



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 06:19 PM UTC

PDB ID : 3ABK / pdb_00003abk
Title : Bovine heart cytochrome c oxidase at the NO-bound fully reduced state (50K)
Authors : Ohta, K.; Muramoto, K.; Shinzawa-Itoh, K.; Yamashita, E.; Yoshikawa, S.;
Tsukihara, T.
Deposited on : 2009-12-16
Resolution : 2.00 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

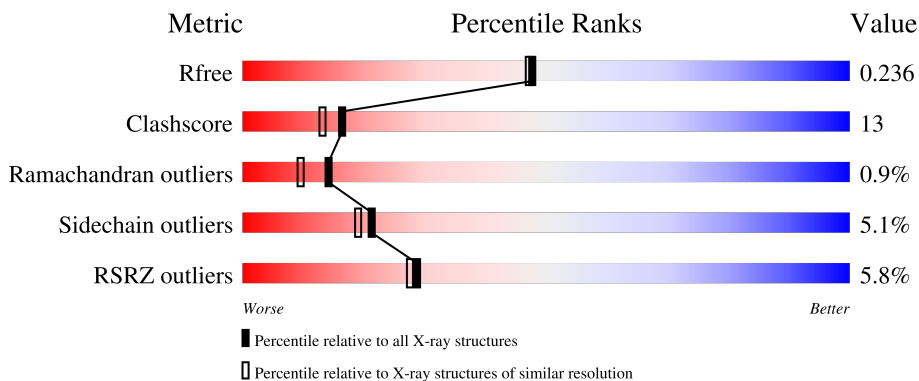
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	514	 68% 27% 5%
1	N	514	 69% 27% 4% ..
2	B	227	 69% 26% 4% ..
2	O	227	 67% 27% 4% ..
3	C	261	 77% 20% ...

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	CHD	C	271	X	-	-	-
23	CHD	J	60	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	CHD	P	1271	X	-	-	-
23	CHD	P	1525	X	-	-	-
23	CHD	W	1059	X	-	-	-
24	UNX	C	262	-	-	-	X
24	UNX	P	262	-	-	-	X
26	CDL	G	269	-	-	X	-
26	CDL	P	1270	-	-	X	-
26	CDL	T	1269	-	-	X	-
27	DMU	C	272	X	-	-	-
27	DMU	M	526	X	-	-	-
27	DMU	P	272	X	-	-	-
27	DMU	Z	1526	X	-	-	-

2 Entry composition [i](#)

There are 29 unique types of molecules in this entry. The entry contains 32382 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
			Total	C	N	O	S			
1	A	514	Total	C	N	O	S	0	5	0
			4060	2712	628	684	36			
1	N	514	Total	C	N	O	S	0	5	0
			4060	2712	628	684	36			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			
4	Q	144	Total	C	N	O	S	0	0	0
			1195	777	196	218	4			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			
6	S	98	Total	C	N	O	S	0	0	0
			748	464	134	145	5			

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

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

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

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

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

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

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

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.

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

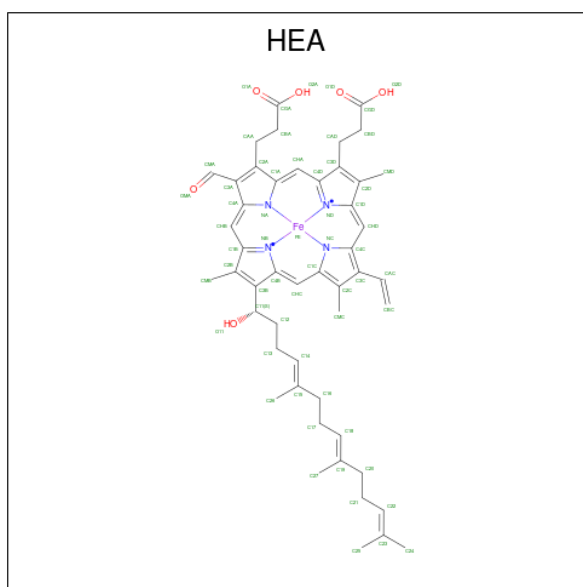
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C.

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.

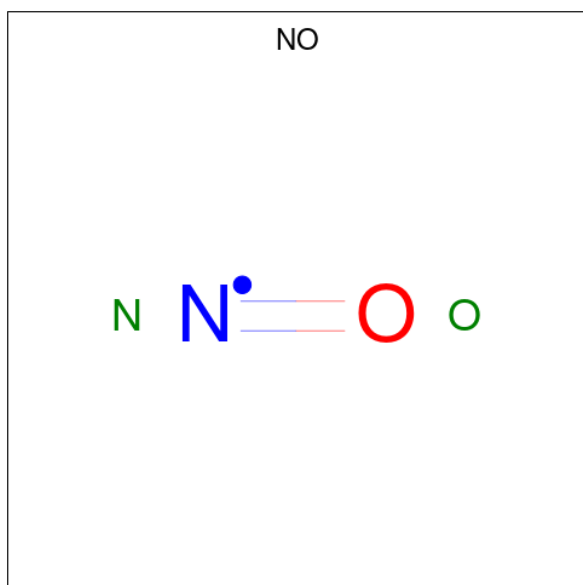
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	43	Total	C	N	O	0	0	0
			335	223	53	59			
13	Z	43	Total	C	N	O	0	0	0
			335	223	53	59			

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



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

- Molecule 15 is NITRIC OXIDE (CCD ID: NO) (formula: NO).



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

- Molecule 16 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

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

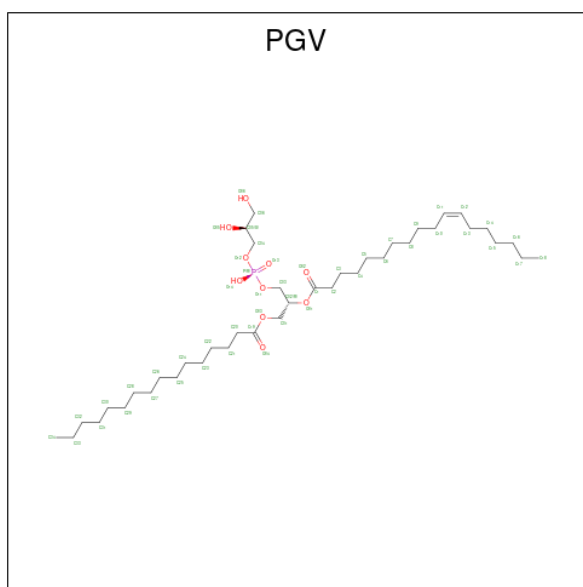
- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 18 is SODIUM ION (CCD ID: NA) (formula: Na).

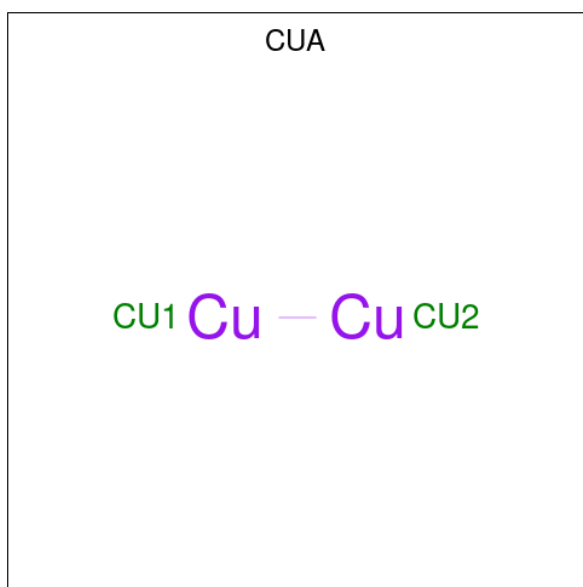
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	A	1	Total Na 1 1	0	0
18	N	1	Total Na 1 1	0	0

- Molecule 19 is (1R)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P).



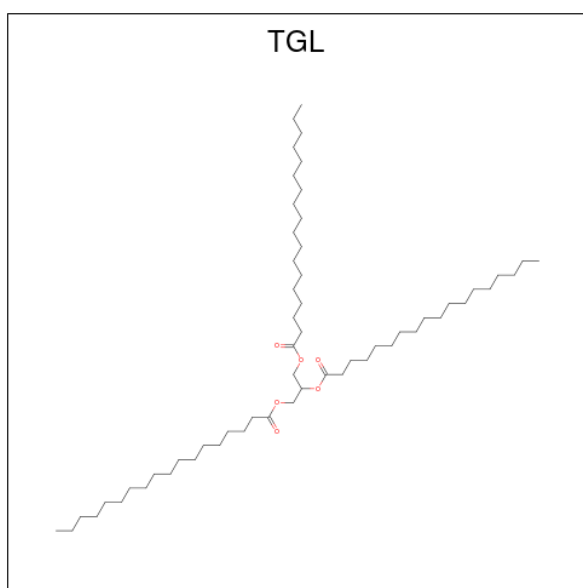
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
19	A	1	51	40	10	1	0	0
19	A	1	51	40	10	1	0	0
19	C	1	51	40	10	1	0	0
19	C	1	51	40	10	1	0	0
19	N	1	51	40	10	1	0	0
19	N	1	51	40	10	1	0	0
19	P	1	51	40	10	1	0	0
19	U	1	51	40	10	1	0	0

- Molecule 20 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



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

- Molecule 21 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: $C_{57}H_{110}O_6$).



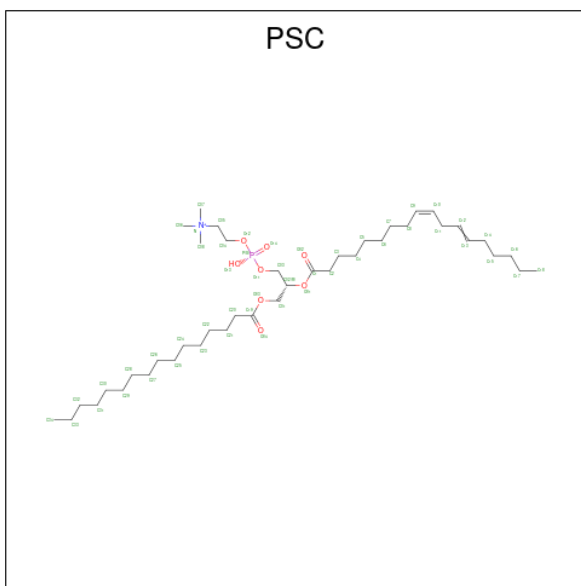
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
21	B	1	Total C O 63 57 6	0	0
21	D	1	Total C O 63 57 6	0	0

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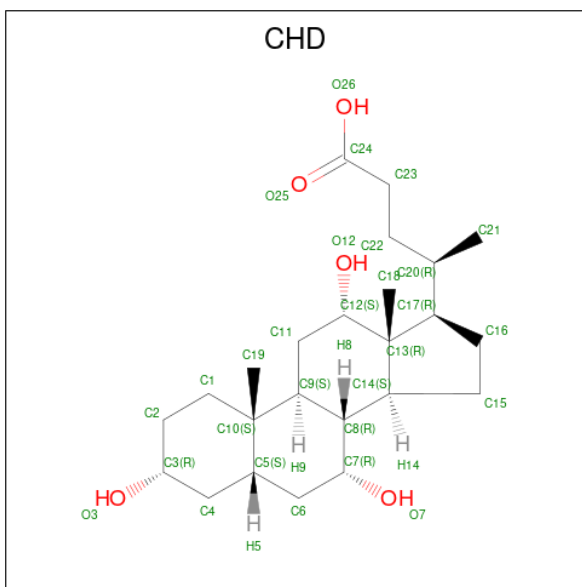
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	L	1	Total	C	O	0	0
			63	57	6		
21	N	1	Total	C	O	0	0
			63	57	6		
21	O	1	Total	C	O	0	0
			63	57	6		
21	Y	1	Total	C	O	0	0
			63	57	6		

- Molecule 22 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (CCD ID: PSC) (formula: $C_{42}H_{81}NO_8P$).



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

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

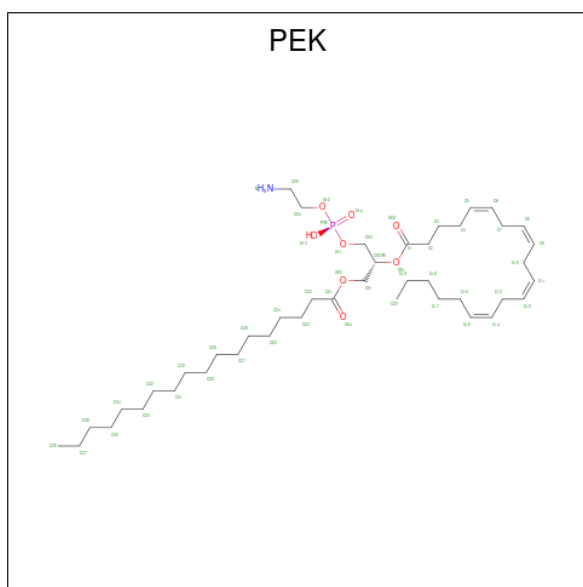


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	B	1	Total C O 29 24 5	0	0
23	C	1	Total C O 29 24 5	0	0
23	C	1	Total C O 29 24 5	0	0
23	J	1	Total C O 29 24 5	0	0
23	O	1	Total C O 29 24 5	0	0
23	P	1	Total C O 29 24 5	0	0
23	P	1	Total C O 29 24 5	0	0
23	W	1	Total C O 29 24 5	0	0

- Molecule 24 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

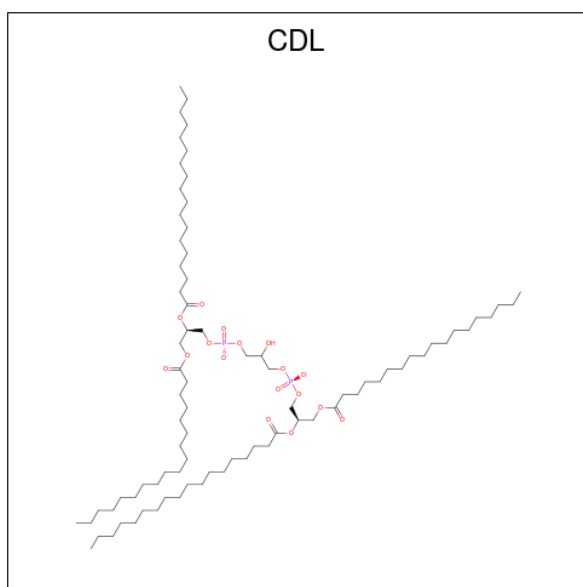
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	C	1	Total X 1 1	0	0
24	P	1	Total X 1 1	0	0

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



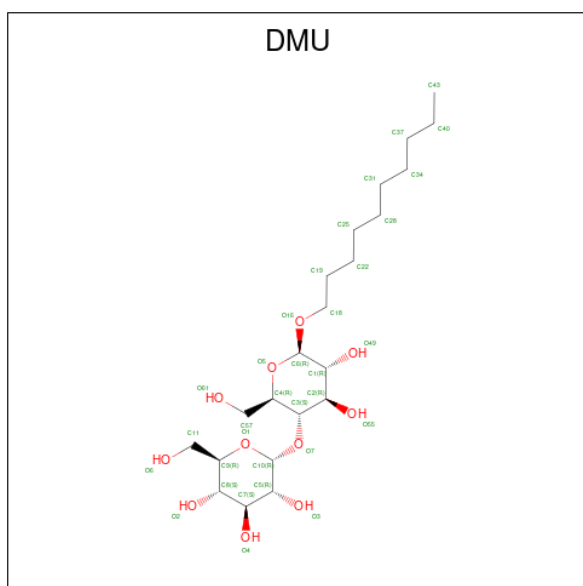
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
25	C	1	Total 53	43	1	8	1	0	0
25	C	1	Total 53	43	1	8	1	0	0
25	G	1	Total 53	43	1	8	1	0	0
25	P	1	Total 53	43	1	8	1	0	0
25	T	1	Total 53	43	1	8	1	0	0
25	T	1	Total 53	43	1	8	1	0	0

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



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

- Molecule 27 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: $C_{22}H_{42}O_{11}$).



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

- Molecule 28 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 29 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	A	217	Total	O	0	0
			217	217		
29	B	127	Total	O	0	0
			127	127		
29	C	93	Total	O	0	0
			93	93		
29	D	86	Total	O	0	0
			86	86		
29	E	52	Total	O	0	0
			52	52		
29	F	72	Total	O	0	0
			72	72		
29	G	42	Total	O	0	0
			42	42		
29	H	46	Total	O	0	0
			46	46		
29	I	31	Total	O	0	0
			31	31		
29	J	28	Total	O	0	0
			28	28		
29	K	27	Total	O	0	0
			27	27		
29	L	16	Total	O	0	0
			16	16		

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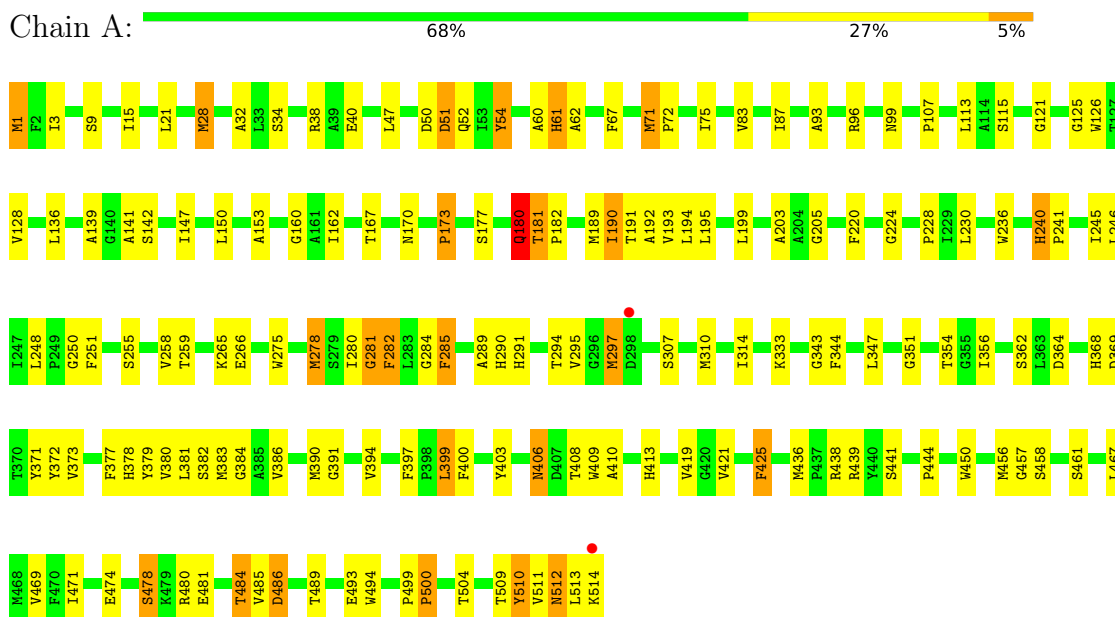
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	M	20	Total 20	O 20	0	0
29	N	207	Total 207	O 207	0	0
29	O	105	Total 105	O 105	0	0
29	P	96	Total 96	O 96	0	0
29	Q	57	Total 57	O 57	0	0
29	R	35	Total 35	O 35	0	0
29	S	63	Total 63	O 63	0	0
29	T	44	Total 44	O 44	0	0
29	U	43	Total 43	O 43	0	0
29	V	20	Total 20	O 20	0	0
29	W	17	Total 17	O 17	0	0
29	X	13	Total 13	O 13	0	0
29	Y	12	Total 12	O 12	0	0
29	Z	11	Total 11	O 11	0	0

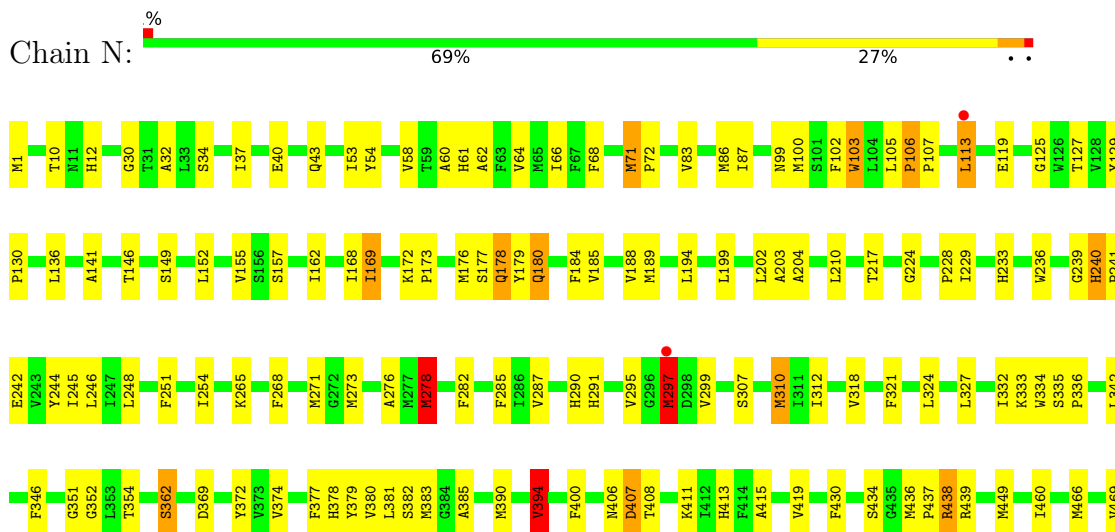
3 Residue-property plots

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

- Molecule 1: Cytochrome c oxidase subunit 1

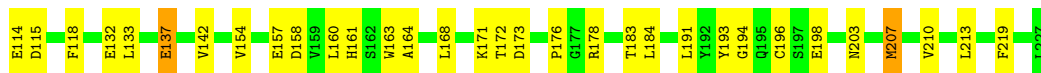


- Molecule 1: Cytochrome c oxidase subunit 1





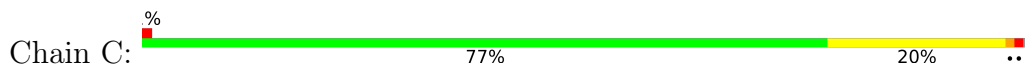
• Molecule 2: Cytochrome c oxidase subunit 2



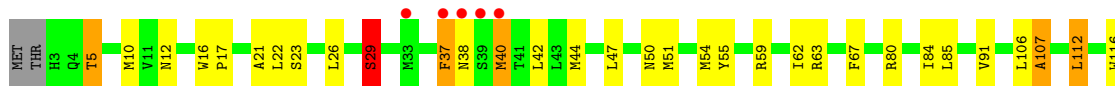
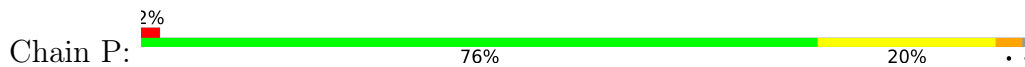
• Molecule 2: Cytochrome c oxidase subunit 2



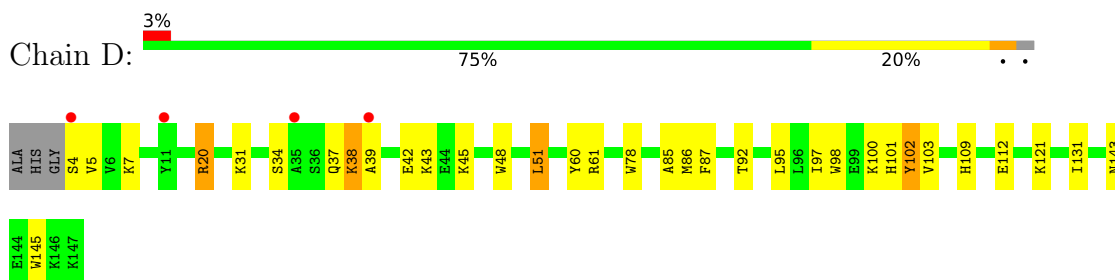
• Molecule 3: Cytochrome c oxidase subunit 3



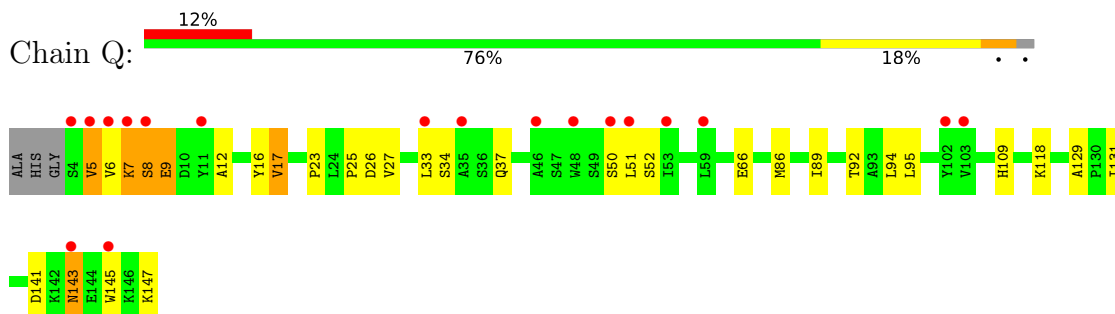
• Molecule 3: Cytochrome c oxidase subunit 3



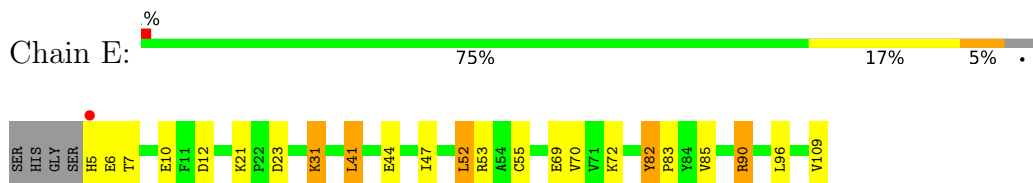
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1



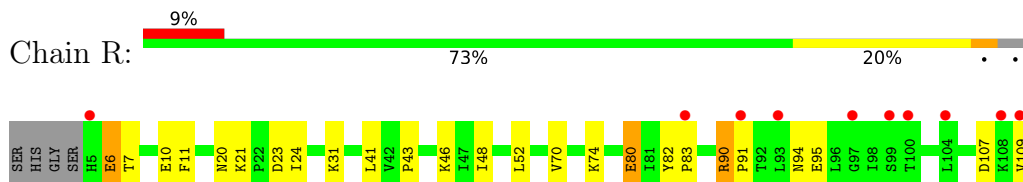
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1



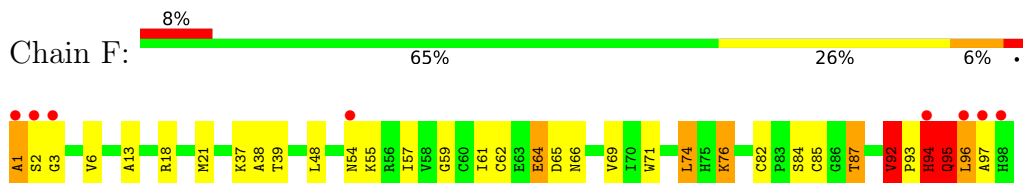
- Molecule 5: Cytochrome c oxidase subunit 5A



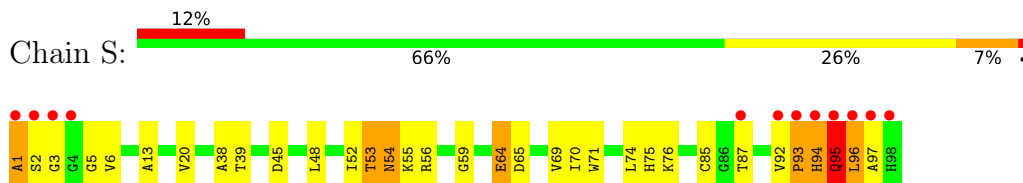
- Molecule 5: Cytochrome c oxidase subunit 5A



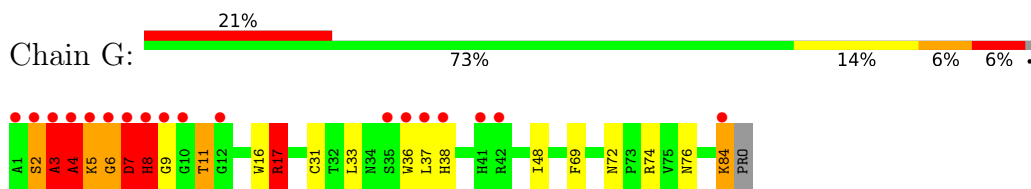
- Molecule 6: Cytochrome c oxidase subunit 5B



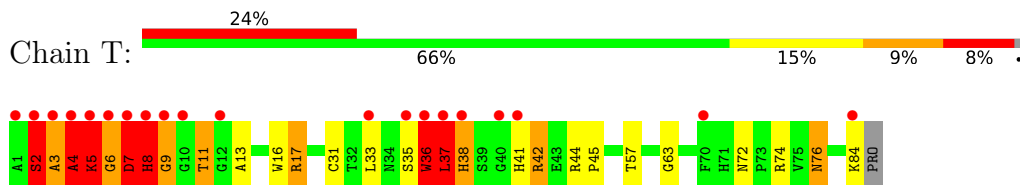
- Molecule 6: Cytochrome c oxidase subunit 5B



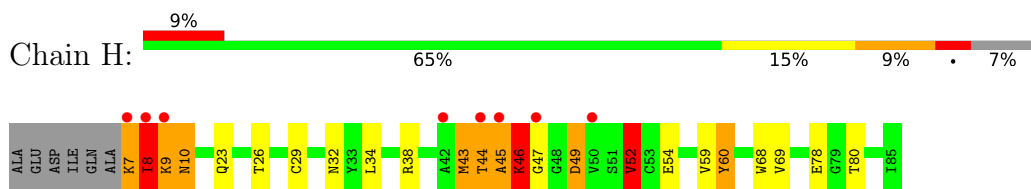
- Molecule 7: Cytochrome c oxidase subunit 6A2



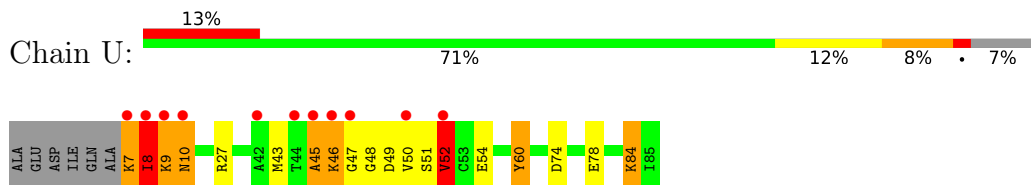
- Molecule 7: Cytochrome c oxidase subunit 6A2



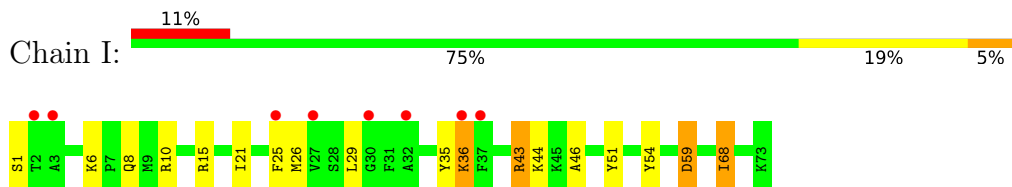
- Molecule 8: Cytochrome c oxidase subunit 6B1



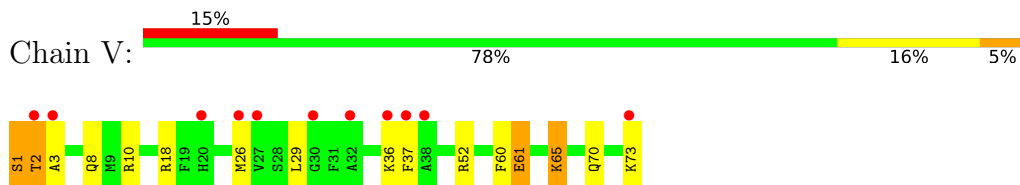
- Molecule 8: Cytochrome c oxidase subunit 6B1



- Molecule 9: Cytochrome c oxidase subunit 6C

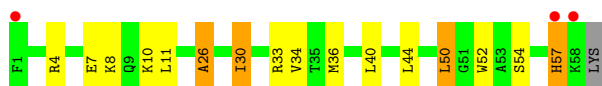


- Molecule 9: Cytochrome c oxidase subunit 6C

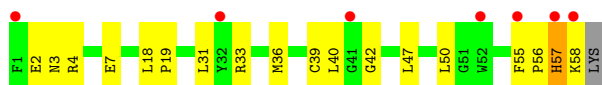


- Molecule 10: Cytochrome c oxidase polypeptide 7A1

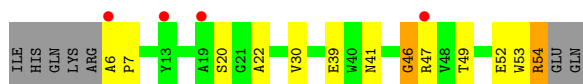




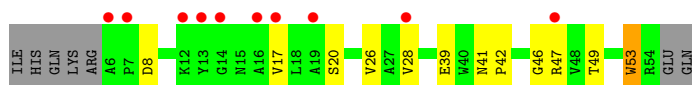
- Molecule 10: Cytochrome c oxidase polypeptide 7A1



- Molecule 11: Cytochrome c oxidase subunit 7B



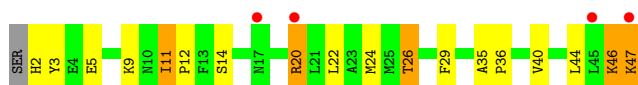
- Molecule 11: Cytochrome c oxidase subunit 7B



- Molecule 12: Cytochrome c oxidase subunit 7C



- Molecule 12: Cytochrome c oxidase subunit 7C

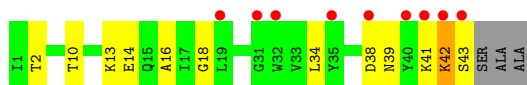


- Molecule 13: Cytochrome c oxidase subunit 8B



- Molecule 13: Cytochrome c oxidase subunit 8B

Chain Z: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	182.25Å 207.94Å 178.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 40.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.00) 98.7 (40.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.3	Depositor
R, R_{free}	0.183 , 0.219 0.201 , 0.236	Depositor DCC
R_{free} test set	22073 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtrriage
Anisotropy	0.521	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.014 for l,-k,h	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	32382	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, HEA, PSC, CU, FME, NO, PEK, NA, PGV, TGL, TPO, DMU, CHD, CUA, UNX, MG, CDL, SAC

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	1.99	77/4189 (1.8%)	1.57	43/5722 (0.8%)
1	N	1.77	43/4189 (1.0%)	1.50	56/5722 (1.0%)
2	B	1.83	28/1860 (1.5%)	1.57	21/2534 (0.8%)
2	O	1.59	10/1860 (0.5%)	1.37	9/2534 (0.4%)
3	C	1.66	15/2197 (0.7%)	1.39	16/3005 (0.5%)
3	P	1.62	16/2197 (0.7%)	1.43	20/3005 (0.7%)
4	D	1.58	5/1229 (0.4%)	1.34	8/1658 (0.5%)
4	Q	1.45	7/1229 (0.6%)	1.30	6/1658 (0.4%)
5	E	1.61	6/871 (0.7%)	1.30	3/1182 (0.3%)
5	R	1.37	0/871	1.30	3/1182 (0.3%)
6	F	1.88	15/765 (2.0%)	1.63	8/1038 (0.8%)
6	S	1.70	11/765 (1.4%)	1.52	9/1038 (0.9%)
7	G	1.64	7/690 (1.0%)	1.40	6/937 (0.6%)
7	T	1.65	9/690 (1.3%)	1.46	10/937 (1.1%)
8	H	1.61	7/682 (1.0%)	1.44	9/921 (1.0%)
8	U	1.46	4/682 (0.6%)	1.27	1/921 (0.1%)
9	I	1.44	3/605 (0.5%)	1.38	6/802 (0.7%)
9	V	1.37	0/605	1.22	0/802
10	J	1.50	4/471 (0.8%)	1.39	2/636 (0.3%)
10	W	1.44	2/471 (0.4%)	1.47	5/636 (0.8%)
11	K	1.64	1/398 (0.3%)	1.56	9/546 (1.6%)
11	X	1.35	4/398 (1.0%)	1.38	4/546 (0.7%)
12	L	1.67	5/393 (1.3%)	1.47	3/526 (0.6%)
12	Y	1.61	2/393 (0.5%)	1.33	3/526 (0.6%)
13	M	1.73	3/345 (0.9%)	1.49	1/470 (0.2%)
13	Z	1.41	1/345 (0.3%)	1.30	0/470
All	All	1.69	285/29390 (1.0%)	1.45	261/39954 (0.7%)

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
5	E	0	1
6	F	0	1
6	S	0	2
12	Y	0	1
All	All	0	5

The worst 5 of 285 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	198	GLU	C-O	14.52	1.40	1.23
1	A	83	VAL	CA-CB	12.32	1.61	1.54
1	N	297	MET	SD-CE	12.21	2.10	1.79
1	N	188	VAL	N-CA	11.60	1.60	1.46
6	F	3	GLY	C-O	9.88	1.32	1.23

The worst 5 of 261 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	181	THR	CA-C-N	10.58	130.66	119.76
1	A	181	THR	C-N-CA	10.58	130.66	119.76
1	A	71	MET	CG-SD-CE	-10.51	77.77	100.90
6	S	2	SER	N-CA-C	9.69	121.54	107.88
1	N	278	MET	CG-SD-CE	-8.99	81.12	100.90

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	5	HIS	Peptide
6	F	93	PRO	Peptide
6	S	93	PRO	Peptide
6	S	95	GLN	Peptide
12	Y	46	LYS	Peptide

5.2 Too-close contacts [i](#)

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4060	0	4037	82	0
1	N	4060	0	4037	94	0
2	B	1824	0	1833	31	0
2	O	1824	0	1833	56	0
3	C	2110	0	2027	25	0
3	P	2110	0	2027	38	0
4	D	1195	0	1183	20	0
4	Q	1195	0	1183	22	0
5	E	852	0	845	10	0
5	R	852	0	845	21	0
6	F	748	0	728	22	0
6	S	748	0	728	39	0
7	G	675	0	643	46	0
7	T	675	0	643	43	0
8	H	662	0	623	21	0
8	U	662	0	623	23	0
9	I	601	0	613	9	0
9	V	601	0	613	9	0
10	J	460	0	459	14	0
10	W	460	0	459	12	0
11	K	384	0	366	3	0
11	X	384	0	366	5	0
12	L	380	0	380	17	0
12	Y	380	0	380	20	0
13	M	335	0	352	13	0
13	Z	335	0	352	6	0
14	A	120	0	108	12	0
14	N	120	0	108	5	0
15	A	2	0	0	0	0
15	N	2	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	1	0	0	0	0
18	N	1	0	0	0	0
19	A	102	0	152	16	0
19	C	102	0	152	10	0
19	N	102	0	152	7	0
19	P	51	0	76	3	0
19	U	51	0	76	4	0
20	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	O	2	0	0	0	0
21	B	63	0	110	4	0
21	D	63	0	110	10	0
21	L	63	0	110	15	0
21	N	63	0	110	14	0
21	O	63	0	110	5	0
21	Y	63	0	110	20	0
22	B	52	0	80	20	0
22	R	52	0	80	20	0
23	B	29	0	37	4	0
23	C	58	0	71	4	0
23	J	29	0	36	8	0
23	O	29	0	37	3	0
23	P	58	0	72	5	0
23	W	29	0	35	3	0
24	C	1	0	0	0	0
24	P	1	0	0	0	0
25	C	106	0	154	22	0
25	G	53	0	77	19	0
25	P	53	0	77	6	0
25	T	106	0	154	33	0
26	C	100	0	156	20	0
26	G	100	0	156	34	0
26	P	100	0	156	27	0
26	T	100	0	156	30	0
27	C	33	0	39	4	0
27	M	33	0	39	0	0
27	P	33	0	38	2	0
27	Z	33	0	38	0	0
28	F	1	0	0	0	0
28	S	1	0	0	0	0
29	A	217	0	0	5	0
29	B	127	0	0	3	0
29	C	93	0	0	4	0
29	D	86	0	0	6	0
29	E	52	0	0	0	0
29	F	72	0	0	3	0
29	G	42	0	0	7	0
29	H	46	0	0	1	0
29	I	31	0	0	3	0
29	J	28	0	0	4	0
29	K	27	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	L	16	0	0	1	0
29	M	20	0	0	0	0
29	N	207	0	0	6	0
29	O	105	0	0	2	0
29	P	96	0	0	3	0
29	Q	57	0	0	4	0
29	R	35	0	0	1	0
29	S	63	0	0	5	0
29	T	44	0	0	5	0
29	U	43	0	0	5	0
29	V	20	0	0	0	0
29	W	17	0	0	2	0
29	X	13	0	0	1	0
29	Y	12	0	0	1	0
29	Z	11	0	0	1	0
All	All	32382	0	31350	808	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 13.

The worst 5 of 808 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)
25:T:1265:PEK:H383	26:T:1269:CDL:C27	1.34	1.51
1:N:297:MET:SD	1:N:297:MET:CE	2.10	1.40
25:T:1265:PEK:C38	26:T:1269:CDL:H273	1.51	1.36
10:W:2:GLU:HB2	10:W:4:ARG:NH1	1.50	1.26
25:T:1265:PEK:C38	26:T:1269:CDL:C27	2.12	1.18

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	517/514 (101%)	502 (97%)	15 (3%)	0	100	100
1	N	517/514 (101%)	495 (96%)	22 (4%)	0	100	100
2	B	225/227 (99%)	217 (96%)	7 (3%)	1 (0%)	30	27
2	O	225/227 (99%)	219 (97%)	5 (2%)	1 (0%)	30	27
3	C	257/261 (98%)	251 (98%)	6 (2%)	0	100	100
3	P	257/261 (98%)	250 (97%)	7 (3%)	0	100	100
4	D	142/147 (97%)	138 (97%)	4 (3%)	0	100	100
4	Q	142/147 (97%)	134 (94%)	8 (6%)	0	100	100
5	E	103/109 (94%)	101 (98%)	2 (2%)	0	100	100
5	R	103/109 (94%)	100 (97%)	2 (2%)	1 (1%)	12	8
6	F	96/98 (98%)	90 (94%)	3 (3%)	3 (3%)	3	1
6	S	96/98 (98%)	88 (92%)	5 (5%)	3 (3%)	3	1
7	G	81/85 (95%)	68 (84%)	7 (9%)	6 (7%)	1	0
7	T	81/85 (95%)	67 (83%)	6 (7%)	8 (10%)	0	0
8	H	77/85 (91%)	68 (88%)	3 (4%)	6 (8%)	1	0
8	U	77/85 (91%)	68 (88%)	5 (6%)	4 (5%)	1	0
9	I	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
9	V	71/73 (97%)	67 (94%)	4 (6%)	0	100	100
10	J	56/59 (95%)	56 (100%)	0	0	100	100
10	W	56/59 (95%)	56 (100%)	0	0	100	100
11	K	47/56 (84%)	44 (94%)	3 (6%)	0	100	100
11	X	47/56 (84%)	45 (96%)	2 (4%)	0	100	100
12	L	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
12	Y	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
13	M	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
13	Z	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
All	All	3514/3614 (97%)	3356 (96%)	125 (4%)	33 (1%)	14	9

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	94	HIS
6	F	95	GLN
7	G	4	ALA

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Mol	Chain	Res	Type
7	G	7	ASP
7	G	8	HIS

5.3.2 Protein sidechains [i](#)

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	430/426 (101%)	420 (98%)	10 (2%)	44	49
1	N	430/426 (101%)	416 (97%)	14 (3%)	33	34
2	B	210/210 (100%)	202 (96%)	8 (4%)	29	29
2	O	210/210 (100%)	197 (94%)	13 (6%)	16	13
3	C	224/226 (99%)	218 (97%)	6 (3%)	39	42
3	P	224/226 (99%)	219 (98%)	5 (2%)	45	50
4	D	128/129 (99%)	122 (95%)	6 (5%)	23	22
4	Q	128/129 (99%)	120 (94%)	8 (6%)	16	13
5	E	92/95 (97%)	86 (94%)	6 (6%)	15	12
5	R	92/95 (97%)	88 (96%)	4 (4%)	26	25
6	F	81/81 (100%)	74 (91%)	7 (9%)	10	6
6	S	81/81 (100%)	77 (95%)	4 (5%)	22	20
7	G	67/68 (98%)	62 (92%)	5 (8%)	12	9
7	T	67/68 (98%)	59 (88%)	8 (12%)	5	3
8	H	71/75 (95%)	64 (90%)	7 (10%)	7	4
8	U	71/75 (95%)	67 (94%)	4 (6%)	19	16
9	I	57/57 (100%)	52 (91%)	5 (9%)	9	6
9	V	57/57 (100%)	46 (81%)	11 (19%)	1	1
10	J	49/50 (98%)	47 (96%)	2 (4%)	27	26
10	W	49/50 (98%)	48 (98%)	1 (2%)	48	54
11	K	39/46 (85%)	36 (92%)	3 (8%)	12	8
11	X	39/46 (85%)	36 (92%)	3 (8%)	12	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	L	39/40 (98%)	36 (92%)	3 (8%)	12 8
12	Y	39/40 (98%)	35 (90%)	4 (10%)	7 4
13	M	37/38 (97%)	34 (92%)	3 (8%)	11 7
13	Z	37/38 (97%)	33 (89%)	4 (11%)	6 3
All	All	3048/3082 (99%)	2894 (95%)	154 (5%)	21 19

5 of 154 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	S	48	LEU
11	X	20	SER
7	T	2	SER
8	U	84	LYS
13	Z	13	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	43	GLN
7	T	76	ASN
1	N	512	ASN
7	T	41	HIS
9	V	8	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	FME	A	1	1	8,9,10	0.59	0	8,9,11	5.13	4 (50%)
9	SAC	I	1	9	7,8,9	2.65	2 (28%)	7,9,11	2.10	3 (42%)
2	FME	O	1	2	8,9,10	1.05	0	8,9,11	4.87	2 (25%)
7	TPO	T	11	7	8,10,11	3.18	4 (50%)	10,14,16	2.00	3 (30%)
7	TPO	G	11	7	8,10,11	2.96	4 (50%)	10,14,16	1.55	3 (30%)
9	SAC	V	1	9	7,8,9	3.34	2 (28%)	7,9,11	1.80	2 (28%)
1	FME	N	1	1	8,9,10	0.59	0	8,9,11	5.70	1 (12%)
2	FME	B	1	2	8,9,10	1.91	3 (37%)	8,9,11	7.60	5 (62%)

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	A	1	1	-	4/7/9/11	-
9	SAC	I	1	9	-	3/7/8/10	-
2	FME	O	1	2	-	1/7/9/11	-
7	TPO	T	11	7	-	3/9/11/13	-
7	TPO	G	11	7	-	4/9/11/13	-
9	SAC	V	1	9	-	3/7/8/10	-
1	FME	N	1	1	-	2/7/9/11	-
2	FME	B	1	2	-	1/7/9/11	-

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	11	TPO	P-OG1	6.97	1.71	1.59
9	V	1	SAC	CA-N	6.07	1.55	1.46
9	V	1	SAC	OAC-C1A	5.84	1.36	1.23
7	G	11	TPO	P-OG1	5.67	1.69	1.59
9	I	1	SAC	OAC-C1A	5.38	1.35	1.23

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	FME	CA-N-CN	-20.70	90.98	122.82
1	N	1	FME	CA-N-CN	-15.77	98.57	122.82
1	A	1	FME	CA-N-CN	-13.36	102.27	122.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	1	FME	CA-N-CN	-13.30	102.36	122.82
1	A	1	FME	CB-CA-N	4.12	118.02	110.52

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	O1-CN-N-CA
1	A	1	FME	N-CA-CB-CG
2	B	1	FME	O1-CN-N-CA
7	G	11	TPO	N-CA-CB-CG2
7	G	11	TPO	N-CA-CB-OG1

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	FME	2	0
2	O	1	FME	1	0
7	T	11	TPO	2	0
7	G	11	TPO	4	0
9	V	1	SAC	1	0
2	B	1	FME	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 56 ligands modelled in this entry, 8 are monoatomic and 2 are unknown - leaving 46 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
19	PGV	A	521	-	50,50,50	1.28	6 (12%)	53,56,56	1.72	14 (26%)
22	PSC	R	1229	-	51,51,51	1.35	3 (5%)	57,59,59	1.31	3 (5%)
14	HEA	A	515	1	67,67,67	2.16	23 (34%)	81,103,103	1.74	20 (24%)
27	DMU	M	526	-	34,34,34	1.11	4 (11%)	45,45,45	3.41	26 (57%)
19	PGV	C	268	-	50,50,50	1.43	4 (8%)	53,56,56	1.67	7 (13%)
19	PGV	N	1266	-	50,50,50	1.00	2 (4%)	53,56,56	1.58	11 (20%)
25	PEK	C	265	-	52,52,52	1.63	6 (11%)	55,57,57	1.64	8 (14%)
26	CDL	C	270	-	99,99,99	1.58	15 (15%)	105,111,111	1.48	17 (16%)
14	HEA	A	516	1	67,67,67	2.00	23 (34%)	81,103,103	2.57	34 (41%)
23	CHD	W	1059	-	32,32,32	1.29	3 (9%)	51,51,51	5.28	32 (62%)
27	DMU	Z	1526	-	34,34,34	1.12	2 (5%)	45,45,45	3.19	25 (55%)
27	DMU	C	272	-	34,34,34	1.53	4 (11%)	45,45,45	3.45	25 (55%)
14	HEA	N	516	15,1	67,67,67	1.99	20 (29%)	81,103,103	2.48	35 (43%)
25	PEK	P	1264	-	52,52,52	0.93	3 (5%)	55,57,57	1.75	15 (27%)
21	TGL	Y	1522	-	62,62,62	1.75	10 (16%)	65,65,65	2.20	18 (27%)
20	CUA	O	228	2	0,1,1	-	-	-	-	-
22	PSC	B	229	-	51,51,51	1.22	3 (5%)	57,59,59	1.36	6 (10%)
19	PGV	P	1267	-	50,50,50	0.94	3 (6%)	53,56,56	1.55	8 (15%)
19	PGV	U	1268	-	50,50,50	1.60	4 (8%)	53,56,56	1.87	10 (18%)
23	CHD	O	229	-	32,32,32	1.64	5 (15%)	51,51,51	5.57	32 (62%)
23	CHD	C	271	-	32,32,32	0.88	1 (3%)	51,51,51	4.86	34 (66%)
20	CUA	B	228	2	0,1,1	-	-	-	-	-
25	PEK	C	264	-	52,52,52	0.92	2 (3%)	55,57,57	1.76	15 (27%)
21	TGL	N	1523	-	62,62,62	1.47	7 (11%)	65,65,65	1.43	10 (15%)
21	TGL	L	522	-	62,62,62	1.64	7 (11%)	65,65,65	2.12	16 (24%)
25	PEK	G	1263	-	52,52,52	1.34	3 (5%)	55,57,57	1.41	5 (9%)
15	NO	A	520	16	0,1,1	-	-	-	-	-
21	TGL	O	1521	-	62,62,62	1.42	6 (9%)	65,65,65	1.62	11 (16%)
21	TGL	B	521	-	62,62,62	1.36	6 (9%)	65,65,65	1.91	14 (21%)
26	CDL	T	1269	-	99,99,99	1.50	12 (12%)	105,111,111	1.55	15 (14%)
15	NO	N	520	16,14	0,1,1	-	-	-	-	-
19	PGV	C	267	-	50,50,50	0.90	3 (6%)	53,56,56	1.38	9 (16%)
19	PGV	N	1524	-	50,50,50	1.10	2 (4%)	53,56,56	1.31	6 (11%)
26	CDL	G	269	-	99,99,99	1.52	12 (12%)	105,111,111	1.54	20 (19%)
25	PEK	T	1265	-	52,52,52	1.44	5 (9%)	55,57,57	1.53	7 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	DMU	P	272	-	34,34,34	1.69	5 (14%)	45,45,45	3.40	25 (55%)
26	CDL	P	1270	-	99,99,99	1.54	12 (12%)	105,111,111	1.71	21 (20%)
23	CHD	C	525	-	32,32,32	1.63	6 (18%)	51,51,51	5.37	38 (74%)
14	HEA	N	515	1	67,67,67	2.13	21 (31%)	81,103,103	1.86	24 (29%)
23	CHD	J	60	-	32,32,32	1.01	0	51,51,51	5.18	35 (68%)
21	TGL	D	523	-	62,62,62	1.65	8 (12%)	65,65,65	1.56	13 (20%)
23	CHD	P	1271	-	32,32,32	0.89	1 (3%)	51,51,51	4.95	34 (66%)
23	CHD	B	1085	-	32,32,32	1.90	7 (21%)	51,51,51	5.60	35 (68%)
19	PGV	A	524	-	50,50,50	1.36	3 (6%)	53,56,56	1.64	9 (16%)
23	CHD	P	1525	-	32,32,32	1.70	8 (25%)	51,51,51	5.51	39 (76%)
25	PEK	T	263	-	52,52,52	1.47	4 (7%)	55,57,57	1.32	7 (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
19	PGV	A	521	-	-	10/55/55/55	-
22	PSC	R	1229	-	-	34/55/55/55	-
14	HEA	A	515	1	-	7/36/76/76	-
27	DMU	M	526	-	4/4/10/10	8/19/59/59	0/2/2/2
19	PGV	C	268	-	-	30/55/55/55	-
19	PGV	N	1266	-	-	14/55/55/55	-
25	PEK	C	265	-	-	25/56/56/56	-
26	CDL	C	270	-	-	58/110/110/110	-
14	HEA	A	516	1	-	9/36/76/76	-
23	CHD	W	1059	-	1/1/12/12	6/9/74/74	0/4/4/4
27	DMU	Z	1526	-	5/5/10/10	10/19/59/59	0/2/2/2
27	DMU	C	272	-	6/6/10/10	12/19/59/59	0/2/2/2
14	HEA	N	516	15,1	-	6/36/76/76	-
25	PEK	P	1264	-	-	28/56/56/56	-
21	TGL	Y	1522	-	-	37/65/65/65	-
22	PSC	B	229	-	-	35/55/55/55	-
19	PGV	P	1267	-	-	15/55/55/55	-
19	PGV	U	1268	-	-	30/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CHD	O	229	-	-	3/9/74/74	0/4/4/4
23	CHD	C	271	-	1/1/12/12	4/9/74/74	0/4/4/4
25	PEK	C	264	-	-	25/56/56/56	-
21	TGL	N	1523	-	-	36/65/65/65	-
21	TGL	L	522	-	-	37/65/65/65	-
25	PEK	G	1263	-	-	26/56/56/56	-
21	TGL	O	1521	-	-	35/65/65/65	-
21	TGL	B	521	-	-	34/65/65/65	-
26	CDL	T	1269	-	-	63/110/110/110	-
19	PGV	C	267	-	-	13/55/55/55	-
19	PGV	N	1524	-	-	31/55/55/55	-
26	CDL	G	269	-	-	61/110/110/110	-
25	PEK	T	1265	-	-	25/56/56/56	-
27	DMU	P	272	-	6/6/10/10	8/19/59/59	0/2/2/2
26	CDL	P	1270	-	-	67/110/110/110	-
23	CHD	C	525	-	-	2/9/74/74	0/4/4/4
14	HEA	N	515	1	-	7/36/76/76	-
23	CHD	J	60	-	2/2/12/12	7/9/74/74	0/4/4/4
21	TGL	D	523	-	-	34/65/65/65	-
23	CHD	P	1271	-	1/1/12/12	3/9/74/74	0/4/4/4
23	CHD	B	1085	-	-	2/9/74/74	0/4/4/4
19	PGV	A	524	-	-	35/55/55/55	-
23	CHD	P	1525	-	1/1/12/12	2/9/74/74	0/4/4/4
25	PEK	T	263	-	-	25/56/56/56	-

The worst 5 of 284 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Y	1522	TGL	OG2-CB1	7.88	1.56	1.34
19	U	1268	PGV	O01-C1	7.26	1.54	1.34
21	L	522	TGL	OG2-CB1	7.25	1.54	1.34
27	P	272	DMU	O16-C6	7.18	1.52	1.40
19	C	268	PGV	O01-C1	6.57	1.52	1.34

The worst 5 of 788 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	B	1085	CHD	C6-C5-C10	15.27	128.91	112.66
23	O	229	CHD	C18-C13-C12	-14.12	94.92	109.06
23	C	271	CHD	C10-C9-C8	14.09	127.55	111.84
23	P	1525	CHD	C1-C10-C5	13.37	126.94	107.75
23	O	229	CHD	C14-C13-C12	13.19	119.47	107.42

5 of 27 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	C	271	CHD	C9
23	J	60	CHD	C17
23	J	60	CHD	C9
23	P	1525	CHD	C9
23	P	1271	CHD	C9

5 of 959 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	N	515	HEA	C2A-C3A-CMA-OMA
19	A	524	PGV	C02-C03-O11-P
19	A	524	PGV	C04-C05-C06-O06
19	A	524	PGV	O02-C1-O01-C02
19	A	524	PGV	O04-C19-O03-C01

There are no ring outliers.

38 monomers are involved in 366 short contacts:

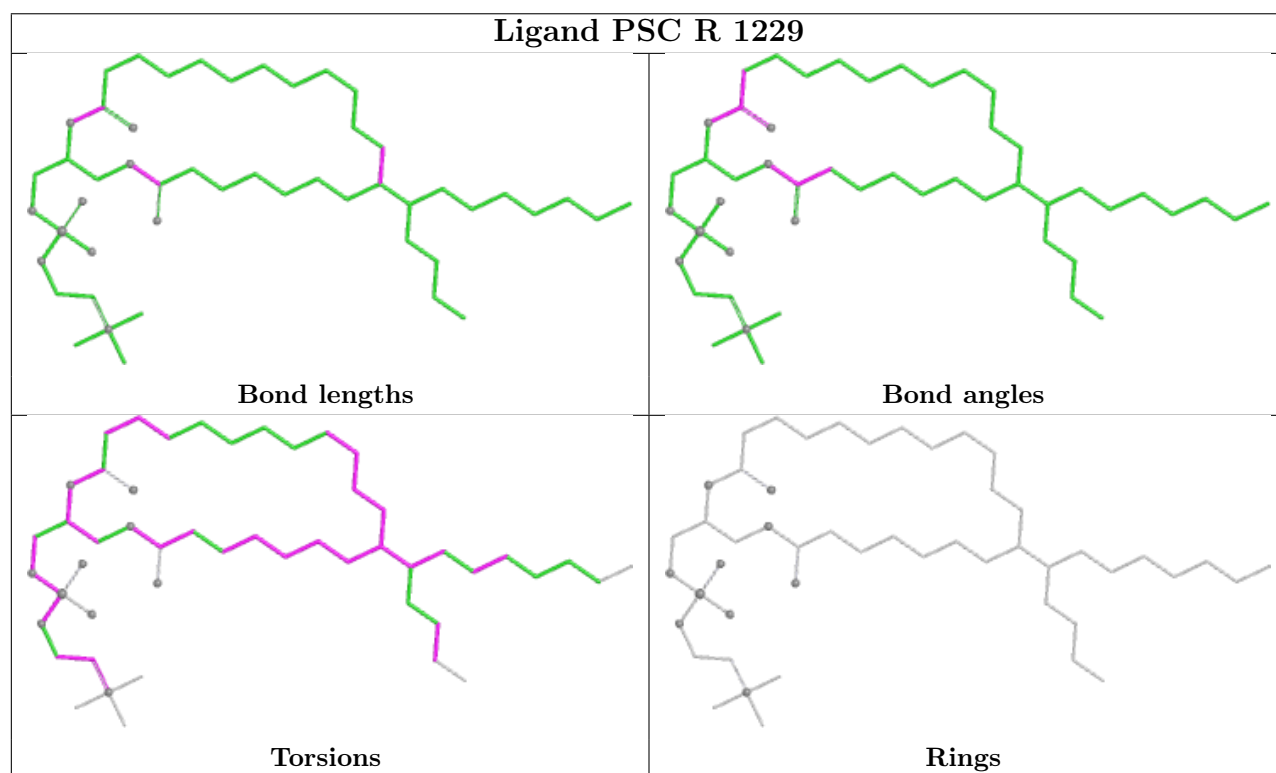
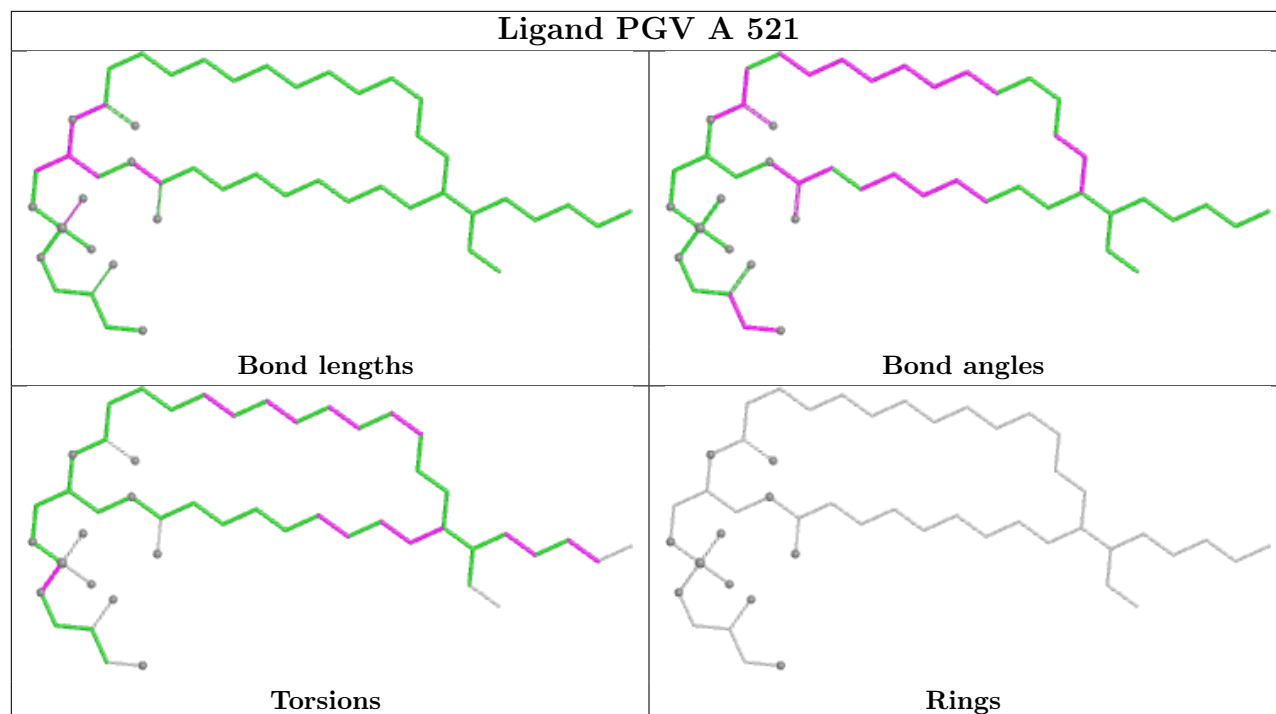
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	A	521	PGV	2	0
22	R	1229	PSC	20	0
14	A	515	HEA	8	0
19	C	268	PGV	6	0
25	C	265	PEK	13	0
26	C	270	CDL	20	0
14	A	516	HEA	4	0
23	W	1059	CHD	3	0
27	C	272	DMU	4	0
14	N	516	HEA	2	0
25	P	1264	PEK	6	0
21	Y	1522	TGL	20	0
22	B	229	PSC	20	0
19	P	1267	PGV	3	0
19	U	1268	PGV	4	0

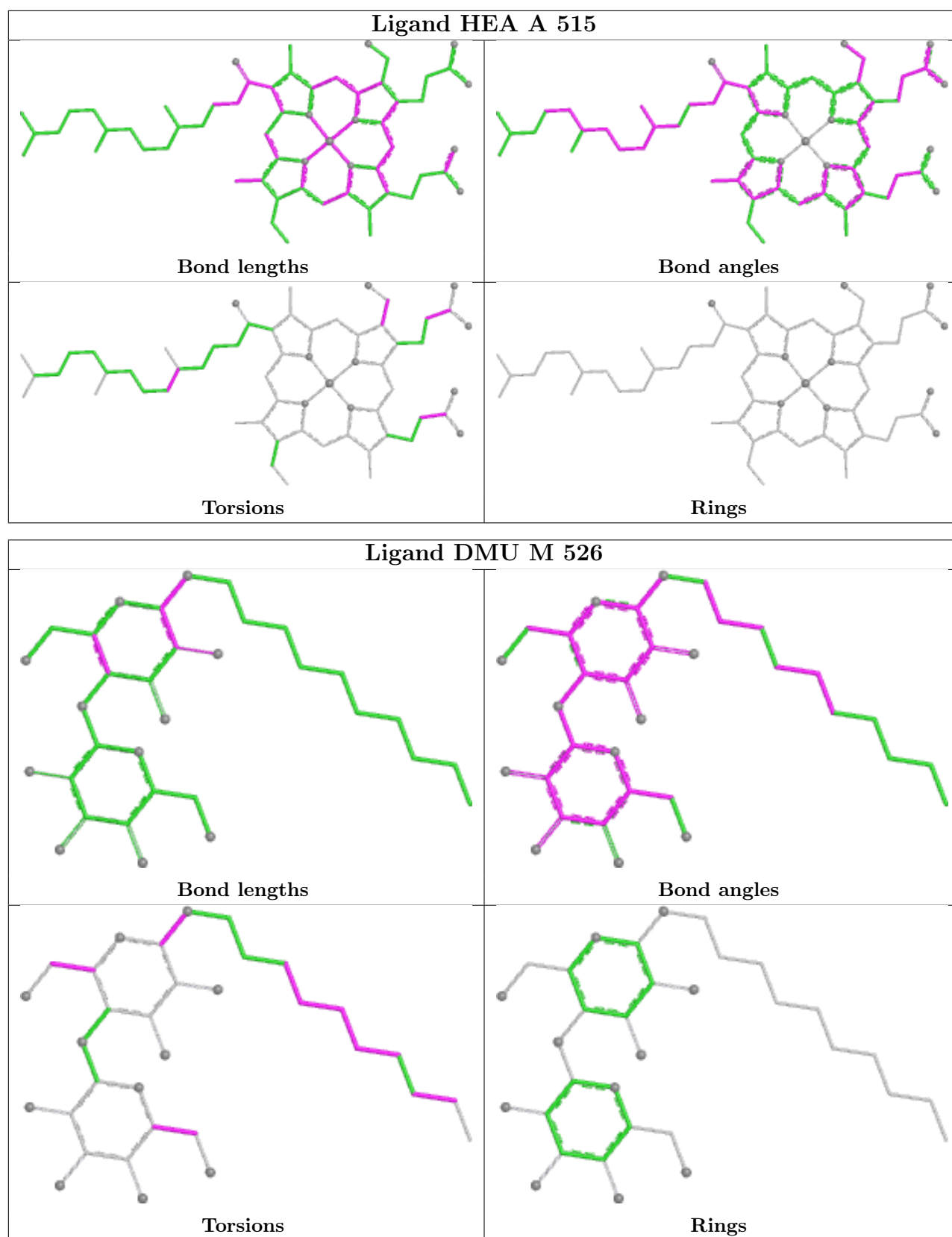
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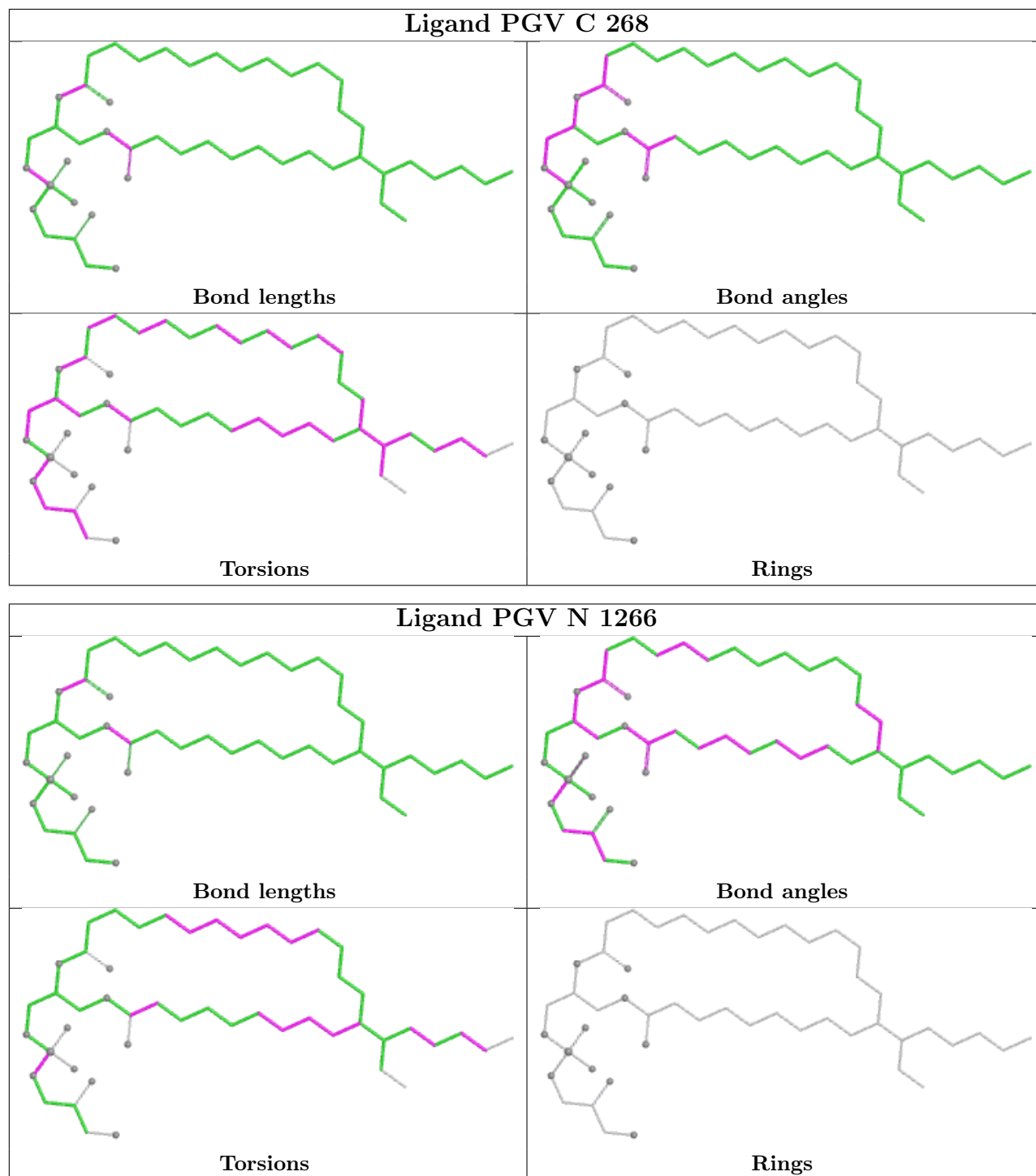
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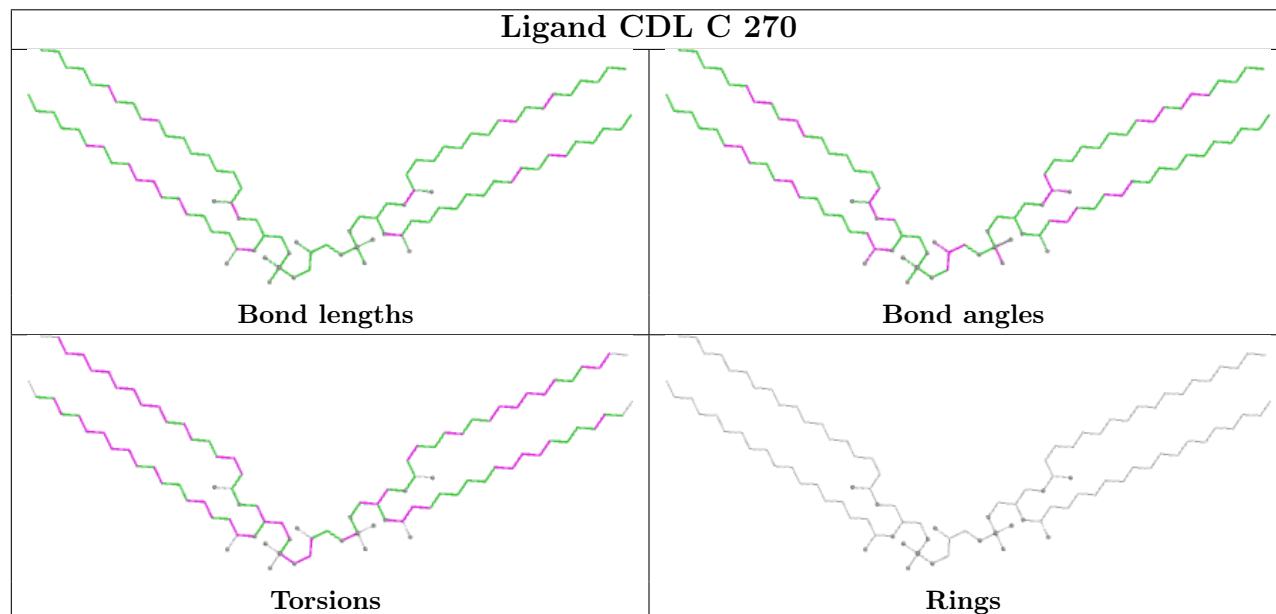
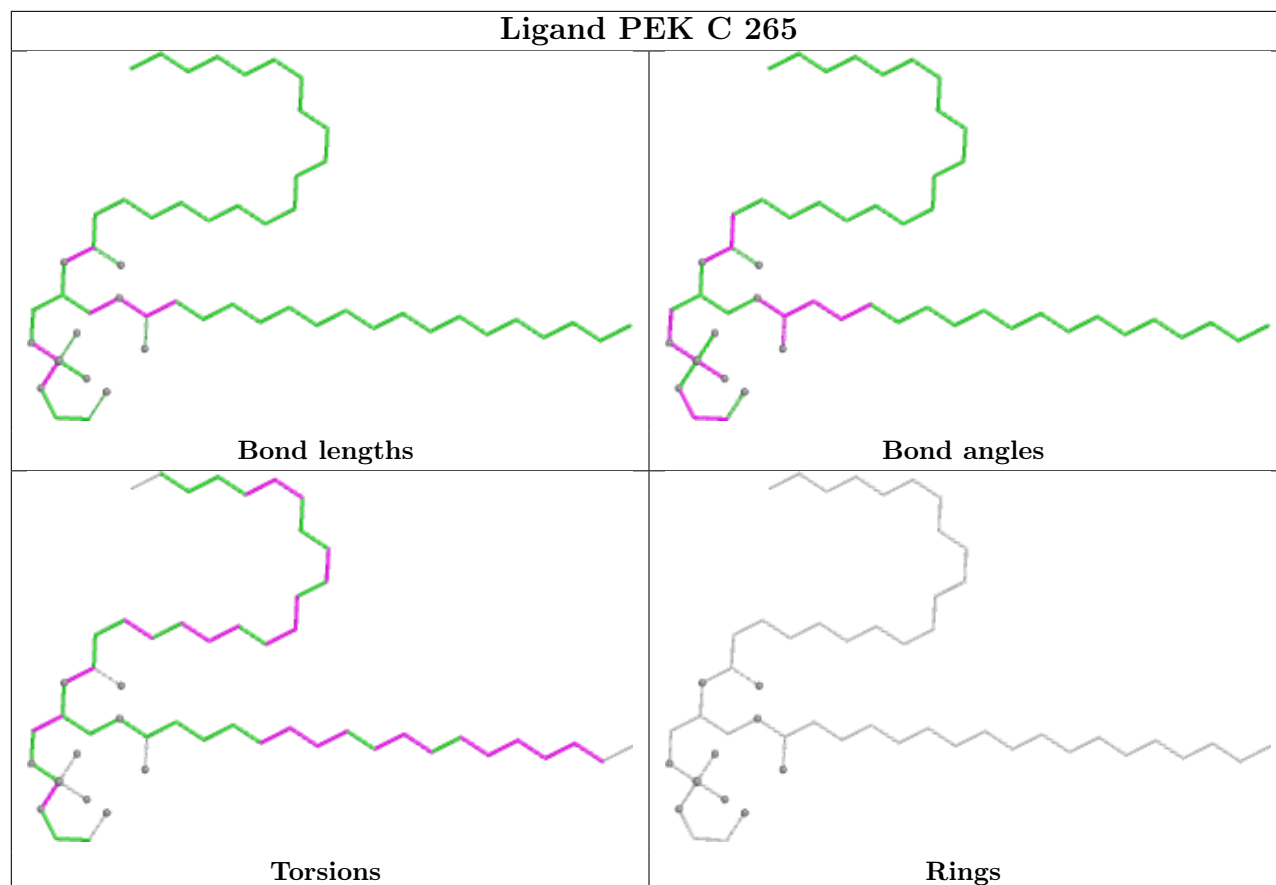
Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	O	229	CHD	3	0
23	C	271	CHD	2	0
25	C	264	PEK	9	0
21	N	1523	TGL	14	0
21	L	522	TGL	15	0
25	G	1263	PEK	19	0
21	O	1521	TGL	5	0
21	B	521	TGL	4	0
26	T	1269	CDL	30	0
19	C	267	PGV	4	0
19	N	1524	PGV	7	0
26	G	269	CDL	34	0
25	T	1265	PEK	19	0
27	P	272	DMU	2	0
26	P	1270	CDL	27	0
23	C	525	CHD	2	0
14	N	515	HEA	3	0
23	J	60	CHD	8	0
21	D	523	TGL	10	0
23	P	1271	CHD	5	0
23	B	1085	CHD	4	0
19	A	524	PGV	14	0
25	T	263	PEK	14	0

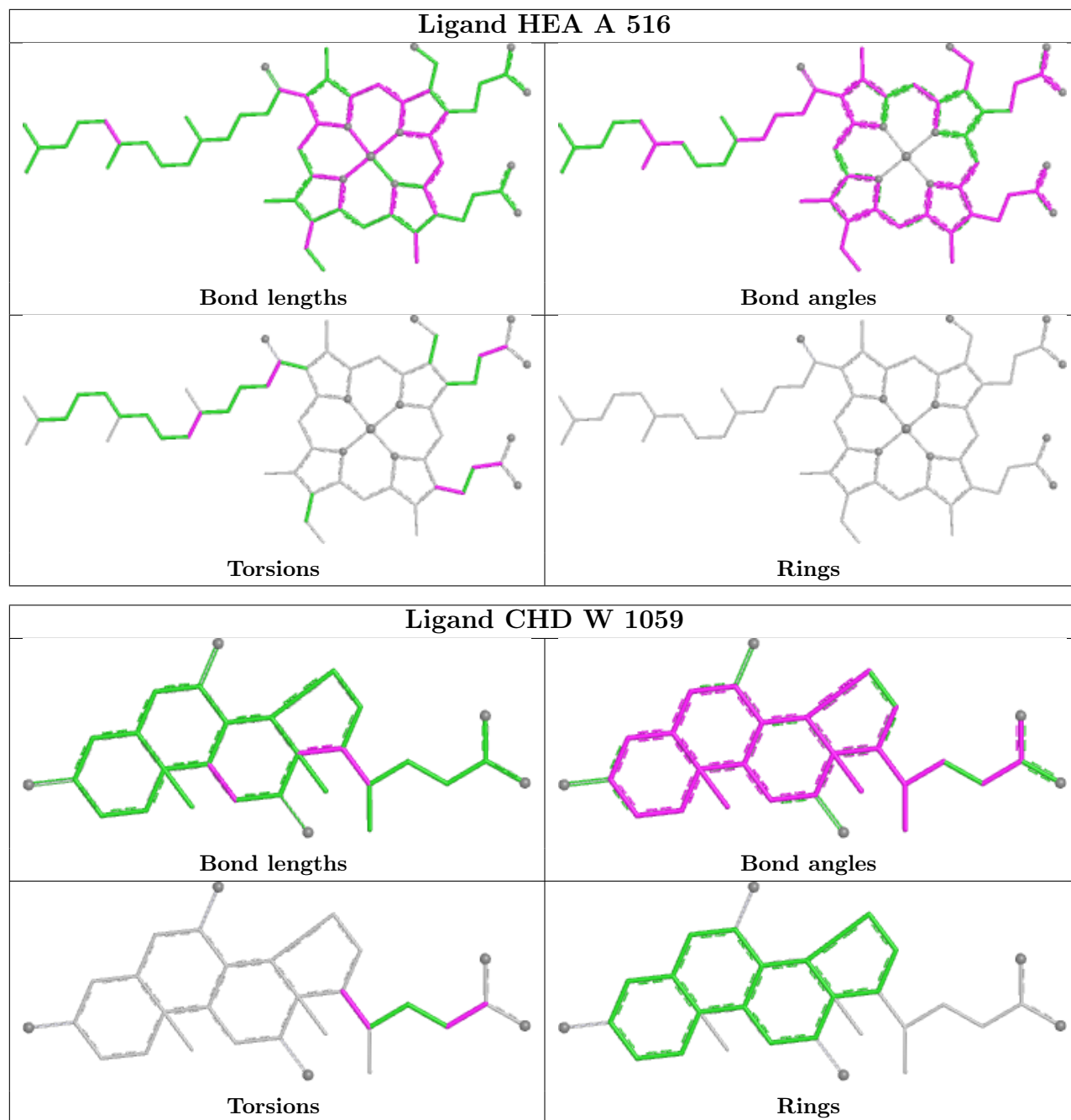
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

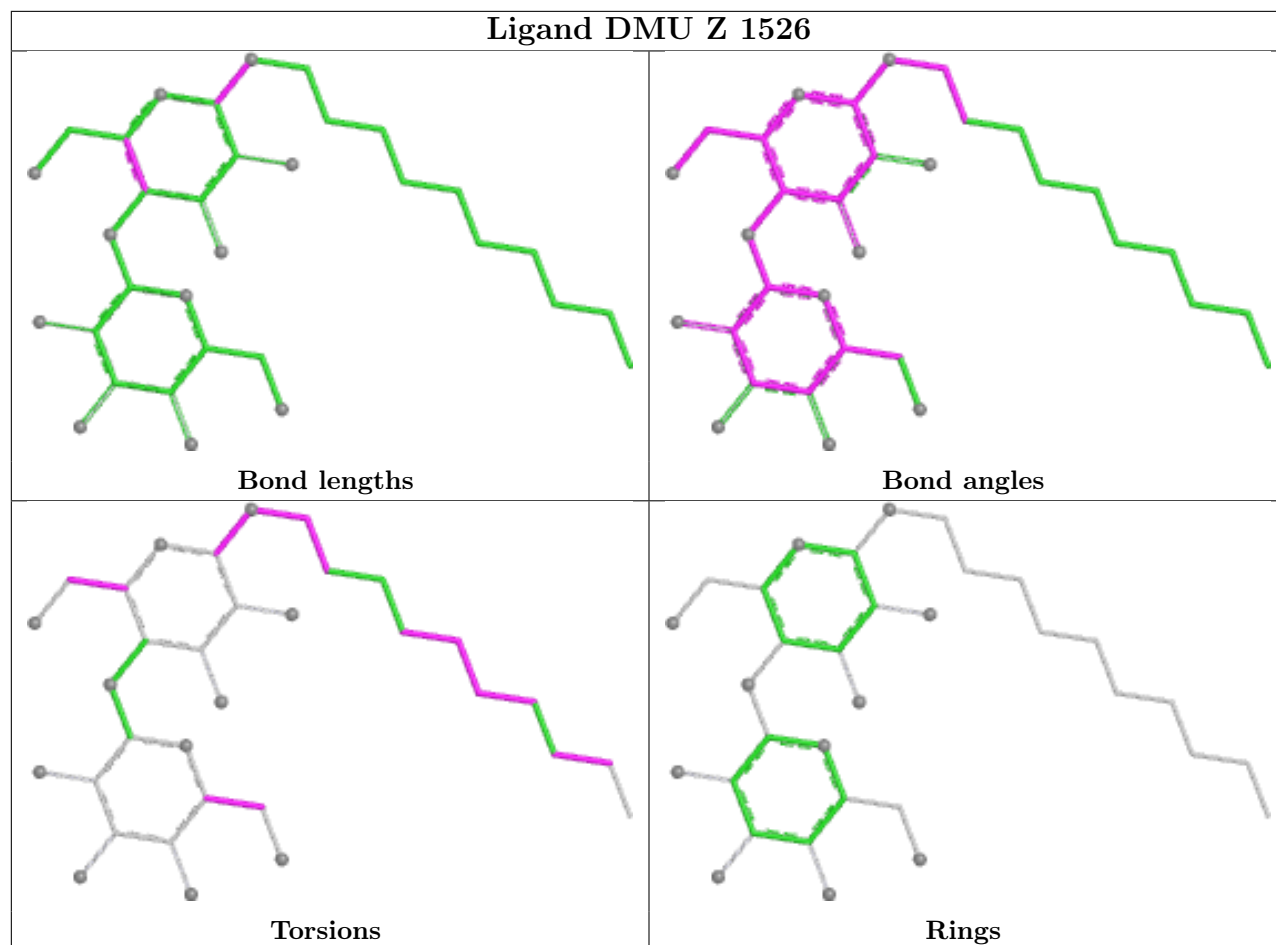


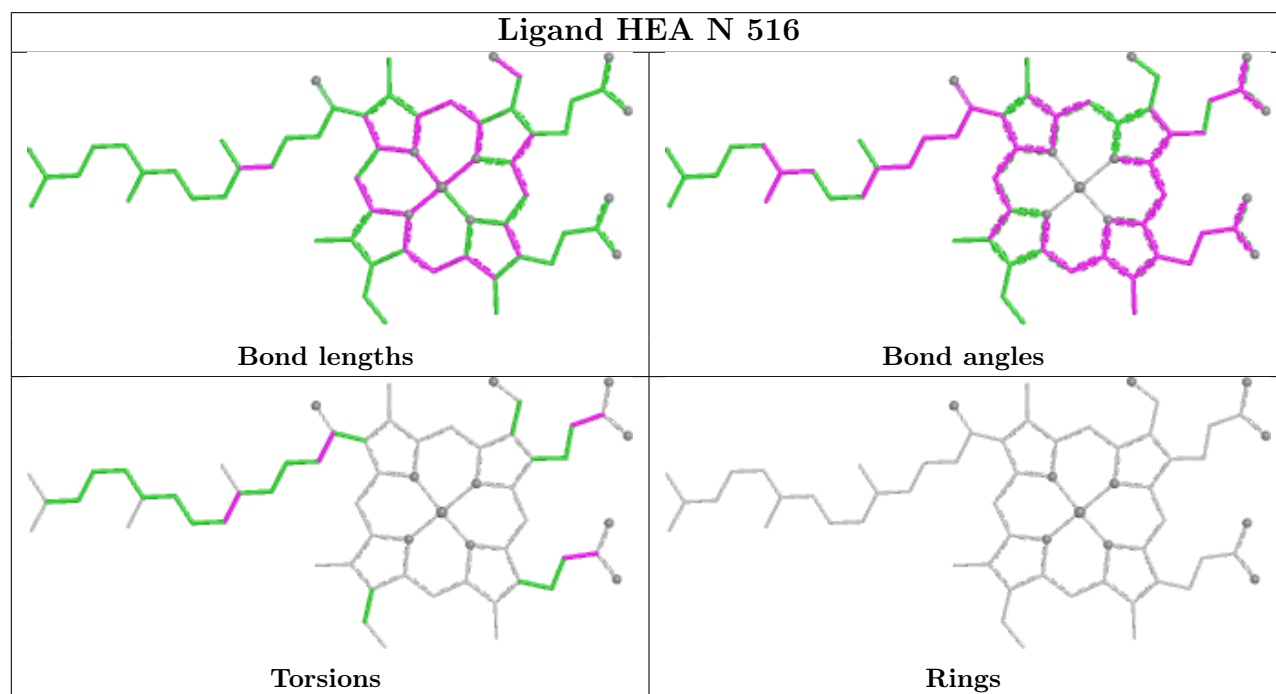
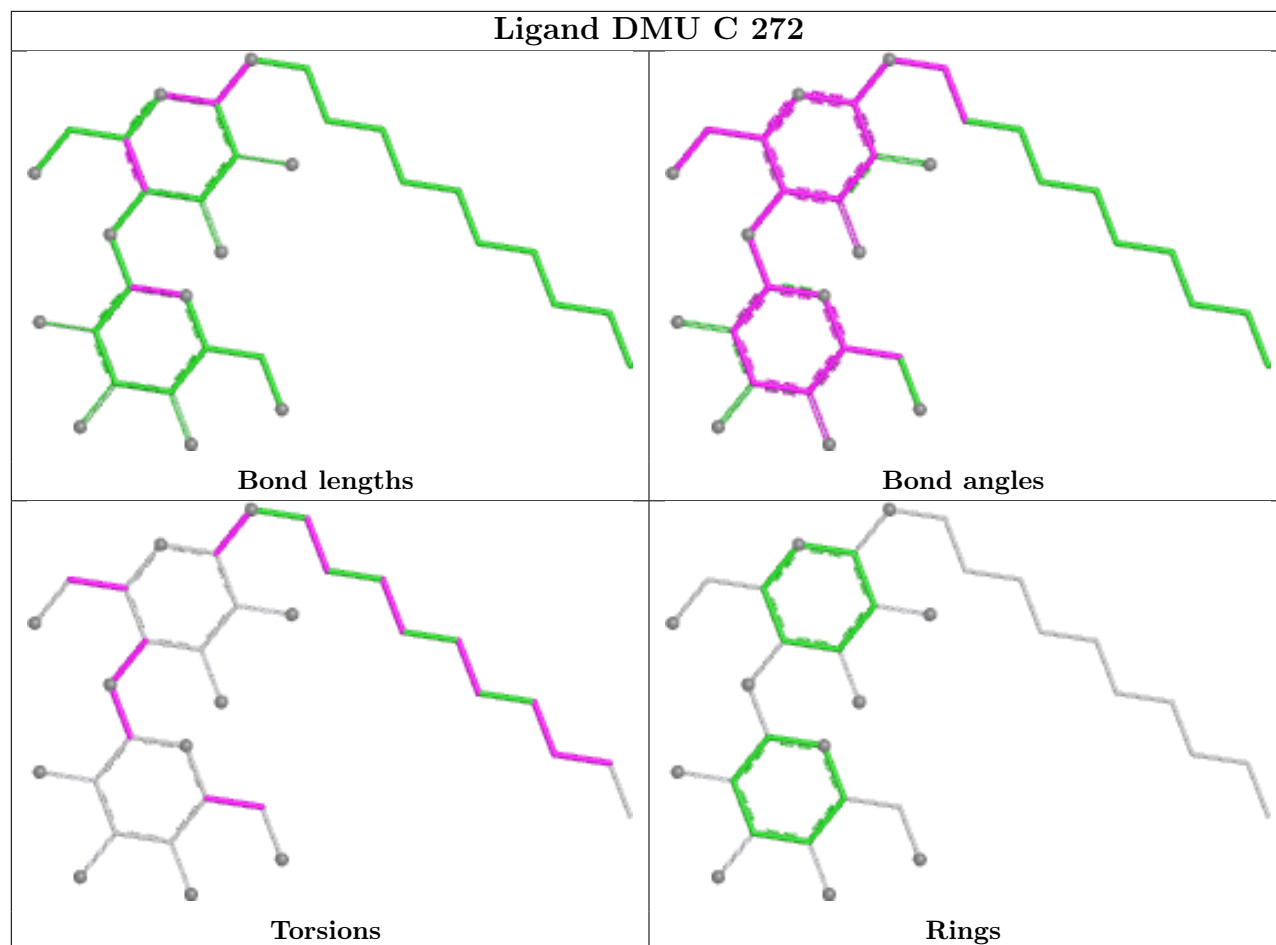


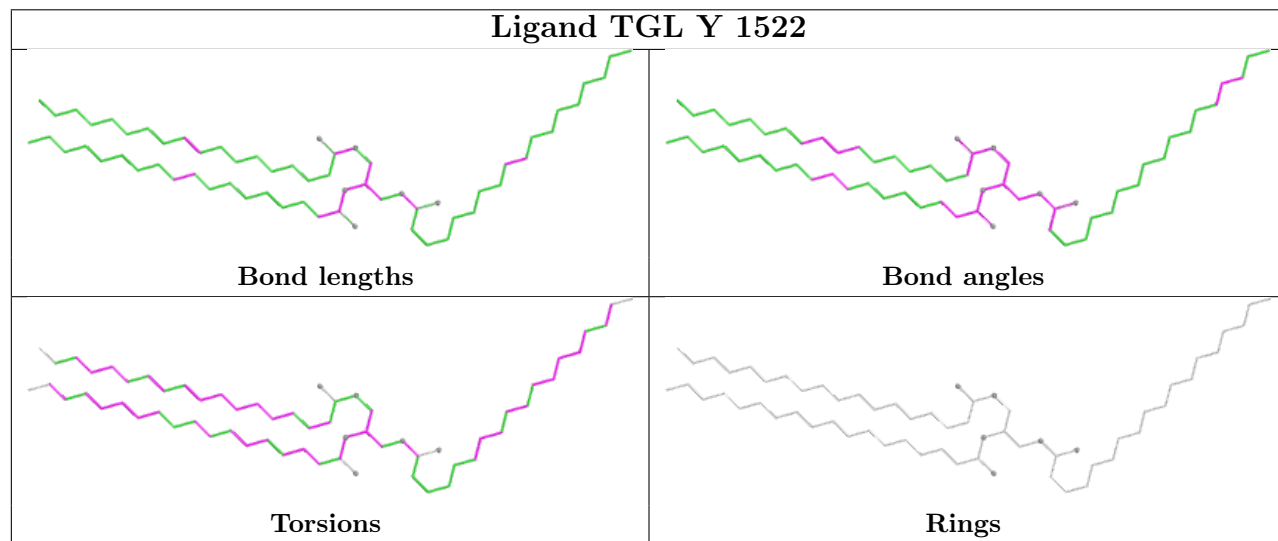
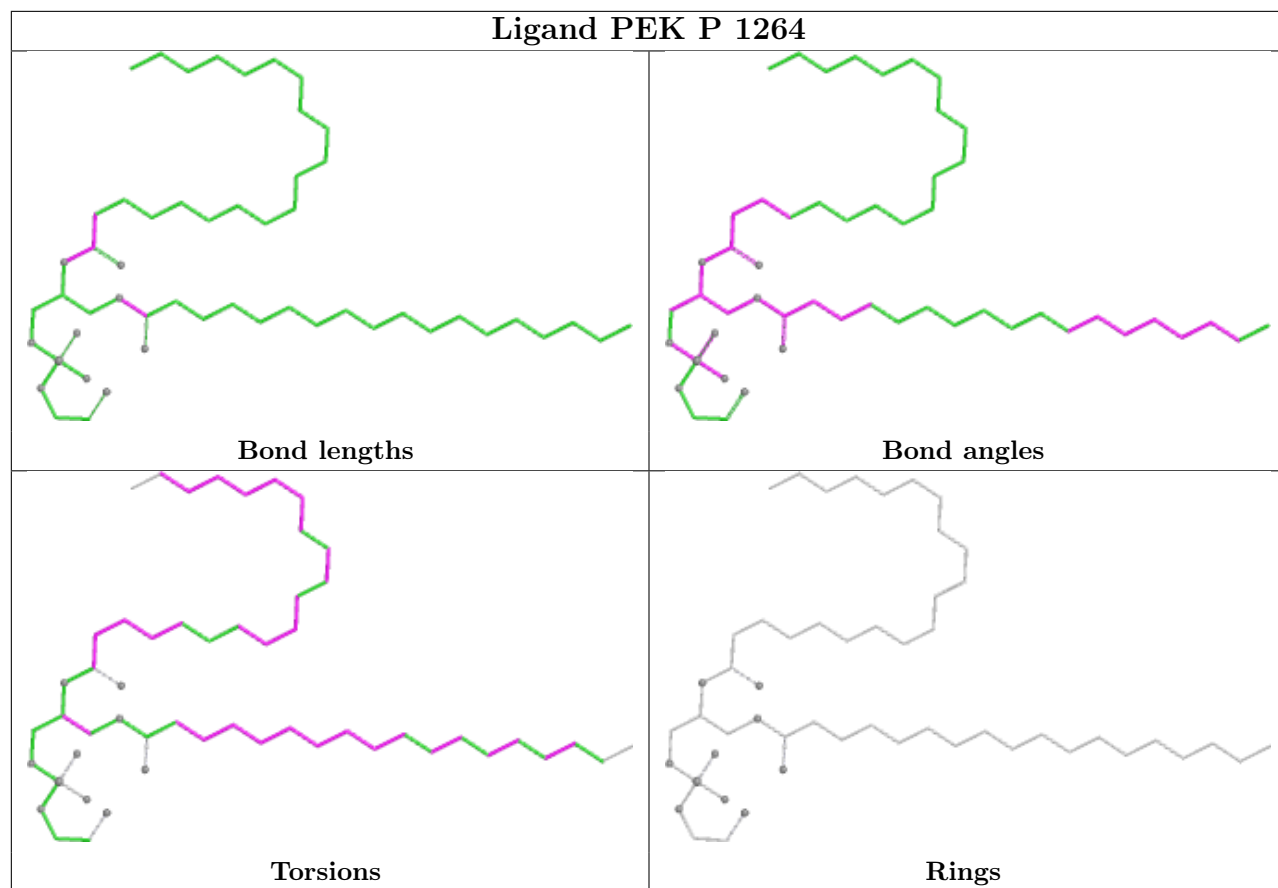


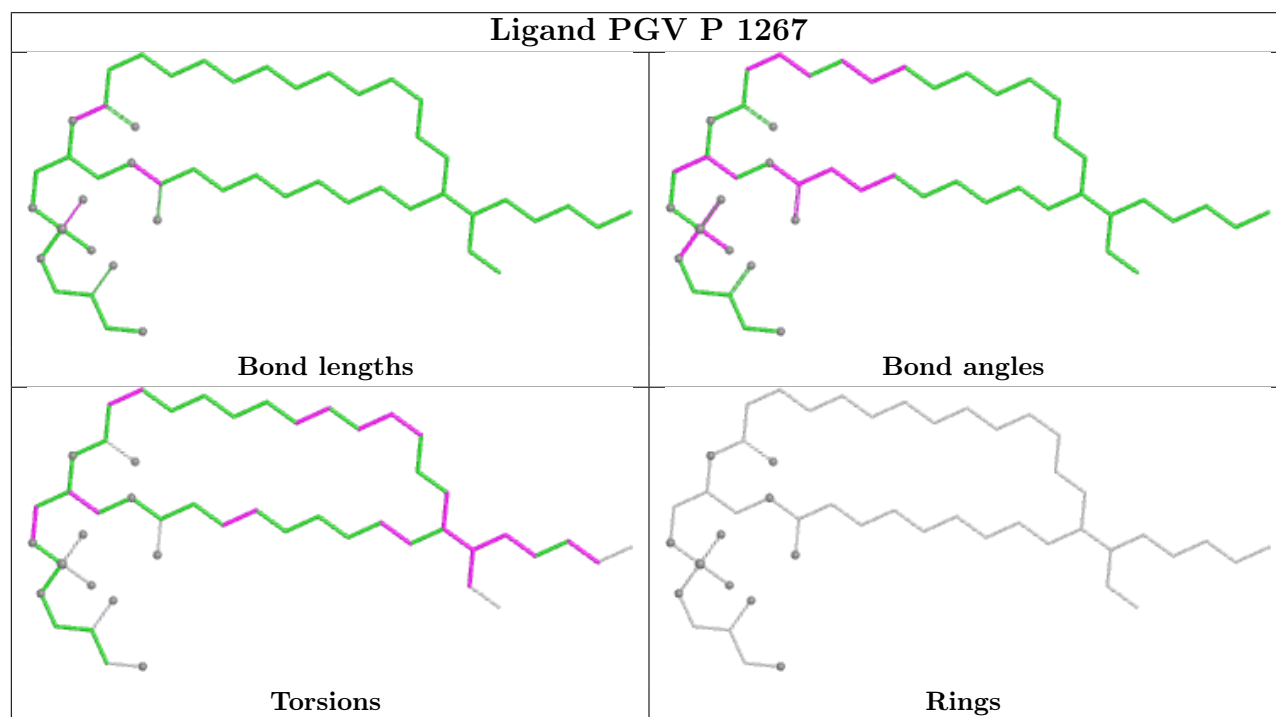
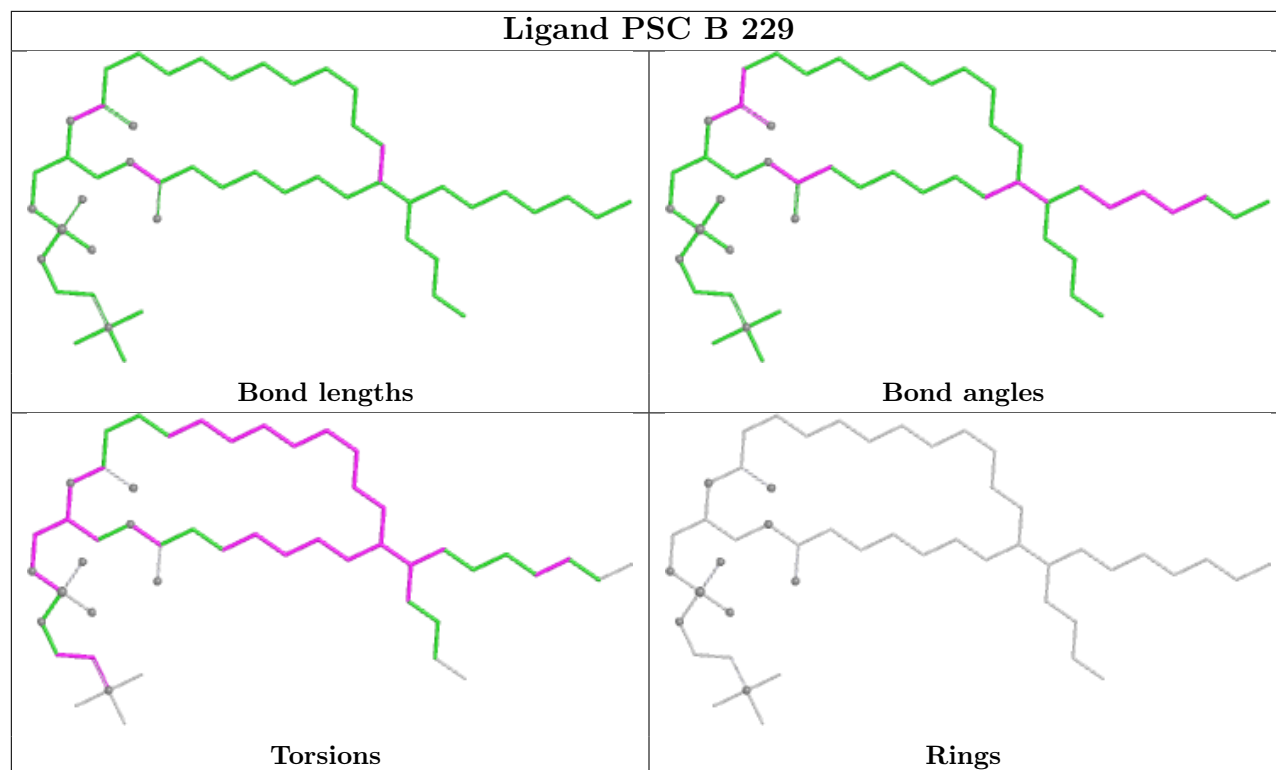


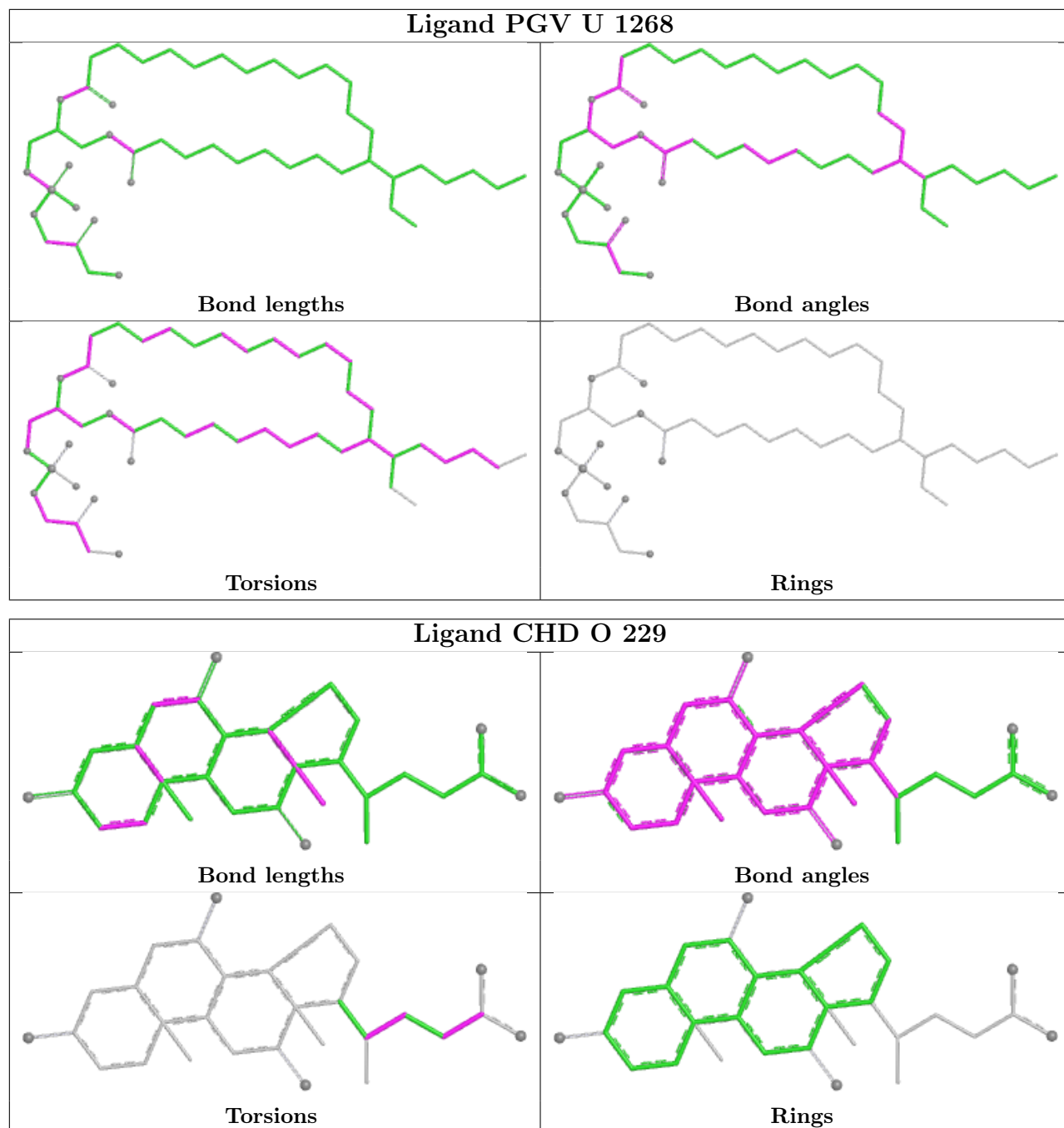


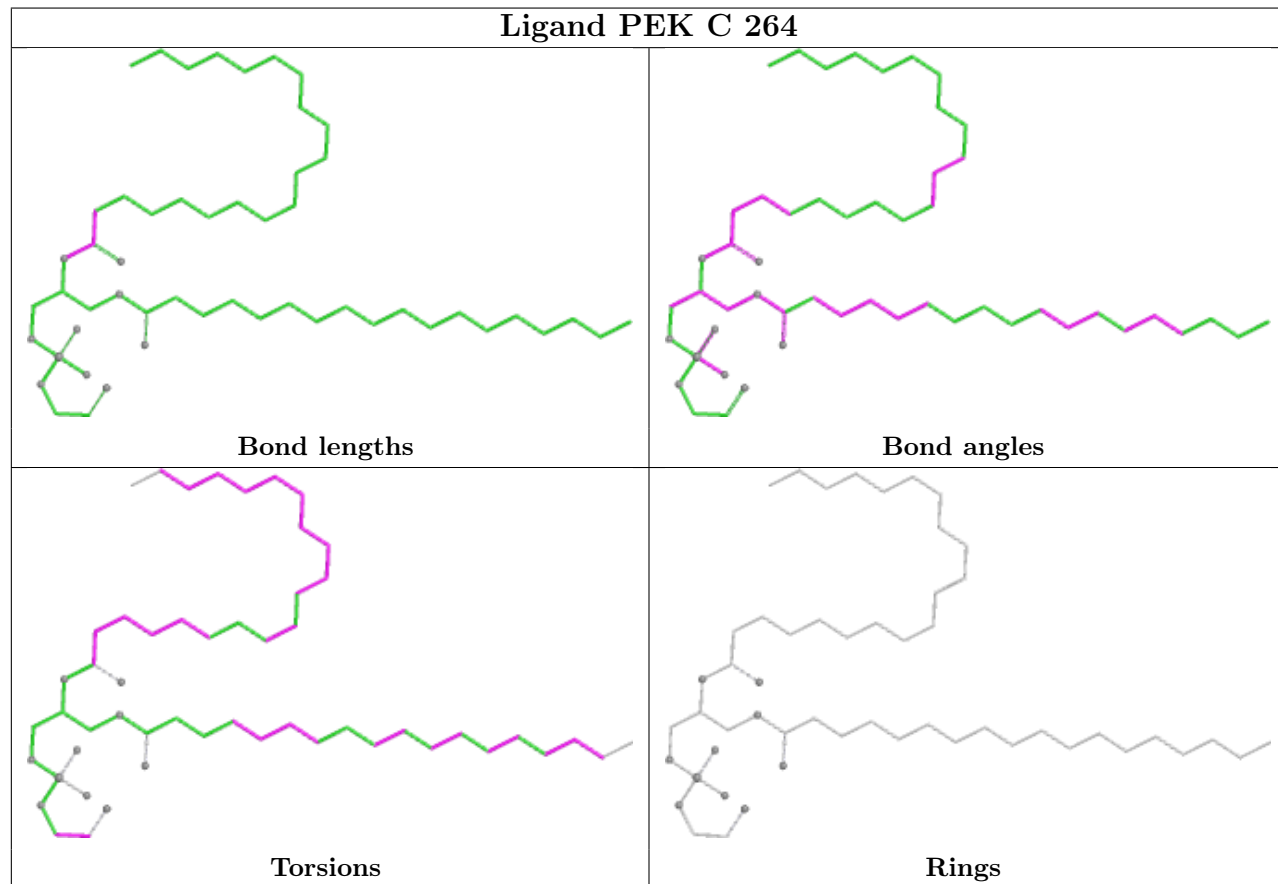
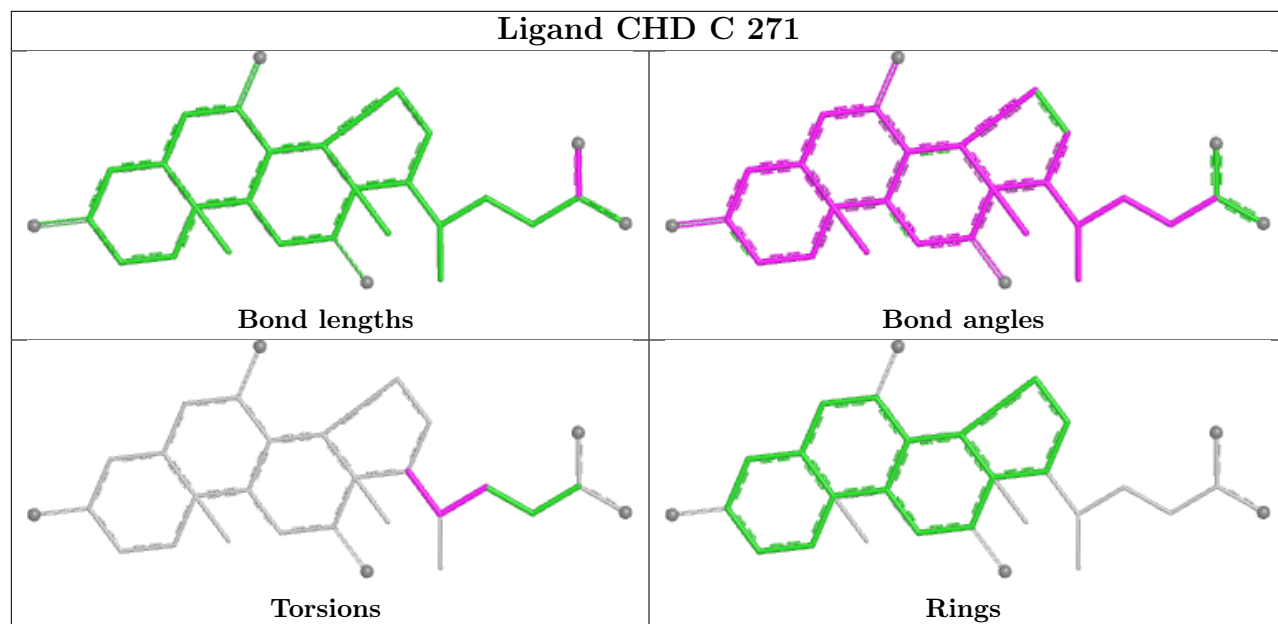


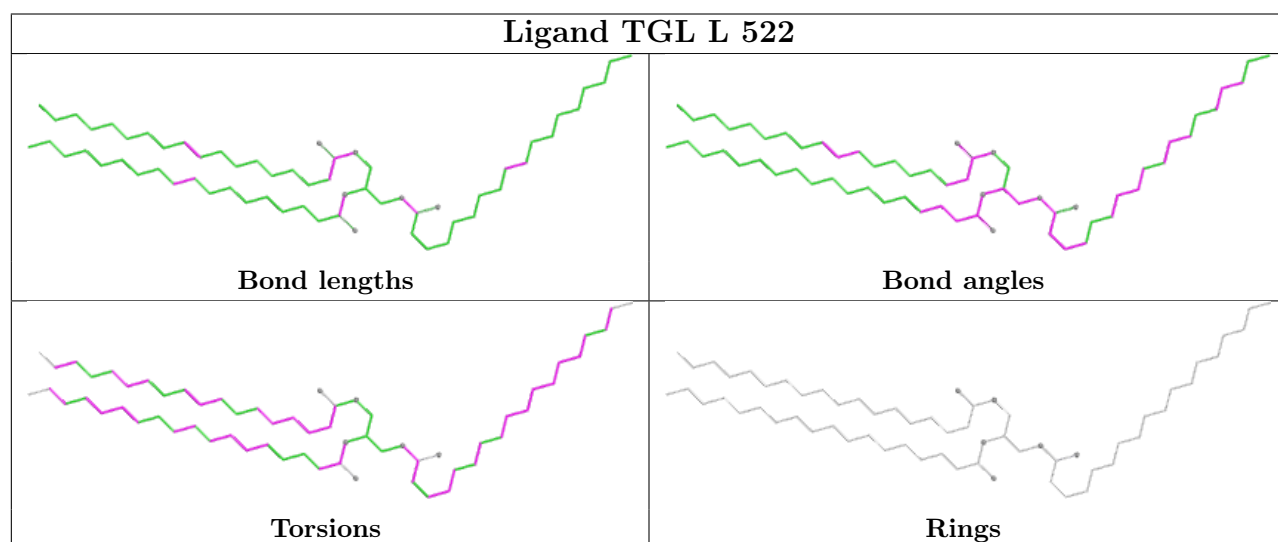
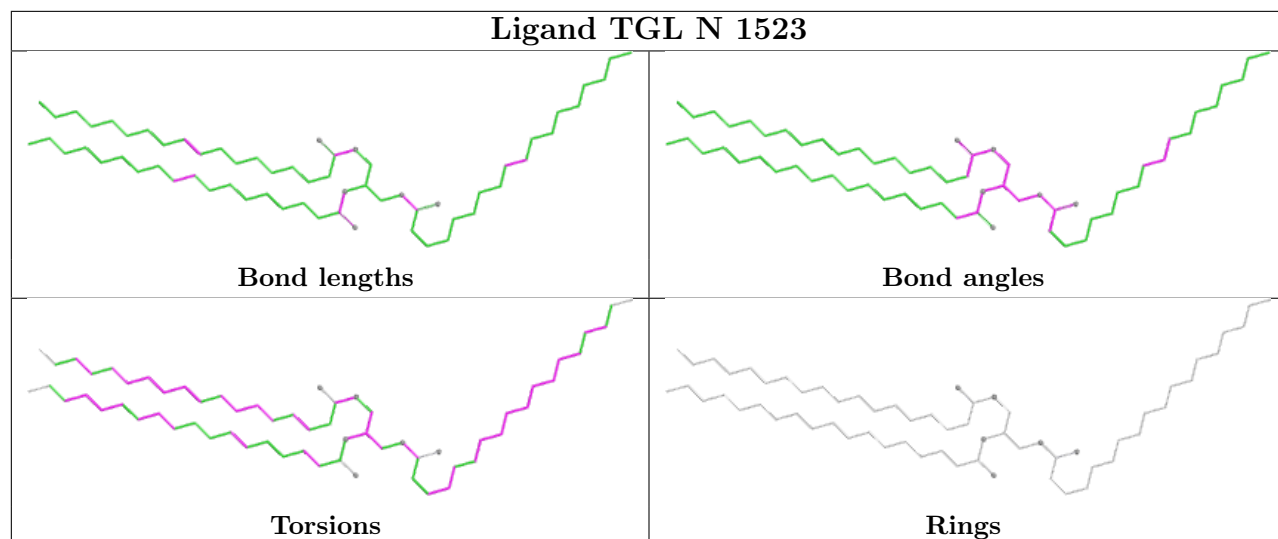


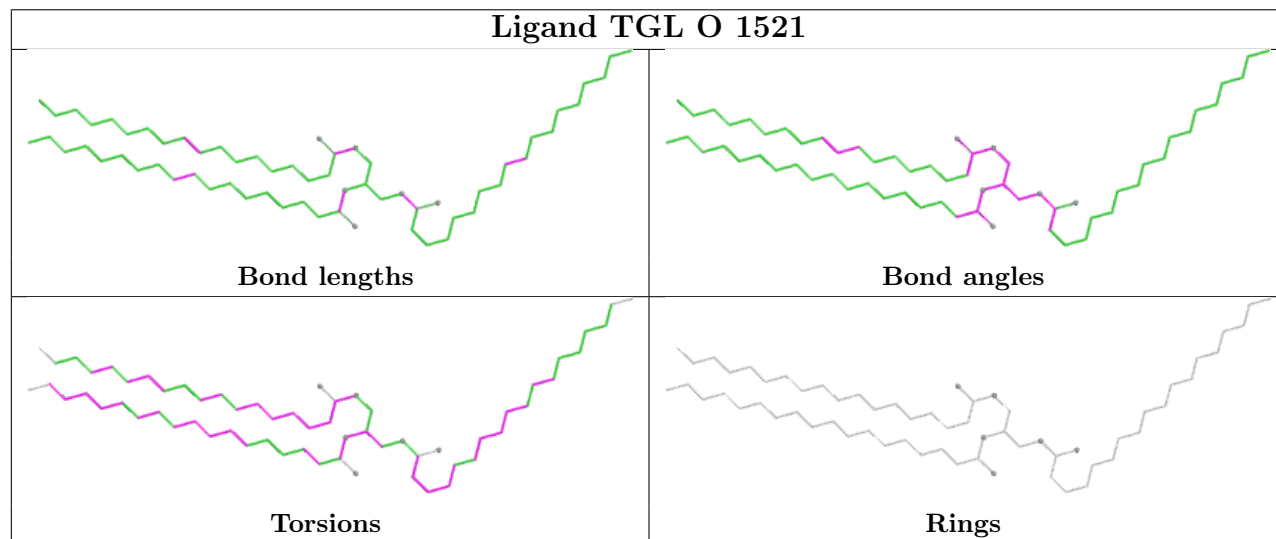
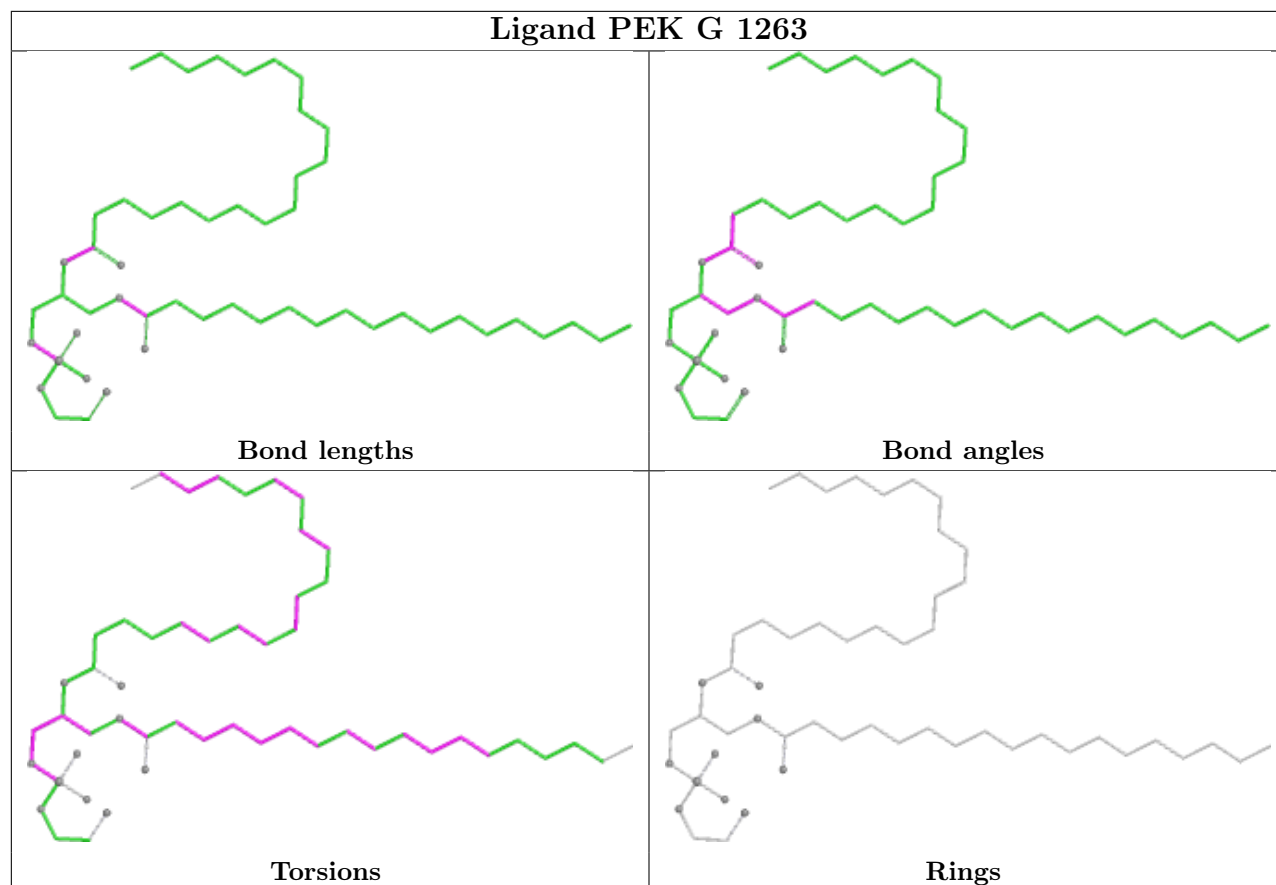


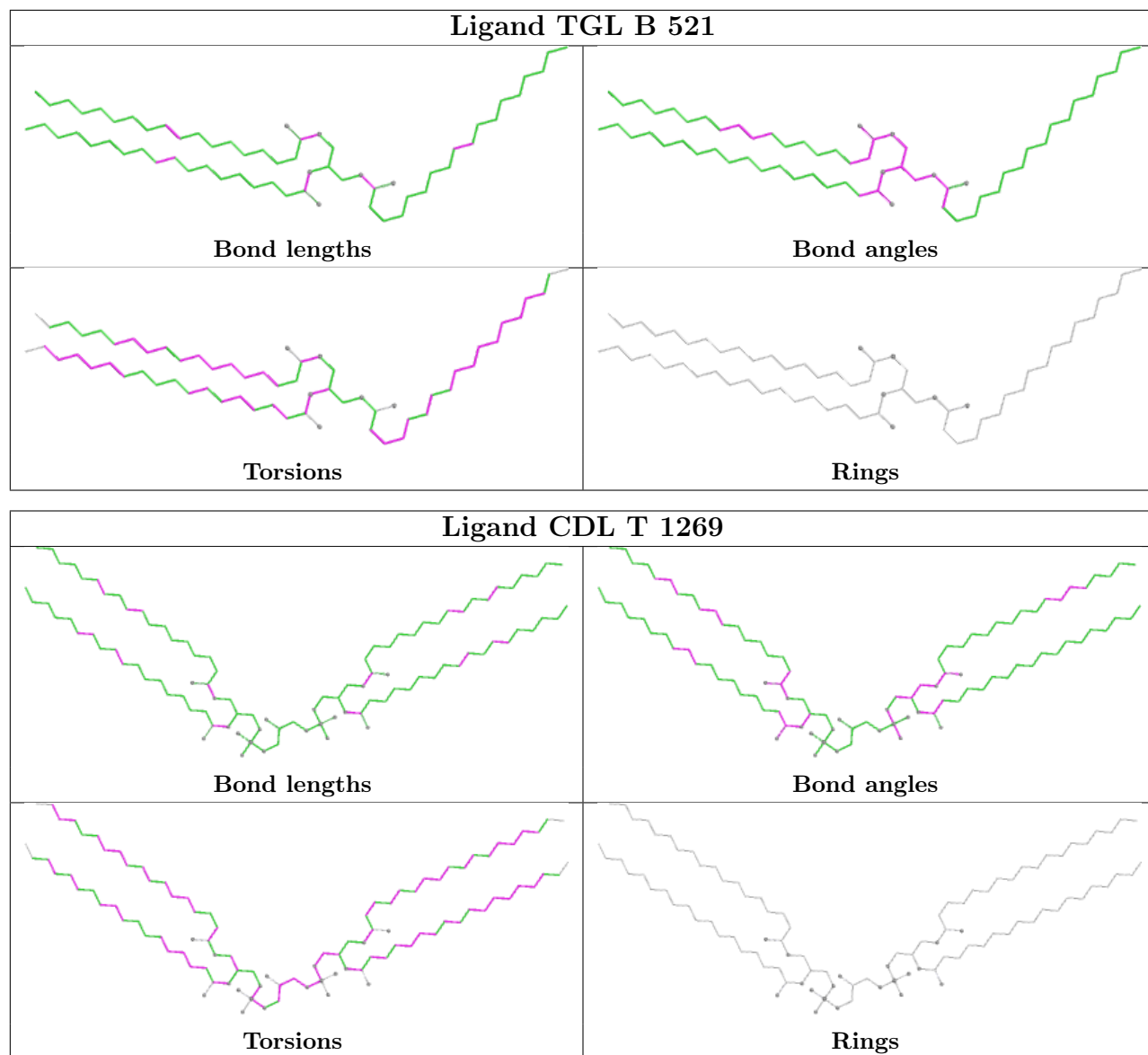


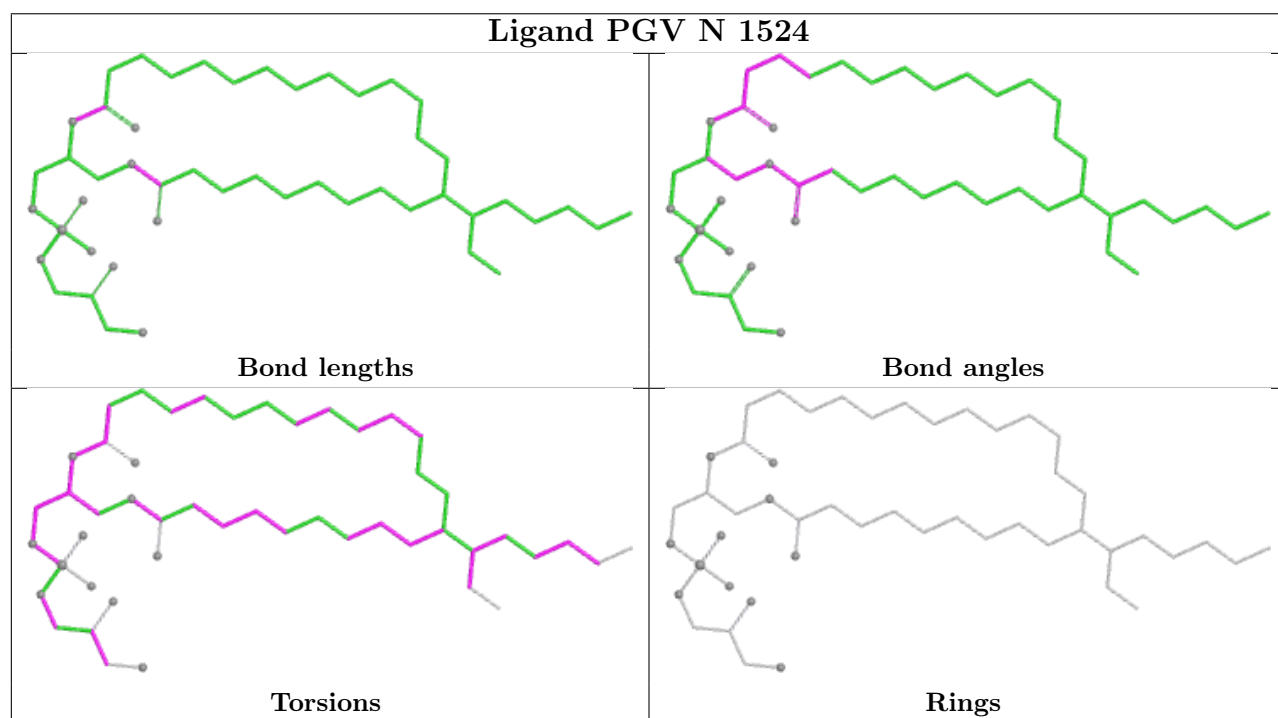
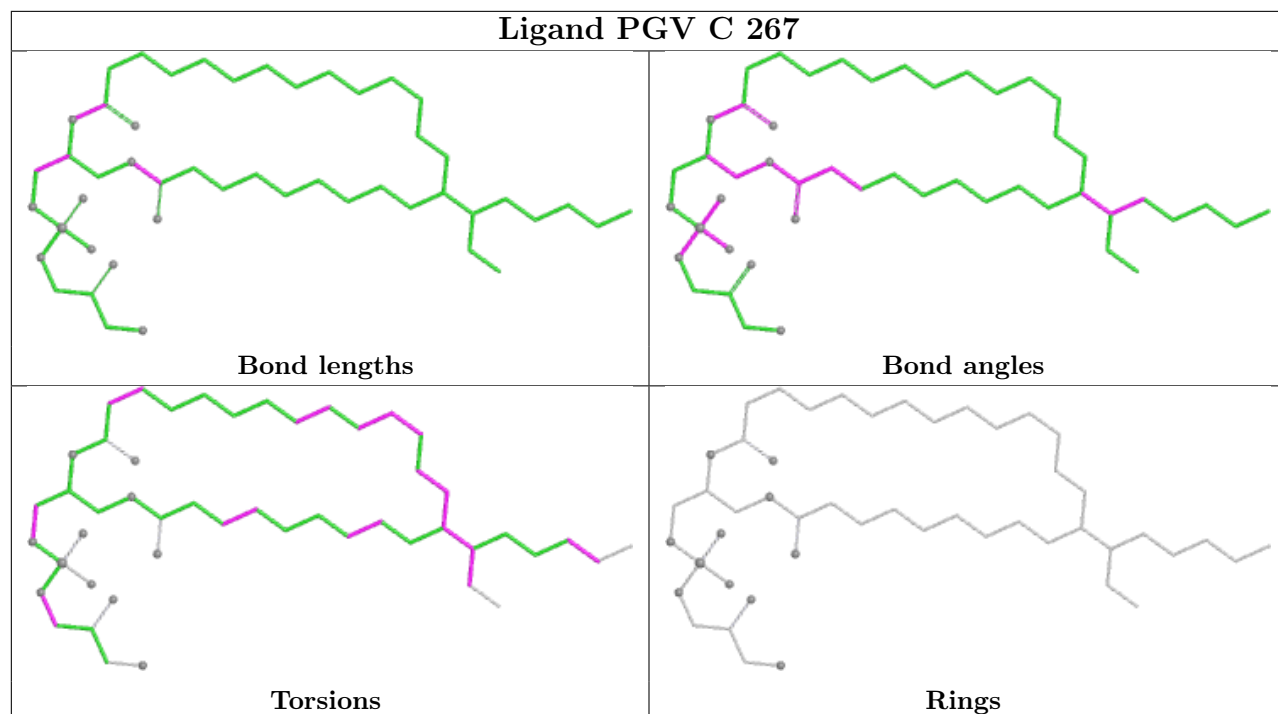


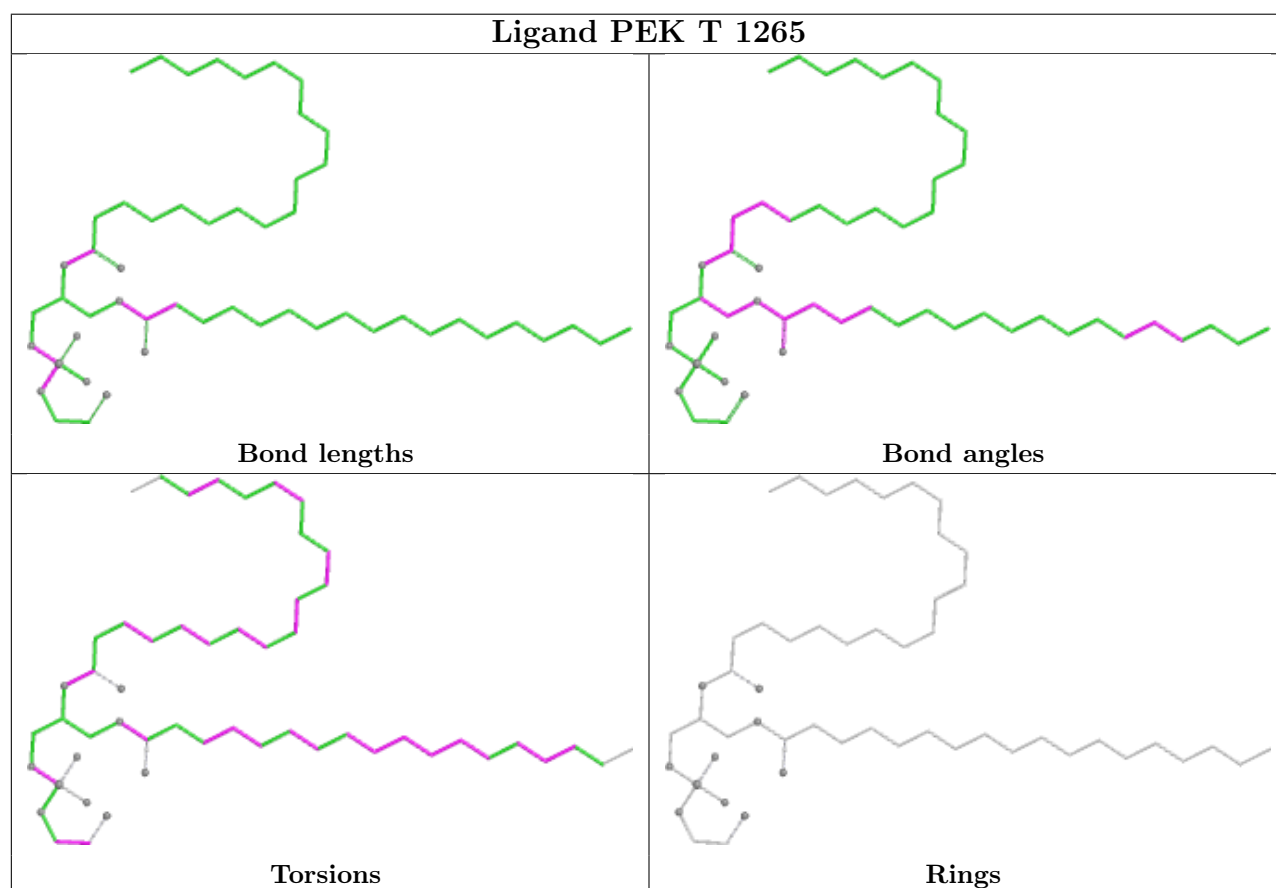
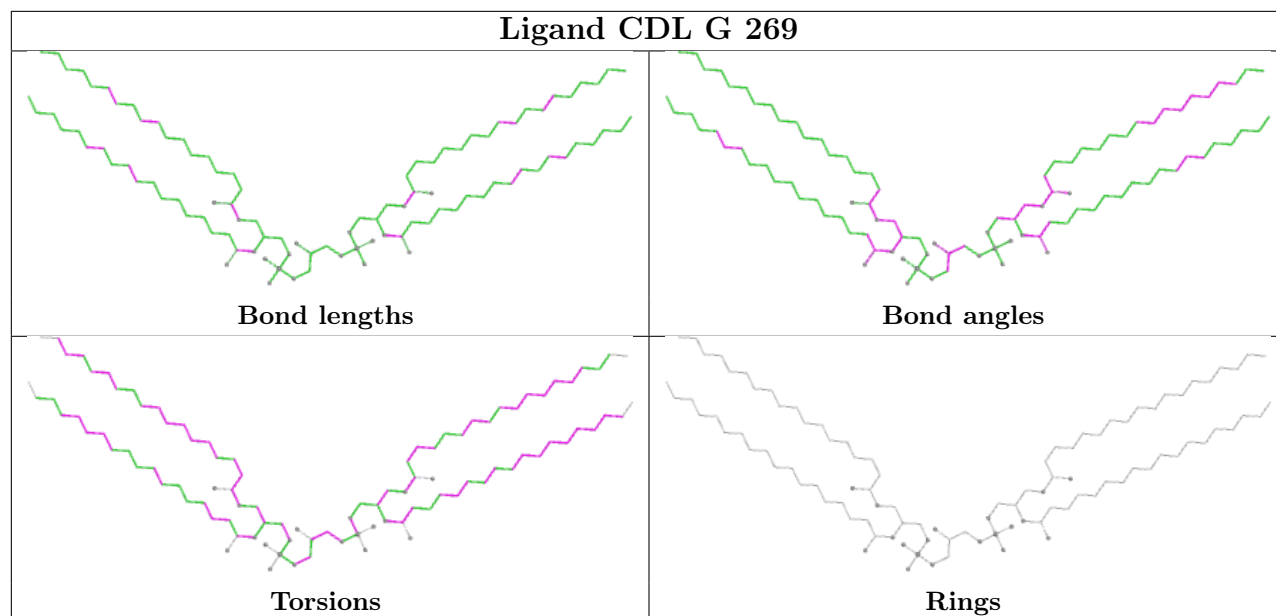


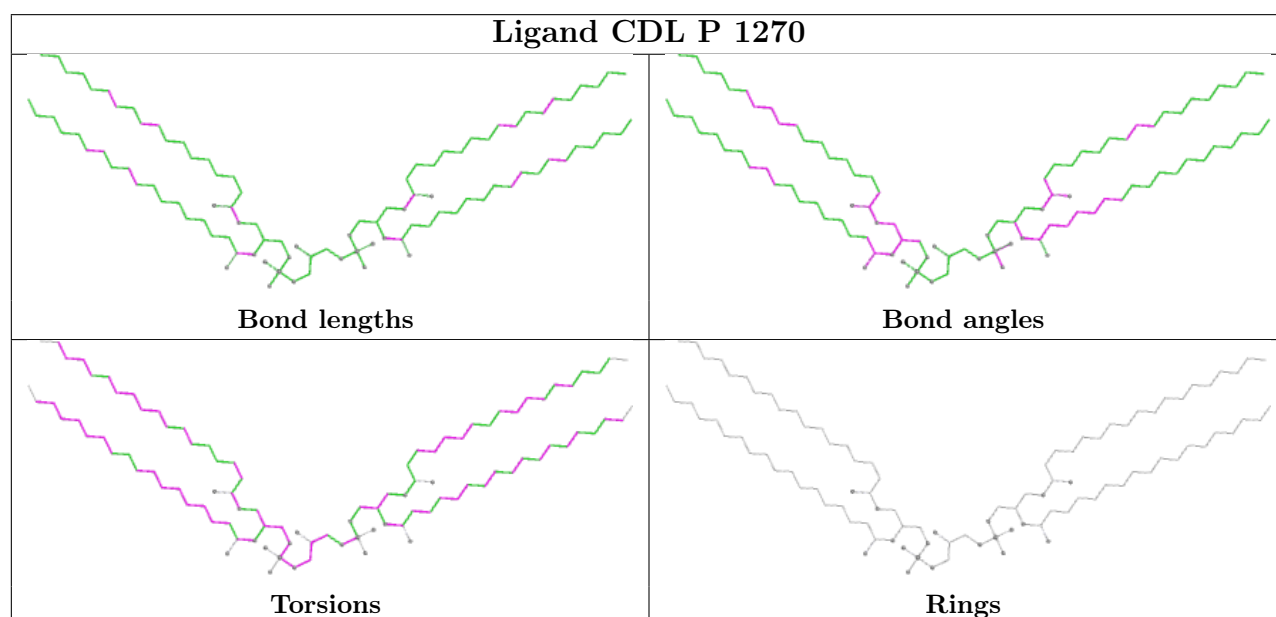
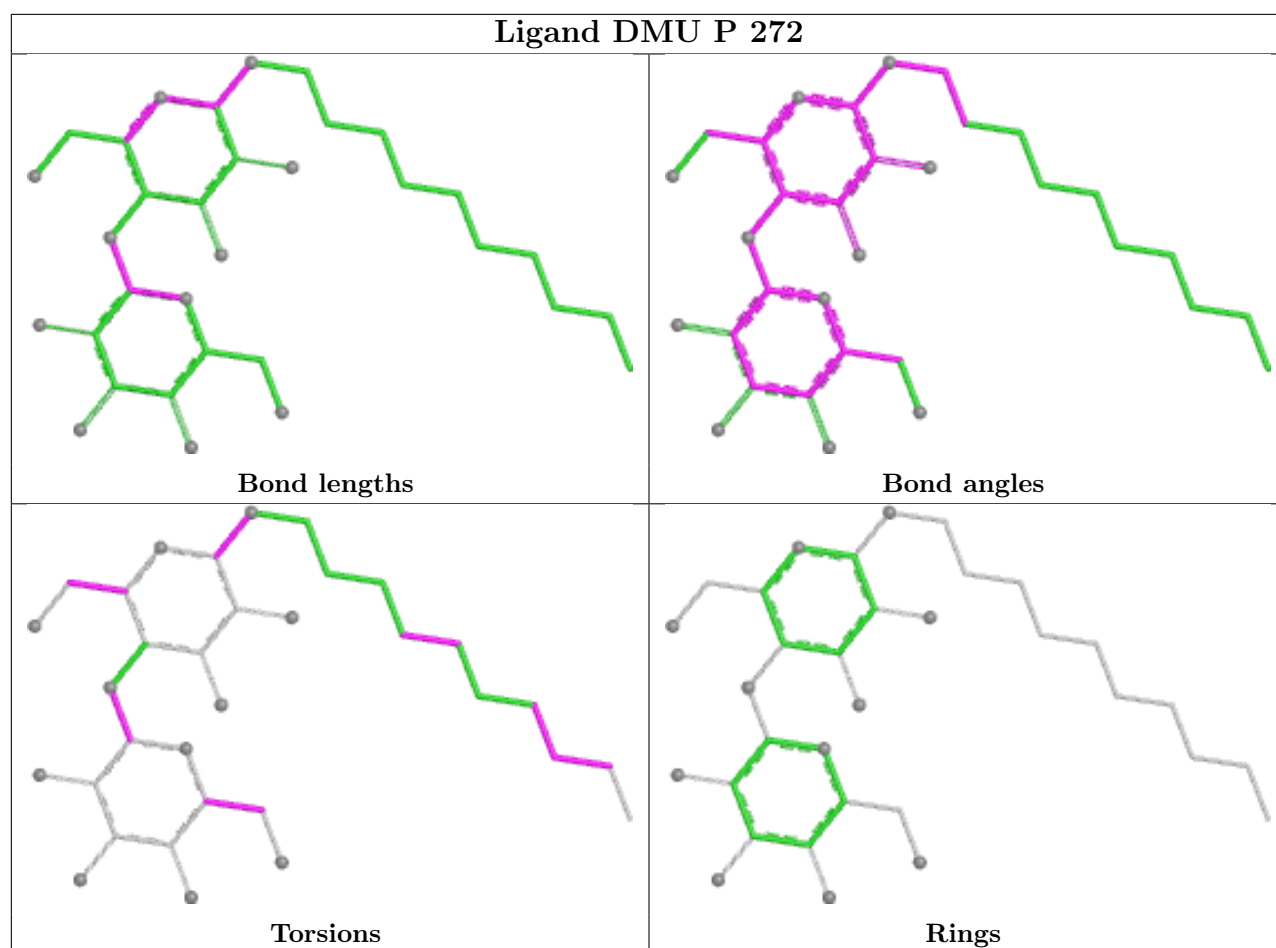


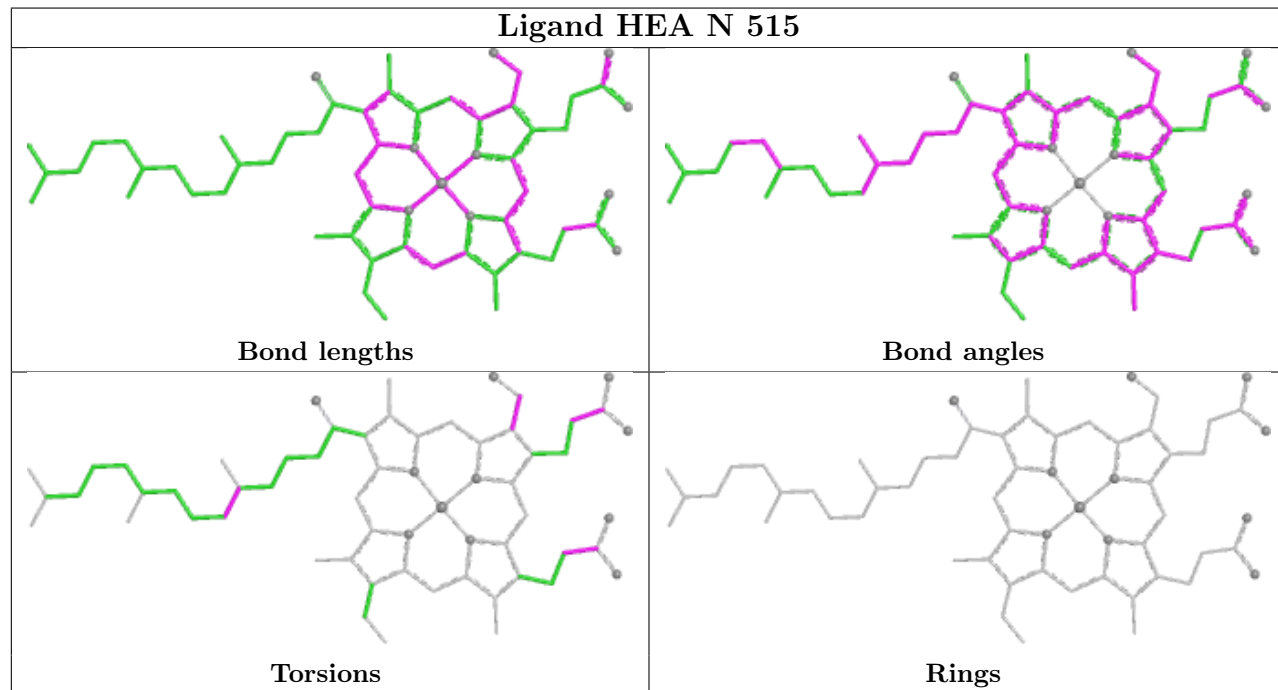
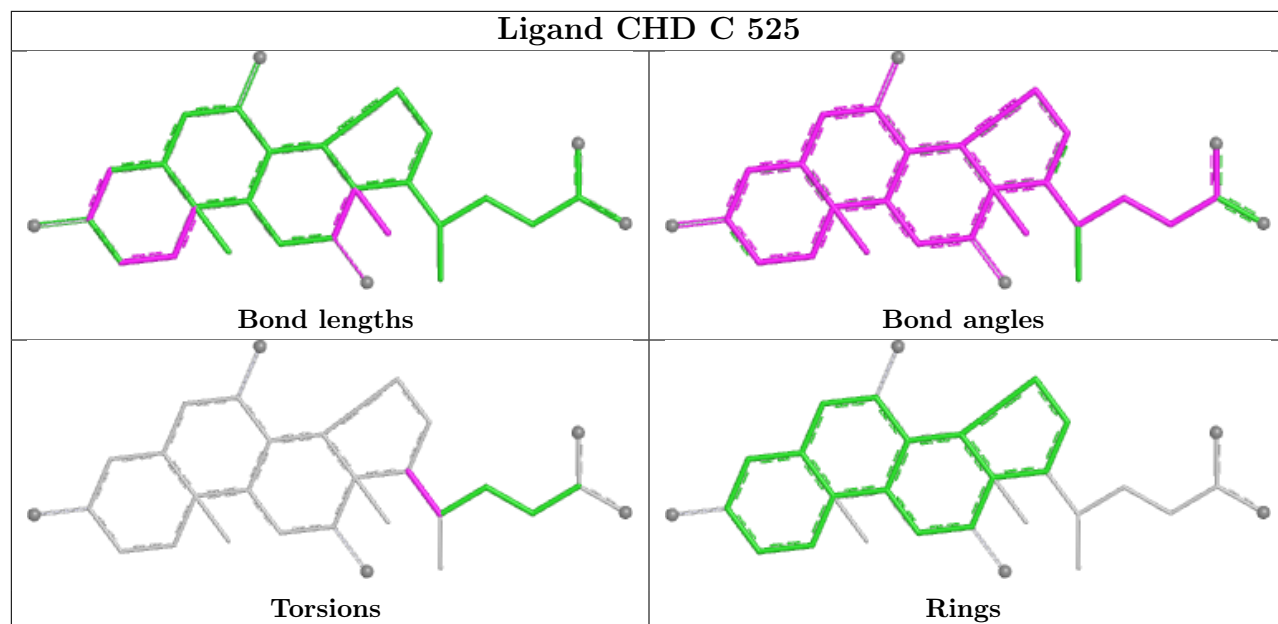


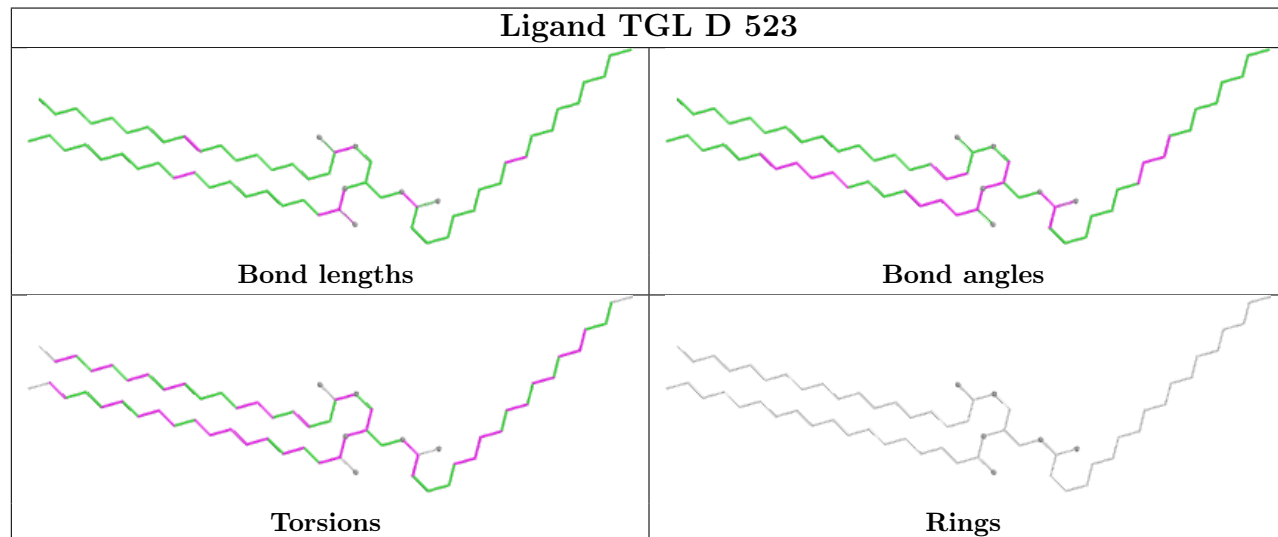
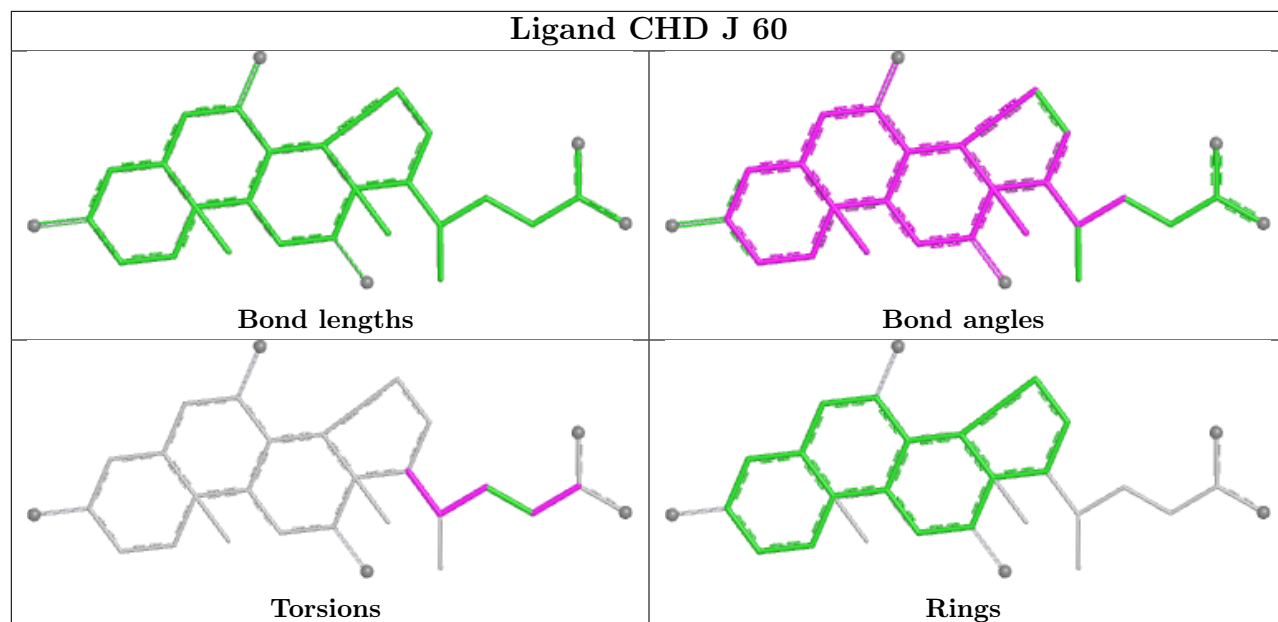


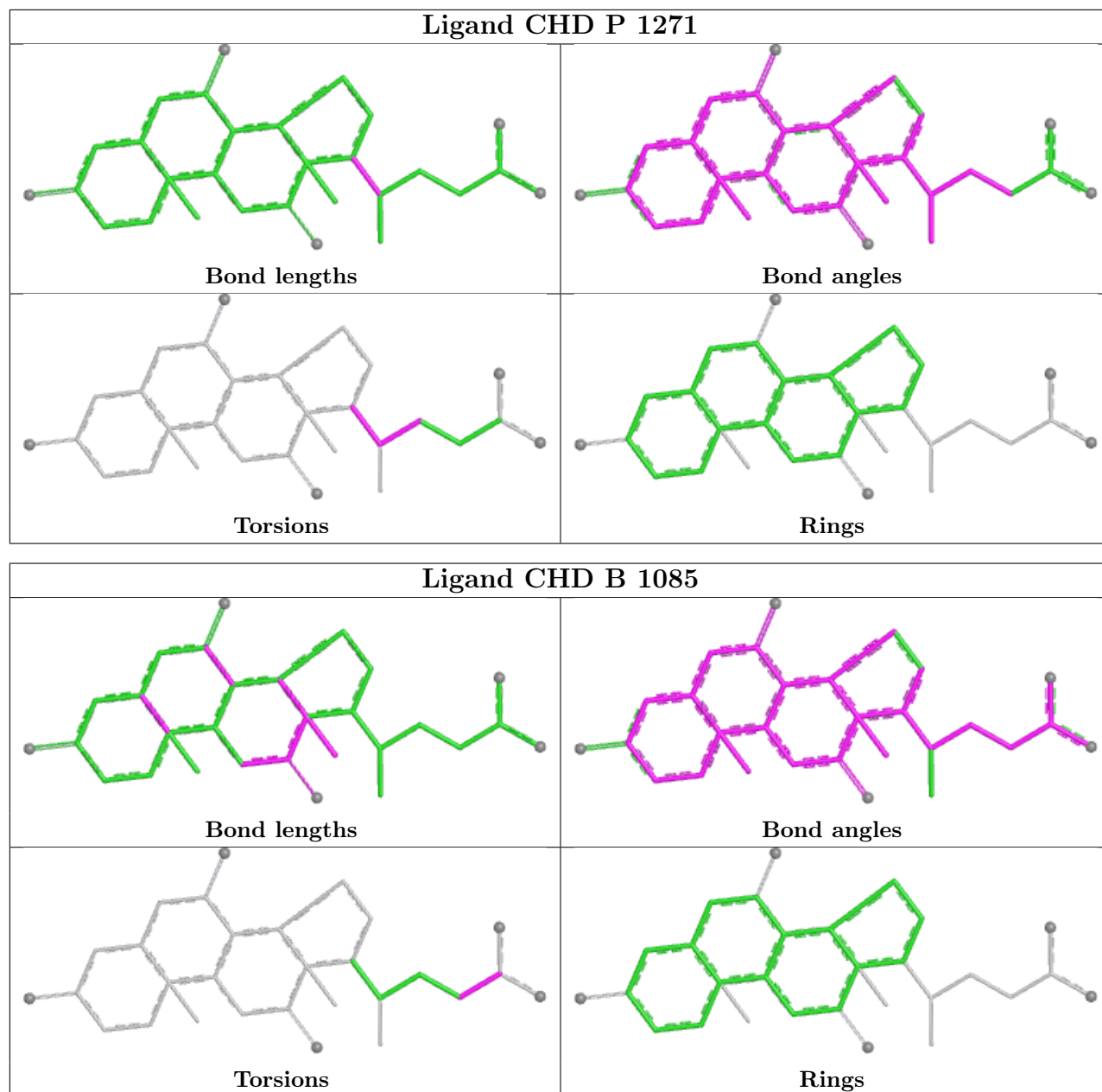


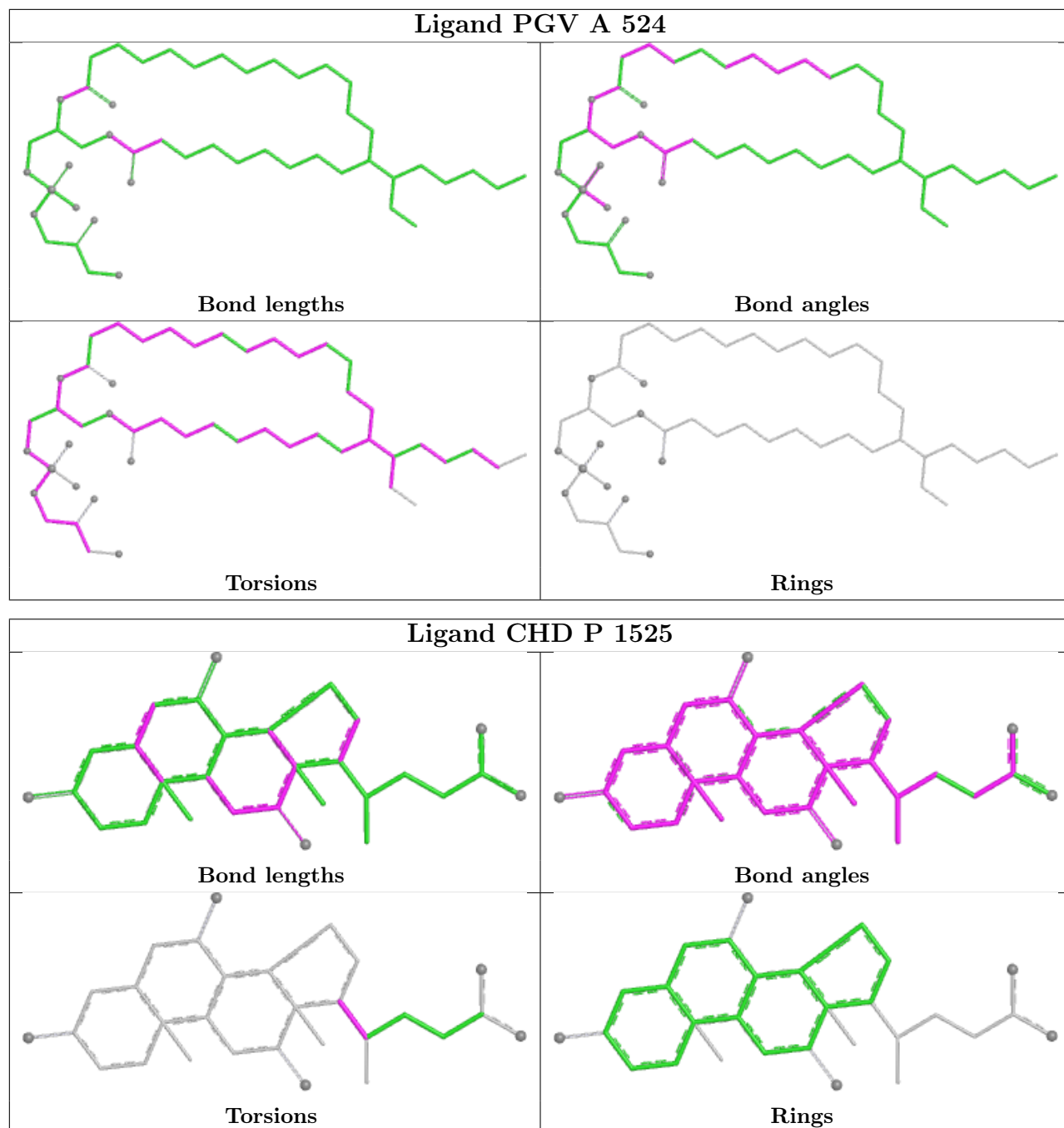


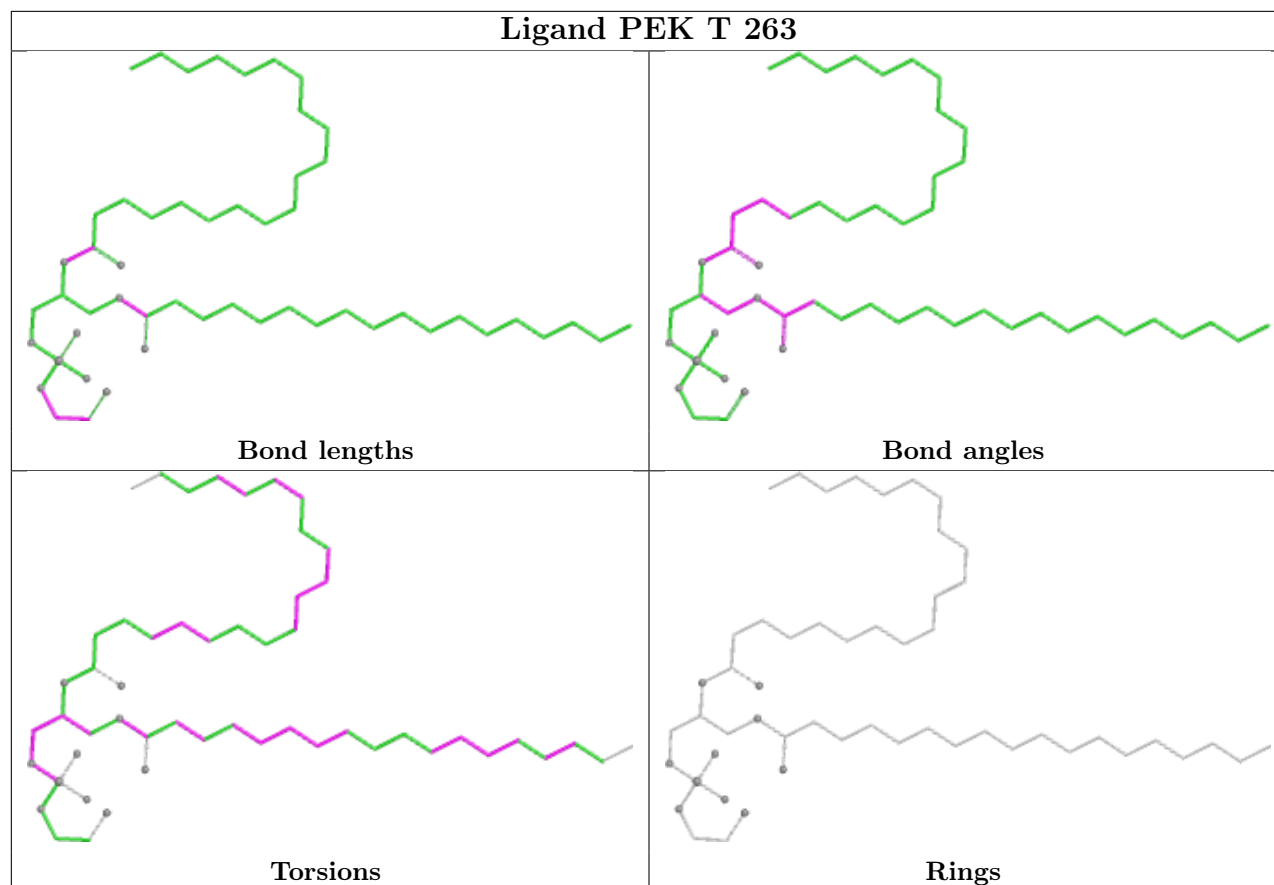












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

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%)	-0.44	2 (0%) 88 88	13, 29, 38, 65	5 (0%)
1	N	513/514 (99%)	0.15	5 (0%) 79 79	16, 35, 44, 71	5 (0%)
2	B	226/227 (99%)	0.01	9 (3%) 42 41	24, 33, 53, 72	0
2	O	226/227 (99%)	0.56	10 (4%) 39 38	31, 42, 64, 81	0
3	C	259/261 (99%)	-0.21	2 (0%) 82 82	26, 32, 43, 66	0
3	P	259/261 (99%)	0.20	5 (1%) 66 66	30, 36, 48, 67	0
4	D	144/147 (97%)	0.36	4 (2%) 55 54	30, 40, 53, 66	0
4	Q	144/147 (97%)	1.20	18 (12%) 8 7	39, 50, 71, 105	0
5	E	105/109 (96%)	0.50	1 (0%) 79 79	33, 40, 64, 97	0
5	R	105/109 (96%)	0.95	10 (9%) 14 12	36, 46, 70, 97	0
6	F	98/98 (100%)	0.69	8 (8%) 17 16	30, 41, 80, 117	0
6	S	98/98 (100%)	0.87	12 (12%) 8 7	34, 46, 80, 113	0
7	G	83/85 (97%)	0.84	18 (21%) 2 2	29, 38, 90, 106	0
7	T	83/85 (97%)	1.11	20 (24%) 2 2	32, 41, 91, 106	0
8	H	79/85 (92%)	0.51	8 (10%) 12 11	29, 41, 81, 101	0
8	U	79/85 (92%)	0.83	11 (13%) 6 5	37, 47, 85, 106	0
9	I	72/73 (98%)	0.76	8 (11%) 10 9	31, 46, 65, 70	0
9	V	72/73 (98%)	1.19	11 (15%) 5 4	36, 52, 67, 77	0
10	J	58/59 (98%)	0.50	3 (5%) 33 31	32, 41, 66, 95	0
10	W	58/59 (98%)	1.10	7 (12%) 8 8	36, 45, 67, 97	0
11	K	49/56 (87%)	0.67	4 (8%) 17 16	31, 39, 54, 64	0
11	X	49/56 (87%)	1.44	10 (20%) 3 2	42, 50, 66, 78	0
12	L	46/47 (97%)	-0.01	2 (4%) 40 39	29, 34, 51, 77	0
12	Y	46/47 (97%)	0.93	4 (8%) 16 15	35, 43, 60, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	43/46 (93%)	0.48	6 (13%) 6 5	31, 34, 72, 96	0
13	Z	43/46 (93%)	1.26	9 (20%) 2 2	39, 44, 81, 104	0
All	All	3550/3614 (98%)	0.35	207 (5%) 29 27	13, 38, 64, 117	10 (0%)

The worst 5 of 207 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	S	1	ALA	13.5
6	F	1	ALA	12.6
4	Q	6	VAL	8.3
6	S	98	HIS	7.5
6	S	97	ALA	7.5

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	0.34	0.24	83,84,85,86	0
9	SAC	I	1	9/10	0.63	0.23	73,76,78,80	0
7	TPO	T	11	11/12	0.66	0.25	75,82,102,103	0
7	TPO	G	11	11/12	0.67	0.29	69,76,102,102	0
1	FME	N	1	10/11	0.83	0.19	46,53,78,82	0
1	FME	A	1	10/11	0.89	0.15	44,51,71,75	0
2	FME	B	1	10/11	0.96	0.08	33,33,41,48	0
2	FME	O	1	10/11	0.96	0.09	40,42,47,55	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column

labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

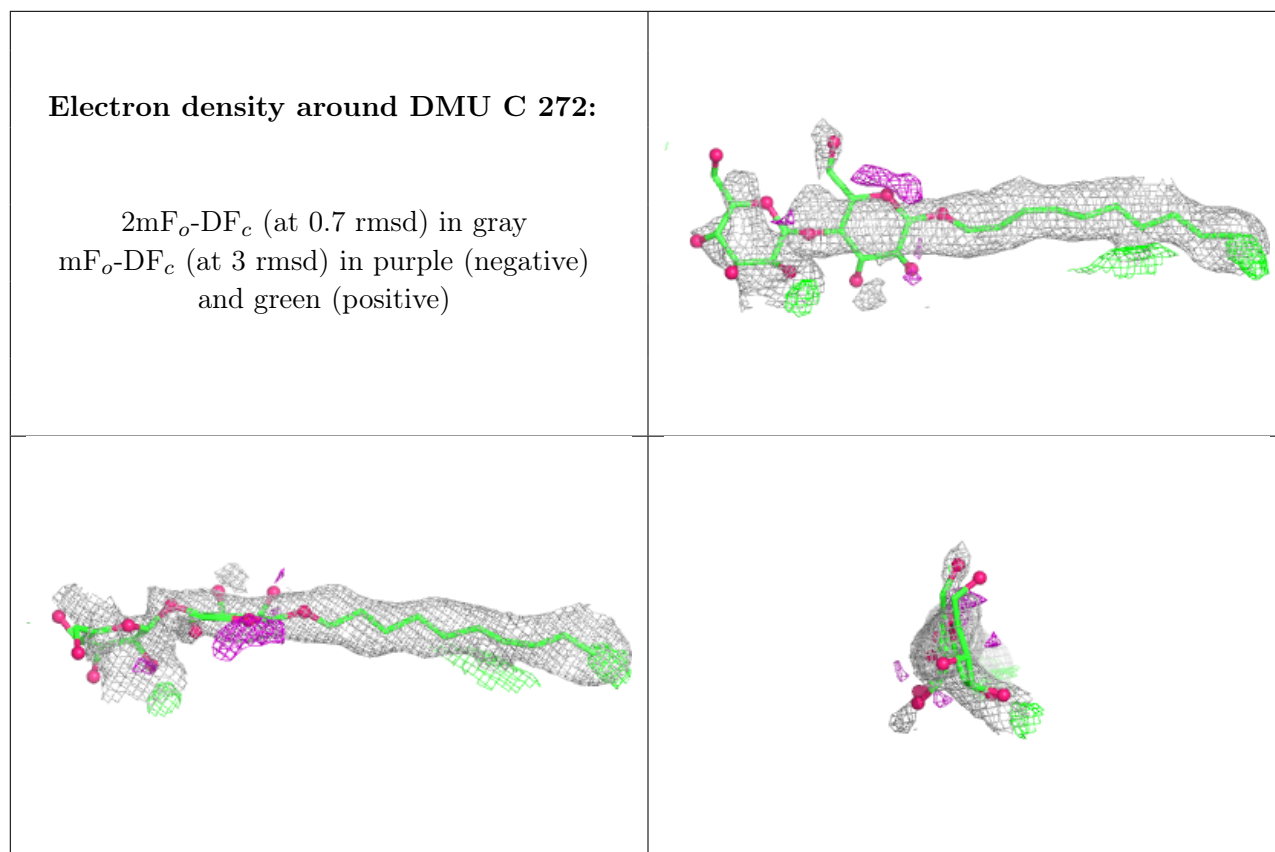
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
24	UNX	C	262	1/1	0.42	0.59	80,80,80,80	0
24	UNX	P	262	1/1	0.47	0.48	79,79,79,79	0
27	DMU	C	272	33/33	0.74	0.20	68,100,115,116	0
27	DMU	P	272	33/33	0.74	0.22	77,107,124,124	0
25	PEK	T	1265	53/53	0.76	0.23	49,79,110,118	0
23	CHD	J	60	29/29	0.77	0.23	99,105,108,110	0
19	PGV	U	1268	51/51	0.77	0.24	60,84,103,105	0
23	CHD	W	1059	29/29	0.78	0.23	101,109,113,115	0
19	PGV	A	524	51/51	0.78	0.20	44,72,112,114	0
21	TGL	Y	1522	63/63	0.79	0.21	51,73,89,92	0
25	PEK	C	265	53/53	0.79	0.23	49,83,106,107	0
25	PEK	T	263	53/53	0.79	0.23	52,103,125,127	0
19	PGV	N	1524	51/51	0.79	0.20	54,74,103,105	0
21	TGL	D	523	63/63	0.79	0.20	48,69,91,91	0
21	TGL	N	1523	63/63	0.79	0.22	61,79,97,99	0
26	CDL	T	1269	100/100	0.80	0.20	58,86,114,118	0
19	PGV	C	268	51/51	0.80	0.23	53,81,98,102	0
21	TGL	O	1521	63/63	0.80	0.20	58,80,95,96	0
22	PSC	R	1229	52/52	0.81	0.21	48,99,136,139	0
26	CDL	G	269	100/100	0.82	0.20	62,86,116,120	0
25	PEK	G	1263	53/53	0.82	0.24	52,103,133,134	0
21	TGL	L	522	63/63	0.82	0.20	43,66,82,89	0
21	TGL	B	521	63/63	0.82	0.21	53,74,88,90	0
26	CDL	P	1270	100/100	0.83	0.20	36,94,119,119	0
26	CDL	C	270	100/100	0.83	0.20	41,91,129,130	0
22	PSC	B	229	52/52	0.84	0.21	43,92,139,143	0
23	CHD	C	271	29/29	0.84	0.17	79,83,85,85	0
23	CHD	P	1271	29/29	0.85	0.20	78,92,94,95	0
27	DMU	Z	1526	33/33	0.86	0.14	49,57,70,70	0
17	MG	N	518	1/1	0.93	0.07	34,34,34,34	0
27	DMU	M	526	33/33	0.93	0.10	33,47,65,71	0
25	PEK	C	264	53/53	0.94	0.12	30,46,78,80	0
25	PEK	P	1264	53/53	0.94	0.13	35,50,86,88	0
23	CHD	O	229	29/29	0.94	0.08	27,32,38,40	0
19	PGV	N	1266	51/51	0.95	0.10	30,42,65,69	0
19	PGV	P	1267	51/51	0.95	0.11	29,40,82,87	0
18	NA	N	519	1/1	0.95	0.15	39,39,39,39	0
15	NO	N	520	2/2	0.95	0.17	39,39,39,42	0
23	CHD	C	525	29/29	0.96	0.06	26,33,39,41	0
23	CHD	P	1525	29/29	0.96	0.08	32,37,43,47	0
19	PGV	C	267	51/51	0.96	0.10	28,40,73,76	0
23	CHD	B	1085	29/29	0.96	0.06	27,31,36,42	0

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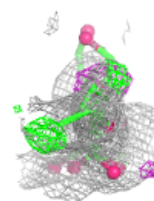
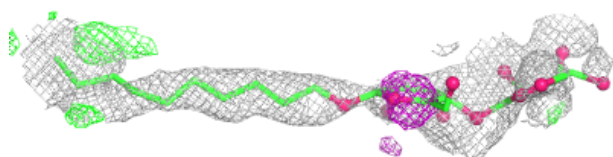
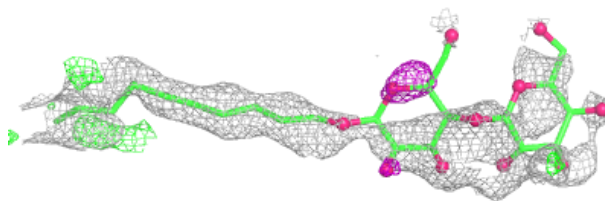
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
15	NO	A	520	2/2	0.97	0.12	32,32,32,36	0
19	PGV	A	521	51/51	0.97	0.09	23,35,63,67	0
18	NA	A	519	1/1	0.97	0.10	32,32,32,32	0
17	MG	A	518	1/1	0.97	0.06	23,23,23,23	0
14	HEA	N	516	60/60	0.98	0.07	27,33,37,40	0
14	HEA	A	515	60/60	0.98	0.06	22,28,41,42	0
14	HEA	N	515	60/60	0.98	0.07	28,36,45,49	0
20	CUA	O	228	2/2	0.98	0.04	34,34,34,36	0
28	ZN	F	99	1/1	0.98	0.03	37,37,37,37	0
16	CU	N	517	1/1	0.99	0.04	35,35,35,35	0
20	CUA	B	228	2/2	0.99	0.03	27,27,27,28	0
14	HEA	A	516	60/60	0.99	0.05	18,26,31,36	0
28	ZN	S	99	1/1	0.99	0.03	43,43,43,43	0
16	CU	A	517	1/1	1.00	0.03	29,29,29,29	0

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

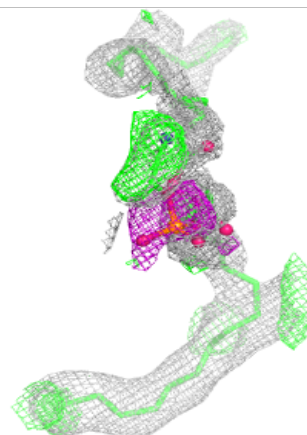
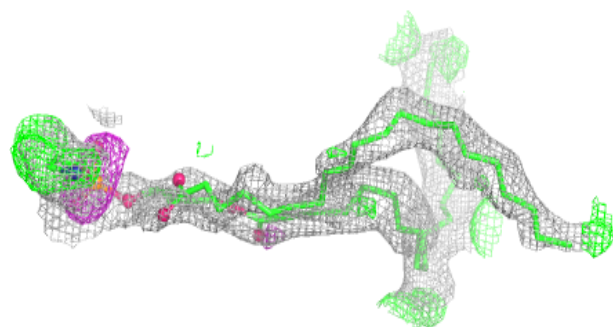
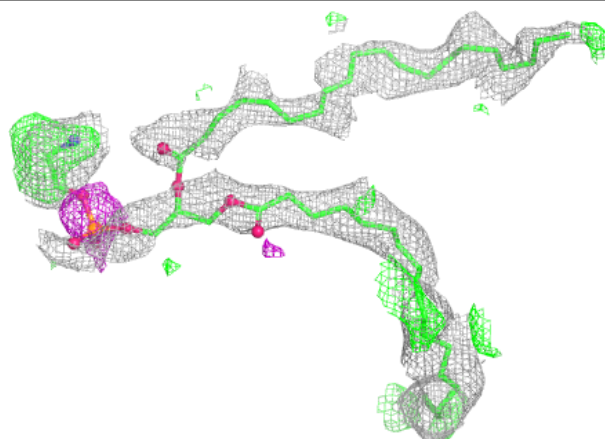


Electron density around DMU P 272:

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

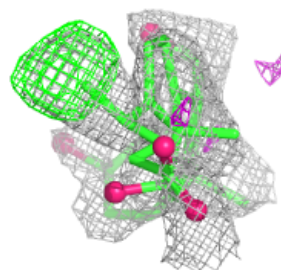
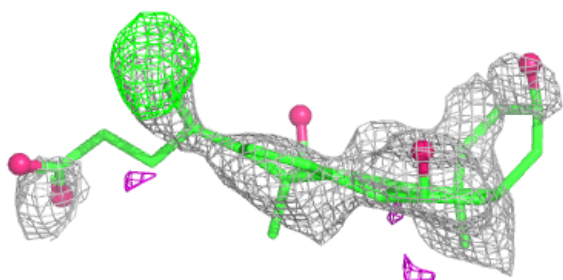
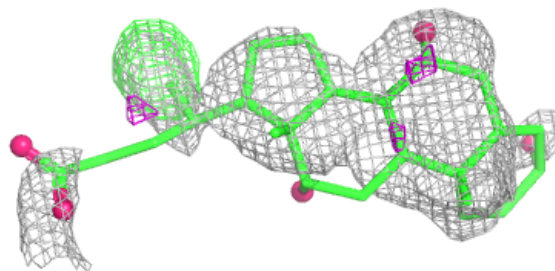
**Electron density around PEK T 1265:**

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

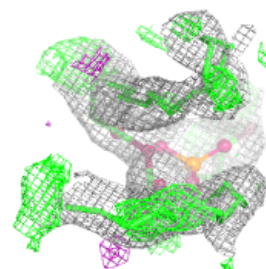
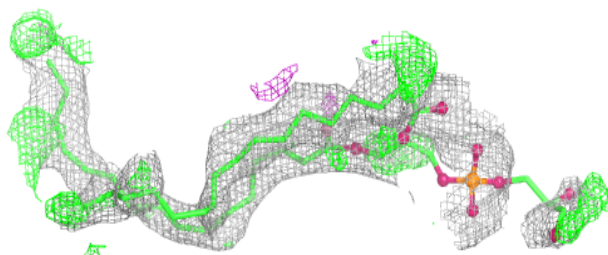
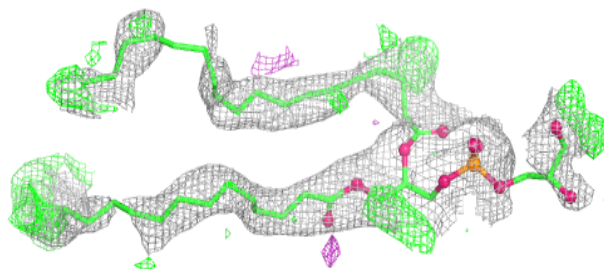


Electron density around CHD J 60:

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

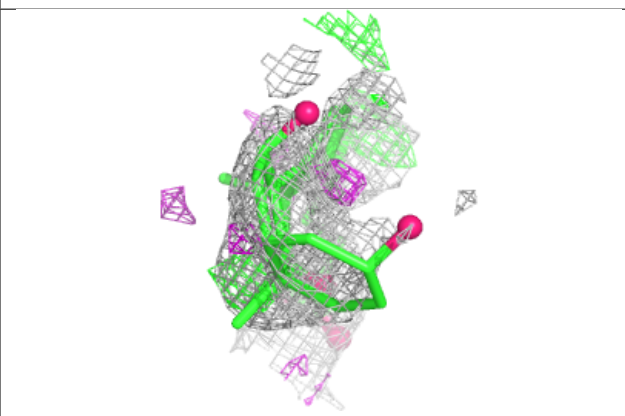
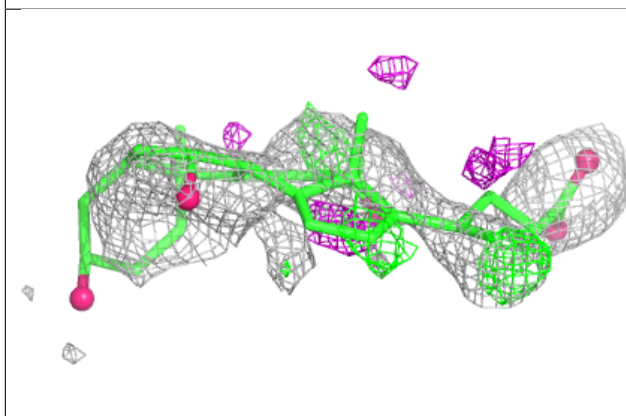
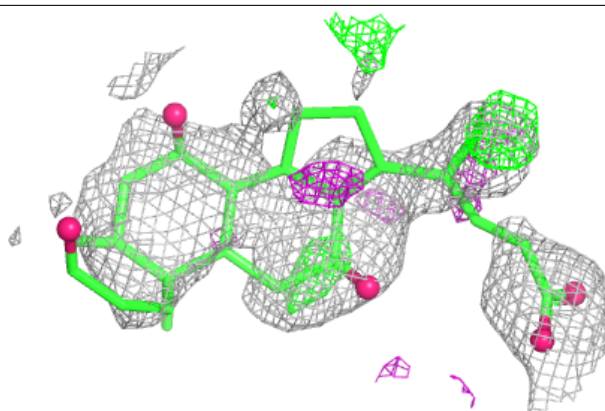
**Electron density around PGV U 1268:**

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and green (positive)

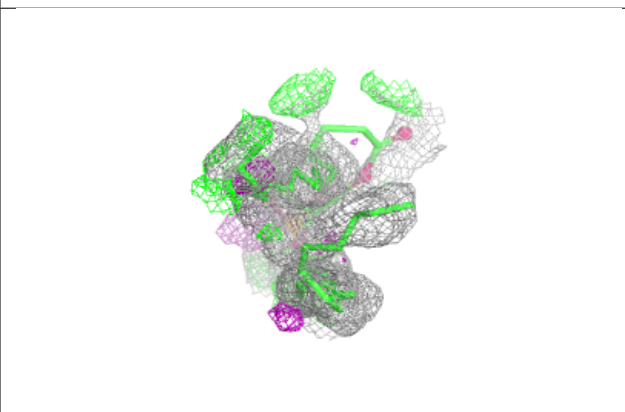
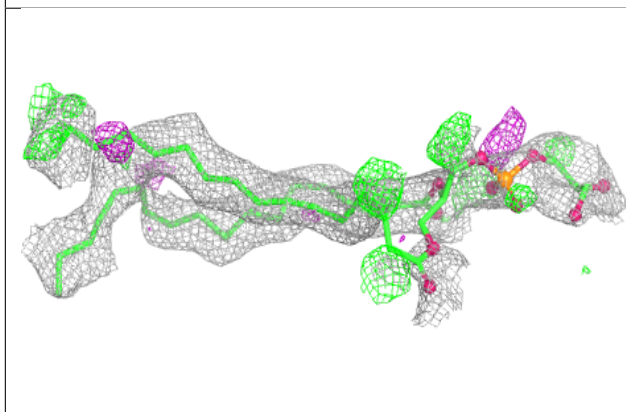
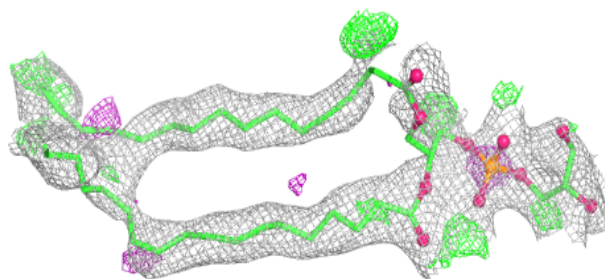


Electron density around CHD W 1059:

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and green (positive)

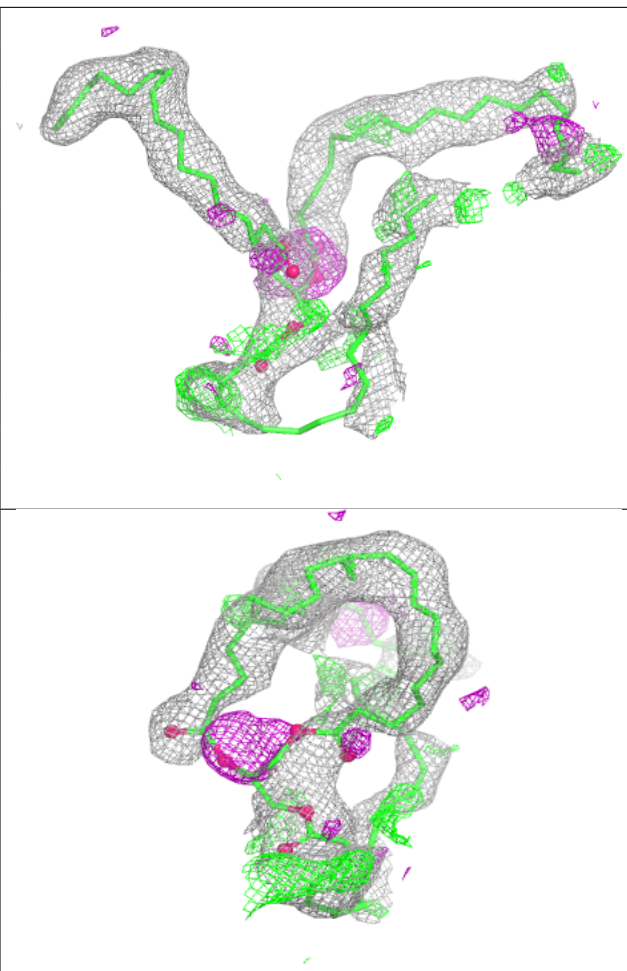
**Electron density around PGV A 524:**

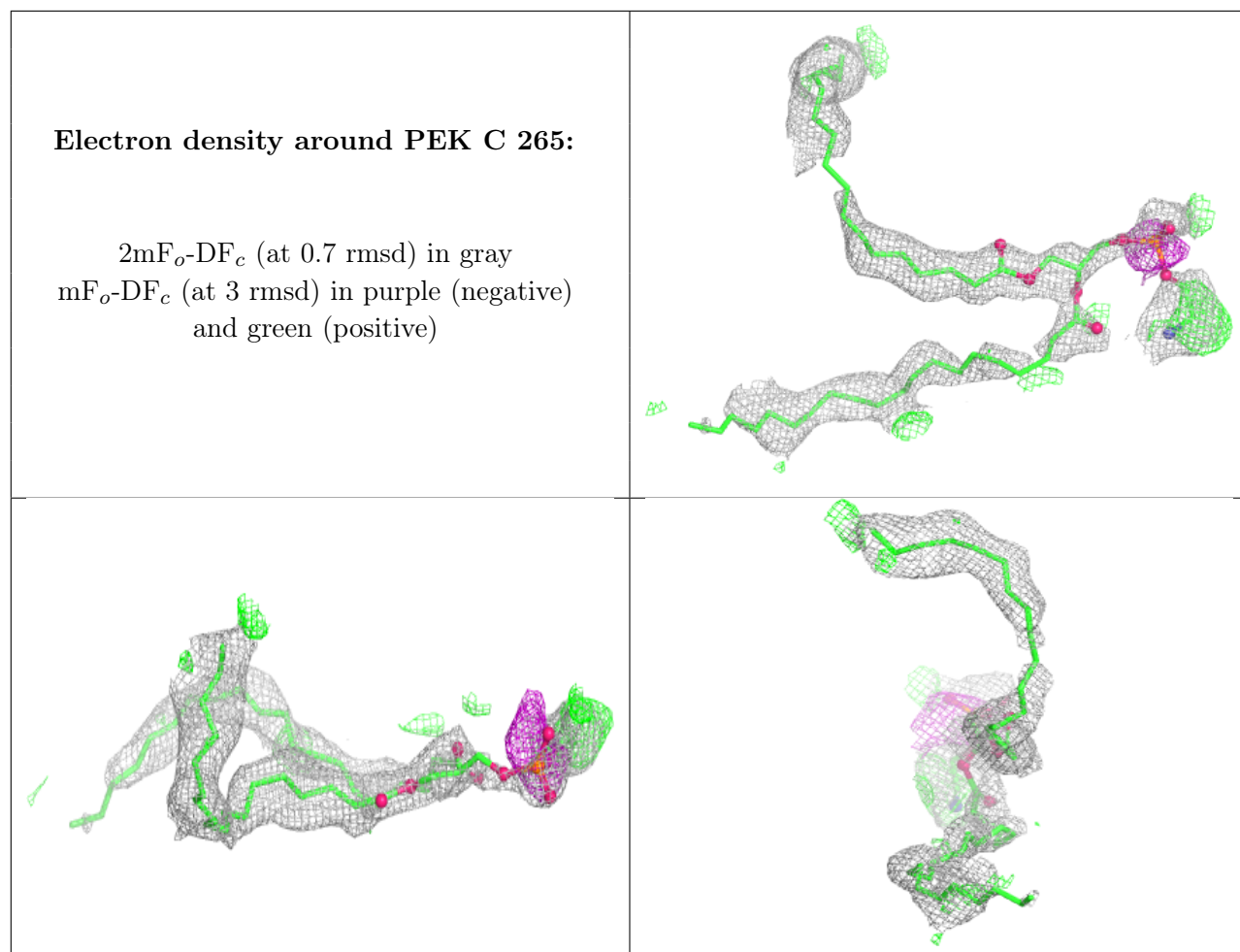
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

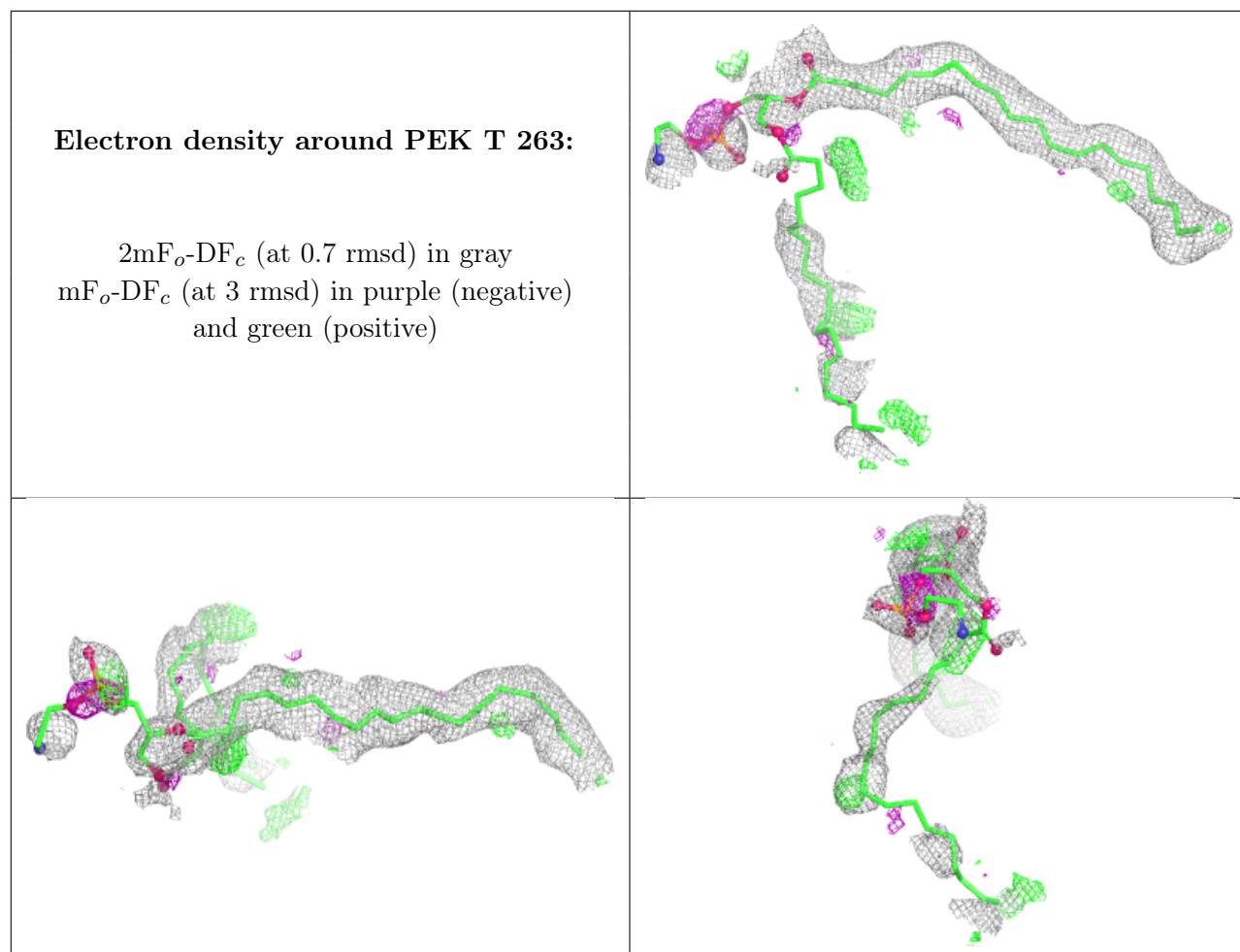


Electron density around TGL Y 1522:

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

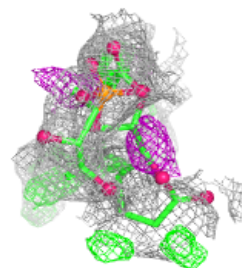
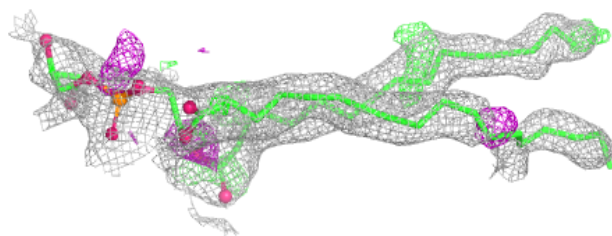
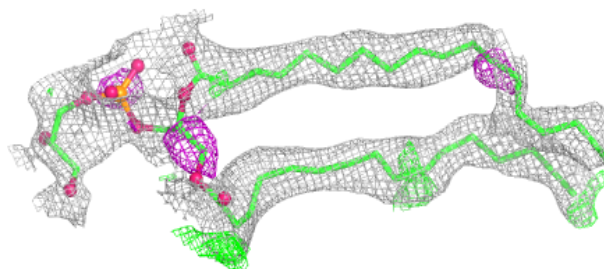




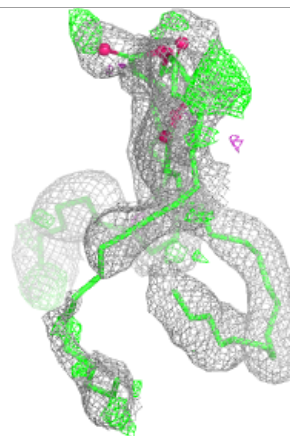
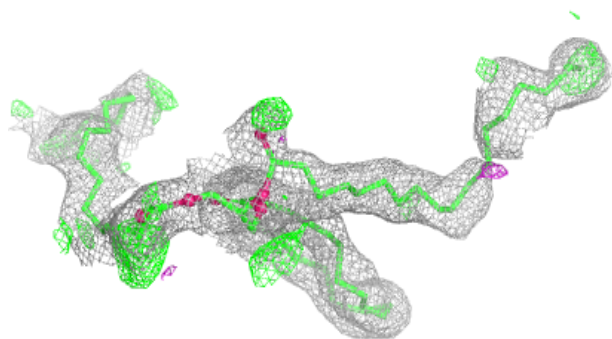
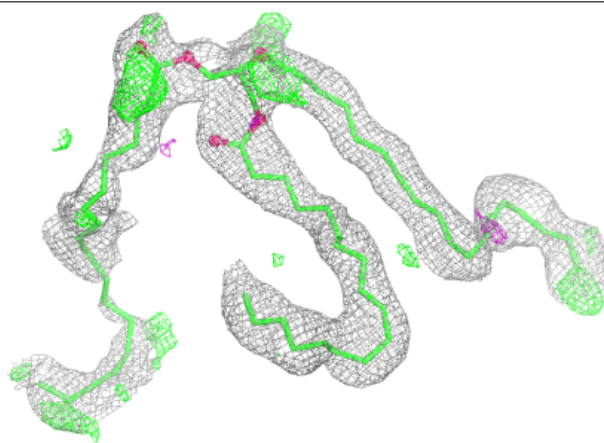


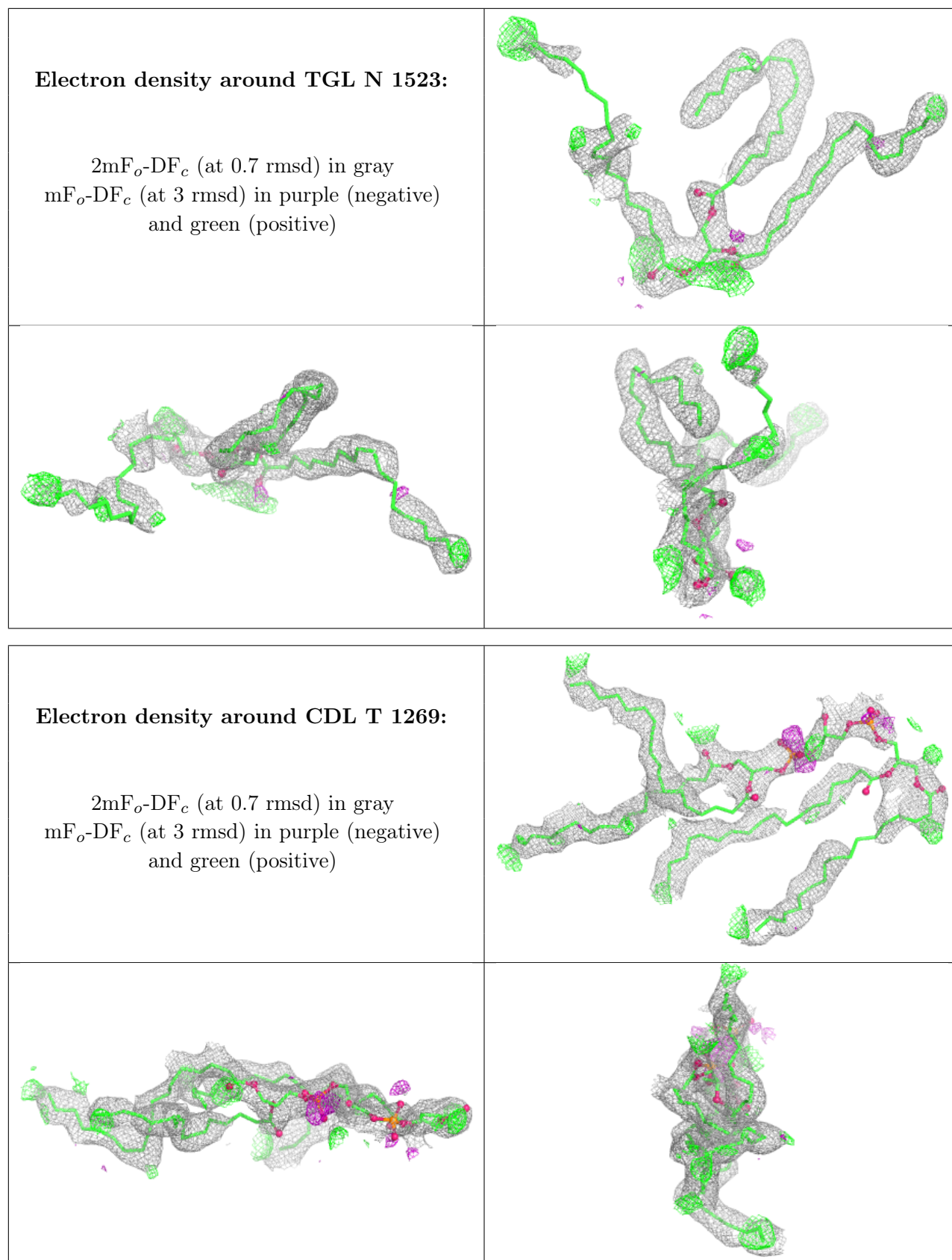
Electron density around PGV N 1524:

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

**Electron density around TGL D 523:**

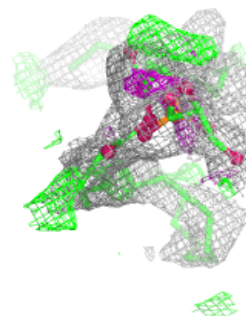
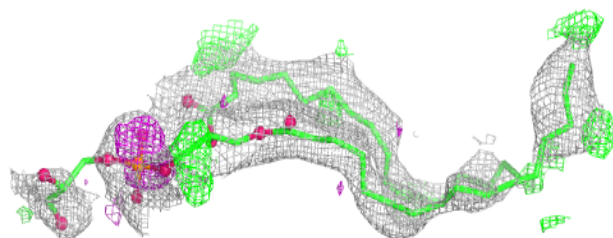
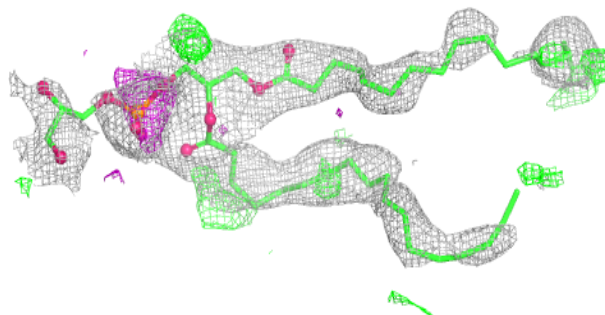
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



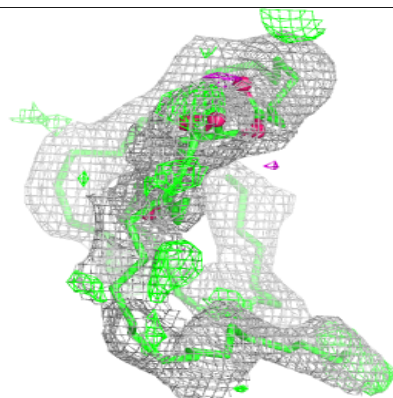
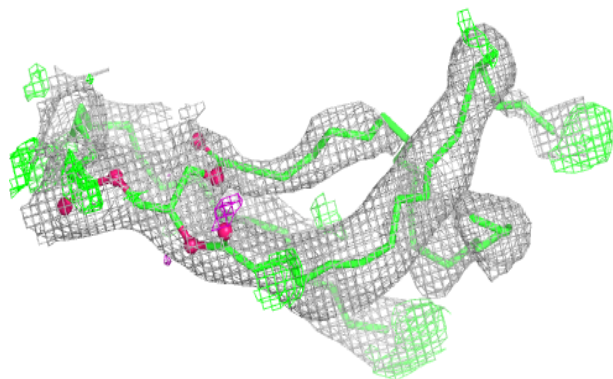
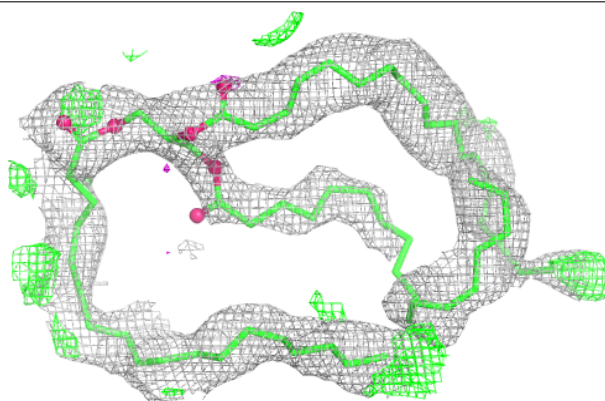


Electron density around PGV C 268:

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

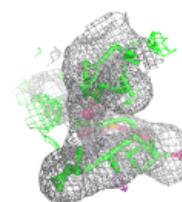
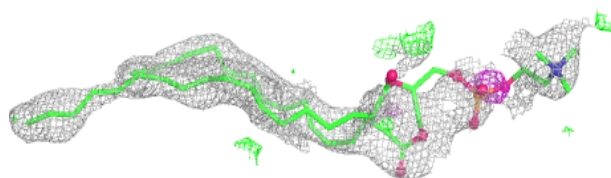
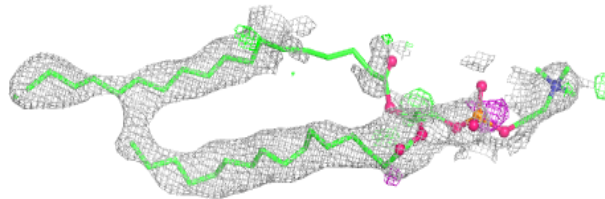
**Electron density around TGL O 1521:**

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

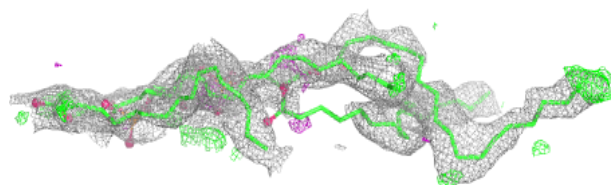
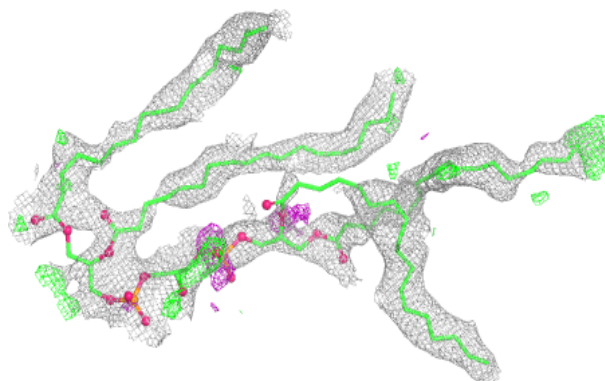


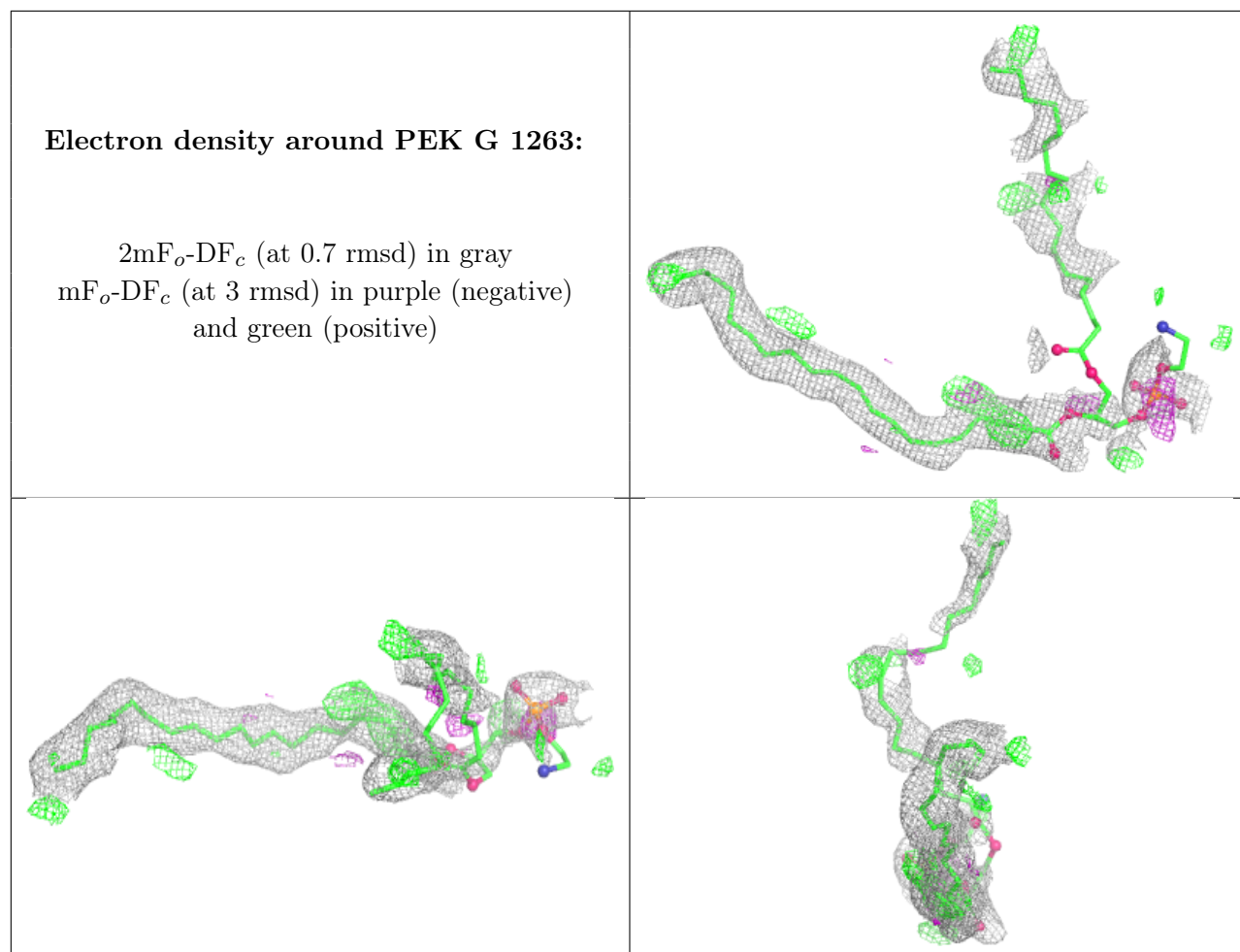
Electron density around PSC R 1229:

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

**Electron density around CDL G 269:**

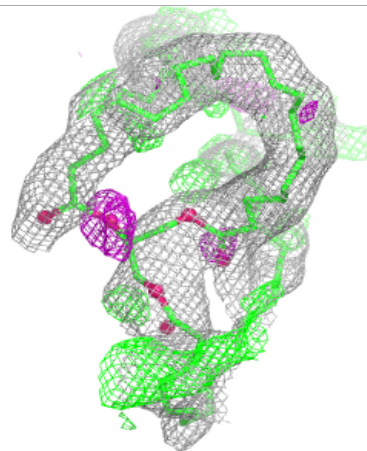
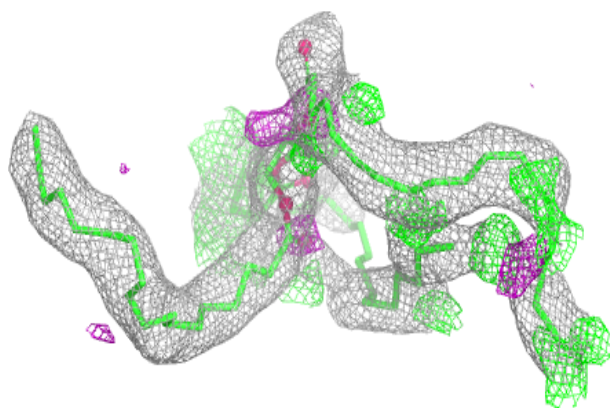
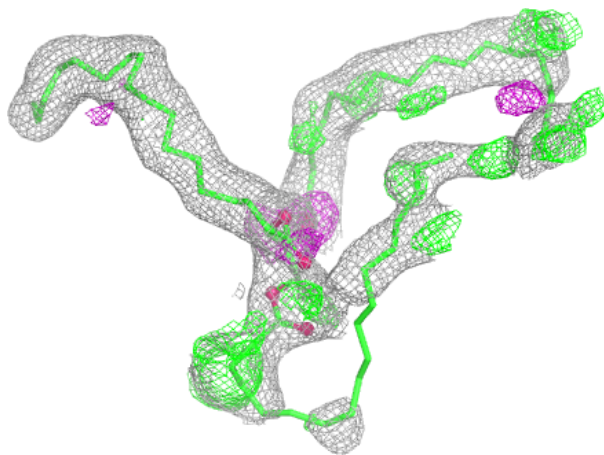
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





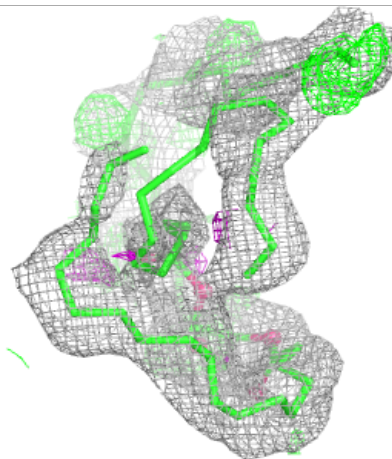
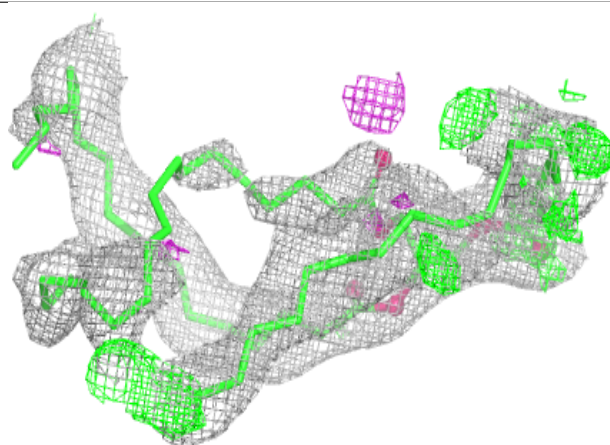
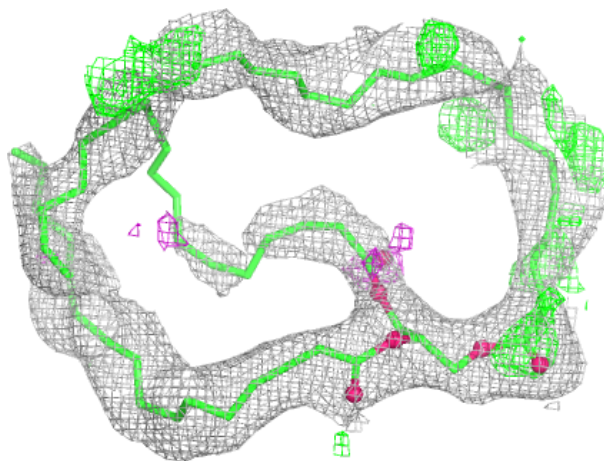
Electron density around TGL L 522:

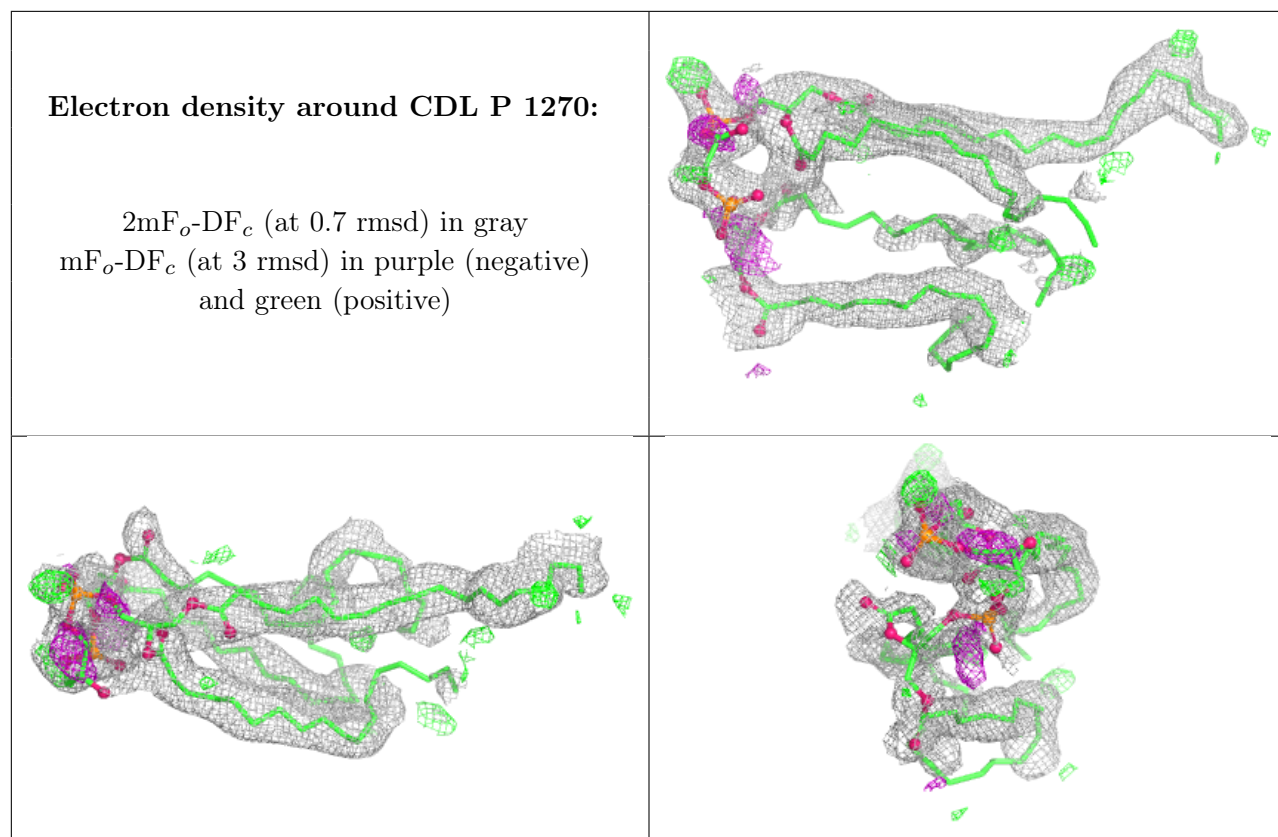
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

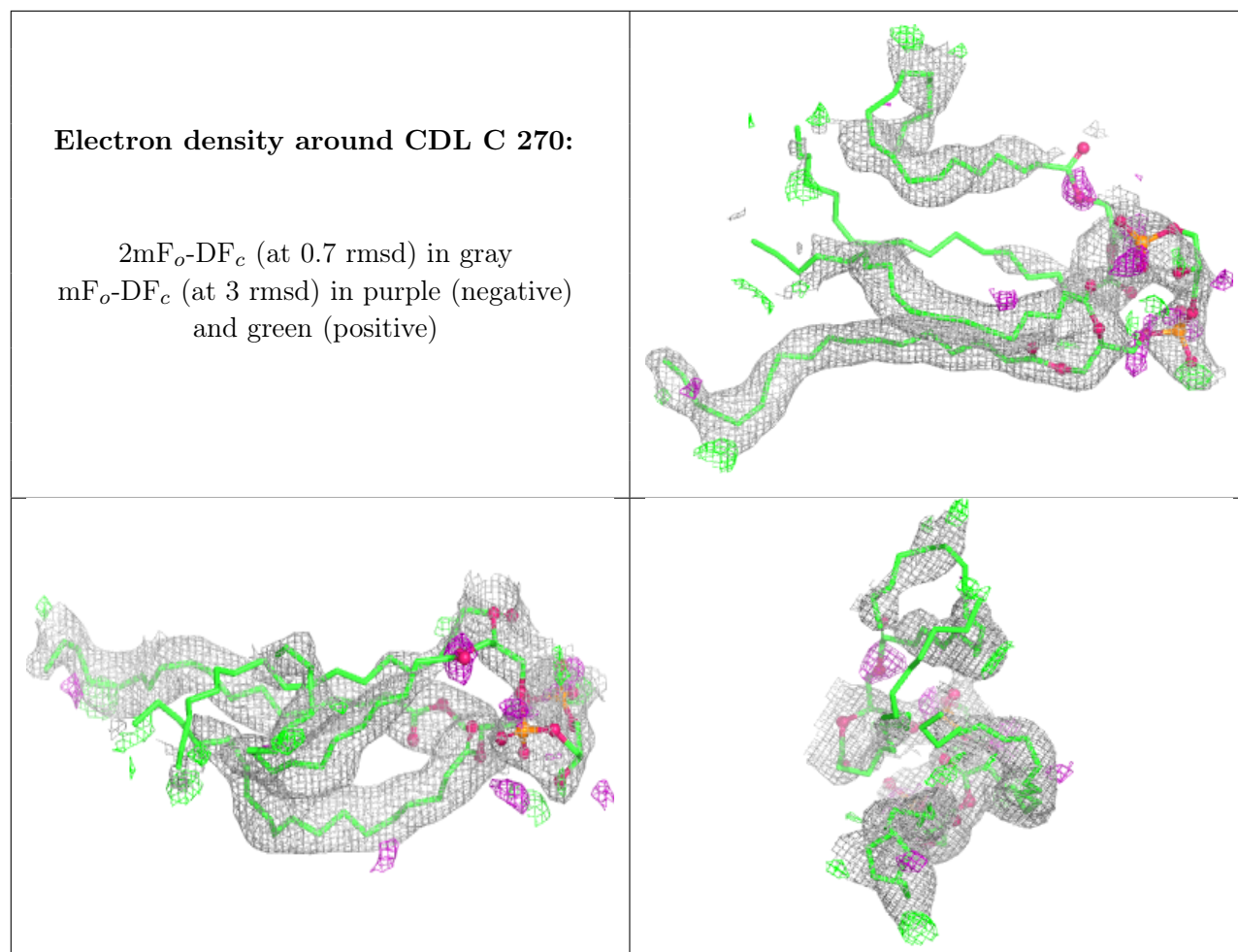


Electron density around TGL B 521:

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

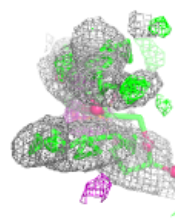
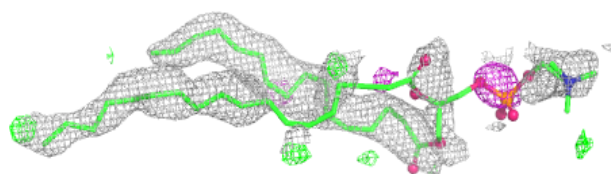
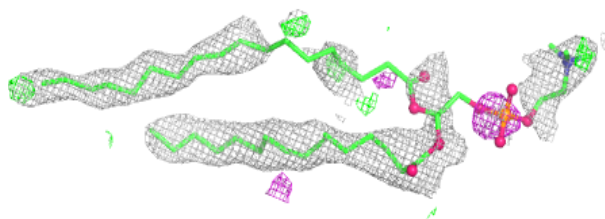




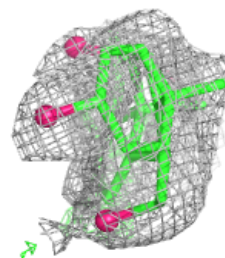
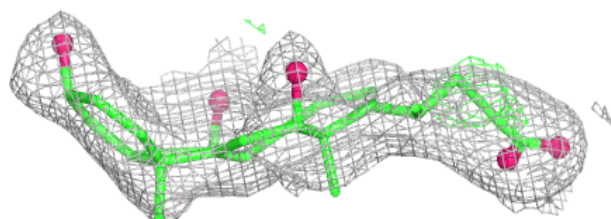
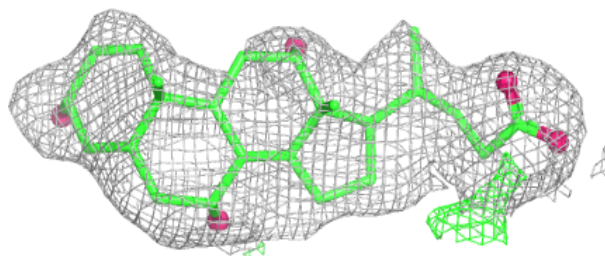


Electron density around PSC B 229:

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

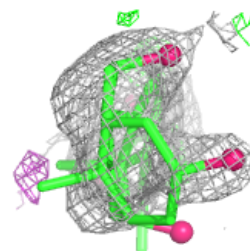
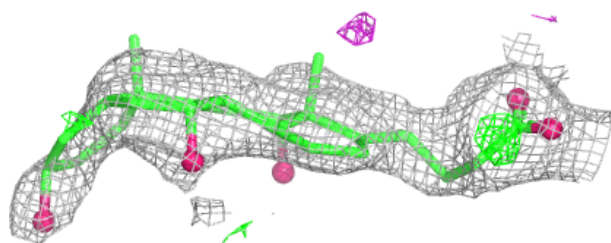
**Electron density around CHD C 271:**

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

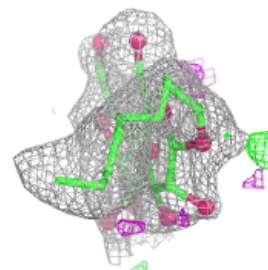
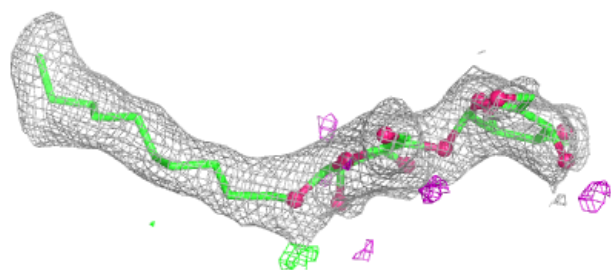


Electron density around CHD P 1271:

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

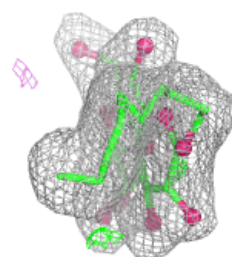
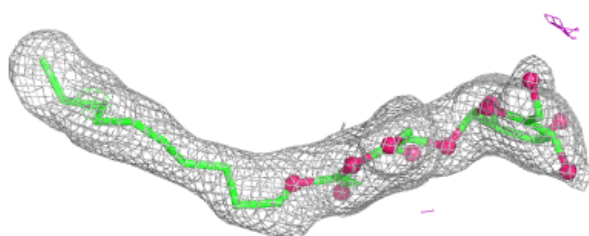
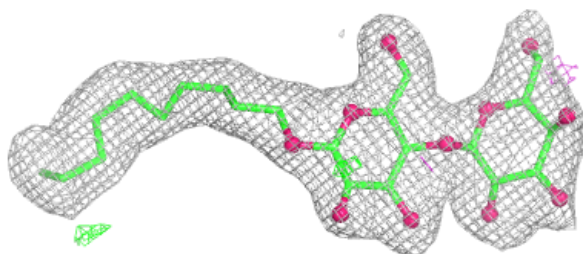
**Electron density around DMU Z 1526:**

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

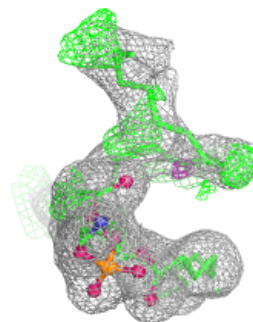
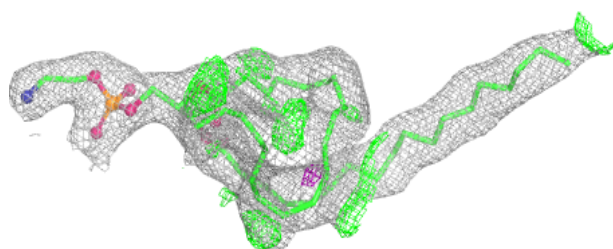
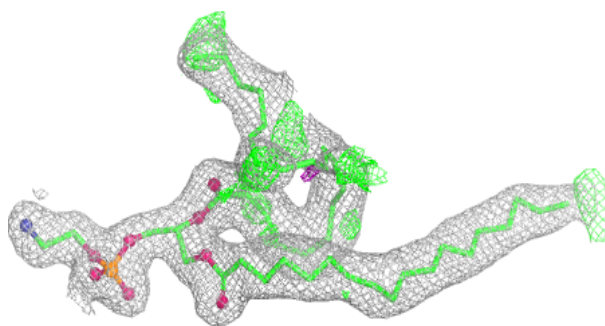


Electron density around DMU M 526:

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

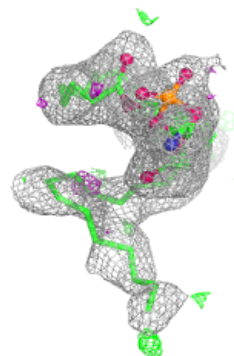
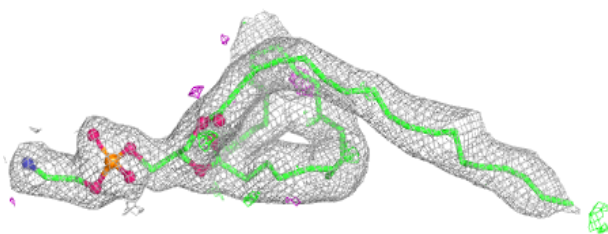
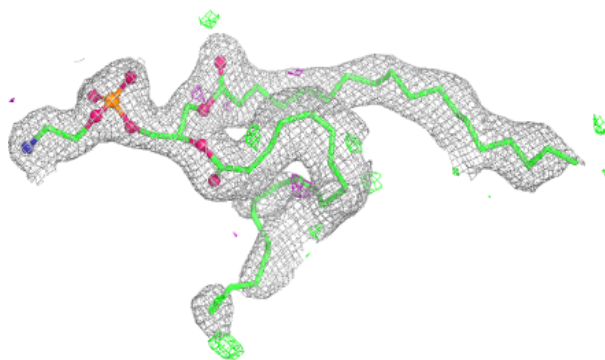
**Electron density around PEK C 264:**

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

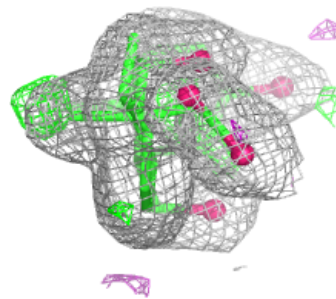
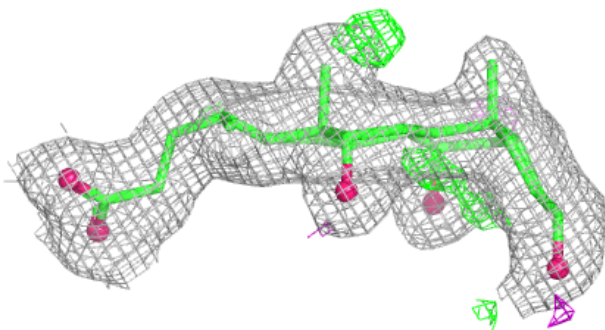
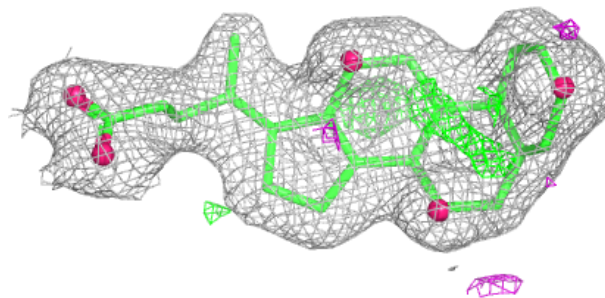


Electron density around PEK P 1264:

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

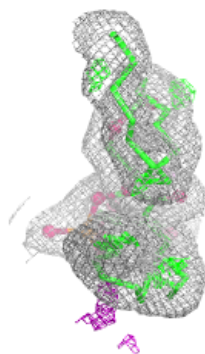
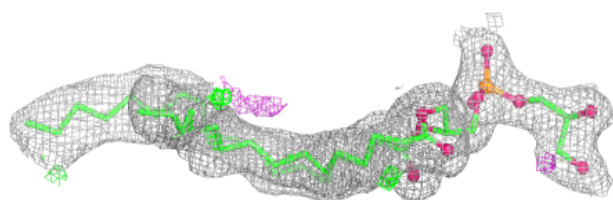
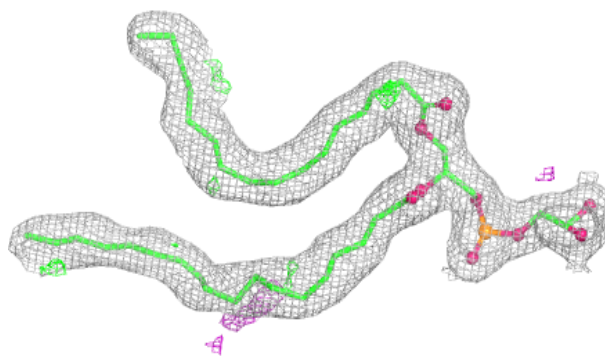
**Electron density around CHD O 229:**

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

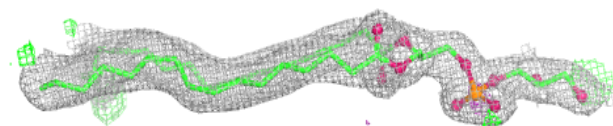
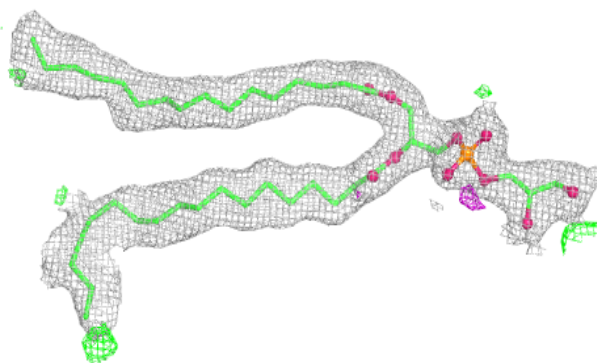


Electron density around PGV N 1266:

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

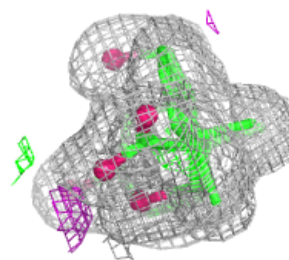
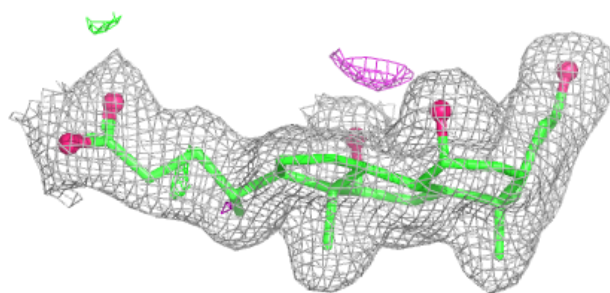
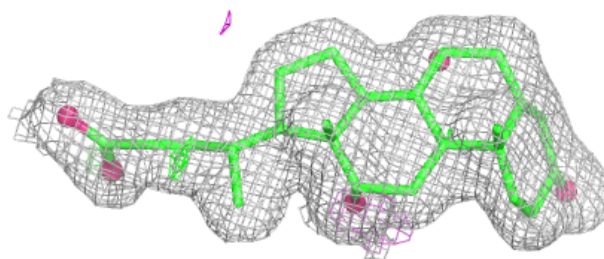
**Electron density around PGV P 1267:**

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

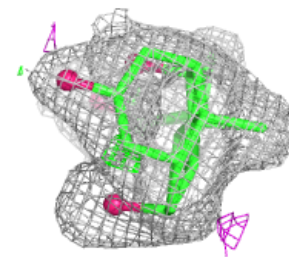
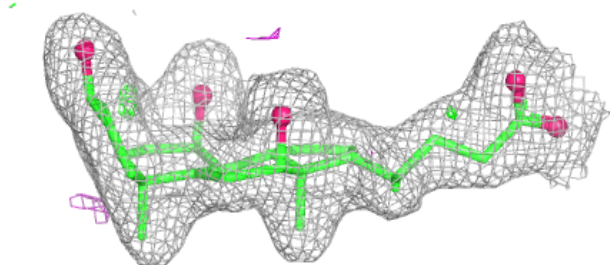
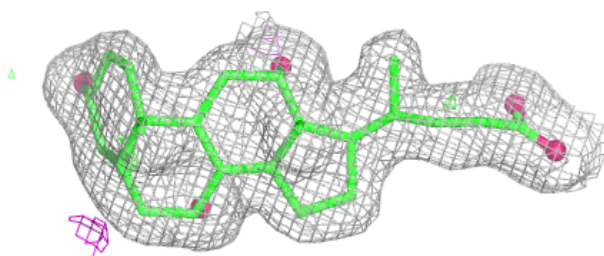


Electron density around CHD C 525:

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

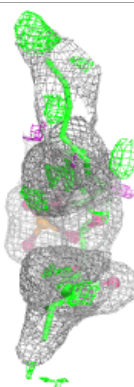
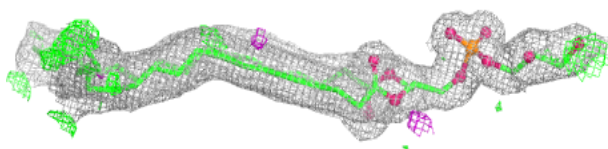
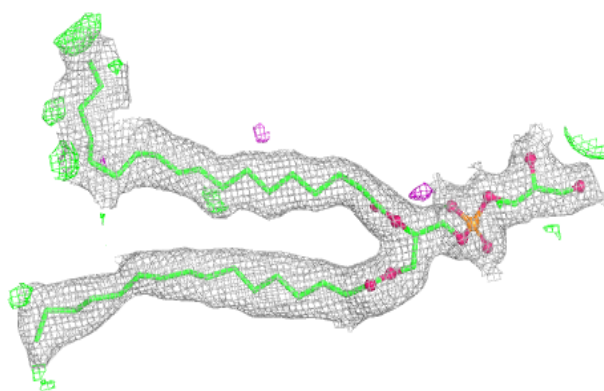
**Electron density around CHD P 1525:**

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

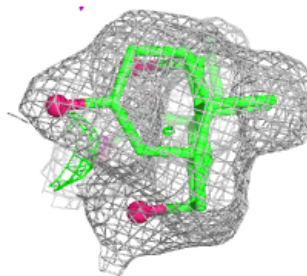
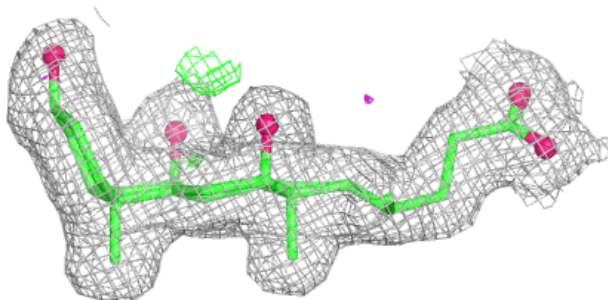
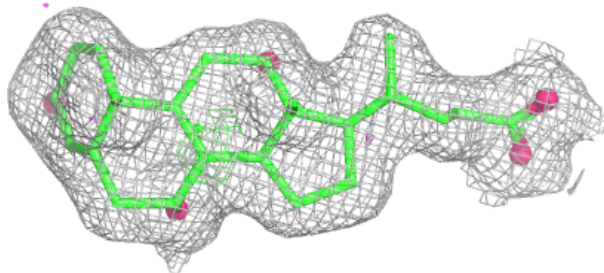


Electron density around PGV C 267:

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

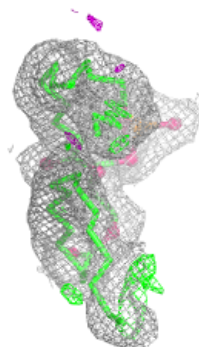
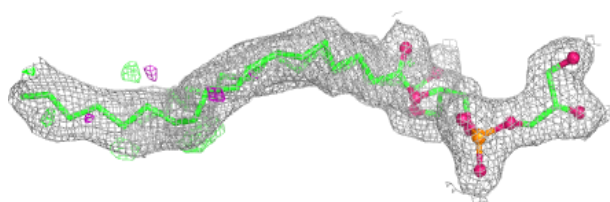
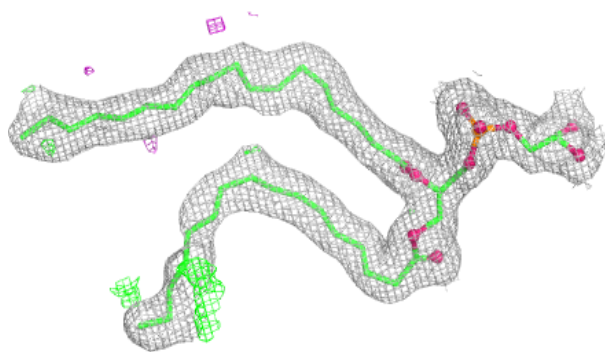
**Electron density around CHD B 1085:**

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

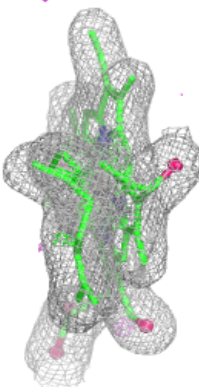
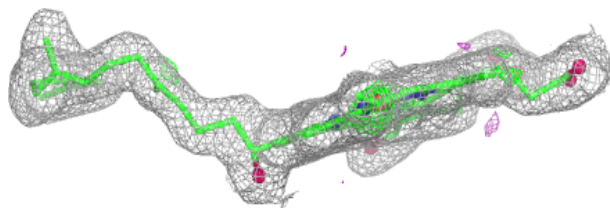
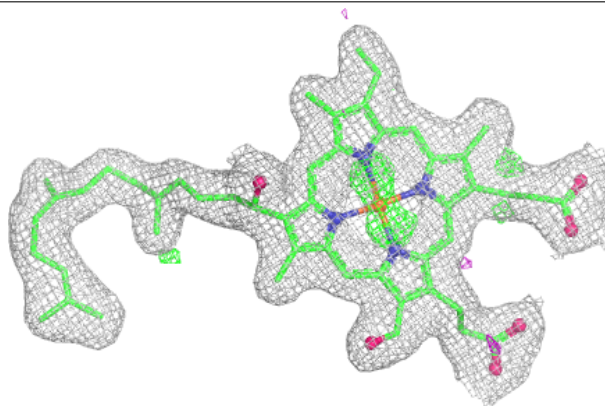


Electron density around PGV A 521:

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

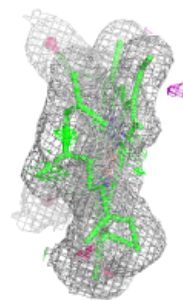
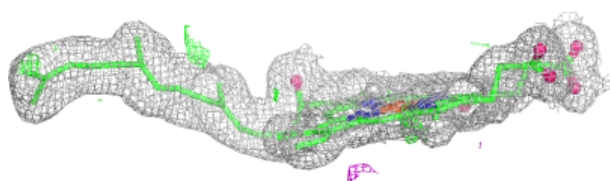
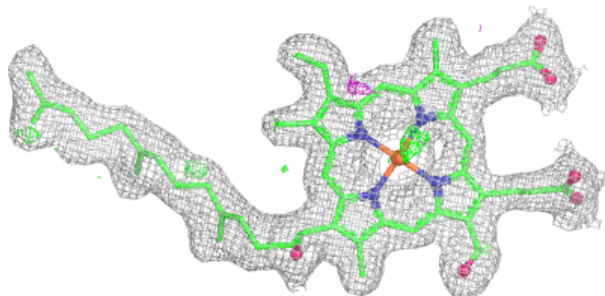
**Electron density around HEA N 516:**

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

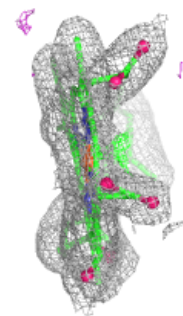
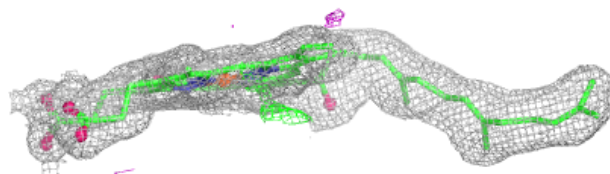
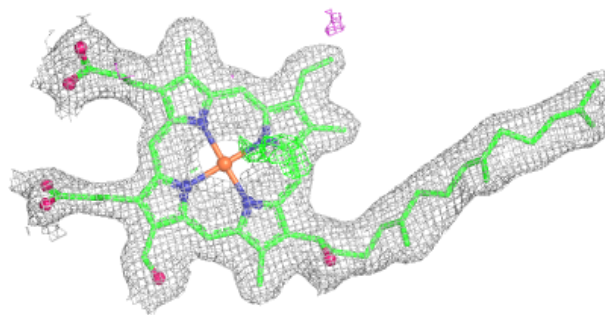


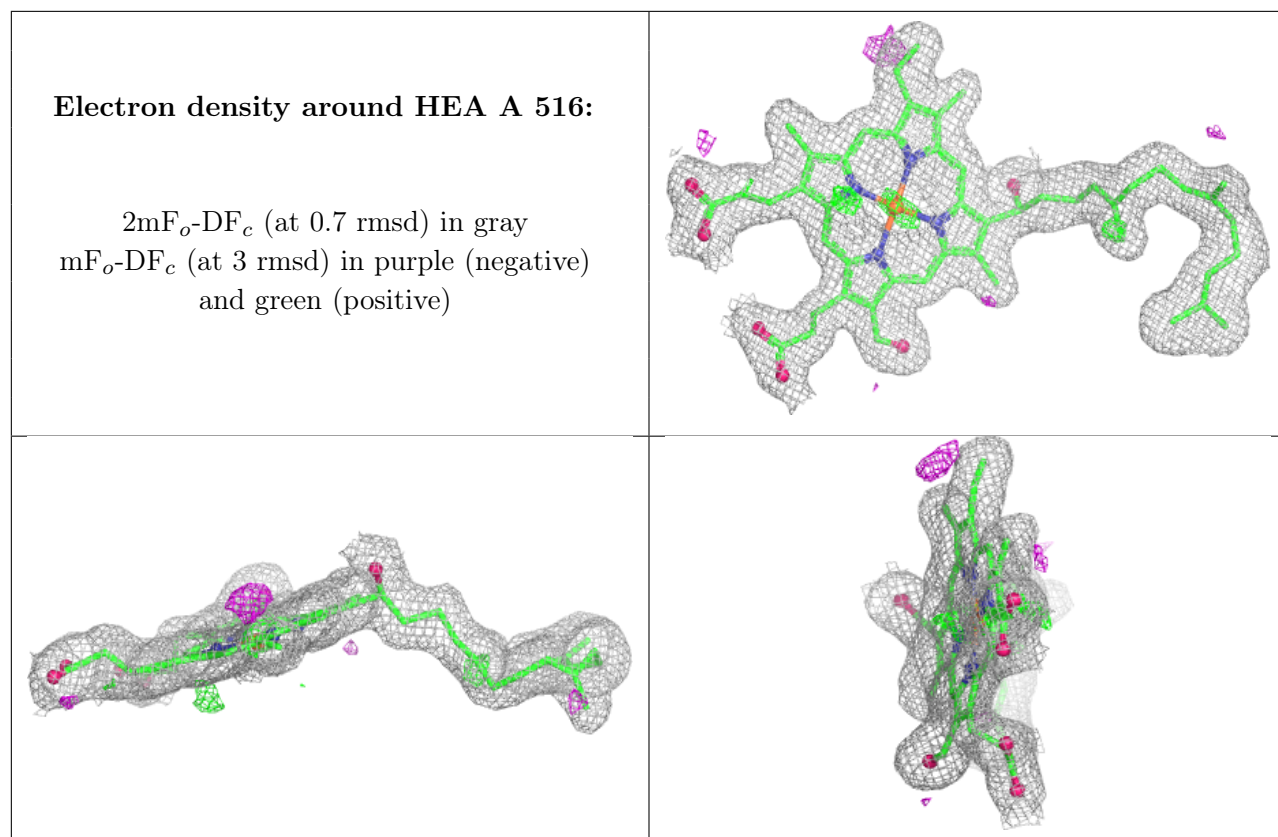
Electron density around HEA A 515:

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

**Electron density around HEA N 515:**

$2mF_o-DF_c$ (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.