wwPDB X-ray Structure Validation Summary Report (i)

Oct 23, 2023 – 11:52 PM EDT

PDB ID	:	3AG1
Title	:	Bovine Heart Cytochrome c Oxidase in the Carbon Monoxide-bound Fully Reduced State at 280 K
Authors	:	Muramoto, K.; Ohta, K.; Shinzawa-Itoh, K.; Kanda, K.; Taniguchi, M.; Nabekura, H.; Yamashita, E.; Tsukihara, T.; Yoshikawa, S.
Deposited on	:	2010-03-19
Resolution	:	2.20 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

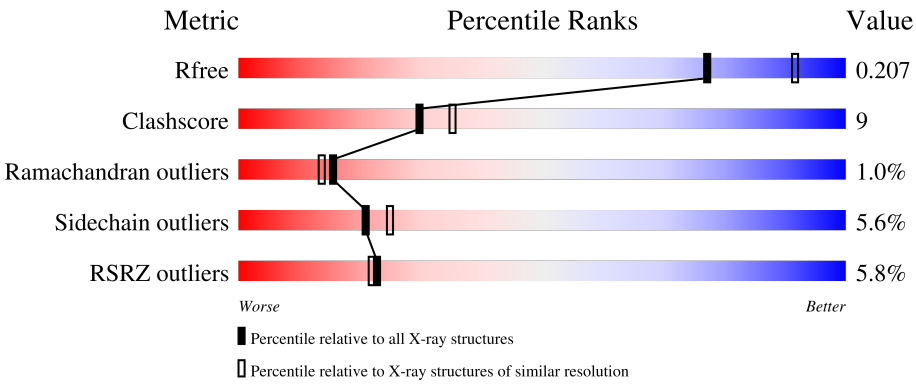
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	3% 85% 13% •
1	N	514	2% 85% 13% •
2	B	227	68% 27% • •
2	O	227	3% 75% 20% 5%

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Mol	Chain	Length	Quality of chain
3	C	261	8% 87% 10%
3	P	261	10% 87% 10%
4	D	147	% 84% 14%
4	Q	147	11% 80% 14%
5	E	109	83% 11%
5	R	109	8% 83% 11%
6	F	98	7% 80% 17%
6	S	98	7% 74% 21%
7	G	85	18% 71% 19% 8%
7	T	85	19% 62% 25% 11%
8	H	85	4% 75% 13% 7%
8	U	85	2% 75% 11% 5% 7%
9	I	73	8% 73% 19% 8%
9	V	73	16% 66% 25% 10%
10	J	59	7% 85% 10%
10	W	59	8% 69% 25%
11	K	56	71% 12% 12%
11	X	56	18% 73% 12% 12%
12	L	47	2% 77% 19%
12	Y	47	6% 74% 17% 6%
13	M	46	2% 72% 15% 7% 7%
13	Z	46	15% 70% 24% 7%

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
20	PGV	C	268	-	-	-	X
20	PGV	P	1268	-	-	-	X
23	CHD	B	1085	X	-	-	-
23	CHD	C	271	X	-	-	-
23	CHD	J	60	X	-	-	-
23	CHD	O	229	X	-	-	-
23	CHD	P	1271	X	-	-	-
23	CHD	W	1059	X	-	-	-
24	UNX	C	262	-	-	-	X
24	UNX	P	262	-	-	-	X
25	CDL	C	270	-	-	X	-
25	CDL	G	269	-	-	X	X
25	CDL	T	1269	-	-	X	X
26	DMU	C	272	X	-	-	-
26	DMU	M	526	X	-	-	-
26	DMU	T	1272	X	-	-	-
26	DMU	Z	1526	X	-	-	-
28	PEK	G	1263	-	-	-	X
28	PEK	T	263	-	-	-	X
7	TPO	G	11	-	-	-	X
7	TPO	T	11	-	-	-	X
9	SAC	I	1	-	-	-	X
9	SAC	V	1	-	X	-	X

2 Entry composition (i)

There are 29 unique types of molecules in this entry. The entry contains 32105 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	4027	2691	623	678	35	0	0	0
1	N	514	4027	2691	623	678	35	0	0	0

- 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	1824	1185	281	340	18	0	0	0
2	O	227	1824	1185	281	340	18	0	0	0

- 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	2110	1412	336	350	12	0	0	0
3	P	259	2110	1412	336	350	12	0	0	0

- 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	1195	777	196	218	4	0	0	0
4	Q	144	1195	777	196	218	4	0	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

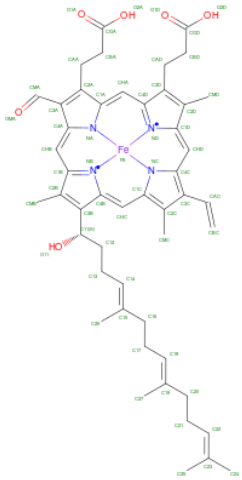
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	46	380	254	64	60	2	0	0	0
			Total	C	N	O	S			
12	Y	46	380	254	64	60	2	0	0	0

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

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

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

HEA



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

- Molecule 15 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).

CMO

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

- Molecule 16 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

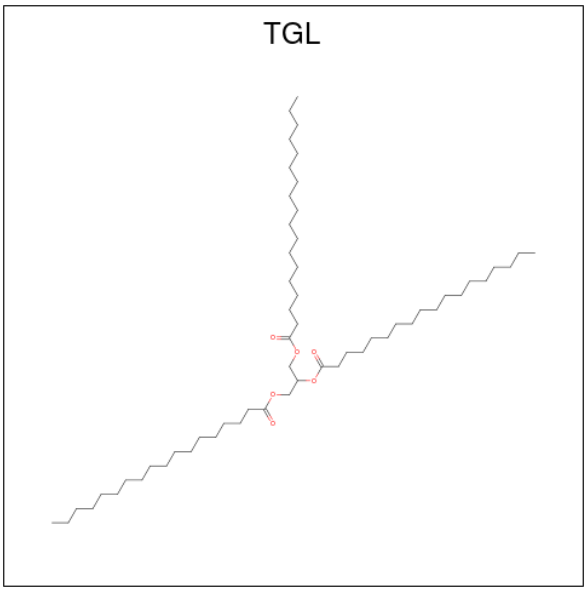
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 18 is SODIUM ION (three-letter code: NA) (formula: Na).

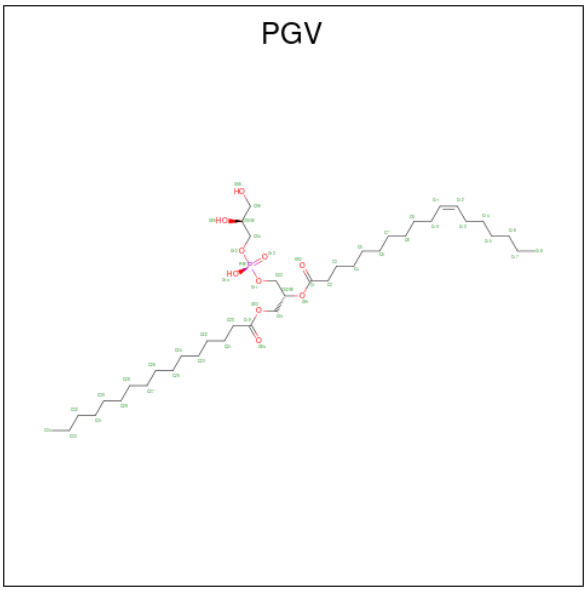
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
18	A	1	1	1	0	0
18	N	1	1	1	0	0

- Molecule 19 is TRISTEAROYLGLYCEROL (three-letter code: TGL) (formula: $C_{57}H_{110}O_6$).



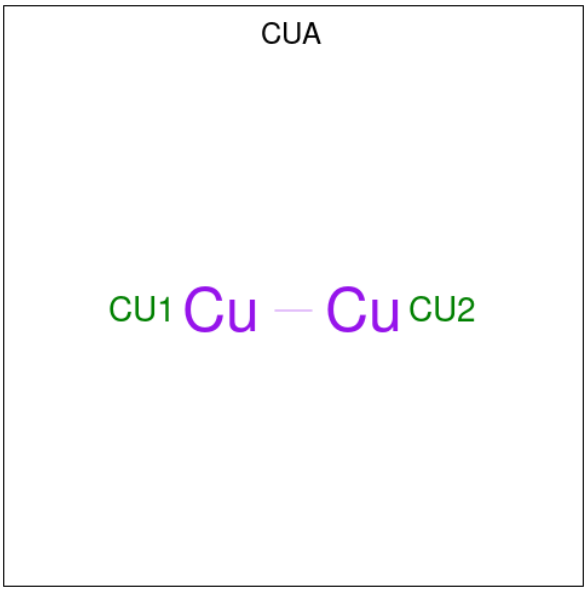
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
19	A	1	63	57	6	0	0
19	B	1	63	57	6	0	0
19	L	1	63	57	6	0	0
19	N	1	63	57	6	0	0
19	N	1	63	57	6	0	0
19	N	1	63	57	6	0	0

- Molecule 20 is (1R)-2-{[{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: $C_{40}H_{77}O_{10}P$).



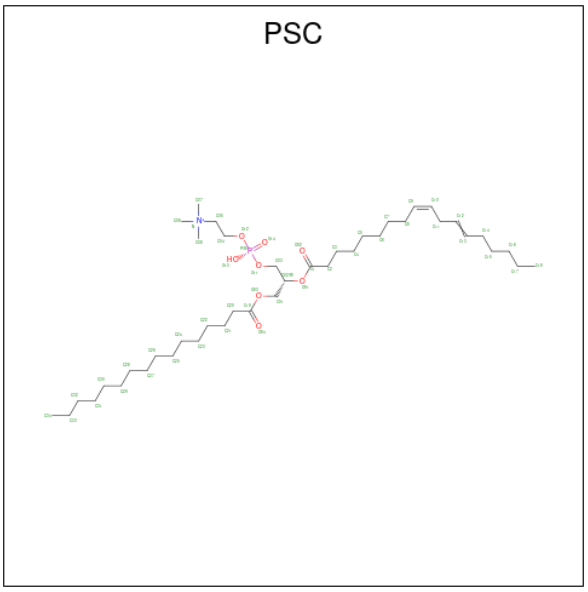
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
20	A	1	51	40	10	1	0	0
			Total	C	O	P		
20	A	1	51	40	10	1	0	0
			Total	C	O	P		
20	C	1	51	40	10	1	0	0
			Total	C	O	P		
20	C	1	51	40	10	1	0	0
			Total	C	O	P		
20	N	1	51	40	10	1	0	0
			Total	C	O	P		
20	N	1	51	40	10	1	0	0
			Total	C	O	P		
20	P	1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

- Molecule 21 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu_2).



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

- 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 (three-letter code: PSC) (formula: $C_{42}H_{81}NO_8P$).



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

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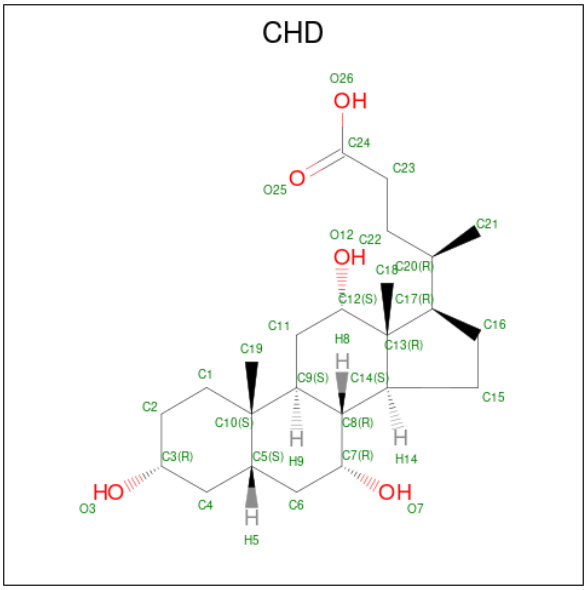
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
22	R	1	52	42	1	8	1	0	0

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

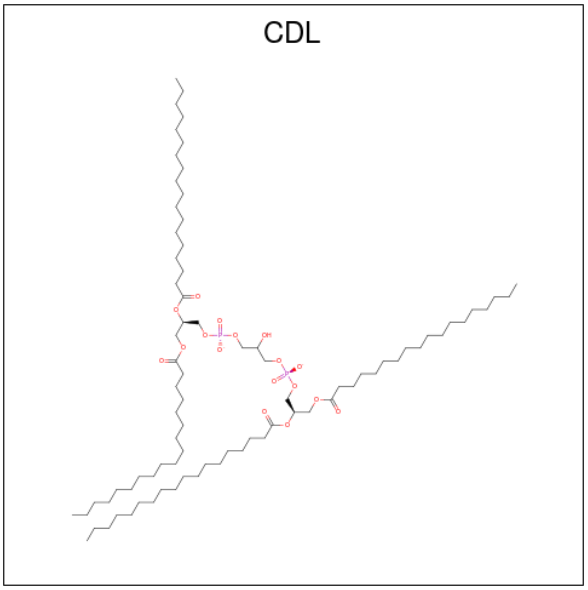


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
23	B	1	29	24	5	0	0
23	C	1	29	24	5	0	0
23	C	1	29	24	5	0	0
23	J	1	29	24	5	0	0
23	O	1	29	24	5	0	0
23	P	1	29	24	5	0	0
23	P	1	29	24	5	0	0
23	W	1	29	24	5	0	0

- Molecule 24 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

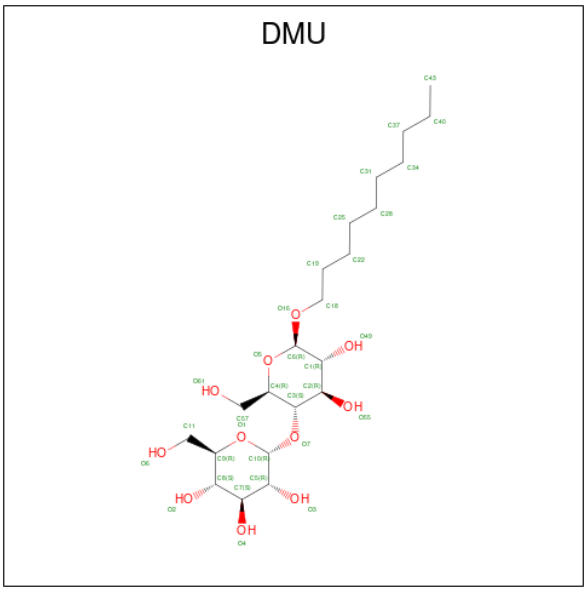
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	X		
24	C	1	1	1	0	0
			Total	X		
24	P	1	1	1	0	0

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



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

- Molecule 26 is DECYL-BETA-D-MALTOPYRANOSIDE (three-letter code: DMU) (formula: $C_{22}H_{42}O_{11}$).

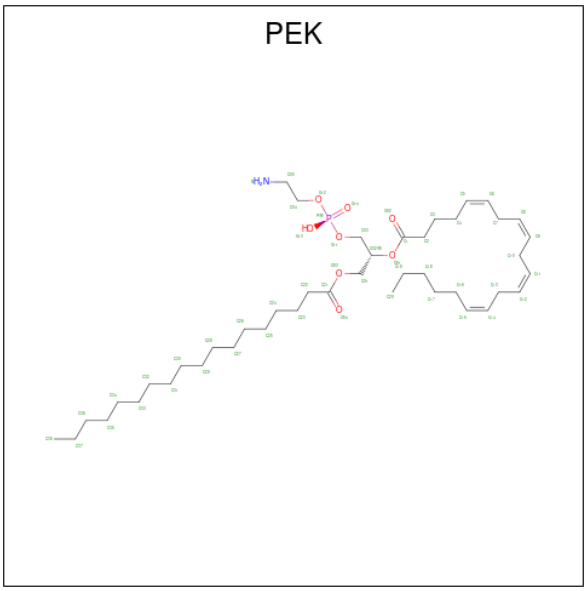


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
26	C	1	33	22	11	0	0
			Total	C	O		
26	M	1	33	22	11	0	0
			Total	C	O		
26	T	1	33	22	11	0	0
			Total	C	O		
26	Z	1	33	22	11	0	0

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 28 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (three-letter code: PEK) (formula: $C_{43}H_{78}NO_8P$).



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

- Molecule 29 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
29	A	205	205	205	0	0
			Total	O		
29	B	121	121	121	0	0
			Total	O		
29	C	80	80	80	0	0
			Total	O		
29	D	75	75	75	0	0
			Total	O		
29	E	39	39	39	0	0
			Total	O		
29	F	70	70	70	0	0

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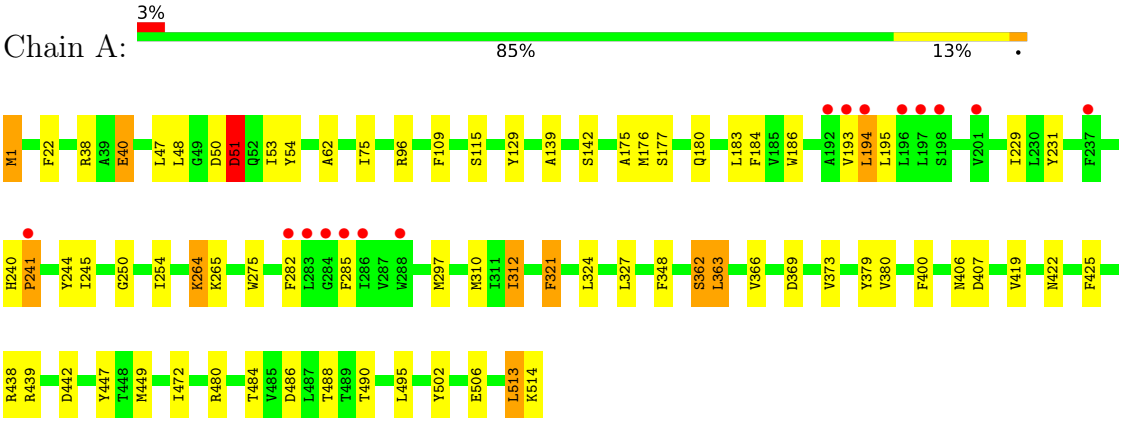
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
29	G	42	Total O 42 42	0	0
29	H	33	Total O 33 33	0	0
29	I	24	Total O 24 24	0	0
29	J	9	Total O 9 9	0	0
29	K	17	Total O 17 17	0	0
29	L	20	Total O 20 20	0	0
29	M	15	Total O 15 15	0	0
29	N	184	Total O 184 184	0	0
29	O	97	Total O 97 97	0	0
29	P	81	Total O 81 81	0	0
29	Q	47	Total O 47 47	0	0
29	R	27	Total O 27 27	0	0
29	S	52	Total O 52 52	0	0
29	T	37	Total O 37 37	0	0
29	U	28	Total O 28 28	0	0
29	V	17	Total O 17 17	0	0
29	W	12	Total O 12 12	0	0
29	X	12	Total O 12 12	0	0
29	Y	16	Total O 16 16	0	0
29	Z	9	Total O 9 9	0	0

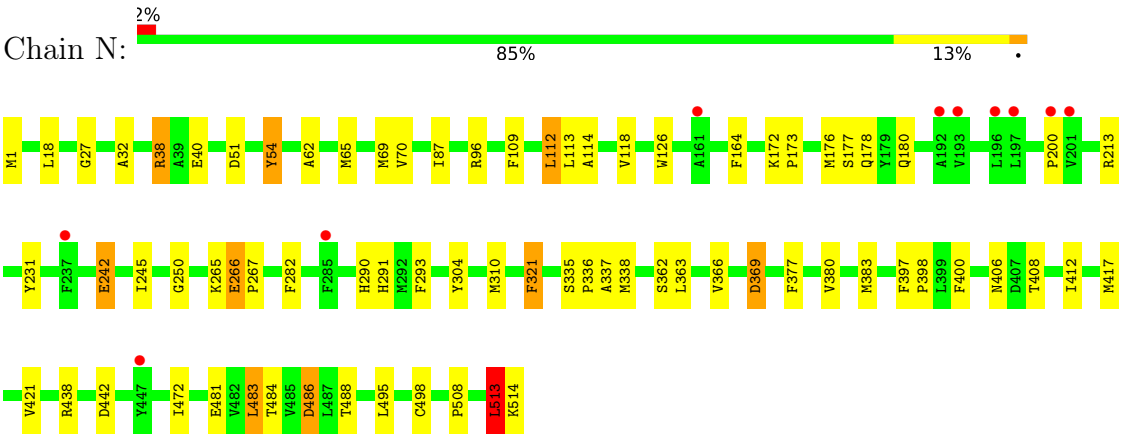
3 Residue-property plots (i)

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.

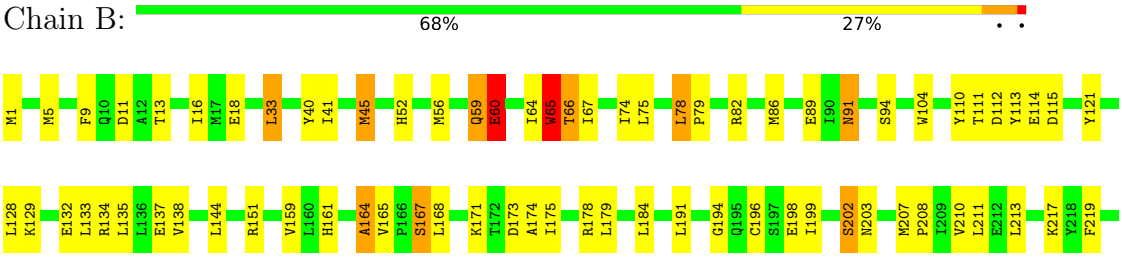
• Molecule 1: Cytochrome c oxidase subunit 1



• Molecule 1: Cytochrome c oxidase subunit 1



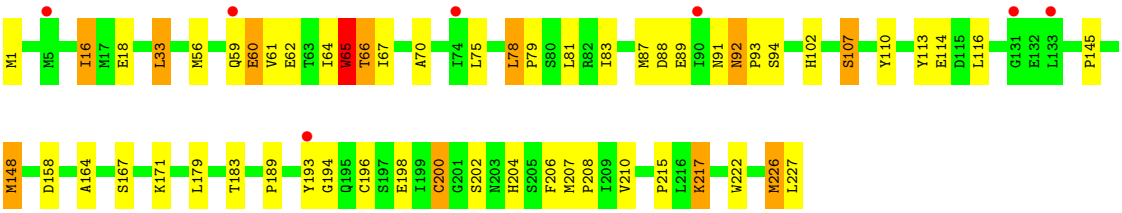
• Molecule 2: Cytochrome c oxidase subunit 2



L227

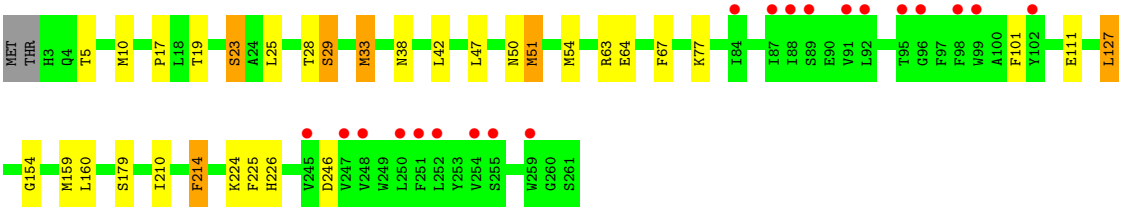
- Molecule 2: Cytochrome c oxidase subunit 2

Chain O:



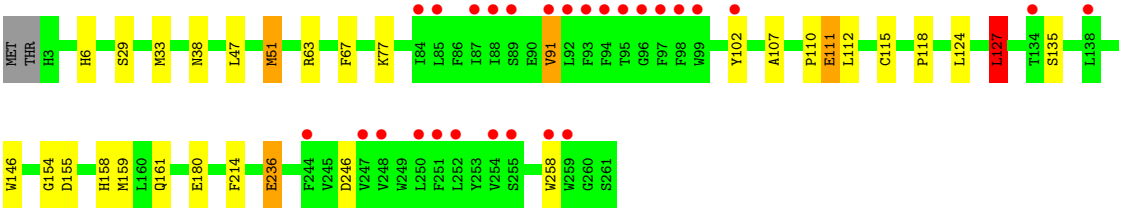
- Molecule 3: Cytochrome c oxidase subunit 3

Chain C:



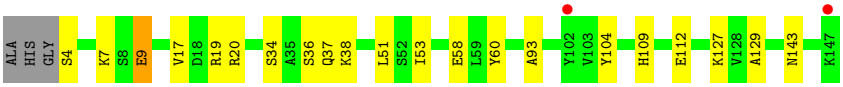
- Molecule 3: Cytochrome c oxidase subunit 3

Chain P:



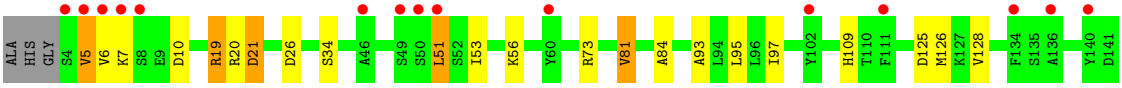
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain D:



- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain Q:

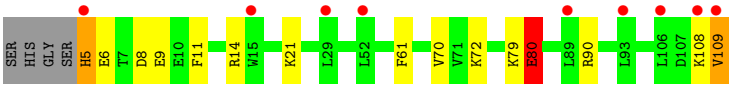


• Molecule 5: Cytochrome c oxidase subunit 5A

Chain E:

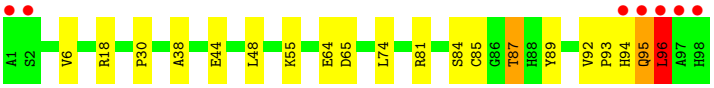
• Molecule 5: Cytochrome c oxidase subunit 5A

Chain R:



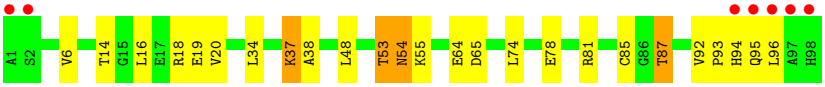
• Molecule 6: Cytochrome c oxidase subunit 5B

Chain F:



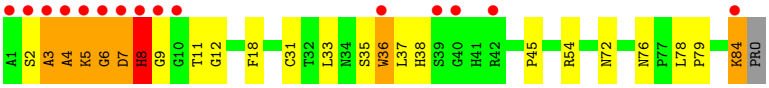
• Molecule 6: Cytochrome c oxidase subunit 5B

Chain S:



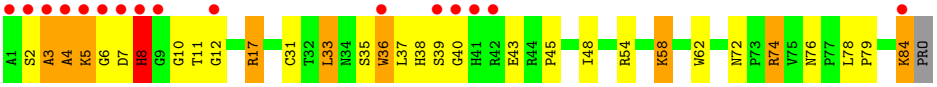
• Molecule 7: Cytochrome c oxidase subunit 6A2

Chain G:



• Molecule 7: Cytochrome c oxidase subunit 6A2

Chain T:

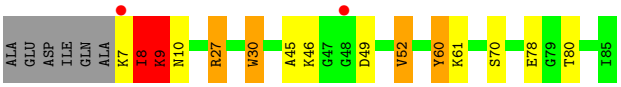


• Molecule 8: Cytochrome c oxidase subunit 6B1

Chain H:

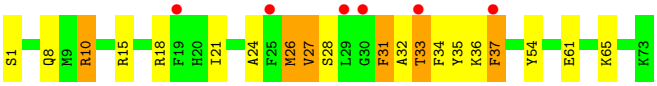
• Molecule 8: Cytochrome c oxidase subunit 6B1

Chain U:



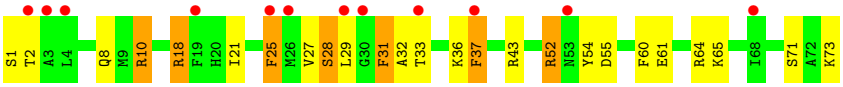
• Molecule 9: Cytochrome c oxidase subunit 6C

Chain I:



• Molecule 9: Cytochrome c oxidase subunit 6C

Chain V:

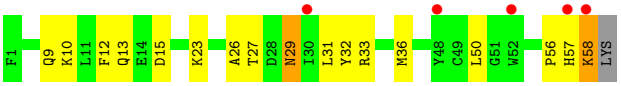


• Molecule 10: Cytochrome c oxidase polypeptide 7A1

Chain J:

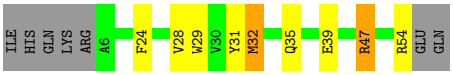
• Molecule 10: Cytochrome c oxidase polypeptide 7A1

Chain W:



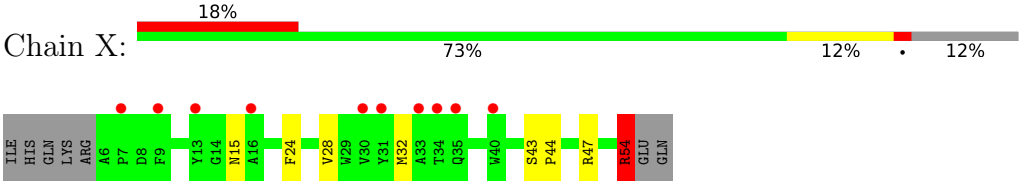
• Molecule 11: Cytochrome c oxidase subunit 7B

Chain K:



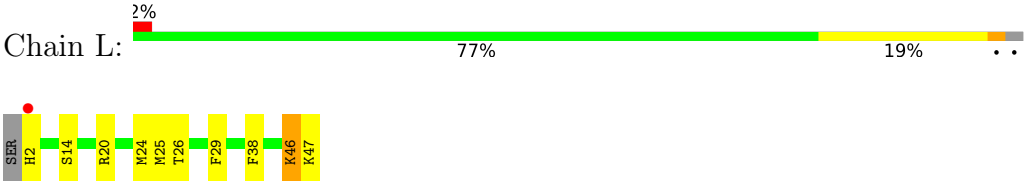
- Molecule 11: Cytochrome c oxidase subunit 7B

Chain X:



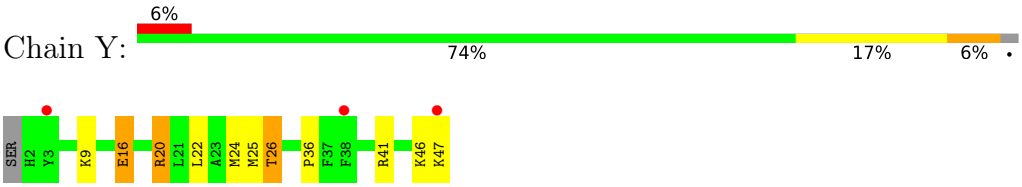
- Molecule 12: Cytochrome c oxidase subunit 7C

Chain L:



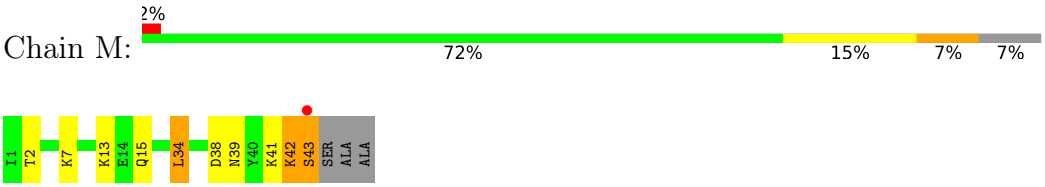
- Molecule 12: Cytochrome c oxidase subunit 7C

Chain Y:



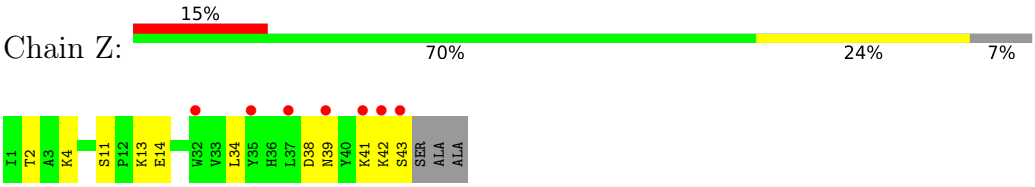
- Molecule 13: Cytochrome c oxidase subunit 8B

Chain M:



- Molecule 13: Cytochrome c oxidase subunit 8B

Chain Z:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	189.49Å 210.89Å 178.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.20 94.75 – 2.21	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.20) 99.2 (94.75-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.3	Depositor
R, R_{free}	0.162 , 0.192 0.180 , 0.207	Depositor DCC
R_{free} test set	17414 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	51.1	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 61.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	32105	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: TGL, CDL, FME, SAC, HEA, PGV, UNX, PSC, DMU, NA, MG, CHD, CMO, CUA, ZN, PEK, CU, TPO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	A	1.52	24/4156 (0.6%)	1.14	17/5678 (0.3%)
1	N	1.30	13/4156 (0.3%)	1.00	9/5678 (0.2%)
2	B	1.52	17/1860 (0.9%)	1.22	15/2534 (0.6%)
2	O	1.19	5/1860 (0.3%)	1.02	3/2534 (0.1%)
3	C	1.44	6/2197 (0.3%)	1.00	2/3005 (0.1%)
3	P	1.26	7/2197 (0.3%)	0.96	4/3005 (0.1%)
4	D	1.42	8/1229 (0.7%)	1.12	1/1658 (0.1%)
4	Q	1.10	2/1229 (0.2%)	0.98	6/1658 (0.4%)
5	E	1.26	2/871 (0.2%)	1.07	3/1182 (0.3%)
5	R	1.03	2/871 (0.2%)	0.93	1/1182 (0.1%)
6	F	1.47	3/765 (0.4%)	1.25	4/1038 (0.4%)
6	S	1.25	2/765 (0.3%)	1.09	3/1038 (0.3%)
7	G	1.38	2/690 (0.3%)	1.12	3/937 (0.3%)
7	T	1.43	4/690 (0.6%)	1.09	4/937 (0.4%)
8	H	1.29	1/682 (0.1%)	1.01	1/921 (0.1%)
8	U	1.09	1/682 (0.1%)	0.94	0/921
9	I	1.45	3/605 (0.5%)	1.13	3/802 (0.4%)
9	V	1.31	2/605 (0.3%)	1.10	4/802 (0.5%)
10	J	1.35	0/471	1.12	2/636 (0.3%)
10	W	1.10	1/471 (0.2%)	0.98	0/636
11	K	1.34	3/398 (0.8%)	1.16	2/546 (0.4%)
11	X	0.97	0/398	0.93	1/546 (0.2%)
12	L	1.49	1/393 (0.3%)	1.07	1/526 (0.2%)
12	Y	1.10	0/393	0.98	1/526 (0.2%)
13	M	1.20	0/345	1.15	2/470 (0.4%)
13	Z	0.98	0/345	0.97	0/470
All	All	1.33	109/29324 (0.4%)	1.06	92/39866 (0.2%)

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
6	F	0	1
6	S	0	1
10	J	0	1
10	W	0	1
All	All	0	4

The worst 5 of 109 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	36	TRP	CB-CG	12.12	1.72	1.50
7	G	36	TRP	CB-CG	10.31	1.68	1.50
7	T	58	LYS	CE-NZ	9.32	1.72	1.49
2	O	198	GLU	C-O	8.13	1.38	1.23
2	B	198	GLU	C-O	7.69	1.38	1.23

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	K	32	MET	CG-SD-CE	8.85	114.36	100.20
6	F	18	ARG	NE-CZ-NH2	-8.74	115.93	120.30
4	D	20	ARG	NE-CZ-NH2	-8.70	115.95	120.30
1	A	176	MET	CG-SD-CE	-8.47	86.66	100.20
2	B	112	ASP	CB-CG-OD2	-8.21	110.91	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	F	93	PRO	Peptide
10	J	57	HIS	Peptide
6	S	93	PRO	Peptide
10	W	57	HIS	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	4027	0	4001	38	0
1	N	4027	0	4001	48	0
2	B	1824	0	1833	34	0
2	O	1824	0	1833	40	0
3	C	2110	0	2027	22	0
3	P	2110	0	2027	22	0
4	D	1195	0	1183	9	0
4	Q	1195	0	1183	15	0
5	E	852	0	845	11	0
5	R	852	0	845	9	0
6	F	748	0	728	10	0
6	S	748	0	728	14	0
7	G	675	0	643	26	0
7	T	675	0	644	41	0
8	H	662	0	623	8	0
8	U	662	0	623	12	0
9	I	601	0	613	22	0
9	V	601	0	613	25	0
10	J	460	0	459	5	0
10	W	460	0	459	12	0
11	K	384	0	366	3	0
11	X	384	0	366	6	0
12	L	380	0	380	14	0
12	Y	380	0	380	9	0
13	M	335	0	352	7	0
13	Z	335	0	352	4	0
14	A	120	0	108	4	0
14	N	120	0	108	7	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	63	0	110	3	0
19	B	63	0	109	9	0
19	L	63	0	110	19	0
19	N	189	0	330	21	0
20	A	102	0	152	13	0
20	C	102	0	152	7	0
20	N	102	0	152	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	P	102	0	152	7	0
21	B	2	0	0	0	0
21	O	2	0	0	0	0
22	B	52	0	80	17	0
22	R	52	0	80	16	0
23	B	29	0	37	3	0
23	C	58	0	71	3	0
23	J	29	0	36	2	0
23	O	29	0	37	1	0
23	P	58	0	72	4	0
23	W	29	0	36	3	0
24	C	1	0	0	0	0
24	P	1	0	0	0	0
25	C	100	0	156	22	0
25	G	100	0	156	24	0
25	P	100	0	156	16	0
25	T	100	0	156	23	0
26	C	33	0	38	2	0
26	M	33	0	38	0	0
26	T	33	0	39	6	0
26	Z	33	0	39	1	0
27	F	1	0	0	0	0
27	S	1	0	0	0	0
28	G	159	0	231	22	0
28	S	53	0	77	6	0
28	T	106	0	154	19	0
29	A	205	0	0	3	0
29	B	121	0	0	3	0
29	C	80	0	0	2	0
29	D	75	0	0	1	0
29	E	39	0	0	1	0
29	F	70	0	0	2	0
29	G	42	0	0	5	0
29	H	33	0	0	5	0
29	I	24	0	0	1	0
29	J	9	0	0	0	0
29	K	17	0	0	0	0
29	L	20	0	0	2	0
29	M	15	0	0	0	0
29	N	184	0	0	6	0
29	O	97	0	0	2	0
29	P	81	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	Q	47	0	0	2	0
29	R	27	0	0	0	0
29	S	52	0	0	1	0
29	T	37	0	0	8	0
29	U	28	0	0	4	0
29	V	17	0	0	4	0
29	W	12	0	0	2	0
29	X	12	0	0	1	0
29	Y	16	0	0	0	0
29	Z	9	0	0	0	0
All	All	32105	0	31279	581	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 9.

The worst 5 of 581 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)
1:A:75:ILE:CD1	1:A:75:ILE:CG1	1.76	1.62
28:G:265:PEK:C7	28:G:265:PEK:C6	1.81	1.53
7:T:58:LYS:CE	7:T:58:LYS:NZ	1.72	1.47
12:L:20:ARG:NH2	19:L:522:TGL:HC32	1.40	1.36
7:T:45:PRO:CD	29:T:3099:HOH:O	1.75	1.35

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	512/514 (100%)	500 (98%)	12 (2%)	0	100	100
1	N	512/514 (100%)	495 (97%)	17 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	225/227 (99%)	213 (95%)	11 (5%)	1 (0%)	34	37
2	O	225/227 (99%)	212 (94%)	12 (5%)	1 (0%)	34	37
3	C	257/261 (98%)	253 (98%)	3 (1%)	1 (0%)	34	37
3	P	257/261 (98%)	252 (98%)	4 (2%)	1 (0%)	34	37
4	D	142/147 (97%)	139 (98%)	3 (2%)	0	100	100
4	Q	142/147 (97%)	132 (93%)	9 (6%)	1 (1%)	22	22
5	E	103/109 (94%)	103 (100%)	0	0	100	100
5	R	103/109 (94%)	102 (99%)	1 (1%)	0	100	100
6	F	96/98 (98%)	88 (92%)	5 (5%)	3 (3%)	4	2
6	S	96/98 (98%)	91 (95%)	3 (3%)	2 (2%)	7	4
7	G	81/85 (95%)	67 (83%)	9 (11%)	5 (6%)	1	0
7	T	81/85 (95%)	65 (80%)	11 (14%)	5 (6%)	1	0
8	H	77/85 (91%)	66 (86%)	5 (6%)	6 (8%)	1	0
8	U	77/85 (91%)	69 (90%)	4 (5%)	4 (5%)	2	0
9	I	71/73 (97%)	63 (89%)	6 (8%)	2 (3%)	5	2
9	V	71/73 (97%)	64 (90%)	4 (6%)	3 (4%)	3	1
10	J	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
10	W	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
11	K	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
11	X	47/56 (84%)	46 (98%)	1 (2%)	0	100	100
12	L	44/47 (94%)	43 (98%)	1 (2%)	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%)	39 (95%)	1 (2%)	1 (2%)	6	3
All	All	3504/3614 (97%)	3339 (95%)	129 (4%)	36 (1%)	15	14

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	94	HIS
7	G	3	ALA
7	G	4	ALA
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	426/426 (100%)	416 (98%)	10 (2%)	50	63
1	N	426/426 (100%)	414 (97%)	12 (3%)	43	56
2	B	210/210 (100%)	199 (95%)	11 (5%)	23	28
2	O	210/210 (100%)	191 (91%)	19 (9%)	9	9
3	C	224/226 (99%)	216 (96%)	8 (4%)	35	45
3	P	224/226 (99%)	220 (98%)	4 (2%)	59	72
4	D	128/129 (99%)	122 (95%)	6 (5%)	26	33
4	Q	128/129 (99%)	121 (94%)	7 (6%)	21	26
5	E	92/95 (97%)	89 (97%)	3 (3%)	38	49
5	R	92/95 (97%)	84 (91%)	8 (9%)	10	10
6	F	81/81 (100%)	76 (94%)	5 (6%)	18	21
6	S	81/81 (100%)	75 (93%)	6 (7%)	13	14
7	G	67/68 (98%)	60 (90%)	7 (10%)	7	6
7	T	67/68 (98%)	59 (88%)	8 (12%)	5	4
8	H	71/75 (95%)	66 (93%)	5 (7%)	15	16
8	U	71/75 (95%)	64 (90%)	7 (10%)	8	7
9	I	57/57 (100%)	50 (88%)	7 (12%)	4	4
9	V	57/57 (100%)	48 (84%)	9 (16%)	2	2
10	J	49/50 (98%)	48 (98%)	1 (2%)	55	69
10	W	49/50 (98%)	43 (88%)	6 (12%)	5	4
11	K	39/46 (85%)	36 (92%)	3 (8%)	13	13
11	X	39/46 (85%)	36 (92%)	3 (8%)	13	13
12	L	39/40 (98%)	37 (95%)	2 (5%)	24	29
12	Y	39/40 (98%)	36 (92%)	3 (8%)	13	13
13	M	37/38 (97%)	32 (86%)	5 (14%)	4	3
13	Z	37/38 (97%)	33 (89%)	4 (11%)	6	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3040/3082 (99%)	2871 (94%)	169 (6%)	21 25

5 of 169 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	R	5	HIS
8	U	70	SER
5	R	80	GLU
7	T	35	SER
9	V	52	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
7	T	76	ASN
8	U	22	ASN
7	G	76	ASN
5	E	94	ASN
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	0.80	0	7,9,11	5.34	3 (42%)
2	FME	B	1	2	8,9,10	1.40	1 (12%)	7,9,11	6.53	3 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
9	SAC	I	1	9	7,8,9	3.80	2 (28%)	8,9,11	5.05	4 (50%)
7	TPO	T	11	7	8,10,11	2.60	5 (62%)	10,14,16	2.20	3 (30%)
9	SAC	V	1	9	7,8,9	3.80	3 (42%)	8,9,11	3.63	5 (62%)
7	TPO	G	11	7	8,10,11	2.47	5 (62%)	10,14,16	2.14	3 (30%)
1	FME	N	1	1	8,9,10	0.92	0	7,9,11	4.46	3 (42%)
2	FME	O	1	2	8,9,10	0.92	0	7,9,11	4.00	4 (57%)

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

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	V	1	SAC	CA-N	7.65	1.57	1.46
9	I	1	SAC	CA-N	7.03	1.56	1.46
9	I	1	SAC	OAC-C1A	6.45	1.37	1.23
9	V	1	SAC	OAC-C1A	5.49	1.35	1.23
7	T	11	TPO	P-OG1	4.26	1.67	1.59

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	FME	CA-N-CN	-16.81	96.98	122.82
1	A	1	FME	CA-N-CN	-12.33	103.86	122.82
1	N	1	FME	CA-N-CN	-10.28	107.00	122.82
9	I	1	SAC	C-CA-N	9.43	126.74	109.73
2	O	1	FME	CA-N-CN	-9.32	108.49	122.82

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	FME	1	0

5.5 Carbohydrates (i)

There are no monosaccharides 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	TGL	N	1521	-	62,62,62	1.43	9 (14%)	65,65,65	2.20	15 (23%)
23	CHD	C	525	-	32,32,32	1.42	4 (12%)	51,51,51	5.00	39 (76%)
19	TGL	N	1522	-	62,62,62	1.65	7 (11%)	65,65,65	1.79	16 (24%)
23	CHD	P	1525	-	32,32,32	1.08	2 (6%)	51,51,51	5.40	38 (74%)
19	TGL	A	523	-	62,62,62	1.43	6 (9%)	65,65,65	1.69	12 (18%)
25	CDL	G	269	-	99,99,99	1.46	13 (13%)	105,111,111	1.43	17 (16%)
20	PGV	C	268	-	50,50,50	1.47	3 (6%)	53,56,56	1.70	7 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
23	CHD	P	1271	-	32,32,32	0.88	1 (3%)	51,51,51	5.18	35 (68%)
23	CHD	B	1085	-	32,32,32	1.59	4 (12%)	51,51,51	5.54	37 (72%)
14	HEA	N	515	1	57,67,67	1.69	15 (26%)	61,103,103	2.00	19 (31%)
26	DMU	T	1272	-	34,34,34	1.37	3 (8%)	45,45,45	3.12	22 (48%)
20	PGV	C	267	-	50,50,50	0.90	2 (4%)	53,56,56	1.20	5 (9%)
26	DMU	Z	1526	-	34,34,34	1.01	3 (8%)	45,45,45	3.11	21 (46%)
14	HEA	A	515	1	57,67,67	1.67	11 (19%)	61,103,103	2.51	20 (32%)
25	CDL	T	1269	-	99,99,99	1.52	13 (13%)	105,111,111	1.49	13 (12%)
22	PSC	R	1229	-	51,51,51	1.36	3 (5%)	57,59,59	1.26	5 (8%)
28	PEK	S	1265	-	52,52,52	1.29	3 (5%)	55,57,57	1.31	5 (9%)
20	PGV	P	1268	-	50,50,50	1.43	2 (4%)	53,56,56	1.60	8 (15%)
23	CHD	J	60	-	32,32,32	1.10	2 (6%)	51,51,51	5.30	37 (72%)
19	TGL	N	1523	-	62,62,62	1.45	7 (11%)	65,65,65	1.43	10 (15%)
28	PEK	G	1263	-	52,52,52	1.41	6 (11%)	55,57,57	1.48	7 (12%)
23	CHD	C	271	-	32,32,32	0.92	3 (9%)	51,51,51	5.00	34 (66%)
25	CDL	P	1270	-	99,99,99	1.47	13 (13%)	105,111,111	1.42	12 (11%)
20	PGV	A	521	-	50,50,50	0.82	2 (4%)	53,56,56	1.73	7 (13%)
25	CDL	C	270	-	99,99,99	1.45	15 (15%)	105,111,111	1.46	15 (14%)
20	PGV	N	1524	-	50,50,50	1.26	2 (4%)	53,56,56	1.21	6 (11%)
23	CHD	W	1059	-	32,32,32	0.78	1 (3%)	51,51,51	5.06	34 (66%)
14	HEA	A	516	1	57,67,67	1.61	11 (19%)	61,103,103	2.42	23 (37%)
20	PGV	N	1266	-	50,50,50	0.85	3 (6%)	53,56,56	1.37	5 (9%)
21	CUA	B	228	2	0,1,1	-	-	-		
23	CHD	O	229	-	32,32,32	1.51	6 (18%)	51,51,51	5.47	37 (72%)
19	TGL	L	522	-	62,62,62	1.72	9 (14%)	65,65,65	1.99	16 (24%)
22	PSC	B	229	-	51,51,51	1.40	3 (5%)	57,59,59	1.29	7 (12%)
28	PEK	T	1264	-	52,52,52	0.90	4 (7%)	55,57,57	1.44	9 (16%)
15	CMO	A	520	-	0,1,1	-	-	-		
19	TGL	B	521	-	62,62,62	1.49	8 (12%)	65,65,65	2.47	18 (27%)
20	PGV	P	1267	-	50,50,50	1.02	2 (4%)	53,56,56	1.01	3 (5%)
26	DMU	C	272	-	34,34,34	1.34	5 (14%)	45,45,45	3.33	21 (46%)
15	CMO	N	520	14	0,1,1	-	-	-		
20	PGV	A	524	-	50,50,50	1.33	3 (6%)	53,56,56	1.40	8 (15%)
14	HEA	N	516	15,1	57,67,67	1.68	12 (21%)	61,103,103	2.28	20 (32%)
28	PEK	G	265	-	52,52,52	1.62	6 (11%)	55,57,57	1.52	11 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
28	PEK	G	264	-	52,52,52	1.04	5 (9%)	55,57,57	1.58	10 (18%)
26	DMU	M	526	-	34,34,34	1.28	2 (5%)	45,45,45	3.40	22 (48%)
21	CUA	O	228	2	0,1,1	-	-	-		
28	PEK	T	263	-	52,52,52	1.42	4 (7%)	55,57,57	1.20	5 (9%)

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	TGL	N	1521	-	-	36/65/65/65	-
23	CHD	C	525	-	-	1/9/74/74	0/4/4/4
19	TGL	N	1522	-	-	34/65/65/65	-
23	CHD	P	1525	-	-	4/9/74/74	0/4/4/4
19	TGL	A	523	-	-	34/65/65/65	-
25	CDL	G	269	-	-	59/110/110/110	-
20	PGV	C	268	-	-	30/55/55/55	-
23	CHD	P	1271	-	1/1/12/12	6/9/74/74	0/4/4/4
23	CHD	B	1085	-	1/1/12/12	2/9/74/74	0/4/4/4
14	HEA	N	515	1	-	4/32/76/76	-
26	DMU	T	1272	-	6/6/10/10	12/19/59/59	0/2/2/2
20	PGV	C	267	-	-	13/55/55/55	-
26	DMU	Z	1526	-	5/5/10/10	10/19/59/59	0/2/2/2
14	HEA	A	515	1	-	4/32/76/76	-
25	CDL	T	1269	-	-	59/110/110/110	-
22	PSC	R	1229	-	-	28/55/55/55	-
28	PEK	S	1265	-	-	27/56/56/56	-
23	CHD	J	60	-	1/1/12/12	7/9/74/74	0/4/4/4
20	PGV	P	1268	-	-	36/55/55/55	-
19	TGL	N	1523	-	-	34/65/65/65	-
28	PEK	G	1263	-	-	32/56/56/56	-
23	CHD	C	271	-	1/1/12/12	7/9/74/74	0/4/4/4
25	CDL	P	1270	-	-	78/110/110/110	-
20	PGV	A	521	-	-	14/55/55/55	-
25	CDL	C	270	-	-	68/110/110/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CHD	W	1059	-	2/2/12/12	6/9/74/74	0/4/4/4
20	PGV	N	1524	-	-	30/55/55/55	-
14	HEA	A	516	1	-	4/32/76/76	-
20	PGV	N	1266	-	-	14/55/55/55	-
23	CHD	O	229	-	1/1/12/12	5/9/74/74	0/4/4/4
19	TGL	L	522	-	-	42/65/65/65	-
22	PSC	B	229	-	-	32/55/55/55	-
28	PEK	T	1264	-	-	22/56/56/56	-
19	TGL	B	521	-	-	35/65/65/65	-
26	DMU	C	272	-	5/5/10/10	12/19/59/59	0/2/2/2
20	PGV	P	1267	-	-	15/55/55/55	-
20	PGV	A	524	-	-	33/55/55/55	-
14	HEA	N	516	15,1	-	6/32/76/76	-
28	PEK	G	265	-	-	24/56/56/56	-
28	PEK	G	264	-	-	23/56/56/56	-
26	DMU	M	526	-	5/5/10/10	8/19/59/59	0/2/2/2
28	PEK	T	263	-	-	26/56/56/56	-

The worst 5 of 238 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	L	522	TGL	OG2-CB1	7.64	1.55	1.34
19	N	1522	TGL	OG2-CB1	7.48	1.55	1.34
20	C	268	PGV	O01-C1	7.21	1.54	1.34
20	P	1268	PGV	O01-C1	7.10	1.54	1.34
28	G	1263	PEK	O03-C21	6.42	1.52	1.33

The worst 5 of 711 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	P	1525	CHD	C6-C5-C10	14.76	128.34	112.66
23	J	60	CHD	C10-C9-C8	13.98	126.83	111.82
23	C	271	CHD	C10-C9-C8	13.67	126.50	111.82
23	B	1085	CHD	C6-C5-C10	13.41	126.90	112.66
23	P	1271	CHD	C10-C9-C8	12.93	125.70	111.82

5 of 28 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	B	1085	CHD	C9
23	C	271	CHD	C9
23	J	60	CHD	C9
23	O	229	CHD	C9
23	P	1271	CHD	C9

5 of 976 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	A	523	TGL	CC2-CC1-OG3-CG3
19	A	523	TGL	OC1-CC1-OG3-CG3
19	N	1521	TGL	CB2-CB1-OG2-CG2
20	A	524	PGV	C03-O11-P-O13
20	A	524	PGV	C04-O12-P-O11

There are no ring outliers.

40 monomers are involved in 272 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	N	1521	TGL	10	0
23	C	525	CHD	1	0
19	N	1522	TGL	6	0
23	P	1525	CHD	1	0
19	A	523	TGL	3	0
25	G	269	CDL	24	0
23	P	1271	CHD	3	0
23	B	1085	CHD	3	0
14	N	515	HEA	5	0
26	T	1272	DMU	6	0
20	C	267	PGV	7	0
26	Z	1526	DMU	1	0
14	A	515	HEA	3	0
25	T	1269	CDL	23	0
22	R	1229	PSC	16	0
28	S	1265	PEK	6	0
20	P	1268	PGV	2	0
23	J	60	CHD	2	0
19	N	1523	TGL	5	0
28	G	1263	PEK	10	0
23	C	271	CHD	2	0
25	P	1270	CDL	16	0
20	A	521	PGV	1	0
25	C	270	CDL	22	0

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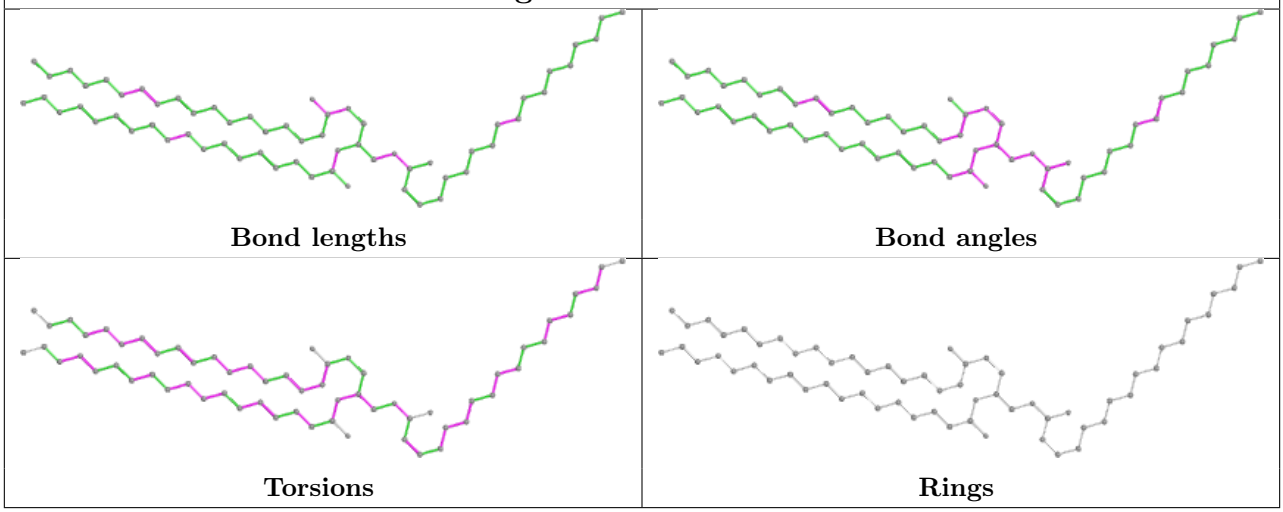
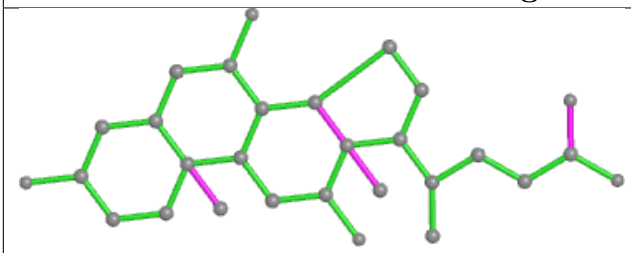
Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	N	1524	PGV	8	0
23	W	1059	CHD	3	0
14	A	516	HEA	1	0
20	N	1266	PGV	1	0
23	O	229	CHD	1	0
19	L	522	TGL	19	0
22	B	229	PSC	17	0
28	T	1264	PEK	4	0
19	B	521	TGL	9	0
20	P	1267	PGV	5	0
26	C	272	DMU	2	0
20	A	524	PGV	12	0
14	N	516	HEA	2	0
28	G	265	PEK	8	0
28	G	264	PEK	4	0
28	T	263	PEK	15	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 then 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.

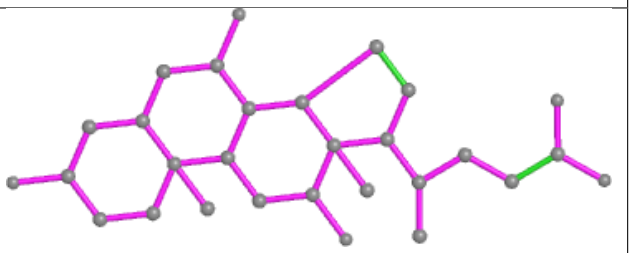
Ligand TGL N 1521



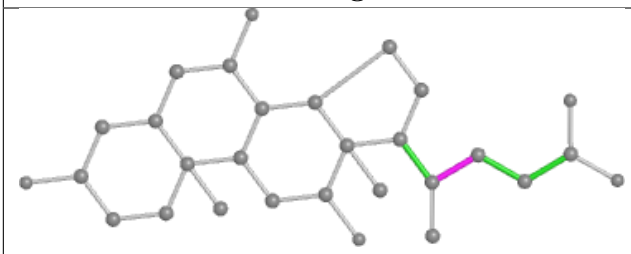
Ligand CHD C 525



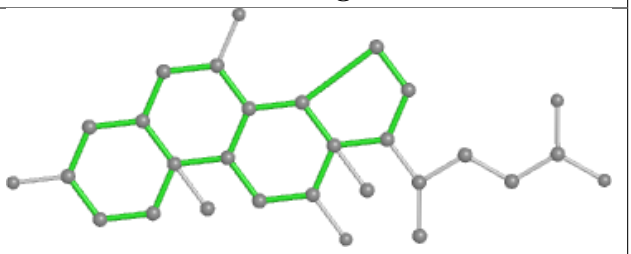
Bond lengths



Bond angles

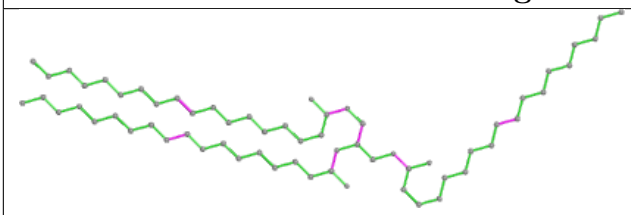


Torsions

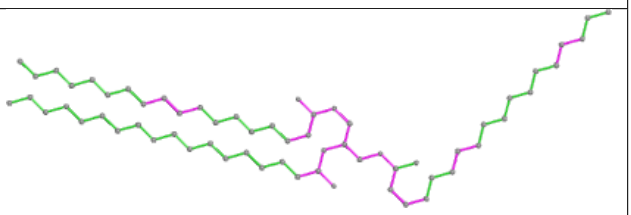


Rings

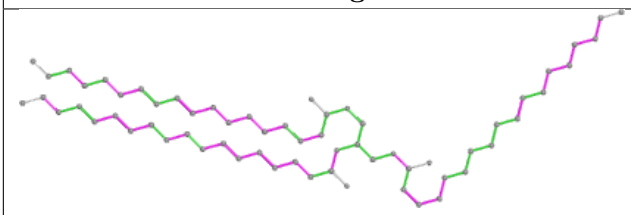
Ligand TGL N 1522



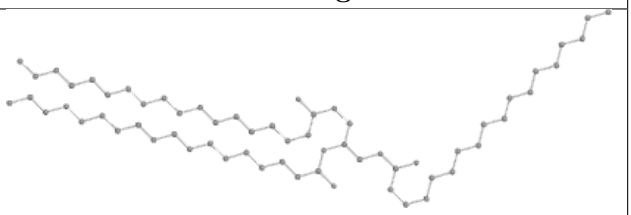
Bond lengths



Bond angles

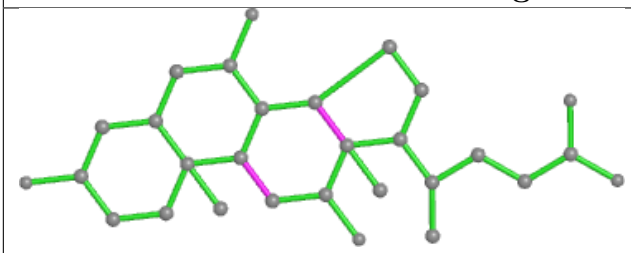


Torsions

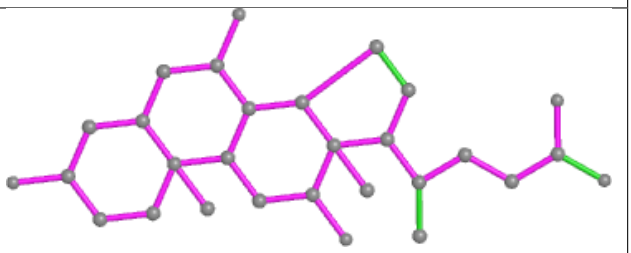


Rings

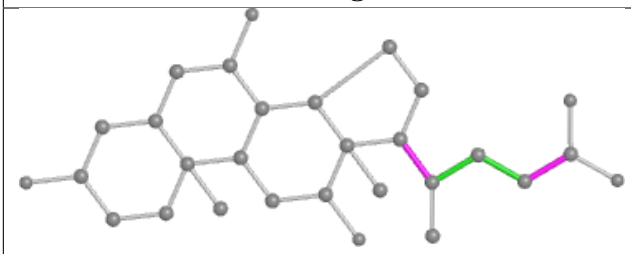
Ligand CHD P 1525



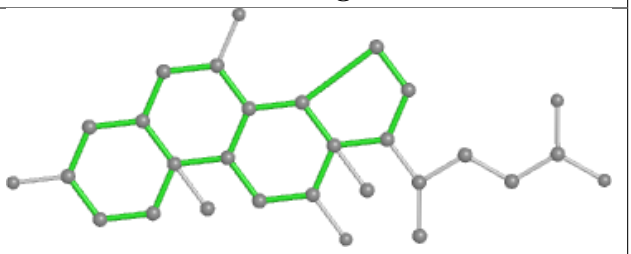
Bond lengths



Bond angles

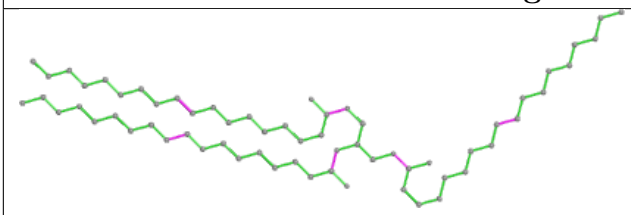


Torsions



Rings

Ligand TGL A 523



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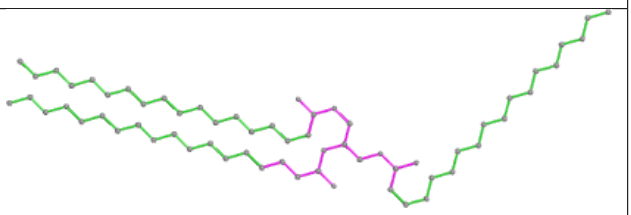
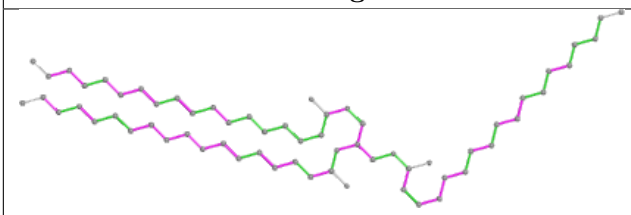
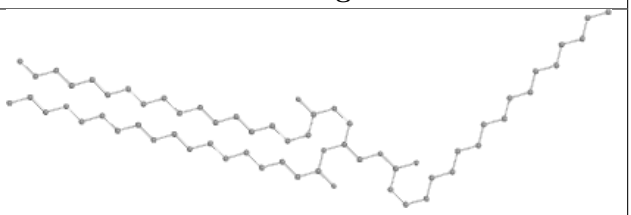


Bond angles

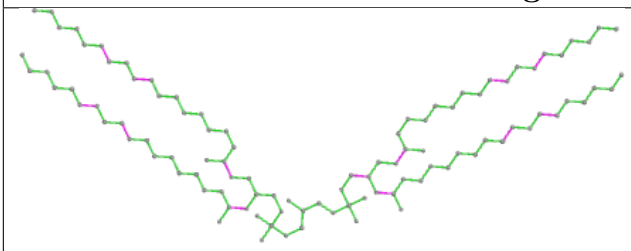


Torsions



Rings

Ligand CDL G 269



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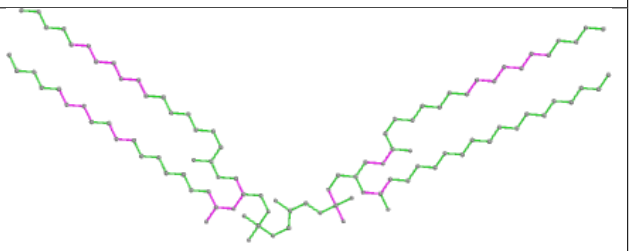
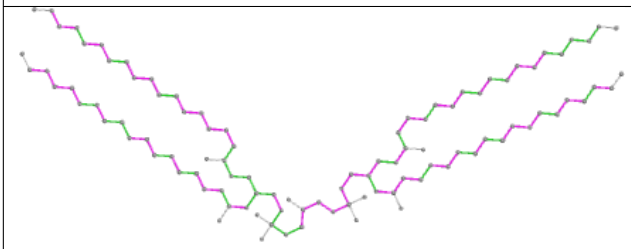


Bond angles



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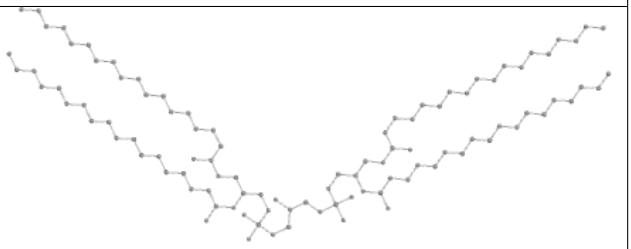
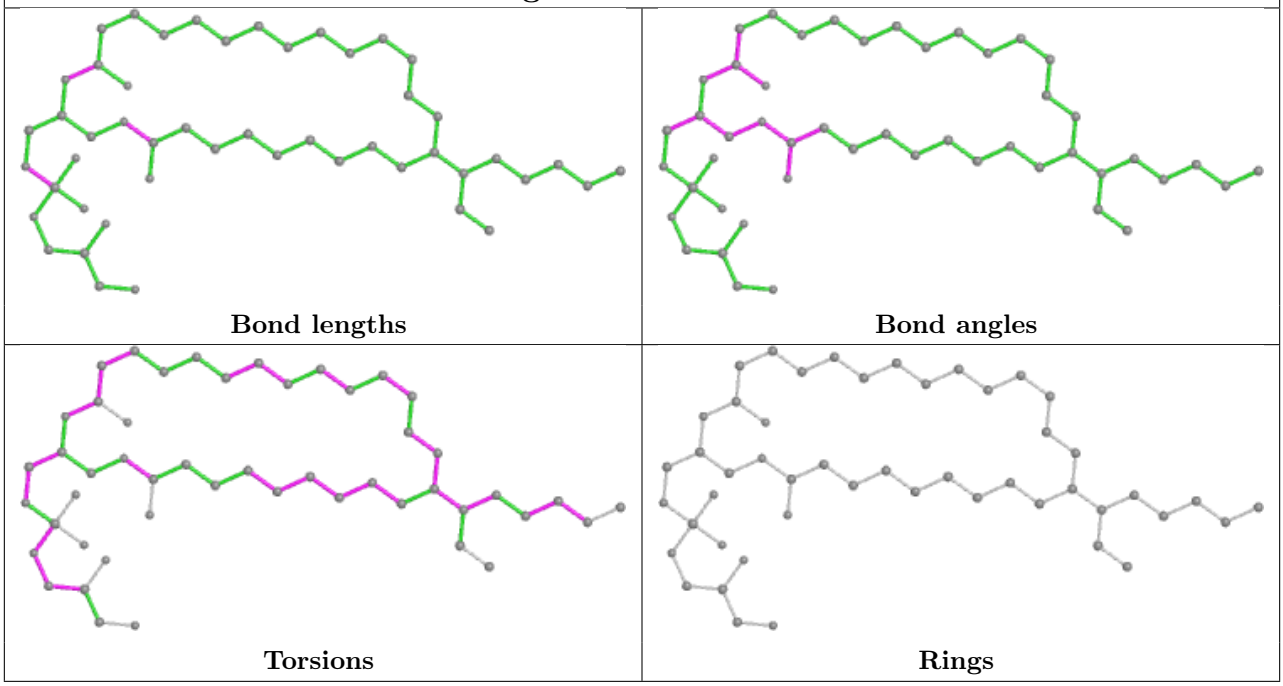
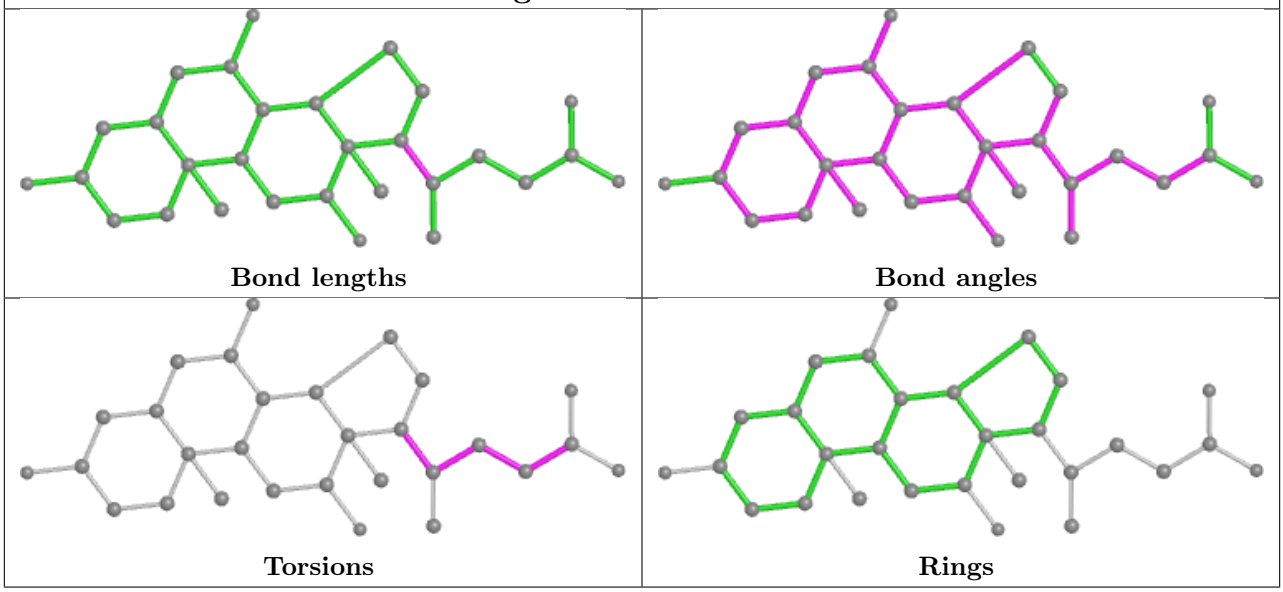


Rings

Ligand PGV C 268



Ligand CHD P 1271



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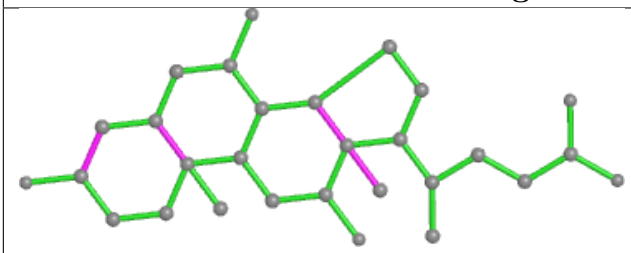
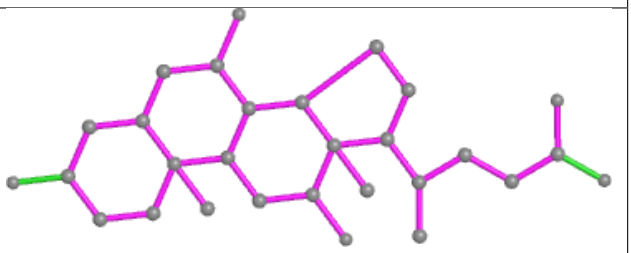
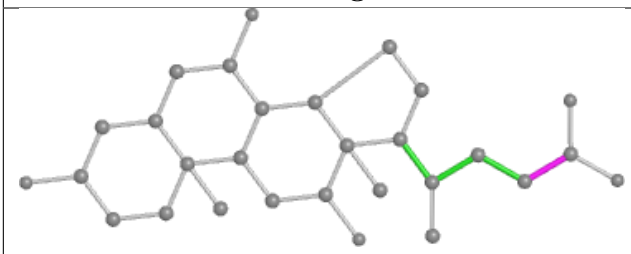


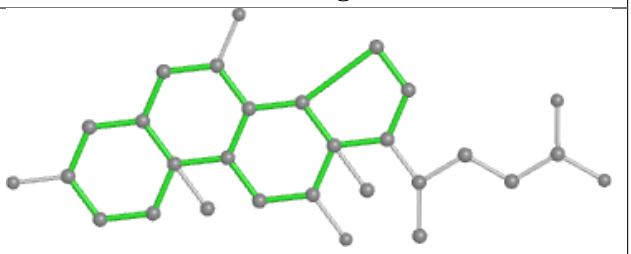
Bond lengths



Bond angles

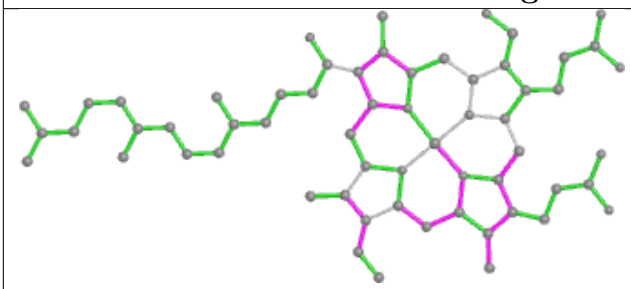


Torsions

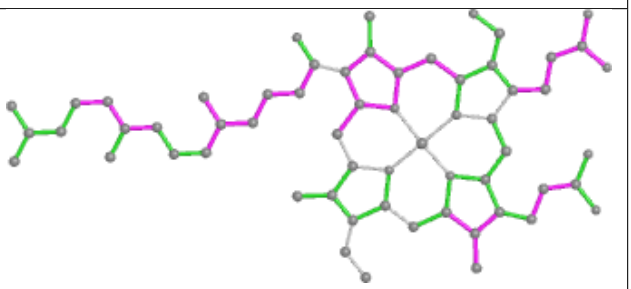


Rings

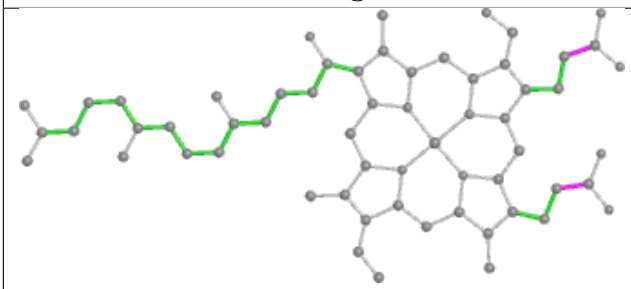
Ligand HEA N 515



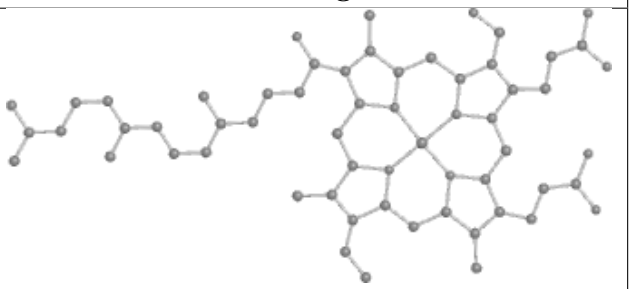
Bond lengths



Bond angles

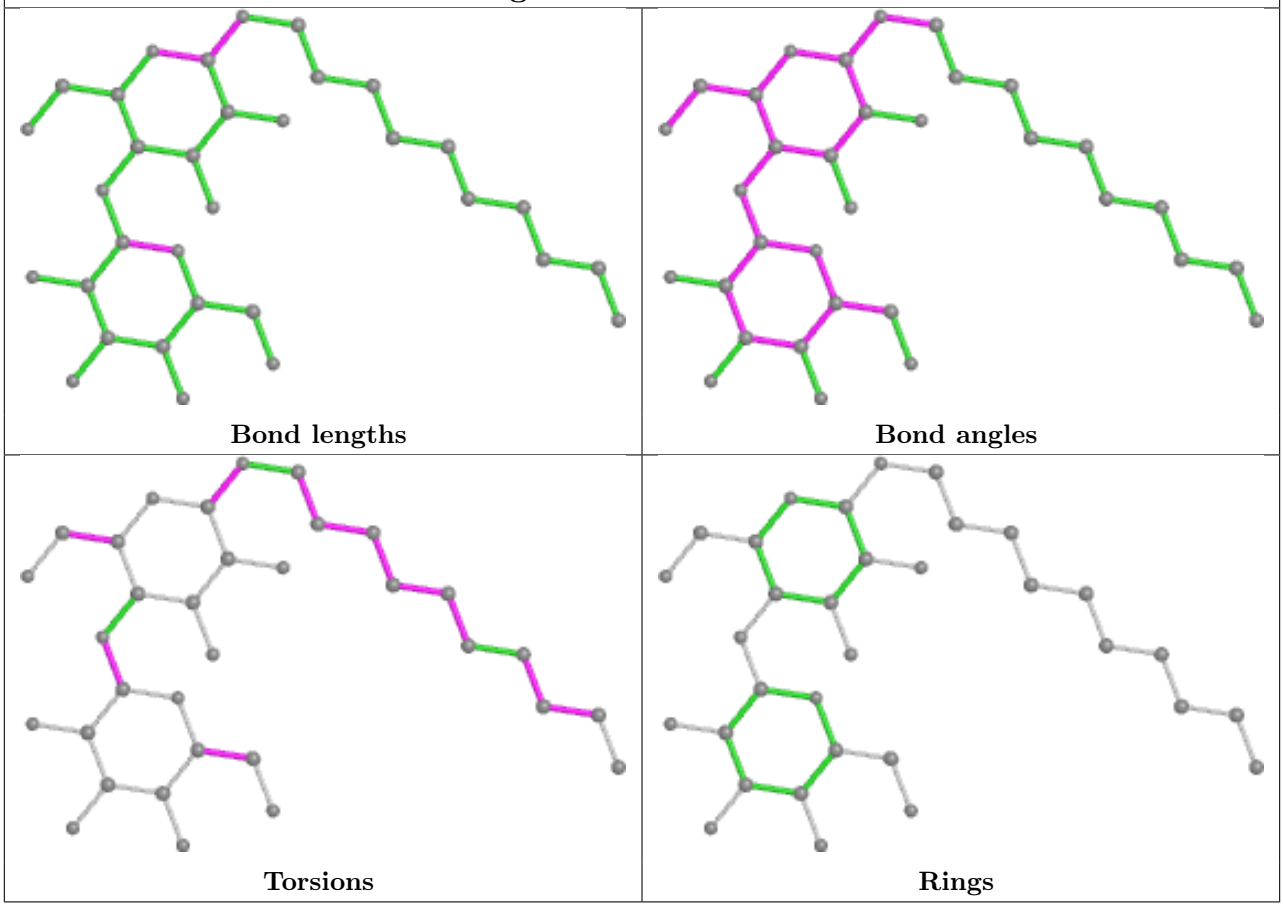


Torsions

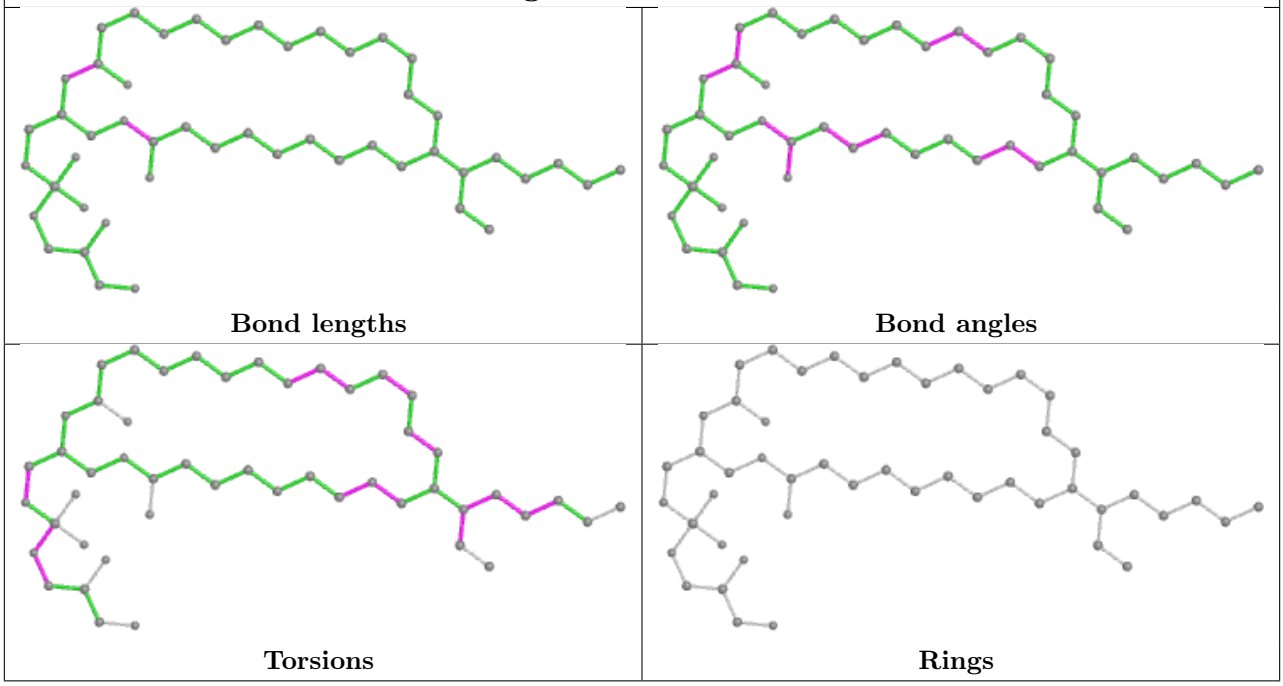


Rings

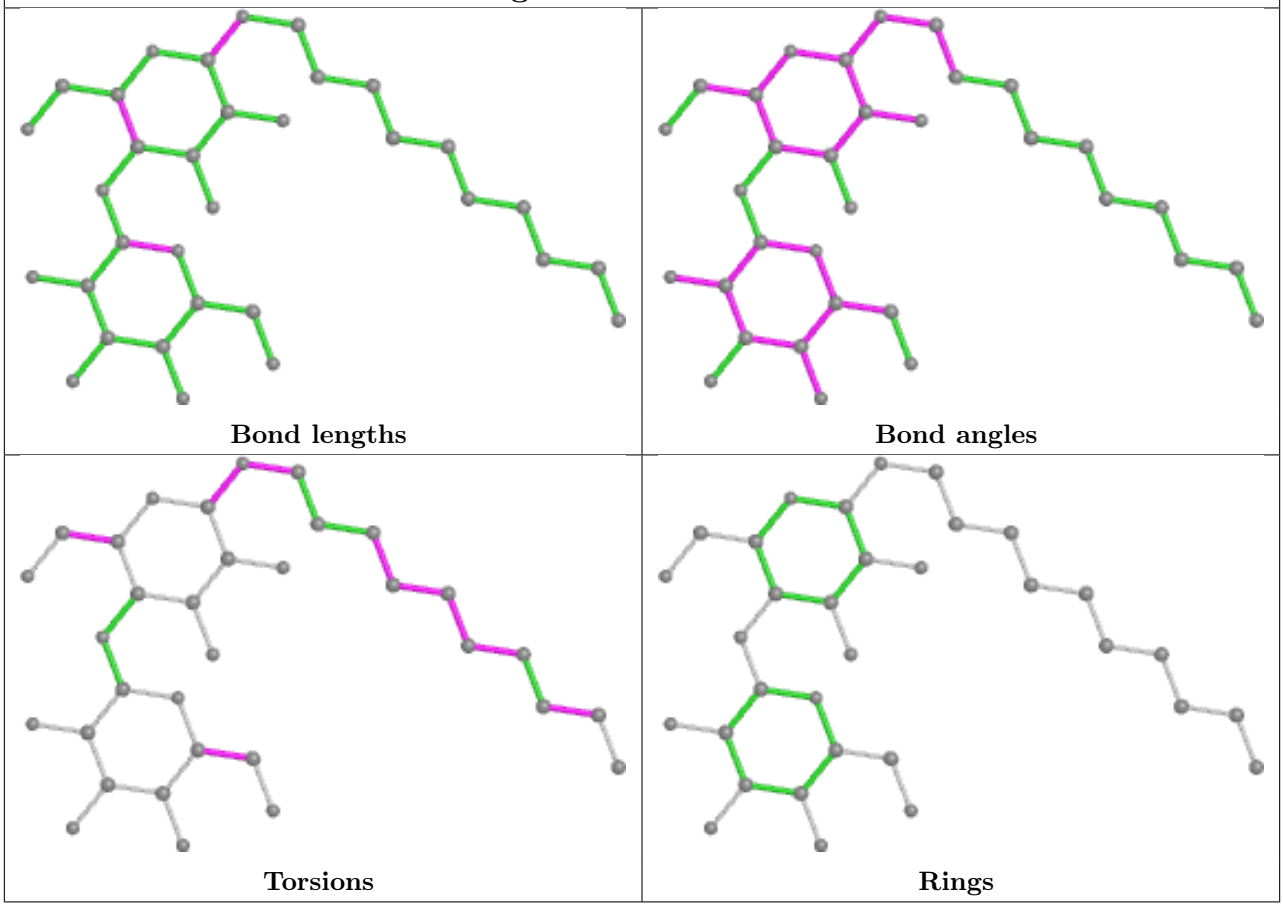
Ligand DMU T 1272



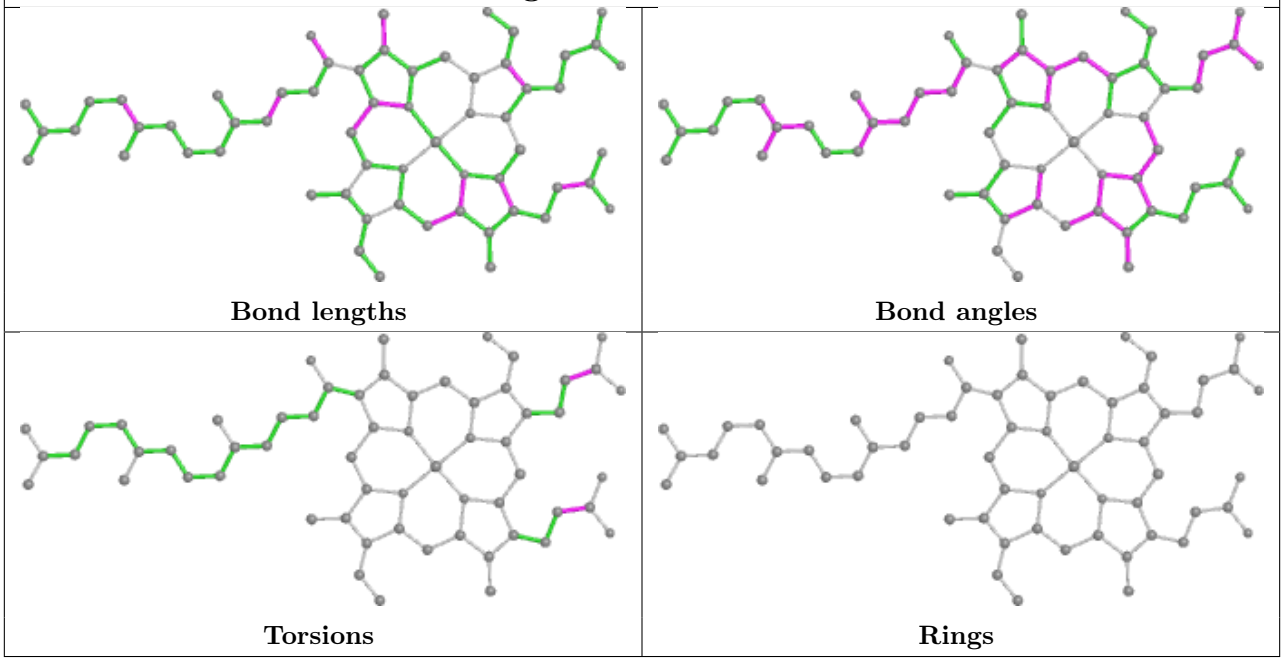
Ligand PGV C 267



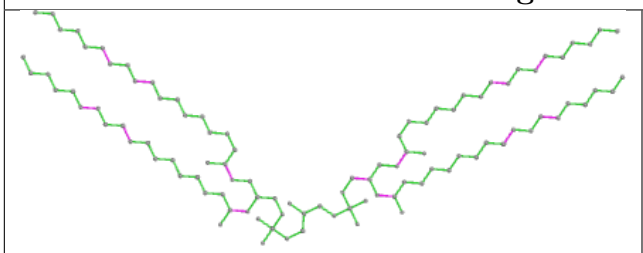
Ligand DMU Z 1526



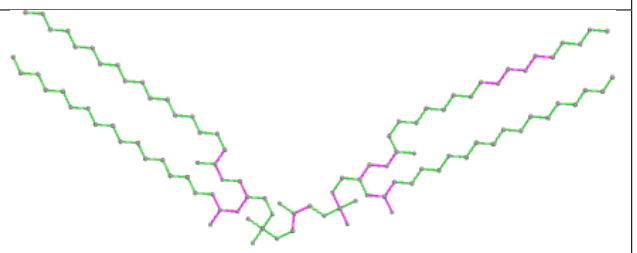
Ligand HEA A 515



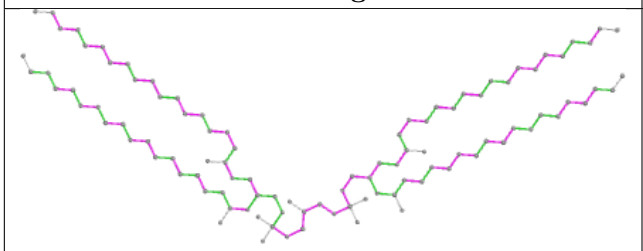
Ligand CDL T 1269



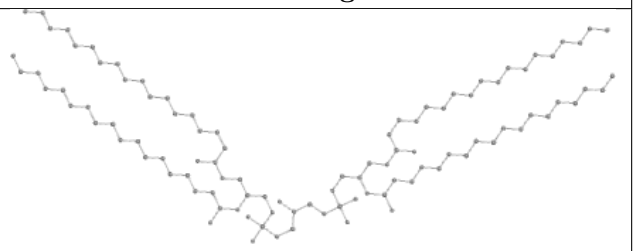
Bond lengths



Bond angles

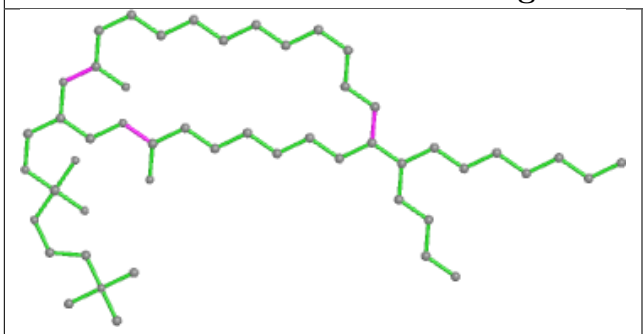


Torsions



Rings

Ligand PSC R 1229



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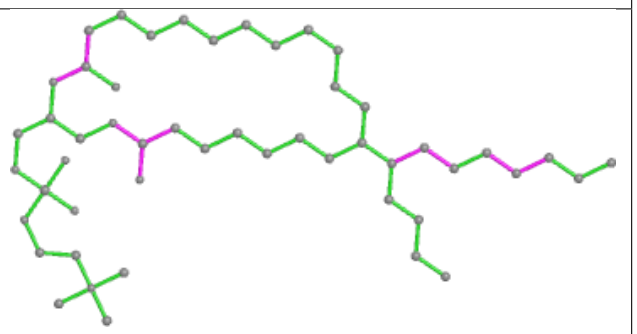
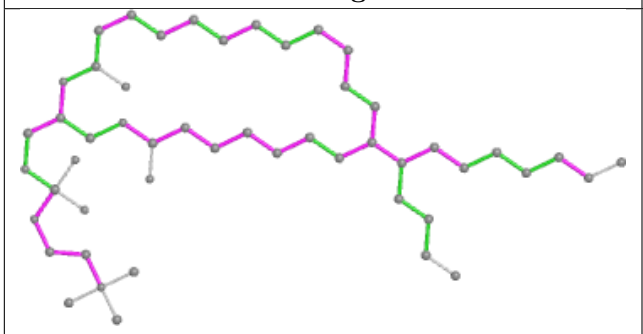
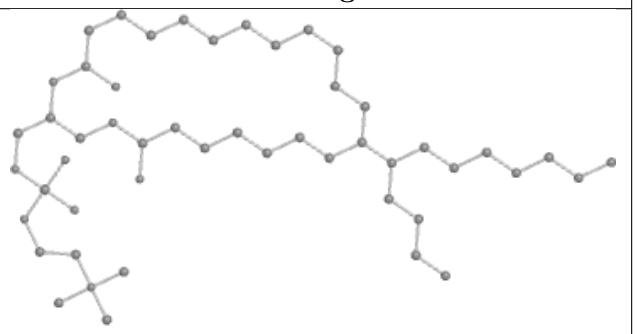


Bond angles

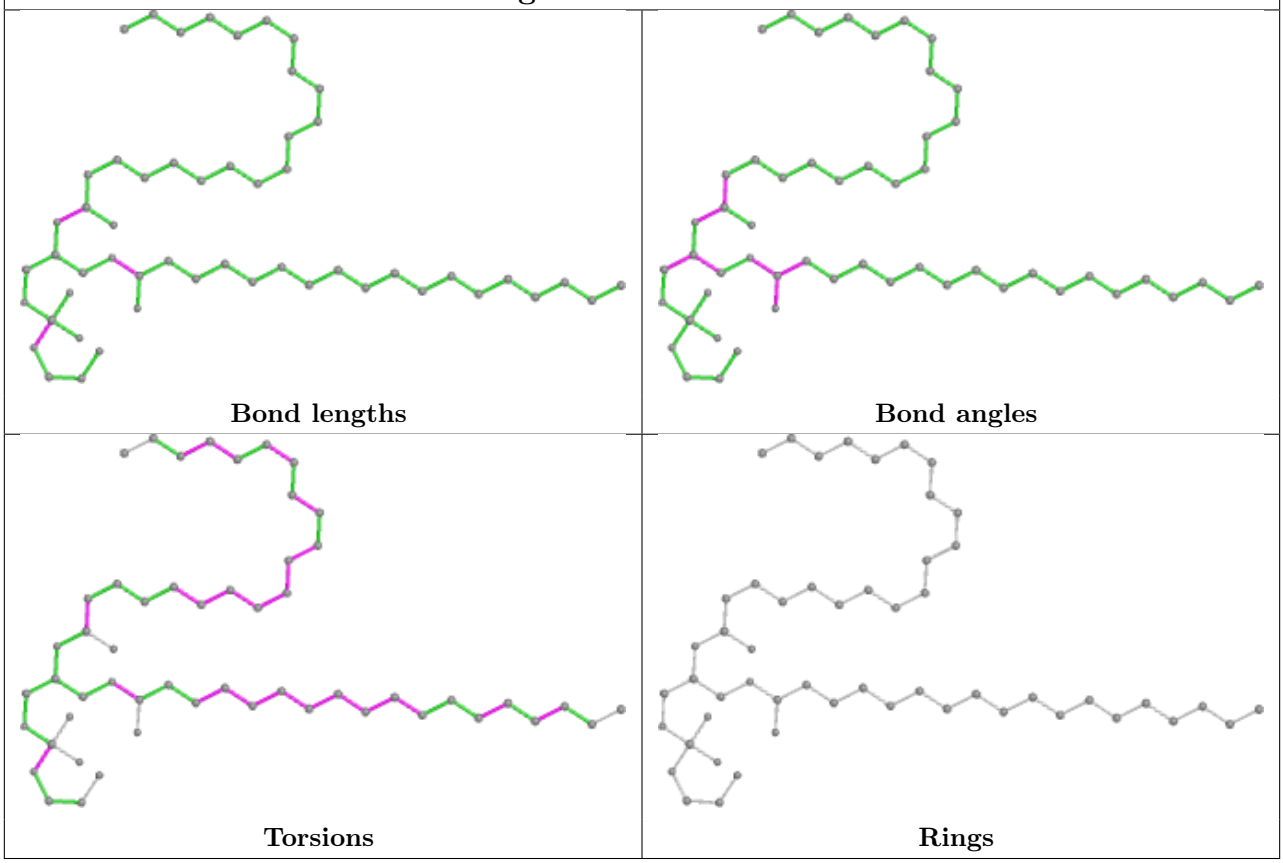


Torsions

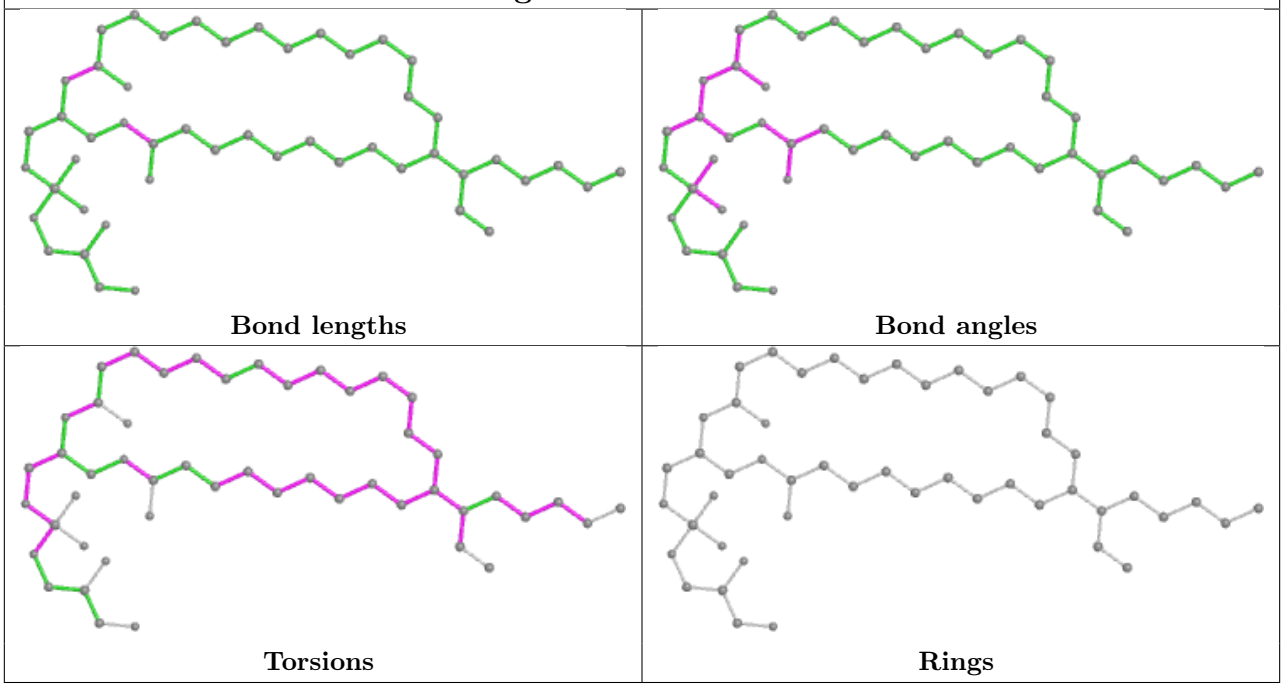


Rings

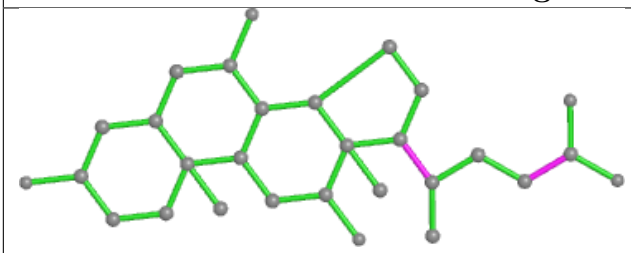
Ligand PEK S 1265



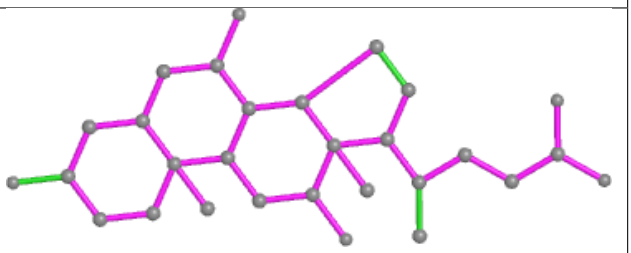
Ligand PGV P 1268



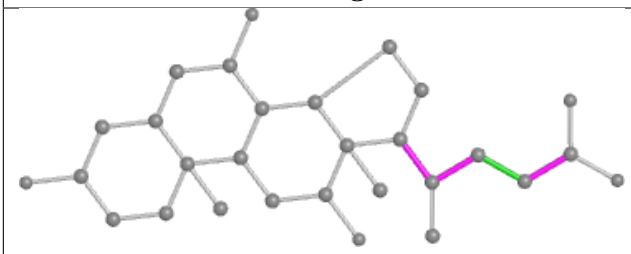
Ligand CHD J 60



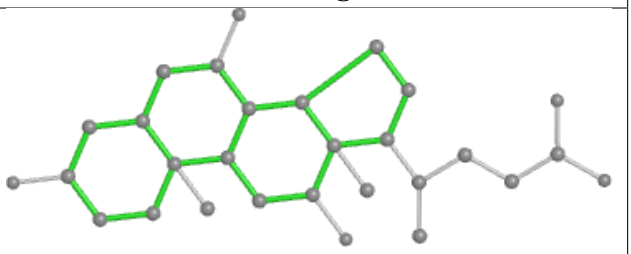
Bond lengths



Bond angles

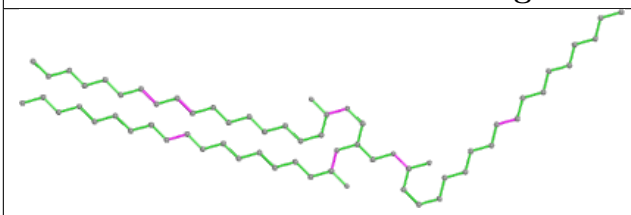


Torsions

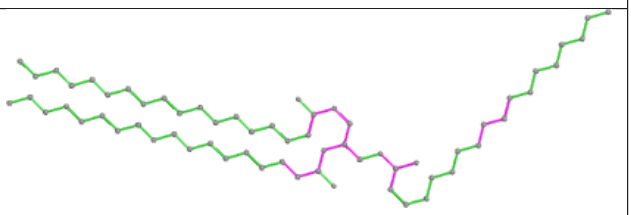


Rings

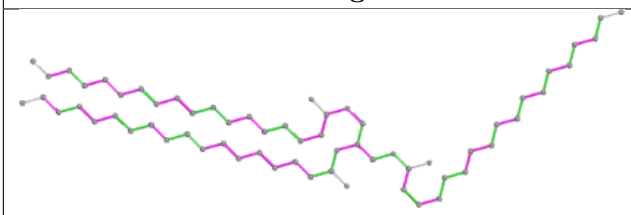
Ligand TGL N 1523



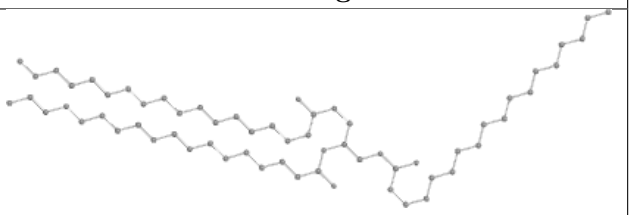
Bond lengths



Bond angles

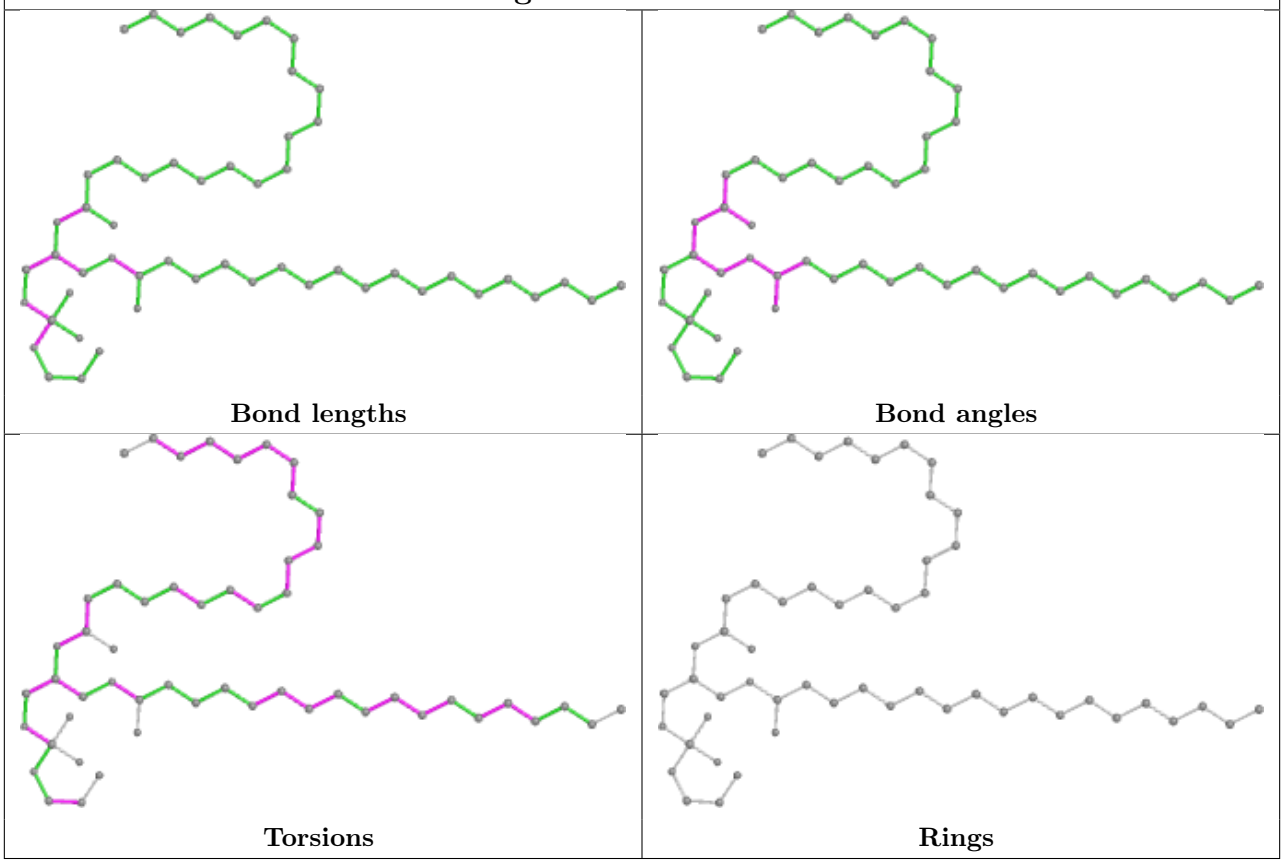


Torsions

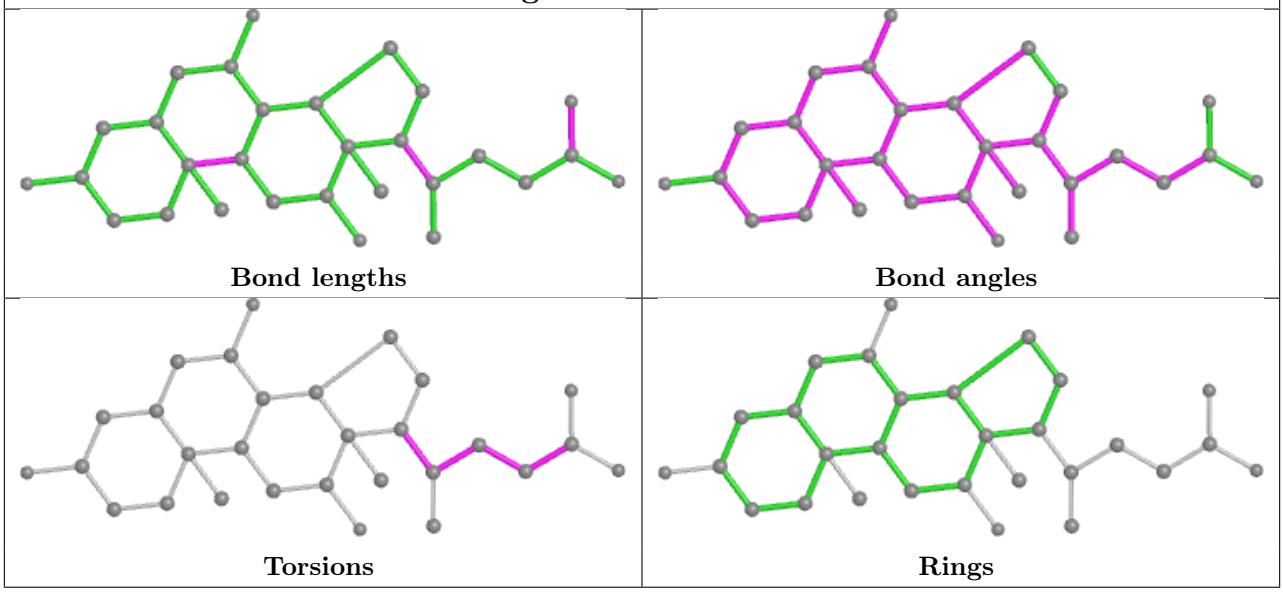


Rings

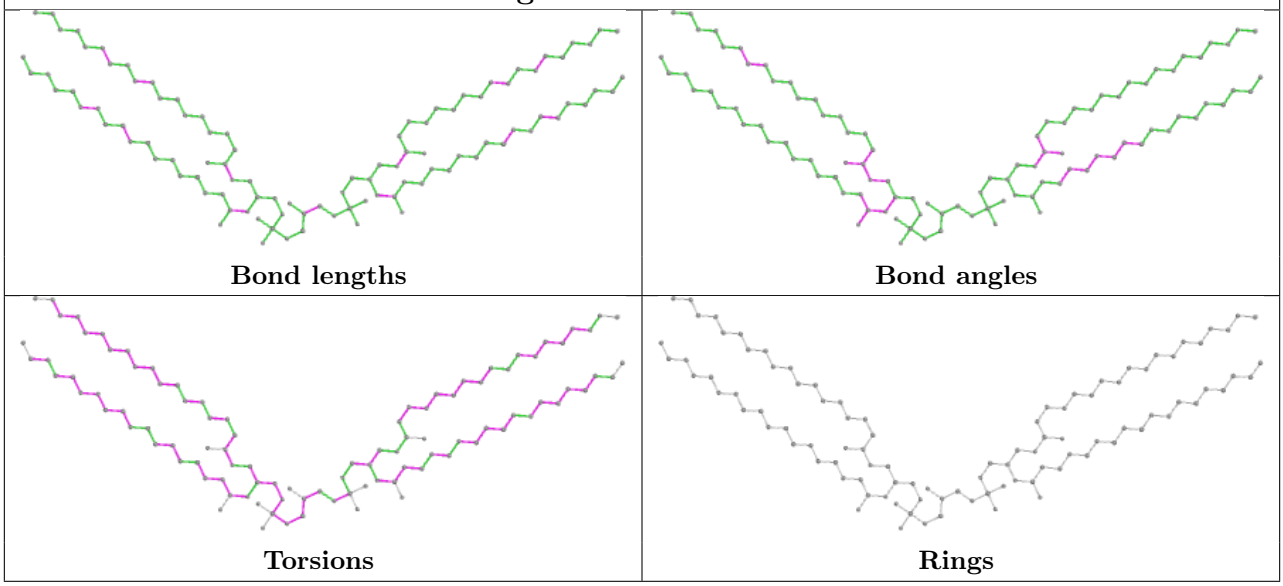
Ligand PEK G 1263



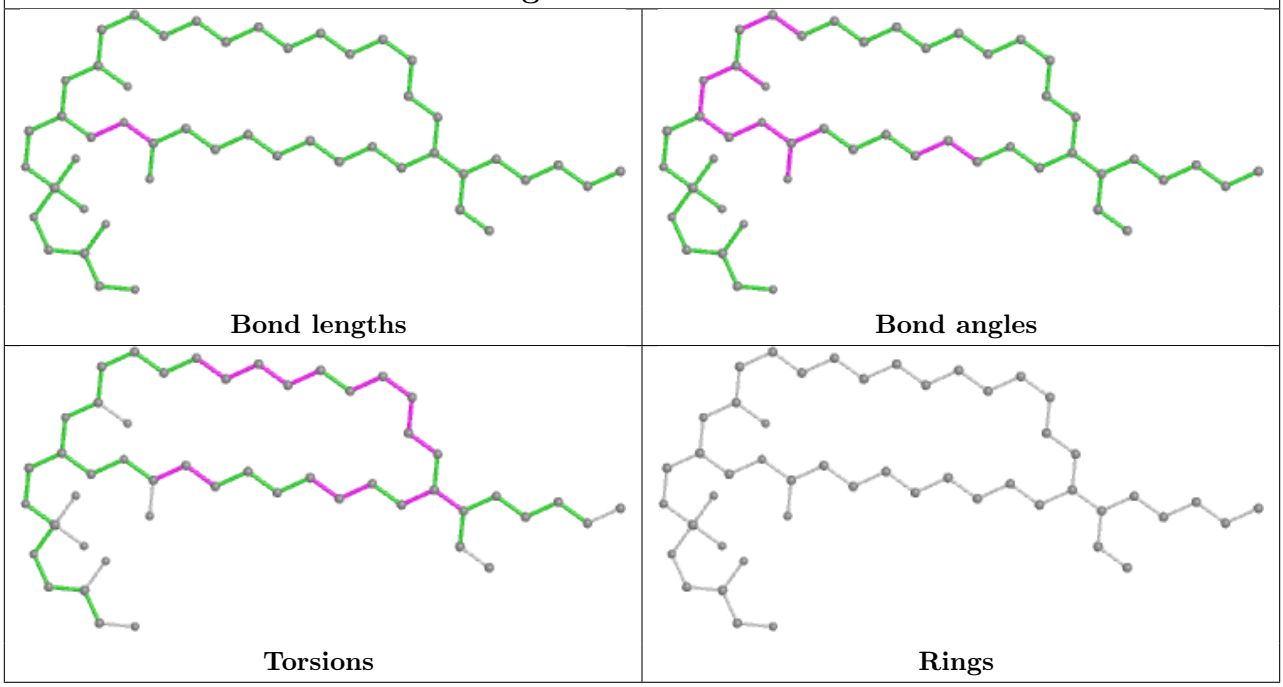
Ligand CHD C 271



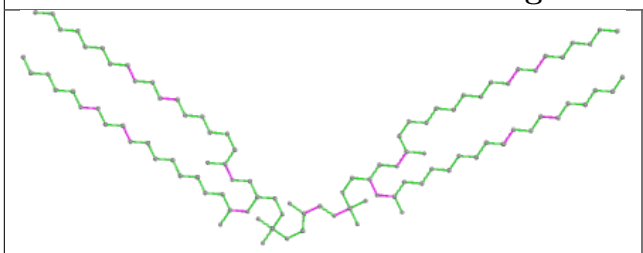
Ligand CDL P 1270



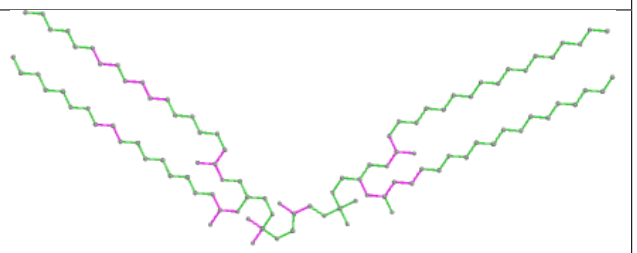
Ligand PGV A 521



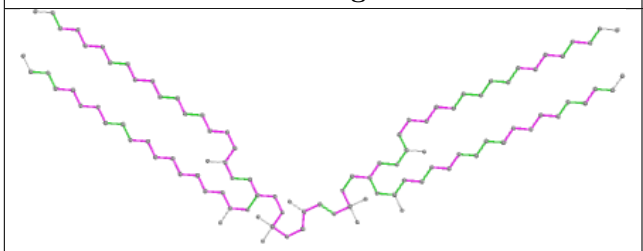
Ligand CDL C 270



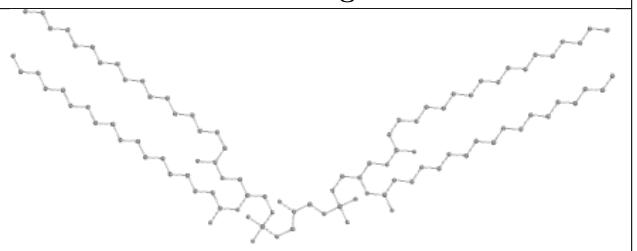
Bond lengths



Bond angles

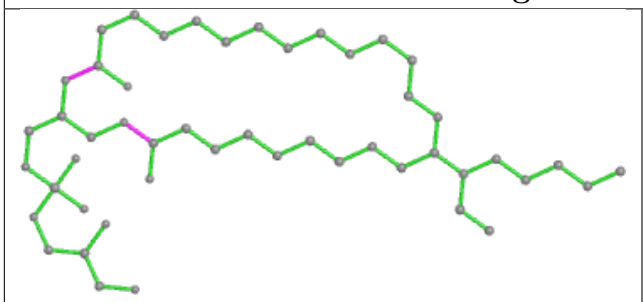


Torsions



Rings

Ligand PGV N 1524



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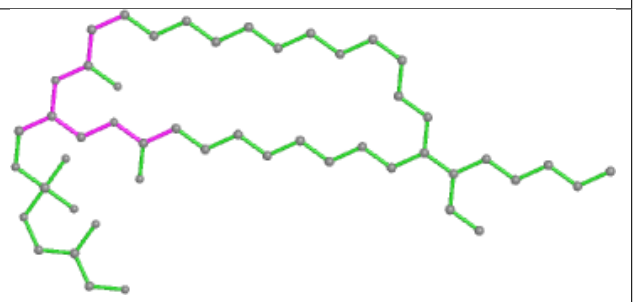
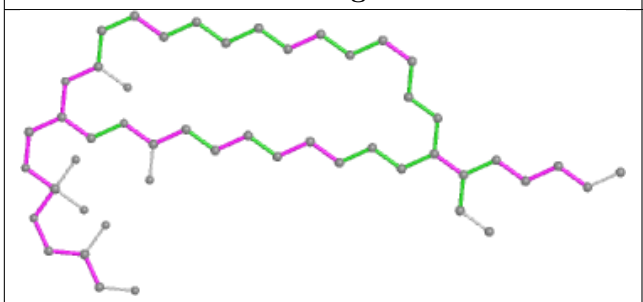


Bond angles



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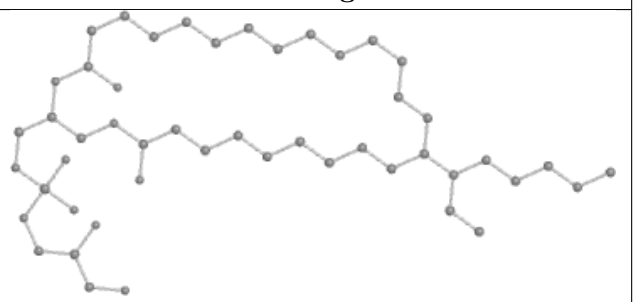
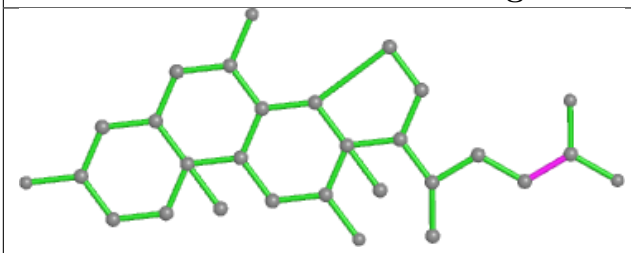


Rings

Ligand CHD W 1059



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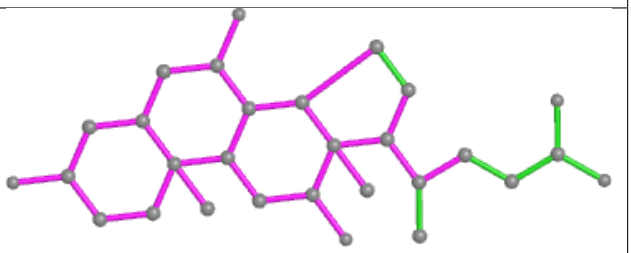
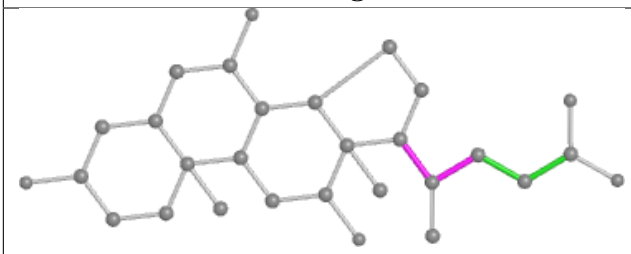


Bond angles



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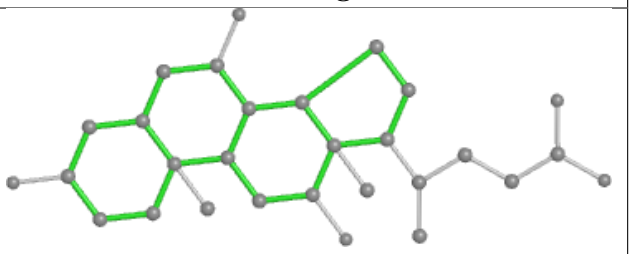
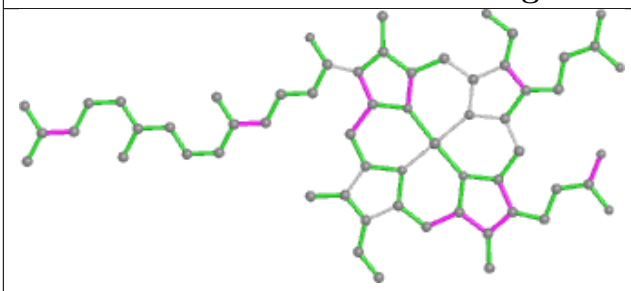


Rings

Ligand HEA A 516



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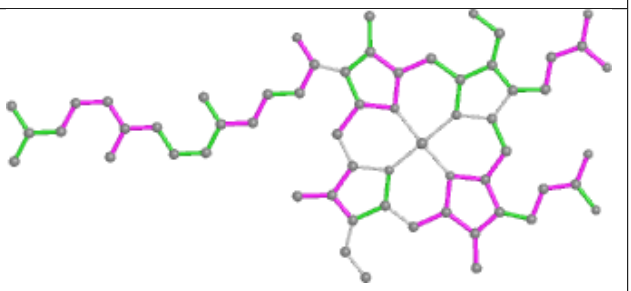
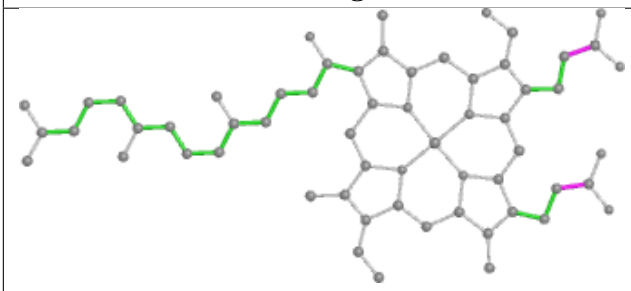


Bond angles



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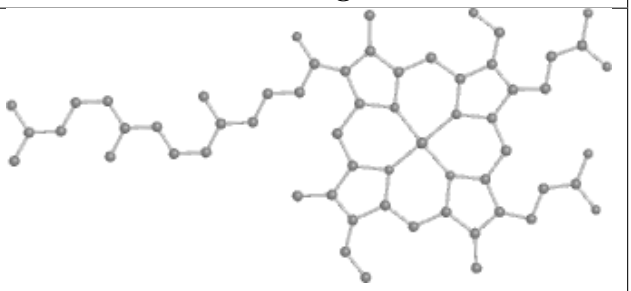
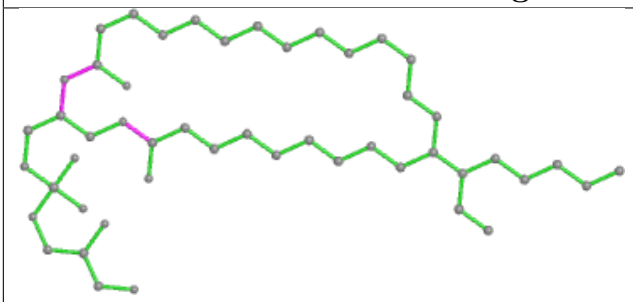


Rings

Ligand PGV N 1266



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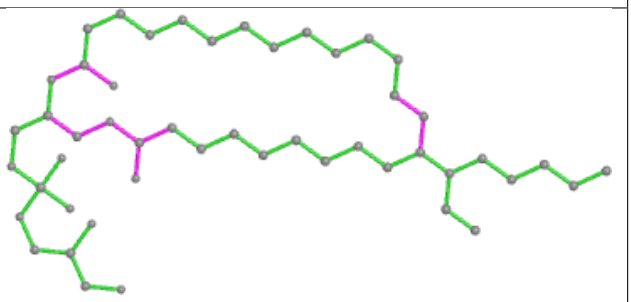
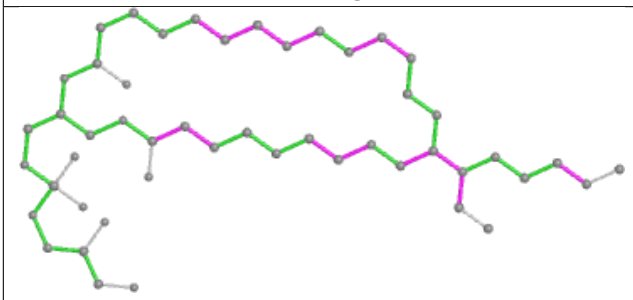


Bond angles



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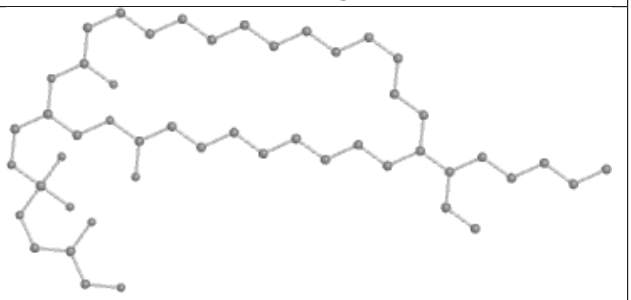
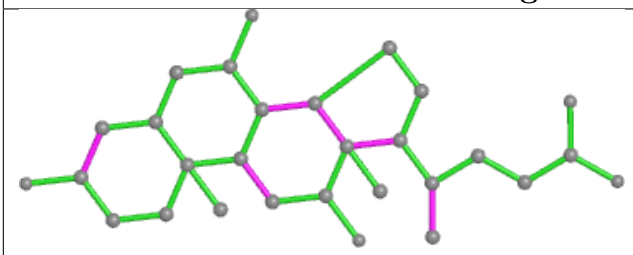
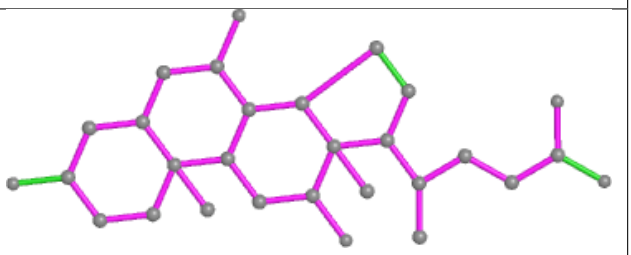


Rings

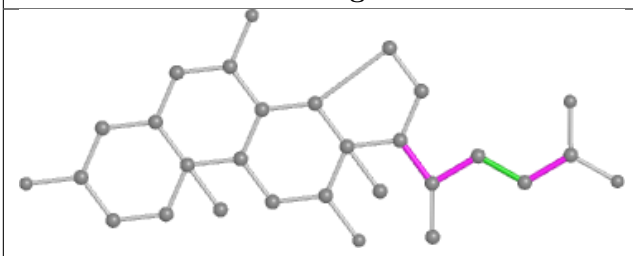
Ligand CHD O 229



Bond lengths



Bond angles



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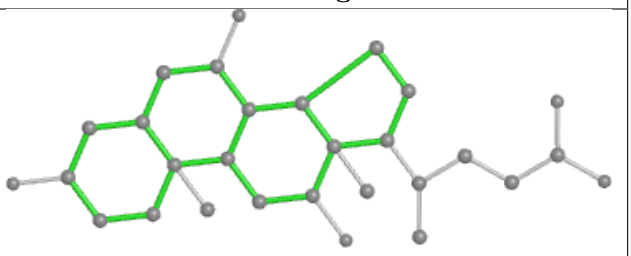
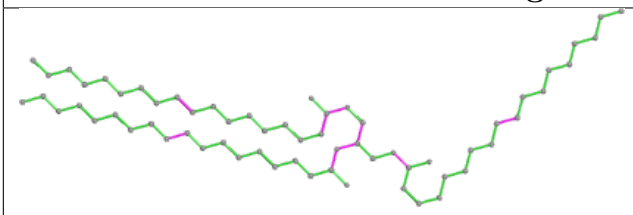


Rings

Ligand TGL L 522



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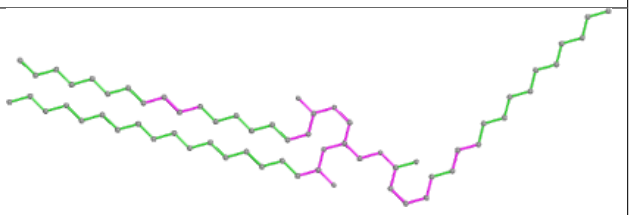
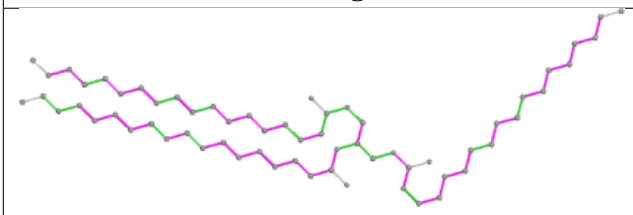
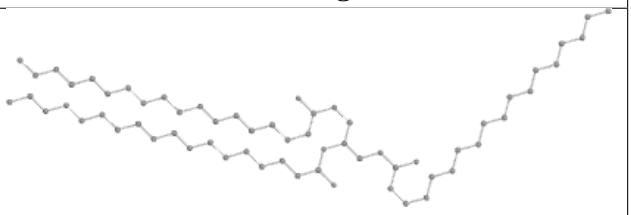


Bond angles

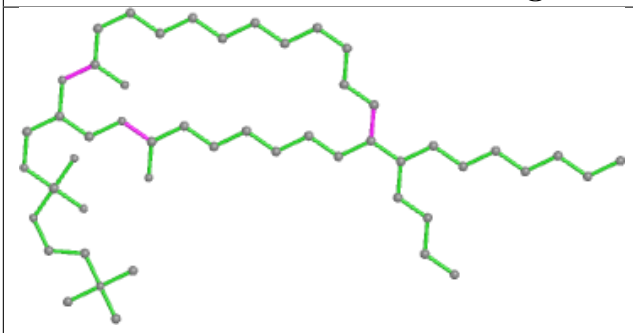


Torsions



Rings

Ligand PSC B 229



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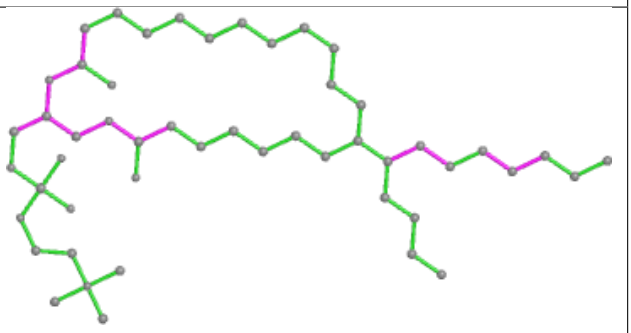
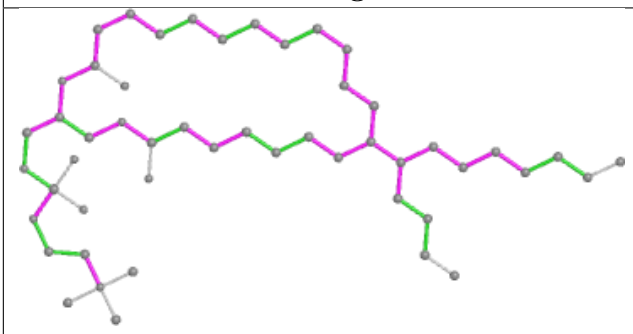


Bond angles



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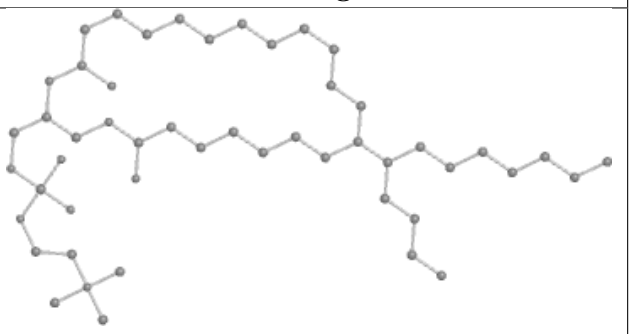
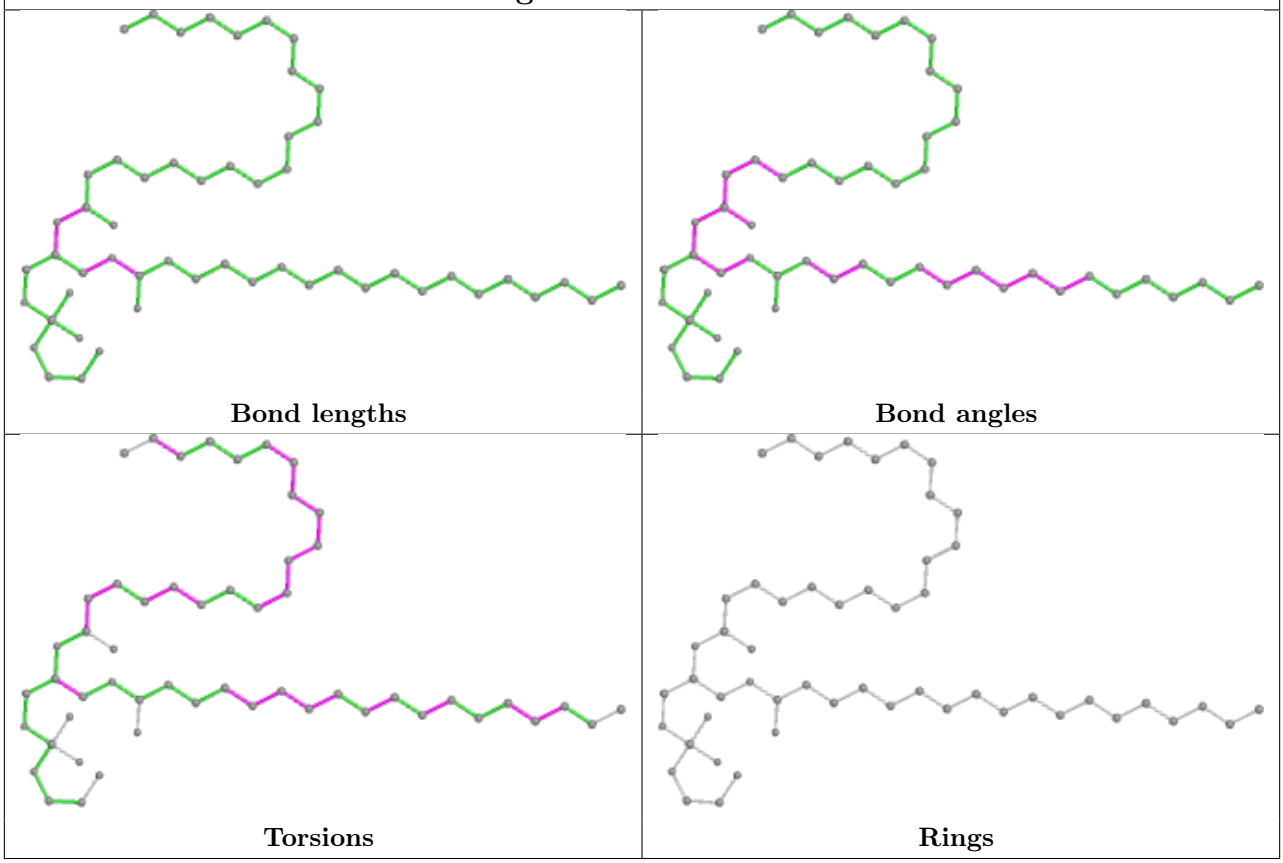
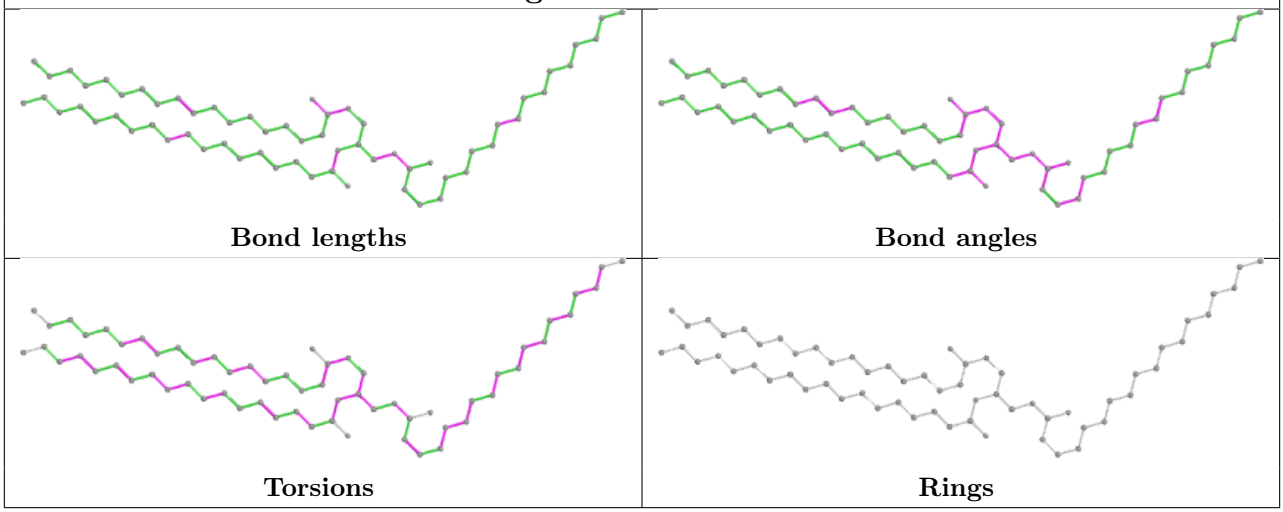


Rings

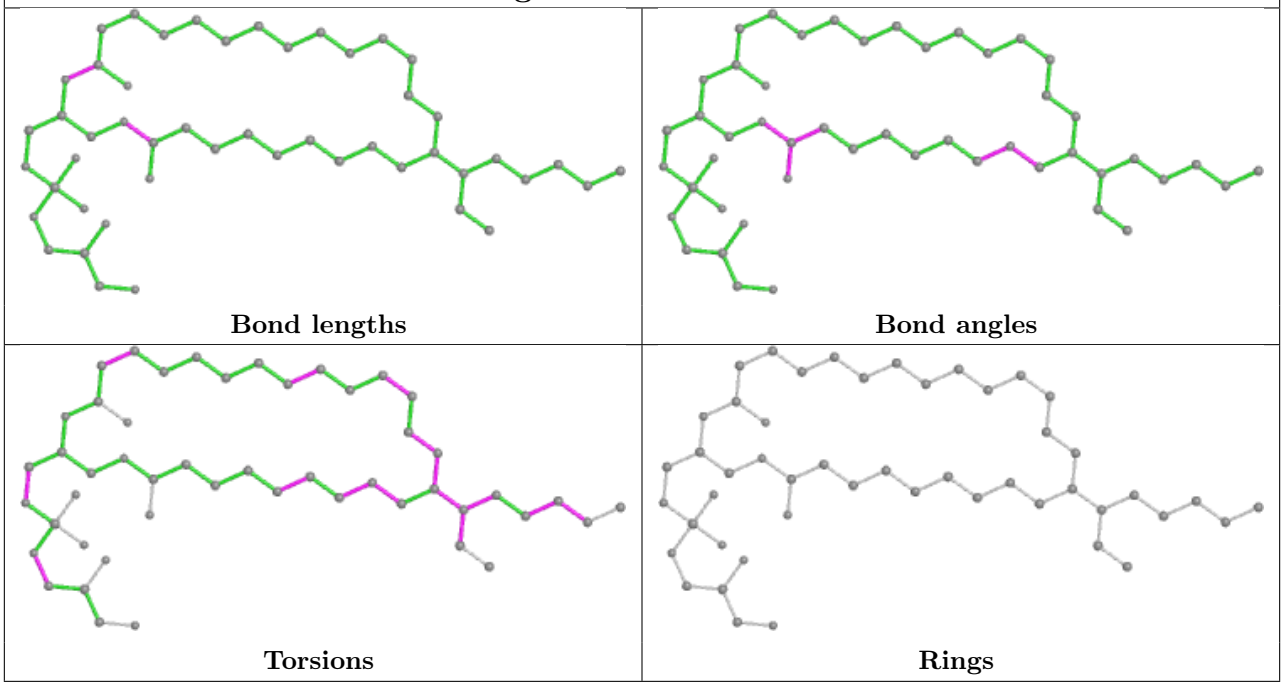
Ligand PEK T 1264



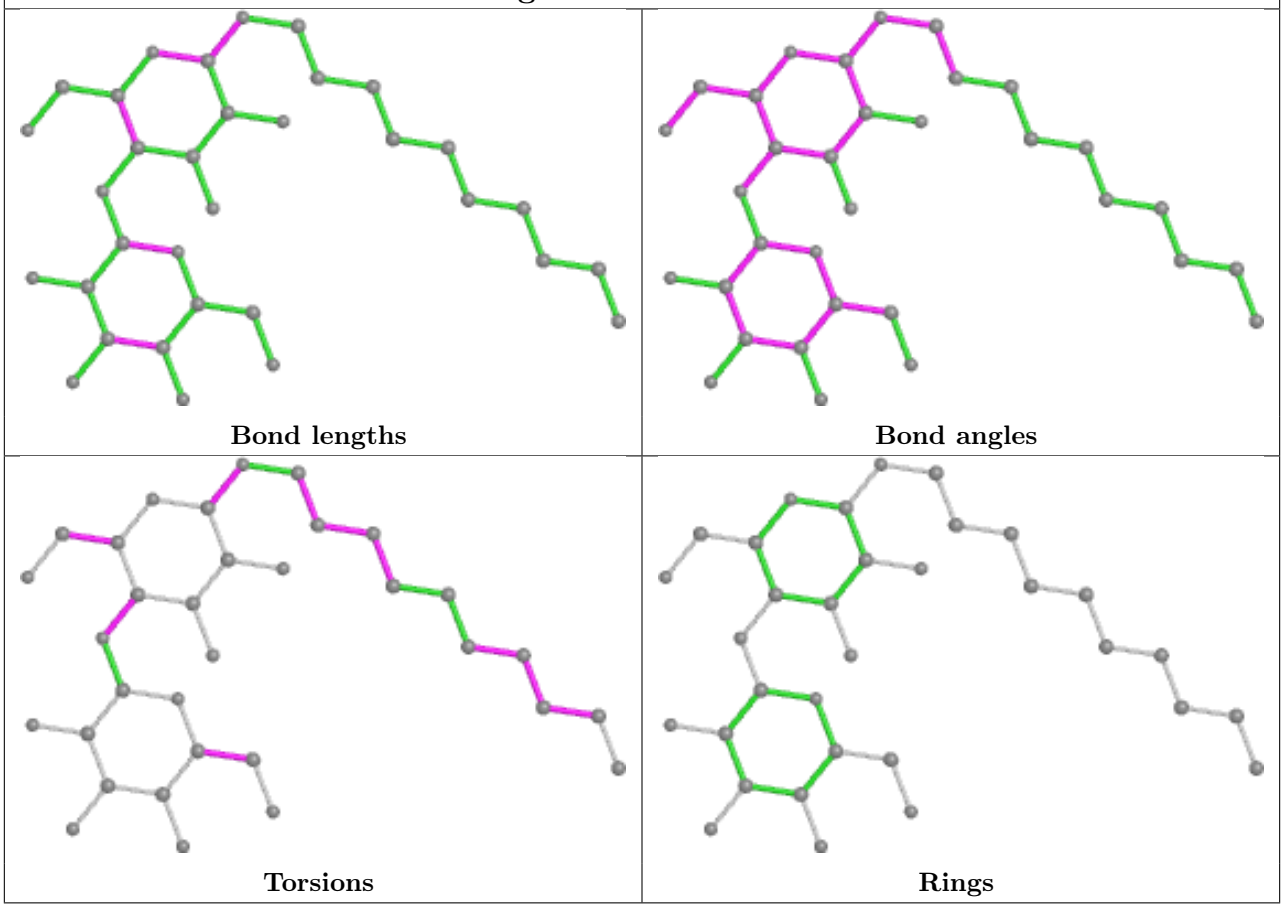
Ligand TGL B 521



Ligand PGV P 1267



Ligand DMU C 272



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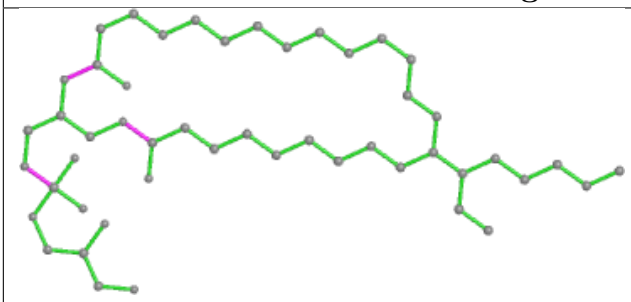
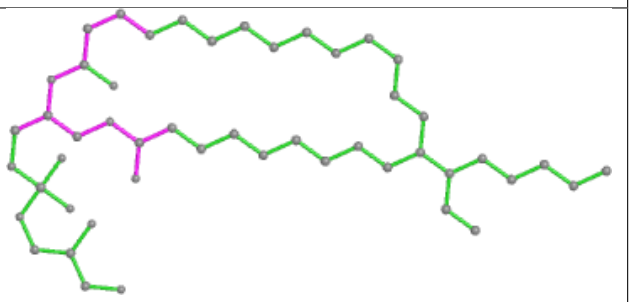
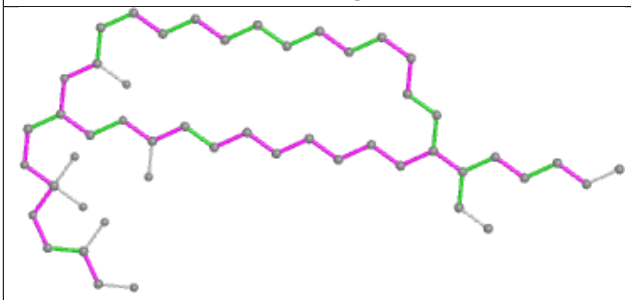


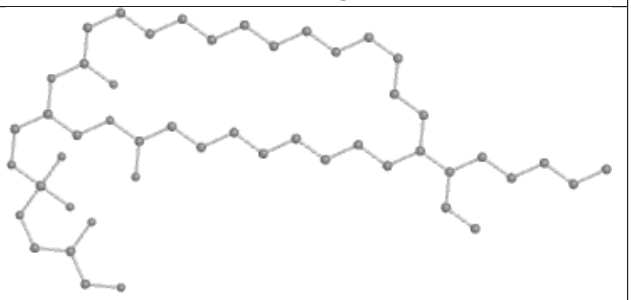
Bond lengths



Bond angles

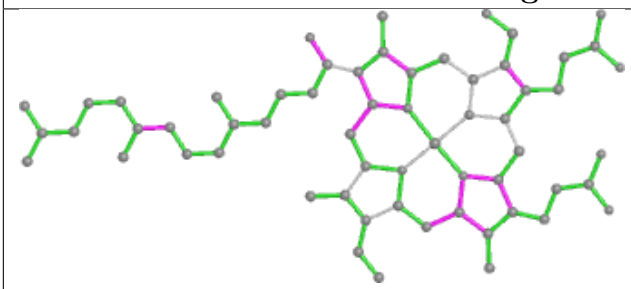


Torsions

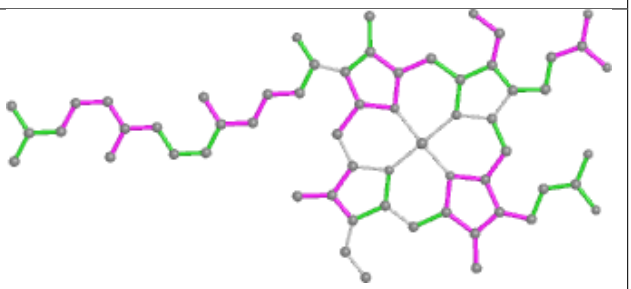


Rings

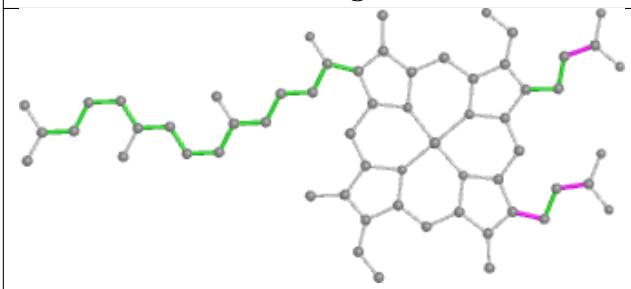
Ligand HEA N 516



Bond lengths



Bond angles



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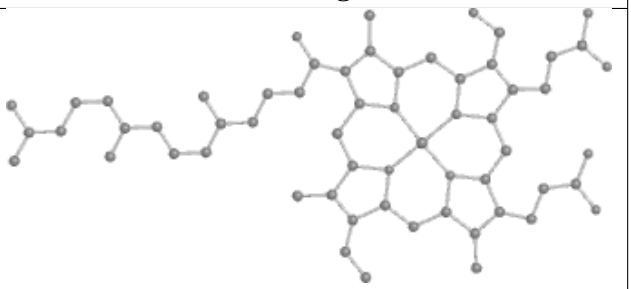
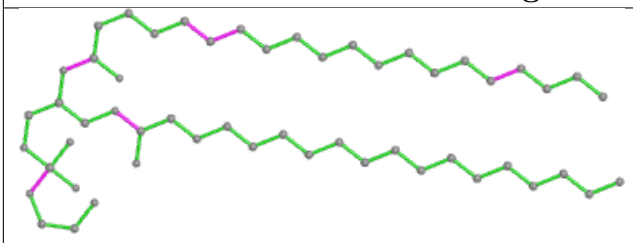
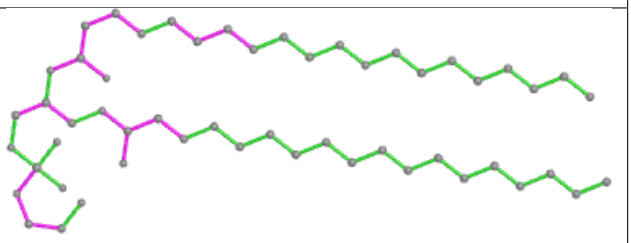


Rings

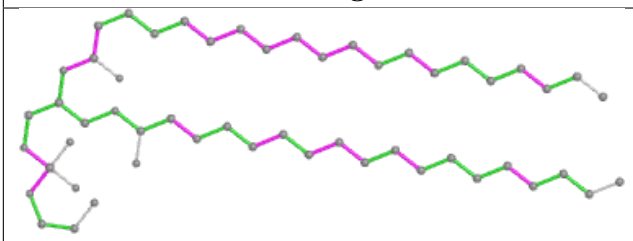
Ligand PEK G 265



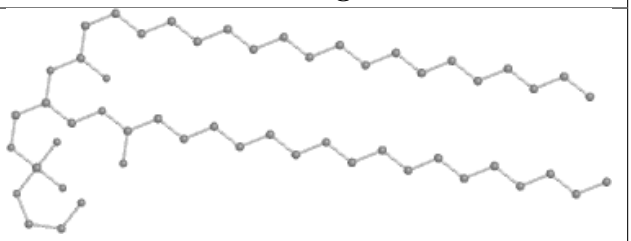
Bond lengths



Bond angles

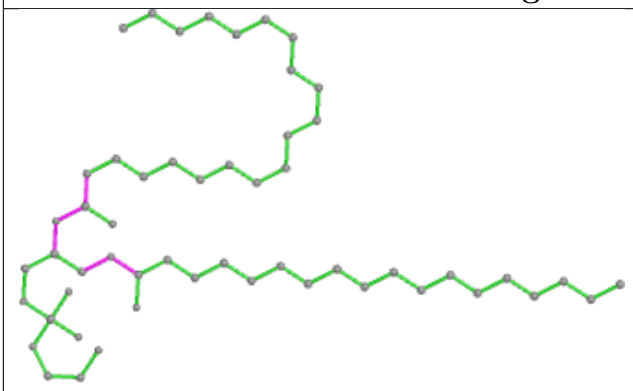


Torsions

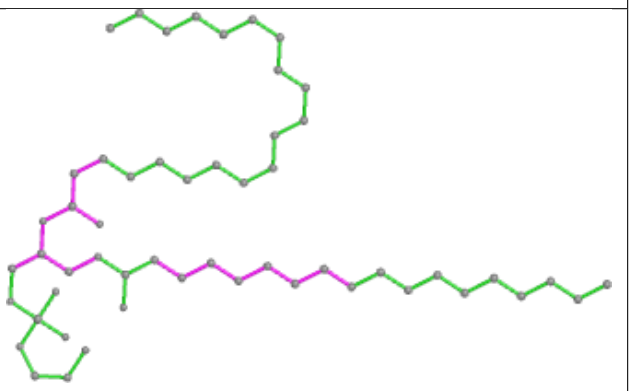


Rings

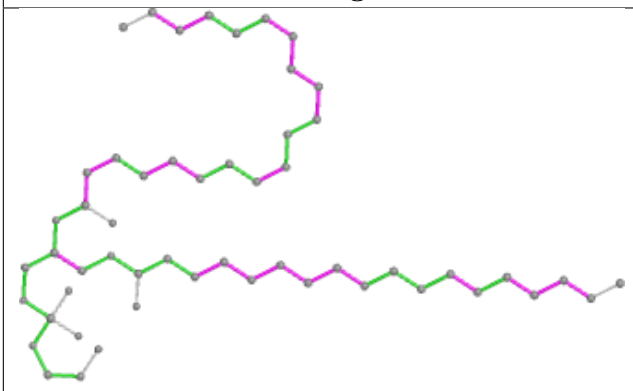
Ligand PEK G 264



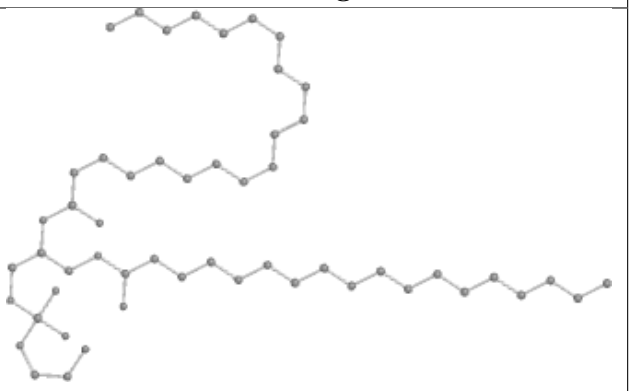
Bond lengths



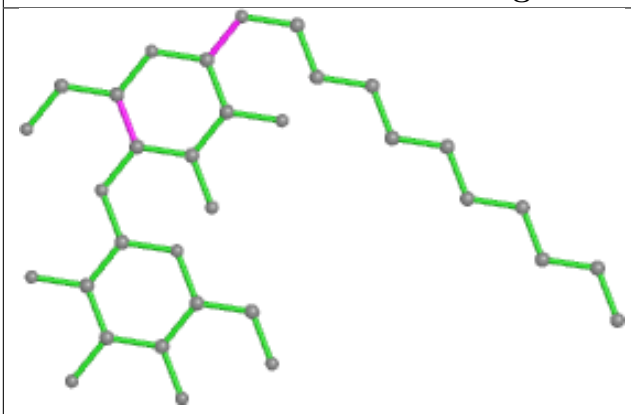
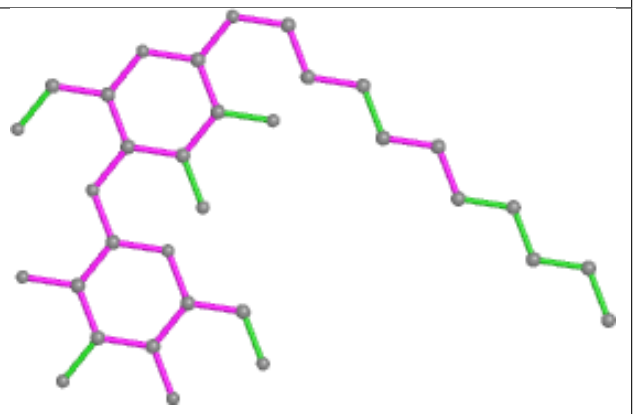
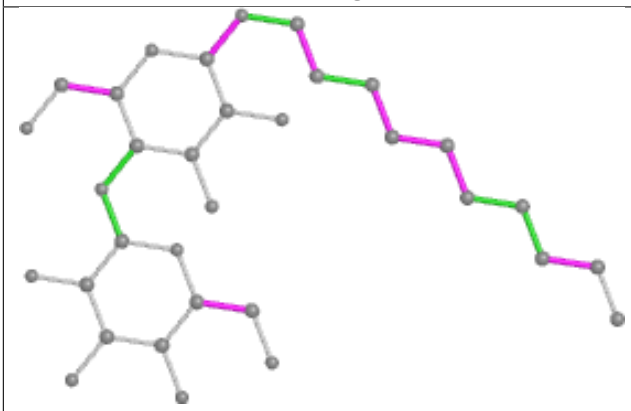
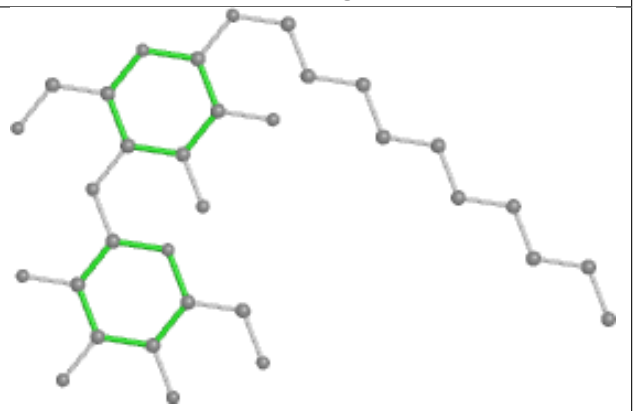
Bond angles



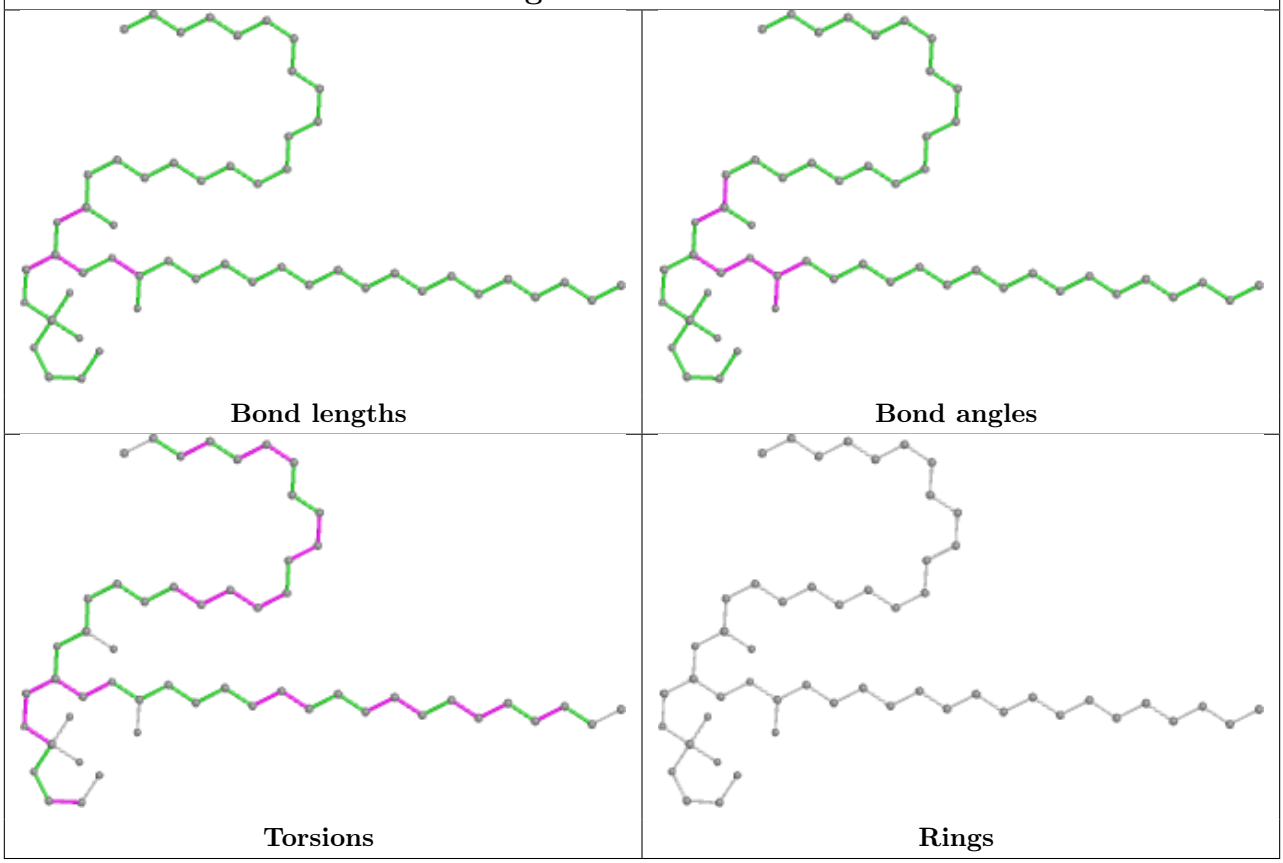
Torsions



Rings

Ligand DMU M 526	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand PEK T 263



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%)	-0.09	15 (2%) 51 49	36, 42, 52, 84	0
1	N	513/514 (99%)	-0.17	10 (1%) 66 65	43, 51, 63, 92	0
2	B	226/227 (99%)	-0.45	0 100 100	36, 48, 78, 111	0
2	O	226/227 (99%)	-0.11	7 (3%) 49 47	49, 61, 93, 120	0
3	C	259/261 (99%)	0.04	20 (7%) 13 12	38, 45, 59, 86	0
3	P	259/261 (99%)	0.36	27 (10%) 6 5	44, 51, 68, 88	0
4	D	144/147 (97%)	-0.58	2 (1%) 75 73	43, 51, 75, 91	0
4	Q	144/147 (97%)	0.70	16 (11%) 5 4	55, 69, 96, 132	0
5	E	105/109 (96%)	-0.35	0 100 100	43, 51, 83, 118	0
5	R	105/109 (96%)	0.71	9 (8%) 10 9	51, 63, 92, 123	0
6	F	98/98 (100%)	-0.16	7 (7%) 16 14	40, 53, 112, 143	0
6	S	98/98 (100%)	-0.20	7 (7%) 16 14	49, 61, 113, 144	0
7	G	83/85 (97%)	0.47	15 (18%) 1 1	42, 55, 123, 129	0
7	T	83/85 (97%)	0.67	16 (19%) 1 1	46, 62, 121, 133	0
8	H	79/85 (92%)	-0.02	3 (3%) 40 38	46, 58, 119, 129	0
8	U	79/85 (92%)	-0.35	2 (2%) 57 55	54, 69, 120, 127	0
9	I	72/73 (98%)	0.20	6 (8%) 11 10	48, 60, 105, 112	0
9	V	72/73 (98%)	0.93	12 (16%) 1 1	52, 74, 109, 112	0
10	J	58/59 (98%)	0.14	4 (6%) 16 15	45, 58, 86, 119	0
10	W	58/59 (98%)	0.41	5 (8%) 10 9	54, 66, 88, 120	0
11	K	49/56 (87%)	-0.42	0 100 100	45, 57, 75, 83	0
11	X	49/56 (87%)	0.84	10 (20%) 1 1	62, 69, 85, 99	0
12	L	46/47 (97%)	-0.38	1 (2%) 62 59	43, 48, 70, 100	0
12	Y	46/47 (97%)	-0.14	3 (6%) 18 17	53, 61, 82, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
13	M	43/46 (93%)	-0.33	1 (2%)	60	58	44, 51, 88, 120	0
13	Z	43/46 (93%)	0.44	7 (16%)	1	1	57, 65, 96, 121	0
All	All	3550/3614 (98%)	0.01	205 (5%)	23	22	36, 53, 92, 144	0

The worst 5 of 205 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	Q	6	VAL	14.6
4	Q	5	VAL	11.0
7	T	1	ALA	10.7
6	F	1	ALA	10.3
4	Q	7	LYS	10.1

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
7	TPO	T	11	11/12	0.34	0.41	97,105,129,130	0
9	SAC	V	1	9/10	0.50	0.62	110,112,114,115	0
7	TPO	G	11	11/12	0.51	0.45	93,102,125,127	0
9	SAC	I	1	9/10	0.58	0.54	99,103,106,106	0
1	FME	N	1	10/11	0.87	0.46	77,82,105,107	0
1	FME	A	1	10/11	0.94	0.21	63,70,93,102	0
2	FME	O	1	10/11	0.94	0.25	59,59,64,64	0
2	FME	B	1	10/11	0.98	0.10	46,48,51,61	0

6.3 Carbohydrates (i)

There are no monosaccharides 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	0.39	0.65	75,75,75,75	0
28	PEK	G	1263	53/53	0.41	0.68	83,126,150,150	0
22	PSC	R	1229	52/52	0.55	0.35	73,120,150,150	0
28	PEK	T	263	53/53	0.55	0.51	78,123,145,149	0
25	CDL	T	1269	100/100	0.58	0.45	92,117,138,143	0
25	CDL	G	269	100/100	0.60	0.40	89,118,138,141	0
26	DMU	T	1272	33/33	0.60	0.37	111,140,141,141	0
26	DMU	C	272	33/33	0.62	0.28	96,129,132,134	0
22	PSC	B	229	52/52	0.62	0.32	70,117,150,150	0
20	PGV	C	268	51/51	0.64	0.66	78,103,119,120	0
19	TGL	N	1522	63/63	0.65	0.30	72,95,111,112	0
24	UNX	P	262	1/1	0.69	0.68	75,75,75,75	0
28	PEK	S	1265	53/53	0.71	0.26	75,112,133,136	0
20	PGV	P	1268	51/51	0.73	0.57	78,108,125,126	0
20	PGV	N	1524	51/51	0.73	0.39	67,106,139,140	0
28	PEK	G	265	53/53	0.74	0.23	70,109,135,138	0
25	CDL	P	1270	100/100	0.76	0.38	69,119,136,137	0
23	CHD	W	1059	29/29	0.77	0.37	110,117,120,122	0
19	TGL	N	1523	63/63	0.77	0.34	84,111,131,133	0
19	TGL	L	522	63/63	0.77	0.25	57,89,109,113	0
20	PGV	A	524	51/51	0.78	0.27	62,101,132,135	0
19	TGL	A	523	63/63	0.78	0.21	78,102,131,132	0
25	CDL	C	270	100/100	0.83	0.34	56,112,137,139	0
23	CHD	J	60	29/29	0.85	0.34	103,112,119,120	0
19	TGL	B	521	63/63	0.86	0.18	54,96,118,120	0
18	NA	N	519	1/1	0.87	0.24	58,58,58,58	0
19	TGL	N	1521	63/63	0.88	0.21	69,101,120,123	0
26	DMU	Z	1526	33/33	0.90	0.28	73,80,94,96	0
17	MG	N	518	1/1	0.92	0.11	50,50,50,50	0
23	CHD	C	271	29/29	0.94	0.19	86,97,99,99	0
23	CHD	P	1271	29/29	0.94	0.13	98,101,103,104	0
26	DMU	M	526	33/33	0.94	0.14	52,63,87,91	0
17	MG	A	518	1/1	0.95	0.17	40,40,40,40	0
28	PEK	T	1264	53/53	0.95	0.17	49,70,109,111	0
23	CHD	P	1525	29/29	0.96	0.27	48,54,57,59	0
28	PEK	G	264	53/53	0.96	0.14	44,65,107,109	0
20	PGV	P	1267	51/51	0.96	0.19	45,56,102,106	0
23	CHD	C	525	29/29	0.96	0.29	38,50,57,65	0
18	NA	A	519	1/1	0.96	0.06	47,47,47,47	0
20	PGV	N	1266	51/51	0.96	0.15	45,60,81,84	0
23	CHD	O	229	29/29	0.96	0.13	45,49,56,62	0

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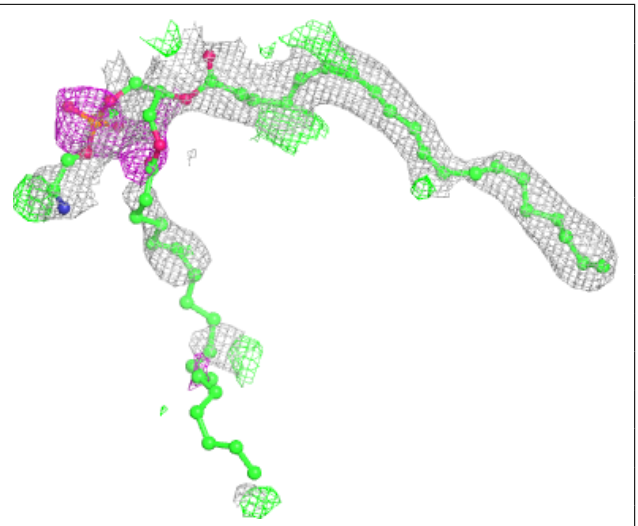
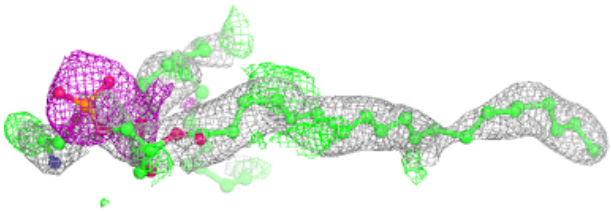
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	CHD	B	1085	29/29	0.97	0.14	46,50,53,59	0
20	PGV	C	267	51/51	0.97	0.14	38,52,95,97	0
20	PGV	A	521	51/51	0.97	0.15	36,53,77,79	0
14	HEA	N	515	60/60	0.98	0.12	47,52,65,66	0
21	CUA	O	228	2/2	0.98	0.11	52,52,52,54	0
15	CMO	A	520	2/2	0.99	0.15	39,39,39,41	0
14	HEA	A	516	60/60	0.99	0.14	32,40,56,64	0
14	HEA	A	515	60/60	0.99	0.12	33,40,54,68	0
21	CUA	B	228	2/2	0.99	0.15	41,41,41,42	0
14	HEA	N	516	60/60	0.99	0.14	42,48,69,74	0
27	ZN	F	99	1/1	0.99	0.15	48,48,48,48	0
16	CU	A	517	1/1	1.00	0.20	40,40,40,40	0
27	ZN	S	99	1/1	1.00	0.11	56,56,56,56	0
16	CU	N	517	1/1	1.00	0.18	49,49,49,49	0
15	CMO	N	520	2/2	1.00	0.14	47,47,47,48	0

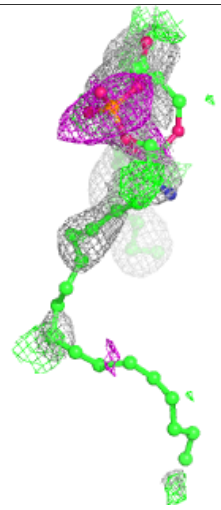
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PEK G 1263:

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

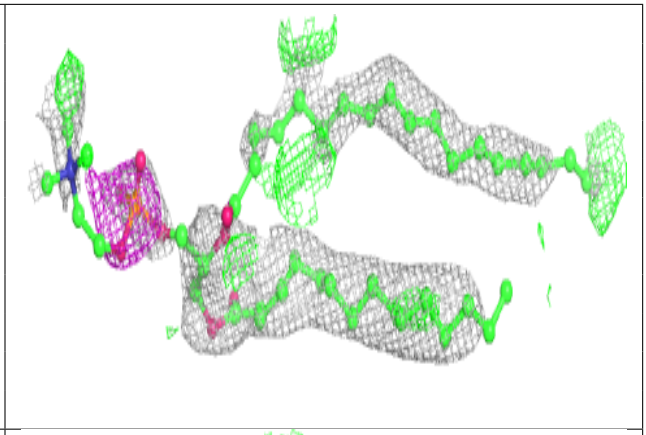


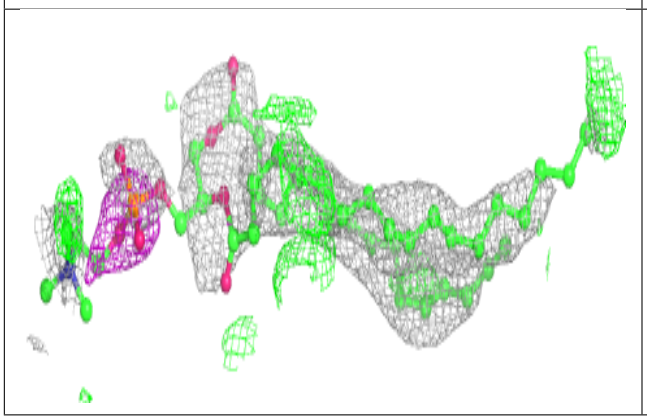


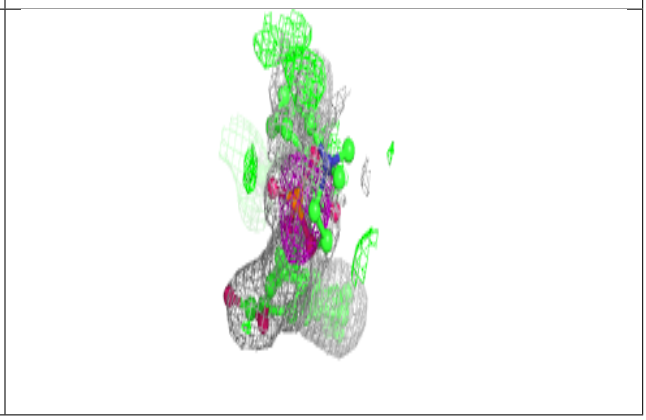


Electron density around PSC R 1229:

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

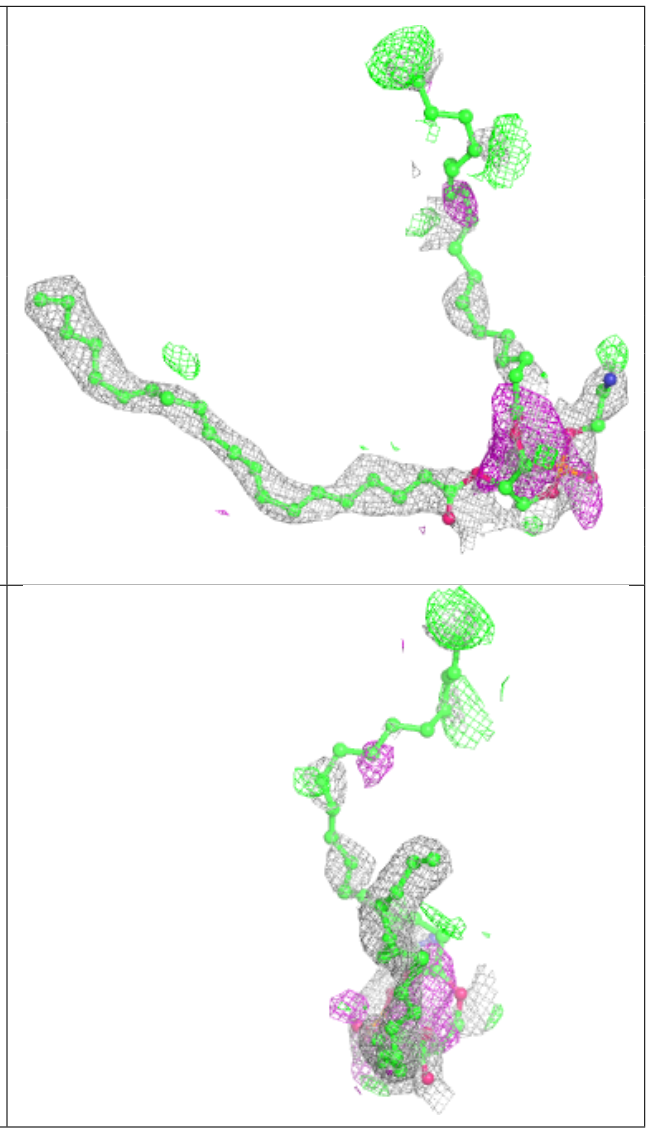






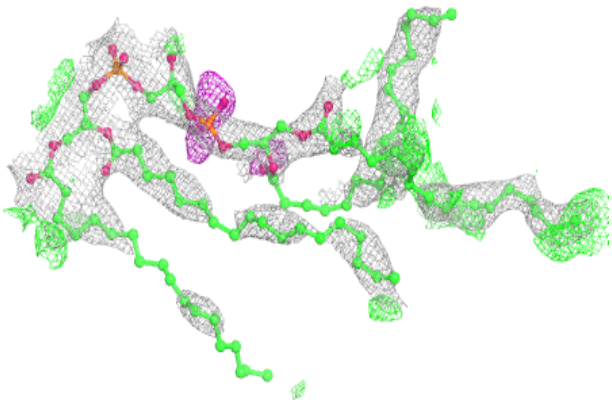
Electron density around PEK T 263:

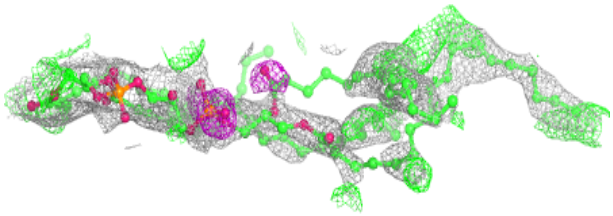
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

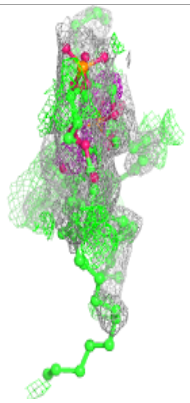


Electron density around CDL T 1269:

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

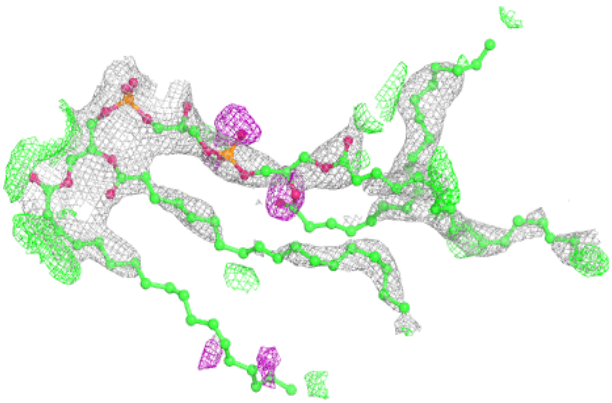


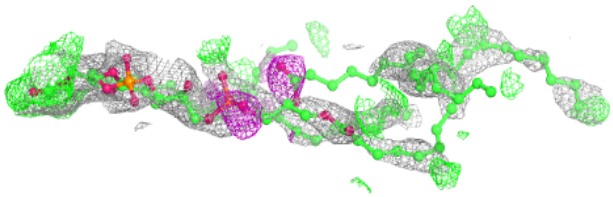


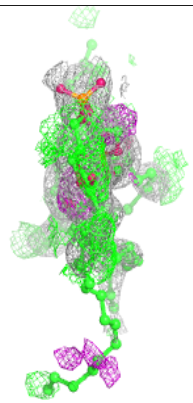


Electron density around CDL G 269:

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

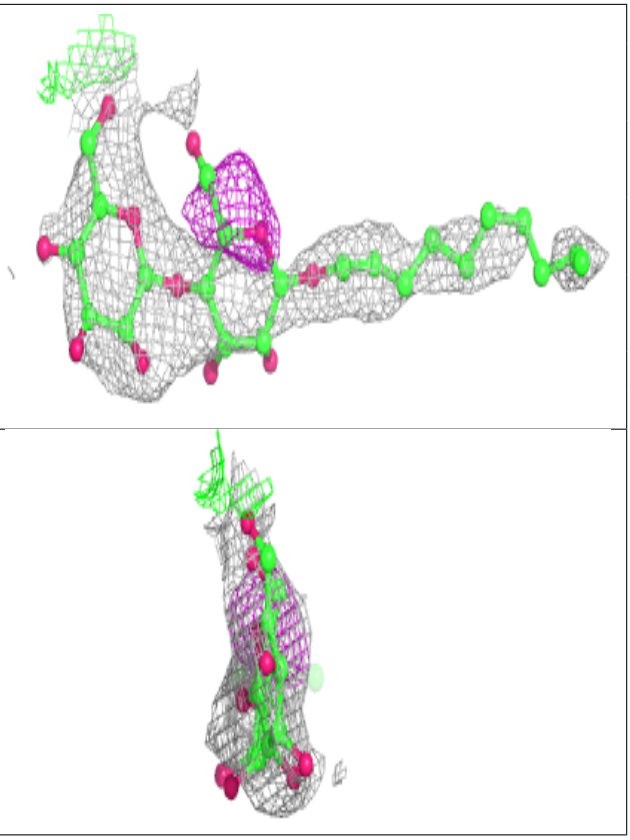






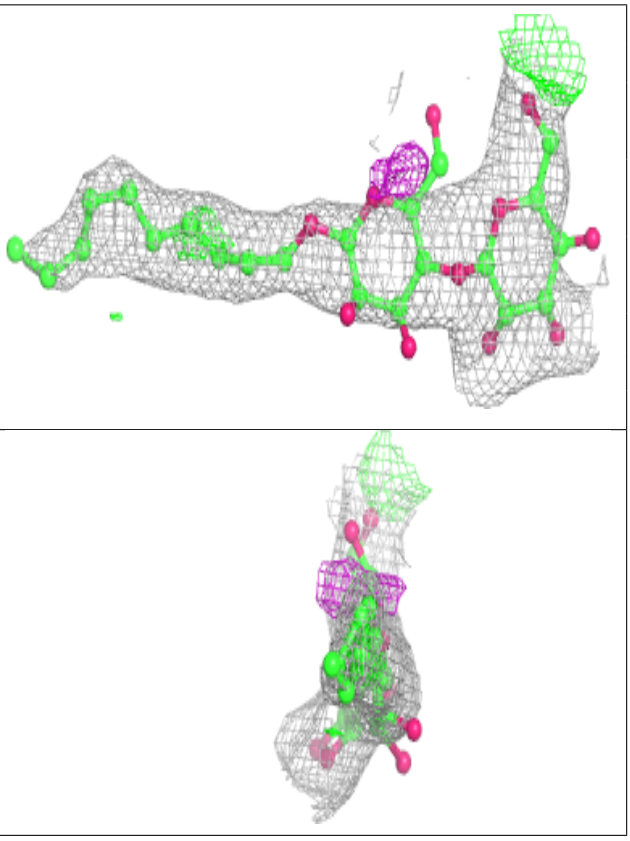
Electron density around DMU T 1272:

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



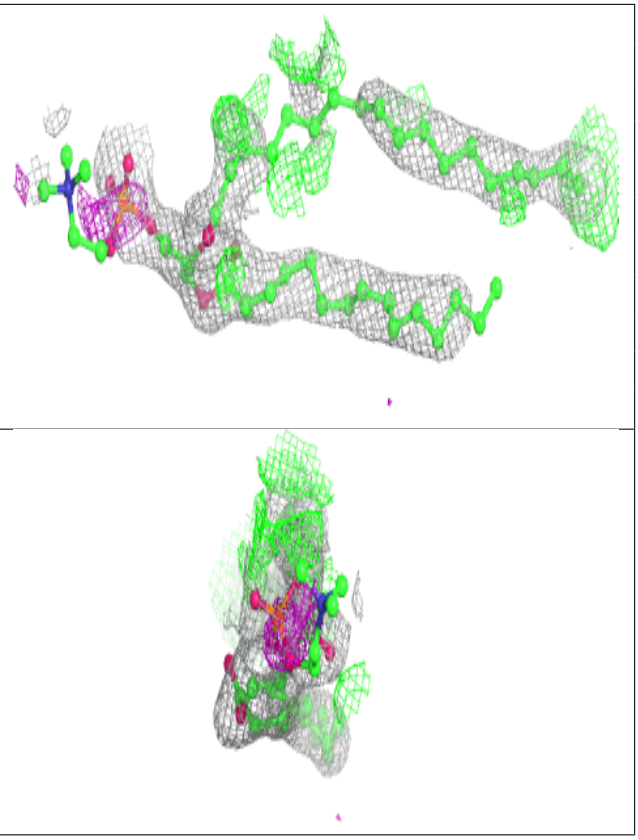
Electron density around DMU C 272:

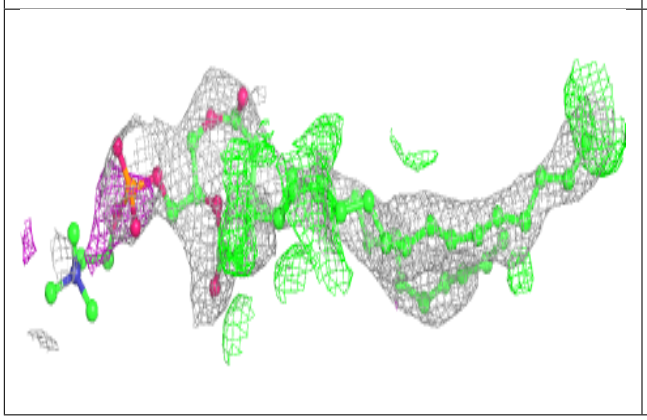
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PSC B 229:

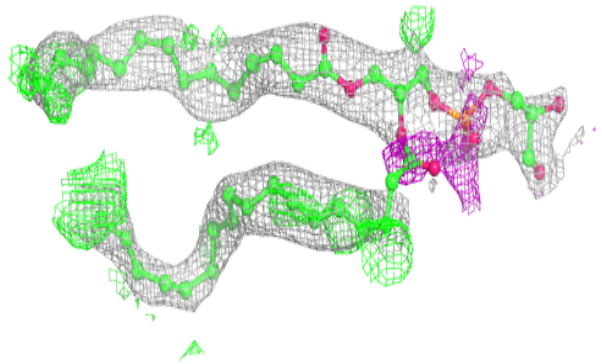
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

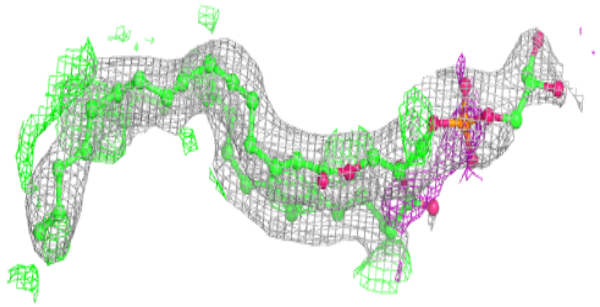


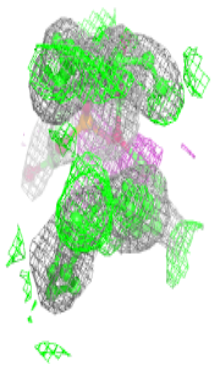


Electron density around PGV C 268:

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

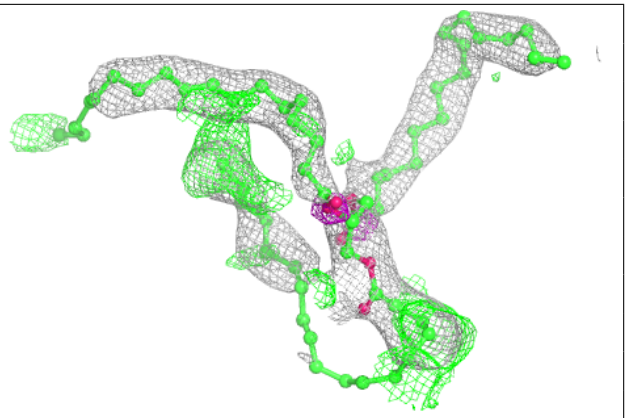


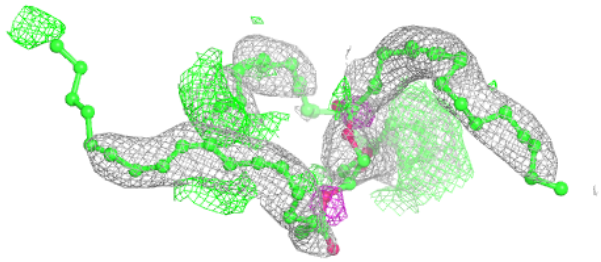


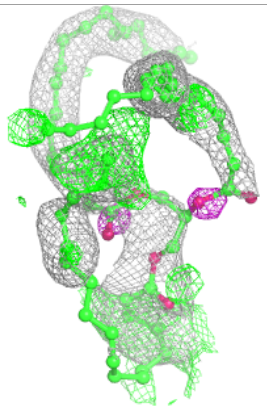


Electron density around TGL N 1522:

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

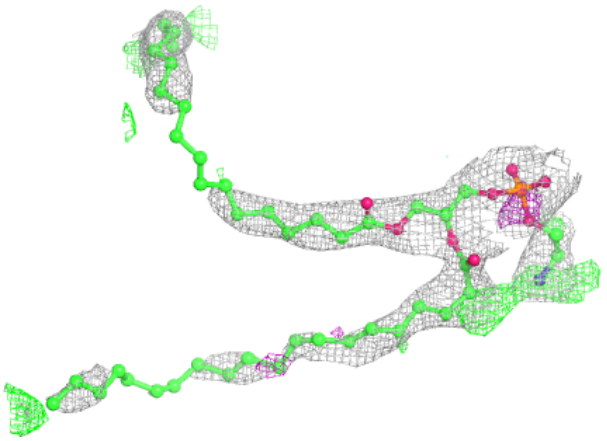


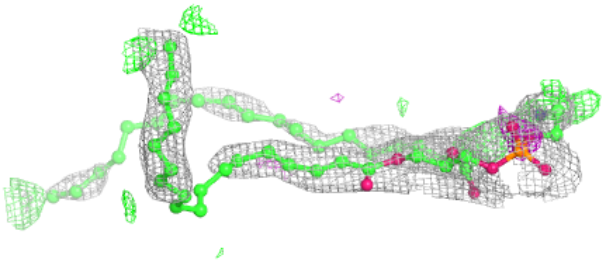


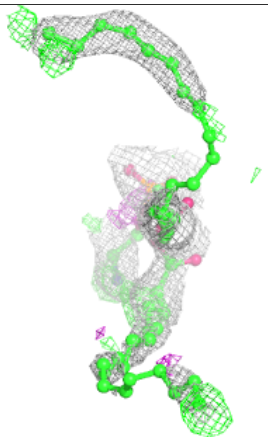


Electron density around PEK S 1265:

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

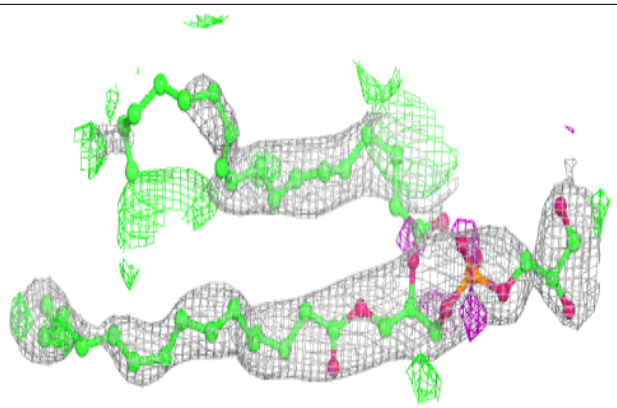


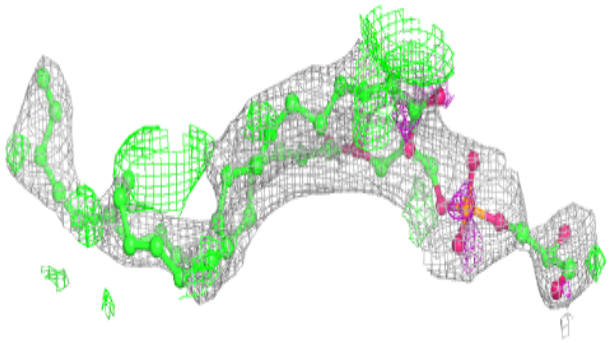


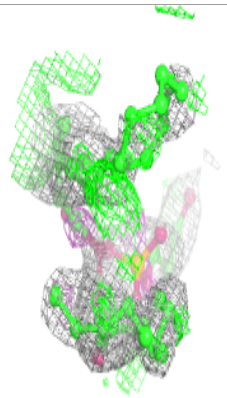


Electron density around PGV P 1268:

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

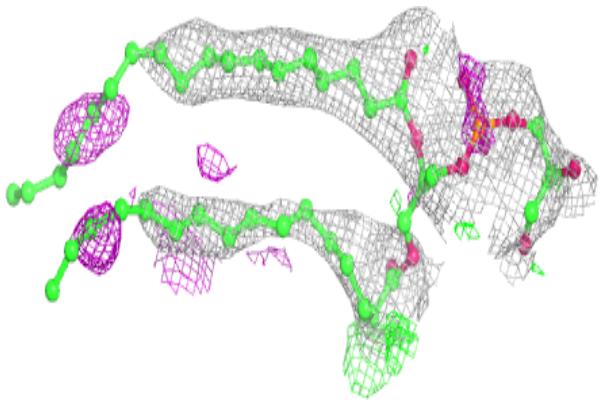


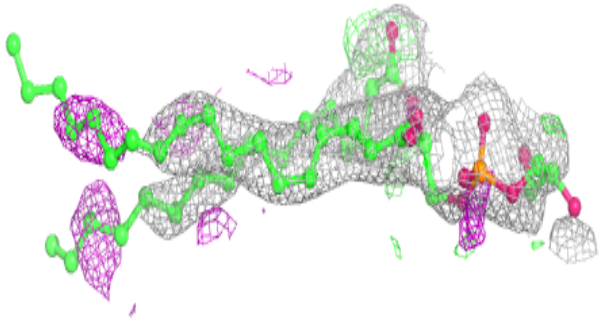


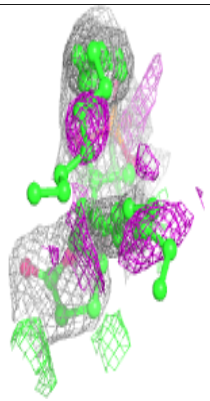


Electron density around PGV N 1524:

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

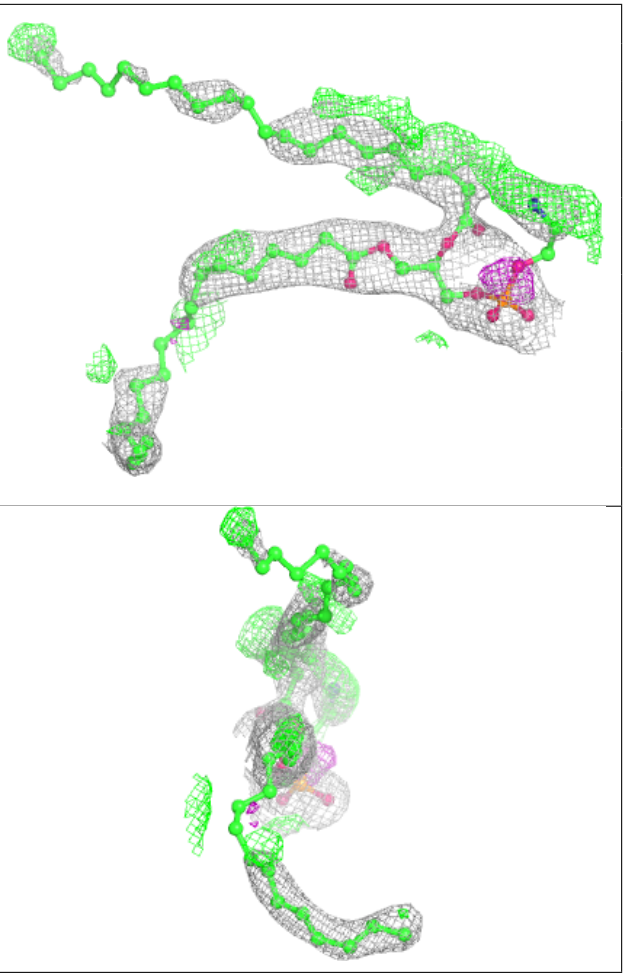






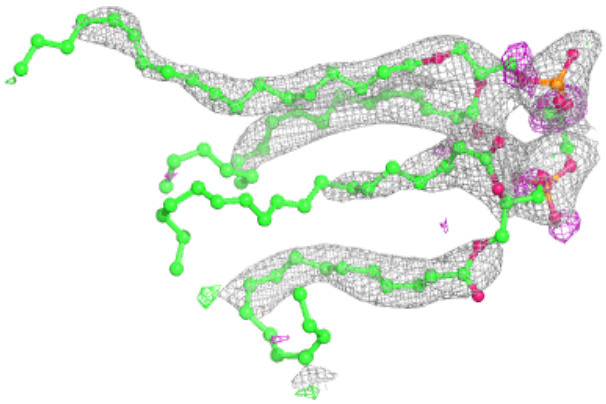
Electron density around PEK G 265:

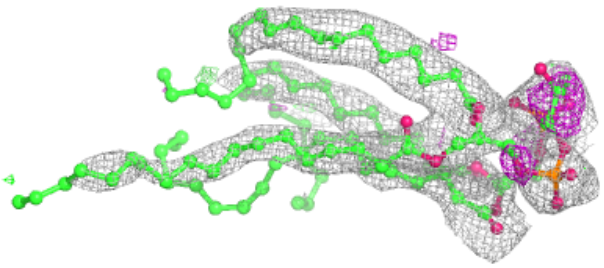
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

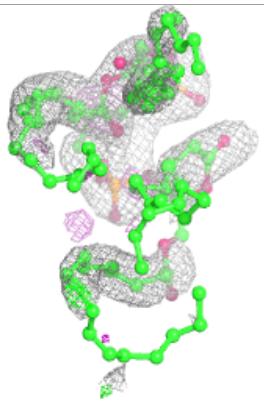


Electron density around CDL P 1270:

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

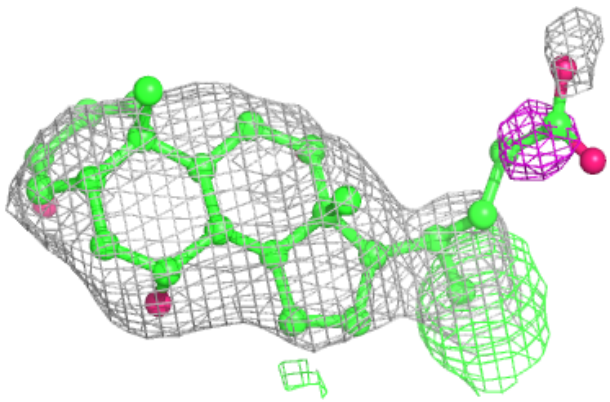


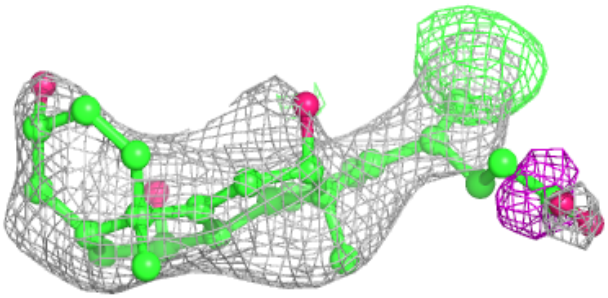


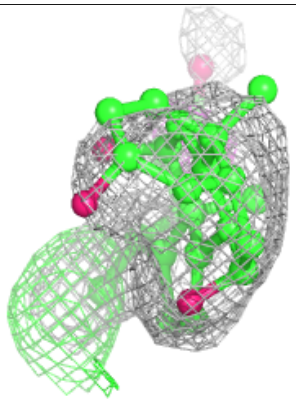


Electron density around CHD W 1059:

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

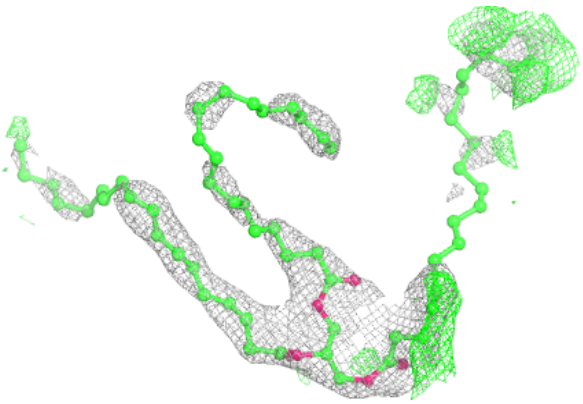


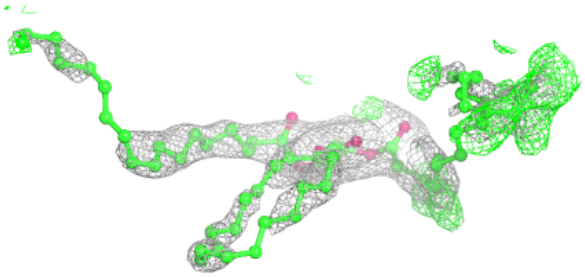


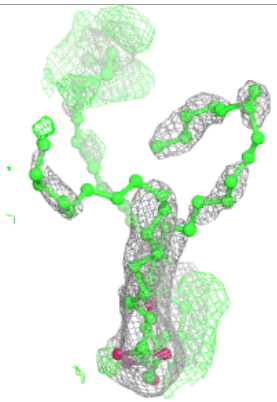


Electron density around TGL N 1523:

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

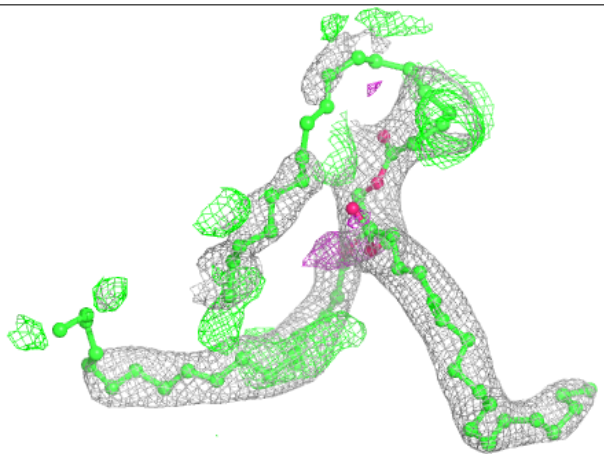


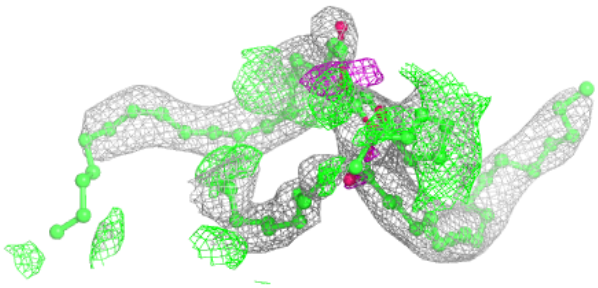


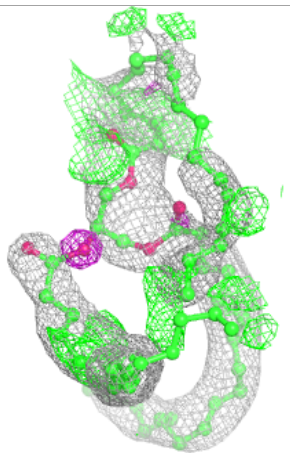


Electron density around TGL L 522:

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

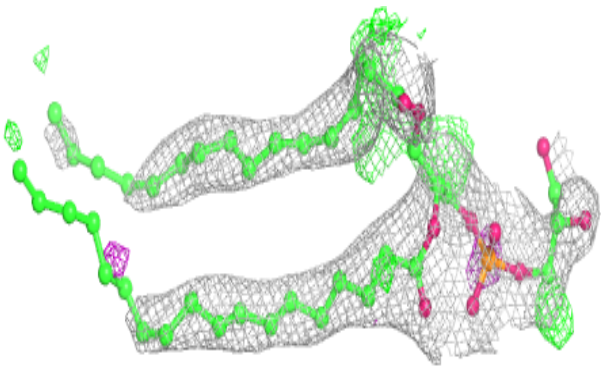


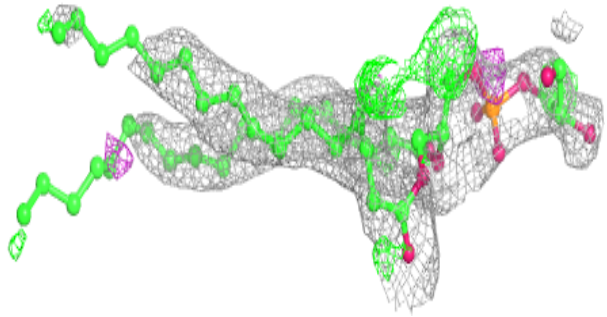


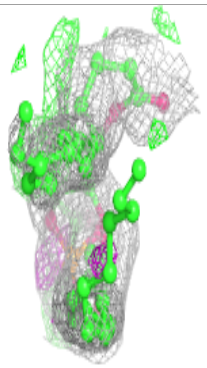


Electron density around PGV A 524:

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

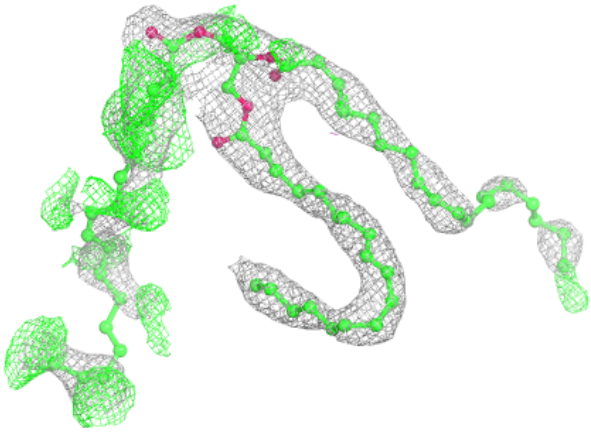


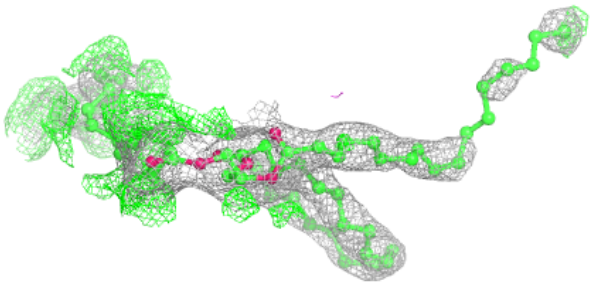


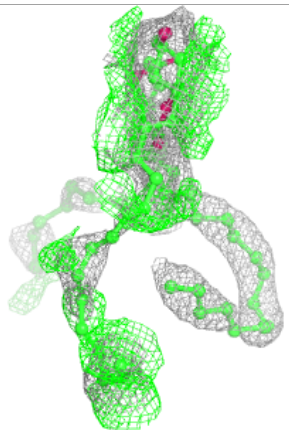


Electron density around TGL A 523:

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

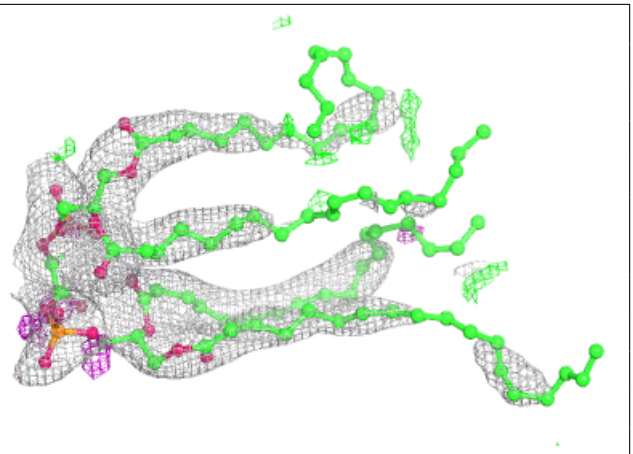


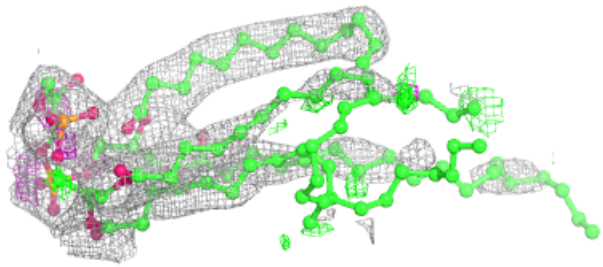


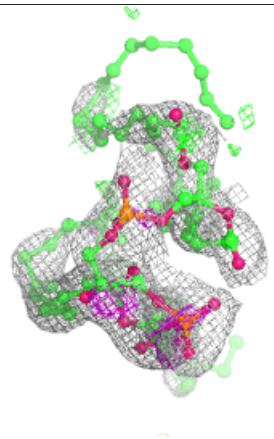


Electron density around CDL C 270:

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

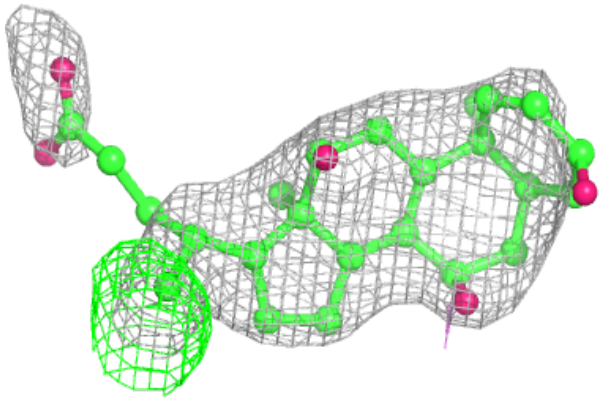


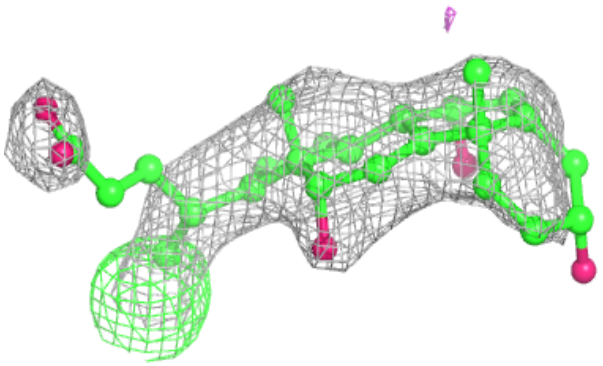


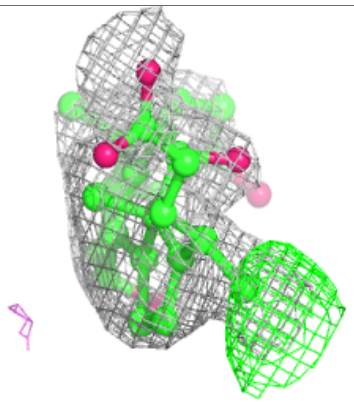


Electron density around CHD J 60:

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

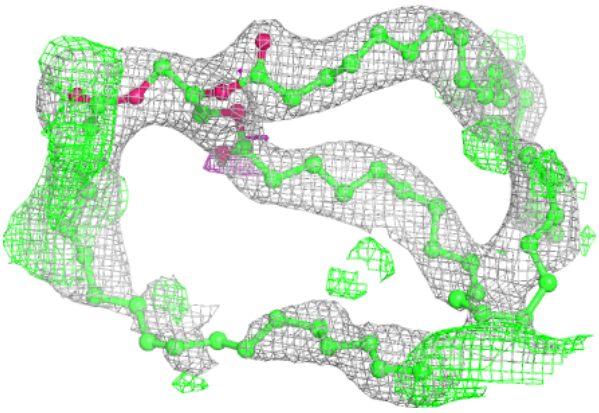


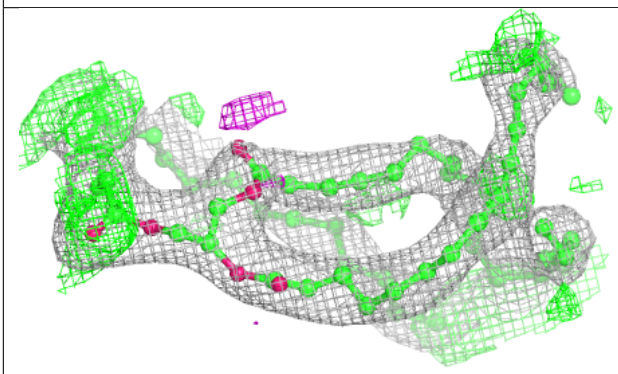


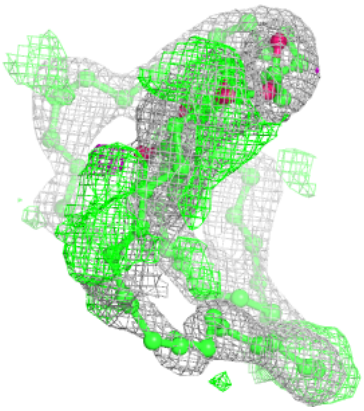


Electron density around TGL B 521:

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

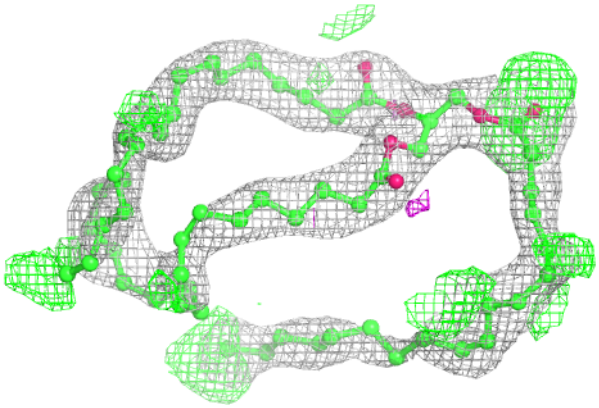


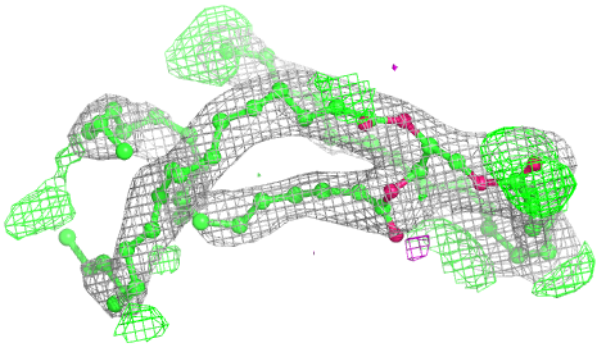


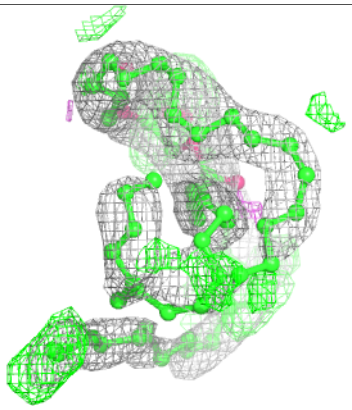


Electron density around TGL N 1521:

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

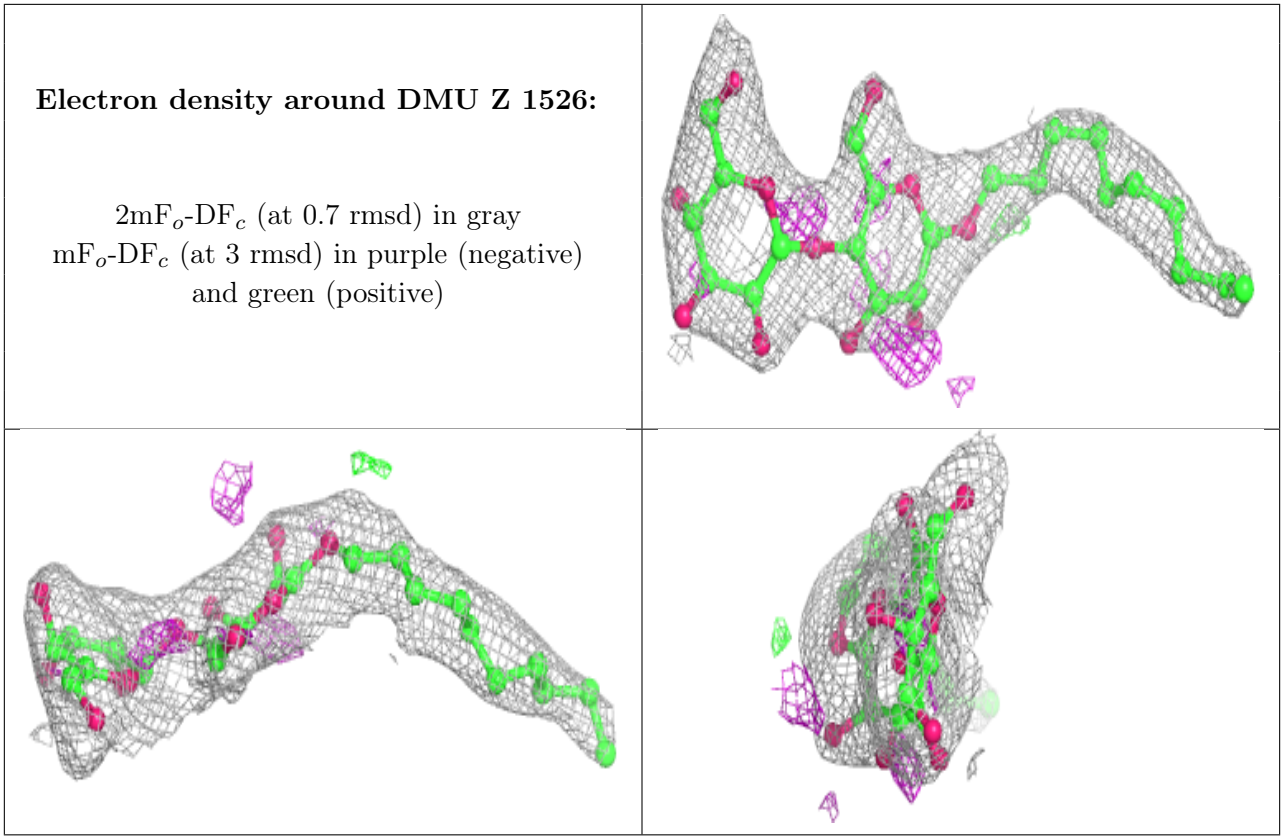






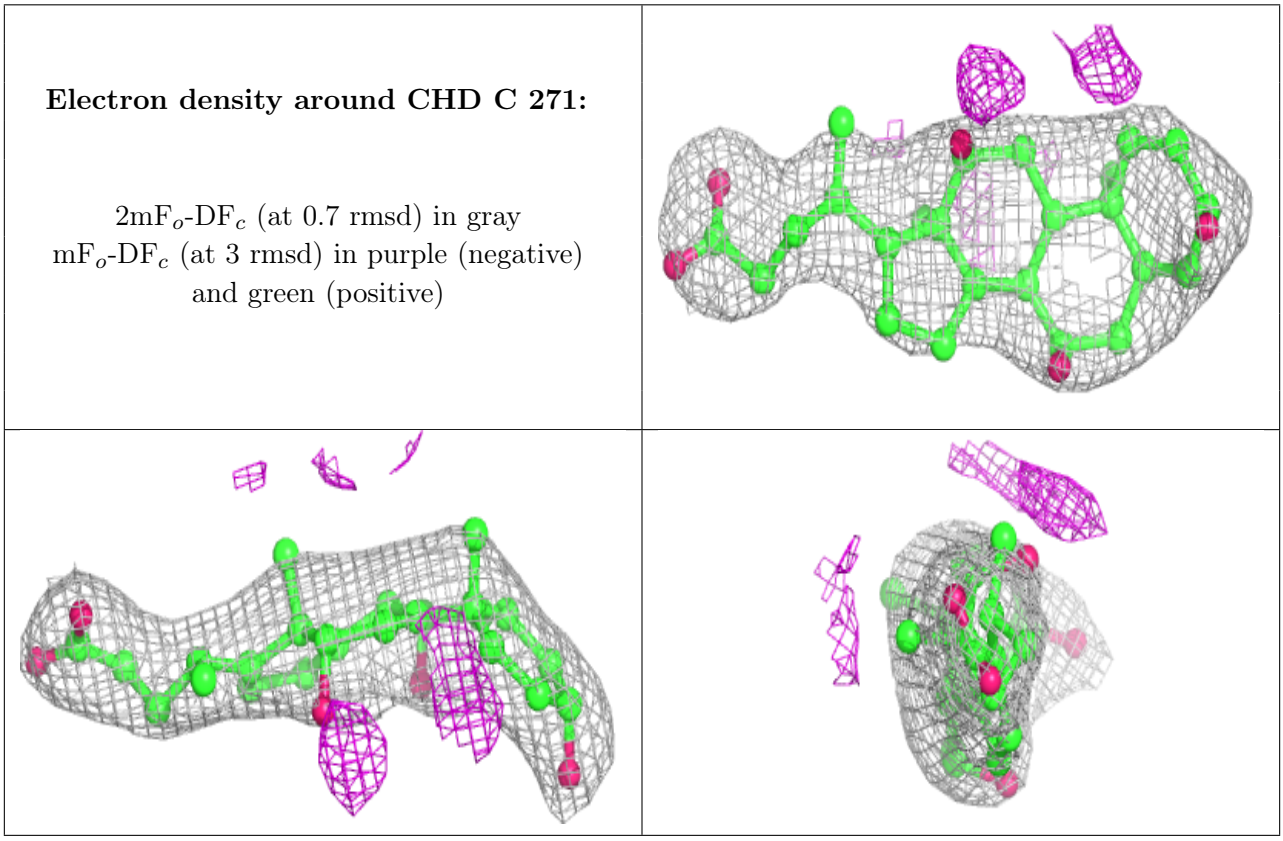
Electron density around DMU Z 1526:

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



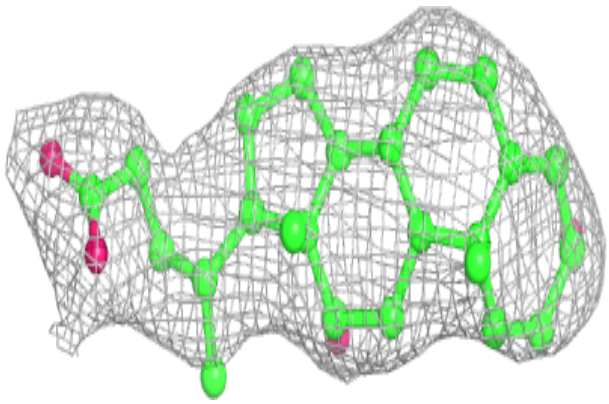
Electron density around CHD C 271:

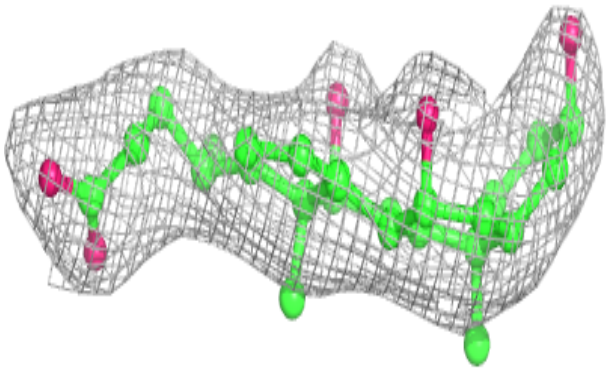
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

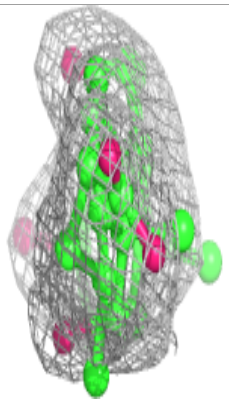


Electron density around CHD P 1271:

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

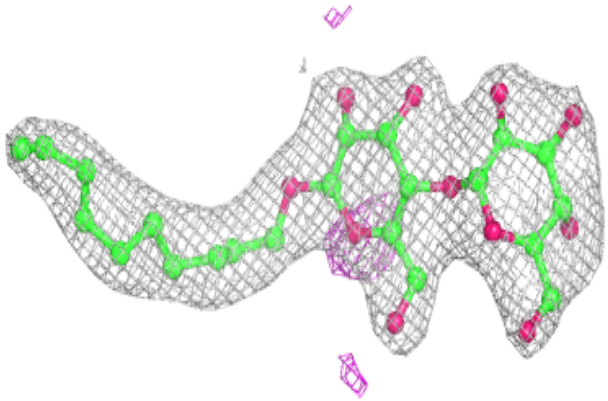


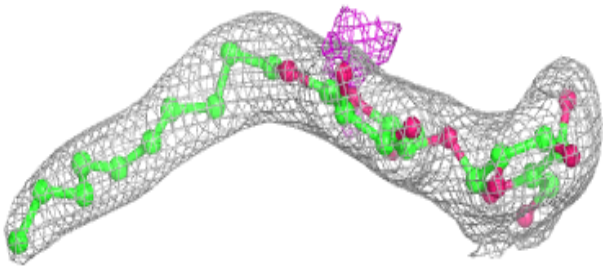


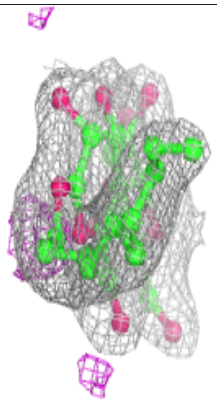


Electron density around DMU M 526:

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

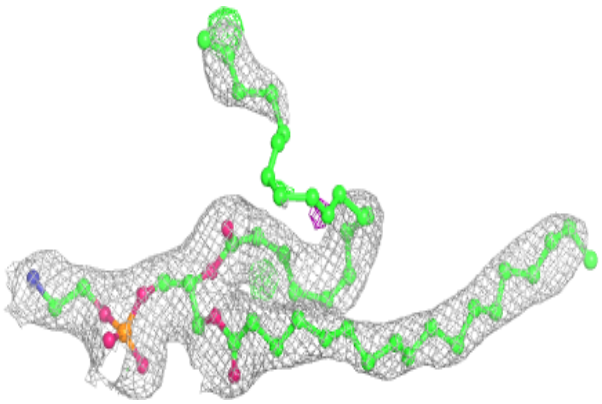


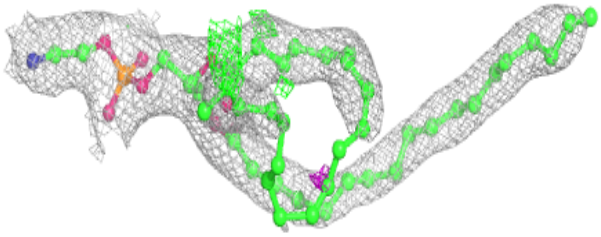


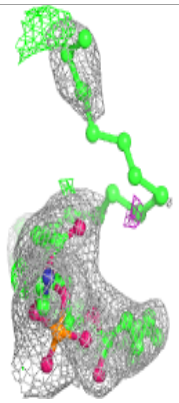


Electron density around PEK T 1264:

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

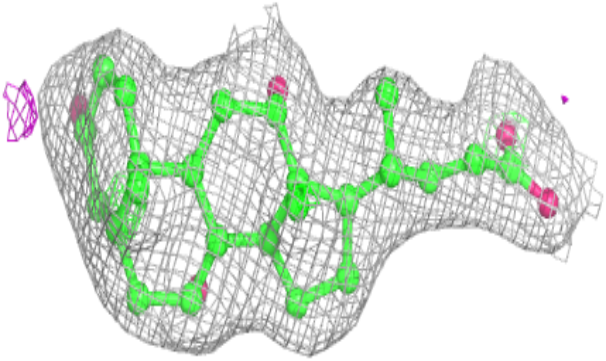


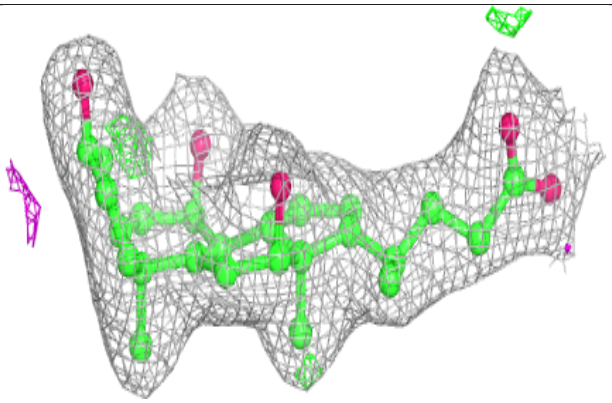


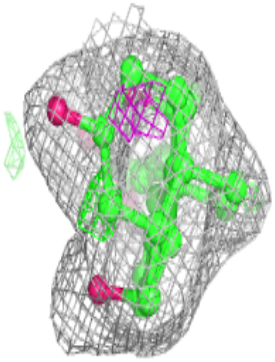


Electron density around CHD P 1525:

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

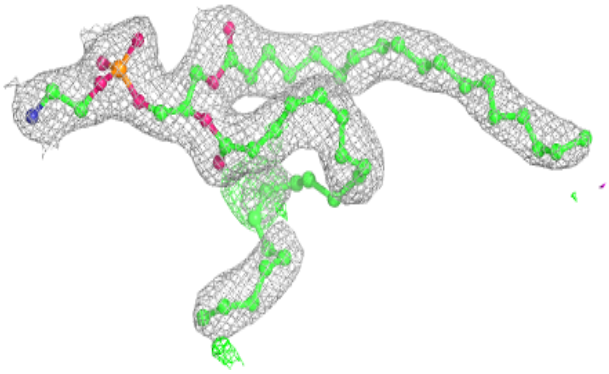


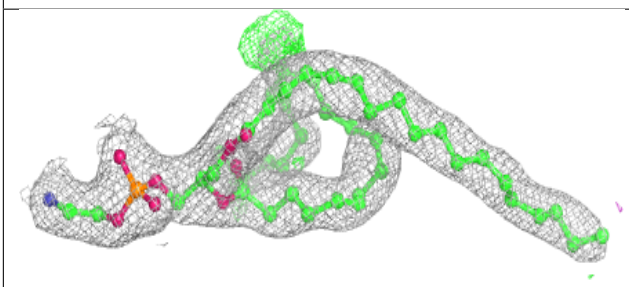


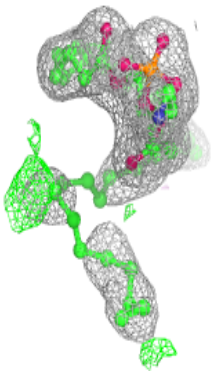


Electron density around PEK G 264:

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

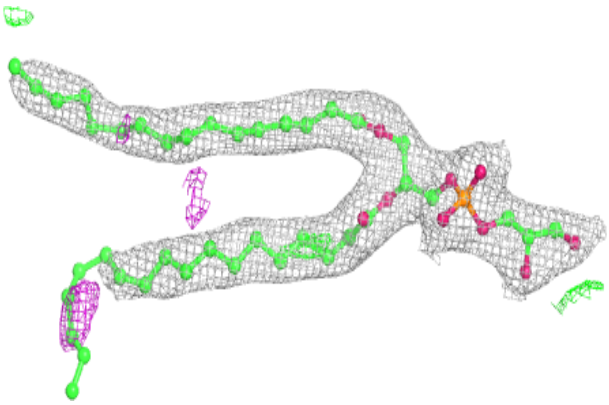


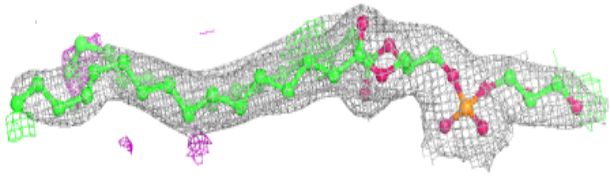


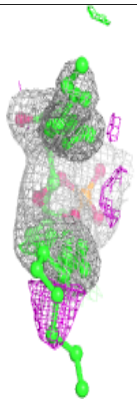


Electron density around PGV P 1267:

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

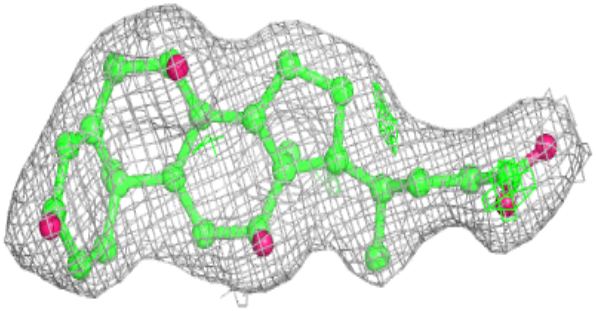


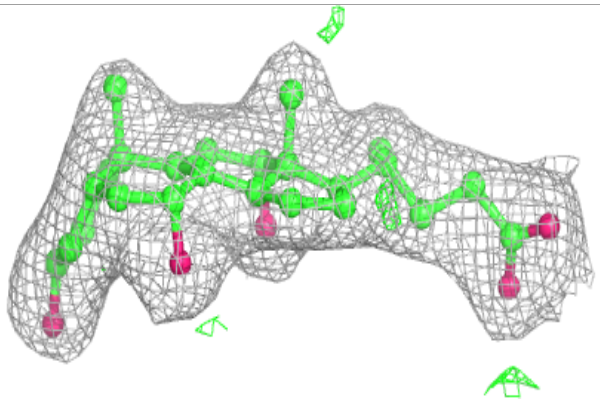


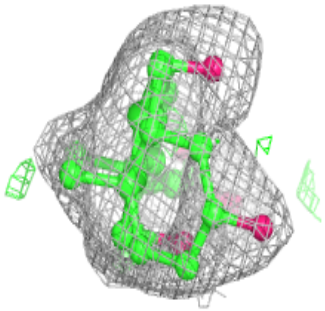


Electron density around CHD C 525:

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

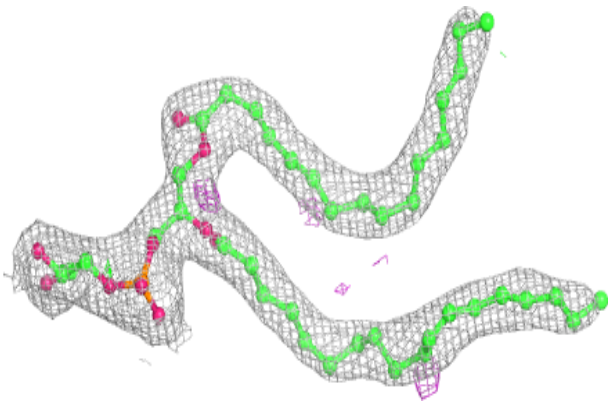


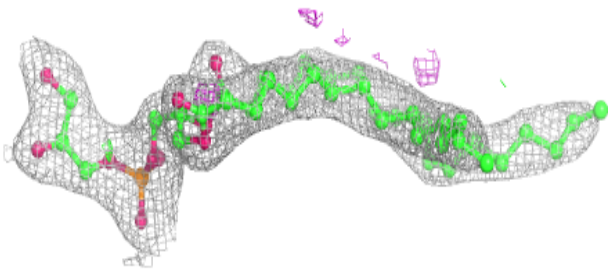


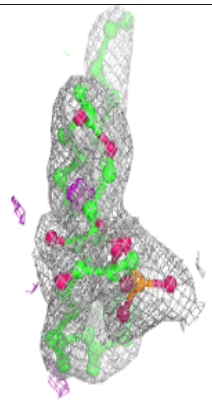


Electron density around PGV N 1266:

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

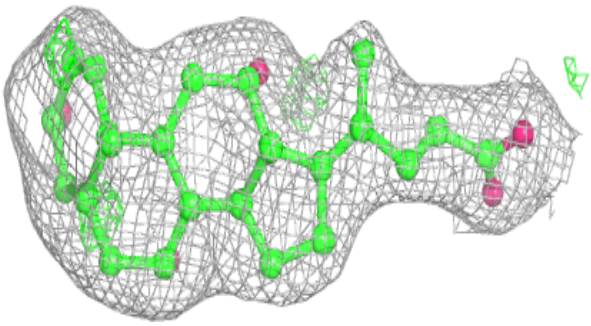


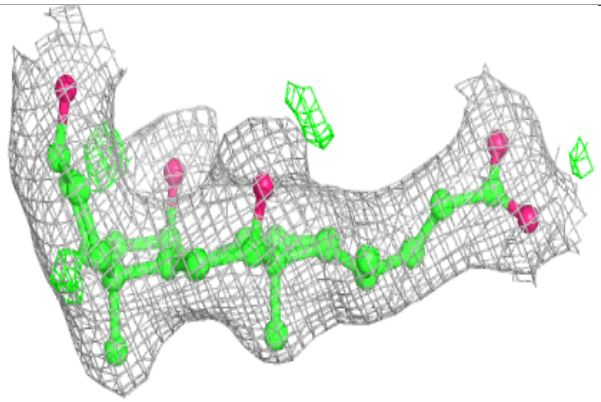


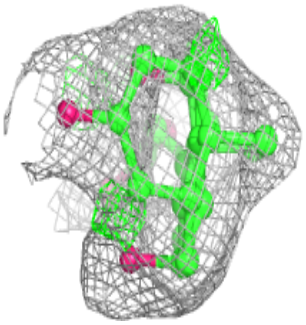


Electron density around CHD O 229:

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

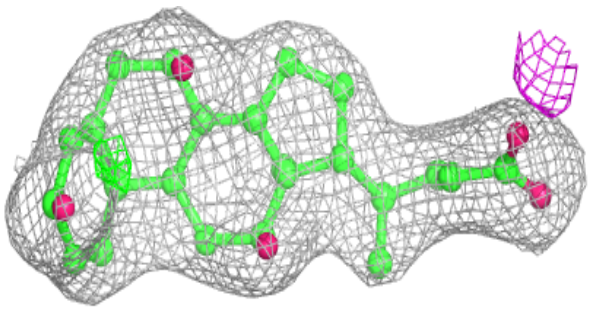


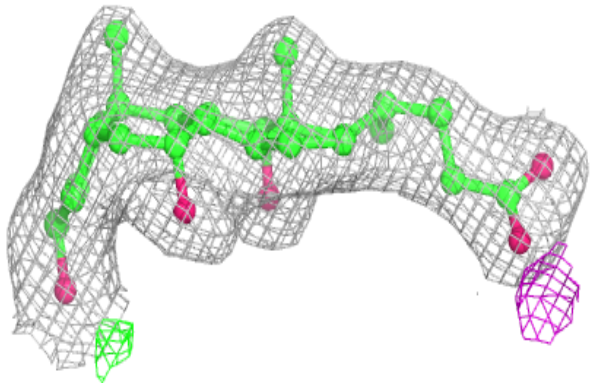


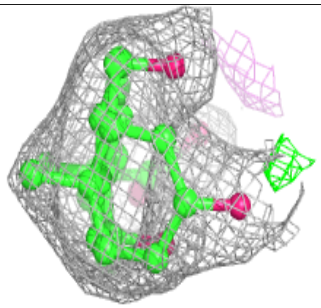


Electron density around CHD B 1085:

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

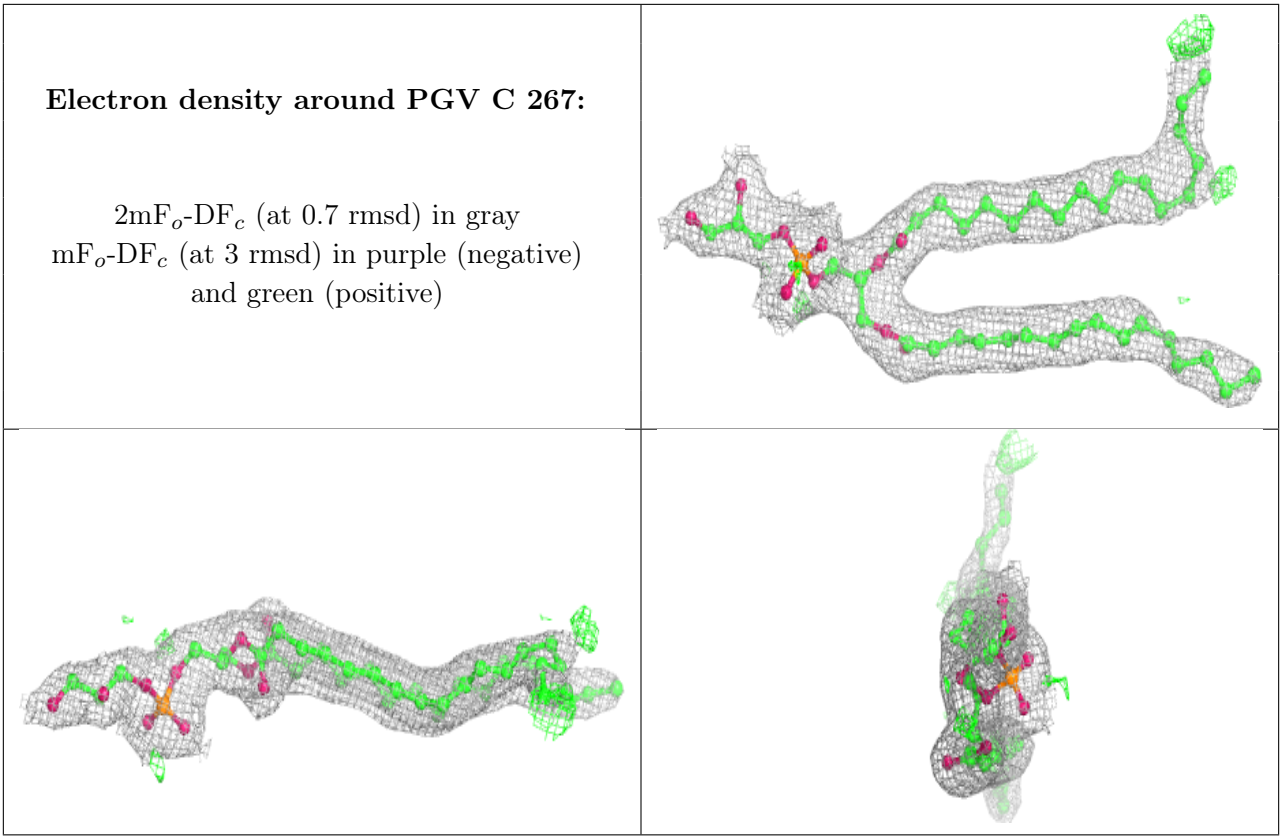






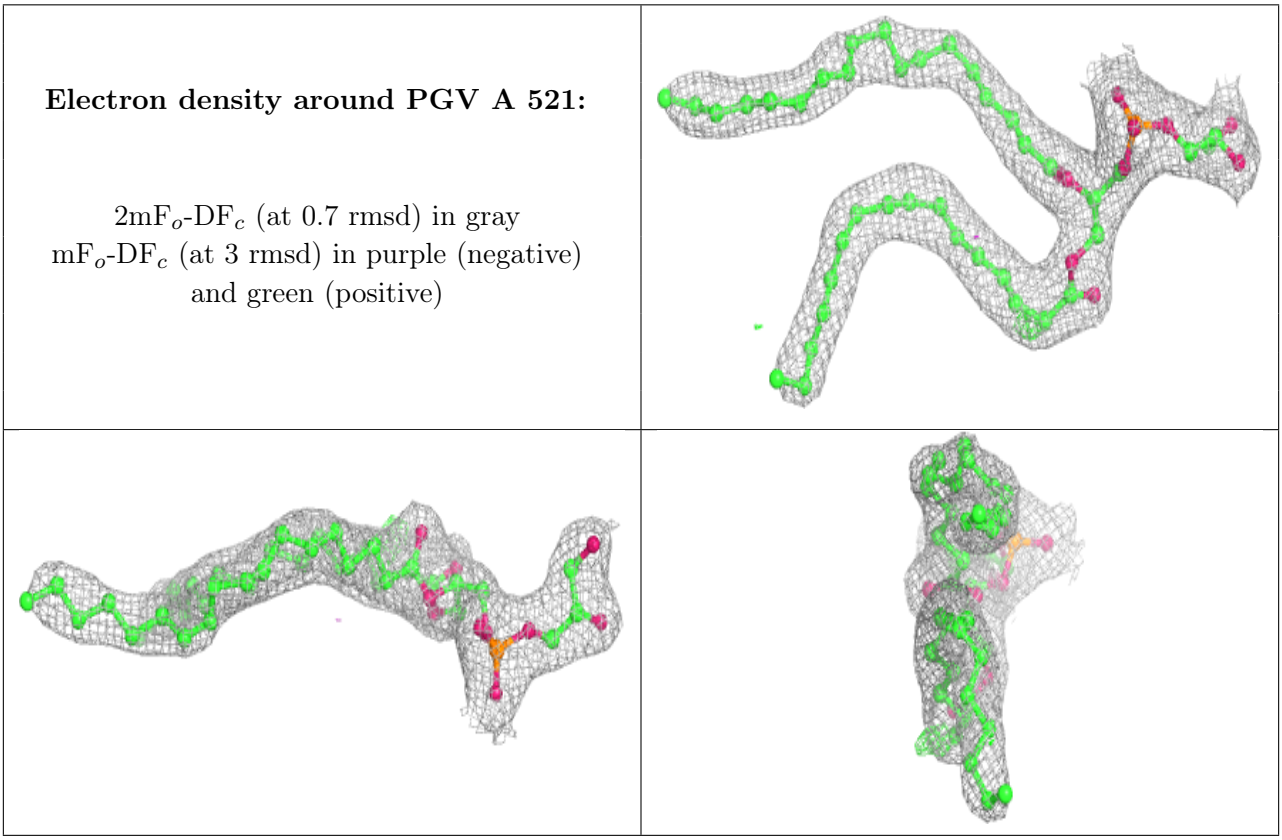
Electron density around PGV C 267:

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



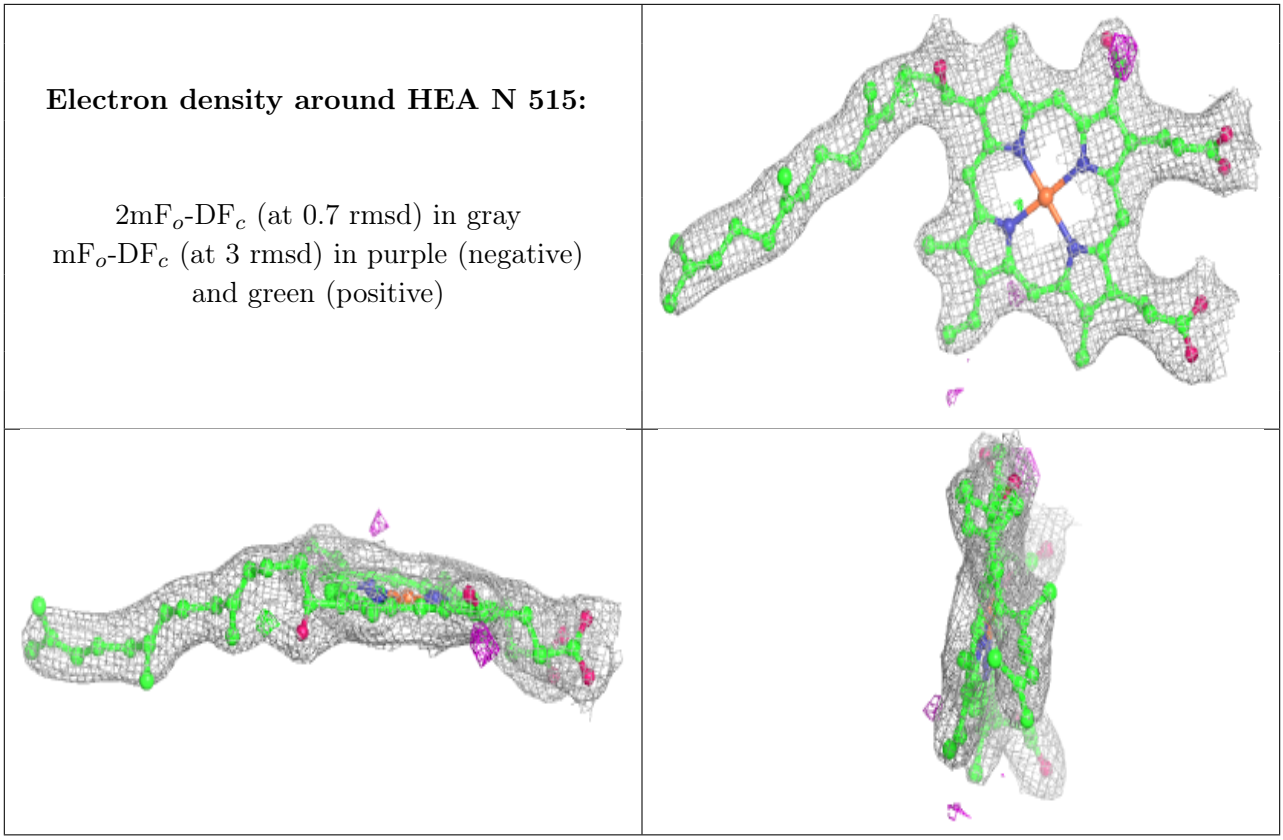
Electron density around PGV A 521:

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



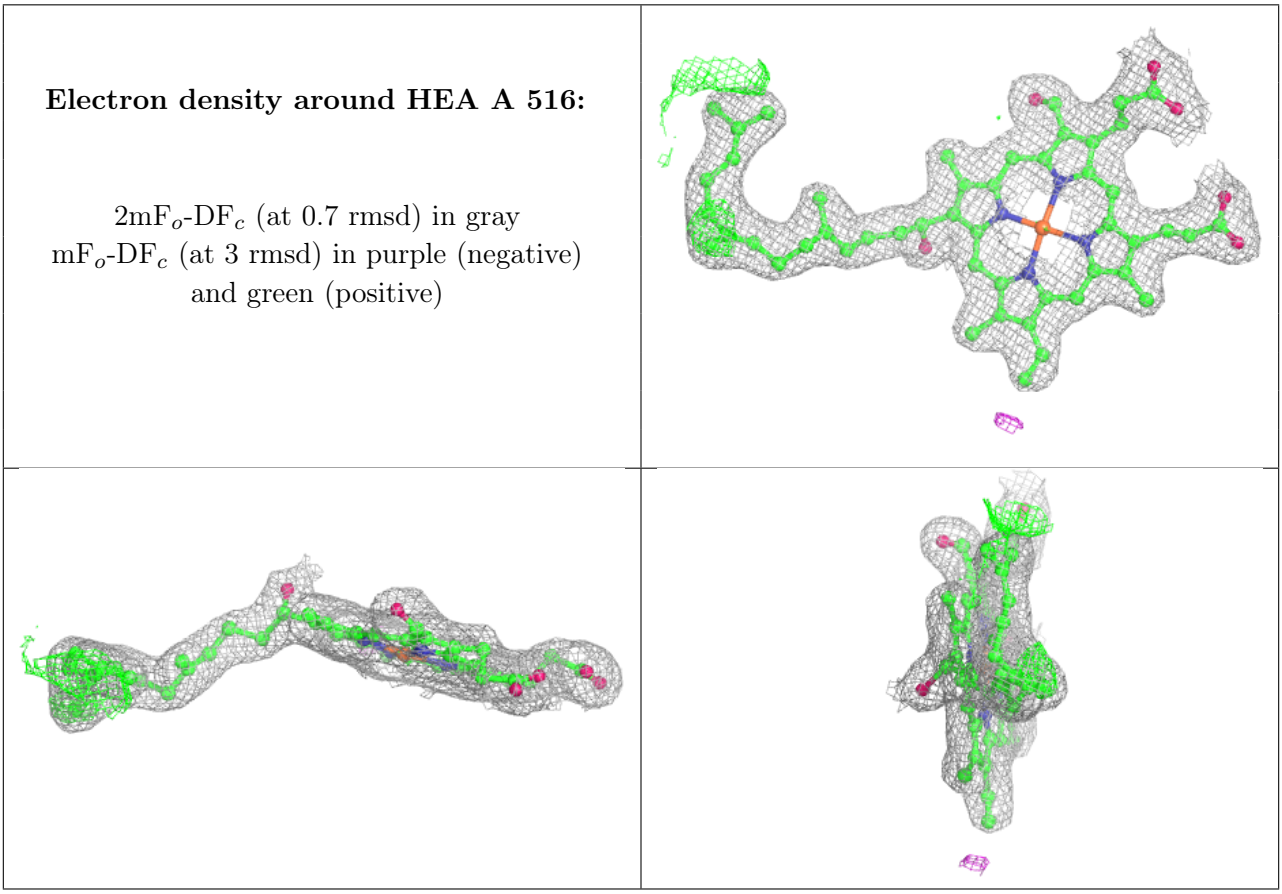
Electron density around HEA N 515:

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



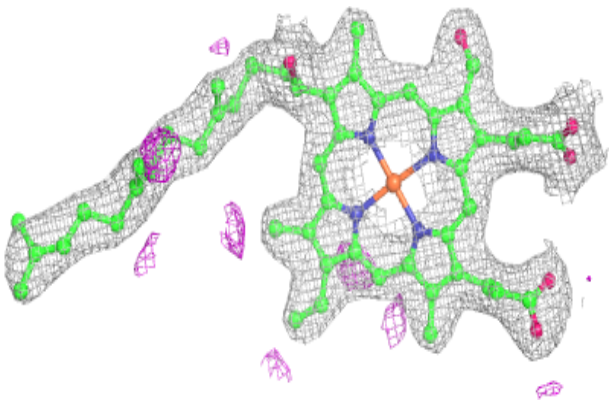
Electron density around HEA A 516:

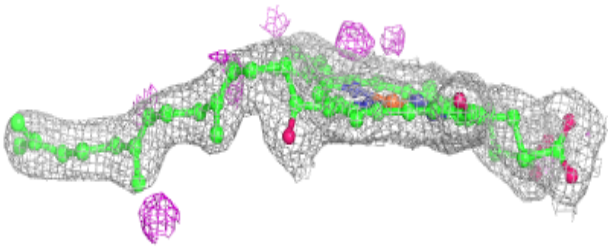
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

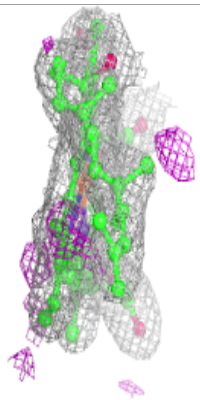


Electron density around HEA A 515:

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

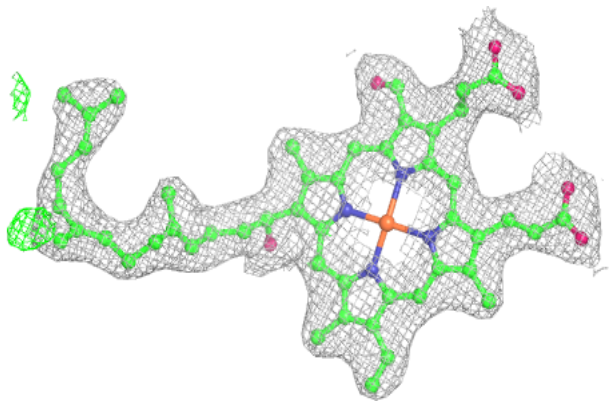


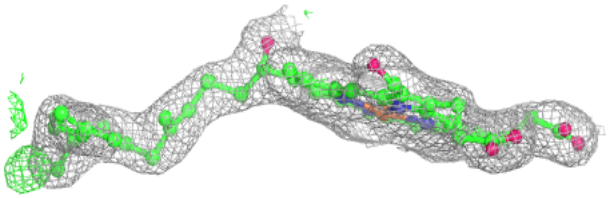


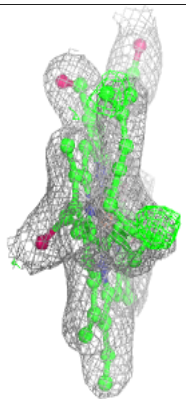


Electron density around HEA N 516:

$2mF_o$-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.