TGL:HB52	2.02	0.40
1:A:236:TRP:CH2	14:A:602:HEA:HBD1	2.56	0.40
1:N:242:GLU:HA	1:N:245:ILE:HD12	2.04	0.40
1:N:383[B]:MET:HA	1:N:387:PHE:CD1	2.57	0.40
19:N:608:TGL:HA91	19:N:608:TGL:H221	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:N:621:EDO:H11	29:O:454:HOH:O	2.22	0.40
24:P:303:DMU:H25	10:W:46:SER:HB2	2.03	0.40
4:Q:51:LEU:HD21	4:Q:59:LEU:HD12	2.03	0.40
25:T:101:CDL:H202	25:T:101:CDL:H531	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	532/514 (104%)	517 (97%)	15 (3%)	0	100	100
1	N	534/514 (104%)	522 (98%)	12 (2%)	0	100	100
2	B	231/227 (102%)	226 (98%)	5 (2%)	0	100	100
2	O	229/227 (101%)	222 (97%)	7 (3%)	0	100	100
3	C	265/259 (102%)	260 (98%)	5 (2%)	0	100	100
3	P	265/259 (102%)	260 (98%)	5 (2%)	0	100	100
4	D	148/144 (103%)	145 (98%)	3 (2%)	0	100	100
4	Q	143/144 (99%)	138 (96%)	5 (4%)	0	100	100
5	E	104/105 (99%)	104 (100%)	0	0	100	100
5	R	103/105 (98%)	103 (100%)	0	0	100	100
6	F	100/98 (102%)	95 (95%)	3 (3%)	2 (2%)	6	1
6	S	97/98 (99%)	90 (93%)	4 (4%)	3 (3%)	3	0
7	G	83/84 (99%)	72 (87%)	10 (12%)	1 (1%)	10	2
7	T	85/84 (101%)	75 (88%)	9 (11%)	1 (1%)	10	2
8	H	77/79 (98%)	72 (94%)	4 (5%)	1 (1%)	9	2
8	U	77/79 (98%)	74 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	71/73 (97%)	70 (99%)	1 (1%)	0	100	100
9	V	72/73 (99%)	69 (96%)	3 (4%)	0	100	100
10	J	56/58 (97%)	56 (100%)	0	0	100	100
10	W	56/58 (97%)	56 (100%)	0	0	100	100
11	K	48/49 (98%)	46 (96%)	2 (4%)	0	100	100
11	X	48/49 (98%)	47 (98%)	1 (2%)	0	100	100
12	L	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
12	Y	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
13	M	41/43 (95%)	40 (98%)	1 (2%)	0	100	100
13	Z	41/43 (95%)	41 (100%)	0	0	100	100
All	All	3594/3558 (101%)	3486 (97%)	100 (3%)	8 (0%)	43	24

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	S	96	LEU
6	F	96	LEU
6	F	95	GLN
6	S	95	GLN
7	G	5	LYS
6	S	94	HIS
7	T	5	LYS
8	H	8	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	444/426 (104%)	438 (99%)	6 (1%)	59	38
1	N	446/426 (105%)	442 (99%)	4 (1%)	70	55
2	B	216/210 (103%)	210 (97%)	6 (3%)	38	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	O	214/210 (102%)	210 (98%)	4 (2%)	50	27
3	C	232/224 (104%)	229 (99%)	3 (1%)	61	40
3	P	232/224 (104%)	229 (99%)	3 (1%)	61	40
4	D	134/128 (105%)	134 (100%)	0	100	100
4	Q	129/128 (101%)	126 (98%)	3 (2%)	44	20
5	E	93/92 (101%)	92 (99%)	1 (1%)	65	46
5	R	92/92 (100%)	91 (99%)	1 (1%)	65	46
6	F	85/81 (105%)	84 (99%)	1 (1%)	63	43
6	S	82/81 (101%)	79 (96%)	3 (4%)	30	10
7	G	69/68 (102%)	66 (96%)	3 (4%)	26	7
7	T	71/68 (104%)	66 (93%)	5 (7%)	14	2
8	H	71/71 (100%)	70 (99%)	1 (1%)	59	38
8	U	71/71 (100%)	68 (96%)	3 (4%)	26	7
9	I	57/57 (100%)	57 (100%)	0	100	100
9	V	58/57 (102%)	57 (98%)	1 (2%)	53	30
10	J	49/49 (100%)	48 (98%)	1 (2%)	48	24
10	W	49/49 (100%)	48 (98%)	1 (2%)	48	24
11	K	40/39 (103%)	40 (100%)	0	100	100
11	X	40/39 (103%)	39 (98%)	1 (2%)	42	18
12	L	39/39 (100%)	36 (92%)	3 (8%)	12	2
12	Y	39/39 (100%)	39 (100%)	0	100	100
13	M	37/37 (100%)	37 (100%)	0	100	100
13	Z	37/37 (100%)	37 (100%)	0	100	100
All	All	3126/3042 (103%)	3072 (98%)	54 (2%)	55	30

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	THR
1	A	128	VAL
1	A	180	GLN
1	A	297[A]	MET
1	A	297[B]	MET
1	A	369	ASP

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Mol	Chain	Res	Type
2	B	33	LEU
2	B	37	LEU
2	B	60	GLU
2	B	75	LEU
2	B	78	LEU
2	B	94	SER
3	C	159	MET
3	C	180[A]	GLU
3	C	180[B]	GLU
5	E	90	ARG
6	F	48	LEU
7	G	8	HIS
7	G	11	THR
7	G	37	LEU
8	H	60	TYR
10	J	29	ASN
12	L	2	HIS
12	L	26	THR
12	L	47	LYS
1	N	128	VAL
1	N	180	GLN
1	N	369	ASP
1	N	504	THR
2	O	33	LEU
2	O	75	LEU
2	O	78	LEU
2	O	217	LYS
3	P	159	MET
3	P	180[A]	GLU
3	P	180[B]	GLU
4	Q	19	ARG
4	Q	20	ARG
4	Q	31	LYS
5	R	108	LYS
6	S	54	ASN
6	S	80	GLN
6	S	96	LEU
7	T	8	HIS
7	T	11	THR
7	T	36[A]	TRP
7	T	36[B]	TRP
7	T	37	LEU

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Mol	Chain	Res	Type
8	U	8	ILE
8	U	60	TYR
8	U	84	LYS
9	V	37	PHE
10	W	50	LEU
11	X	52	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	80	ASN
1	A	98	ASN
1	A	170	ASN
1	A	178	GLN
1	A	180	GLN
1	A	422	ASN
1	A	512	ASN
2	B	59	GLN
2	B	140	ASN
3	C	50	ASN
3	C	68	GLN
3	C	76	GLN
4	D	76	ASN
4	D	119	GLN
5	E	94	ASN
8	H	23	GLN
8	H	28	ASN
8	H	32	ASN
8	H	37	HIS
10	J	29	ASN
10	J	57	HIS
11	K	35	GLN
1	N	80	ASN
1	N	98	ASN
1	N	170	ASN
1	N	180	GLN
1	N	422	ASN
1	N	512	ASN
2	O	59	GLN
2	O	91	ASN
2	O	140	ASN

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Mol	Chain	Res	Type
2	O	181	GLN
3	P	3	HIS
3	P	50	ASN
3	P	68	GLN
3	P	76	GLN
4	Q	32	ASN
4	Q	76	ASN
4	Q	101	HIS
4	Q	109	HIS
5	R	94	ASN
6	S	54	ASN
8	U	10	ASN
8	U	12	GLN
8	U	37	HIS
11	X	15	ASN
11	X	35	GLN
13	Z	39	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	FME	N	1	1	8,9,10	0.55	0	8,9,11	1.43	2 (25%)
2	FME	B	1	2	8,9,10	2.49	2 (25%)	8,9,11	2.66	3 (37%)
1	FME	A	1	1	8,9,10	0.61	0	8,9,11	1.39	2 (25%)
9	SAC	V	1	9	7,8,9	0.63	0	7,9,11	0.93	0
9	SAC	I	1	9	7,8,9	0.68	0	7,9,11	0.86	0
2	FME	O	1	2	8,9,10	0.91	0	8,9,11	1.05	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	-	1/7/9/11	-
2	FME	B	1	2	-	0/7/9/11	-
1	FME	A	1	1	-	5/7/9/11	-
9	SAC	V	1	9	-	3/7/8/10	-
9	SAC	I	1	9	-	3/7/8/10	-
2	FME	O	1	2	-	0/7/9/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	FME	CN-N	6.10	1.53	1.33
2	B	1	FME	CG-SD	-2.06	1.70	1.81

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	FME	CA-N-CN	-5.90	113.75	122.82
2	B	1	FME	C-CA-N	3.78	116.80	109.50
1	N	1	FME	O-C-CA	-2.73	117.76	124.77
2	O	1	FME	O-C-CA	-2.35	118.71	124.77
2	B	1	FME	O-C-CA	-2.13	119.30	124.77
1	A	1	FME	O1-CN-N	-2.08	119.94	125.32
1	A	1	FME	C-CA-N	2.07	113.49	109.50
1	N	1	FME	CG-CB-CA	-2.02	106.69	112.87

There are no chirality outliers.

All (12) torsion outliers are listed below:

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

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Mol	Chain	Res	Type	Atoms
9	V	1	SAC	O-C-CA-CB
1	A	1	FME	CA-CB-CG-SD
1	A	1	FME	C-CA-CB-CG
1	A	1	FME	CB-CA-N-CN

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	FME	1	0
9	V	1	SAC	1	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 - leaving 127 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
21	EDO	B	306	-	3,3,3	0.86	0	2,2,2	0.62	0
21	EDO	Q	203	-	3,3,3	0.33	0	2,2,2	0.76	0
25	CDL	T	101	-	76,76,99	1.53	12 (15%)	77,77,111	1.34	3 (3%)
24	DMU	X	102	-	9,9,34	0.24	0	8,8,45	0.51	0
21	EDO	A	610	-	3,3,3	0.92	0	2,2,2	1.17	0
21	EDO	N	621	-	3,3,3	0.73	0	2,2,2	0.25	0
18	PGV	P	304	-	49,49,50	1.08	4 (8%)	52,55,56	2.09	8 (15%)
21	EDO	A	612	-	3,3,3	0.61	0	2,2,2	0.19	0
21	EDO	N	610	-	3,3,3	1.03	0	2,2,2	0.63	0
19	TGL	A	608	-	61,61,62	0.85	2 (3%)	63,63,65	1.24	4 (6%)
20	PSC	O	303	-	22,22,51	0.83	1 (4%)	20,20,59	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	PGV	N	607	-	50,50,50	1.08	4 (8%)	53,56,56	1.13	4 (7%)
21	EDO	B	303	-	3,3,3	0.53	0	2,2,2	0.37	0
21	EDO	J	104	-	3,3,3	0.35	0	2,2,2	0.52	0
24	DMU	K	102	-	8,8,34	0.26	0	7,7,45	0.49	0
23	CHD	P	307	-	32,32,32	0.97	1 (3%)	51,51,51	1.26	7 (13%)
14	HEA	N	601[B]	-	67,67,67	1.81	16 (23%)	81,103,103	2.03	23 (28%)
26	PEK	P	308	-	52,52,52	0.74	2 (3%)	55,57,57	1.55	7 (12%)
14	HEA	N	601[A]	-	67,67,67	1.83	17 (25%)	81,103,103	2.01	27 (33%)
21	EDO	F	106	-	3,3,3	0.81	0	2,2,2	0.47	0
24	DMU	O	304	-	9,9,34	0.22	0	8,8,45	0.48	0
19	TGL	O	301	-	56,56,62	1.07	3 (5%)	58,58,65	1.32	5 (8%)
21	EDO	S	106	-	3,3,3	0.34	0	2,2,2	0.22	0
22	CUA	B	301	2	0,1,1	-	-	-	-	-
21	EDO	R	201	-	3,3,3	0.77	0	2,2,2	0.46	0
21	EDO	Q	204	-	3,3,3	0.44	0	2,2,2	0.46	0
24	DMU	X	105	-	9,9,34	0.22	0	8,8,45	0.57	0
21	EDO	N	615	-	3,3,3	0.50	0	2,2,2	0.73	0
23	CHD	G	103	-	32,32,32	0.89	1 (3%)	51,51,51	1.46	6 (11%)
28	PO4	U	101	-	4,4,4	1.07	0	6,6,6	0.38	0
18	PGV	A	606	-	50,50,50	0.90	2 (4%)	53,56,56	0.86	1 (1%)
21	EDO	T	102	-	3,3,3	0.62	0	2,2,2	0.31	0
19	TGL	L	101	-	58,58,62	1.08	3 (5%)	61,61,65	1.34	9 (14%)
24	DMU	P	310	-	10,10,34	0.28	0	9,9,45	0.53	0
24	DMU	K	101	-	8,8,34	0.22	0	7,7,45	0.59	0
21	EDO	P	311	-	3,3,3	0.53	0	2,2,2	0.26	0
21	EDO	J	103	-	3,3,3	0.57	0	2,2,2	0.21	0
14	HEA	A	601[B]	-	67,67,67	1.72	17 (25%)	81,103,103	1.96	22 (27%)
21	EDO	Q	202	-	3,3,3	0.50	0	2,2,2	0.09	0
14	HEA	A	601[A]	-	67,67,67	1.80	19 (28%)	81,103,103	1.77	20 (24%)
21	EDO	P	313	-	3,3,3	0.80	0	2,2,2	0.40	0
21	EDO	C	309	-	3,3,3	0.60	0	2,2,2	1.05	0
26	PEK	C	305	-	35,35,52	0.24	0	33,33,57	0.52	0
21	EDO	T	103	-	3,3,3	0.38	0	2,2,2	0.55	0
21	EDO	Y	101	-	3,3,3	0.53	0	2,2,2	0.47	0
21	EDO	A	619	-	3,3,3	1.16	0	2,2,2	0.90	0
23	CHD	B	302	-	32,32,32	1.23	3 (9%)	51,51,51	1.76	13 (25%)
24	DMU	X	101	-	34,34,34	0.43	0	45,45,45	0.80	1 (2%)
21	EDO	N	613	-	3,3,3	0.62	0	2,2,2	0.35	0
18	PGV	P	302	-	40,40,50	1.12	2 (5%)	42,42,56	1.47	6 (14%)
21	EDO	O	306	-	3,3,3	0.59	0	2,2,2	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CHD	P	306	-	32,32,32	0.77	0	51,51,51	1.34	8 (15%)
21	EDO	N	620	-	3,3,3	0.42	0	2,2,2	0.63	0
21	EDO	N	619	-	3,3,3	0.28	0	2,2,2	1.45	0
24	DMU	C	301	-	8,8,34	0.34	0	7,7,45	0.37	0
21	EDO	E	201	-	3,3,3	0.54	0	2,2,2	0.49	0
25	CDL	C	303	-	52,52,99	1.26	7 (13%)	50,50,111	1.07	2 (4%)
23	CHD	J	101	-	32,32,32	0.68	0	51,51,51	1.25	5 (9%)
24	DMU	X	103	-	8,8,34	0.27	0	7,7,45	0.51	0
24	DMU	C	308	-	11,11,34	0.33	0	10,10,45	0.51	0
21	EDO	S	103	-	3,3,3	0.61	0	2,2,2	0.77	0
21	EDO	W	103	-	3,3,3	0.43	0	2,2,2	0.22	0
25	CDL	G	102	-	59,60,99	1.36	8 (13%)	55,56,111	0.78	0
21	EDO	N	616	-	3,3,3	0.99	0	2,2,2	0.94	0
24	DMU	L	102	-	21,21,34	0.50	0	24,25,45	1.10	3 (12%)
21	EDO	F	105	-	3,3,3	0.52	0	2,2,2	0.70	0
20	PSC	A	609	-	23,23,51	0.83	1 (4%)	21,21,59	0.81	0
21	EDO	O	305	-	3,3,3	0.66	0	2,2,2	0.47	0
21	EDO	F	102	-	3,3,3	0.63	0	2,2,2	0.54	0
24	DMU	W	101	-	8,8,34	0.21	0	7,7,45	0.52	0
21	EDO	S	102	-	3,3,3	0.48	0	2,2,2	0.76	0
21	EDO	N	617	-	3,3,3	0.46	0	2,2,2	0.25	0
21	EDO	G	104	-	3,3,3	0.73	0	2,2,2	0.56	0
24	DMU	D	203	-	8,8,34	0.28	0	7,7,45	0.49	0
21	EDO	N	609	-	3,3,3	0.69	0	2,2,2	0.09	0
21	EDO	P	312	-	3,3,3	0.30	0	2,2,2	0.77	0
19	TGL	Q	201	-	62,62,62	1.01	3 (4%)	65,65,65	1.05	6 (9%)
21	EDO	B	304	-	3,3,3	0.59	0	2,2,2	0.65	0
19	TGL	N	608	-	53,54,62	0.66	1 (1%)	51,52,65	0.80	1 (1%)
18	PGV	C	306	-	34,34,50	0.93	1 (2%)	33,33,56	1.08	2 (6%)
21	EDO	C	313	-	3,3,3	0.63	0	2,2,2	0.51	0
21	EDO	A	611	-	3,3,3	0.55	0	2,2,2	0.66	0
21	EDO	S	105	-	3,3,3	0.62	0	2,2,2	0.56	0
21	EDO	C	311	-	3,3,3	0.67	0	2,2,2	0.18	0
21	EDO	N	611	-	3,3,3	0.63	0	2,2,2	0.66	0
24	DMU	J	102	-	10,10,34	0.23	0	9,9,45	0.60	0
19	TGL	D	201	-	62,62,62	1.08	3 (4%)	65,65,65	1.17	6 (9%)
21	EDO	F	104	-	3,3,3	0.90	0	2,2,2	0.33	0
21	EDO	N	614	-	3,3,3	0.47	0	2,2,2	0.34	0
28	PO4	H	101	-	4,4,4	1.15	0	6,6,6	0.51	0
21	EDO	A	616	-	3,3,3	0.45	0	2,2,2	0.51	0
21	EDO	C	312	-	3,3,3	0.59	0	2,2,2	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	EDO	W	102	-	3,3,3	0.43	0	2,2,2	1.01	0
24	DMU	P	303	-	34,34,34	0.53	1 (2%)	45,45,45	0.81	0
21	EDO	A	617	-	3,3,3	0.49	0	2,2,2	0.57	0
24	DMU	D	202	-	11,11,34	0.28	0	10,10,45	0.30	0
18	PGV	C	302	-	50,50,50	0.82	1 (2%)	53,56,56	0.88	2 (3%)
21	EDO	N	618	-	3,3,3	0.41	0	2,2,2	0.44	0
24	DMU	M	101	-	34,34,34	0.47	0	45,45,45	1.17	3 (6%)
21	EDO	A	615	-	3,3,3	0.64	0	2,2,2	0.67	0
24	DMU	Z	101	-	34,34,34	0.56	1 (2%)	45,45,45	0.85	0
21	EDO	E	202	-	3,3,3	0.54	0	2,2,2	0.27	0
24	DMU	K	106	-	8,8,34	0.26	0	7,7,45	0.53	0
26	PEK	G	101	-	52,52,52	0.98	4 (7%)	55,57,57	1.62	8 (14%)
26	PEK	C	307	-	24,24,52	0.30	0	22,22,57	0.46	0
24	DMU	K	105	-	8,8,34	0.24	0	7,7,45	0.57	0
23	CHD	C	304	-	32,32,32	1.09	1 (3%)	51,51,51	1.82	17 (33%)
22	CUA	O	302	2	0,1,1	-	-	-	-	-
18	PGV	A	607	-	34,35,50	0.94	1 (2%)	33,34,56	0.84	0
21	EDO	A	613	-	3,3,3	0.60	0	2,2,2	0.61	0
24	DMU	X	104	-	9,9,34	0.30	0	8,8,45	0.50	0
21	EDO	O	307	-	3,3,3	0.58	0	2,2,2	0.28	0
14	HEA	A	602	1	67,67,67	1.85	19 (28%)	81,103,103	2.17	31 (38%)
24	DMU	K	103	-	34,34,34	0.55	1 (2%)	45,45,45	0.98	2 (4%)
14	HEA	N	602	1	67,67,67	1.88	23 (34%)	81,103,103	1.92	26 (32%)
21	EDO	F	103	-	3,3,3	0.55	0	2,2,2	0.39	0
21	EDO	S	104	-	3,3,3	0.53	0	2,2,2	0.75	0
26	PEK	P	301	-	19,19,52	0.24	0	18,18,57	0.53	0
21	EDO	B	305	-	3,3,3	0.60	0	2,2,2	0.42	0
26	PEK	P	309	-	37,37,52	0.76	1 (2%)	36,36,57	0.85	1 (2%)
24	DMU	K	104	-	8,8,34	0.23	0	7,7,45	0.44	0
21	EDO	N	612	-	3,3,3	0.50	0	2,2,2	0.48	0
21	EDO	C	310	-	3,3,3	0.77	0	2,2,2	0.23	0
21	EDO	A	618	-	3,3,3	0.35	0	2,2,2	0.59	0
18	PGV	N	606	-	39,39,50	1.09	2 (5%)	40,40,56	1.17	4 (10%)
25	CDL	P	305	-	66,66,99	1.48	9 (13%)	65,65,111	1.01	1 (1%)
21	EDO	A	614	-	3,3,3	0.83	0	2,2,2	0.82	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	EDO	B	306	-	-	0/1/1/1	-
21	EDO	Q	203	-	-	0/1/1/1	-
25	CDL	T	101	-	-	19/73/73/110	-
24	DMU	X	102	-	-	1/7/7/59	-
21	EDO	A	610	-	-	1/1/1/1	-
21	EDO	N	621	-	-	0/1/1/1	-
18	PGV	P	304	-	-	9/54/54/55	-
21	EDO	A	612	-	-	0/1/1/1	-
21	EDO	N	610	-	-	0/1/1/1	-
19	TGL	A	608	-	-	18/63/63/65	-
20	PSC	O	303	-	-	5/18/18/55	-
18	PGV	N	607	-	-	4/55/55/55	-
21	EDO	B	303	-	-	0/1/1/1	-
21	EDO	J	104	-	-	0/1/1/1	-
24	DMU	K	102	-	-	3/6/6/59	-
23	CHD	P	307	-	-	2/9/74/74	0/4/4/4
14	HEA	N	601[B]	-	-	7/36/76/76	-
26	PEK	P	308	-	-	16/56/56/56	-
14	HEA	N	601[A]	-	-	6/36/76/76	-
21	EDO	F	106	-	-	0/1/1/1	-
24	DMU	O	304	-	-	2/7/7/59	-
19	TGL	O	301	-	-	14/57/57/65	-
21	EDO	S	106	-	-	0/1/1/1	-
21	EDO	R	201	-	-	0/1/1/1	-
21	EDO	Q	204	-	-	1/1/1/1	-
24	DMU	X	105	-	-	2/7/7/59	-
21	EDO	N	615	-	-	0/1/1/1	-
23	CHD	G	103	-	-	2/9/74/74	0/4/4/4
18	PGV	A	606	-	-	6/55/55/55	-
21	EDO	T	102	-	-	1/1/1/1	-
19	TGL	L	101	-	-	19/61/61/65	-
24	DMU	P	310	-	-	0/8/8/59	-
24	DMU	K	101	-	-	1/6/6/59	-
21	EDO	P	311	-	-	0/1/1/1	-
21	EDO	J	103	-	-	0/1/1/1	-
14	HEA	A	601[B]	-	-	8/36/76/76	-
21	EDO	Q	202	-	-	1/1/1/1	-
14	HEA	A	601[A]	-	-	5/36/76/76	-
21	EDO	P	313	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	EDO	C	309	-	-	0/1/1/1	-
26	PEK	C	305	-	-	13/31/31/56	-
21	EDO	T	103	-	-	0/1/1/1	-
21	EDO	Y	101	-	-	0/1/1/1	-
21	EDO	A	619	-	-	1/1/1/1	-
23	CHD	B	302	-	-	2/9/74/74	0/4/4/4
24	DMU	X	101	-	-	1/19/59/59	0/2/2/2
21	EDO	N	613	-	-	1/1/1/1	-
18	PGV	P	302	-	-	9/41/41/55	-
21	EDO	O	306	-	-	0/1/1/1	-
23	CHD	P	306	-	-	0/9/74/74	0/4/4/4
21	EDO	N	620	-	-	0/1/1/1	-
21	EDO	N	619	-	-	1/1/1/1	-
24	DMU	C	301	-	-	3/6/6/59	-
21	EDO	E	201	-	-	0/1/1/1	-
25	CDL	C	303	-	-	6/47/47/110	-
23	CHD	J	101	-	-	5/9/74/74	0/4/4/4
24	DMU	X	103	-	-	1/6/6/59	-
24	DMU	C	308	-	-	0/9/9/59	-
21	EDO	S	103	-	-	0/1/1/1	-
21	EDO	W	103	-	-	1/1/1/1	-
25	CDL	G	102	-	-	8/52/52/110	-
21	EDO	N	616	-	-	0/1/1/1	-
24	DMU	L	102	-	-	7/13/29/59	0/1/1/2
21	EDO	F	105	-	-	0/1/1/1	-
20	PSC	A	609	-	-	5/19/19/55	-
21	EDO	O	305	-	-	0/1/1/1	-
21	EDO	F	102	-	-	0/1/1/1	-
24	DMU	W	101	-	-	1/6/6/59	-
21	EDO	S	102	-	-	0/1/1/1	-
21	EDO	N	617	-	-	0/1/1/1	-
21	EDO	G	104	-	-	0/1/1/1	-
24	DMU	D	203	-	-	1/6/6/59	-
21	EDO	N	609	-	-	0/1/1/1	-
21	EDO	P	312	-	-	1/1/1/1	-
19	TGL	Q	201	-	-	17/65/65/65	-
21	EDO	B	304	-	-	0/1/1/1	-
19	TGL	N	608	-	-	13/49/49/65	-
18	PGV	C	306	-	-	6/31/31/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	EDO	C	313	-	-	0/1/1/1	-
21	EDO	A	611	-	-	0/1/1/1	-
21	EDO	S	105	-	-	0/1/1/1	-
21	EDO	C	311	-	-	1/1/1/1	-
21	EDO	N	611	-	-	0/1/1/1	-
24	DMU	J	102	-	-	2/8/8/59	-
19	TGL	D	201	-	-	16/65/65/65	-
21	EDO	F	104	-	-	0/1/1/1	-
21	EDO	N	614	-	-	0/1/1/1	-
21	EDO	A	616	-	-	0/1/1/1	-
21	EDO	C	312	-	-	0/1/1/1	-
21	EDO	W	102	-	-	0/1/1/1	-
24	DMU	P	303	-	-	5/19/59/59	0/2/2/2
21	EDO	A	617	-	-	0/1/1/1	-
24	DMU	D	202	-	-	5/9/9/59	-
18	PGV	C	302	-	-	7/55/55/55	-
21	EDO	N	618	-	-	0/1/1/1	-
24	DMU	M	101	-	-	4/19/59/59	0/2/2/2
21	EDO	A	615	-	-	0/1/1/1	-
24	DMU	Z	101	-	-	5/19/59/59	0/2/2/2
21	EDO	E	202	-	-	1/1/1/1	-
24	DMU	K	106	-	-	1/6/6/59	-
26	PEK	G	101	-	-	14/56/56/56	-
26	PEK	C	307	-	-	10/20/20/56	-
24	DMU	K	105	-	-	0/6/6/59	-
23	CHD	C	304	-	-	2/9/74/74	0/4/4/4
18	PGV	A	607	-	-	10/31/31/55	-
21	EDO	A	613	-	-	1/1/1/1	-
24	DMU	X	104	-	-	1/7/7/59	-
21	EDO	O	307	-	-	0/1/1/1	-
14	HEA	A	602	1	-	7/36/76/76	-
24	DMU	K	103	-	-	9/19/59/59	0/2/2/2
14	HEA	N	602	1	-	7/36/76/76	-
21	EDO	F	103	-	-	0/1/1/1	-
21	EDO	S	104	-	-	0/1/1/1	-
26	PEK	P	301	-	-	11/17/17/56	-
21	EDO	B	305	-	-	0/1/1/1	-
26	PEK	P	309	-	-	16/34/34/56	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	DMU	K	104	-	-	1/6/6/59	-
21	EDO	N	612	-	-	0/1/1/1	-
21	EDO	C	310	-	-	0/1/1/1	-
21	EDO	A	618	-	-	1/1/1/1	-
18	PGV	N	606	-	-	11/39/39/55	-
25	CDL	P	305	-	-	11/62/62/110	-
21	EDO	A	614	-	-	0/1/1/1	-

All (197) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	C	306	PGV	O03-C19	5.10	1.48	1.33
14	N	601[A]	HEA	CHB-C4A	5.10	1.48	1.38
14	N	601[B]	HEA	CHB-C4A	5.10	1.48	1.38
18	A	607	PGV	O01-C1	4.97	1.47	1.30
25	P	305	CDL	OB6-CB5	4.93	1.47	1.33
25	P	305	CDL	OB8-CB7	4.93	1.47	1.33
19	D	201	TGL	OG3-CC1	4.87	1.47	1.33
25	T	101	CDL	OB8-CB7	4.75	1.47	1.33
25	T	101	CDL	OA8-CA7	4.74	1.46	1.30
18	N	606	PGV	O03-C19	4.74	1.47	1.33
14	N	601[A]	HEA	CHA-C1A	4.70	1.47	1.38
14	N	601[B]	HEA	CHA-C1A	4.70	1.47	1.38
19	L	101	TGL	OG3-CC1	4.70	1.47	1.33
19	O	301	TGL	OG1-CA1	4.67	1.46	1.33
18	P	302	PGV	O01-C1	4.64	1.47	1.34
18	P	304	PGV	O03-C01	-4.56	1.35	1.45
19	A	608	TGL	OG2-CB1	4.53	1.47	1.34
25	C	303	CDL	OB6-CB5	4.52	1.46	1.33
18	P	302	PGV	O03-C19	4.47	1.46	1.33
14	N	602	HEA	CHB-C4A	4.44	1.47	1.38
18	N	606	PGV	O01-C1	4.41	1.46	1.33
19	O	301	TGL	OG3-CC1	4.33	1.46	1.33
19	L	101	TGL	OG2-CB1	4.27	1.46	1.34
19	L	101	TGL	OG1-CA1	4.26	1.45	1.33
19	N	608	TGL	OG3-CC1	4.26	1.46	1.33
19	Q	201	TGL	OG1-CA1	4.26	1.45	1.33
19	D	201	TGL	OG2-CB1	4.26	1.46	1.34
19	O	301	TGL	OG2-CB1	4.24	1.46	1.34
19	D	201	TGL	OG1-CA1	4.23	1.45	1.33
19	Q	201	TGL	OG3-CC1	4.20	1.45	1.33
19	Q	201	TGL	OG2-CB1	4.20	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	601[A]	HEA	C1A-C2A	-4.19	1.37	1.45
14	A	601[B]	HEA	C1A-C2A	-4.19	1.37	1.45
14	N	601[A]	HEA	C3A-C4A	-4.17	1.38	1.46
14	N	601[B]	HEA	C3A-C4A	-4.17	1.38	1.46
14	A	602	HEA	CHD-C1D	4.13	1.46	1.38
26	P	309	PEK	O03-C21	4.10	1.45	1.33
25	T	101	CDL	OB6-CB5	4.08	1.45	1.34
19	A	608	TGL	OG3-CC1	4.07	1.45	1.33
14	N	602	HEA	C1D-ND	-3.99	1.33	1.40
14	A	602	HEA	CHC-C4B	3.98	1.46	1.38
25	P	305	CDL	C82-C81	-3.95	1.32	1.51
25	C	303	CDL	C82-C81	-3.84	1.32	1.51
25	G	102	CDL	C59-C58	-3.83	1.32	1.51
14	A	602	HEA	FE-NC	3.81	2.07	1.95
20	A	609	PSC	C13-C12	3.79	1.53	1.31
14	A	602	HEA	C4A-NA	-3.76	1.32	1.39
25	C	303	CDL	C79-C78	-3.75	1.33	1.51
25	T	101	CDL	C62-C61	-3.72	1.33	1.51
25	P	305	CDL	C79-C78	-3.71	1.33	1.51
14	A	601[A]	HEA	CHA-C1A	3.71	1.45	1.38
14	A	601[B]	HEA	CHA-C1A	3.71	1.45	1.38
25	P	305	CDL	C22-C21	-3.69	1.33	1.51
25	P	305	CDL	C19-C18	-3.69	1.33	1.51
14	A	601[A]	HEA	C4D-C3D	-3.68	1.38	1.45
14	A	601[B]	HEA	C4D-C3D	-3.68	1.38	1.45
25	G	102	CDL	C22-C21	-3.67	1.33	1.51
25	T	101	CDL	C82-C81	-3.67	1.33	1.51
14	N	602	HEA	FE-NB	3.65	2.06	1.94
25	G	102	CDL	C19-C18	-3.63	1.33	1.51
25	G	102	CDL	C62-C61	-3.63	1.33	1.51
25	P	305	CDL	C42-C41	-3.62	1.33	1.51
25	P	305	CDL	C39-C38	-3.61	1.33	1.51
20	O	303	PSC	C13-C12	3.61	1.52	1.31
25	G	102	CDL	C39-C38	-3.60	1.33	1.51
25	T	101	CDL	C19-C18	-3.60	1.33	1.51
25	G	102	CDL	C42-C41	-3.60	1.33	1.51
25	T	101	CDL	C59-C58	-3.59	1.33	1.51
25	G	102	CDL	C82-C81	-3.58	1.34	1.51
25	T	101	CDL	C22-C21	-3.58	1.34	1.51
25	T	101	CDL	C39-C38	-3.57	1.34	1.51
25	T	101	CDL	C79-C78	-3.56	1.34	1.51
25	T	101	CDL	C42-C41	-3.51	1.34	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	C	303	CDL	C59-C58	-3.50	1.34	1.51
25	G	102	CDL	C79-C78	-3.50	1.34	1.51
26	G	101	PEK	O04-C21	3.50	1.32	1.22
26	G	101	PEK	O03-C01	-3.48	1.37	1.45
14	A	602	HEA	C1A-C2A	-3.45	1.39	1.45
14	A	602	HEA	C11-C3B	3.43	1.55	1.51
14	N	601[A]	HEA	CMD-C2D	3.42	1.57	1.50
14	N	601[B]	HEA	CMD-C2D	3.42	1.57	1.50
14	A	602	HEA	C1D-C2D	-3.39	1.37	1.44
18	P	304	PGV	O03-C19	3.30	1.43	1.33
14	N	601[A]	HEA	C4B-NB	-3.21	1.34	1.40
14	N	601[B]	HEA	C4B-NB	-3.21	1.34	1.40
14	A	601[A]	HEA	CHD-C4C	3.21	1.46	1.39
14	A	601[B]	HEA	CHD-C4C	3.21	1.46	1.39
14	N	602	HEA	CHB-C1B	3.21	1.46	1.39
14	N	602	HEA	FE-NC	3.19	2.05	1.95
14	N	602	HEA	FE-ND	3.18	2.04	1.94
14	A	601[A]	HEA	O11-C11	3.18	1.49	1.42
14	N	602	HEA	C1A-C2A	-3.17	1.39	1.45
14	N	601[A]	HEA	O11-C11	3.16	1.49	1.42
18	N	607	PGV	O01-C02	-3.07	1.39	1.46
14	N	602	HEA	O11-C11	3.07	1.49	1.42
14	A	601[A]	HEA	C3A-C4A	-3.03	1.40	1.46
14	A	601[B]	HEA	C3A-C4A	-3.03	1.40	1.46
14	N	601[A]	HEA	CHC-C4B	3.02	1.44	1.38
14	N	601[B]	HEA	CHC-C4B	3.02	1.44	1.38
18	N	607	PGV	O01-C1	2.99	1.42	1.34
14	A	602	HEA	FE-NB	2.95	2.04	1.94
14	N	602	HEA	CHD-C1D	2.95	1.44	1.38
14	N	602	HEA	CHD-C4C	2.91	1.45	1.39
25	P	305	CDL	C59-C58	-2.88	1.33	1.51
14	N	602	HEA	CHA-C1A	2.87	1.44	1.38
23	B	302	CHD	C11-C12	2.82	1.57	1.53
14	N	601[A]	HEA	CMB-C2B	2.81	1.56	1.50
14	N	601[B]	HEA	CMB-C2B	2.81	1.56	1.50
23	C	304	CHD	O12-C12	2.81	1.48	1.43
14	N	602	HEA	C4A-NA	-2.80	1.34	1.39
18	N	607	PGV	O03-C01	2.80	1.51	1.45
14	N	601[A]	HEA	CHA-C4D	2.78	1.45	1.39
14	N	601[B]	HEA	CHA-C4D	2.78	1.45	1.39
14	N	602	HEA	FE-NA	2.76	2.04	1.95
14	A	601[A]	HEA	CHC-C4B	2.74	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	601[B]	HEA	CHC-C4B	2.74	1.44	1.38
14	A	601[A]	HEA	CHD-C1D	2.69	1.43	1.38
14	A	601[B]	HEA	CHD-C1D	2.69	1.43	1.38
14	N	602	HEA	C3A-C4A	-2.68	1.41	1.46
14	A	601[A]	HEA	C1C-C2C	-2.67	1.36	1.43
14	A	601[B]	HEA	C1C-C2C	-2.67	1.36	1.43
14	N	602	HEA	C1D-C2D	-2.65	1.39	1.44
14	A	602	HEA	C1C-C2C	-2.62	1.37	1.43
14	N	601[A]	HEA	O1A-CGA	2.61	1.30	1.22
14	N	601[B]	HEA	O1A-CGA	2.61	1.30	1.22
14	A	602	HEA	CHA-C4D	2.60	1.45	1.39
18	C	302	PGV	O03-C01	2.57	1.50	1.45
14	N	601[A]	HEA	CHD-C4C	2.56	1.45	1.39
14	N	601[B]	HEA	CHD-C4C	2.56	1.45	1.39
14	A	602	HEA	CHB-C4A	2.55	1.43	1.38
14	A	602	HEA	C1D-ND	-2.54	1.35	1.40
26	P	308	PEK	O03-C21	2.50	1.40	1.33
23	B	302	CHD	C10-C9	-2.49	1.51	1.56
18	P	304	PGV	P-O14	-2.47	1.43	1.55
14	N	602	HEA	C4C-NC	-2.44	1.35	1.39
23	B	302	CHD	O12-C12	2.43	1.47	1.43
14	A	601[A]	HEA	CMC-C2C	2.43	1.55	1.50
14	A	601[B]	HEA	CMC-C2C	2.43	1.55	1.50
14	N	601[A]	HEA	C1D-C2D	-2.42	1.39	1.44
14	N	601[B]	HEA	C1D-C2D	-2.42	1.39	1.44
14	N	602	HEA	C1C-C2C	-2.42	1.37	1.43
14	A	602	HEA	FE-NA	2.41	2.03	1.95
26	G	101	PEK	O03-C21	2.41	1.40	1.33
14	A	602	HEA	CMC-C2C	2.39	1.55	1.50
14	A	601[A]	HEA	CHB-C4A	2.38	1.43	1.38
14	A	601[B]	HEA	CHB-C4A	2.38	1.43	1.38
25	C	303	CDL	C39-C38	-2.37	1.33	1.50
25	C	303	CDL	C62-C61	-2.36	1.33	1.50
18	N	607	PGV	C03-C02	2.36	1.58	1.50
14	A	602	HEA	CHD-C4C	2.36	1.44	1.39
14	N	601[A]	HEA	CBD-CGD	2.36	1.56	1.50
14	N	601[B]	HEA	CBD-CGD	2.36	1.56	1.50
14	A	601[A]	HEA	C4B-NB	-2.34	1.36	1.40
14	A	601[B]	HEA	C4B-NB	-2.34	1.36	1.40
14	A	601[A]	HEA	C12-C13	2.34	1.61	1.53
14	N	602	HEA	C4B-C3B	-2.34	1.40	1.44
23	P	307	CHD	O12-C12	2.33	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	601[A]	HEA	CBD-CGD	2.33	1.56	1.50
14	A	601[B]	HEA	CBD-CGD	2.33	1.56	1.50
25	C	303	CDL	C19-C18	-2.32	1.33	1.50
25	T	101	CDL	OB6-CB4	-2.31	1.43	1.47
26	G	101	PEK	O01-C1	2.30	1.40	1.34
18	A	606	PGV	O01-C02	-2.30	1.41	1.46
24	Z	101	DMU	O16-C6	2.27	1.44	1.40
18	A	606	PGV	O01-C1	2.25	1.40	1.34
14	A	602	HEA	O11-C11	2.25	1.47	1.42
24	P	303	DMU	O16-C6	2.23	1.43	1.40
26	P	308	PEK	C05-C04	2.23	1.59	1.49
14	A	601[A]	HEA	CMB-C2B	2.22	1.55	1.50
14	A	601[B]	HEA	CMB-C2B	2.22	1.55	1.50
14	N	601[A]	HEA	OMA-CMA	2.22	1.26	1.22
14	N	601[B]	HEA	OMA-CMA	2.22	1.26	1.22
18	P	304	PGV	C20-C19	2.18	1.57	1.50
24	K	103	DMU	O16-C6	2.17	1.43	1.40
14	A	602	HEA	O2D-CGD	-2.17	1.23	1.30
14	A	601[A]	HEA	FE-ND	2.16	2.01	1.94
14	A	601[B]	HEA	FE-ND	2.16	2.01	1.94
14	N	602	HEA	CHC-C1C	2.15	1.44	1.39
14	N	601[A]	HEA	FE-ND	2.11	2.01	1.94
14	N	601[B]	HEA	FE-ND	2.11	2.01	1.94
14	A	602	HEA	CBC-CAC	2.11	1.40	1.30
23	G	103	CHD	C10-C9	-2.11	1.52	1.56
14	N	602	HEA	C4D-C3D	-2.10	1.41	1.45
14	N	601[A]	HEA	C1D-ND	-2.08	1.36	1.40
14	N	601[B]	HEA	C1D-ND	-2.08	1.36	1.40
14	N	602	HEA	C12-C11	2.08	1.56	1.53
14	A	602	HEA	O1A-CGA	2.07	1.28	1.22
14	A	601[A]	HEA	CHB-C1B	2.04	1.43	1.39
14	A	601[B]	HEA	CHB-C1B	2.04	1.43	1.39
14	A	601[A]	HEA	FE-NA	2.03	2.01	1.95
14	A	601[B]	HEA	FE-NA	2.03	2.01	1.95
14	N	602	HEA	CBA-CGA	2.03	1.55	1.50
14	N	602	HEA	C1B-C2B	-2.02	1.40	1.44
14	A	601[A]	HEA	CAD-C3D	2.01	1.56	1.51
14	A	601[B]	HEA	CAD-C3D	2.01	1.56	1.51
14	N	601[A]	HEA	C1A-C2A	-2.00	1.41	1.45
14	N	601[B]	HEA	C1A-C2A	-2.00	1.41	1.45

All (294) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	P	304	PGV	O03-C19-O04	-9.09	100.89	123.63
18	P	304	PGV	O03-C19-C20	8.17	136.76	111.83
14	A	602	HEA	C2D-C1D-ND	6.85	117.71	109.84
14	A	601[B]	HEA	C12-C11-C3B	6.09	121.65	112.12
19	A	608	TGL	OG2-CB1-CB2	6.09	124.66	111.48
14	N	602	HEA	O2D-CGD-O1D	6.07	138.95	123.33
14	N	601[B]	HEA	C13-C12-C11	-6.07	104.70	114.39
19	O	301	TGL	OG2-CB1-CB2	5.97	124.40	111.48
14	N	601[A]	HEA	C3C-C4C-NC	5.87	114.74	109.80
14	N	601[B]	HEA	C3C-C4C-NC	5.87	114.74	109.80
25	T	101	CDL	CB4-OB6-CB5	-5.87	109.31	117.78
26	G	101	PEK	O03-C21-C22	5.60	128.90	111.83
25	T	101	CDL	OB6-CB5-C51	5.32	123.00	111.48
26	G	101	PEK	O03-C21-O04	-5.01	111.10	123.63
19	L	101	TGL	OG2-CB1-CB2	4.95	122.20	111.48
14	N	602	HEA	CBD-CAD-C3D	4.81	125.84	112.53
19	D	201	TGL	OG3-CC1-CC2	4.71	126.18	111.83
23	B	302	CHD	C11-C9-C10	-4.69	108.94	113.70
26	P	308	PEK	O03-C21-C22	4.68	126.09	111.83
18	P	304	PGV	C03-C02-C01	4.67	122.68	111.78
14	A	602	HEA	C3C-C4C-NC	4.65	113.72	109.80
26	P	308	PEK	C02-O01-C1	-4.60	106.79	117.80
18	P	302	PGV	O01-C1-C2	4.60	121.43	111.48
26	G	101	PEK	C02-O01-C1	-4.54	106.94	117.80
14	A	601[A]	HEA	C3D-C4D-ND	4.46	114.67	110.35
14	A	601[B]	HEA	C3D-C4D-ND	4.46	114.67	110.35
14	N	602	HEA	C2D-C1D-ND	4.35	114.84	109.84
14	N	602	HEA	C2B-C1B-NB	4.31	114.88	109.90
14	A	601[A]	HEA	C17-C18-C19	-4.24	117.92	127.62
14	A	602	HEA	C13-C12-C11	-4.21	107.67	114.39
14	N	601[A]	HEA	C3A-C2A-C1A	-4.20	103.07	107.05
14	N	601[B]	HEA	C3A-C2A-C1A	-4.20	103.07	107.05
14	A	602	HEA	CMD-C2D-C1D	4.18	131.56	125.03
26	P	308	PEK	C01-O03-C21	4.09	132.06	117.12
14	A	601[A]	HEA	CMB-C2B-C1B	-4.04	118.71	125.03
14	A	601[B]	HEA	CMB-C2B-C1B	-4.04	118.71	125.03
23	C	304	CHD	C14-C8-C7	-4.02	106.52	111.85
14	A	601[B]	HEA	C13-C12-C11	-4.00	108.00	114.39
18	P	302	PGV	O03-C19-C20	3.97	123.95	111.83
14	N	601[A]	HEA	CAA-CBA-CGA	-3.95	103.19	113.67
14	N	601[B]	HEA	CAA-CBA-CGA	-3.95	103.19	113.67
14	A	602	HEA	C2B-C1B-NB	3.92	114.43	109.90
14	A	602	HEA	O2D-CGD-O1D	3.84	133.21	123.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	P	308	PEK	O03-C21-O04	-3.79	114.14	123.63
23	B	302	CHD	C19-C10-C5	-3.79	104.10	110.44
23	G	103	CHD	C4-C3-C2	-3.79	106.00	110.62
18	C	306	PGV	O03-C19-C20	3.74	123.24	111.83
23	C	304	CHD	C1-C2-C3	-3.71	105.57	110.48
18	N	607	PGV	O01-C1-O02	-3.68	115.11	123.70
26	P	308	PEK	C03-C02-C01	3.66	120.31	111.78
23	B	302	CHD	C6-C5-C4	-3.65	107.06	111.23
14	A	602	HEA	C4C-C3C-C2C	-3.64	102.77	107.30
14	A	601[B]	HEA	C17-C18-C19	-3.63	119.32	127.62
19	D	201	TGL	OG3-CC1-OC1	-3.62	114.58	123.63
19	Q	201	TGL	OG2-CB1-CB2	3.61	119.29	111.48
14	A	602	HEA	C2A-C1A-NA	3.57	113.77	110.32
14	A	601[A]	HEA	C3B-C4B-NB	3.56	113.94	109.84
14	A	601[B]	HEA	C3B-C4B-NB	3.56	113.94	109.84
18	N	606	PGV	O01-C1-C2	3.54	122.62	111.83
14	N	601[A]	HEA	C1A-CHA-C4D	-3.51	118.57	126.02
14	N	601[B]	HEA	C1A-CHA-C4D	-3.51	118.57	126.02
18	P	304	PGV	C01-O03-C19	3.49	129.88	117.12
14	N	602	HEA	C3C-C4C-NC	3.49	112.74	109.80
18	P	302	PGV	O01-C02-C01	3.47	114.19	106.21
14	N	601[A]	HEA	C2A-C1A-NA	3.43	113.64	110.32
14	N	601[B]	HEA	C2A-C1A-NA	3.43	113.64	110.32
23	P	306	CHD	C13-C17-C20	-3.40	115.37	119.48
23	J	101	CHD	C22-C20-C17	3.38	117.34	110.33
14	N	601[A]	HEA	C27-C19-C20	3.37	121.08	115.23
14	N	601[B]	HEA	C27-C19-C20	3.37	121.08	115.23
14	A	601[B]	HEA	O11-C11-C3B	-3.36	105.09	111.26
25	C	303	CDL	OB6-CB5-C51	3.29	121.88	111.83
24	K	103	DMU	C10-O7-C3	-3.28	110.19	117.98
24	M	101	DMU	C18-O16-C6	-3.28	108.07	113.68
14	N	601[A]	HEA	O2A-CGA-CBA	3.28	124.35	114.00
14	N	601[B]	HEA	O2A-CGA-CBA	3.28	124.35	114.00
23	C	304	CHD	C1-C10-C5	3.26	112.42	107.75
14	N	601[A]	HEA	OMA-CMA-C3A	-3.25	118.28	125.62
14	N	601[B]	HEA	OMA-CMA-C3A	-3.25	118.28	125.62
14	A	602	HEA	C3A-C2A-C1A	-3.24	103.97	107.05
14	A	601[A]	HEA	C3C-C4C-NC	3.24	112.53	109.80
14	A	601[B]	HEA	C3C-C4C-NC	3.24	112.53	109.80
23	G	103	CHD	C21-C20-C17	-3.22	108.04	112.88
14	A	602	HEA	CHB-C4A-NA	3.20	127.94	124.45
14	N	601[A]	HEA	CHA-C1A-C2A	-3.20	119.82	124.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	601[B]	HEA	CHA-C1A-C2A	-3.20	119.82	124.86
23	C	304	CHD	C14-C13-C12	3.18	110.32	107.42
23	G	103	CHD	C6-C5-C4	-3.15	107.63	111.23
23	P	306	CHD	C17-C13-C14	3.14	103.27	100.11
26	G	101	PEK	O03-C01-C02	-3.14	99.35	108.40
23	P	307	CHD	C22-C20-C17	-3.13	103.85	110.33
23	C	304	CHD	C6-C7-C8	-3.11	108.10	111.50
23	G	103	CHD	C2-C1-C10	-3.11	107.50	112.74
14	A	601[A]	HEA	C4B-NB-C1B	-3.10	101.54	105.21
14	A	601[B]	HEA	C4B-NB-C1B	-3.10	101.54	105.21
14	A	602	HEA	C1D-C2D-C3D	-3.09	103.73	106.98
23	P	307	CHD	C22-C23-C24	-3.08	104.28	112.49
19	Q	201	TGL	OG1-CA1-CA2	3.07	121.21	111.83
24	K	103	DMU	C7-C8-C9	-3.06	104.69	110.23
23	B	302	CHD	C16-C17-C20	-3.03	107.59	112.18
14	N	601[A]	HEA	C27-C19-C18	-3.03	115.85	123.63
25	P	305	CDL	OB8-CB7-C71	3.02	121.05	111.83
14	N	602	HEA	C4B-NB-C1B	-3.02	101.64	105.21
14	N	601[A]	HEA	C4C-NC-C1C	-3.00	100.93	105.82
14	N	601[B]	HEA	C4C-NC-C1C	-3.00	100.93	105.82
23	J	101	CHD	C15-C14-C13	2.98	106.43	103.54
14	A	601[A]	HEA	CHA-C4D-C3D	-2.97	120.44	124.77
14	A	601[B]	HEA	CHA-C4D-C3D	-2.97	120.44	124.77
19	A	608	TGL	OG3-CC1-CC2	2.97	120.88	111.83
14	N	602	HEA	C27-C19-C20	2.96	120.36	115.23
19	Q	201	TGL	CG2-OG2-CB1	-2.95	110.72	117.80
14	A	601[A]	HEA	C2B-C1B-NB	2.95	113.31	109.90
14	A	601[B]	HEA	C2B-C1B-NB	2.95	113.31	109.90
26	P	308	PEK	O11-P-O14	-2.95	97.25	108.94
14	N	602	HEA	O2D-CGD-CBD	-2.94	104.72	114.00
23	C	304	CHD	C4-C3-C2	2.93	114.19	110.62
18	C	306	PGV	O03-C19-O04	-2.92	116.31	123.63
14	A	601[A]	HEA	C3C-C2C-C1C	2.92	110.61	107.17
14	A	601[B]	HEA	C3C-C2C-C1C	2.92	110.61	107.17
23	C	304	CHD	C4-C5-C10	-2.91	109.56	112.66
23	C	304	CHD	C18-C13-C12	2.90	111.96	109.06
18	N	606	PGV	O03-C19-C20	2.89	120.63	111.83
19	O	301	TGL	OG3-CC1-CC2	2.88	120.62	111.83
14	N	601[A]	HEA	C3B-C4B-NB	2.88	113.15	109.84
14	N	601[B]	HEA	C3B-C4B-NB	2.88	113.15	109.84
23	P	306	CHD	C13-C14-C8	-2.87	111.08	114.72
19	L	101	TGL	OG1-CA1-CA2	2.87	120.59	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	602	HEA	CHB-C1B-NB	-2.86	121.34	124.42
23	P	306	CHD	C11-C9-C10	-2.86	110.80	113.70
24	M	101	DMU	O5-C6-O16	-2.85	103.31	110.04
14	A	602	HEA	C25-C23-C22	-2.84	114.13	122.66
14	A	602	HEA	CBD-CAD-C3D	2.84	120.39	112.53
14	N	601[A]	HEA	C13-C12-C11	-2.82	109.89	114.39
19	D	201	TGL	CG2-OG2-CB1	-2.82	111.05	117.80
14	N	601[A]	HEA	C17-C18-C19	-2.82	121.18	127.62
14	A	601[A]	HEA	C4C-C3C-C2C	-2.81	103.81	107.30
14	A	601[B]	HEA	C4C-C3C-C2C	-2.81	103.81	107.30
14	A	602	HEA	O11-C11-C3B	-2.80	106.11	111.26
23	P	307	CHD	C21-C20-C22	-2.77	106.05	110.34
19	O	301	TGL	CG2-OG2-CB1	-2.77	111.17	117.80
24	L	102	DMU	C3-C4-C57	-2.75	107.40	112.50
14	A	601[A]	HEA	CAA-CBA-CGA	-2.73	106.41	113.67
14	A	601[B]	HEA	CAA-CBA-CGA	-2.73	106.41	113.67
23	B	302	CHD	O12-C12-C13	-2.73	106.41	111.02
19	O	301	TGL	OG1-CA1-CA2	2.73	120.16	111.83
14	A	602	HEA	C1D-ND-C4D	-2.73	101.98	105.21
23	C	304	CHD	C13-C14-C8	-2.72	111.27	114.72
18	C	302	PGV	C21-C20-C19	-2.72	103.74	113.69
19	D	201	TGL	OG1-CA1-CA2	2.70	120.08	111.83
14	N	601[A]	HEA	C26-C15-C14	-2.70	116.69	123.63
18	P	302	PGV	O03-C19-O04	-2.70	116.87	123.63
14	A	602	HEA	CAD-C3D-C4D	-2.69	120.01	124.70
14	A	601[A]	HEA	CHB-C1B-NB	-2.68	121.53	124.42
14	A	601[B]	HEA	CHB-C1B-NB	-2.68	121.53	124.42
23	B	302	CHD	C19-C10-C9	2.67	114.76	111.18
18	P	302	PGV	C01-O03-C19	2.66	126.85	117.12
14	N	601[A]	HEA	CHA-C4D-C3D	-2.65	120.91	124.77
14	N	601[B]	HEA	CHA-C4D-C3D	-2.65	120.91	124.77
14	N	602	HEA	C2C-C1C-NC	2.65	114.39	110.14
14	A	602	HEA	CAD-C3D-C2D	2.65	132.83	127.87
19	O	301	TGL	OG2-CB1-OB1	-2.63	117.55	123.70
25	T	101	CDL	OB6-CB5-OB7	-2.63	117.55	123.70
19	A	608	TGL	OG3-CC1-OC1	-2.63	117.04	123.63
14	N	601[A]	HEA	C12-C11-C3B	2.62	116.22	112.12
18	N	606	PGV	O01-C1-O02	-2.62	117.06	123.63
14	N	602	HEA	CMD-C2D-C1D	2.62	129.12	125.03
23	P	306	CHD	C16-C17-C13	2.61	106.08	103.54
14	A	602	HEA	CHA-C1A-NA	-2.58	121.64	124.45
14	N	601[A]	HEA	CHA-C4D-ND	2.58	127.20	124.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	601[B]	HEA	CHA-C4D-ND	2.58	127.20	124.42
14	N	602	HEA	CMB-C2B-C1B	2.58	129.06	125.03
23	P	307	CHD	C19-C10-C1	-2.58	104.21	108.31
23	P	306	CHD	C22-C23-C24	-2.58	105.62	112.49
23	B	302	CHD	C10-C9-C8	2.57	114.71	111.84
14	N	602	HEA	CHC-C1C-NC	-2.57	119.19	123.86
14	N	602	HEA	CHA-C1A-NA	-2.57	121.65	124.45
19	L	101	TGL	CG2-OG2-CB1	-2.57	111.64	117.80
14	A	602	HEA	C4B-NB-C1B	-2.57	102.17	105.21
14	N	602	HEA	CHA-C4D-ND	2.57	127.19	124.42
26	G	101	PEK	C23-C22-C21	-2.54	104.38	113.69
18	P	302	PGV	C03-C02-C01	-2.54	105.55	112.69
14	A	601[A]	HEA	CHC-C4B-C3B	-2.54	119.39	125.80
14	A	601[B]	HEA	CHC-C4B-C3B	-2.54	119.39	125.80
14	A	602	HEA	C4C-NC-C1C	-2.54	101.68	105.82
19	L	101	TGL	OG3-CC1-CC2	2.54	119.58	111.83
18	P	304	PGV	O03-C01-C02	-2.54	101.08	108.40
14	N	601[B]	HEA	C12-C11-C3B	2.53	116.08	112.12
23	G	103	CHD	C4-C5-C10	-2.51	109.99	112.66
26	P	309	PEK	O03-C21-C22	2.51	121.61	112.14
23	P	307	CHD	O12-C12-C13	-2.50	106.80	111.02
19	L	101	TGL	CB3-CB2-CB1	-2.50	104.54	113.69
14	N	602	HEA	CHB-C1B-NB	-2.50	121.74	124.42
14	A	601[A]	HEA	C4C-CHD-C1D	-2.48	120.41	126.25
14	A	601[B]	HEA	C4C-CHD-C1D	-2.48	120.41	126.25
26	P	308	PEK	C23-C22-C21	-2.48	104.61	113.69
23	C	304	CHD	C19-C10-C1	-2.46	104.39	108.31
14	N	601[B]	HEA	C17-C18-C19	-2.46	122.00	127.62
14	N	601[A]	HEA	CMB-C2B-C1B	-2.45	121.20	125.03
14	N	601[B]	HEA	CMB-C2B-C1B	-2.45	121.20	125.03
14	A	602	HEA	CHD-C1D-C2D	-2.44	120.01	126.95
14	A	602	HEA	C27-C19-C20	2.43	119.45	115.23
14	A	601[A]	HEA	O2A-CGA-CBA	2.43	121.67	114.00
14	A	601[B]	HEA	O2A-CGA-CBA	2.43	121.67	114.00
14	A	601[A]	HEA	C13-C12-C11	-2.43	110.52	114.39
25	C	303	CDL	CB7-OB8-CB6	2.42	123.84	113.26
26	G	101	PEK	C03-C02-C01	2.42	117.42	111.78
23	B	302	CHD	C13-C14-C8	-2.41	111.66	114.72
14	A	601[B]	HEA	C26-C15-C16	2.41	119.41	115.23
19	D	201	TGL	CG3-CG2-CG1	-2.40	106.19	111.78
14	A	601[A]	HEA	C1D-ND-C4D	-2.38	102.39	105.21
14	A	601[B]	HEA	C1D-ND-C4D	-2.38	102.39	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	601[A]	HEA	O1D-CGD-CBD	-2.37	115.57	123.09
14	N	601[B]	HEA	O1D-CGD-CBD	-2.37	115.57	123.09
14	A	602	HEA	C13-C14-C15	-2.37	122.21	127.62
14	A	602	HEA	O2A-CGA-CBA	2.36	121.47	114.00
23	G	103	CHD	C19-C10-C5	-2.36	106.49	110.44
14	A	601[A]	HEA	CHB-C4A-NA	2.35	127.02	124.45
14	A	601[B]	HEA	CHB-C4A-NA	2.35	127.02	124.45
23	C	304	CHD	C21-C20-C17	2.35	116.41	112.88
14	N	602	HEA	C4C-NC-C1C	-2.34	102.00	105.82
23	J	101	CHD	C13-C14-C8	-2.34	111.76	114.72
14	N	601[A]	HEA	C13-C14-C15	-2.33	122.28	127.62
14	N	602	HEA	CHB-C4A-C3A	-2.32	121.29	125.21
19	L	101	TGL	CG3-CG2-CG1	-2.32	106.37	111.78
14	A	601[A]	HEA	C13-C14-C15	-2.31	122.33	127.62
24	L	102	DMU	O5-C4-C57	2.31	110.54	106.83
19	Q	201	TGL	OG3-CC1-CC2	2.31	118.88	111.83
14	A	601[A]	HEA	C4B-C3B-C2B	-2.31	103.55	107.44
14	A	601[B]	HEA	C4B-C3B-C2B	-2.31	103.55	107.44
26	G	101	PEK	O11-P-O14	-2.30	99.80	108.94
23	B	302	CHD	C17-C13-C12	2.30	119.74	117.67
14	N	602	HEA	C13-C12-C11	-2.30	110.72	114.39
14	N	602	HEA	CHD-C1D-ND	-2.29	121.53	124.37
18	A	606	PGV	C4-C3-C2	-2.29	104.73	113.13
14	N	601[A]	HEA	C4C-C3C-C2C	-2.27	104.47	107.30
14	N	601[B]	HEA	C4C-C3C-C2C	-2.27	104.47	107.30
14	A	602	HEA	CHB-C4A-C3A	-2.27	121.38	125.21
23	J	101	CHD	C16-C17-C13	2.27	105.74	103.54
14	N	602	HEA	C3B-C4B-NB	2.27	112.45	109.84
23	C	304	CHD	C21-C20-C22	-2.26	106.84	110.34
23	P	306	CHD	C19-C10-C9	-2.26	108.15	111.18
23	B	302	CHD	C16-C17-C13	2.25	105.72	103.54
18	P	304	PGV	C22-C21-C20	-2.25	104.86	113.13
14	N	602	HEA	C1D-C2D-C3D	-2.24	104.62	106.98
14	N	602	HEA	C1B-C2B-C3B	-2.24	104.20	106.80
23	C	304	CHD	C11-C9-C10	-2.23	111.44	113.70
19	D	201	TGL	OG1-CA1-OA1	-2.23	118.04	123.63
26	G	101	PEK	O12-C04-C05	-2.23	101.01	109.17
23	B	302	CHD	C1-C10-C5	2.22	110.93	107.75
19	L	101	TGL	C20-CA9-CA8	-2.22	103.17	114.37
19	Q	201	TGL	OG1-CA1-OA1	-2.21	118.10	123.63
23	B	302	CHD	C5-C4-C3	-2.20	109.38	112.71
24	M	101	DMU	C11-C9-C8	-2.19	107.64	113.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	X	101	DMU	C10-O7-C3	-2.19	112.78	117.98
19	A	608	TGL	OG2-CB1-OB1	-2.17	118.62	123.70
14	N	601[A]	HEA	C1C-CHC-C4B	-2.17	121.14	126.25
14	N	601[B]	HEA	C1C-CHC-C4B	-2.17	121.14	126.25
23	B	302	CHD	C22-C23-C24	-2.17	106.71	112.49
14	A	602	HEA	O1A-CGA-CBA	-2.17	116.22	123.09
18	N	607	PGV	C01-O03-C19	-2.16	109.24	117.12
18	P	304	PGV	C24-C23-C22	-2.15	103.48	114.37
19	Q	201	TGL	OG2-CB1-OB1	-2.15	118.68	123.70
19	N	608	TGL	OG3-CC1-CC2	2.15	120.26	112.14
14	N	601[A]	HEA	O11-C11-C3B	-2.14	107.34	111.26
19	L	101	TGL	OG1-CA1-OA1	-2.14	118.28	123.63
14	N	602	HEA	O1D-CGD-CBD	-2.13	116.33	123.09
14	N	602	HEA	CHD-C4C-NC	2.12	127.71	123.86
14	A	602	HEA	CAA-CBA-CGA	-2.12	108.04	113.67
23	J	101	CHD	C13-C17-C20	2.11	122.04	119.48
18	N	607	PGV	C4-C3-C2	-2.11	105.36	113.13
18	N	606	PGV	C02-O01-C1	-2.11	110.31	116.90
14	N	601[B]	HEA	O11-C11-C3B	-2.09	107.42	111.26
23	C	304	CHD	O3-C3-C2	-2.09	104.69	110.17
23	C	304	CHD	C22-C20-C17	-2.09	105.99	110.33
24	L	102	DMU	C6-O5-C4	2.08	115.44	113.13
18	C	302	PGV	O14-P-O13	2.07	122.10	112.44
14	N	601[A]	HEA	C26-C15-C16	2.07	118.83	115.23
14	A	602	HEA	CBC-CAC-C3C	-2.07	117.19	127.53
23	P	306	CHD	O25-C24-C23	-2.07	116.53	123.09
14	N	601[A]	HEA	CHC-C4B-C3B	-2.06	120.60	125.80
14	N	601[B]	HEA	CHC-C4B-C3B	-2.06	120.60	125.80
14	A	602	HEA	C12-C13-C14	-2.06	106.75	112.16
23	C	304	CHD	C22-C23-C24	-2.03	107.09	112.49
23	P	307	CHD	O7-C7-C8	2.02	114.16	109.52
18	P	304	PGV	O01-C1-O02	-2.02	118.98	123.70
14	A	602	HEA	C21-C20-C19	2.02	119.88	113.19
19	L	101	TGL	OG2-CB1-OB1	-2.02	118.99	123.70
14	N	601[A]	HEA	CHD-C1D-C2D	-2.02	121.22	126.95
14	N	601[B]	HEA	CHD-C1D-C2D	-2.02	121.22	126.95
14	N	602	HEA	C21-C22-C23	-2.01	120.93	127.64
18	N	607	PGV	O02-C1-C2	2.01	131.65	123.78
23	C	304	CHD	C2-C1-C10	2.01	116.14	112.74
23	P	307	CHD	C16-C17-C20	-2.01	109.14	112.18
14	N	602	HEA	C4A-C3A-C2A	-2.00	105.08	106.81

There are no chirality outliers.

All (415) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	602	HEA	C2D-C3D-CAD-CBD
14	A	602	HEA	C4D-C3D-CAD-CBD
18	A	606	PGV	C10-C11-C12-C13
18	A	607	PGV	O04-C19-C20-C21
18	C	302	PGV	C10-C11-C12-C13
18	C	306	PGV	O04-C19-O03-C01
18	C	306	PGV	C20-C19-O03-C01
18	N	606	PGV	O04-C19-O03-C01
18	N	606	PGV	C20-C19-O03-C01
18	P	302	PGV	O04-C19-O03-C01
18	P	302	PGV	C20-C19-O03-C01
18	P	304	PGV	O04-C19-O03-C01
18	P	304	PGV	C20-C19-O03-C01
23	J	101	CHD	C13-C17-C20-C22
24	L	102	DMU	C1-C6-O16-C18
24	L	102	DMU	O5-C6-O16-C18
25	T	101	CDL	OB6-CB4-CB6-OB8
26	C	307	PEK	C9-C10-C11-C12
26	G	101	PEK	C22-C21-O03-C01
26	P	301	PEK	C9-C10-C11-C12
26	G	101	PEK	O04-C21-O03-C01
26	P	308	PEK	O04-C21-O03-C01
26	P	309	PEK	O04-C21-O03-C01
24	K	103	DMU	O5-C4-C57-O61
26	P	309	PEK	C22-C21-O03-C01
14	A	601[A]	HEA	C26-C15-C16-C17
14	N	601[A]	HEA	C26-C15-C16-C17
14	A	601[A]	HEA	C14-C15-C16-C17
14	N	601[A]	HEA	C14-C15-C16-C17
26	P	308	PEK	C22-C21-O03-C01
18	P	302	PGV	C10-C11-C12-C13
18	P	304	PGV	C10-C11-C12-C13
26	P	301	PEK	C4-C5-C6-C7
26	P	309	PEK	C7-C8-C9-C10
14	A	601[B]	HEA	C15-C16-C17-C18
24	K	103	DMU	C3-C4-C57-O61
18	A	607	PGV	C10-C11-C12-C13
26	G	101	PEK	C10-C11-C12-C13
26	P	309	PEK	C4-C5-C6-C7
23	J	101	CHD	C16-C17-C20-C21
24	M	101	DMU	C28-C31-C34-C37
24	Z	101	DMU	C19-C22-C25-C28

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Mol	Chain	Res	Type	Atoms
19	D	201	TGL	C21-C22-C23-C24
26	C	305	PEK	C13-C14-C15-C16
14	N	601[B]	HEA	C15-C16-C17-C18
25	T	101	CDL	C40-C41-C42-C43
19	O	301	TGL	CC1-CC2-CC3-CC4
19	L	101	TGL	CA1-CA2-CA3-CA4
19	Q	201	TGL	CC5-CC6-CC7-CC8
18	P	302	PGV	C1-C2-C3-C4
23	J	101	CHD	C16-C17-C20-C22
26	C	305	PEK	C7-C8-C9-C10
18	N	606	PGV	O03-C01-C02-O01
19	A	608	TGL	CB1-CB2-CB3-CB4
23	J	101	CHD	C13-C17-C20-C21
26	C	305	PEK	C10-C11-C12-C13
26	C	307	PEK	C7-C8-C9-C10
19	O	301	TGL	C18-C19-C33-C34
24	J	102	DMU	C31-C34-C37-C40
25	T	101	CDL	C20-C21-C22-C23
19	N	608	TGL	C12-C13-C14-C29
25	G	102	CDL	C40-C41-C42-C43
26	P	308	PEK	C23-C24-C25-C26
18	N	607	PGV	C10-C11-C12-C13
19	L	101	TGL	CB2-CB3-CB4-CB5
24	K	106	DMU	C28-C31-C34-C37
25	T	101	CDL	C60-C61-C62-C63
25	C	303	CDL	C80-C81-C82-C83
25	T	101	CDL	C77-C78-C79-C80
24	L	102	DMU	C18-C19-C22-C25
19	D	201	TGL	CA7-CA8-CA9-C20
25	C	303	CDL	OB6-CB4-CB6-OB8
19	L	101	TGL	CC9-C15-C16-C17
19	D	201	TGL	C22-C23-C24-C25
19	Q	201	TGL	C21-C20-CA9-CA8
19	Q	201	TGL	CC2-CC3-CC4-CC5
24	P	303	DMU	C22-C25-C28-C31
21	A	610	EDO	O1-C1-C2-O2
24	M	101	DMU	C19-C22-C25-C28
24	O	304	DMU	C22-C25-C28-C31
18	N	606	PGV	C01-C02-O01-C1
26	C	307	PEK	C4-C5-C6-C7
19	D	201	TGL	C20-C21-C22-C23
19	O	301	TGL	CB9-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
19	Q	201	TGL	CC7-CC8-CC9-C15
20	O	303	PSC	C22-C23-C24-C25
25	P	305	CDL	C20-C21-C22-C23
18	N	606	PGV	C2-C1-O01-C02
25	G	102	CDL	C57-C58-C59-C60
20	O	303	PSC	C23-C24-C25-C26
19	O	301	TGL	CB7-CB8-CB9-C10
24	K	103	DMU	C2-C3-O7-C10
24	K	103	DMU	O16-C18-C19-C22
19	L	101	TGL	CB5-CB6-CB7-CB8
18	N	606	PGV	O02-C1-O01-C02
24	K	103	DMU	C22-C25-C28-C31
24	P	303	DMU	O16-C18-C19-C22
19	L	101	TGL	CA5-CA6-CA7-CA8
24	K	103	DMU	C4-C3-O7-C10
18	P	304	PGV	C7-C8-C9-C10
19	Q	201	TGL	CB2-CB1-OG2-CG2
25	P	305	CDL	C77-C78-C79-C80
25	P	305	CDL	C37-C38-C39-C40
25	G	102	CDL	C37-C38-C39-C40
19	L	101	TGL	CA3-CA4-CA5-CA6
19	N	608	TGL	CC5-CC6-CC7-CC8
26	P	309	PEK	C25-C26-C27-C28
26	P	308	PEK	C7-C8-C9-C10
19	A	608	TGL	C25-C26-C27-C28
24	J	102	DMU	C28-C31-C34-C37
19	A	608	TGL	CA2-CA3-CA4-CA5
19	Q	201	TGL	C20-C21-C22-C23
25	P	305	CDL	C17-C18-C19-C20
24	P	303	DMU	O6-C11-C9-O1
19	L	101	TGL	CB7-CB8-CB9-C10
25	T	101	CDL	C80-C81-C82-C83
25	C	303	CDL	C72-C73-C74-C75
19	N	608	TGL	CB9-C10-C11-C12
14	N	602	HEA	C4D-C3D-CAD-CBD
18	N	606	PGV	C10-C11-C12-C13
26	G	101	PEK	C7-C8-C9-C10
26	P	309	PEK	C13-C14-C15-C16
18	A	607	PGV	C2-C3-C4-C5
19	O	301	TGL	OG1-CG1-CG2-CG3
24	K	103	DMU	C18-C19-C22-C25
19	Q	201	TGL	CB7-CB8-CB9-C10

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Mol	Chain	Res	Type	Atoms
19	O	301	TGL	CC9-C15-C16-C17
26	G	101	PEK	C4-C5-C6-C7
26	P	308	PEK	C10-C11-C12-C13
25	G	102	CDL	C60-C61-C62-C63
18	C	306	PGV	C24-C25-C26-C27
24	Z	101	DMU	C34-C37-C40-C43
19	Q	201	TGL	CA1-CA2-CA3-CA4
24	D	202	DMU	C28-C31-C34-C37
25	P	305	CDL	OB6-CB4-CB6-OB8
19	Q	201	TGL	C29-C30-C31-C32
26	P	308	PEK	C4-C5-C6-C7
24	K	104	DMU	C28-C31-C34-C37
18	P	304	PGV	C02-C03-O11-P
24	X	102	DMU	C34-C37-C40-C43
19	A	608	TGL	C15-C16-C17-C18
19	Q	201	TGL	CA6-CA7-CA8-CA9
19	D	201	TGL	CB2-CB3-CB4-CB5
18	A	607	PGV	C3-C4-C5-C6
19	L	101	TGL	C21-C22-C23-C24
19	L	101	TGL	CC2-CC3-CC4-CC5
25	T	101	CDL	C37-C38-C39-C40
25	T	101	CDL	CB3-CB4-CB6-OB8
19	Q	201	TGL	CB9-C10-C11-C12
25	C	303	CDL	C57-C58-C59-C60
19	Q	201	TGL	OB1-CB1-OG2-CG2
26	P	308	PEK	O03-C01-C02-C03
24	X	104	DMU	C31-C34-C37-C40
19	N	608	TGL	CB2-CB3-CB4-CB5
24	C	301	DMU	C22-C25-C28-C31
24	K	102	DMU	C31-C34-C37-C40
14	N	602	HEA	C2D-C3D-CAD-CBD
19	A	608	TGL	OG1-CG1-CG2-OG2
26	P	308	PEK	O03-C01-C02-O01
20	A	609	PSC	C9-C10-C11-C12
20	A	609	PSC	C10-C11-C12-C13
20	O	303	PSC	C10-C11-C12-C13
26	C	305	PEK	C5-C6-C7-C8
26	C	305	PEK	C6-C7-C8-C9
26	C	305	PEK	C11-C10-C9-C8
26	C	305	PEK	C9-C10-C11-C12
26	C	305	PEK	C11-C12-C13-C14
26	C	305	PEK	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
26	C	307	PEK	C5-C6-C7-C8
26	C	307	PEK	C6-C7-C8-C9
26	C	307	PEK	C11-C10-C9-C8
26	C	307	PEK	C11-C12-C13-C14
26	C	307	PEK	C12-C13-C14-C15
26	G	101	PEK	C6-C7-C8-C9
26	G	101	PEK	C9-C10-C11-C12
26	G	101	PEK	C11-C12-C13-C14
26	G	101	PEK	C12-C13-C14-C15
26	P	301	PEK	C5-C6-C7-C8
26	P	301	PEK	C6-C7-C8-C9
26	P	301	PEK	C11-C10-C9-C8
26	P	301	PEK	C11-C12-C13-C14
26	P	301	PEK	C12-C13-C14-C15
26	P	308	PEK	C9-C10-C11-C12
26	P	308	PEK	C11-C12-C13-C14
26	P	308	PEK	C12-C13-C14-C15
26	P	309	PEK	C5-C6-C7-C8
26	P	309	PEK	C6-C7-C8-C9
26	P	309	PEK	C11-C10-C9-C8
26	P	309	PEK	C9-C10-C11-C12
26	P	309	PEK	C11-C12-C13-C14
26	P	309	PEK	C12-C13-C14-C15
25	C	303	CDL	C82-C83-C84-C85
25	T	101	CDL	CA7-C31-C32-C33
19	D	201	TGL	C23-C24-C25-C26
19	L	101	TGL	C17-C18-C19-C33
20	A	609	PSC	C7-C8-C9-C10
24	O	304	DMU	C18-C19-C22-C25
24	L	102	DMU	O16-C18-C19-C22
19	O	301	TGL	C11-C10-CB9-CB8
19	N	608	TGL	C25-C26-C27-C28
20	O	303	PSC	C9-C10-C11-C12
18	N	607	PGV	C26-C27-C28-C29
19	A	608	TGL	CG1-CG2-CG3-OG3
19	A	608	TGL	OG2-CG2-CG3-OG3
19	N	608	TGL	CA2-CA3-CA4-CA5
26	P	309	PEK	C30-C31-C32-C33
19	L	101	TGL	CA2-CA3-CA4-CA5
25	G	102	CDL	C77-C78-C79-C80
19	D	201	TGL	C11-C10-CB9-CB8
19	Q	201	TGL	CA3-CA4-CA5-CA6

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Mol	Chain	Res	Type	Atoms
18	A	606	PGV	C29-C30-C31-C32
18	P	302	PGV	C14-C15-C16-C17
25	T	101	CDL	OB9-CB7-OB8-CB6
24	K	101	DMU	C22-C25-C28-C31
26	P	309	PEK	C33-C34-C35-C36
24	W	101	DMU	C28-C31-C34-C37
14	N	601[B]	HEA	C26-C15-C16-C17
20	O	303	PSC	C12-C13-C14-C15
19	D	201	TGL	C24-C25-C26-C27
19	D	201	TGL	C21-C20-CA9-CA8
19	O	301	TGL	C17-C18-C19-C33
24	L	102	DMU	C31-C34-C37-C40
24	D	202	DMU	C18-C19-C22-C25
25	P	305	CDL	C57-C58-C59-C60
26	P	308	PEK	C27-C28-C29-C30
19	N	608	TGL	CA6-CA7-CA8-CA9
19	O	301	TGL	OG1-CG1-CG2-OG2
18	P	304	PGV	O03-C01-C02-C03
19	A	608	TGL	OG1-CG1-CG2-CG3
25	T	101	CDL	C71-CB7-OB8-CB6
18	N	606	PGV	C11-C12-C13-C14
26	C	305	PEK	C3-C4-C5-C6
24	Z	101	DMU	C18-C19-C22-C25
14	A	601[B]	HEA	O11-C11-C3B-C2B
18	P	302	PGV	C01-C02-O01-C1
26	C	305	PEK	C29-C30-C31-C32
18	C	302	PGV	C02-C03-O11-P
19	D	201	TGL	CC3-CC4-CC5-CC6
24	K	103	DMU	C19-C22-C25-C28
19	A	608	TGL	CC9-C15-C16-C17
24	Z	101	DMU	C28-C31-C34-C37
14	A	601[B]	HEA	C12-C13-C14-C15
18	C	306	PGV	C11-C12-C13-C14
18	N	607	PGV	C11-C12-C13-C14
19	N	608	TGL	C23-C24-C25-C26
19	Q	201	TGL	C16-C15-CC9-CC8
26	P	309	PEK	C3-C4-C5-C6
19	Q	201	TGL	CB1-CB2-CB3-CB4
24	P	303	DMU	C19-C22-C25-C28
24	D	202	DMU	C31-C34-C37-C40
25	T	101	CDL	C17-C18-C19-C20
20	A	609	PSC	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
26	P	308	PEK	C14-C15-C16-C17
21	N	619	EDO	O1-C1-C2-O2
14	A	601[B]	HEA	C26-C15-C16-C17
14	N	601[B]	HEA	C14-C15-C16-C17
24	M	101	DMU	C34-C37-C40-C43
25	T	101	CDL	C53-C54-C55-C56
24	X	105	DMU	C25-C28-C31-C34
24	X	105	DMU	C31-C34-C37-C40
24	P	303	DMU	C34-C37-C40-C43
26	P	301	PEK	C13-C14-C15-C16
18	P	302	PGV	C23-C24-C25-C26
25	G	102	CDL	C43-C44-C45-C46
26	P	309	PEK	C14-C15-C16-C17
25	P	305	CDL	OB7-CB5-OB6-CB4
19	D	201	TGL	OG1-CG1-CG2-OG2
19	O	301	TGL	OG2-CG2-CG3-OG3
19	N	608	TGL	CA7-CA8-CA9-C20
26	P	301	PEK	C7-C8-C9-C10
19	A	608	TGL	OB1-CB1-OG2-CG2
18	C	302	PGV	C11-C12-C13-C14
24	K	103	DMU	C25-C28-C31-C34
18	C	302	PGV	C20-C21-C22-C23
19	Q	201	TGL	CB3-CB4-CB5-CB6
18	N	606	PGV	C20-C21-C22-C23
23	G	103	CHD	C22-C23-C24-O25
19	D	201	TGL	OG1-CG1-CG2-CG3
19	D	201	TGL	CB6-CB7-CB8-CB9
19	O	301	TGL	C16-C15-CC9-CC8
24	L	102	DMU	C19-C22-C25-C28
24	K	102	DMU	C19-C22-C25-C28
18	C	306	PGV	C10-C11-C12-C13
25	T	101	CDL	OB7-CB5-OB6-CB4
21	A	613	EDO	O1-C1-C2-O2
21	A	618	EDO	O1-C1-C2-O2
14	A	601[B]	HEA	C14-C15-C16-C17
26	G	101	PEK	C22-C23-C24-C25
19	L	101	TGL	CA4-CA5-CA6-CA7
14	A	601[A]	HEA	CAD-CBD-CGD-O1D
14	A	601[B]	HEA	CAD-CBD-CGD-O1D
14	N	602	HEA	CAA-CBA-CGA-O1A
23	B	302	CHD	C22-C23-C24-O26
18	A	607	PGV	C9-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
18	P	304	PGV	O03-C01-C02-O01
26	G	101	PEK	C5-C6-C7-C8
26	G	101	PEK	C11-C10-C9-C8
26	P	308	PEK	C6-C7-C8-C9
26	P	308	PEK	C11-C10-C9-C8
19	O	301	TGL	CC2-CC1-OG3-CG3
14	A	602	HEA	CAA-CBA-CGA-O1A
14	N	601[A]	HEA	CAD-CBD-CGD-O1D
14	N	601[B]	HEA	CAD-CBD-CGD-O1D
26	C	305	PEK	C26-C27-C28-C29
19	A	608	TGL	C11-C12-C13-C14
14	N	602	HEA	C26-C15-C16-C17
14	N	602	HEA	CAD-CBD-CGD-O2D
23	G	103	CHD	C22-C23-C24-O26
14	N	602	HEA	CAA-CBA-CGA-O2A
23	B	302	CHD	C22-C23-C24-O25
19	N	608	TGL	C21-C22-C23-C24
19	Q	201	TGL	C21-C22-C23-C24
24	K	102	DMU	C28-C31-C34-C37
14	N	601[A]	HEA	CAD-CBD-CGD-O2D
14	N	601[B]	HEA	CAD-CBD-CGD-O2D
25	G	102	CDL	C80-C81-C82-C83
19	A	608	TGL	C21-C20-CA9-CA8
14	A	601[A]	HEA	CAD-CBD-CGD-O2D
14	A	601[B]	HEA	CAD-CBD-CGD-O2D
23	P	307	CHD	C22-C23-C24-O25
19	L	101	TGL	CB4-CB5-CB6-CB7
18	A	607	PGV	C7-C8-C9-C10
25	T	101	CDL	C57-C58-C59-C60
24	C	301	DMU	C25-C28-C31-C34
18	N	607	PGV	O03-C19-C20-C21
19	L	101	TGL	CB1-CB2-CB3-CB4
25	C	303	CDL	C77-C78-C79-C80
24	Z	101	DMU	O16-C18-C19-C22
18	A	606	PGV	C11-C12-C13-C14
18	A	607	PGV	C11-C12-C13-C14
18	P	302	PGV	C11-C12-C13-C14
26	C	307	PEK	C3-C4-C5-C6
26	G	101	PEK	C14-C15-C16-C17
19	N	608	TGL	C24-C25-C26-C27
18	A	606	PGV	O03-C19-C20-C21
26	P	301	PEK	C14-C15-C16-C17

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Mol	Chain	Res	Type	Atoms
14	N	601[B]	HEA	C12-C13-C14-C15
25	P	305	CDL	C53-C54-C55-C56
25	P	305	CDL	C81-C82-C83-C84
18	A	606	PGV	C23-C24-C25-C26
24	D	203	DMU	C25-C28-C31-C34
18	P	302	PGV	C9-C10-C11-C12
18	P	304	PGV	C9-C10-C11-C12
14	A	602	HEA	CAA-CBA-CGA-O2A
14	N	602	HEA	CAD-CBD-CGD-O1D
18	A	607	PGV	C21-C22-C23-C24
18	N	606	PGV	C9-C10-C11-C12
18	P	304	PGV	C11-C12-C13-C14
26	P	301	PEK	C3-C4-C5-C6
14	A	602	HEA	CAD-CBD-CGD-O2D
18	A	607	PGV	O01-C1-C2-C3
18	A	607	PGV	O02-C1-C2-C3
23	C	304	CHD	C22-C23-C24-O25
26	C	307	PEK	C14-C15-C16-C17
25	G	102	CDL	C72-C73-C74-C75
14	A	602	HEA	CAD-CBD-CGD-O1D
19	A	608	TGL	CB6-CB7-CB8-CB9
21	A	619	EDO	O1-C1-C2-O2
21	C	311	EDO	O1-C1-C2-O2
21	N	613	EDO	O1-C1-C2-O2
21	P	312	EDO	O1-C1-C2-O2
21	Q	204	EDO	O1-C1-C2-O2
21	T	102	EDO	O1-C1-C2-O2
21	W	103	EDO	O1-C1-C2-O2
18	C	306	PGV	C9-C10-C11-C12
23	C	304	CHD	C22-C23-C24-O26
18	C	302	PGV	C25-C26-C27-C28
25	T	101	CDL	C32-C31-CA7-OA8
23	J	101	CHD	C21-C20-C22-C23
25	T	101	CDL	C51-CB5-OB6-CB4
25	P	305	CDL	C51-CB5-OB6-CB4
26	C	305	PEK	C14-C15-C16-C17
25	P	305	CDL	C14-C15-C16-C17
19	A	608	TGL	C24-C25-C26-C27
24	X	103	DMU	C34-C37-C40-C43
24	C	301	DMU	C19-C22-C25-C28
24	D	202	DMU	C22-C25-C28-C31
19	D	201	TGL	OG1-CA1-CA2-CA3

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Mol	Chain	Res	Type	Atoms
19	O	301	TGL	CG1-CG2-CG3-OG3
26	G	101	PEK	O03-C01-C02-C03
18	A	606	PGV	C26-C27-C28-C29
19	L	101	TGL	C16-C17-C18-C19
25	T	101	CDL	C32-C31-CA7-OA9
24	X	101	DMU	C34-C37-C40-C43
19	N	608	TGL	CB3-CB4-CB5-CB6
23	P	307	CHD	C22-C23-C24-O26
19	O	301	TGL	OC1-CC1-OG3-CG3
21	E	202	EDO	O1-C1-C2-O2
19	A	608	TGL	C29-C30-C31-C32
19	L	101	TGL	C18-C19-C33-C34
24	M	101	DMU	O6-C11-C9-O1
19	A	608	TGL	CB2-CB3-CB4-CB5
19	L	101	TGL	C20-C21-C22-C23
14	N	601[A]	HEA	C15-C16-C17-C18
19	L	101	TGL	CC6-CC7-CC8-CC9
18	C	302	PGV	C24-C25-C26-C27
18	C	302	PGV	C9-C10-C11-C12
26	P	308	PEK	C22-C23-C24-C25
19	N	608	TGL	CB6-CB7-CB8-CB9
14	N	601[A]	HEA	CAA-CBA-CGA-O2A
14	N	601[B]	HEA	CAA-CBA-CGA-O2A
20	A	609	PSC	C24-C25-C26-C27
19	L	101	TGL	OG3-CC1-CC2-CC3
14	A	602	HEA	C26-C15-C16-C17
24	L	102	DMU	C34-C37-C40-C43
25	T	101	CDL	C43-C44-C45-C46
14	A	601[A]	HEA	CAA-CBA-CGA-O2A
14	A	601[B]	HEA	CAA-CBA-CGA-O2A
24	D	202	DMU	C34-C37-C40-C43
19	A	608	TGL	CC2-CC1-OG3-CG3
19	D	201	TGL	OA1-CA1-CA2-CA3
21	Q	202	EDO	O1-C1-C2-O2
19	A	608	TGL	CB2-CB1-OG2-CG2
18	N	606	PGV	O03-C19-C20-C21
19	D	201	TGL	OG3-CC1-CC2-CC3

There are no ring outliers.

53 monomers are involved in 139 short contacts:

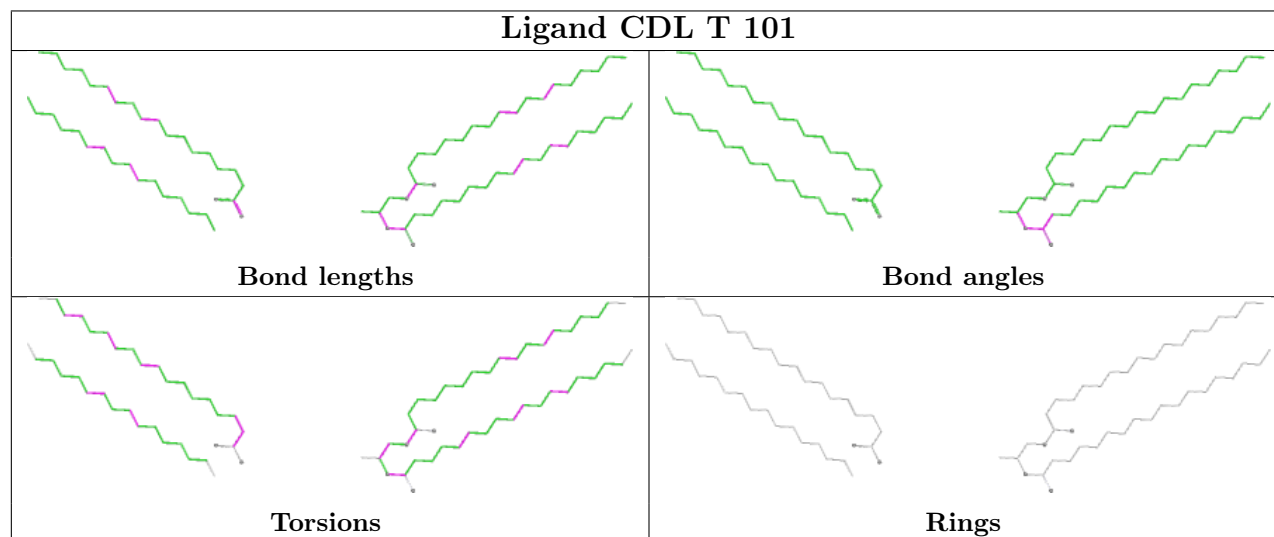
Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	T	101	CDL	12	0
24	X	102	DMU	1	0
21	A	610	EDO	1	0
21	N	621	EDO	2	0
18	P	304	PGV	2	0
19	A	608	TGL	1	0
14	N	601[B]	HEA	1	0
26	P	308	PEK	7	0
19	O	301	TGL	1	0
24	X	105	DMU	1	0
23	G	103	CHD	1	0
18	A	606	PGV	2	0
19	L	101	TGL	6	0
24	P	310	DMU	1	0
26	C	305	PEK	1	0
18	P	302	PGV	1	0
23	P	306	CHD	1	0
24	C	301	DMU	2	0
25	C	303	CDL	7	0
23	J	101	CHD	1	0
24	X	103	DMU	1	0
21	S	103	EDO	4	0
25	G	102	CDL	9	0
24	L	102	DMU	4	0
21	F	105	EDO	2	0
20	A	609	PSC	3	0
21	N	617	EDO	1	0
24	D	203	DMU	1	0
19	Q	201	TGL	7	0
21	B	304	EDO	2	0
19	N	608	TGL	6	0
18	C	306	PGV	2	0
21	N	611	EDO	1	0
19	D	201	TGL	5	0
21	A	616	EDO	2	0
24	P	303	DMU	3	0
18	C	302	PGV	4	0
21	A	615	EDO	3	0
24	Z	101	DMU	1	0
26	G	101	PEK	5	0
26	C	307	PEK	2	0
18	A	607	PGV	4	0
21	O	307	EDO	1	0

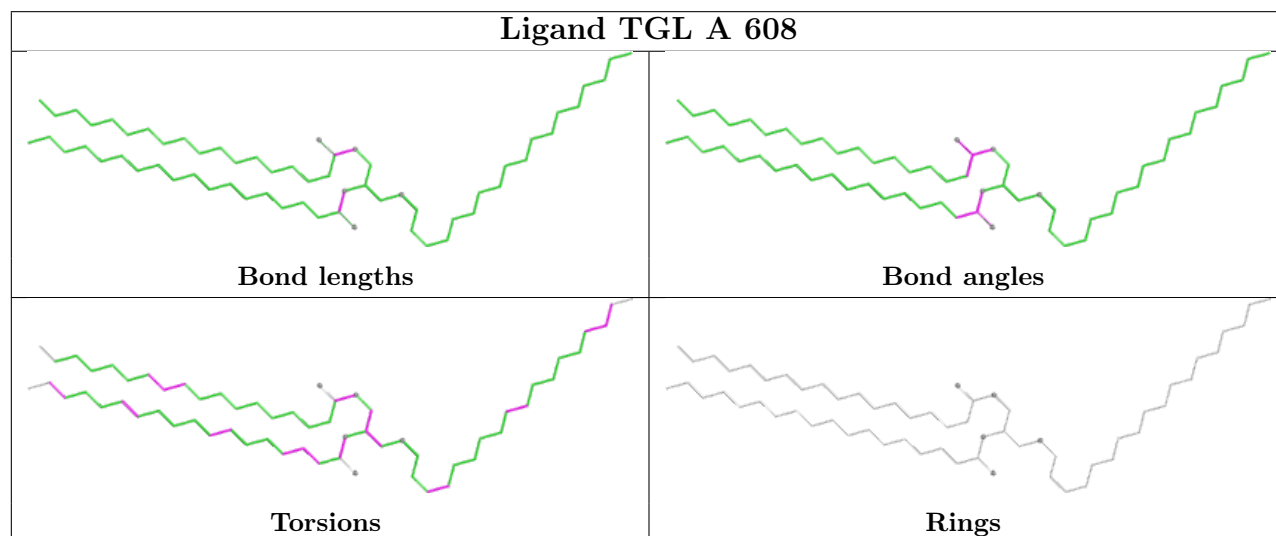
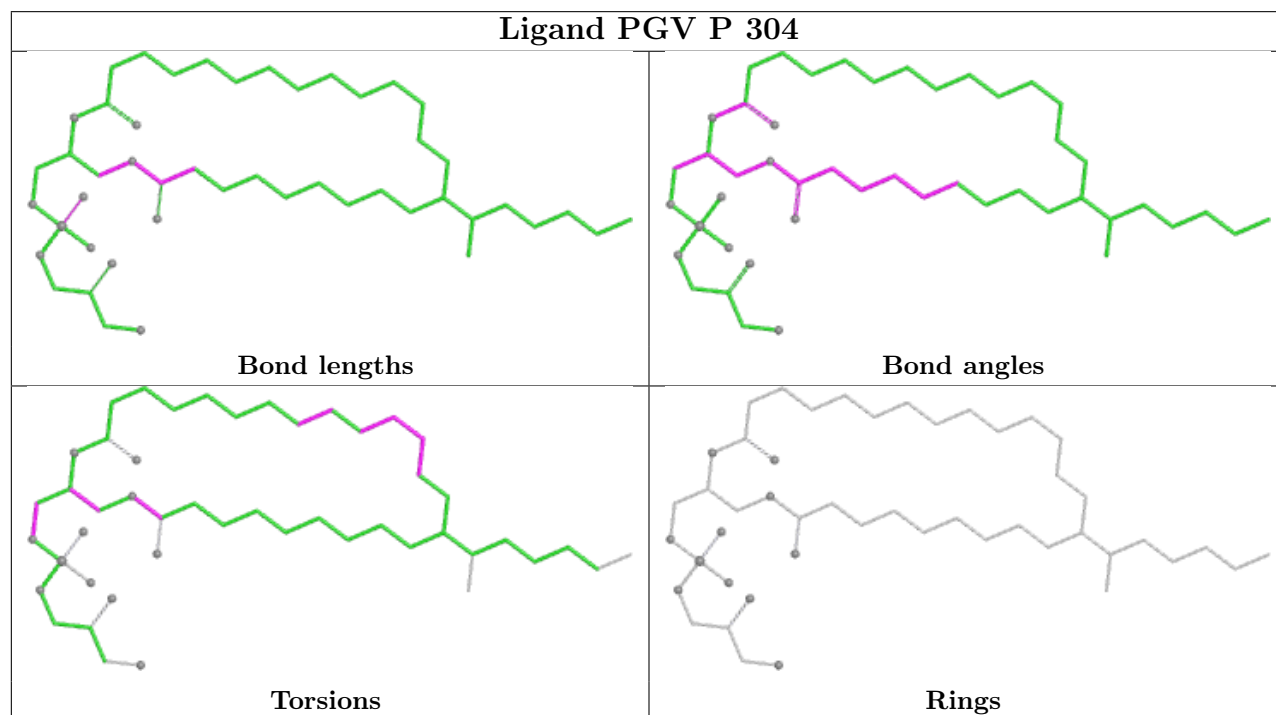
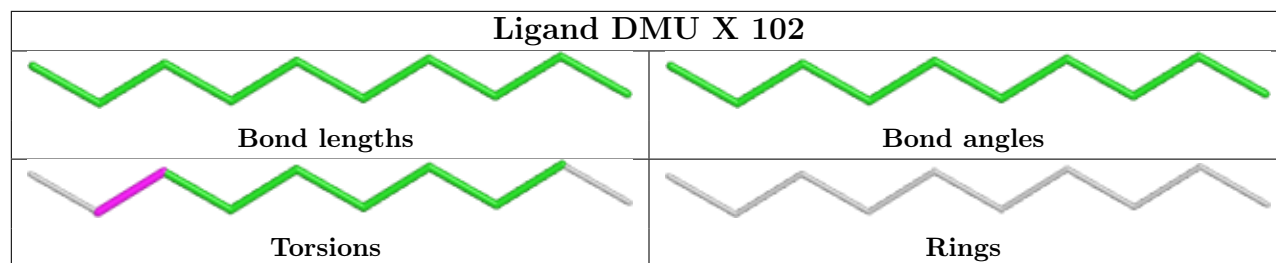
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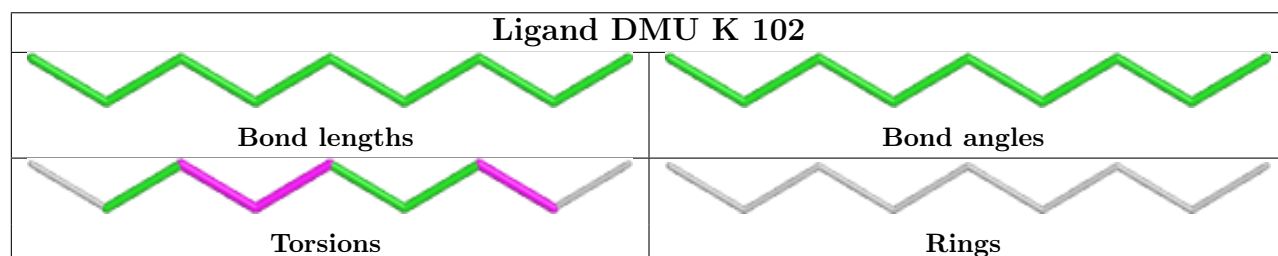
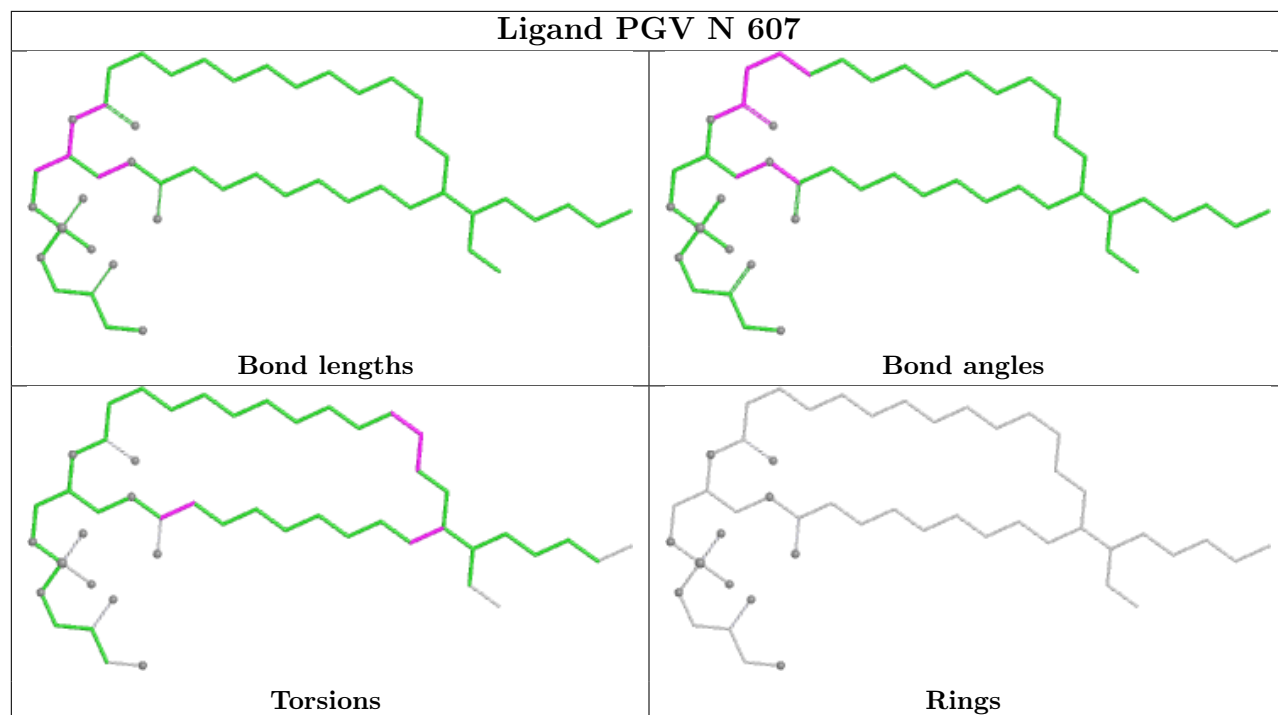
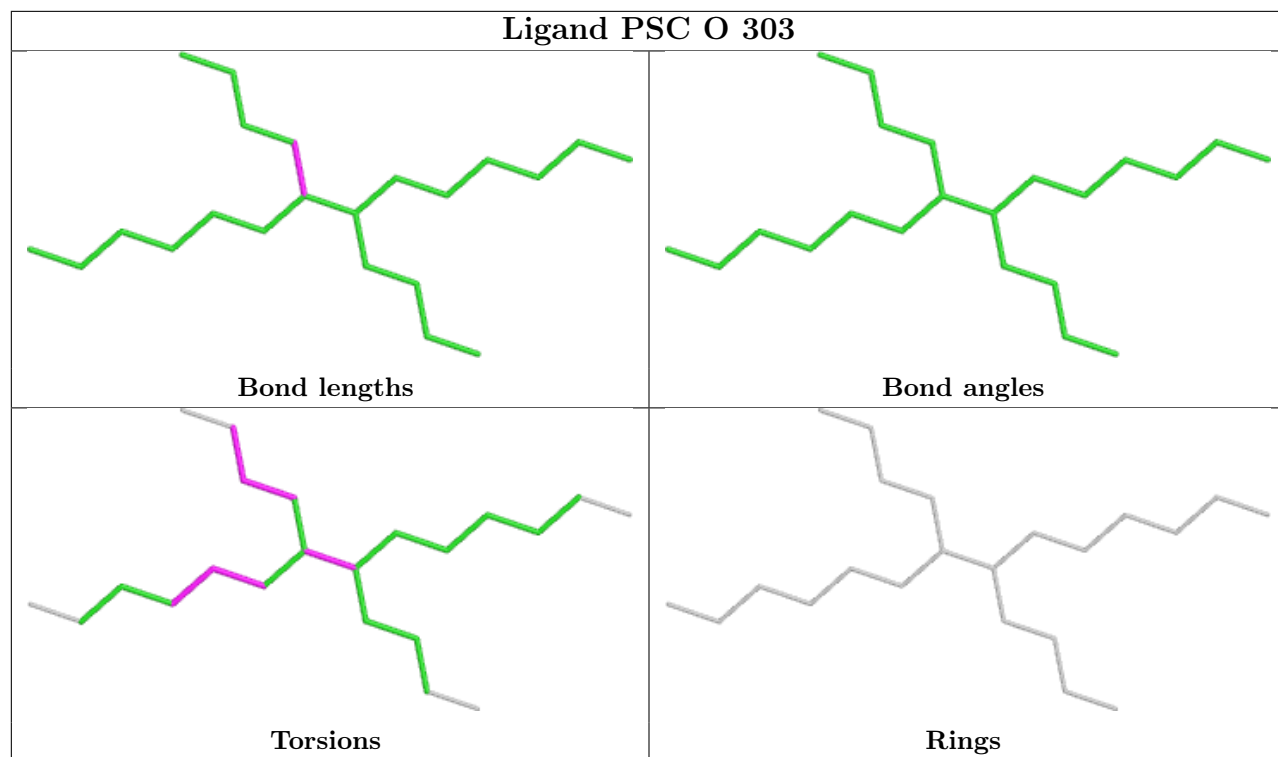
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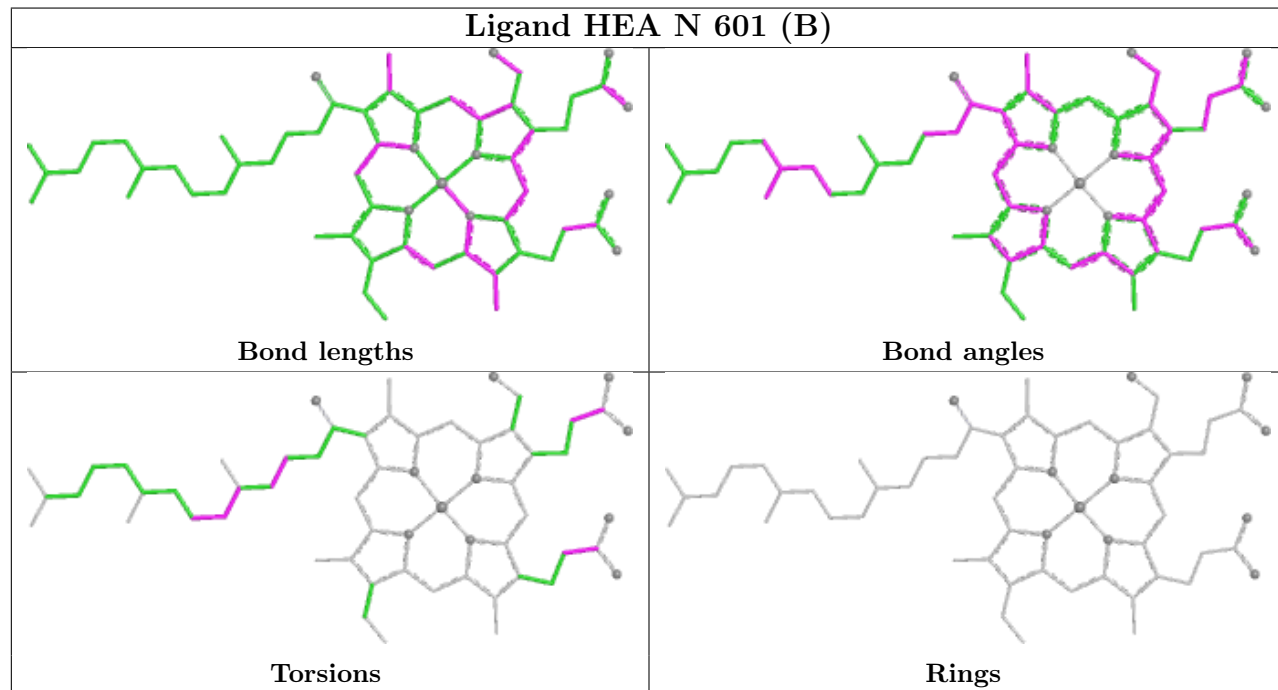
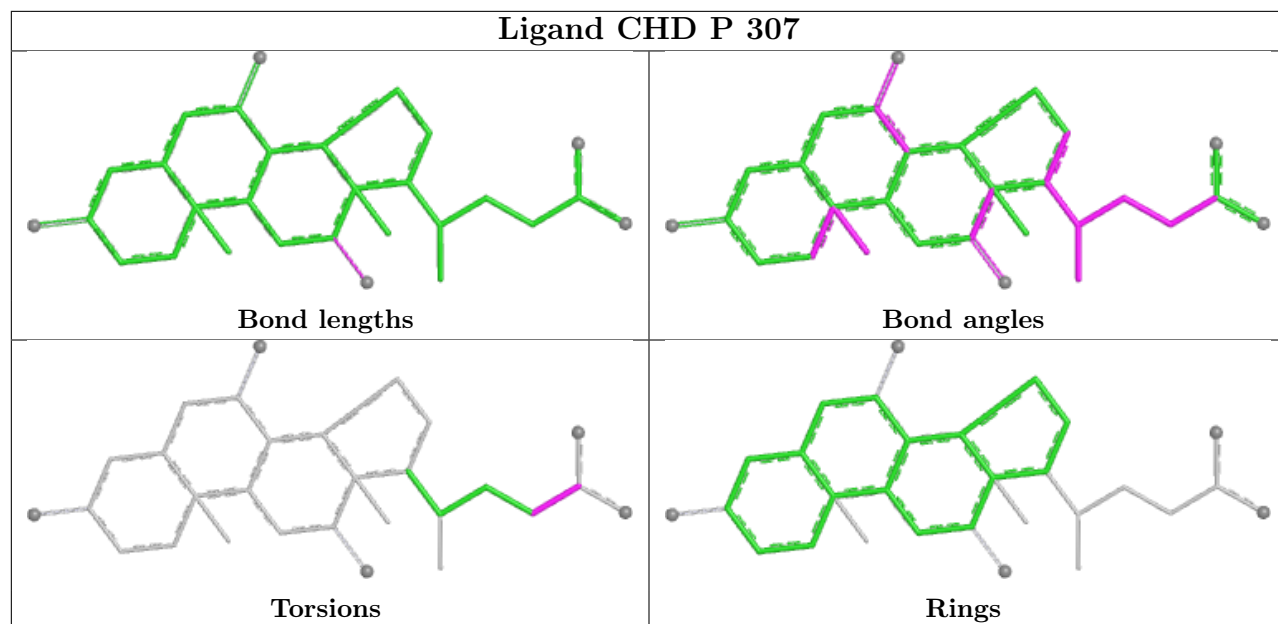
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	A	602	HEA	3	0
24	K	103	DMU	2	0
14	N	602	HEA	4	0
21	F	103	EDO	1	0
26	P	301	PEK	1	0
26	P	309	PEK	3	0
21	N	612	EDO	1	0
18	N	606	PGV	2	0
25	P	305	CDL	2	0
21	A	614	EDO	1	0

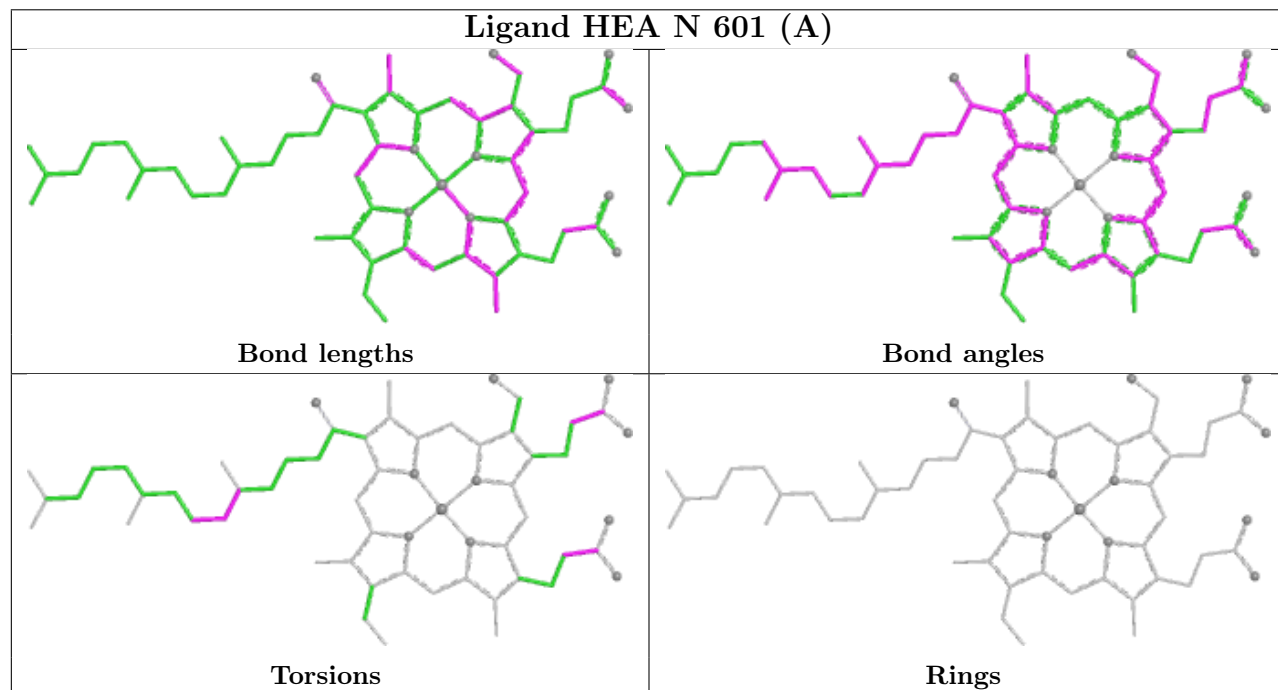
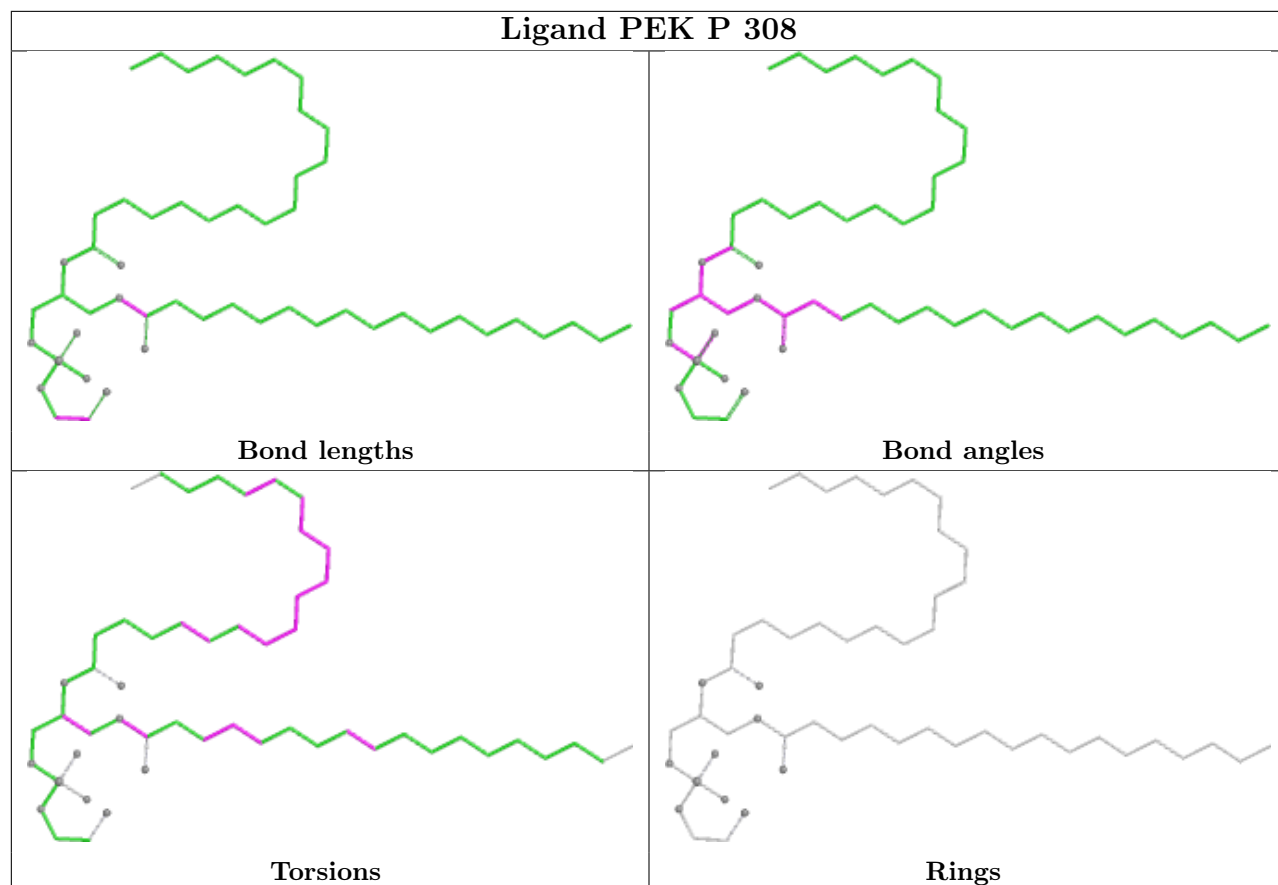
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

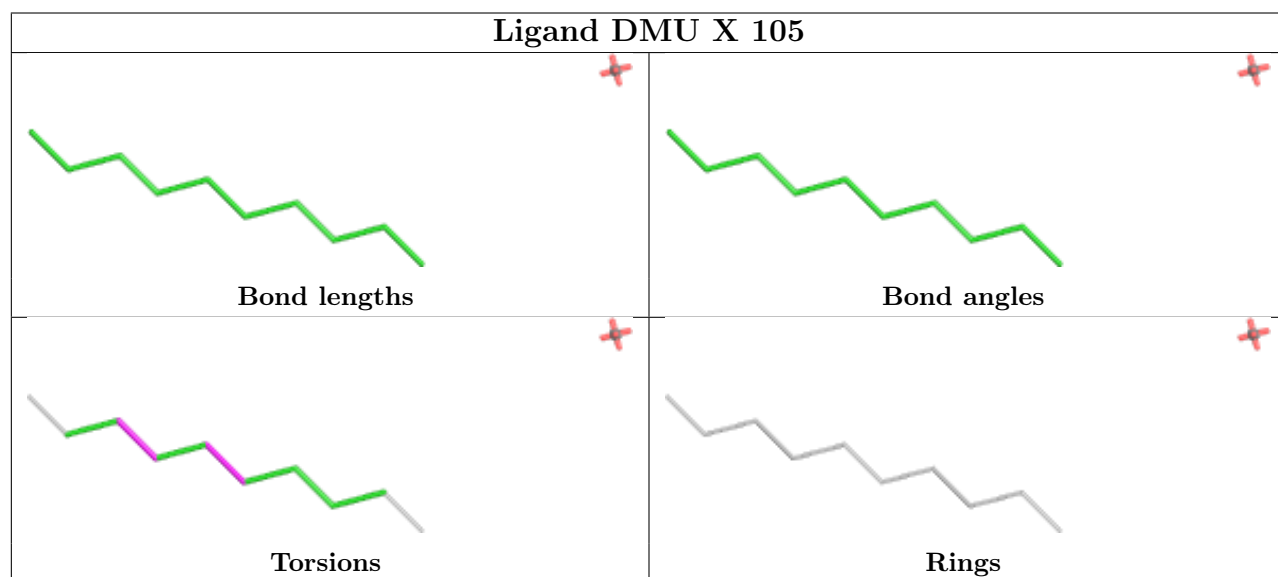
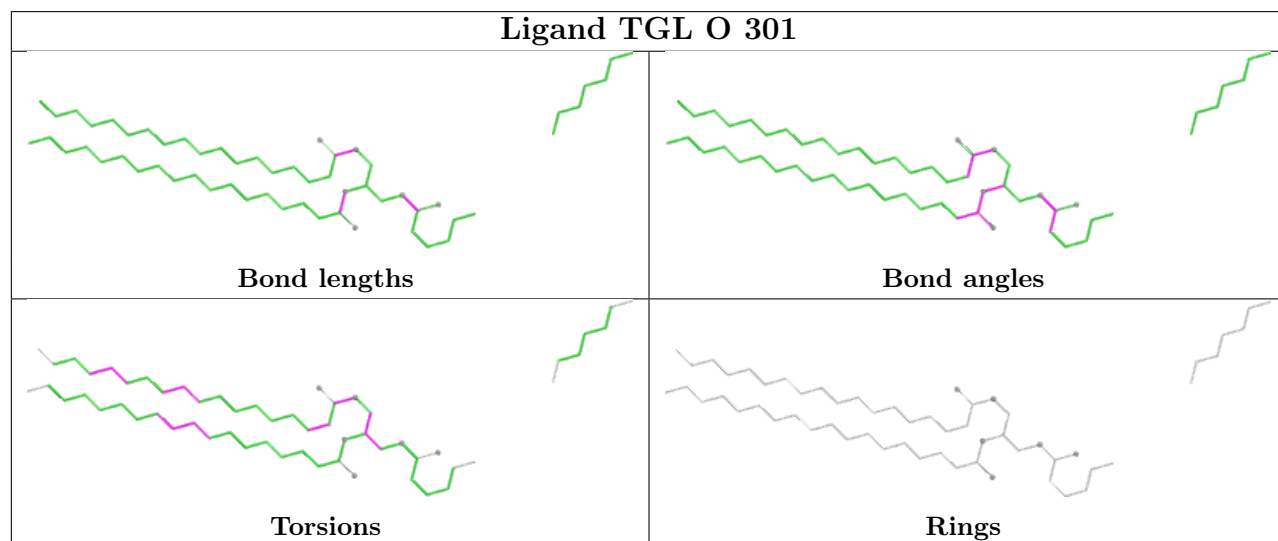
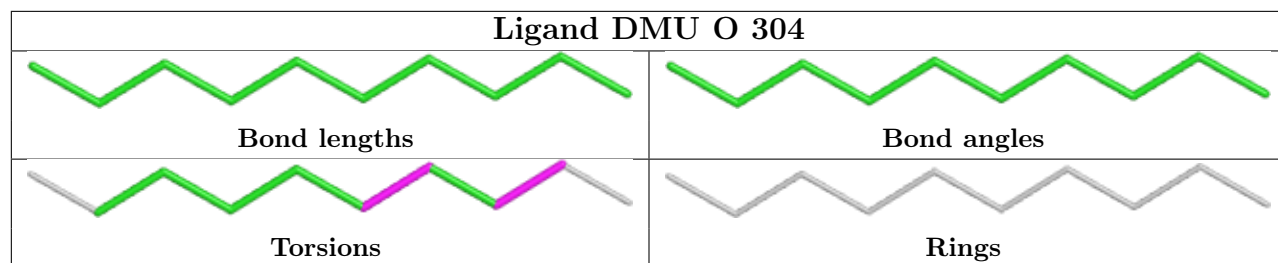


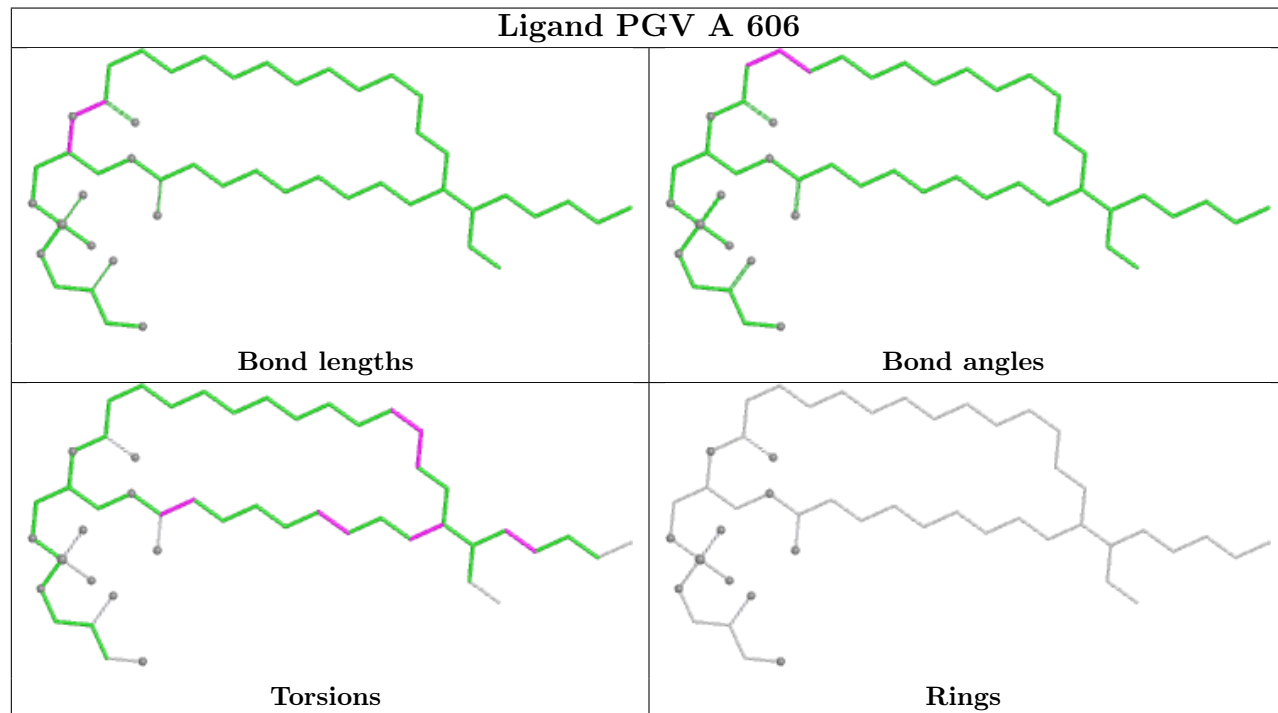
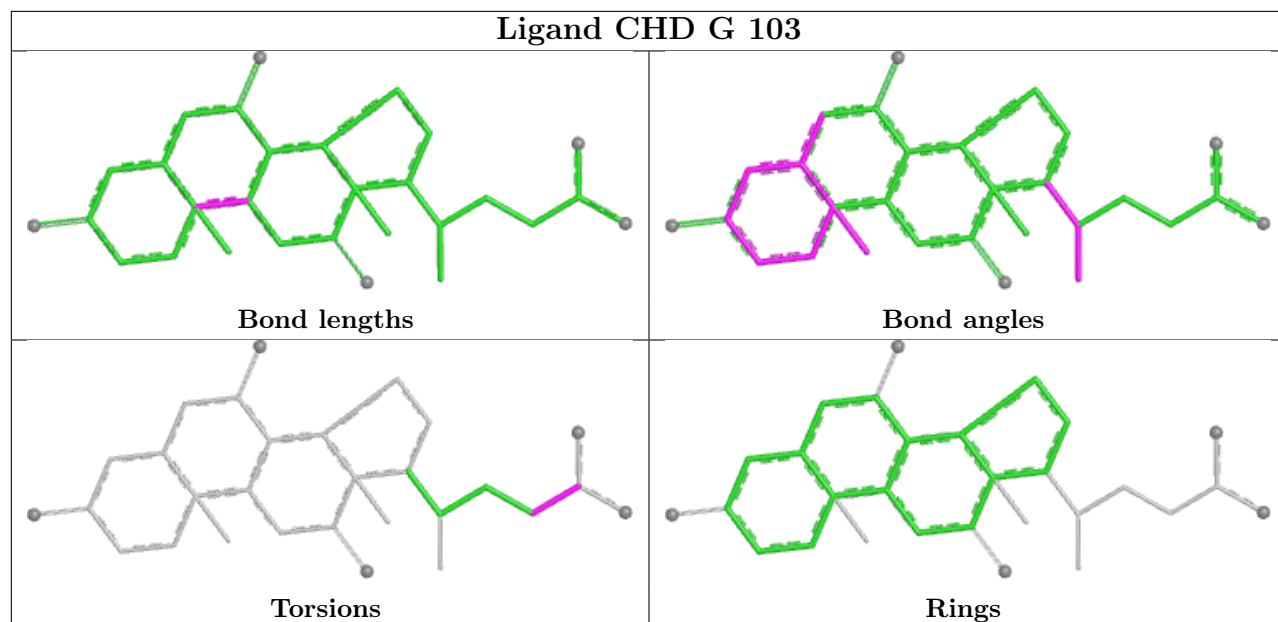


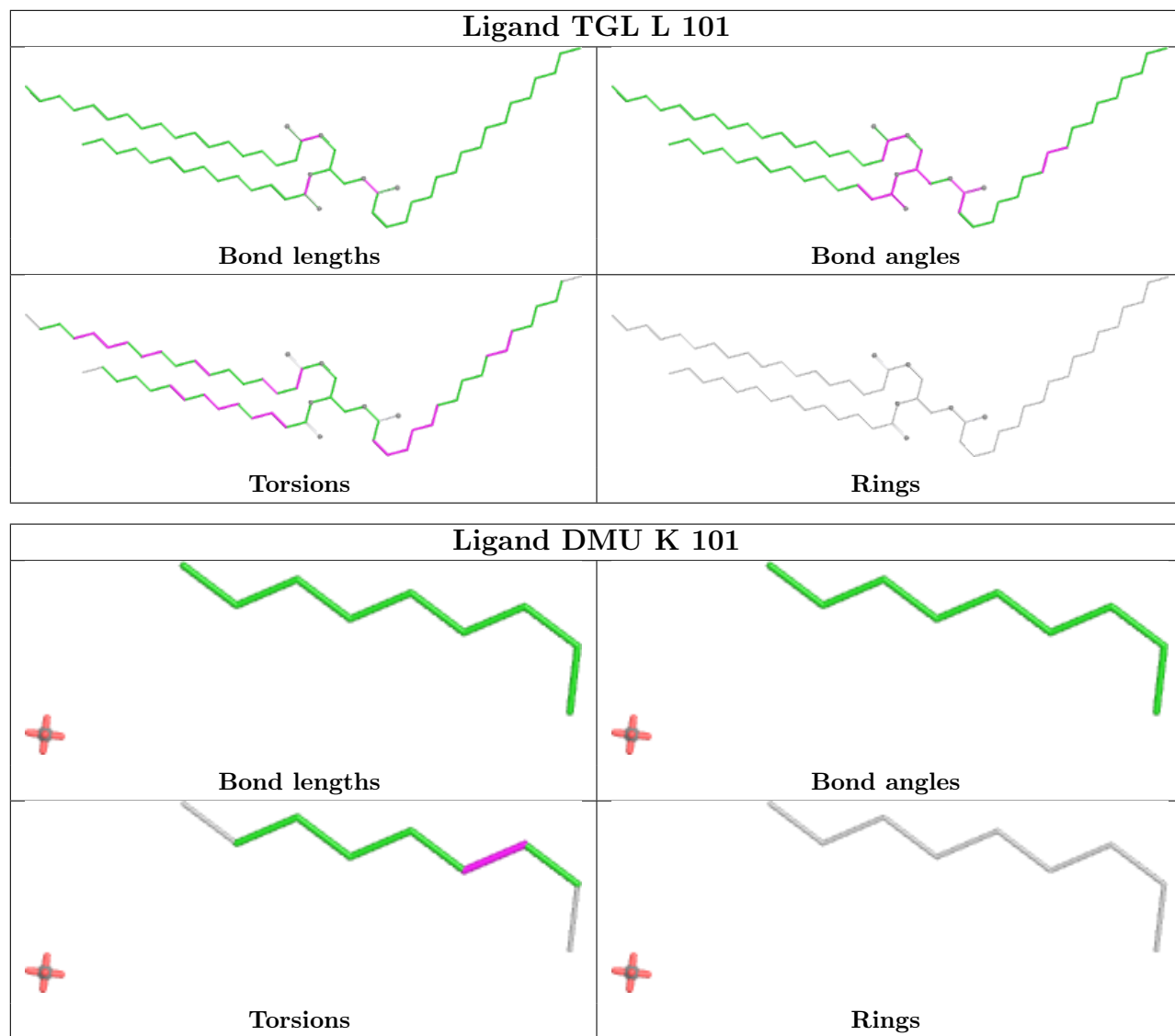


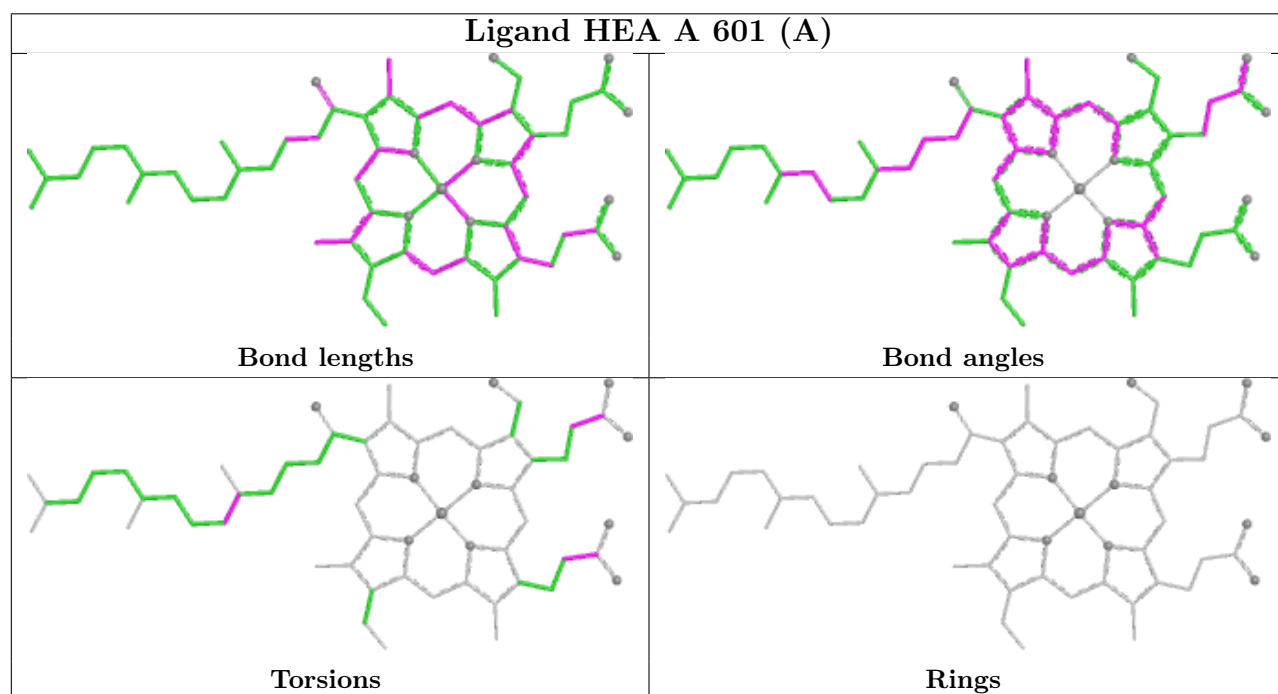
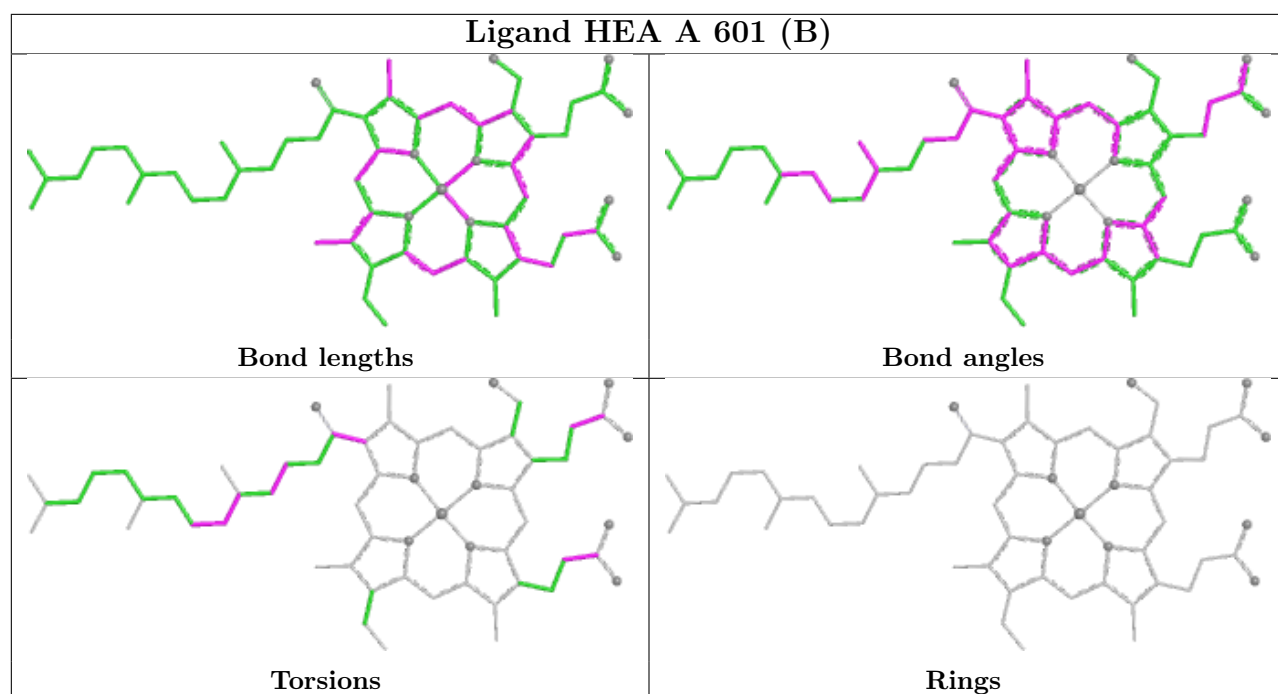


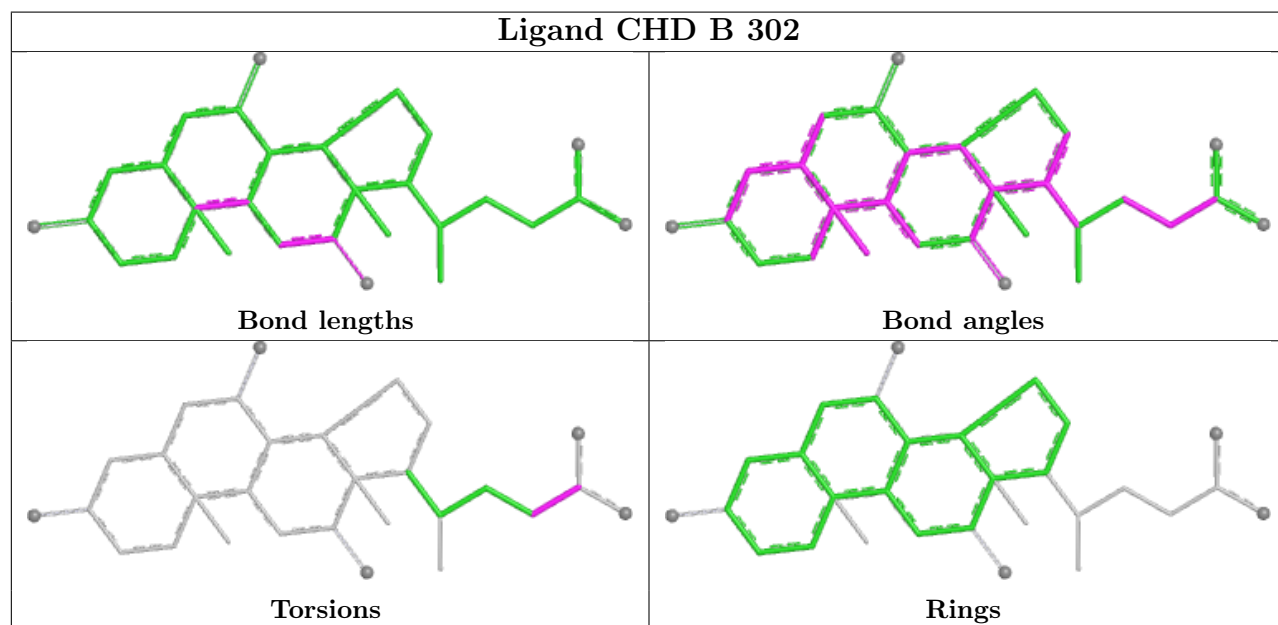
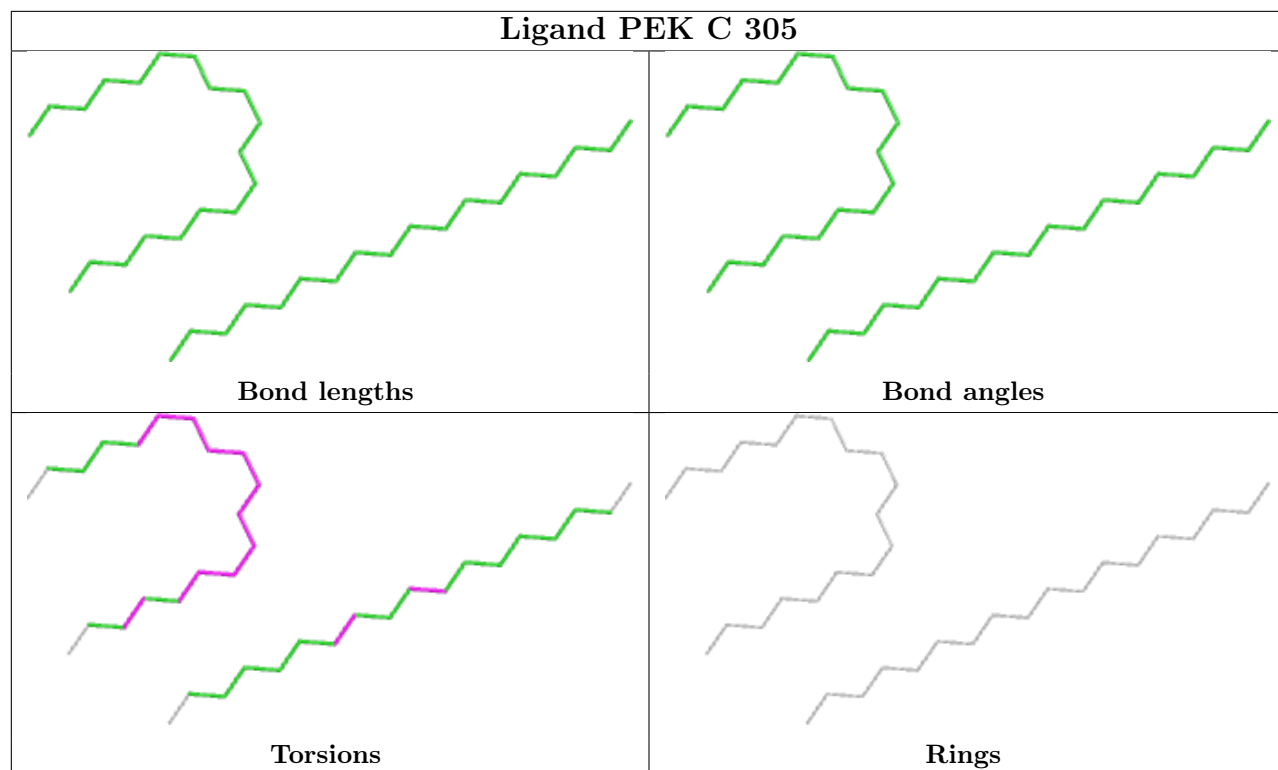


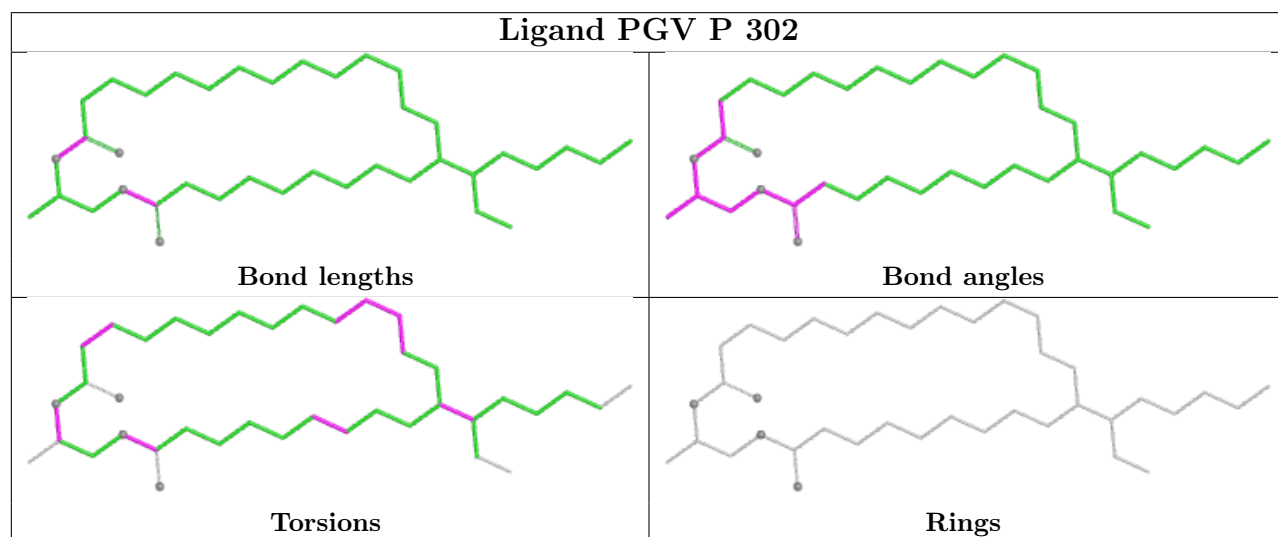
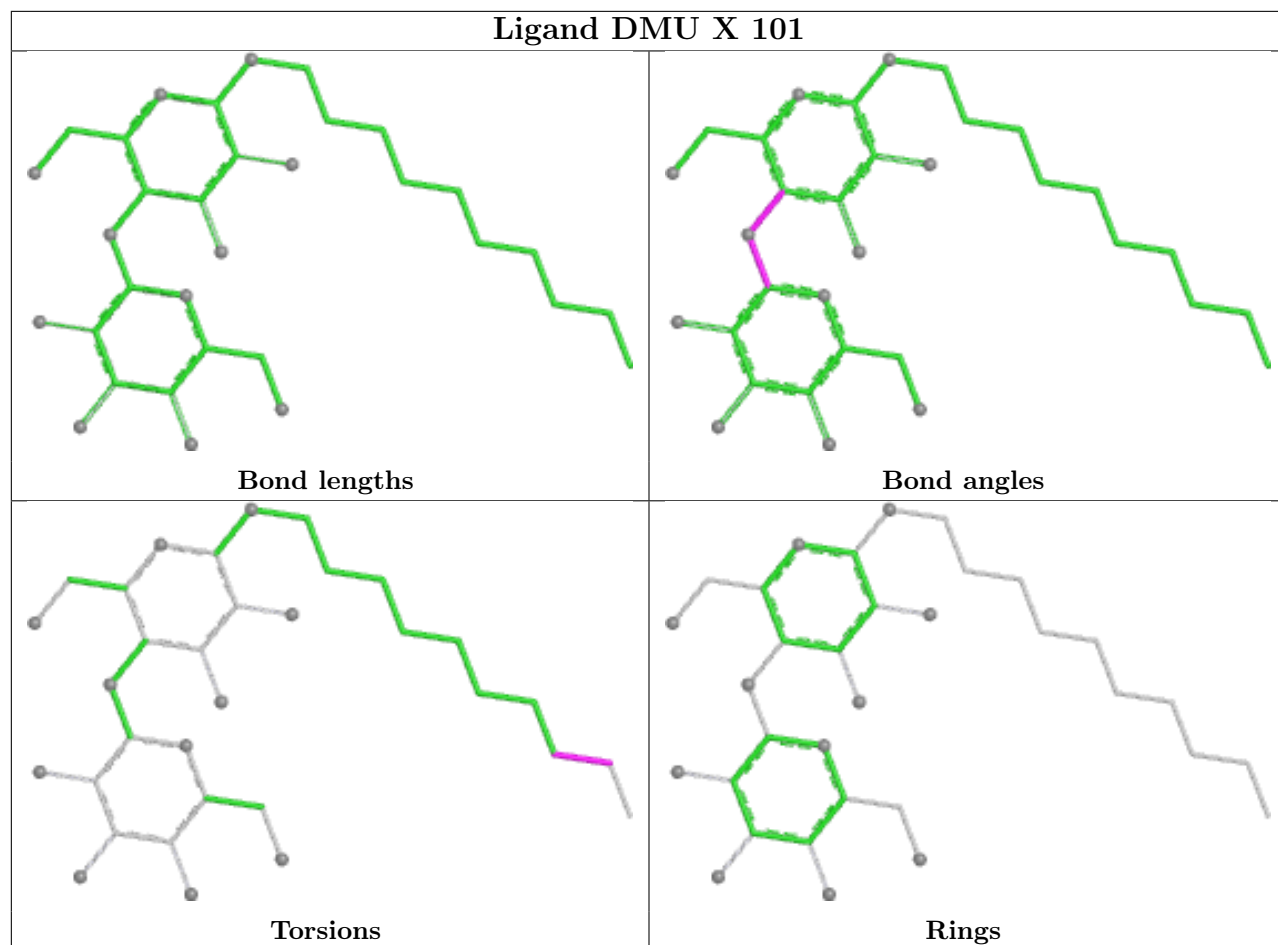


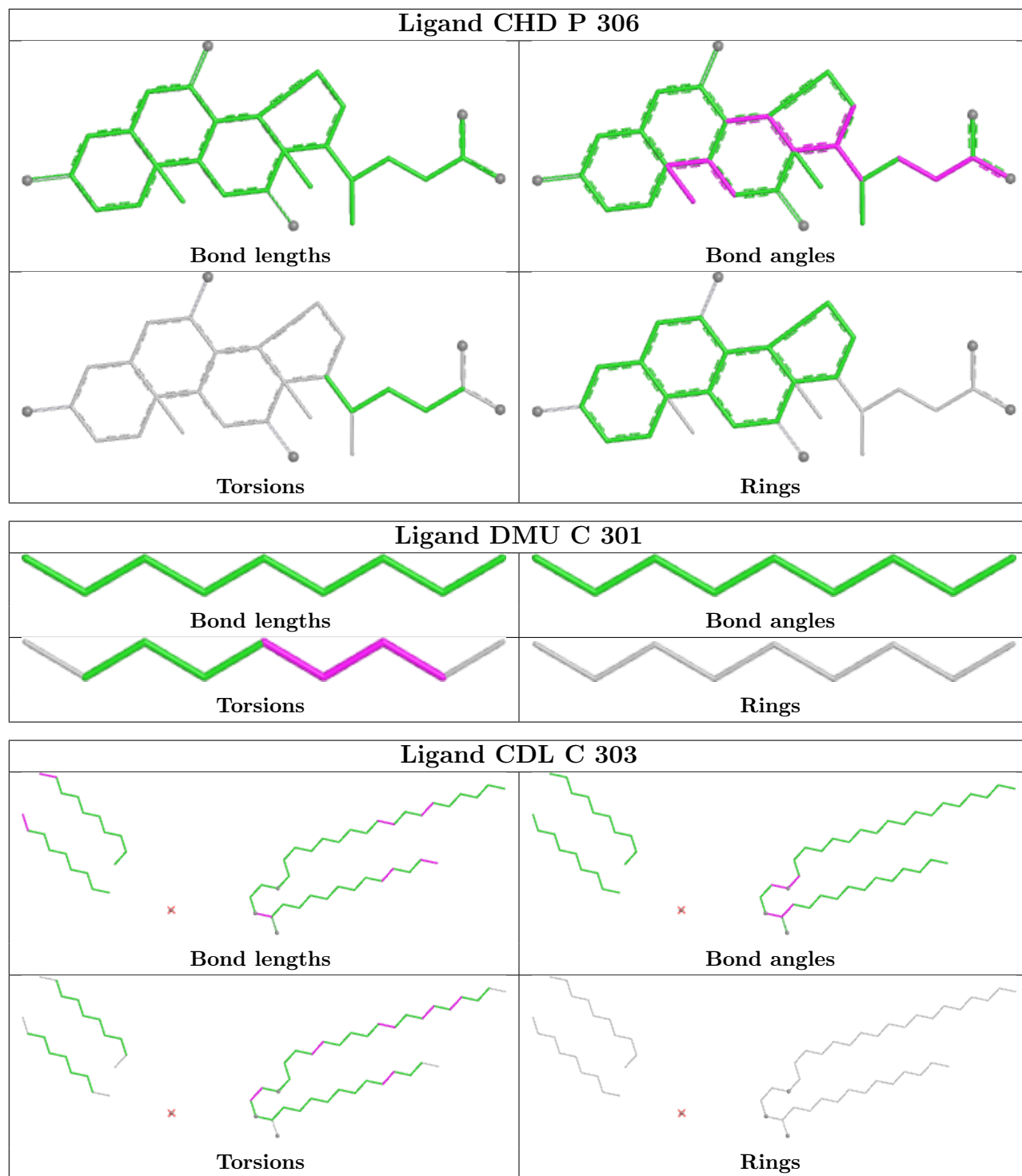


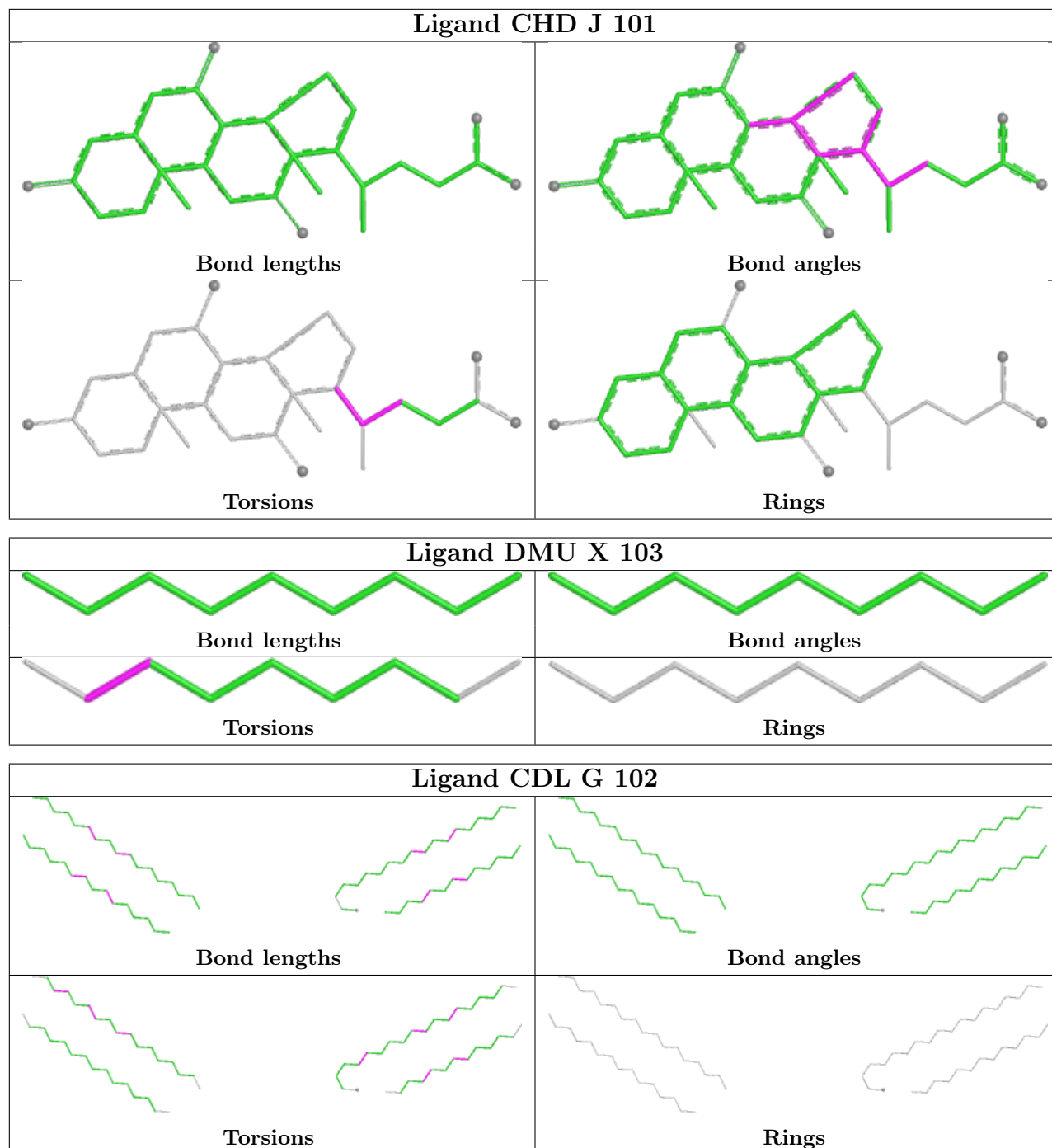


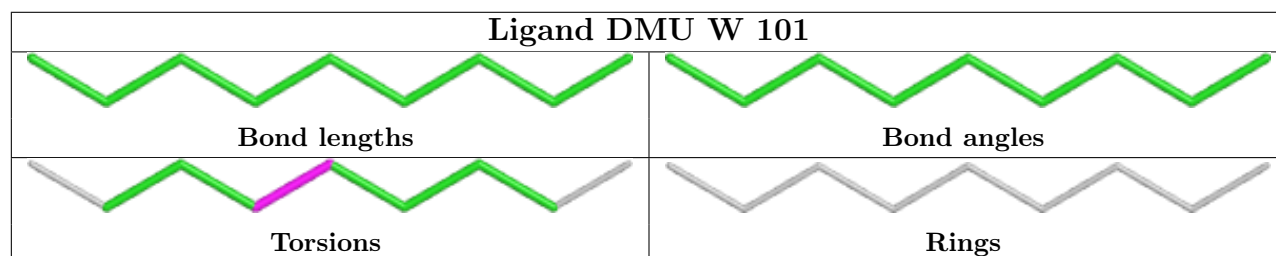
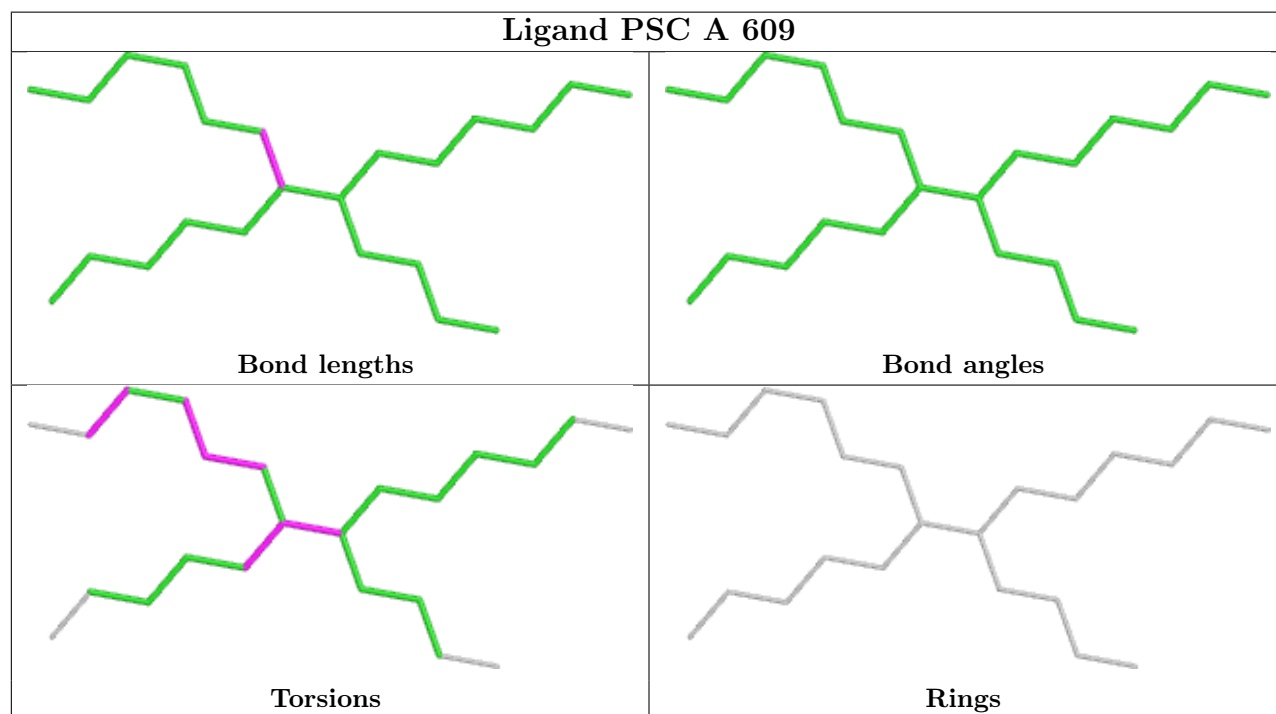
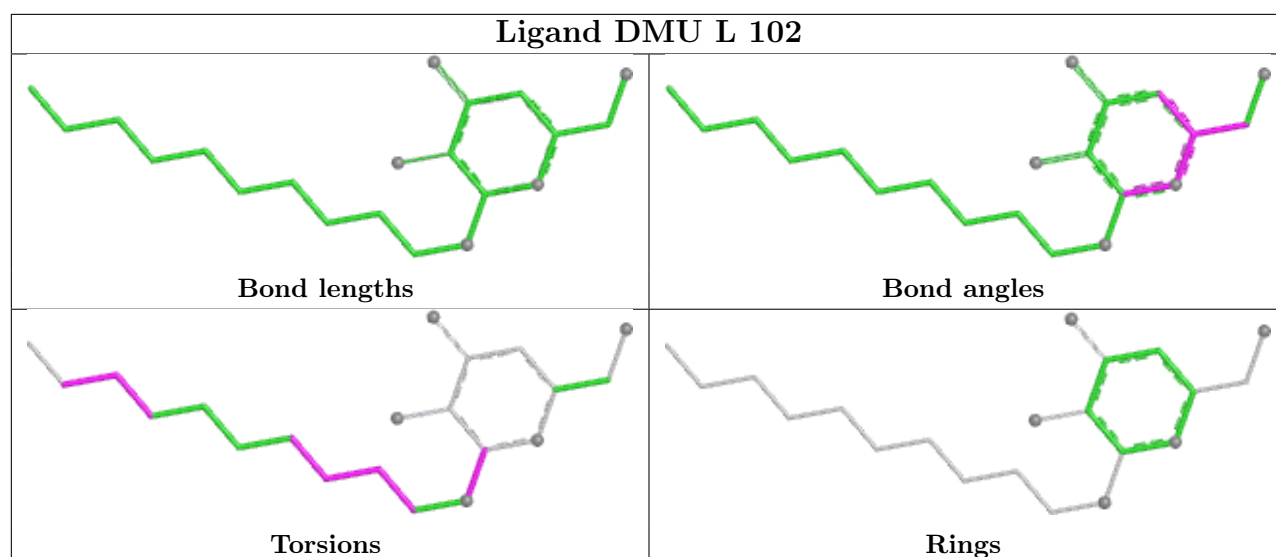


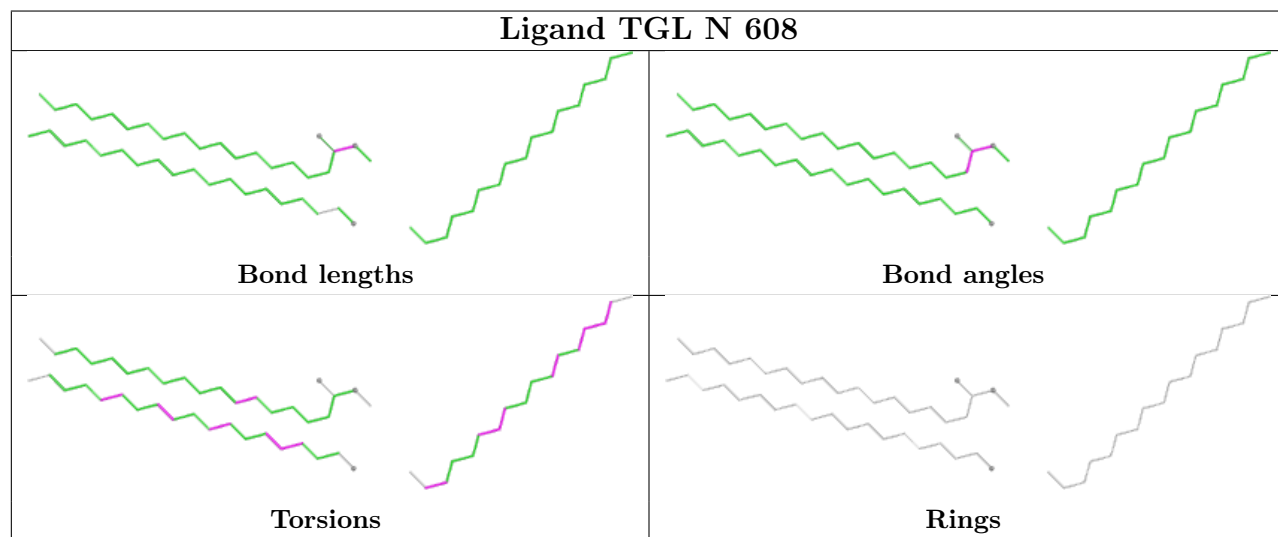
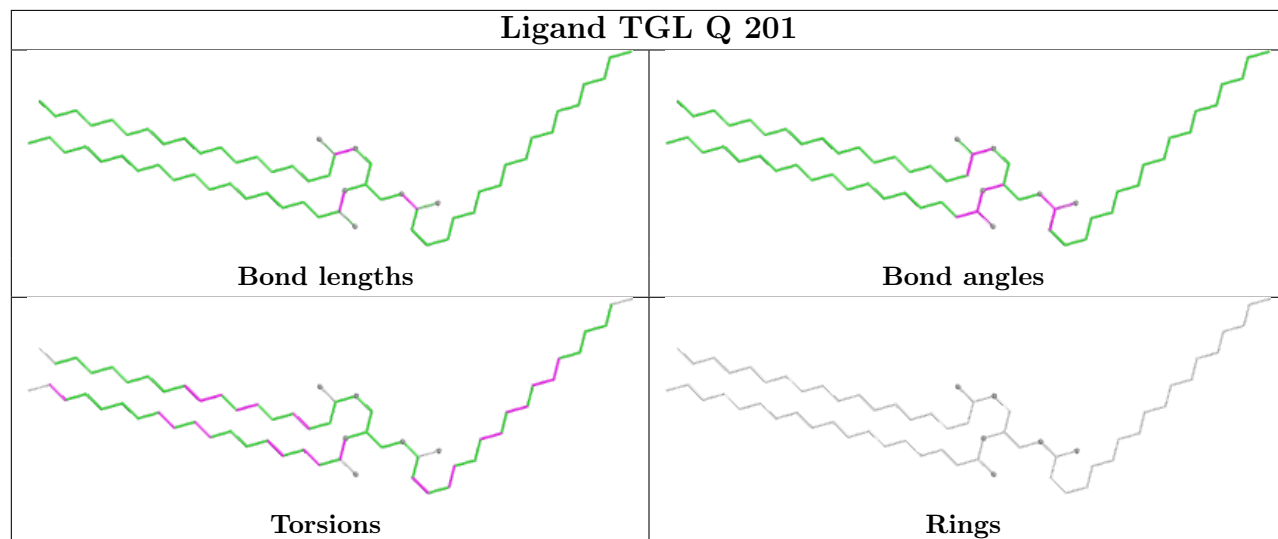
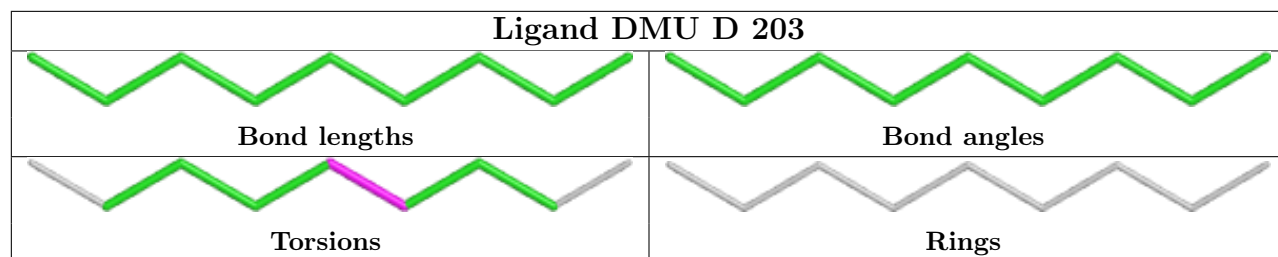


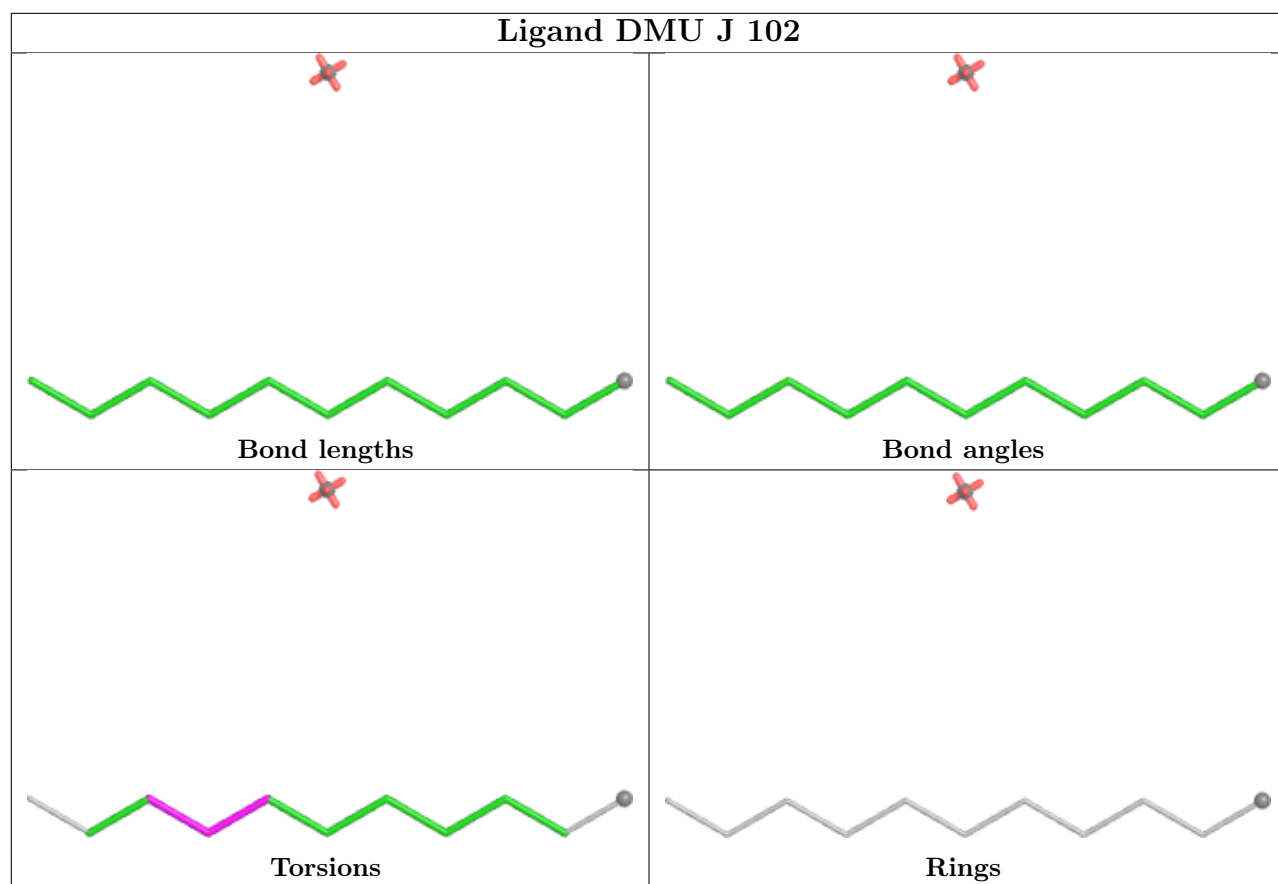
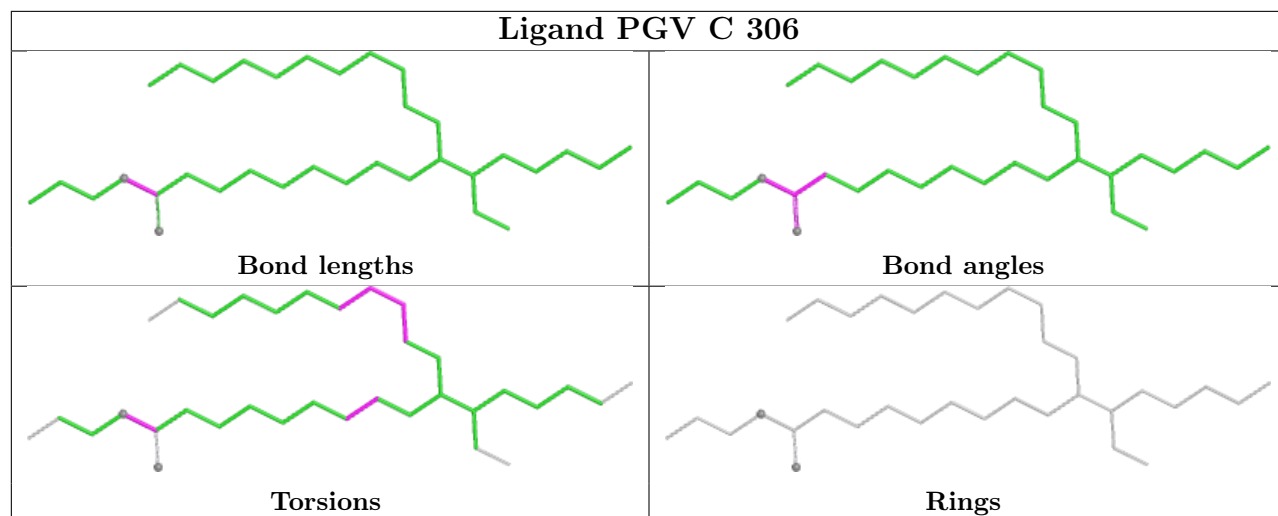


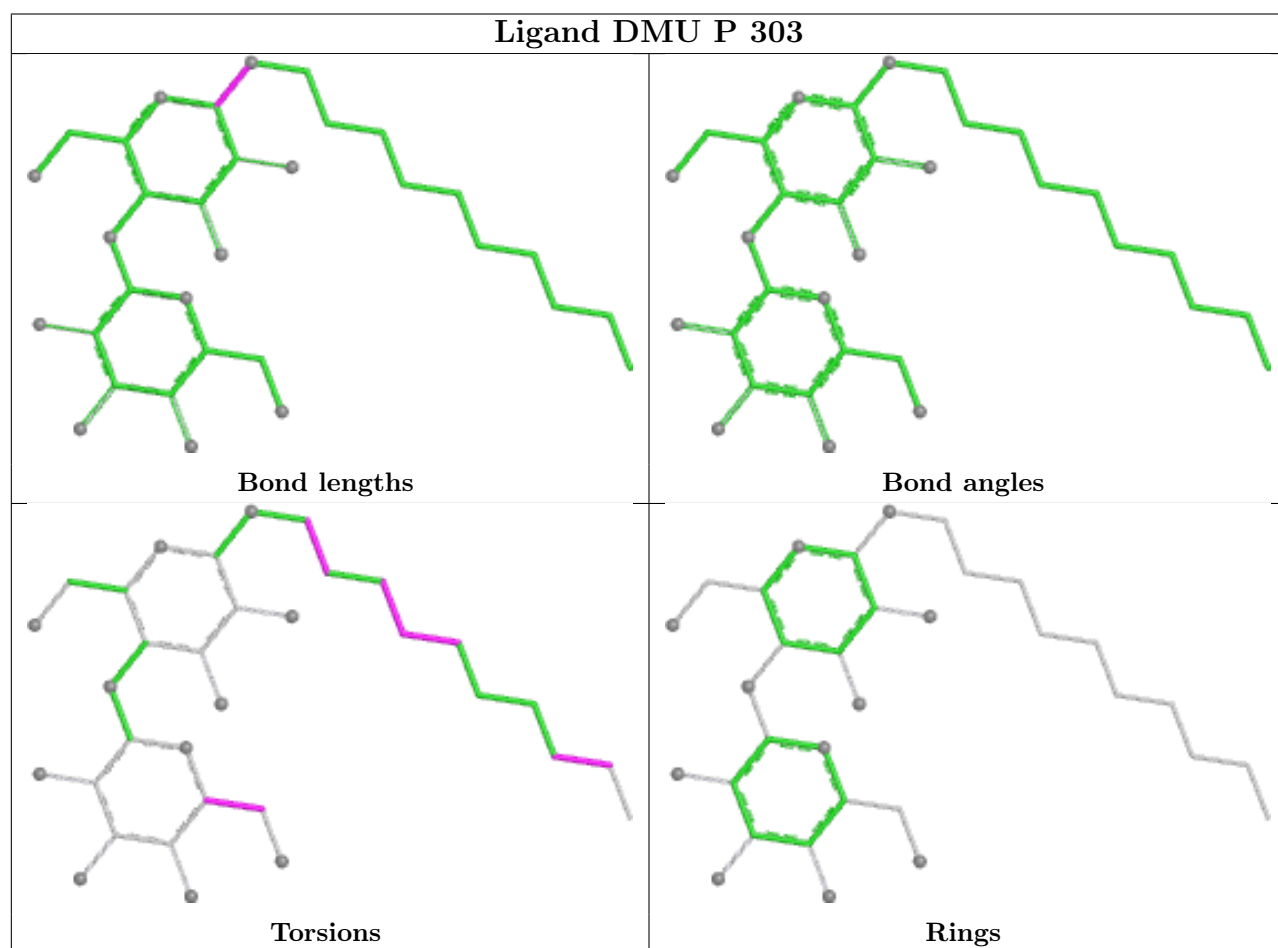
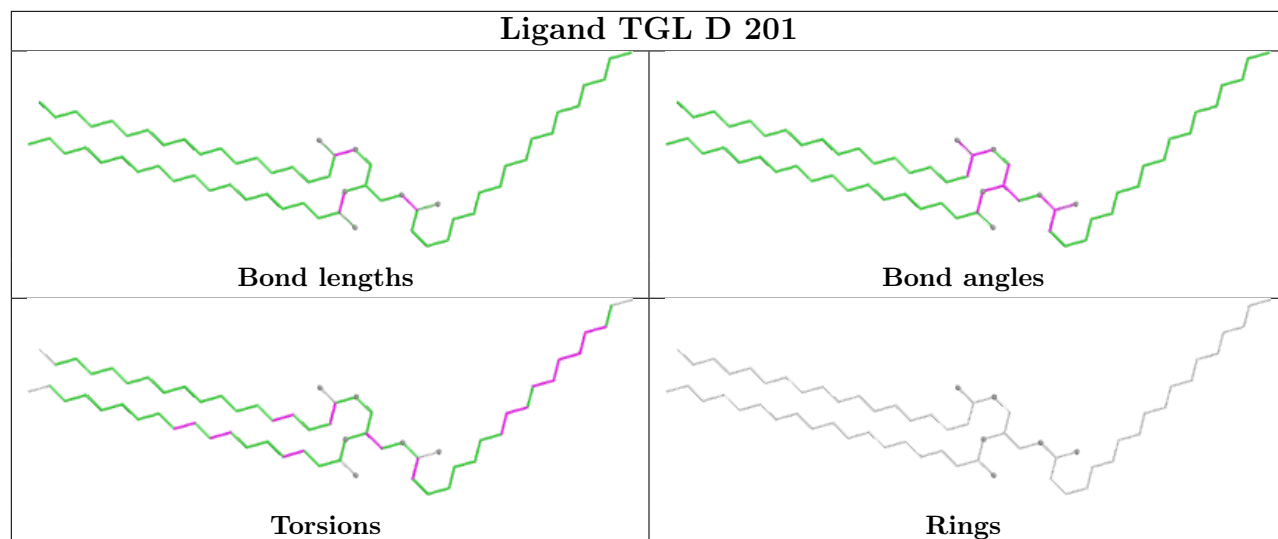


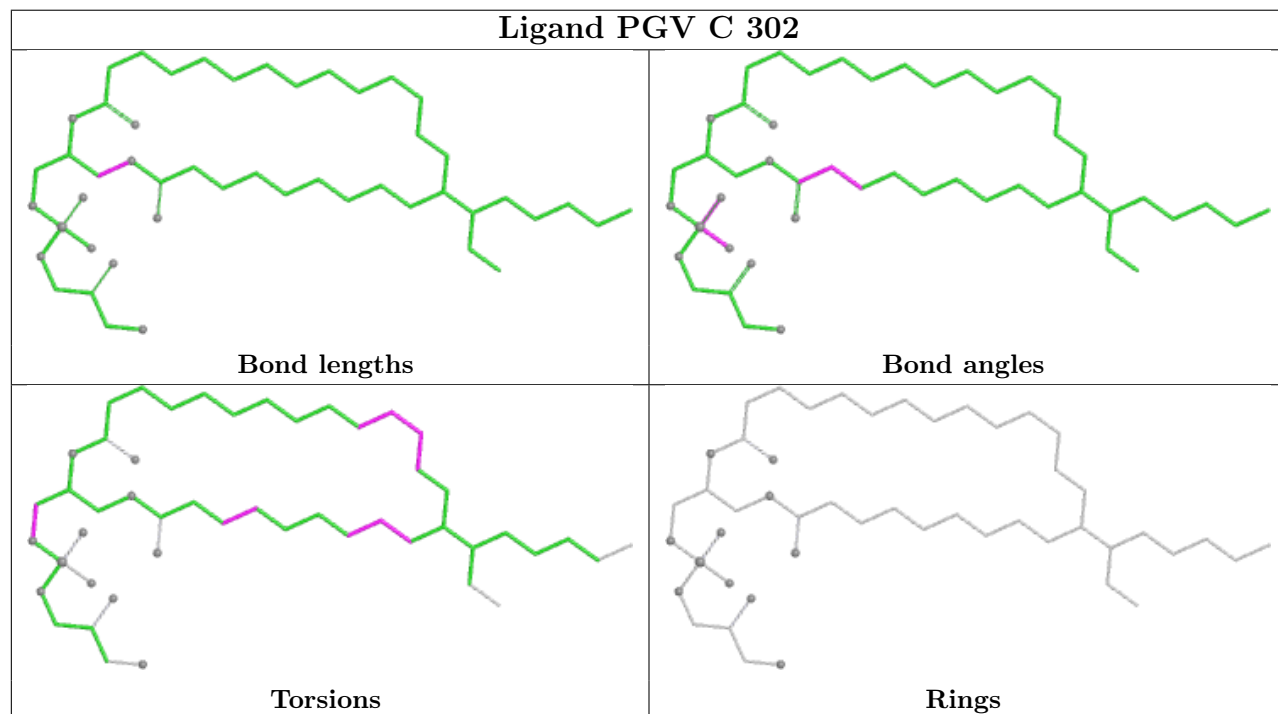
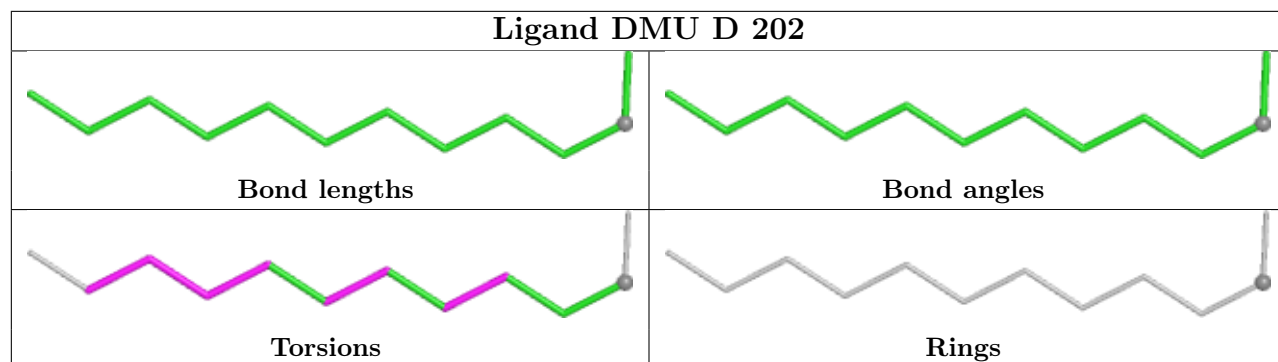


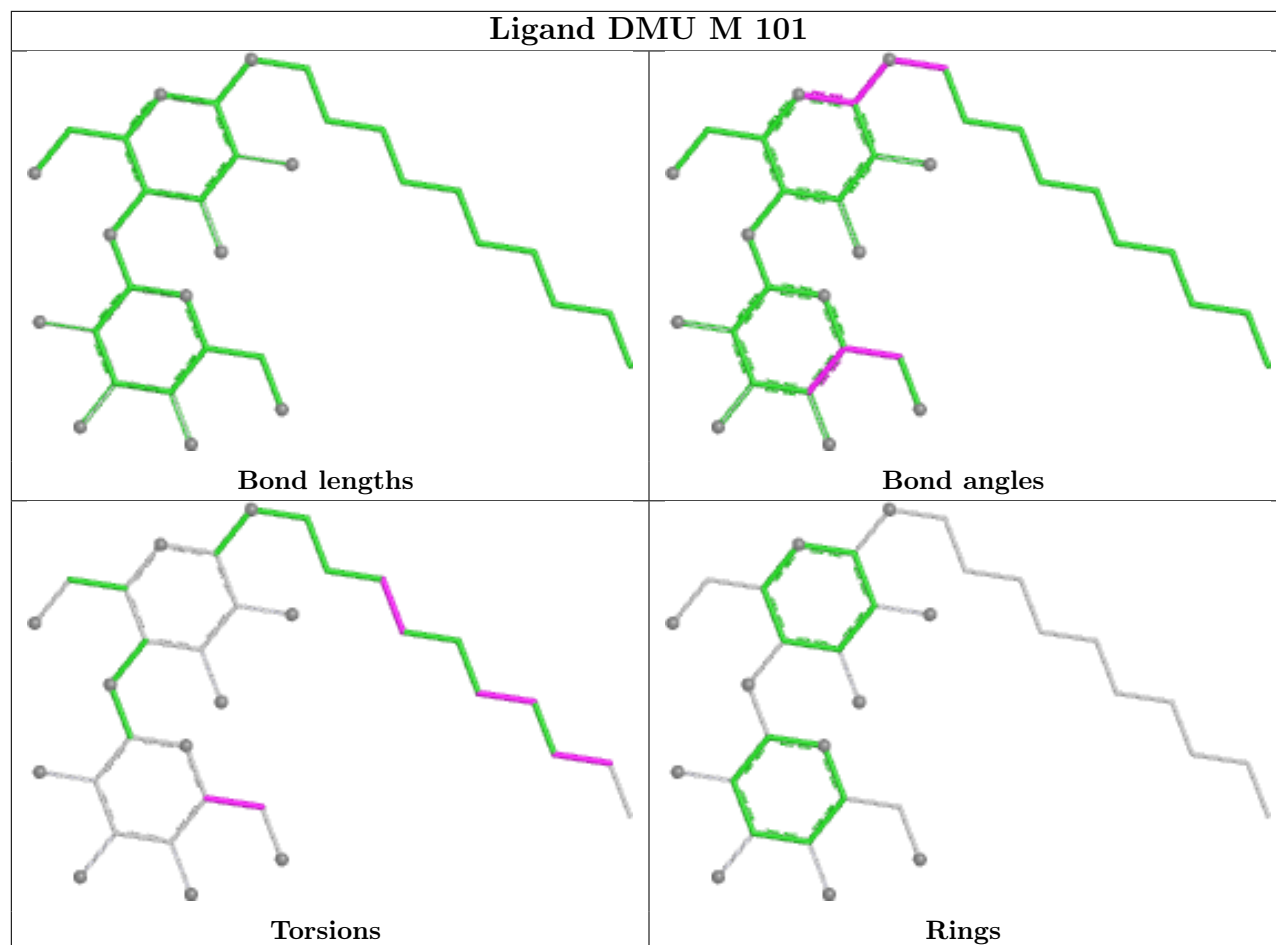


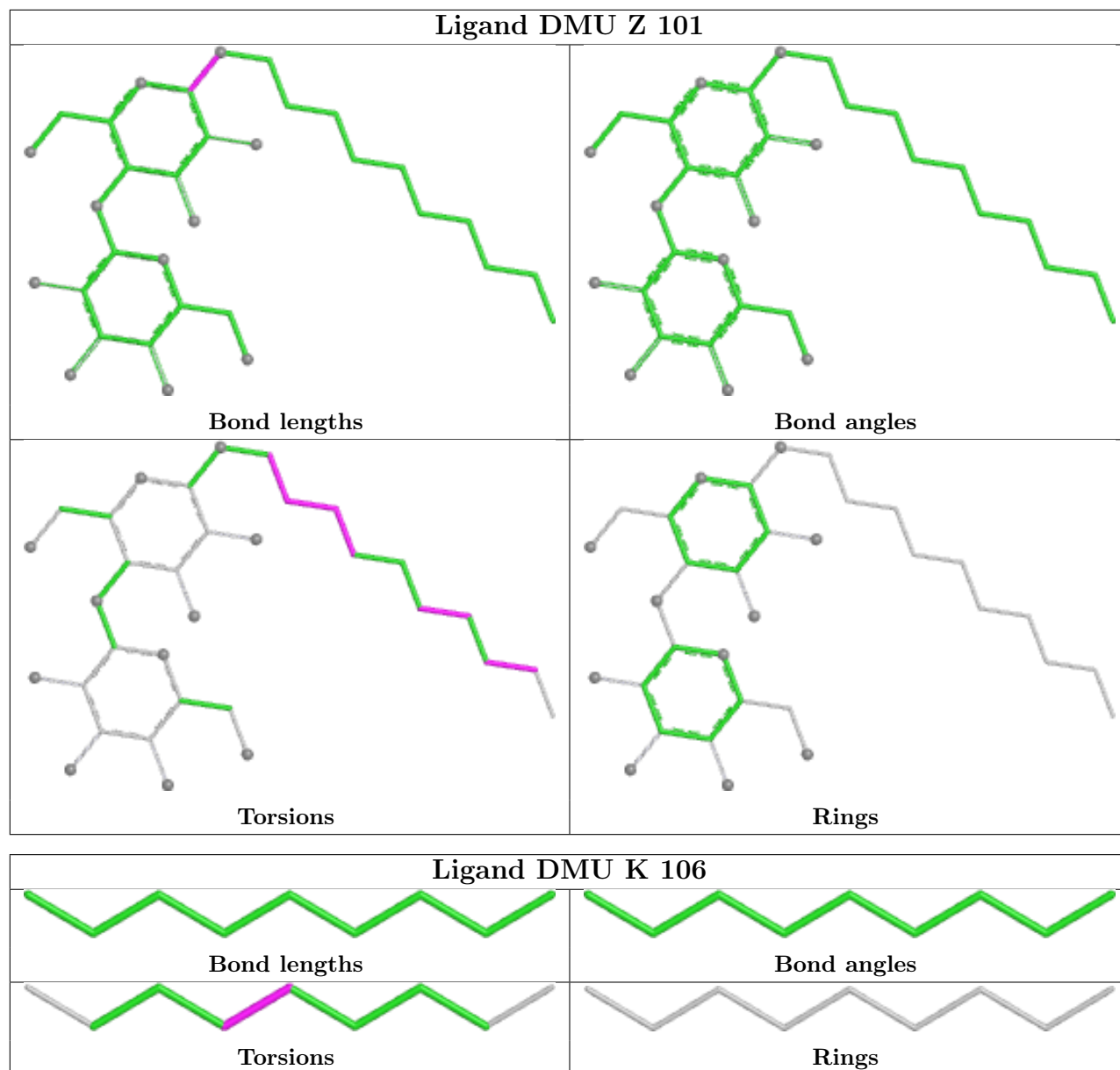


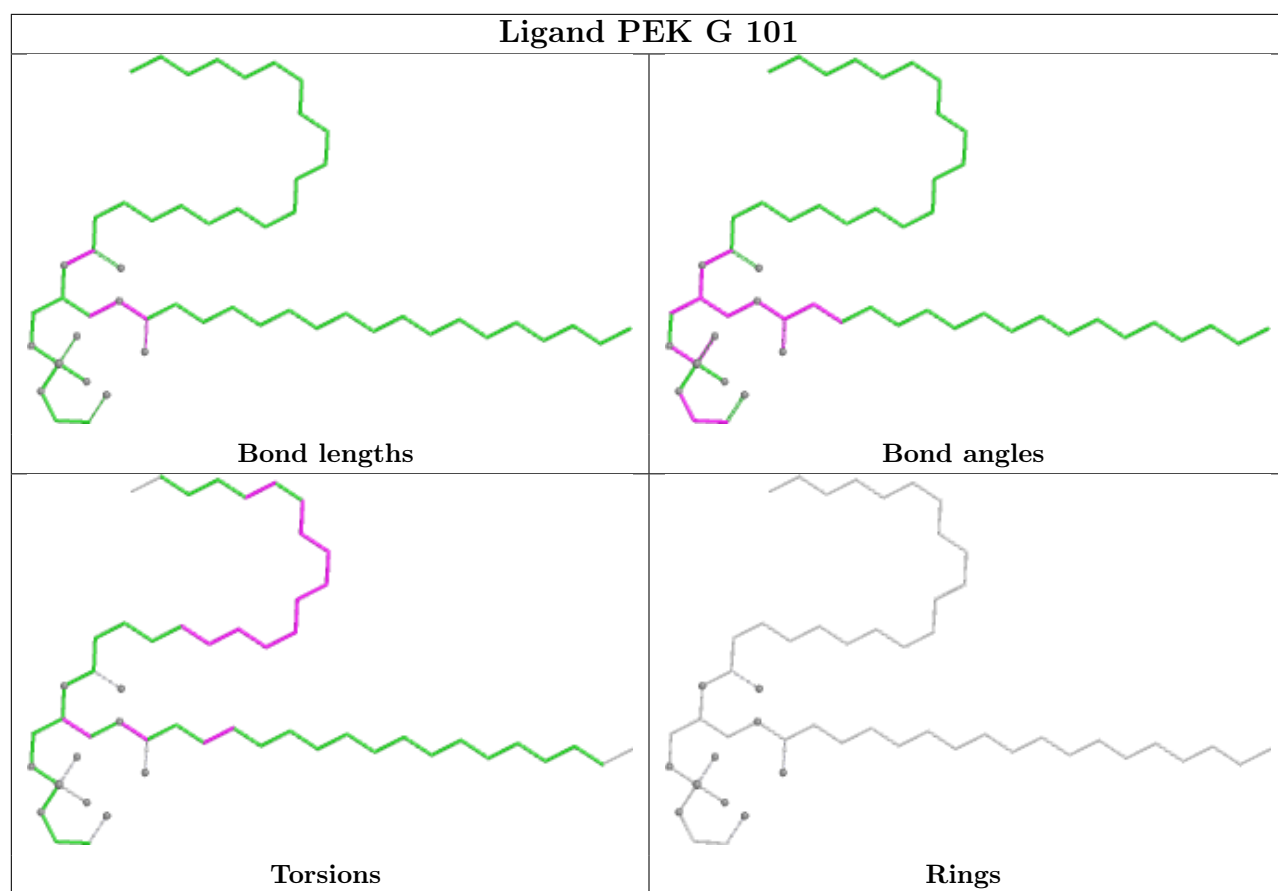


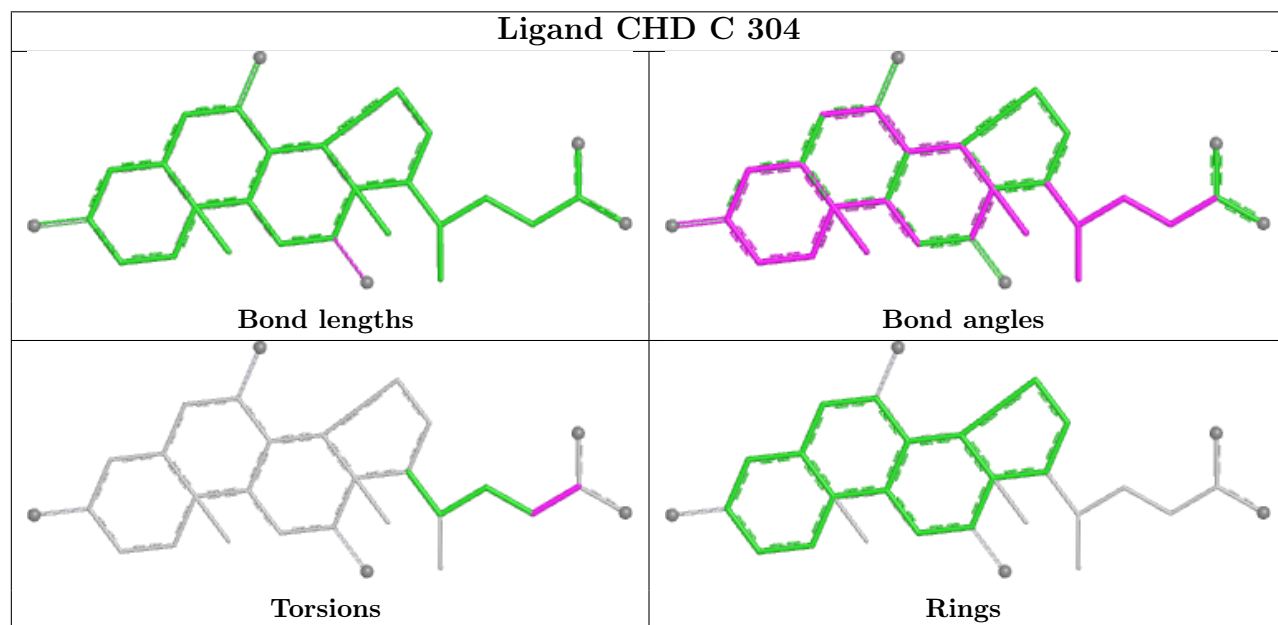
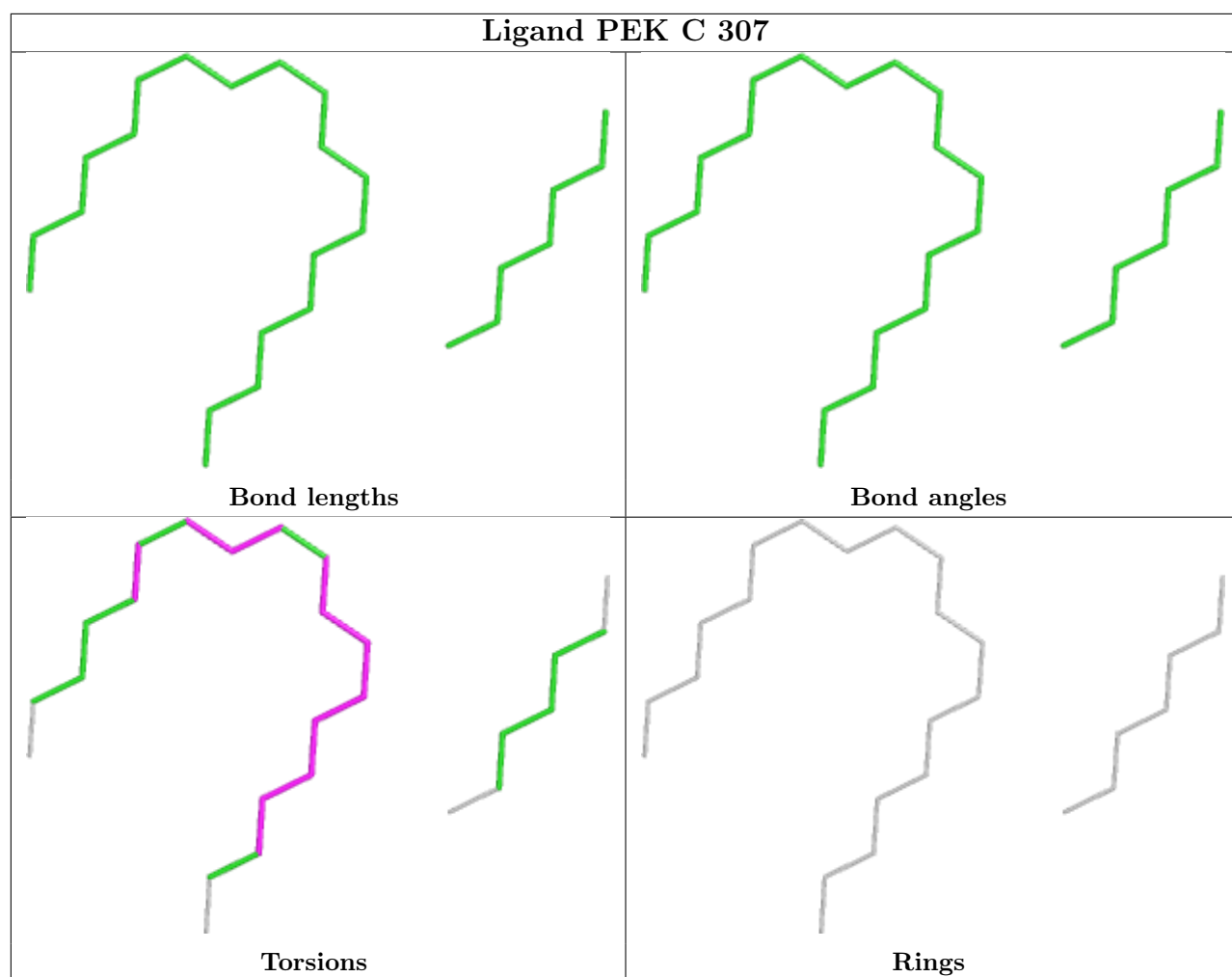


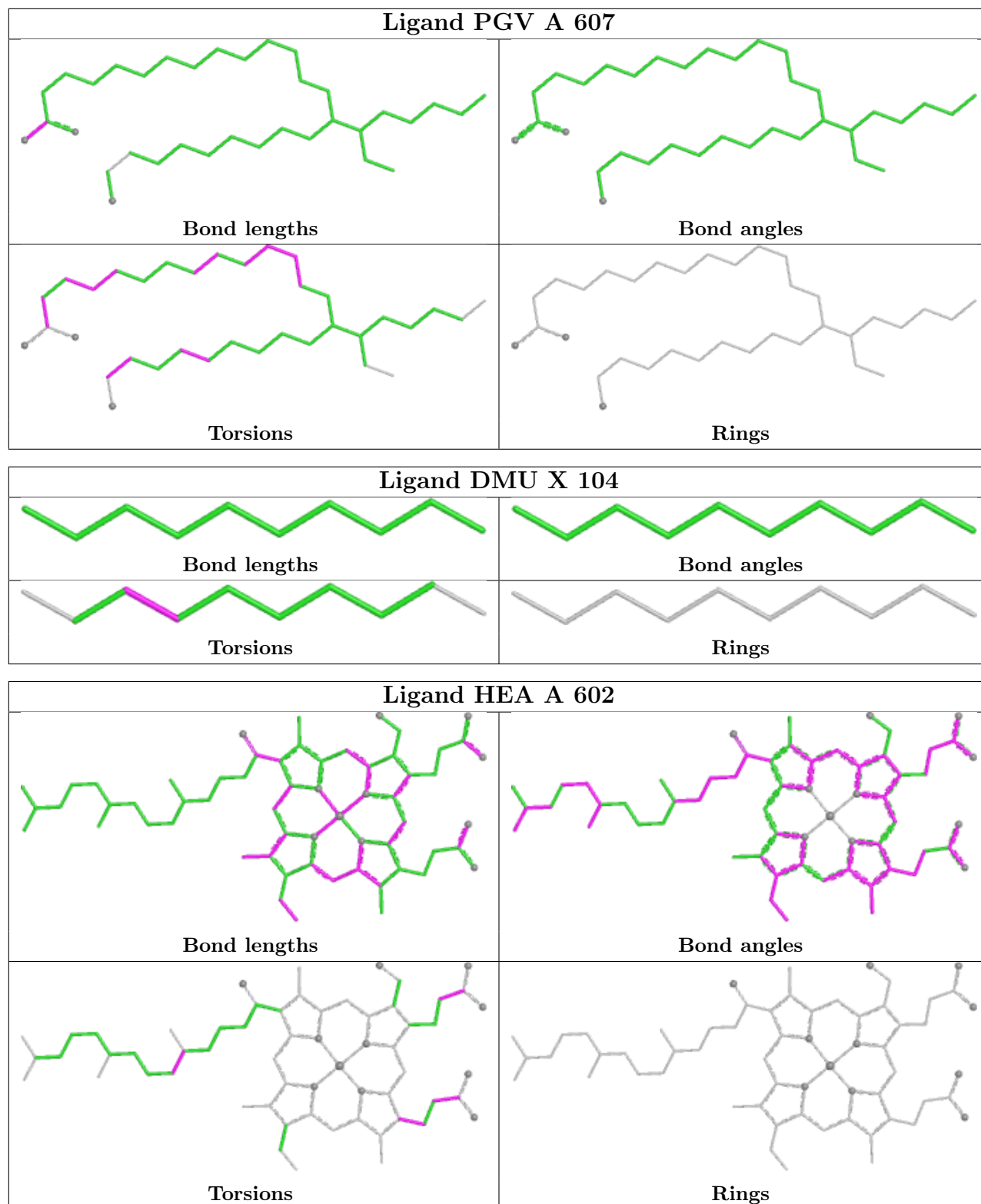




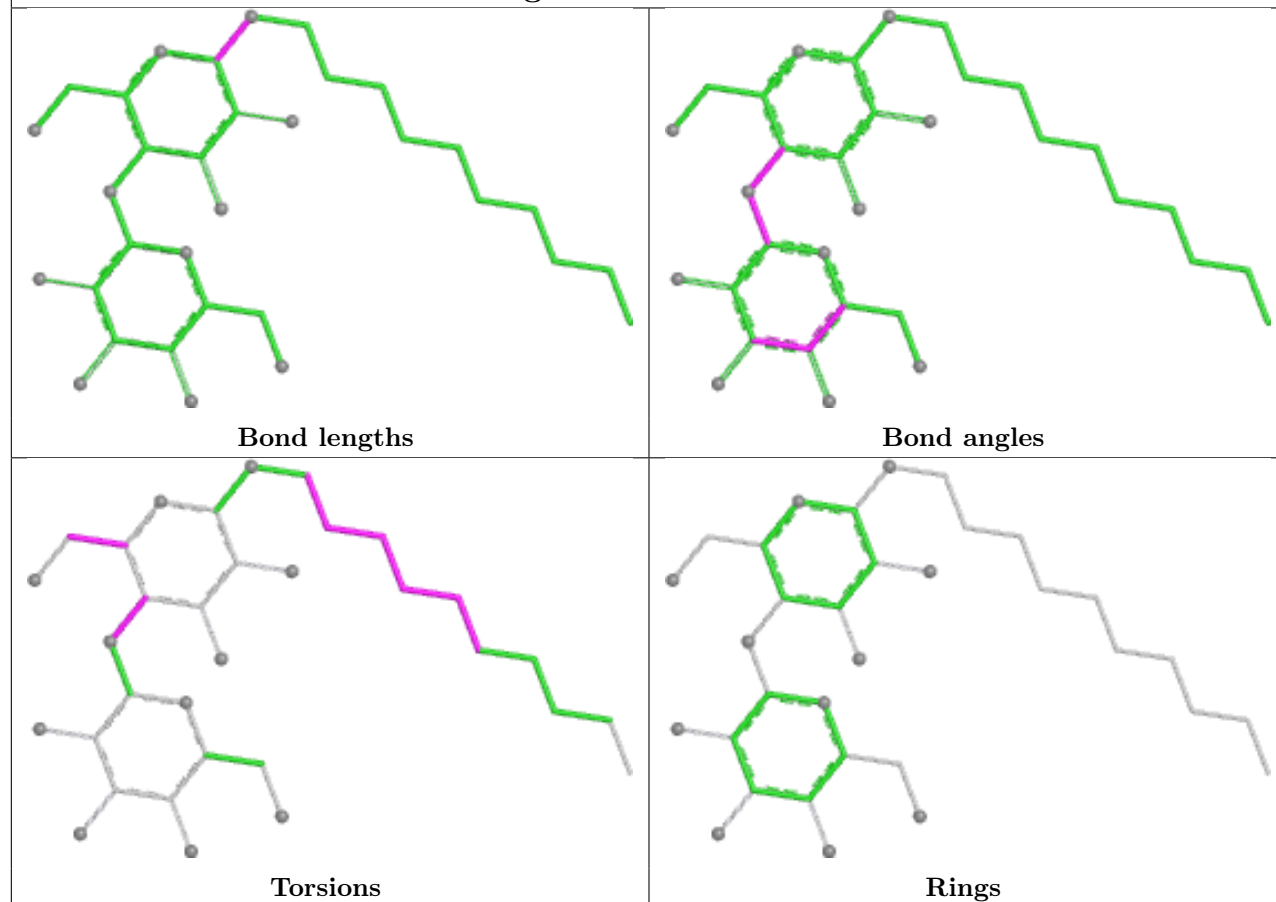




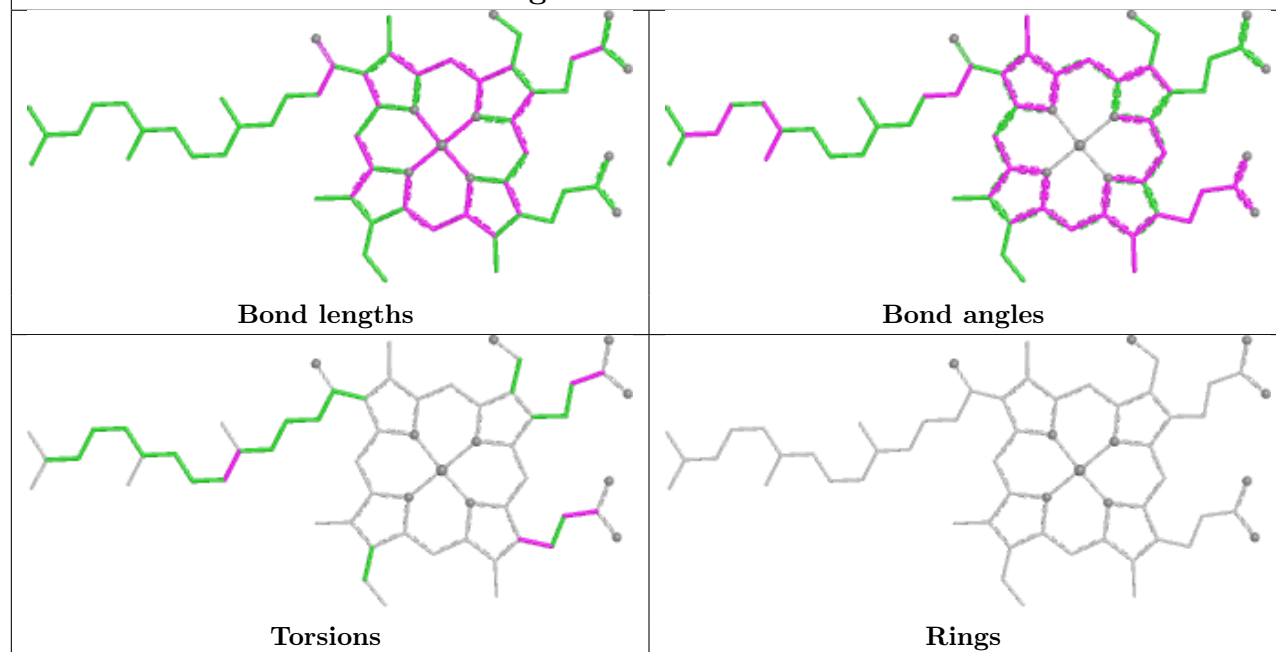


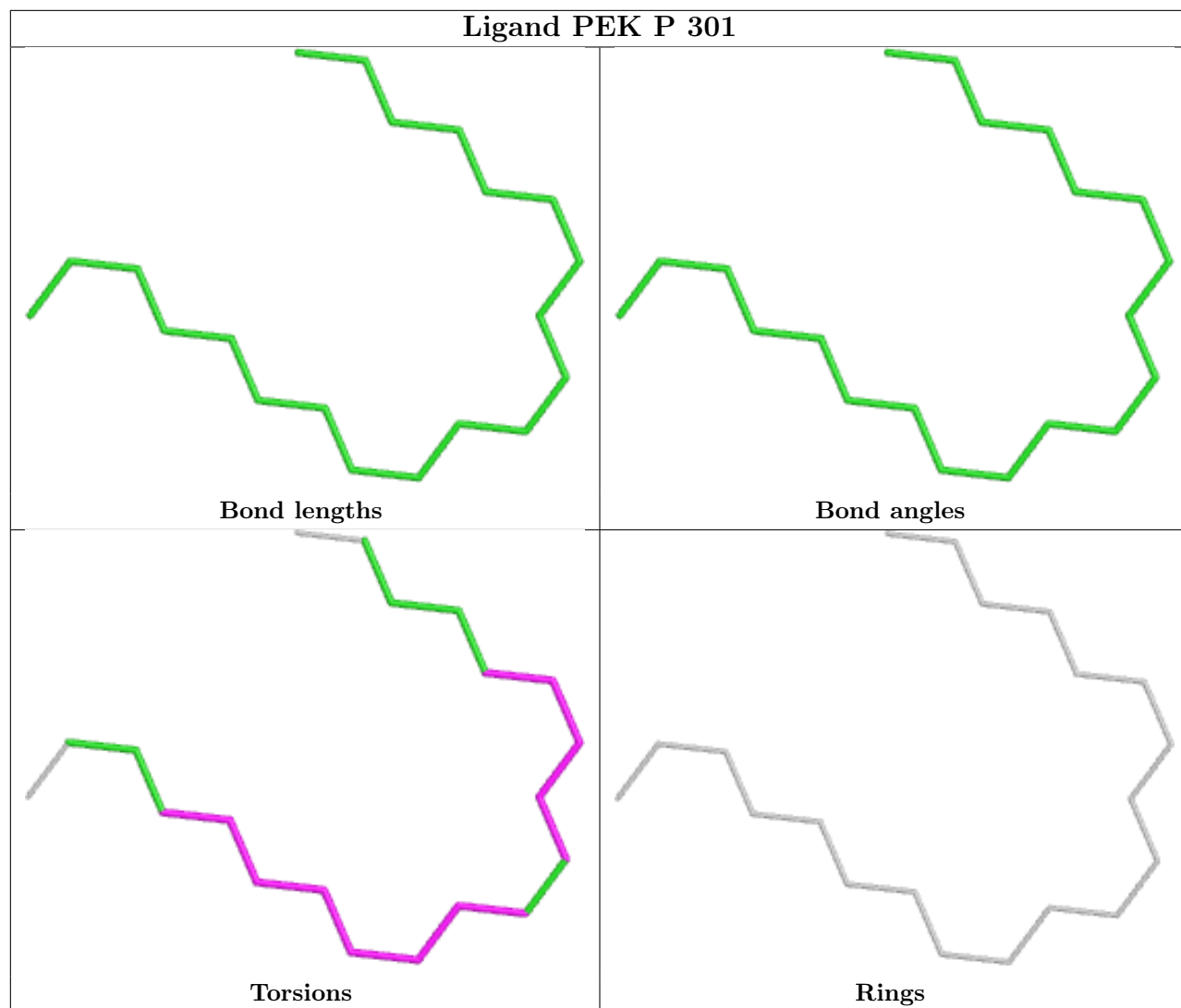


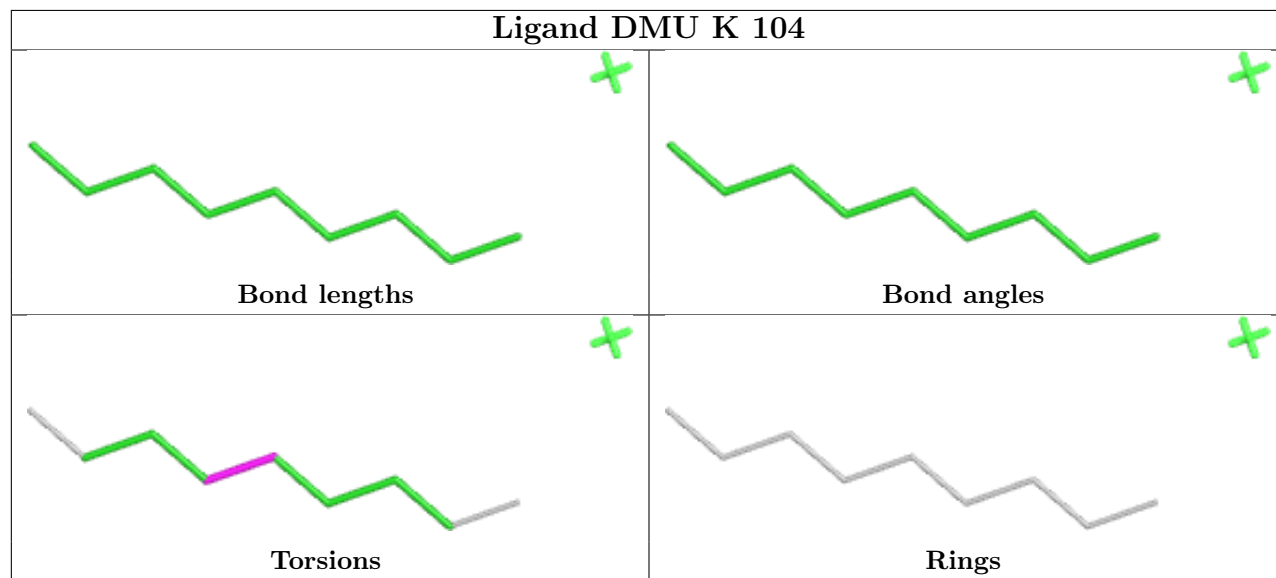
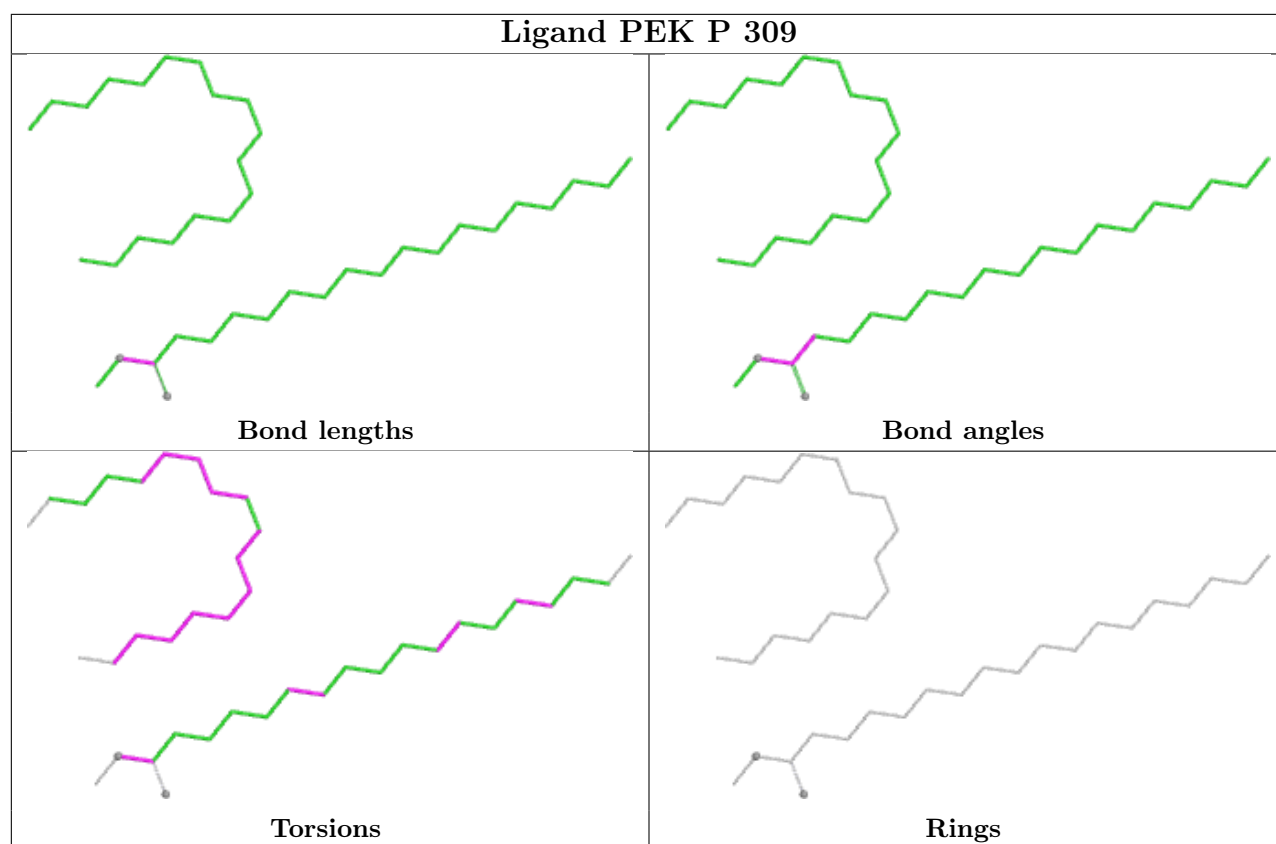
Ligand DMU K 103

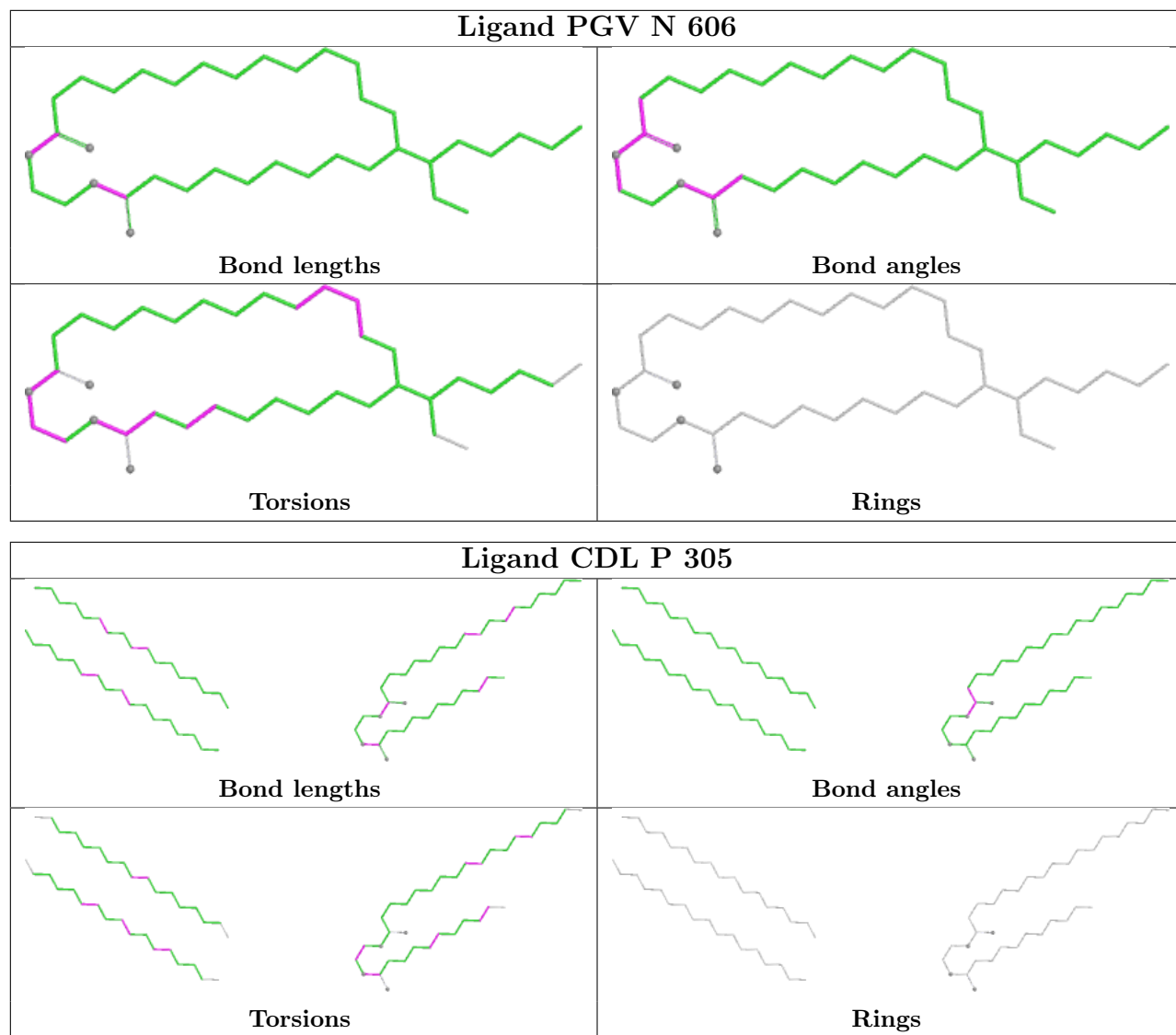


Ligand HEA N 602









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	513/514 (99%)	-0.38	4 (0%) 82 86	9, 20, 28, 79	20 (3%)
1	N	513/514 (99%)	-0.28	6 (1%) 76 80	10, 23, 32, 82	21 (4%)
2	B	226/227 (99%)	0.35	22 (9%) 13 13	19, 27, 57, 115	6 (2%)
2	O	226/227 (99%)	0.49	22 (9%) 13 13	23, 33, 77, 129	4 (1%)
3	C	259/259 (100%)	-0.14	6 (2%) 61 64	16, 24, 41, 82	8 (3%)
3	P	259/259 (100%)	-0.18	6 (2%) 61 64	16, 25, 38, 87	8 (3%)
4	D	144/144 (100%)	0.25	7 (4%) 35 36	18, 30, 53, 94	5 (3%)
4	Q	144/144 (100%)	1.30	28 (19%) 3 3	28, 44, 92, 221	1 (0%)
5	E	105/105 (100%)	0.35	7 (6%) 24 24	23, 30, 62, 164	1 (0%)
5	R	105/105 (100%)	0.53	7 (6%) 24 24	26, 36, 79, 178	0
6	F	98/98 (100%)	0.56	11 (11%) 10 10	18, 30, 118, 222	4 (4%)
6	S	98/98 (100%)	0.91	12 (12%) 8 8	20, 29, 143, 247	1 (1%)
7	G	84/84 (100%)	1.80	25 (29%) 1 1	16, 32, 149, 231	1 (1%)
7	T	84/84 (100%)	1.64	23 (27%) 1 1	21, 34, 132, 230	3 (3%)
8	H	79/79 (100%)	1.14	15 (18%) 3 3	24, 34, 153, 180	0
8	U	79/79 (100%)	1.21	16 (20%) 3 2	29, 39, 141, 209	0
9	I	72/73 (98%)	1.10	18 (25%) 2 1	26, 41, 76, 101	0
9	V	72/73 (98%)	1.77	27 (37%) 1 0	27, 50, 95, 229	1 (1%)
10	J	58/58 (100%)	0.82	10 (17%) 4 3	25, 34, 92, 143	0
10	W	58/58 (100%)	0.74	7 (12%) 8 8	25, 36, 99, 164	0
11	K	49/49 (100%)	0.55	4 (8%) 17 17	23, 34, 60, 64	1 (2%)
11	X	49/49 (100%)	1.18	8 (16%) 4 4	28, 44, 91, 111	1 (2%)
12	L	46/46 (100%)	0.20	3 (6%) 25 25	21, 25, 53, 114	0
12	Y	46/46 (100%)	0.60	7 (15%) 5 5	25, 32, 73, 145	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	43/43 (100%)	0.34	4 (9%) 14 14	22, 26, 75, 150	0
13	Z	43/43 (100%)	0.98	8 (18%) 3 3	30, 35, 128, 256	0
All	All	3552/3558 (99%)	0.33	313 (8%) 15 15	9, 28, 76, 256	86 (2%)

All (313) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	S	97	ALA	12.6
7	G	3	ALA	12.2
4	Q	6	VAL	12.0
7	T	3	ALA	11.5
6	S	94	HIS	11.4
7	G	6	GLY	11.2
4	Q	5	VAL	11.1
7	T	6	GLY	11.1
6	S	1	ALA	10.9
7	T	9	GLY	10.3
10	J	1	PHE	10.1
7	G	1	ALA	9.6
6	S	96	LEU	9.6
7	G	11	THR	9.4
8	H	47	GLY	9.3
8	U	8	ILE	9.1
8	H	8	ILE	8.9
7	T	8	HIS	8.9
4	Q	7	LYS	8.6
8	H	45	ALA	8.6
7	G	8	HIS	8.3
6	S	93	PRO	8.2
4	D	4	SER	8.1
7	G	7	ASP	8.0
7	G	9	GLY	7.9
7	T	1	ALA	7.9
7	T	2	SER	7.9
6	S	95	GLN	7.9
7	G	36	TRP	7.8
9	V	2	THR	7.8
8	H	46	LYS	7.8
7	T	5	LYS	7.6
7	T	11	THR	7.5
8	U	46	LYS	7.4

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Mol	Chain	Res	Type	RSRZ
9	V	37	PHE	7.4
7	G	4	ALA	7.3
7	T	36[A]	TRP	7.2
7	G	10	GLY	7.2
7	G	5	LYS	7.2
7	T	7	ASP	7.0
6	F	1	ALA	6.8
8	U	45	ALA	6.7
6	F	96	LEU	6.5
6	S	98	HIS	6.4
6	S	2	SER	6.4
8	U	9	LYS	6.3
11	X	54	ARG	6.3
2	B	90	ILE	6.2
7	T	10	GLY	6.2
6	F	2	SER	6.0
7	G	2	SER	6.0
4	Q	8	SER	6.0
2	O	227	LEU	5.9
3	P	3	HIS	5.9
13	Z	42	LYS	5.9
6	F	97	ALA	5.8
9	V	3	ALA	5.7
8	H	9	LYS	5.6
6	F	3	GLY	5.6
2	B	87	MET	5.6
7	T	4	ALA	5.5
2	O	113	TYR	5.5
12	Y	47	LYS	5.5
9	I	29	LEU	5.4
10	W	1	PHE	5.4
12	Y	2	HIS	5.4
7	G	84	LYS	5.3
2	O	90	ILE	5.3
6	F	98	HIS	5.3
12	L	2	HIS	5.3
11	X	6	ALA	5.3
9	V	26	MET	5.2
6	F	94	HIS	5.2
7	T	84	LYS	5.2
5	R	109	VAL	5.2
9	I	37	PHE	5.2

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Mol	Chain	Res	Type	RSRZ
5	R	80	GLU	5.1
4	Q	4	SER	5.1
5	E	6	GLU	5.1
2	O	226	MET	5.0
8	U	7	LYS	4.9
4	Q	43	LYS	4.8
1	N	513	LEU	4.8
8	U	47	GLY	4.8
2	B	59	GLN	4.8
2	O	65	TRP	4.8
7	G	38	HIS	4.7
8	H	7	LYS	4.7
5	E	5	HIS	4.7
12	L	47	LYS	4.7
3	C	3	HIS	4.7
2	O	217	LYS	4.6
8	H	48	GLY	4.6
10	W	58	LYS	4.5
2	O	91	ASN	4.4
8	U	61	LYS	4.4
2	B	65	TRP	4.3
2	B	91	ASN	4.3
5	R	5	HIS	4.3
9	V	29	LEU	4.3
1	N	514	LYS	4.3
9	V	65	LYS	4.3
9	I	2	THR	4.3
6	F	95	GLN	4.3
4	Q	9	GLU	4.3
7	T	38	HIS	4.1
13	M	40	TYR	4.1
13	Z	38	ASP	4.1
10	J	58	LYS	4.1
9	V	73	LYS	4.0
8	U	10	ASN	4.0
5	R	79	LYS	4.0
5	E	39	TYR	4.0
5	R	108	LYS	4.0
8	U	50	VAL	4.0
6	S	3	GLY	4.0
1	A	514	LYS	3.9
13	M	43	SER	3.9

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Mol	Chain	Res	Type	RSRZ
10	J	4	ARG	3.9
4	Q	51	LEU	3.9
11	K	6	ALA	3.9
12	Y	20	ARG	3.9
4	Q	39	ALA	3.9
2	B	16	ILE	3.8
7	T	37	LEU	3.8
11	K	54	ARG	3.8
7	G	37	LEU	3.8
11	X	51	LYS	3.8
13	Z	41	LYS	3.8
8	H	44	THR	3.8
13	Z	40	TYR	3.8
8	U	48	GLY	3.7
2	O	87	MET	3.7
11	X	52	GLU	3.7
5	E	109	VAL	3.6
11	X	7	PRO	3.6
1	A	513	LEU	3.6
10	W	48	TYR	3.6
7	G	35	SER	3.5
7	T	33	LEU	3.5
2	B	113	TYR	3.5
13	Z	43	SER	3.5
4	Q	10	ASP	3.5
13	Z	39	ASN	3.5
10	J	48	TYR	3.5
4	Q	35	ALA	3.5
8	U	51	SER	3.5
8	U	44	THR	3.5
7	G	39	SER	3.4
11	X	47	ARG	3.4
2	B	88	ASP	3.4
8	H	10	ASN	3.4
13	M	42	LYS	3.3
9	V	15	ARG	3.3
4	Q	50	SER	3.3
8	U	49	ASP	3.3
1	N	113[A]	LEU	3.3
2	O	59	GLN	3.2
8	U	12	GLN	3.2
8	H	23	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
2	O	92	ASN	3.2
10	J	56	PRO	3.1
3	C	127	LEU	3.1
9	V	25	PHE	3.1
4	Q	140	TYR	3.1
10	W	44	LEU	3.1
5	R	90	ARG	3.1
2	O	114	GLU	3.1
7	T	39	SER	3.1
2	B	61	VAL	3.0
2	B	92	ASN	3.0
10	J	57	HIS	3.0
4	D	5	VAL	3.0
2	B	183	THR	3.0
2	B	60	GLU	3.0
6	F	64	GLU	3.0
8	U	52	VAL	2.9
4	Q	73	ARG	2.9
9	I	18	ARG	2.9
4	Q	31	LYS	2.9
4	Q	147	LYS	2.9
8	U	84	LYS	2.9
10	J	52	TRP	2.9
7	G	33	LEU	2.9
9	V	52	ARG	2.9
6	S	76	LYS	2.9
10	W	57	HIS	2.9
2	O	183	THR	2.9
3	C	44	MET	2.9
2	B	129	LYS	2.9
2	O	221	LYS	2.9
2	O	89	GLU	2.9
4	D	147	LYS	2.9
13	Z	32	TRP	2.9
4	Q	143	ASN	2.9
9	V	53	ASN	2.9
9	V	31	PHE	2.8
7	G	42	ARG	2.8
7	T	40	GLY	2.8
3	P	37	PHE	2.8
4	Q	87	PHE	2.8
2	O	225	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	N	484	THR	2.8
4	D	31	LYS	2.8
8	H	49	ASP	2.8
9	I	52	ARG	2.8
9	V	34	PHE	2.7
9	V	6	LYS	2.7
1	N	512	ASN	2.7
4	D	143	ASN	2.7
4	D	142	LYS	2.7
9	V	58	LYS	2.7
9	I	15	ARG	2.7
4	Q	53	ILE	2.7
6	S	64	GLU	2.7
7	G	12	GLY	2.7
2	B	217	LYS	2.7
3	C	224	LYS	2.7
9	I	41	GLU	2.7
4	Q	33	LEU	2.7
7	T	35	SER	2.6
9	V	28	SER	2.6
9	V	45	LYS	2.6
7	G	70	PHE	2.6
10	J	27	THR	2.6
12	L	26	THR	2.6
8	H	84	LYS	2.6
9	I	26	MET	2.6
4	Q	141	ASP	2.5
5	E	108	LYS	2.5
3	C	230	ASN	2.5
11	K	47	ARG	2.5
9	I	21	ILE	2.5
6	S	37	LYS	2.5
4	D	9	GLU	2.5
7	T	43	GLU	2.5
9	V	21	ILE	2.5
2	O	129	LYS	2.5
2	B	37	LEU	2.5
2	B	115	ASP	2.5
9	I	34	PHE	2.5
2	B	13	THR	2.5
9	V	64	ARG	2.5
9	I	19	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
8	H	52	VAL	2.4
9	V	33	THR	2.4
3	P	230	ASN	2.4
7	T	42	ARG	2.4
1	A	297[A]	MET	2.4
9	V	19	PHE	2.4
4	Q	72	ASN	2.4
2	O	16	ILE	2.4
7	G	41	HIS	2.4
2	B	33	LEU	2.4
10	J	2	GLU	2.4
9	V	68	ILE	2.4
13	Z	1	ILE	2.4
4	Q	58	GLU	2.3
2	B	57	ASP	2.3
5	R	7	THR	2.3
11	X	13	TYR	2.3
12	Y	4	GLU	2.3
2	B	82	ARG	2.3
2	O	115	ASP	2.3
6	F	37	LYS	2.3
7	G	45	PRO	2.3
9	I	73	LYS	2.3
9	V	36	LYS	2.3
2	B	55	THR	2.3
9	I	25	PHE	2.3
3	P	258	TRP	2.3
11	X	20	SER	2.3
4	Q	20	ARG	2.3
9	V	18	ARG	2.3
10	W	2	GLU	2.3
4	Q	11	TYR	2.3
4	Q	121	LYS	2.3
10	W	15	ASP	2.3
1	N	297[A]	MET	2.3
5	E	7	THR	2.2
9	I	33	THR	2.2
3	C	38	ASN	2.2
4	Q	142	LYS	2.2
3	P	122	HIS	2.2
10	J	33	ARG	2.2
12	Y	46	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
6	F	25	ARG	2.2
2	O	130	PRO	2.2
13	M	39	ASN	2.2
4	Q	74	SER	2.2
9	V	72	ALA	2.2
7	G	30	LEU	2.2
7	G	40	GLY	2.2
7	T	41	HIS	2.2
2	O	32[A]	PHE	2.2
11	K	51	LYS	2.2
1	A	113[A]	LEU	2.1
12	Y	45	LEU	2.1
9	I	44	LYS	2.1
8	H	50	VAL	2.1
9	I	39	VAL	2.1
2	O	68	LEU	2.1
2	O	78	LEU	2.1
9	I	36	LYS	2.1
2	B	32[A]	PHE	2.1
3	P	38	ASN	2.0
9	V	57	MET	2.0
12	Y	24	MET	2.0
5	E	14[A]	ARG	2.0
7	T	12	GLY	2.0
8	H	51	SER	2.0
9	I	22	VAL	2.0
9	V	44	LYS	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
9	SAC	V	1	9/10	0.25	0.24	178,202,219,230	0
9	SAC	I	1	9/10	0.61	0.29	102,127,159,160	0
1	FME	A	1	10/11	0.92	0.14	31,42,90,117	0
1	FME	N	1	10/11	0.93	0.15	31,37,74,75	0
2	FME	B	1	10/11	0.94	0.16	17,27,59,100	0
2	FME	O	1	10/11	0.97	0.09	30,34,37,88	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	CHD	J	101	29/29	0.47	0.25	59,123,157,161	0
24	DMU	K	103	33/33	0.49	0.25	53,116,180,196	0
24	DMU	D	203	9/33	0.56	0.41	67,73,89,108	0
24	DMU	K	104	10/33	0.56	0.46	46,68,94,156	0
21	EDO	N	621	4/4	0.66	0.25	40,55,66,68	0
24	DMU	X	101	33/33	0.66	0.24	56,111,187,198	0
18	PGV	C	306	36/51	0.68	0.36	35,74,108,121	0
24	DMU	X	104	10/33	0.68	0.38	60,65,106,130	0
26	PEK	C	305	37/53	0.68	0.32	41,67,97,107	0
18	PGV	P	302	41/51	0.69	0.35	46,78,111,124	0
23	CHD	P	306	29/29	0.69	0.23	59,87,115,124	0
25	CDL	G	102	64/100	0.70	0.35	50,77,106,116	0
26	PEK	P	309	39/53	0.70	0.33	36,74,102,104	0
21	EDO	A	615	4/4	0.71	0.34	36,37,51,110	0
25	CDL	T	101	79/100	0.72	0.32	49,80,113,135	0
24	DMU	X	103	9/33	0.72	0.46	71,75,93,95	0
25	CDL	P	305	69/100	0.72	0.34	41,76,134,145	0
19	TGL	D	201	63/63	0.73	0.31	30,73,104,130	0
21	EDO	C	311	4/4	0.73	0.40	31,70,77,85	0
19	TGL	Q	201	63/63	0.74	0.28	41,73,102,123	0
21	EDO	T	102	4/4	0.75	0.26	36,52,64,76	0
19	TGL	O	301	58/63	0.75	0.33	46,69,105,116	0
24	DMU	C	308	12/33	0.76	0.30	55,59,89,91	0
24	DMU	D	202	12/33	0.76	0.30	43,67,98,130	0
24	DMU	X	105	11/33	0.76	0.29	49,80,93,110	0
26	PEK	P	301	20/53	0.76	0.24	41,52,86,90	0
21	EDO	C	312	4/4	0.76	0.35	38,70,75,119	0
25	CDL	C	303	56/100	0.77	0.32	37,62,94,99	0
26	PEK	C	307	26/53	0.77	0.32	40,56,95,102	0
19	TGL	A	608	62/63	0.78	0.28	36,70,100,112	0
24	DMU	K	101	10/33	0.78	0.25	43,70,82,180	0
19	TGL	L	101	59/63	0.78	0.27	26,59,112,149	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
20	PSC	A	609	25/52	0.78	0.33	44,68,88,93	0
18	PGV	N	606	40/51	0.79	0.29	37,69,127,133	0
21	EDO	W	102	4/4	0.79	0.28	39,55,67,102	0
21	EDO	W	103	4/4	0.80	0.22	55,62,82,96	0
24	DMU	P	303	33/33	0.80	0.19	46,92,140,148	0
28	PO4	U	101	5/5	0.80	0.47	72,73,93,94	5
20	PSC	O	303	24/52	0.81	0.32	35,62,98,102	0
21	EDO	O	307	4/4	0.81	0.28	31,64,82,96	0
24	DMU	W	101	9/33	0.81	0.26	61,64,72,87	0
19	TGL	N	608	57/63	0.81	0.27	37,67,99,118	0
24	DMU	O	304	10/33	0.82	0.24	41,49,79,82	0
24	DMU	K	102	9/33	0.82	0.30	59,68,90,92	0
24	DMU	P	310	11/33	0.82	0.26	47,64,82,98	0
21	EDO	C	309	4/4	0.82	0.26	44,49,70,77	0
18	PGV	A	607	37/51	0.82	0.28	33,60,113,122	0
24	DMU	X	102	10/33	0.82	0.29	48,60,96,115	0
21	EDO	J	104	4/4	0.83	0.25	39,44,62,104	0
24	DMU	L	102	21/33	0.83	0.24	46,81,117,144	0
24	DMU	K	105	9/33	0.84	0.25	59,82,91,107	0
21	EDO	J	103	4/4	0.84	0.26	60,61,61,99	0
21	EDO	T	103	4/4	0.84	0.27	52,69,83,104	0
28	PO4	H	101	5/5	0.84	0.52	57,64,83,100	5
21	EDO	Y	101	4/4	0.84	0.22	43,48,52,89	0
21	EDO	S	103	4/4	0.86	0.26	28,55,84,92	0
21	EDO	F	102	4/4	0.86	0.27	42,45,57,87	0
21	EDO	F	103	4/4	0.87	0.20	33,39,61,104	0
21	EDO	Q	203	4/4	0.87	0.22	33,38,60,65	0
21	EDO	S	102	4/4	0.87	0.15	40,42,47,64	0
21	EDO	N	612	4/4	0.87	0.23	44,59,71,81	0
24	DMU	J	102	12/33	0.87	0.20	51,62,91,111	0
21	EDO	B	304	4/4	0.87	0.26	50,51,53,97	0
21	EDO	Q	204	4/4	0.88	0.15	49,51,59,60	0
21	EDO	R	201	4/4	0.88	0.15	43,47,48,52	0
24	DMU	K	106	9/33	0.89	0.20	36,50,95,95	0
24	DMU	Z	101	33/33	0.89	0.13	35,46,65,75	0
21	EDO	A	613	4/4	0.89	0.14	32,34,37,41	0
21	EDO	F	105	4/4	0.90	0.18	29,42,54,61	0
21	EDO	B	306	4/4	0.90	0.15	27,39,40,47	0
21	EDO	A	617	4/4	0.90	0.15	35,40,42,43	0
21	EDO	A	612	4/4	0.90	0.22	30,34,72,79	0
24	DMU	C	301	9/33	0.90	0.21	25,44,63,71	0
21	EDO	N	617	4/4	0.90	0.22	40,72,73,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
21	EDO	P	312	4/4	0.91	0.23	47,57,60,67	0
21	EDO	N	609	4/4	0.91	0.15	36,36,41,47	0
21	EDO	N	619	4/4	0.91	0.20	29,40,56,95	0
21	EDO	A	618	4/4	0.92	0.19	28,35,67,106	0
21	EDO	N	615	4/4	0.92	0.20	25,34,70,102	0
21	EDO	P	311	4/4	0.92	0.15	26,28,38,61	0
24	DMU	M	101	33/33	0.92	0.11	31,36,67,74	0
21	EDO	B	305	4/4	0.92	0.14	32,43,44,54	0
21	EDO	A	619	4/4	0.92	0.21	25,30,35,41	0
21	EDO	F	104	4/4	0.93	0.11	30,33,35,44	0
26	PEK	P	308	53/53	0.93	0.18	26,43,95,124	0
21	EDO	N	613	4/4	0.93	0.15	33,38,40,69	0
21	EDO	S	106	4/4	0.93	0.20	29,57,60,67	0
26	PEK	G	101	53/53	0.93	0.20	23,42,90,126	0
21	EDO	N	611	4/4	0.94	0.14	27,36,42,77	0
21	EDO	N	614	4/4	0.94	0.17	28,30,58,80	0
21	EDO	C	313	4/4	0.94	0.14	27,28,38,68	0
21	EDO	P	313	4/4	0.94	0.11	31,34,37,39	0
21	EDO	E	202	4/4	0.95	0.08	33,36,38,41	0
21	EDO	O	306	4/4	0.95	0.09	37,37,40,43	0
21	EDO	Q	202	4/4	0.95	0.12	26,33,55,56	0
21	EDO	A	614	4/4	0.95	0.09	22,23,25,26	0
23	CHD	C	304	29/29	0.95	0.07	22,26,31,32	0
21	EDO	A	610	4/4	0.95	0.13	28,28,35,77	0
23	CHD	P	307	29/29	0.96	0.07	22,27,31,36	0
21	EDO	S	105	4/4	0.96	0.08	30,32,35,35	0
21	EDO	N	616	4/4	0.96	0.07	22,23,24,26	0
21	EDO	N	610	4/4	0.96	0.11	30,32,32,33	0
18	PGV	P	304	50/51	0.96	0.12	19,30,70,100	0
21	EDO	G	104	4/4	0.96	0.09	27,29,33,35	0
21	EDO	O	305	4/4	0.96	0.10	28,28,29,32	0
18	PGV	N	607	51/51	0.96	0.12	20,25,70,93	0
23	CHD	B	302	29/29	0.96	0.07	20,24,28,37	0
17	NA	N	605	1/1	0.96	0.08	27,27,27,27	0
21	EDO	E	201	4/4	0.96	0.09	33,35,35,36	0
21	EDO	S	104	4/4	0.96	0.07	20,21,21,22	0
18	PGV	A	606	51/51	0.97	0.12	18,24,66,83	0
21	EDO	C	310	4/4	0.97	0.08	28,30,31,34	0
18	PGV	C	302	51/51	0.97	0.12	19,26,75,97	0
23	CHD	G	103	29/29	0.97	0.06	20,23,27,34	0
21	EDO	N	618	4/4	0.97	0.09	29,37,44,45	0
21	EDO	A	616	4/4	0.97	0.08	26,33,34,42	0

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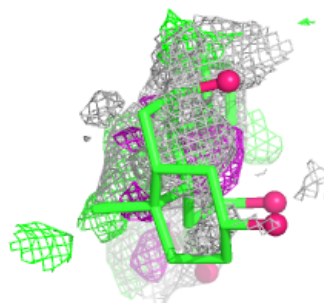
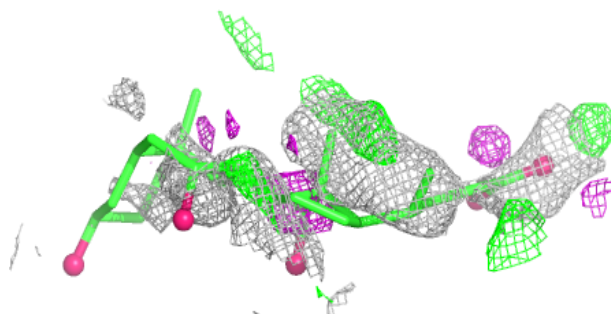
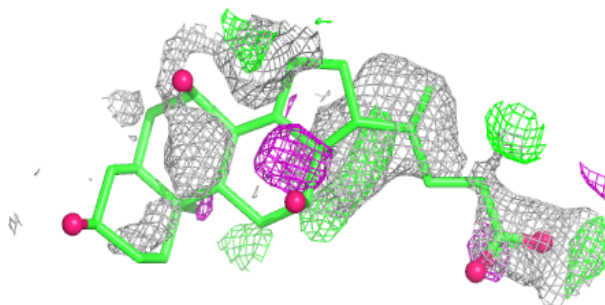
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
21	EDO	B	303	4/4	0.98	0.07	21,23,23,26	0
21	EDO	N	620	4/4	0.98	0.06	21,24,24,28	0
21	EDO	F	106	4/4	0.98	0.05	19,20,20,22	0
14	HEA	A	602	60/60	0.98	0.06	15,18,26,31	0
14	HEA	N	602	60/60	0.99	0.05	16,20,28,30	0
16	MG	A	604	1/1	0.99	0.04	17,17,17,17	0
16	MG	N	604	1/1	0.99	0.04	20,20,20,20	0
17	NA	A	605	1/1	0.99	0.09	22,22,22,22	0
14	HEA	A	601[B]	60/60	0.99	0.06	10,18,32,53	10
14	HEA	A	601[A]	60/60	0.99	0.06	15,18,28,40	10
21	EDO	A	611	4/4	0.99	0.07	19,20,20,25	0
14	HEA	N	601[A]	60/60	0.99	0.06	19,22,34,44	10
14	HEA	N	601[B]	60/60	0.99	0.06	12,22,35,46	10
15	CU	N	603	1/1	1.00	0.02	20,20,20,20	0
22	CUA	B	301	2/2	1.00	0.01	20,20,20,20	0
27	ZN	F	101	1/1	1.00	0.03	23,23,23,23	0
27	ZN	S	101	1/1	1.00	0.03	24,24,24,24	0
22	CUA	O	302	2/2	1.00	0.02	24,24,24,25	0
15	CU	A	603	1/1	1.00	0.02	17,17,17,17	0

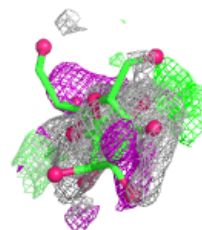
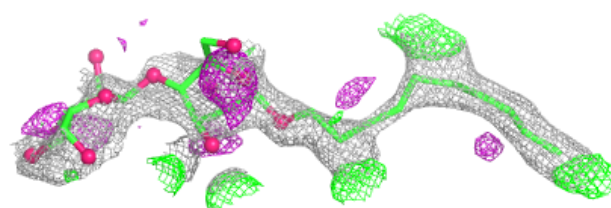
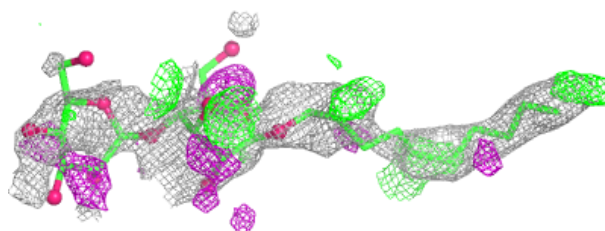
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CHD 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)

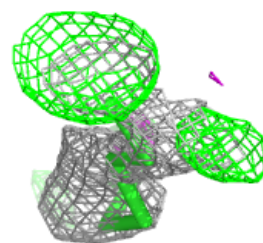
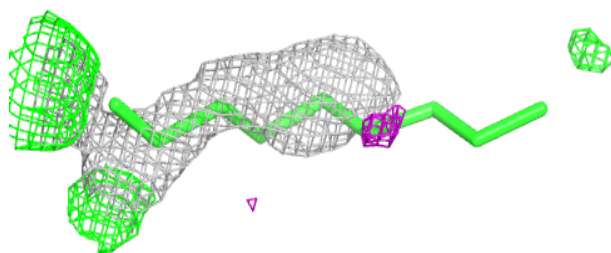
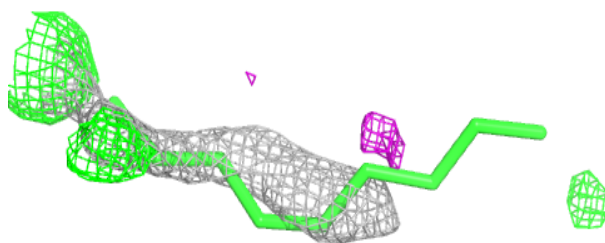
**Electron density around DMU K 103:**

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

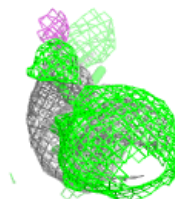
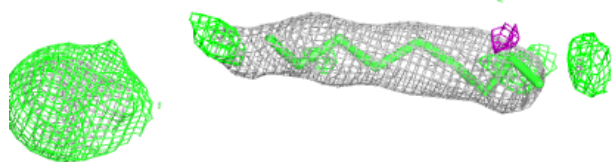
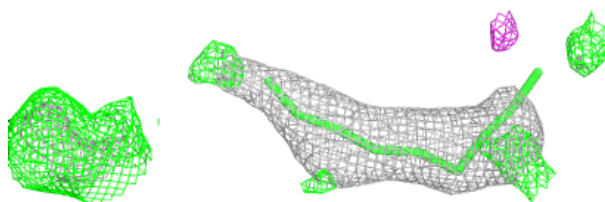


Electron density around DMU D 203:

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

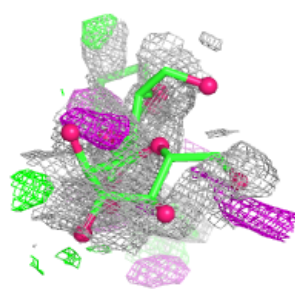
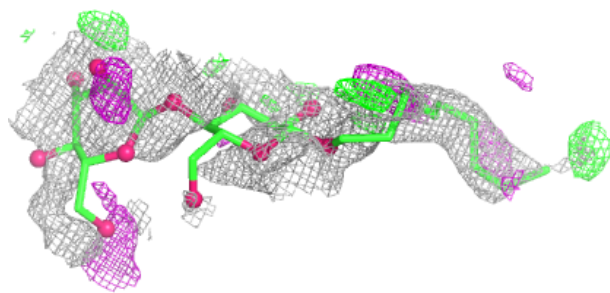
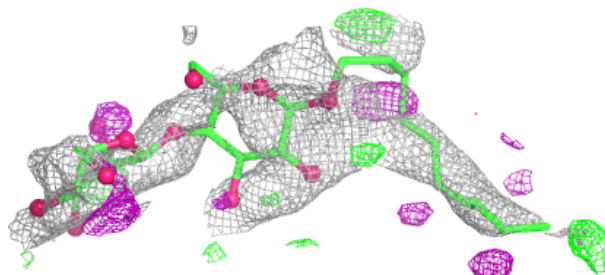
**Electron density around DMU K 104:**

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

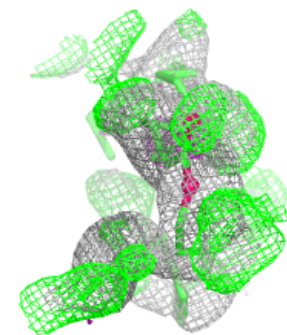
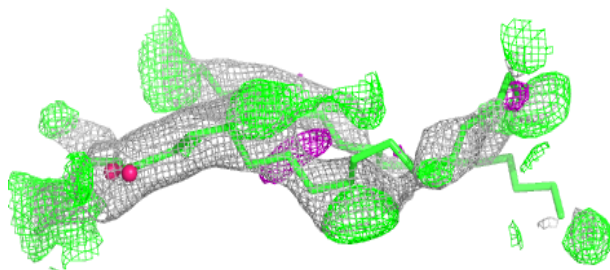
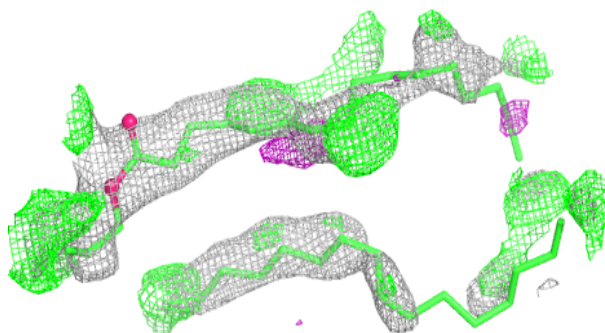


Electron density around DMU X 101:

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

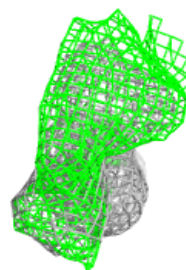
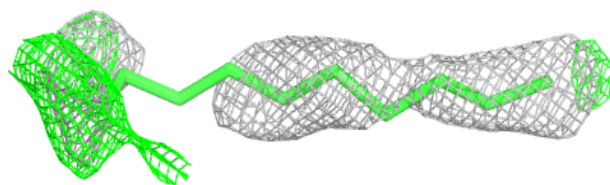
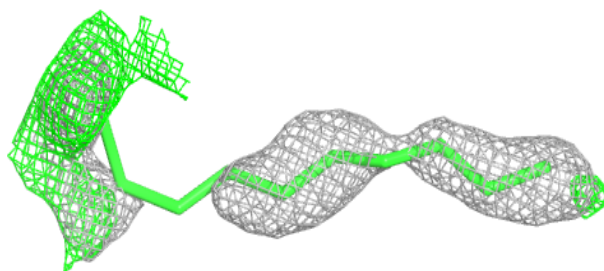
**Electron density around PGV C 306:**

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



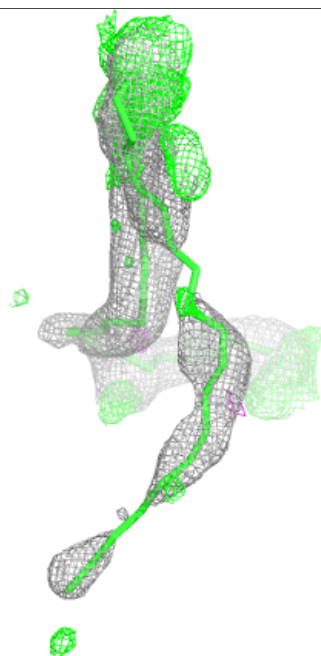
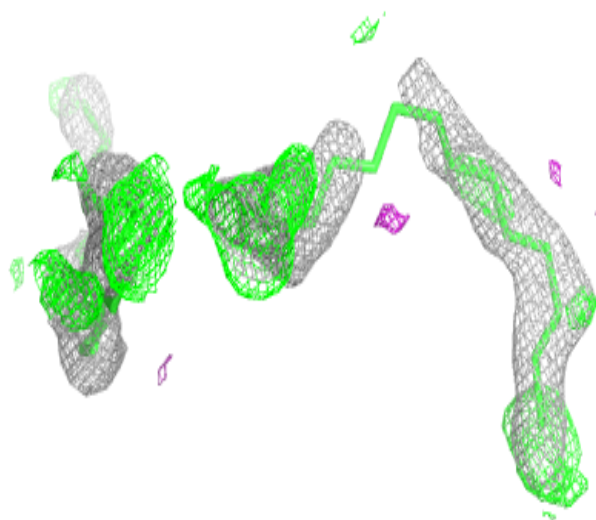
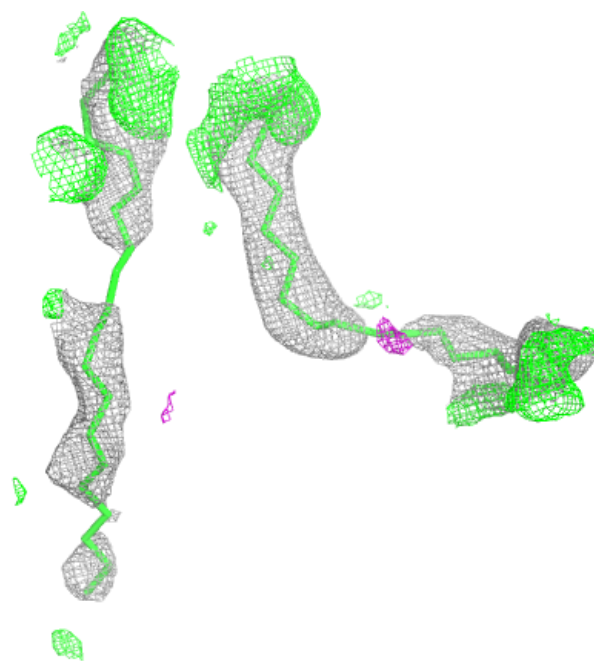
Electron density around DMU X 104:

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



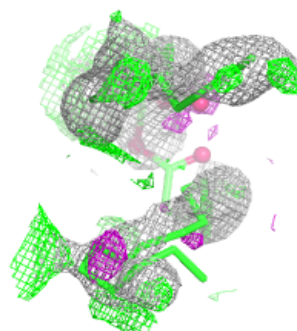
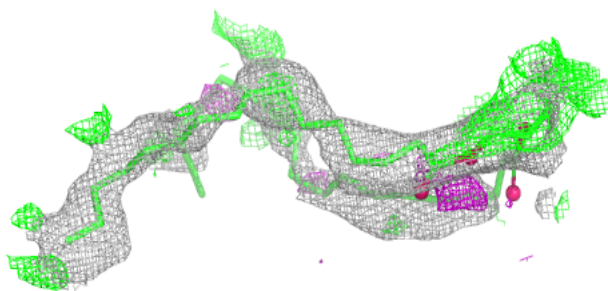
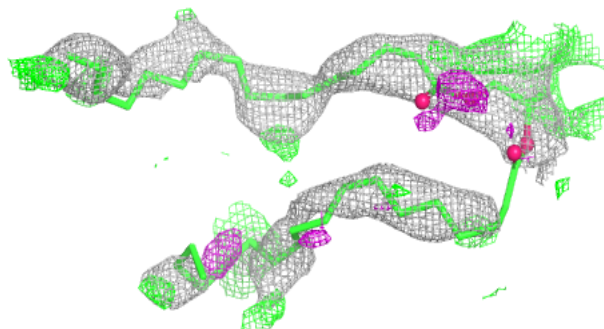
Electron density around PEK C 305:

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

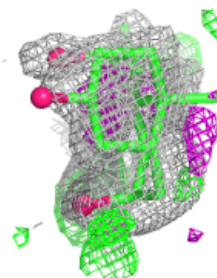
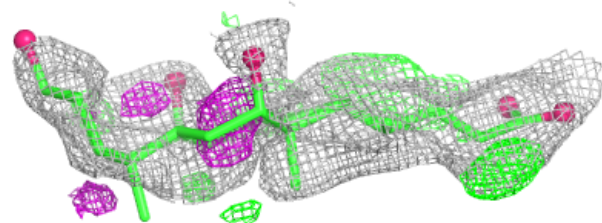
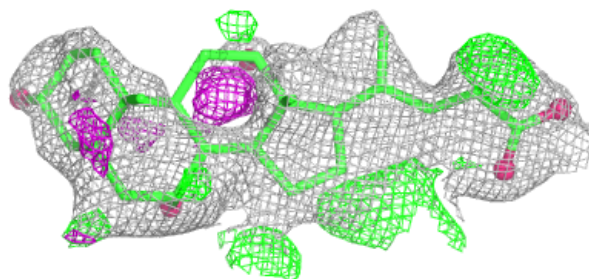


Electron density around PGV P 302:

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

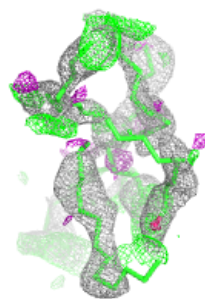
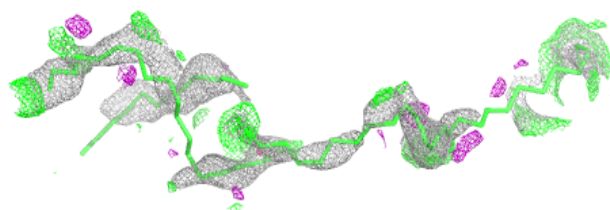
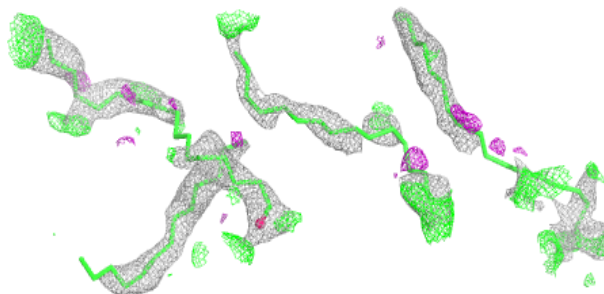
**Electron density around CHD P 306:**

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



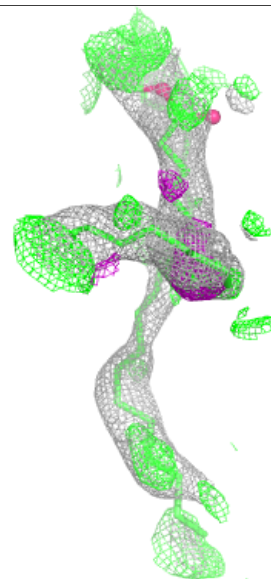
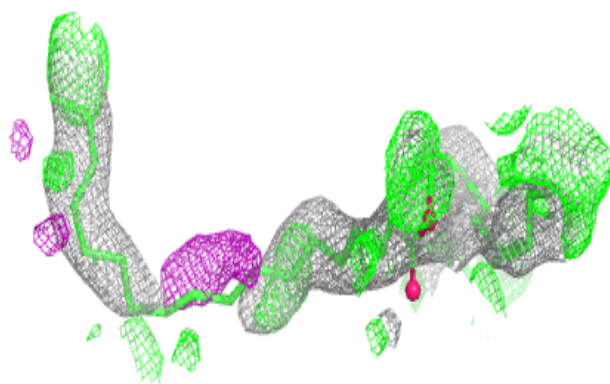
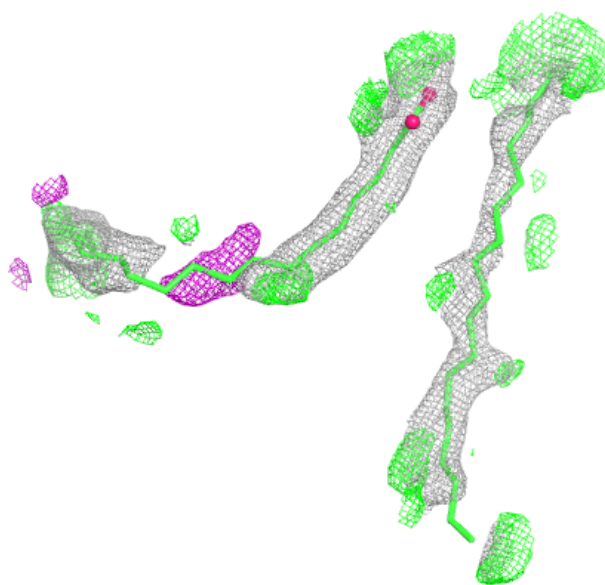
Electron density around CDL G 102:

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



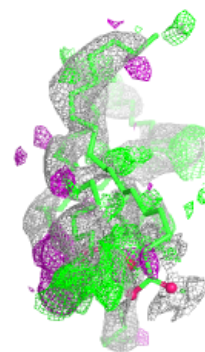
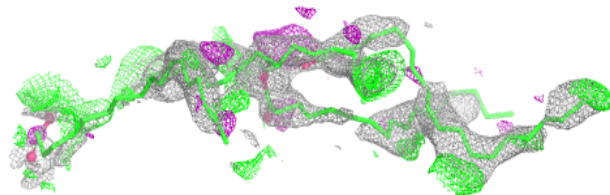
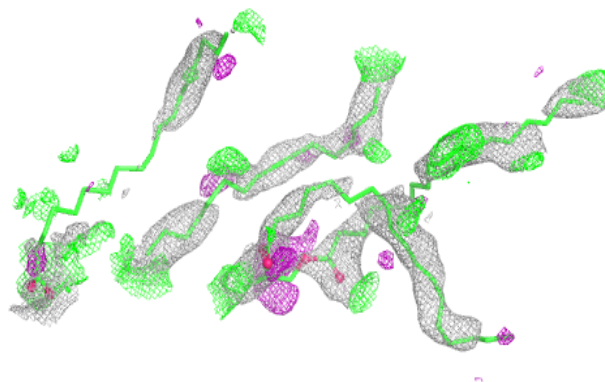
Electron density around PEK P 309:

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

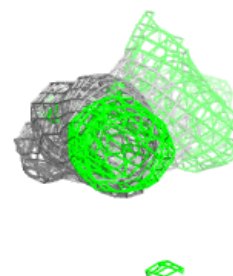
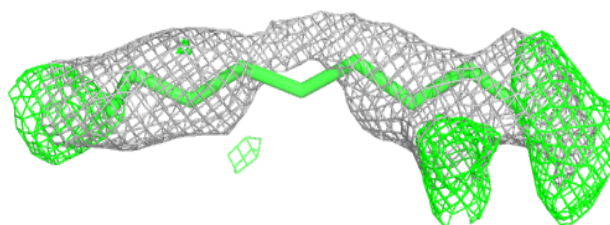
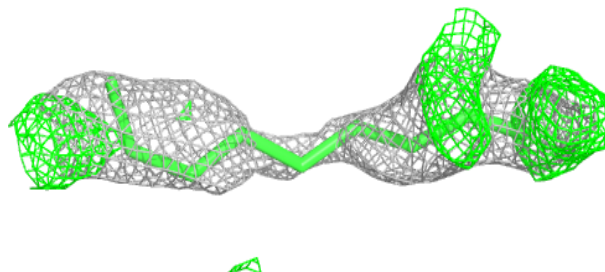


Electron density around CDL T 101:

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

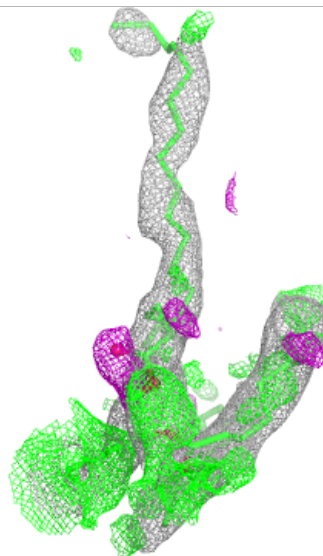
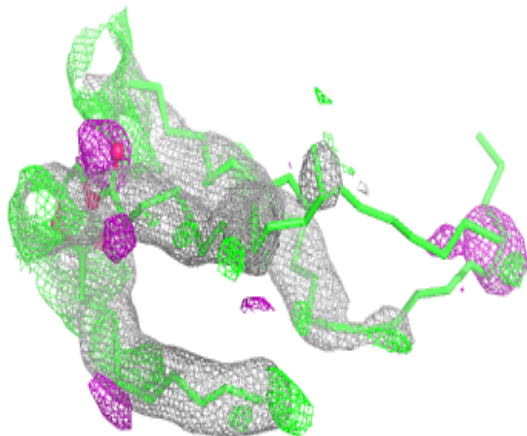
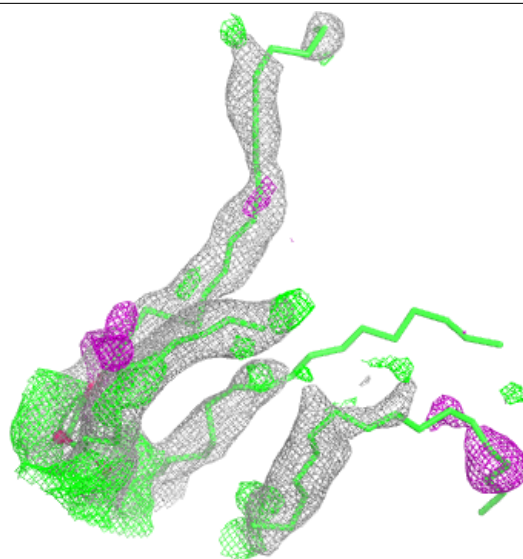
**Electron density around DMU X 103:**

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



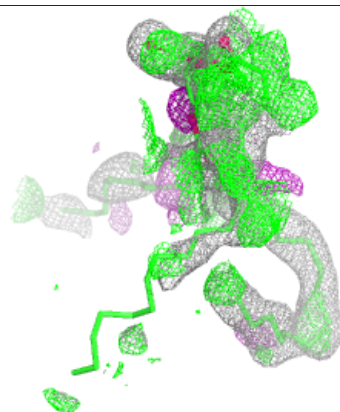
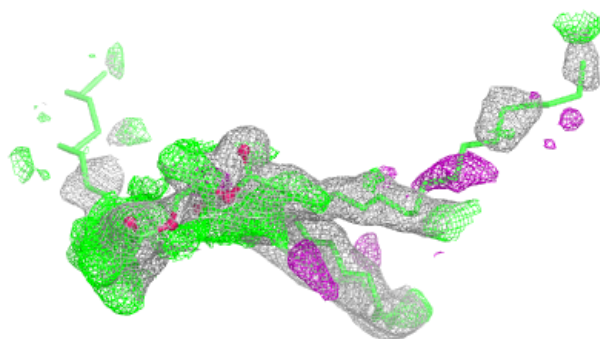
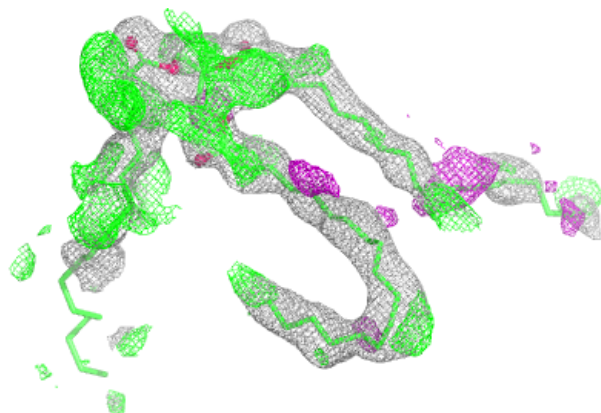
Electron density around CDL P 305:

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

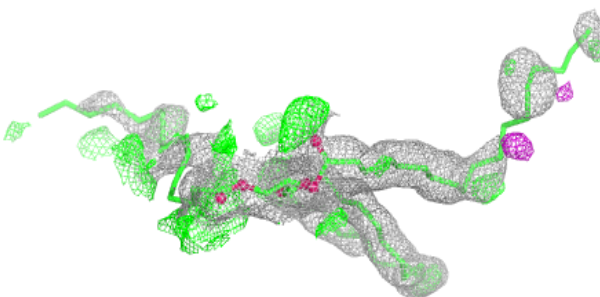
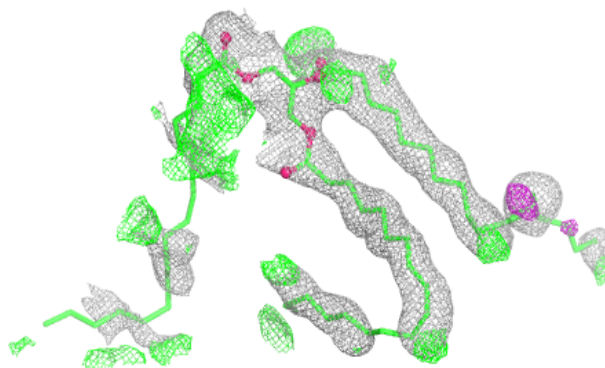


Electron density around TGL D 201:

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

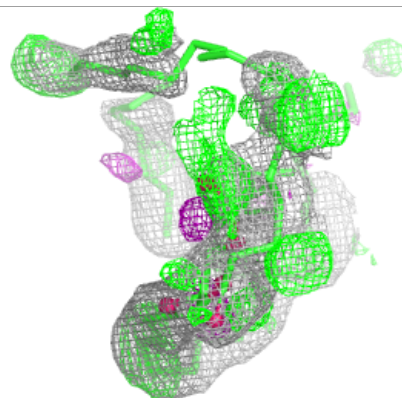
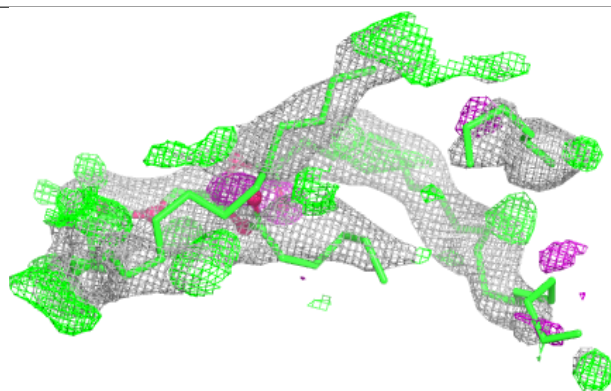
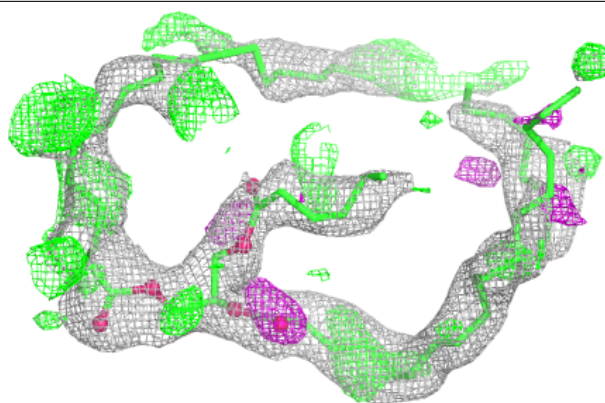
**Electron density around TGL Q 201:**

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

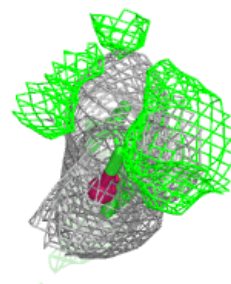
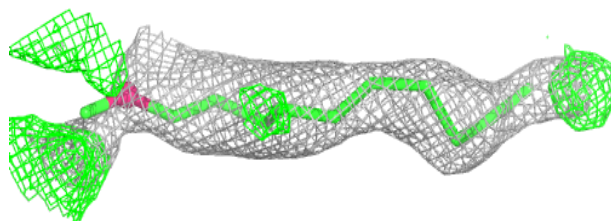
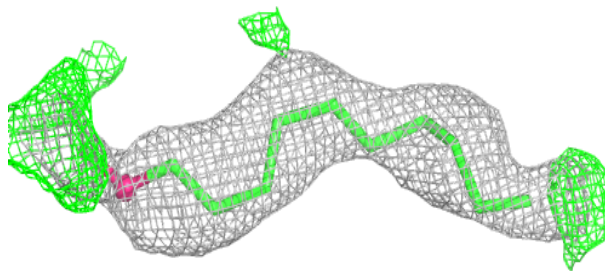


Electron density around TGL O 301:

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

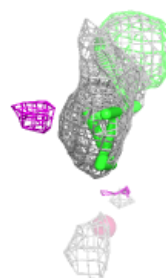
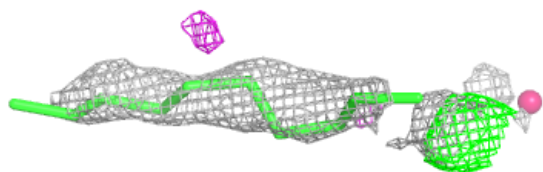
**Electron density around DMU D 202:**

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

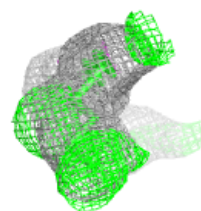
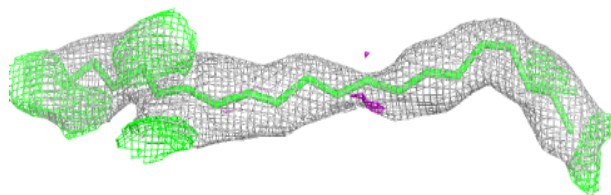
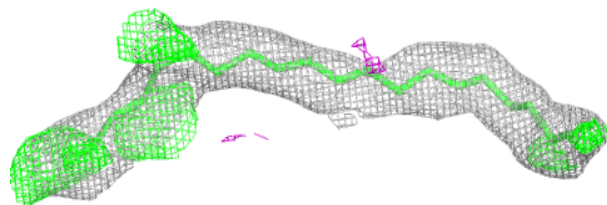


Electron density around DMU X 105:

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

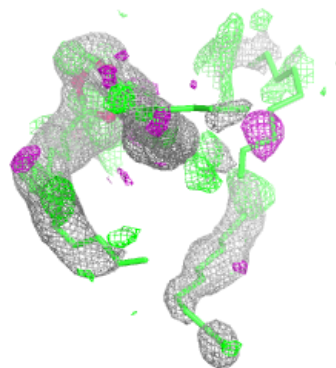
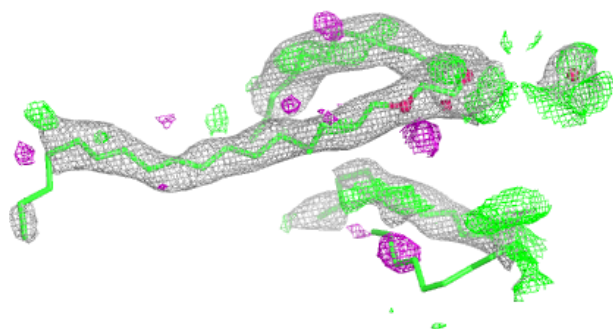
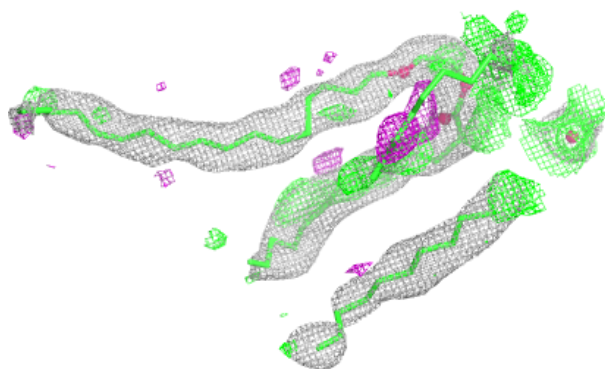
**Electron density around PEK P 301:**

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

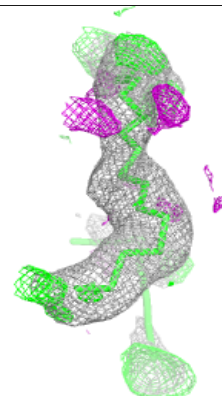
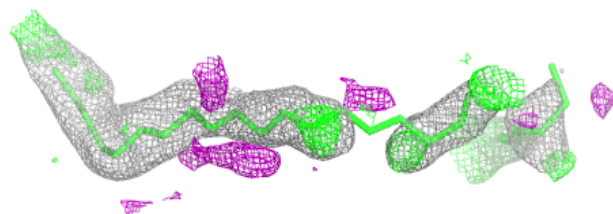
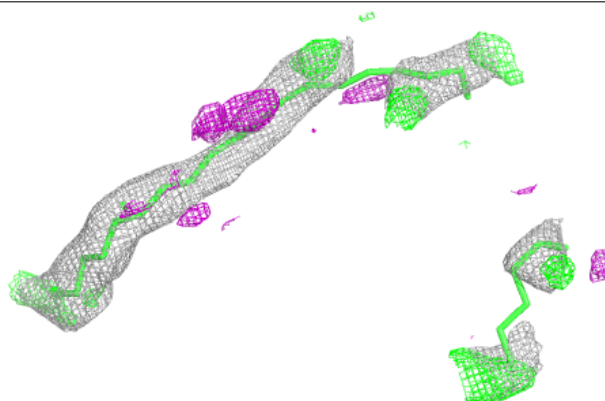


Electron density around CDL C 303:

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

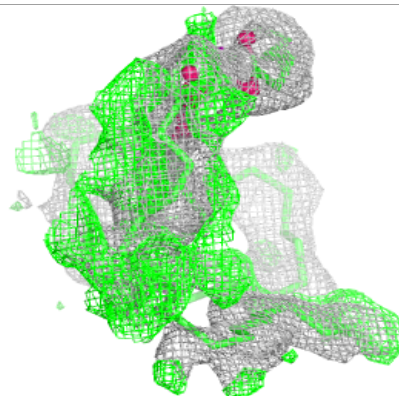
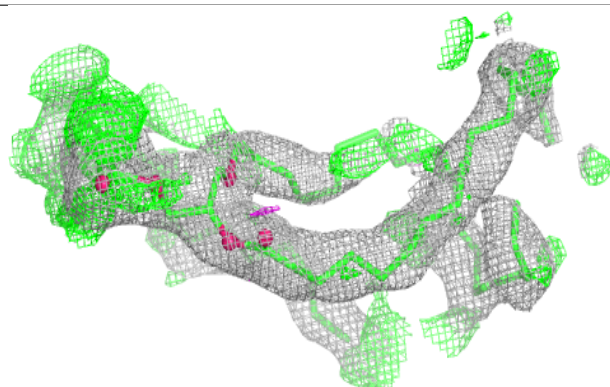
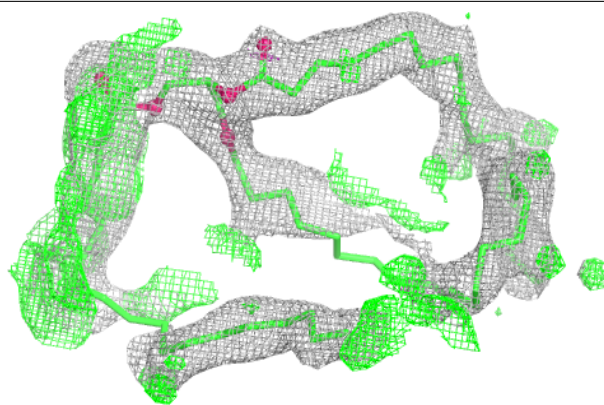
**Electron density around PEK C 307:**

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

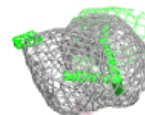
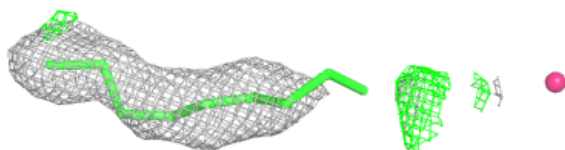
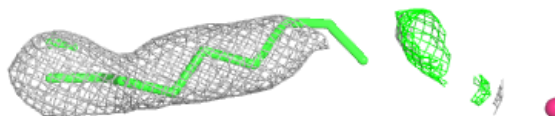


Electron density around TGL A 608:

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

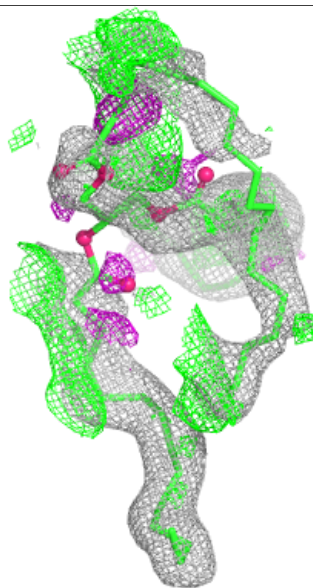
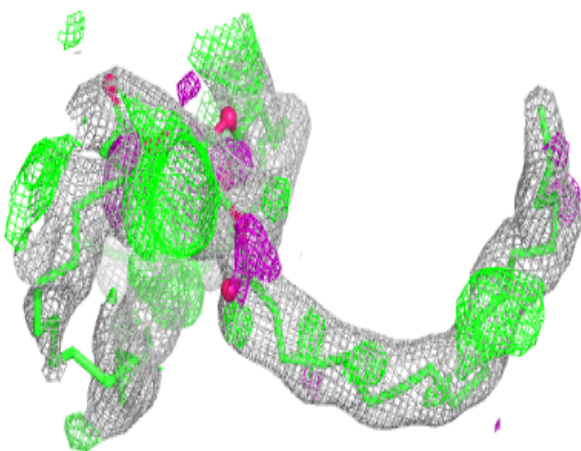
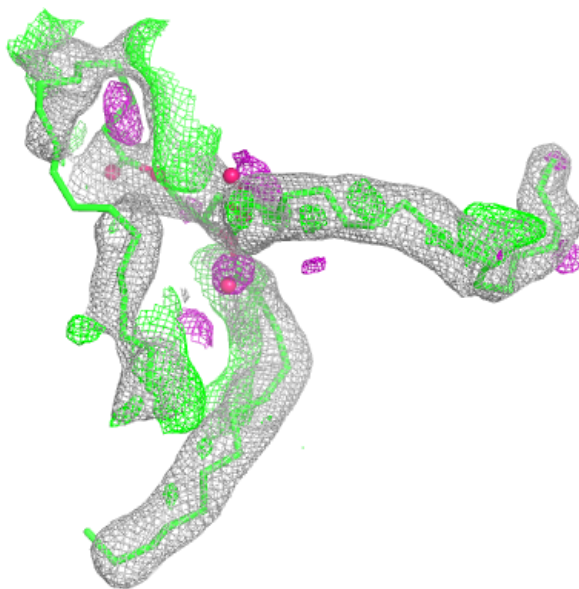
**Electron density around DMU K 101:**

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



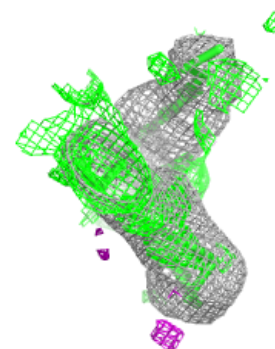
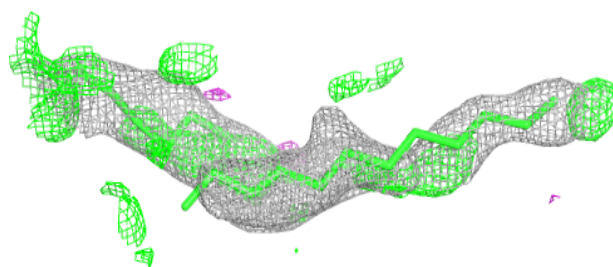
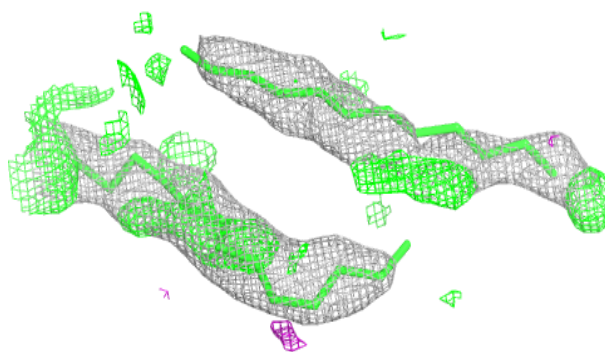
Electron density around TGL L 101:

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

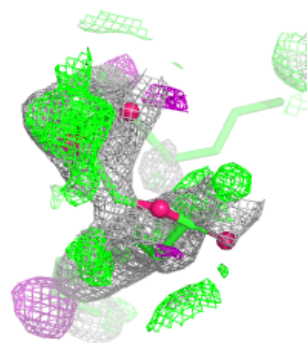
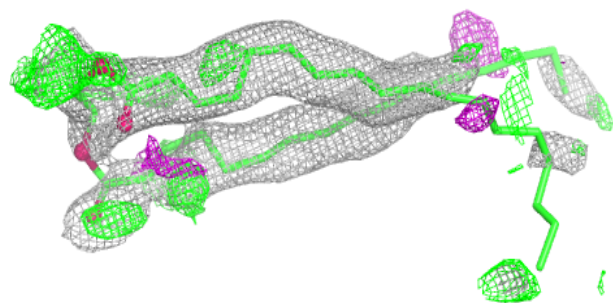
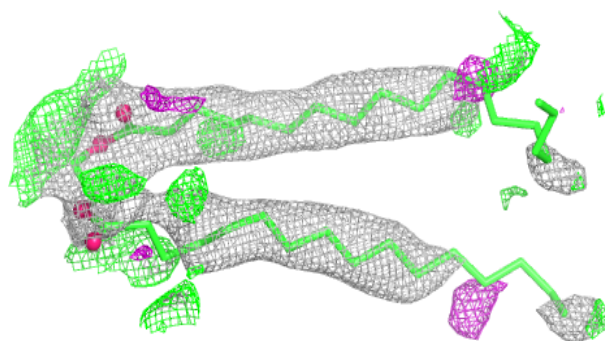


Electron density around PSC A 609:

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

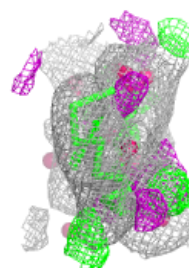
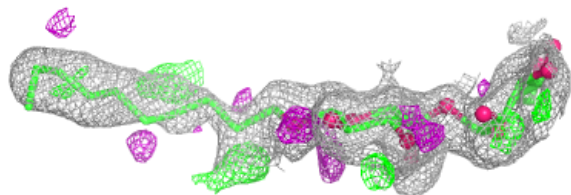
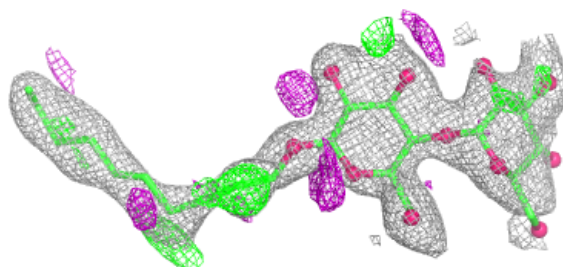
**Electron density around PGV N 606:**

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

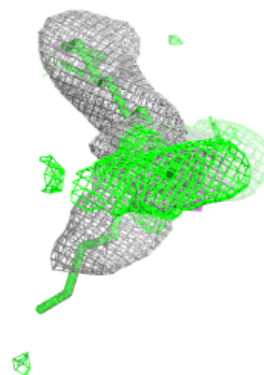
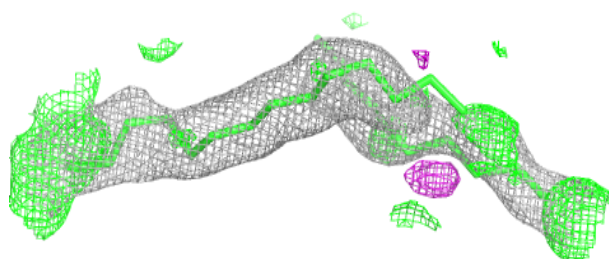
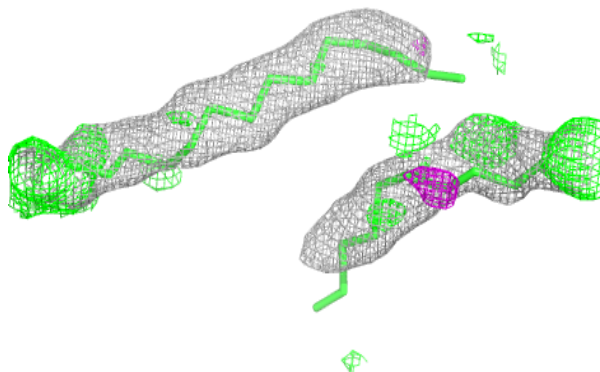


Electron density around DMU P 303:

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

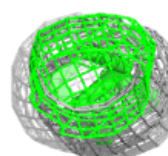
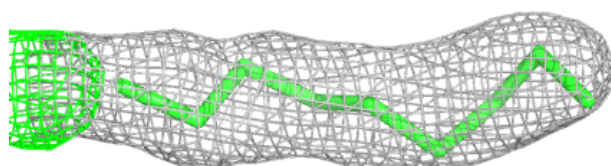
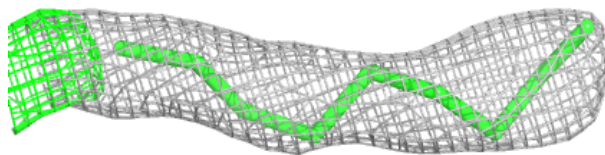
**Electron density around PSC O 303:**

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



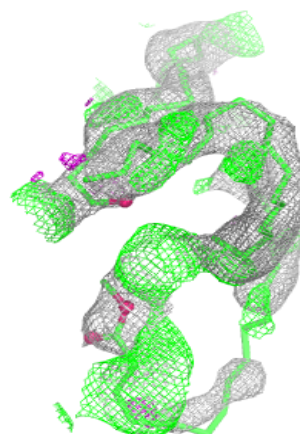
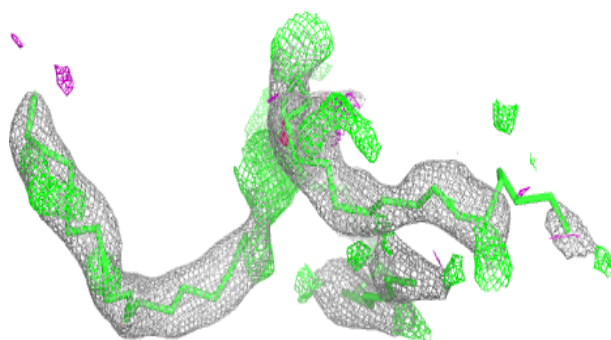
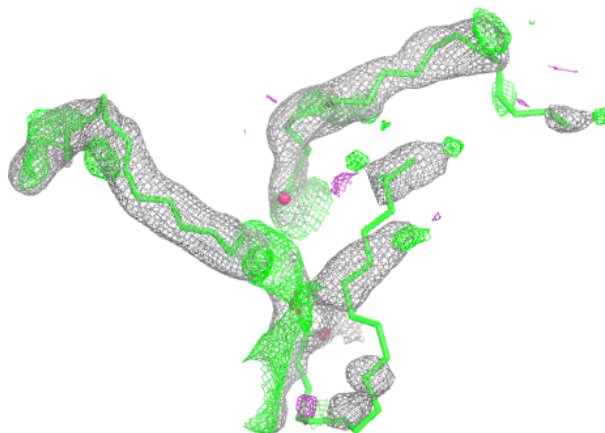
Electron density around DMU W 101:

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



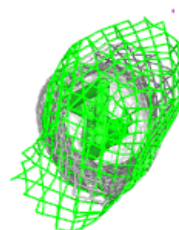
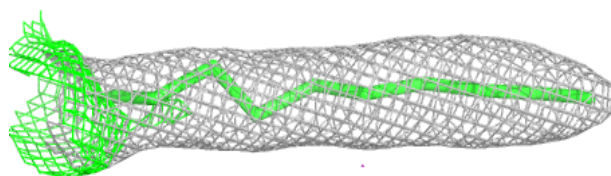
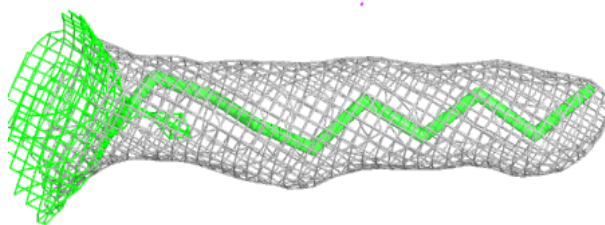
Electron density around TGL N 608:

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

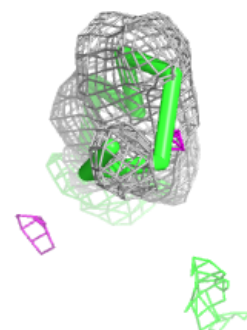
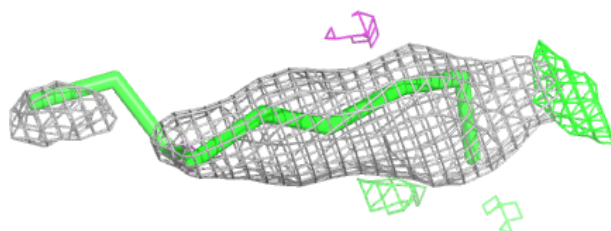
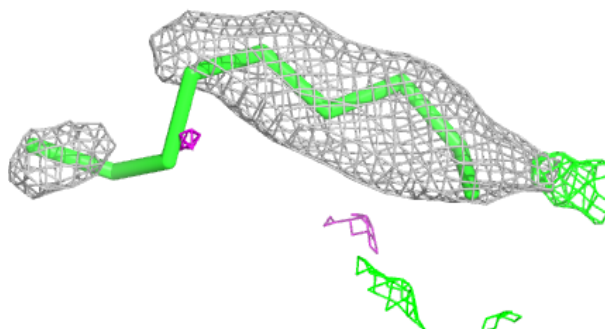


Electron density around DMU O 304:

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

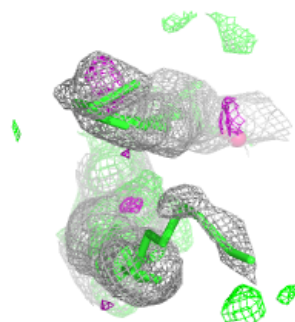
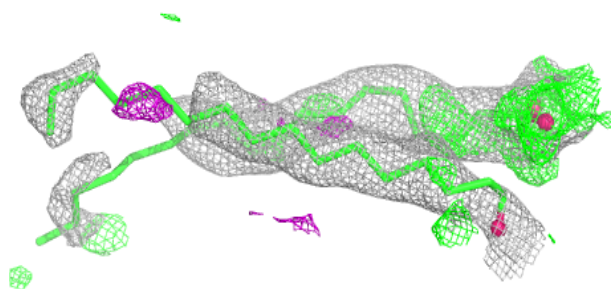
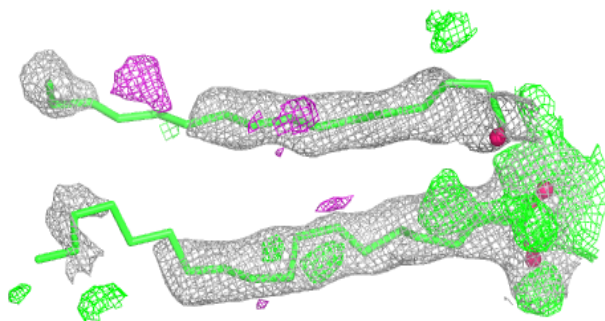
**Electron density around DMU K 102:**

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

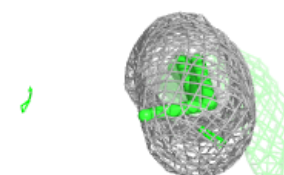
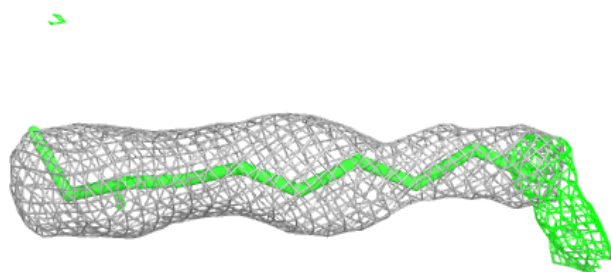
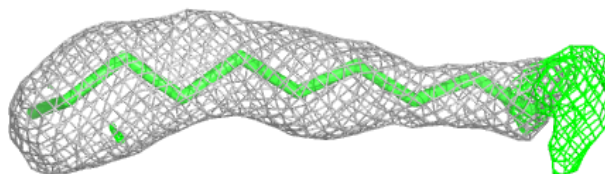


Electron density around PGV A 607:

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

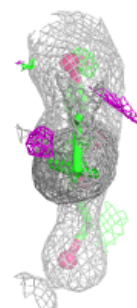
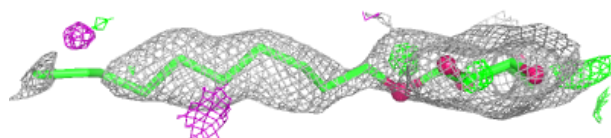
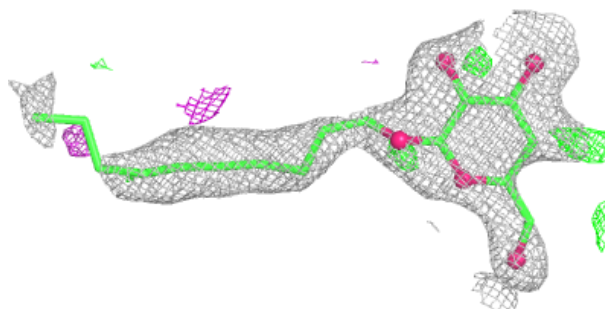
**Electron density around DMU X 102:**

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

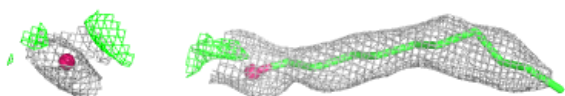
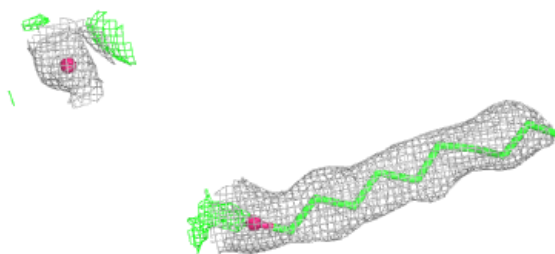


Electron density around DMU L 102:

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

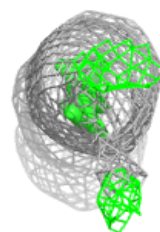
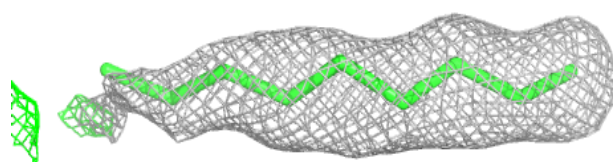
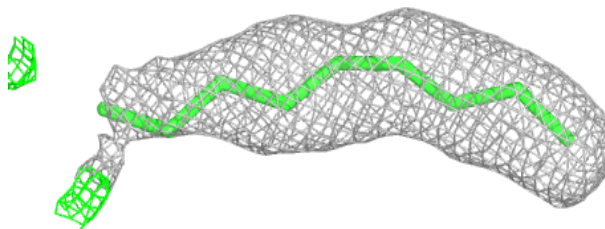
**Electron density around DMU J 102:**

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

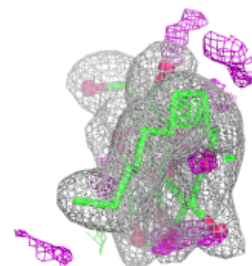
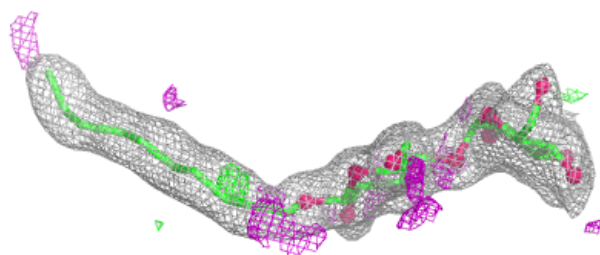
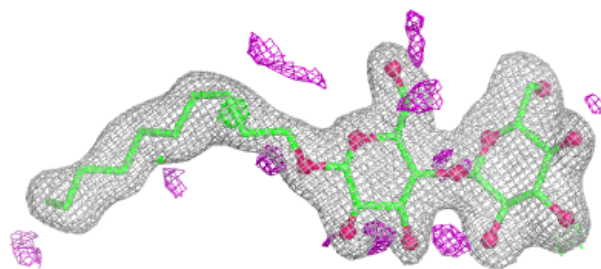


Electron density around DMU K 106:

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

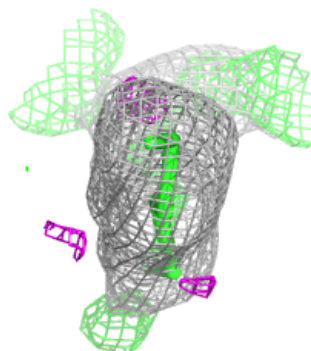
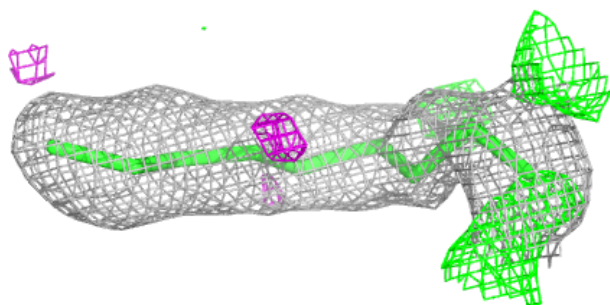
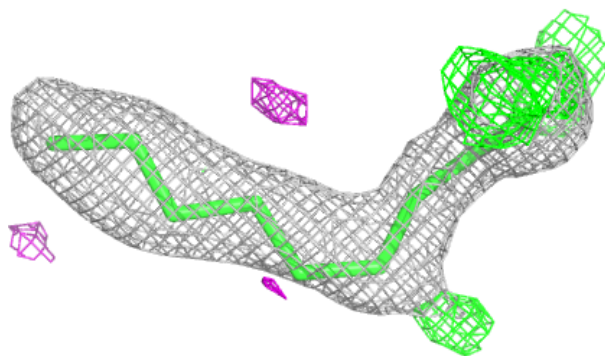
**Electron density around DMU Z 101:**

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

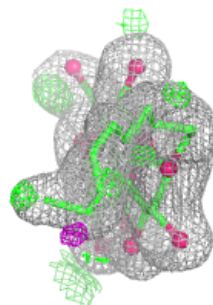
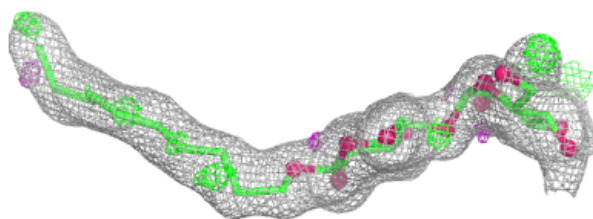
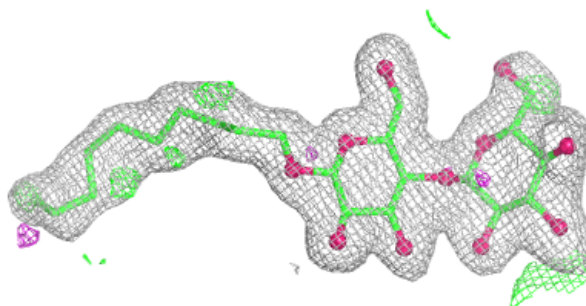


Electron density around DMU C 301:

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

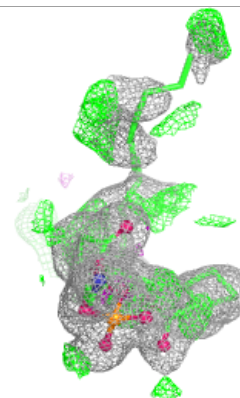
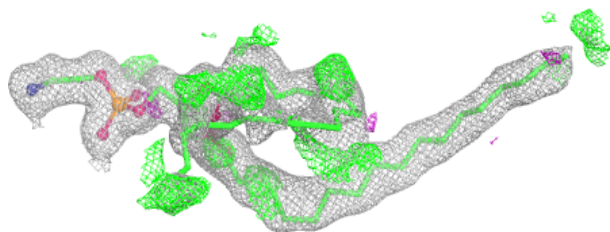
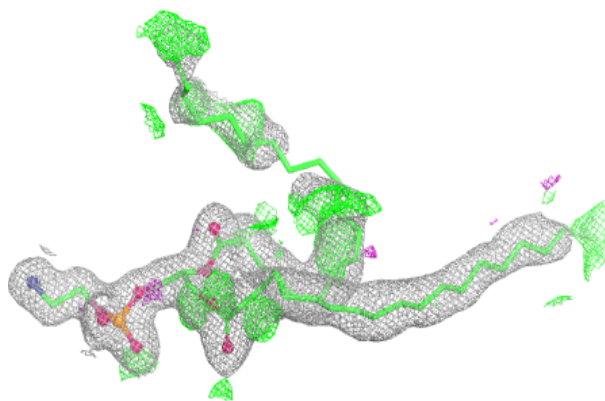
**Electron density around DMU M 101:**

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

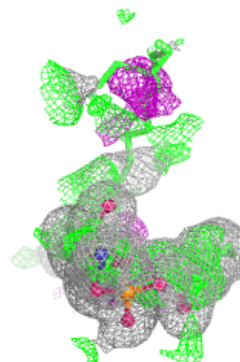
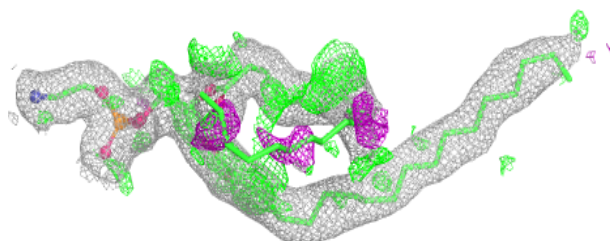
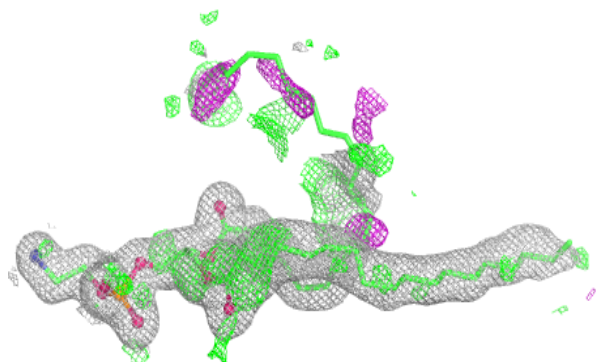


Electron density around PEK P 308:

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

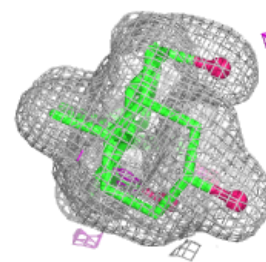
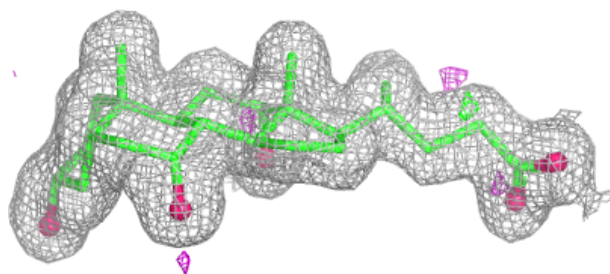
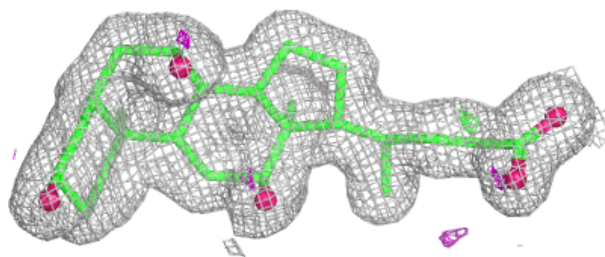
**Electron density around PEK G 101:**

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

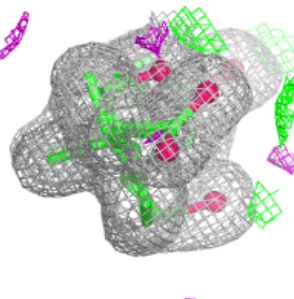
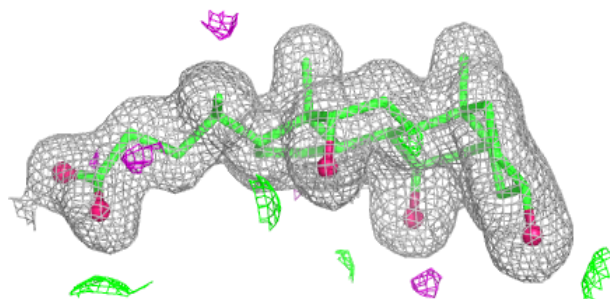
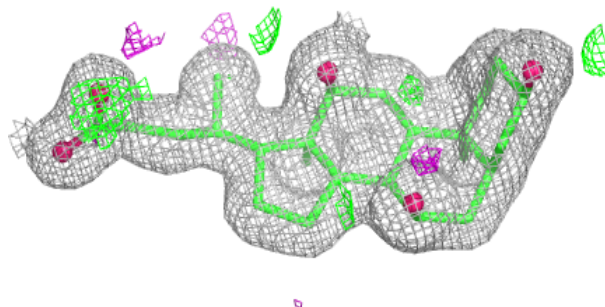


Electron density around CHD C 304:

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

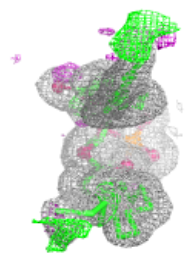
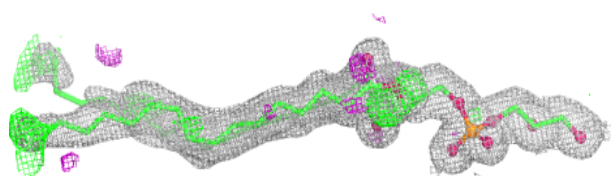
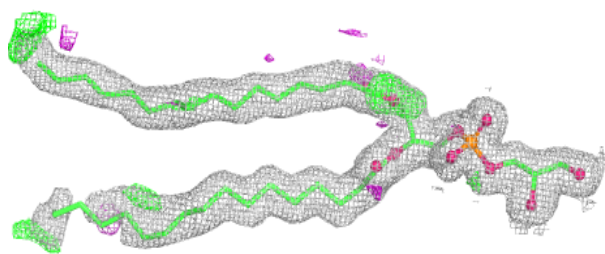
**Electron density around CHD P 307:**

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

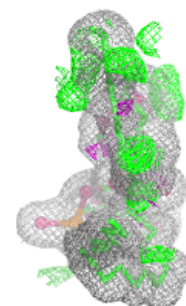
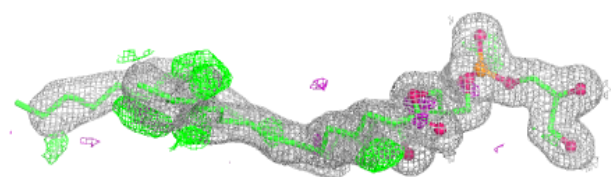
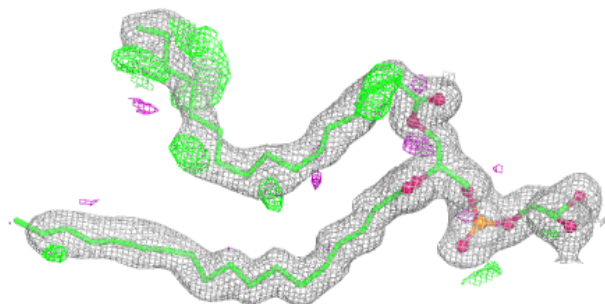


Electron density around PGV P 304:

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

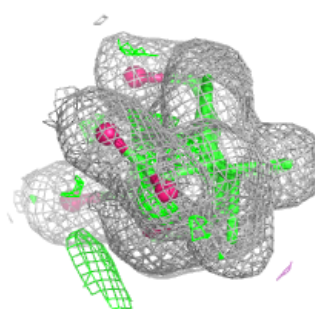
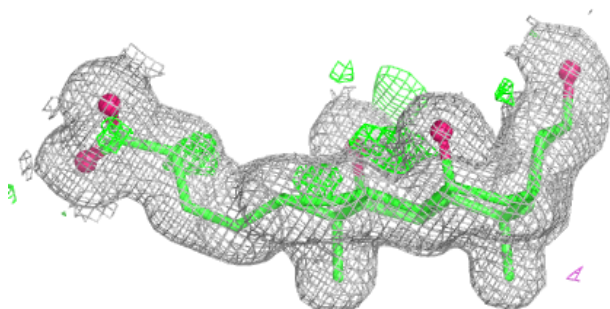
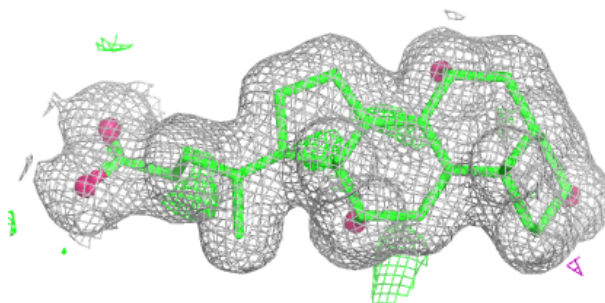
**Electron density around PGV N 607:**

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

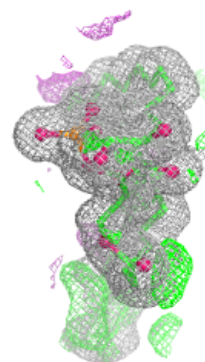
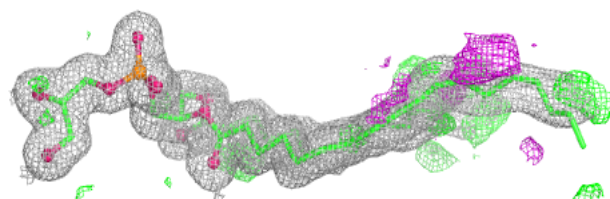
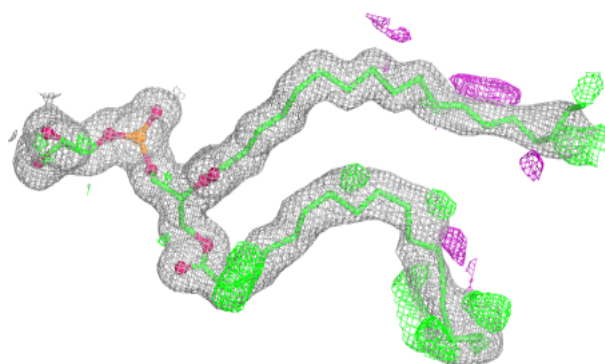


Electron density around CHD B 302:

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

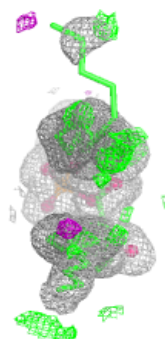
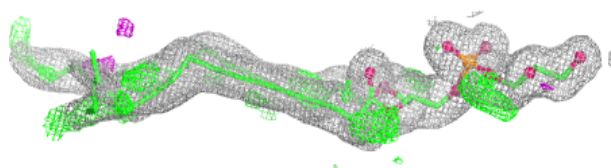
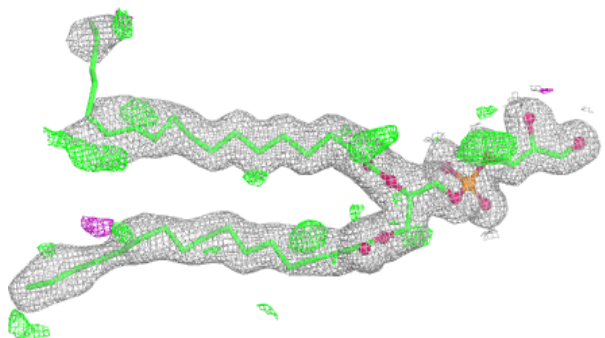
**Electron density around PGV A 606:**

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

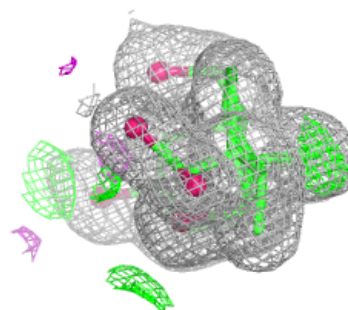
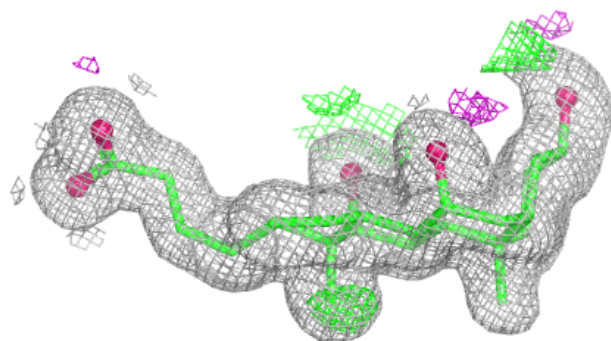
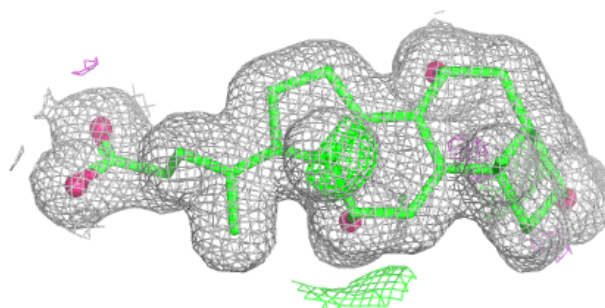


Electron density around PGV C 302:

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

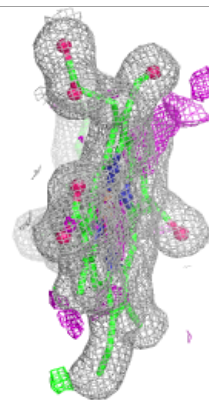
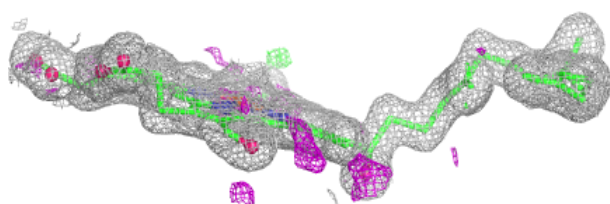
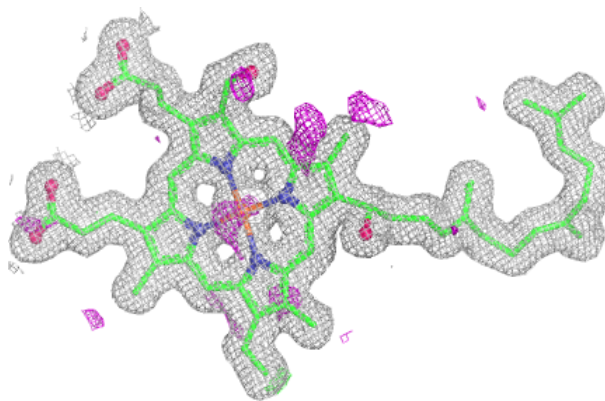
**Electron density around CHD G 103:**

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

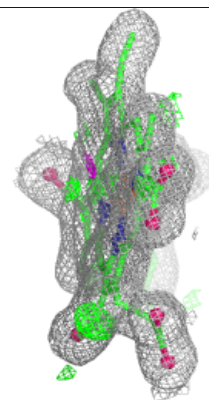
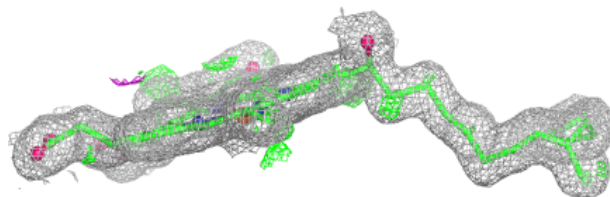
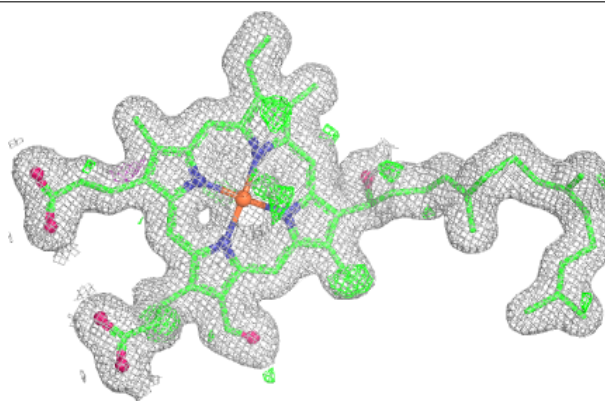


Electron density around HEA A 602:

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

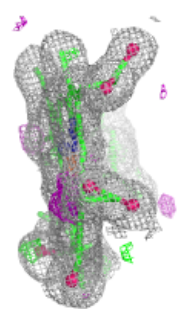
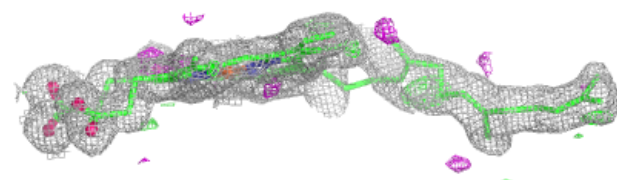
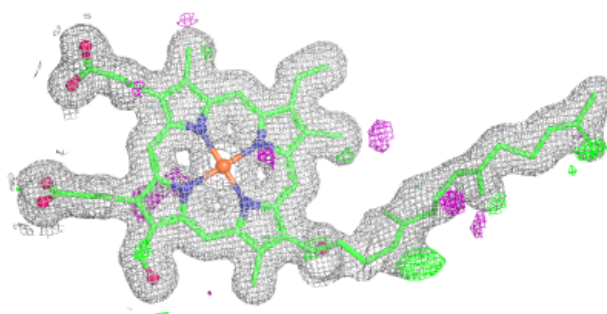
**Electron density around HEA N 602:**

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

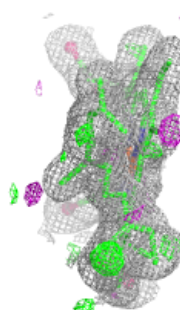
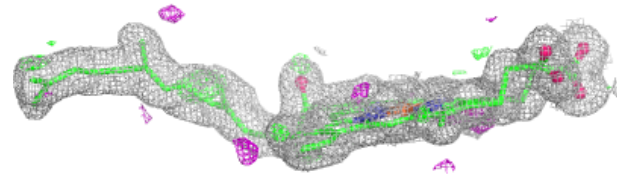
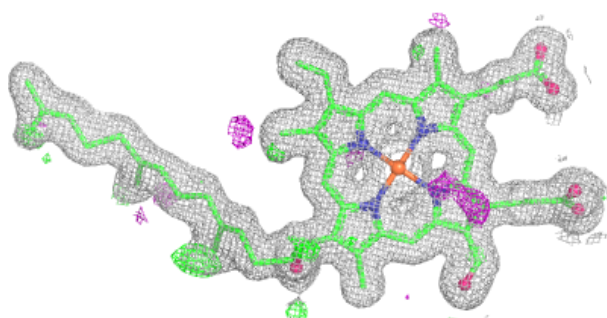


Electron density around HEA A 601 (B):

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

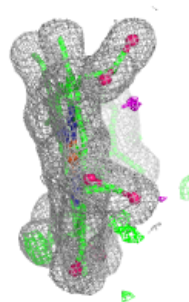
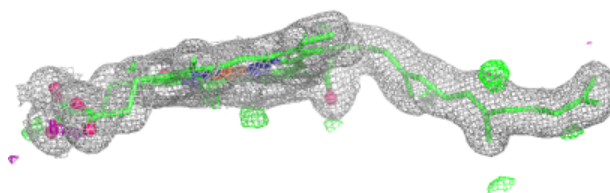
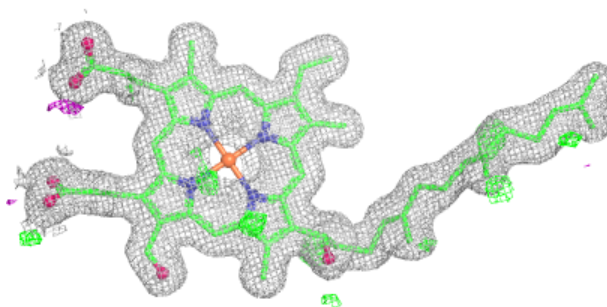
**Electron density around HEA A 601 (A):**

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

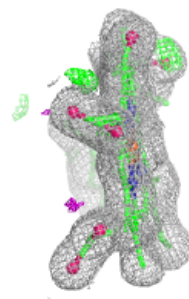
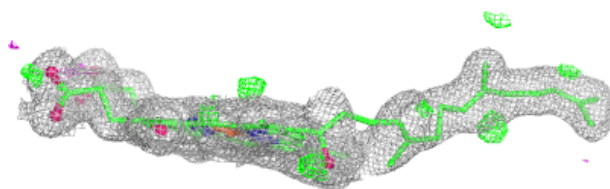
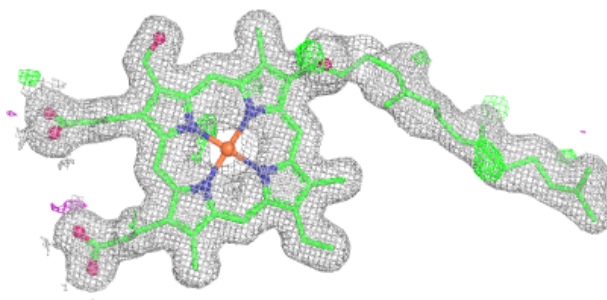


Electron density around HEA N 601 (A):

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

**Electron density around HEA N 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.