wwPDB X-ray Structure Validation Summary Report (i)

Oct 24, 2023 – 02:09 PM EDT

PDB ID	:	3ASO
Title	:	Bovine heart cytochrome C oxidase in the fully oxidized state measured at 0.9 angstrom wavelength
Authors	:	Suga, M.; Yano, N.; Muramoto, K.; Shinzawa-Itoh, K.; Maeda, T.; Yamashita, E.; Tsukihara, T.; Yoshikawa, S.
Deposited on	:	2010-12-17
Resolution	:	2.30 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:

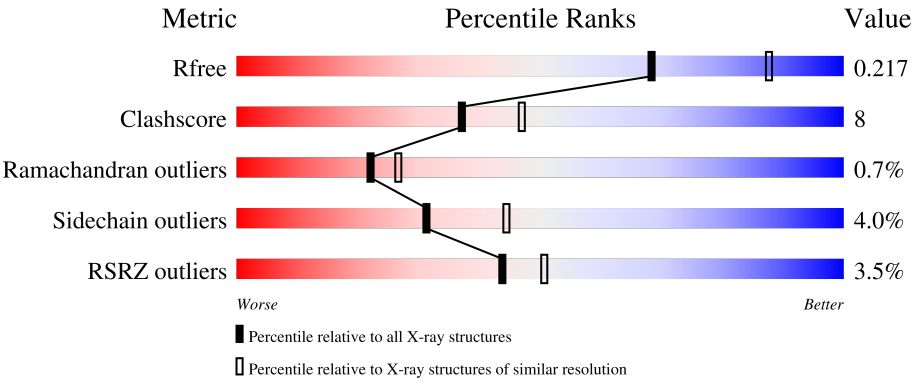
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	87% 12%
1	N	514	85% 14%
2	B	227	81% 18%
2	O	227	4% 78% 20%

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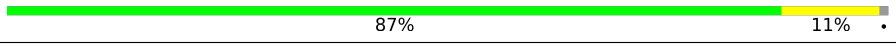
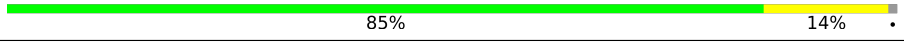
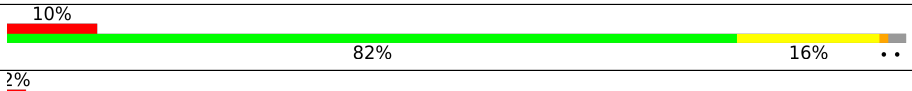
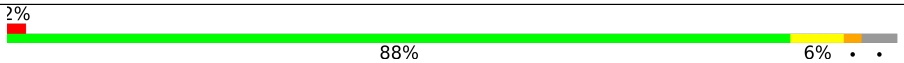
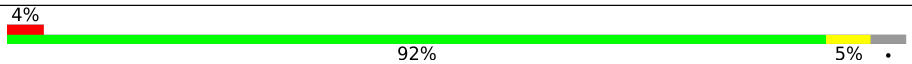
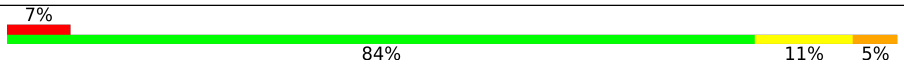
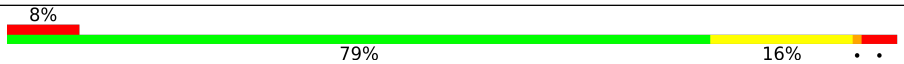
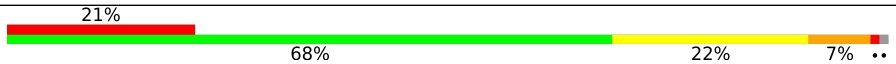
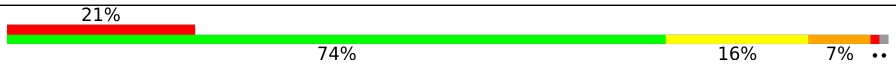
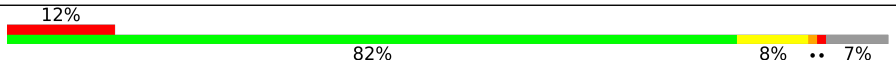
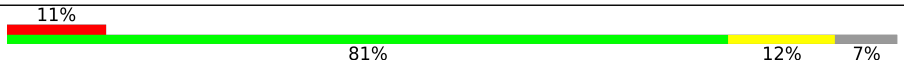
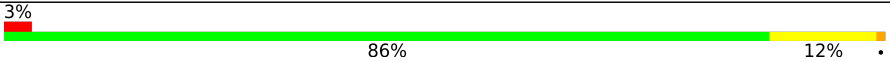
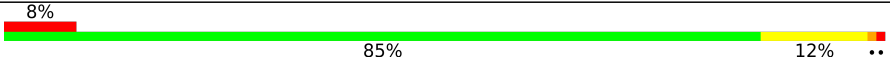
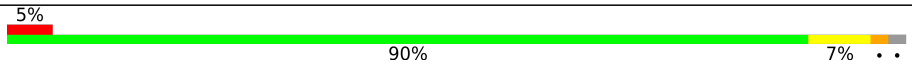
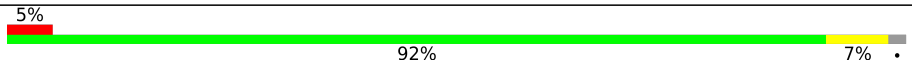
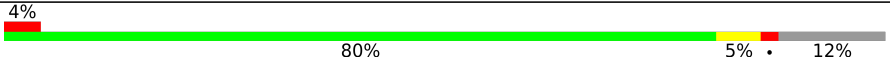
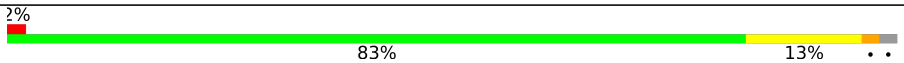
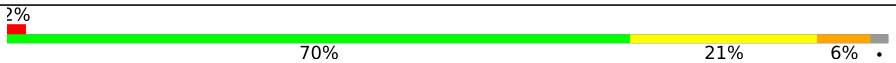
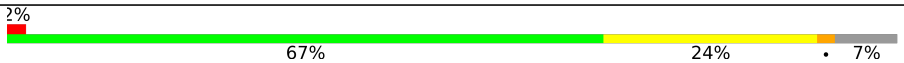
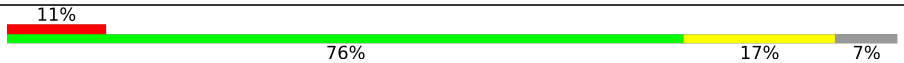
Mol	Chain	Length	Quality of chain
3	C	261	
3	P	261	
4	D	147	
4	Q	147	
5	E	109	
5	R	109	
6	F	98	
6	S	98	
7	G	85	
7	T	85	
8	H	85	
8	U	85	
9	I	73	
9	V	73	
10	J	59	
10	W	59	
11	K	56	
11	X	56	
12	L	47	
12	Y	47	
13	M	46	
13	Z	46	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	CHD	J	60	-	-	-	X
22	CHD	W	1059	-	-	-	X
23	UNX	C	262	-	-	-	X
24	PEK	T	263	-	-	-	X
25	CDL	T	1269	-	-	X	-
27	DMU	M	526	X	-	-	-
27	DMU	Z	1526	X	-	-	-
9	SAC	I	1	-	-	-	X
9	SAC	V	1	-	-	-	X

2 Entry composition (i)

There are 28 unique types of molecules in this entry. The entry contains 32377 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			
1	N	514	Total	C	N	O	S	0	0	0
			4027	2691	623	678	35			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

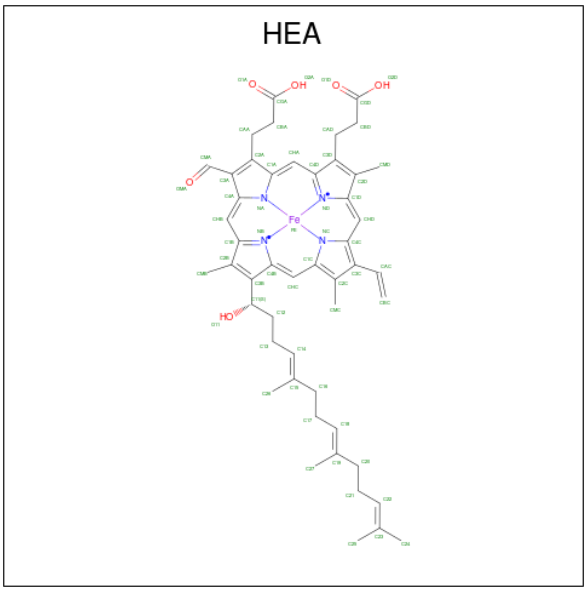
- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C.

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

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

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

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



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

- Molecule 15 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

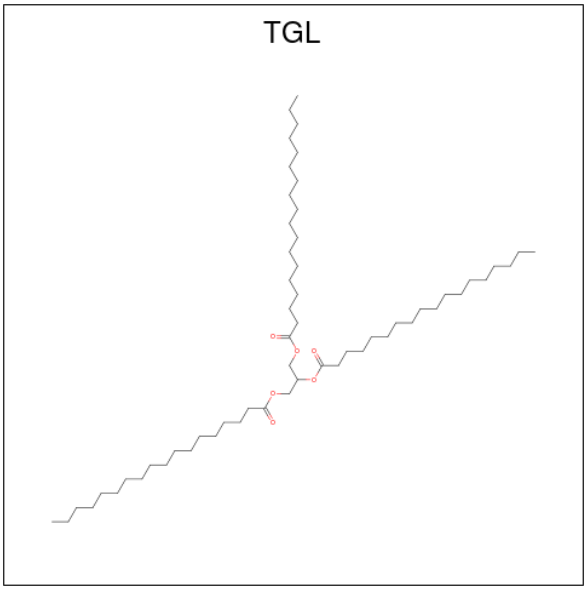
- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 17 is SODIUM ION (three-letter code: NA) (formula: Na).

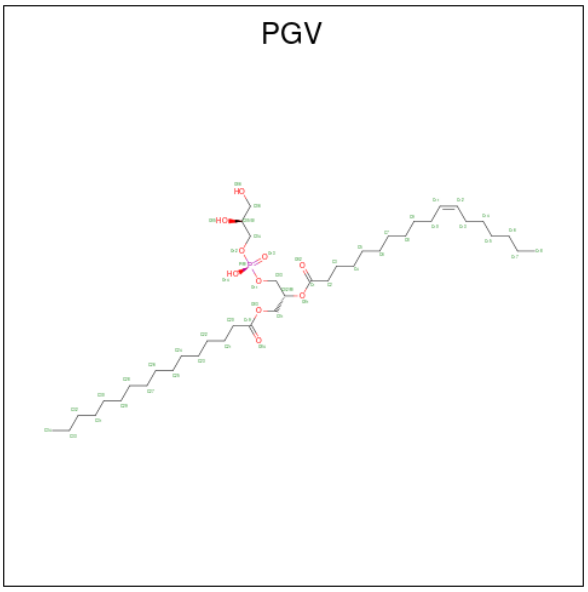
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	1	Total Na 1 1	0	0
17	N	1	Total Na 1 1	0	0

- Molecule 18 is TRISTEAROYLGLYCEROL (three-letter code: TGL) (formula: $C_{57}H_{110}O_6$).



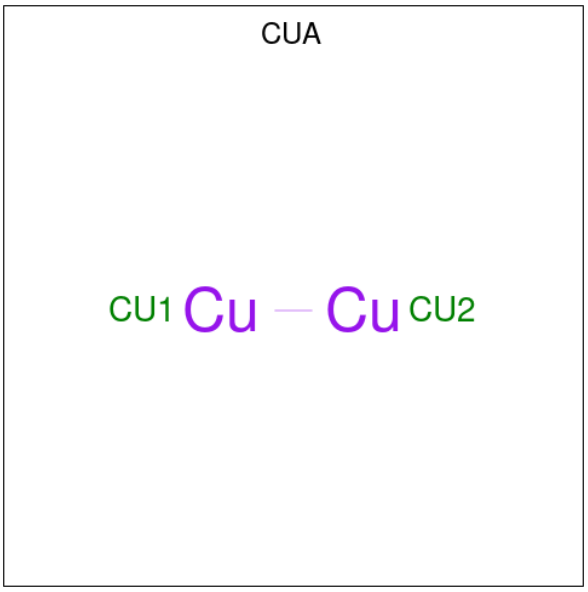
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	A	1	Total C O 63 57 6	0	0
18	D	1	Total C O 63 57 6	0	0
18	L	1	Total C O 63 57 6	0	0
18	N	1	Total C O 63 57 6	0	0
18	N	1	Total C O 63 57 6	0	0
18	Q	1	Total C O 63 57 6	0	0

- Molecule 19 is (1R)-2-{[{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: $C_{40}H_{77}O_{10}P$).



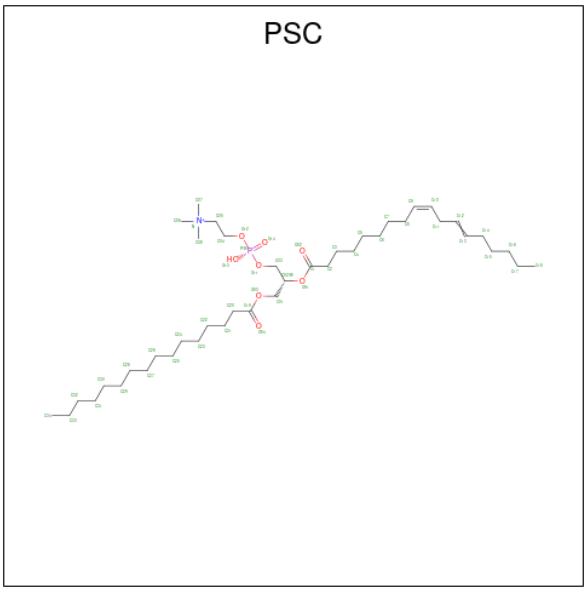
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
19	A	1	Total	C	O	P	0	0
			51	40	10	1		
19	A	1	Total	C	O	P	0	0
			51	40	10	1		
19	C	1	Total	C	O	P	0	0
			51	40	10	1		
19	C	1	Total	C	O	P	0	0
			51	40	10	1		
19	N	1	Total	C	O	P	0	0
			51	40	10	1		
19	N	1	Total	C	O	P	0	0
			51	40	10	1		
19	P	1	Total	C	O	P	0	0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

- Molecule 20 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu_2).



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

- Molecule 21 is (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
21	B	1	Total C N O P 52 42 1 8 1	0	0

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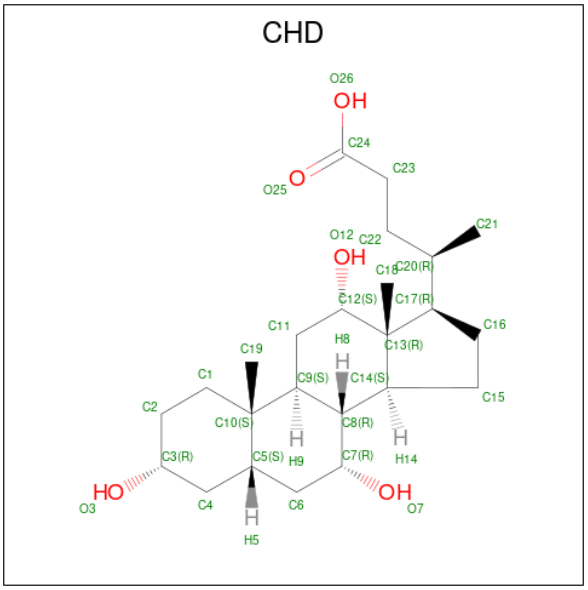
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
21	O	1	Total	C	N	O	P	0	0
			52	42	1	8	1		

- Molecule 22 is CHOLIC ACID (three-letter code: CHD) (formula: $C_{24}H_{40}O_5$).

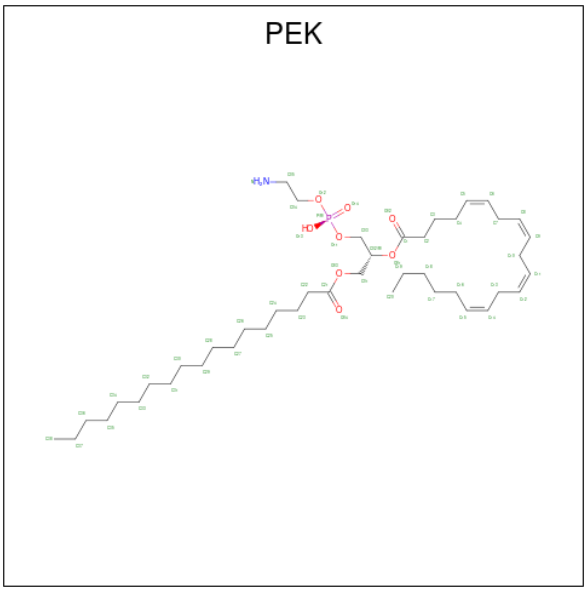


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
22	B	1	Total	C	O		0	0
			29	24	5			
22	C	1	Total	C	O		0	0
			29	24	5			
22	C	1	Total	C	O		0	0
			29	24	5			
22	G	1	Total	C	O		0	0
			29	24	5			
22	J	1	Total	C	O		0	0
			29	24	5			
22	P	1	Total	C	O		0	0
			29	24	5			
22	P	1	Total	C	O		0	0
			29	24	5			
22	W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

- Molecule 23 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

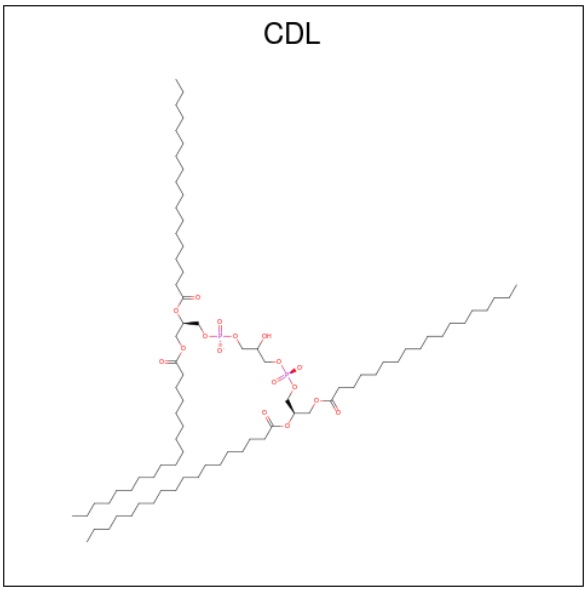
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
23	C	1	Total X 1 1	0	0
23	P	1	Total X 1 1	0	0

- Molecule 24 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
24	C	1	Total C N O P 53 43 1 8 1	0	0
24	G	1	Total C N O P 53 43 1 8 1	0	0
24	G	1	Total C N O P 53 43 1 8 1	0	0
24	T	1	Total C N O P 53 43 1 8 1	0	0
24	T	1	Total C N O P 53 43 1 8 1	0	0
24	T	1	Total C N O P 53 43 1 8 1	0	0

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

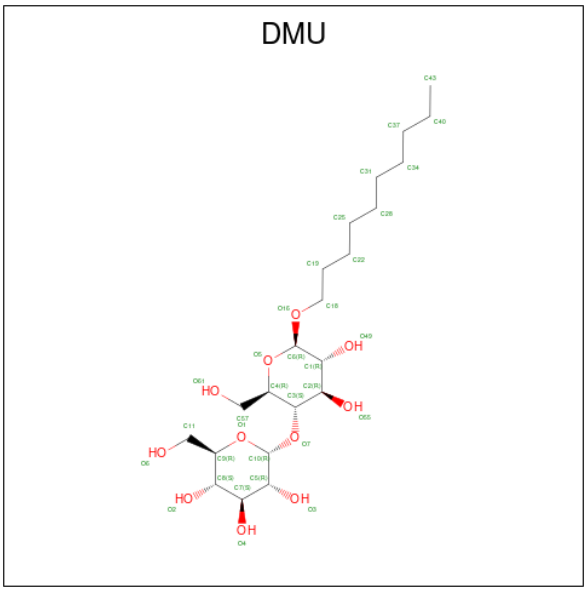


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
25	C	1	Total	C	O	P	0	0
			100	81	17	2		
25	G	1	Total	C	O	P	0	0
			100	81	17	2		
25	P	1	Total	C	O	P	0	0
			100	81	17	2		
25	T	1	Total	C	O	P	0	0
			100	81	17	2		

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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



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

- Molecule 28 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
28	A	215	Total O 215 215	0	0
28	B	124	Total O 124 124	0	0
28	C	109	Total O 109 109	0	0
28	D	102	Total O 102 102	0	0
28	E	67	Total O 67 67	0	0
28	F	81	Total O 81 81	0	0
28	G	48	Total O 48 48	0	0
28	H	48	Total O 48 48	0	0
28	I	31	Total O 31 31	0	0
28	J	16	Total O 16 16	0	0

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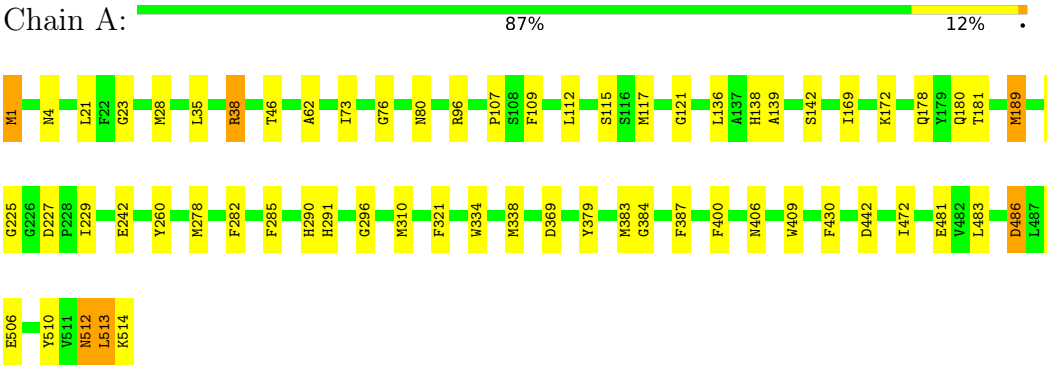
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
28	K	26	Total O 26 26	0	0
28	L	28	Total O 28 28	0	0
28	M	20	Total O 20 20	0	0
28	N	220	Total O 220 220	0	0
28	O	114	Total O 114 114	0	0
28	P	109	Total O 109 109	0	0
28	Q	60	Total O 60 60	0	0
28	R	45	Total O 45 45	0	0
28	S	77	Total O 77 77	0	0
28	T	39	Total O 39 39	0	0
28	U	45	Total O 45 45	0	0
28	V	21	Total O 21 21	0	0
28	W	16	Total O 16 16	0	0
28	X	17	Total O 17 17	0	0
28	Y	19	Total O 19 19	0	0
28	Z	14	Total O 14 14	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.

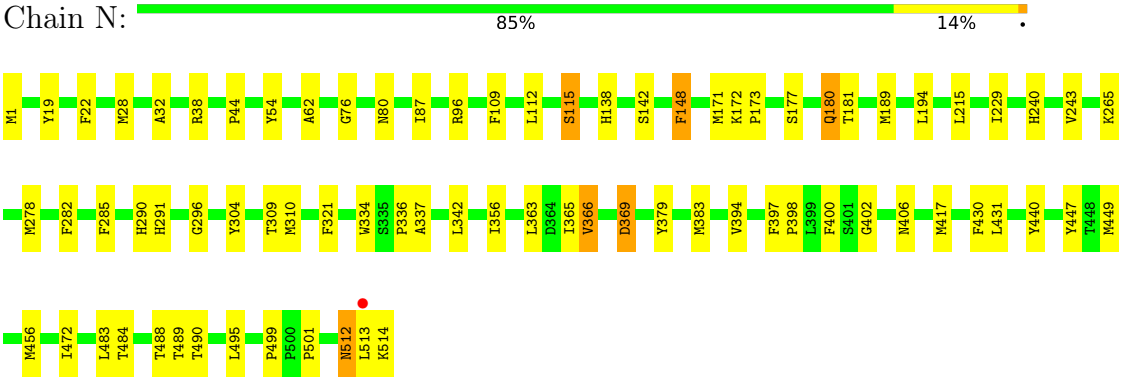
• Molecule 1: Cytochrome c oxidase subunit 1

Chain A:



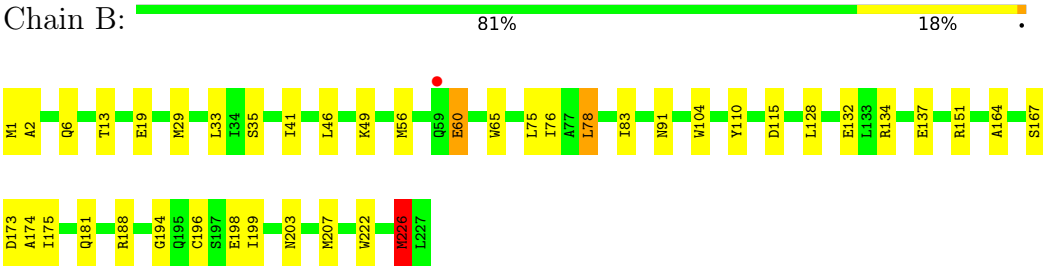
• Molecule 1: Cytochrome c oxidase subunit 1

Chain N:



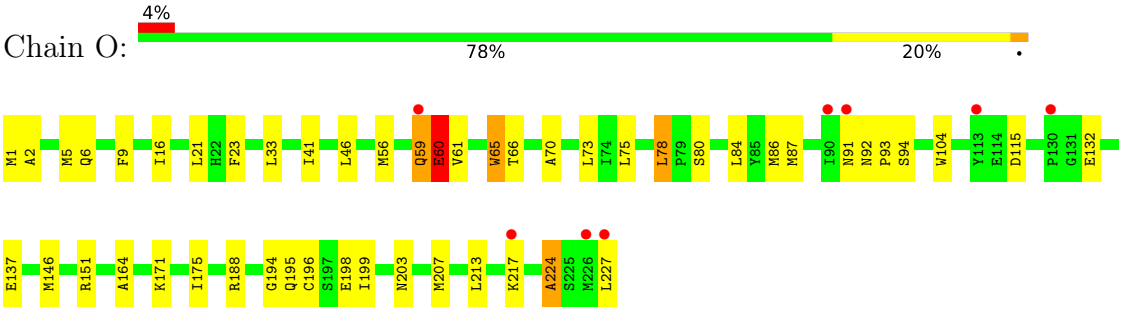
• Molecule 2: Cytochrome c oxidase subunit 2

Chain B:



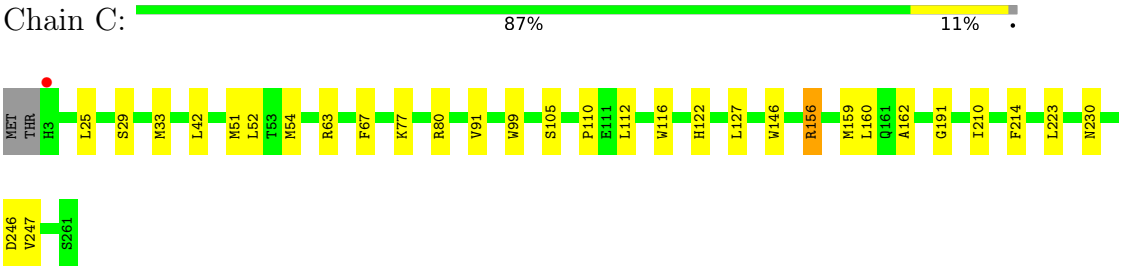
• Molecule 2: Cytochrome c oxidase subunit 2

Chain O:



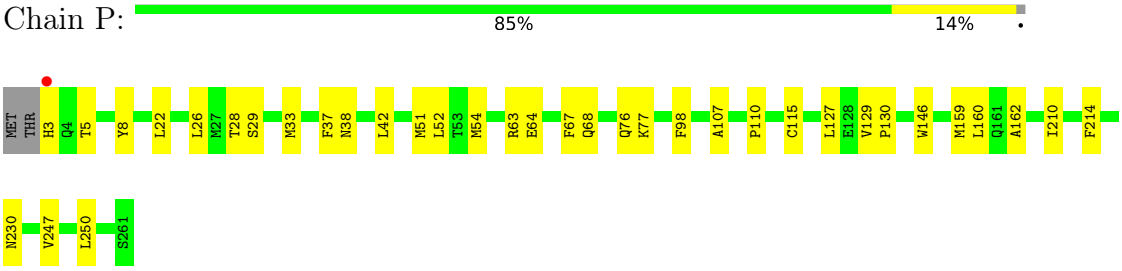
• Molecule 3: Cytochrome c oxidase subunit 3

Chain C:



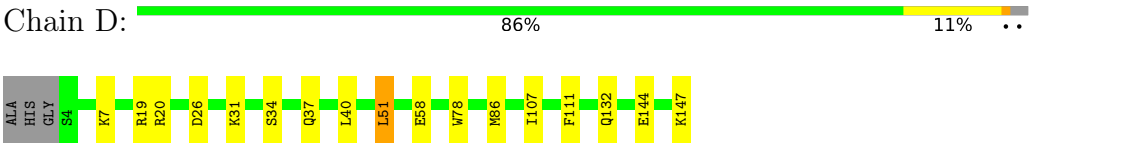
• Molecule 3: Cytochrome c oxidase subunit 3

Chain P:



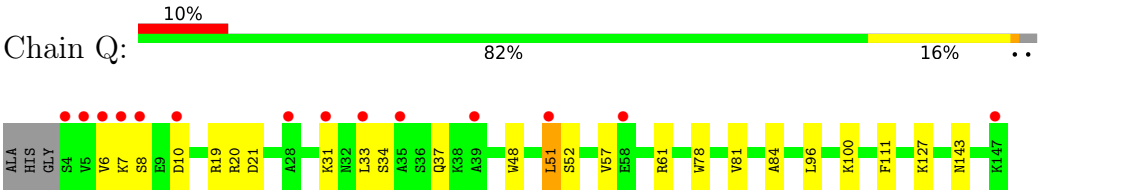
• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

Chain D:



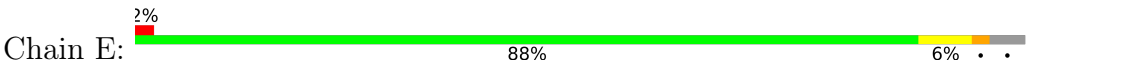
• Molecule 4: Cytochrome c oxidase subunit 4 isoform 1

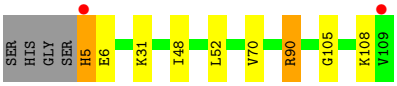
Chain Q:



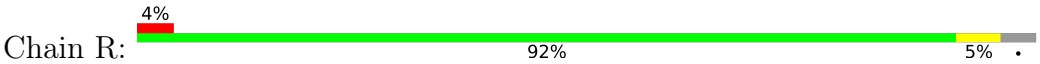
• Molecule 5: Cytochrome c oxidase subunit 5A

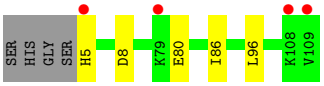
Chain E:



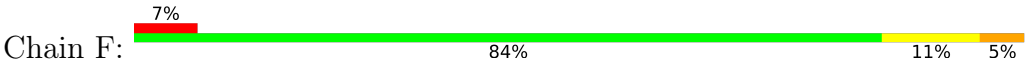


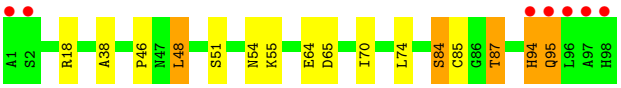
• Molecule 5: Cytochrome c oxidase subunit 5A



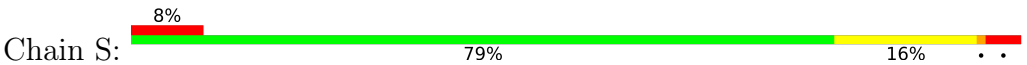


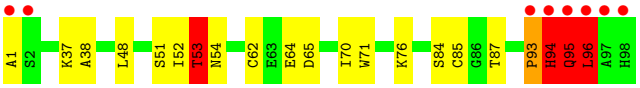
• Molecule 6: Cytochrome c oxidase subunit 5B



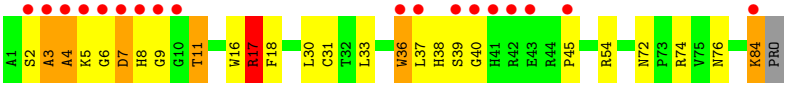


• Molecule 6: Cytochrome c oxidase subunit 5B

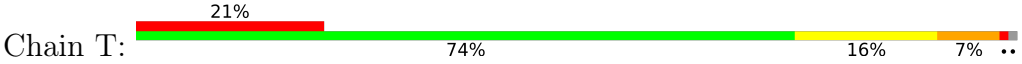


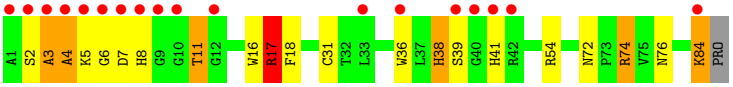


• Molecule 7: Cytochrome c oxidase subunit 6A2

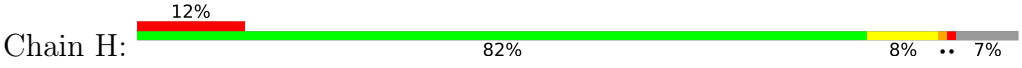


• Molecule 7: Cytochrome c oxidase subunit 6A2



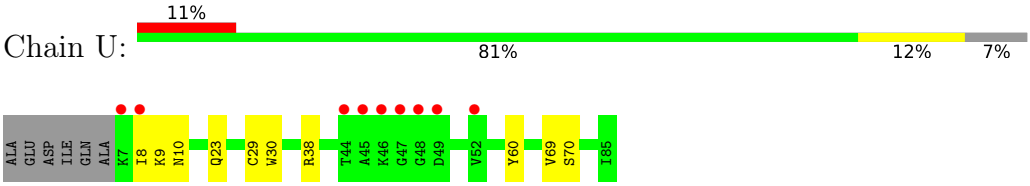


• Molecule 8: Cytochrome c oxidase subunit 6B1



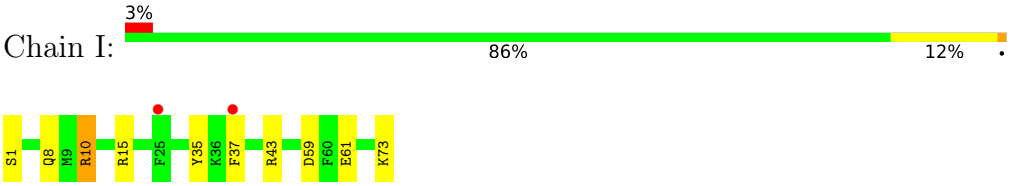
• Molecule 8: Cytochrome c oxidase subunit 6B1

Chain U:



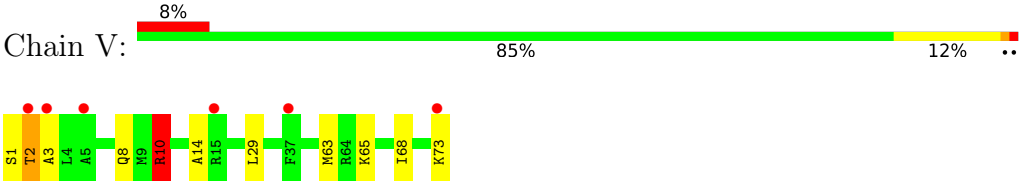
• Molecule 9: Cytochrome c oxidase subunit 6C

Chain I:



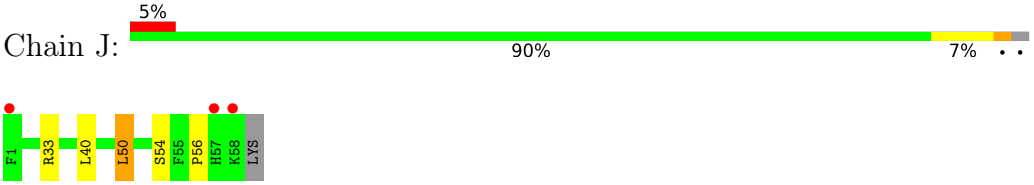
• Molecule 9: Cytochrome c oxidase subunit 6C

Chain V:



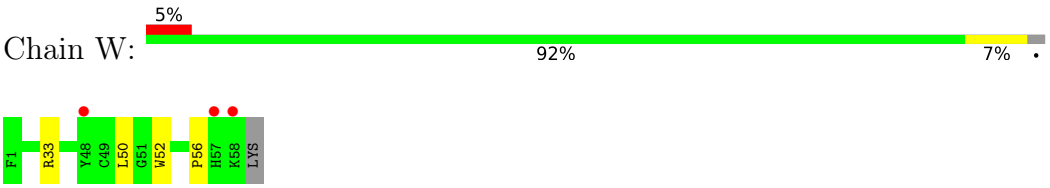
• Molecule 10: Cytochrome c oxidase subunit 7A1

Chain J:



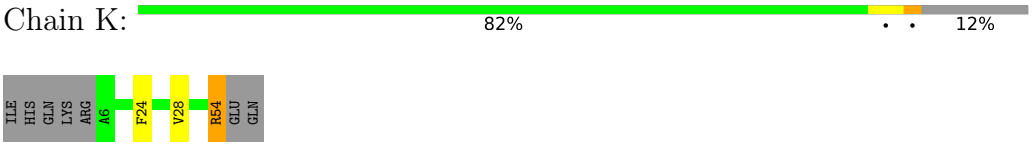
• Molecule 10: Cytochrome c oxidase subunit 7A1

Chain W:



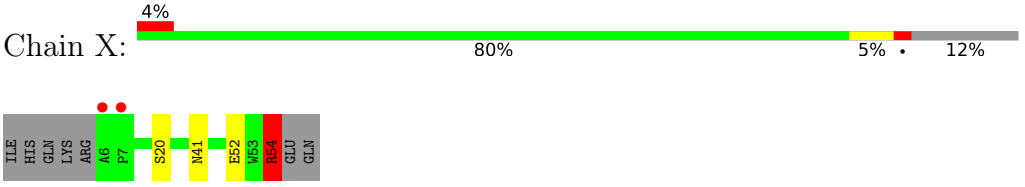
• Molecule 11: Cytochrome c oxidase subunit 7B

Chain K:



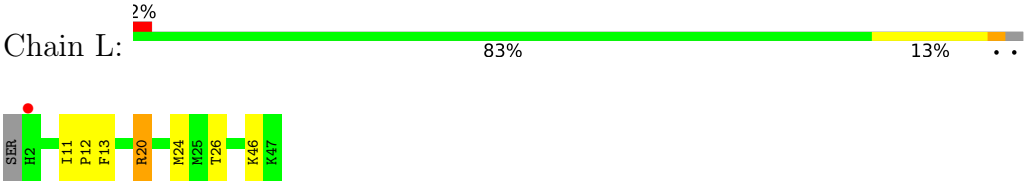
• Molecule 11: Cytochrome c oxidase subunit 7B

Chain X:



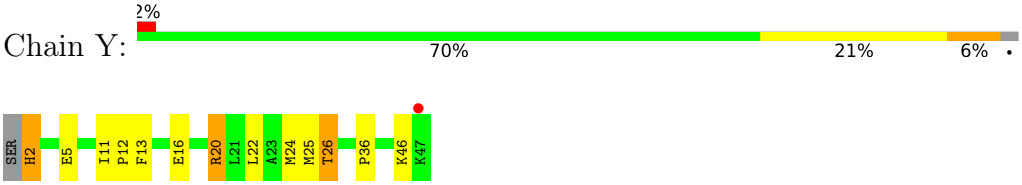
• Molecule 12: Cytochrome c oxidase subunit 7C

Chain L:



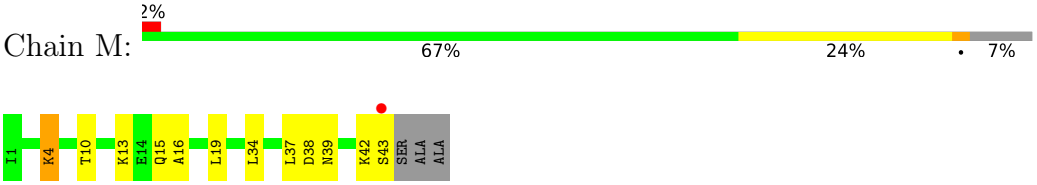
• Molecule 12: Cytochrome c oxidase subunit 7C

Chain Y:



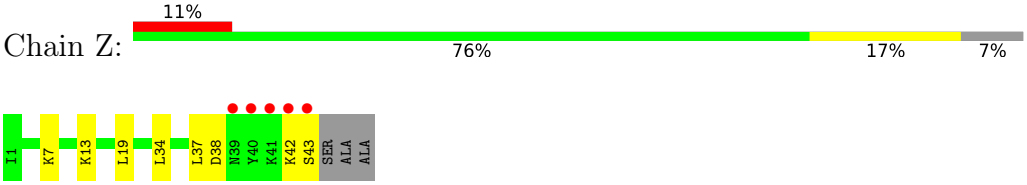
• Molecule 13: Cytochrome c oxidase subunit 8B

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	181.87Å 204.11Å 177.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30 107.93 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (15.00-2.30) 99.7 (107.93-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.96 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5	Depositor
R, R_{free}	0.169 , 0.205 0.184 , 0.217	Depositor DCC
R_{free} test set	14532 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	25.7	Xtriage
Anisotropy	0.564	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 51.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.005 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	32377	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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

5.1 Standard geometry

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

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	1.14	4/4156 (0.1%)	0.90	15/5678 (0.3%)
1	N	1.07	2/4156 (0.0%)	0.83	3/5678 (0.1%)
2	B	1.12	2/1860 (0.1%)	0.93	3/2534 (0.1%)
2	O	0.98	2/1860 (0.1%)	0.92	1/2534 (0.0%)
3	C	1.04	0/2197	0.79	2/3005 (0.1%)
3	P	1.04	1/2197 (0.0%)	0.79	0/3005
4	D	1.07	0/1229	0.92	3/1658 (0.2%)
4	Q	0.91	0/1229	0.79	2/1658 (0.1%)
5	E	1.04	0/871	0.92	2/1182 (0.2%)
5	R	0.94	0/871	0.84	0/1182
6	F	1.03	0/765	0.95	2/1038 (0.2%)
6	S	1.08	1/765 (0.1%)	1.03	3/1038 (0.3%)
7	G	1.10	1/690 (0.1%)	0.93	1/937 (0.1%)
7	T	1.02	1/690 (0.1%)	0.89	1/937 (0.1%)
8	H	1.00	0/682	0.80	0/921
8	U	0.91	1/682 (0.1%)	0.83	1/921 (0.1%)
9	I	0.99	0/605	0.83	2/802 (0.2%)
9	V	0.94	0/605	0.90	1/802 (0.1%)
10	J	0.91	0/471	0.78	0/636
10	W	0.91	0/471	0.80	0/636
11	K	1.02	0/398	0.86	1/546 (0.2%)
11	X	0.92	0/398	0.76	1/546 (0.2%)
12	L	1.02	0/393	0.84	1/526 (0.2%)
12	Y	1.10	1/393 (0.3%)	0.74	0/526
13	M	1.03	0/345	0.85	0/470
13	Z	0.87	0/345	0.79	0/470
All	All	1.04	16/29324 (0.1%)	0.86	45/39866 (0.1%)

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	S	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	139	ALA	CA-CB	8.23	1.69	1.52
7	T	36	TRP	CB-CG	7.35	1.63	1.50
7	G	36	TRP	CB-CG	7.22	1.63	1.50
6	S	54	ASN	CB-CG	-7.02	1.34	1.51
1	A	260	TYR	CD1-CE1	6.95	1.49	1.39

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	90	ARG	NE-CZ-NH1	10.61	125.61	120.30
4	D	20	ARG	NE-CZ-NH2	-10.49	115.06	120.30
7	G	17	ARG	NE-CZ-NH2	-9.43	115.58	120.30
2	B	188	ARG	NE-CZ-NH2	-8.84	115.88	120.30
7	T	17	ARG	NE-CZ-NH2	-8.10	116.25	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	S	93	PRO	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	48	0
1	N	4027	0	4001	70	0
2	B	1824	0	1833	27	0
2	O	1824	0	1833	32	0
3	C	2110	0	2027	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	P	2110	0	2027	33	0
4	D	1195	0	1183	13	0
4	Q	1195	0	1183	18	0
5	E	852	0	845	3	0
5	R	852	0	845	5	0
6	F	748	0	728	9	0
6	S	748	0	728	27	0
7	G	675	0	644	27	0
7	T	675	0	644	28	0
8	H	662	0	623	7	0
8	U	662	0	623	2	0
9	I	601	0	613	8	0
9	V	601	0	613	9	0
10	J	460	0	459	7	0
10	W	460	0	459	4	0
11	K	384	0	366	1	0
11	X	384	0	366	6	0
12	L	380	0	380	10	0
12	Y	380	0	380	11	0
13	M	335	0	352	7	0
13	Z	335	0	352	3	0
14	A	120	0	108	6	0
14	N	120	0	108	9	0
15	A	1	0	0	0	0
15	N	1	0	0	0	0
16	A	1	0	0	0	0
16	N	1	0	0	0	0
17	A	1	0	0	0	0
17	N	1	0	0	0	0
18	A	63	0	110	6	0
18	D	63	0	110	6	0
18	L	63	0	110	15	0
18	N	126	0	220	21	0
18	Q	63	0	110	4	0
19	A	102	0	152	10	0
19	C	102	0	152	8	0
19	N	102	0	152	10	0
19	P	102	0	152	6	0
20	B	2	0	0	0	0
20	O	2	0	0	0	0
21	B	52	0	80	13	0
21	O	52	0	80	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	B	29	0	39	1	0
22	C	58	0	78	3	0
22	G	29	0	39	0	0
22	J	29	0	38	3	0
22	P	58	0	78	1	0
22	W	29	0	38	3	0
23	C	1	0	0	0	0
23	P	1	0	0	0	0
24	C	53	0	77	5	0
24	G	106	0	154	12	0
24	T	159	0	231	21	0
25	C	100	0	156	17	0
25	G	100	0	156	18	0
25	P	100	0	156	14	0
25	T	100	0	156	22	0
26	F	1	0	0	0	0
26	S	1	0	0	0	0
27	M	33	0	41	0	0
27	Z	33	0	40	0	0
28	A	215	0	0	7	0
28	B	124	0	0	2	0
28	C	109	0	0	2	0
28	D	102	0	0	3	0
28	E	67	0	0	1	0
28	F	81	0	0	1	0
28	G	48	0	0	5	0
28	H	48	0	0	2	0
28	I	31	0	0	1	0
28	J	16	0	0	0	0
28	K	26	0	0	2	0
28	L	28	0	0	1	0
28	M	20	0	0	0	0
28	N	220	0	0	6	0
28	O	114	0	0	0	0
28	P	109	0	0	4	0
28	Q	60	0	0	3	0
28	R	45	0	0	0	0
28	S	77	0	0	4	0
28	T	39	0	0	2	0
28	U	45	0	0	0	0
28	V	21	0	0	2	0
28	W	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	X	17	0	0	2	0
28	Y	19	0	0	1	0
28	Z	14	0	0	1	0
All	All	32377	0	31229	485	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 8.

The worst 5 of 485 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:52:ILE:O	6:S:94:HIS:CE1	1.76	1.38
6:S:52:ILE:O	6:S:94:HIS:NE2	1.66	1.26
7:T:84:LYS:H	7:T:84:LYS:HD2	0.95	1.12
1:N:513:LEU:O	1:N:514:LYS:HB2	1.47	1.11
24:T:1265:PEK:H383	25:T:1269:CDL:C27	1.81	1.10

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%)	496 (97%)	15 (3%)	1 (0%)	47 58
1	N	512/514 (100%)	499 (98%)	13 (2%)	0	100 100
2	B	225/227 (99%)	217 (96%)	7 (3%)	1 (0%)	34 42
2	O	225/227 (99%)	214 (95%)	8 (4%)	3 (1%)	12 12
3	C	257/261 (98%)	252 (98%)	5 (2%)	0	100 100
3	P	257/261 (98%)	250 (97%)	6 (2%)	1 (0%)	34 42
4	D	142/147 (97%)	138 (97%)	4 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Q	142/147 (97%)	138 (97%)	4 (3%)	0	100	100
5	E	103/109 (94%)	103 (100%)	0	0	100	100
5	R	103/109 (94%)	103 (100%)	0	0	100	100
6	F	96/98 (98%)	91 (95%)	4 (4%)	1 (1%)	15	17
6	S	96/98 (98%)	88 (92%)	5 (5%)	3 (3%)	4	2
7	G	81/85 (95%)	66 (82%)	8 (10%)	7 (9%)	1	0
7	T	81/85 (95%)	66 (82%)	9 (11%)	6 (7%)	1	0
8	H	77/85 (91%)	70 (91%)	6 (8%)	1 (1%)	12	12
8	U	77/85 (91%)	71 (92%)	4 (5%)	2 (3%)	5	4
9	I	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
9	V	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
10	J	56/59 (95%)	56 (100%)	0	0	100	100
10	W	56/59 (95%)	56 (100%)	0	0	100	100
11	K	47/56 (84%)	47 (100%)	0	0	100	100
11	X	47/56 (84%)	47 (100%)	0	0	100	100
12	L	44/47 (94%)	41 (93%)	3 (7%)	0	100	100
12	Y	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
13	M	41/46 (89%)	41 (100%)	0	0	100	100
13	Z	41/46 (89%)	41 (100%)	0	0	100	100
All	All	3504/3614 (97%)	3371 (96%)	107 (3%)	26 (1%)	22	26

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	95	GLN
7	G	4	ALA
7	G	7	ASP
7	G	8	HIS
7	G	39	SER

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%)	418 (98%)	8 (2%)	57 73
1	N	426/426 (100%)	415 (97%)	11 (3%)	46 63
2	B	210/210 (100%)	199 (95%)	11 (5%)	23 32
2	O	210/210 (100%)	197 (94%)	13 (6%)	18 25
3	C	224/226 (99%)	218 (97%)	6 (3%)	44 61
3	P	224/226 (99%)	218 (97%)	6 (3%)	44 61
4	D	128/129 (99%)	127 (99%)	1 (1%)	81 91
4	Q	128/129 (99%)	124 (97%)	4 (3%)	40 55
5	E	92/95 (97%)	88 (96%)	4 (4%)	29 40
5	R	92/95 (97%)	91 (99%)	1 (1%)	73 86
6	F	81/81 (100%)	78 (96%)	3 (4%)	34 48
6	S	81/81 (100%)	76 (94%)	5 (6%)	18 25
7	G	67/68 (98%)	60 (90%)	7 (10%)	7 8
7	T	67/68 (98%)	61 (91%)	6 (9%)	9 11
8	H	71/75 (95%)	68 (96%)	3 (4%)	30 42
8	U	71/75 (95%)	67 (94%)	4 (6%)	21 29
9	I	57/57 (100%)	53 (93%)	4 (7%)	15 19
9	V	57/57 (100%)	53 (93%)	4 (7%)	15 19
10	J	49/50 (98%)	48 (98%)	1 (2%)	55 72
10	W	49/50 (98%)	48 (98%)	1 (2%)	55 72
11	K	39/46 (85%)	38 (97%)	1 (3%)	46 63
11	X	39/46 (85%)	37 (95%)	2 (5%)	24 33
12	L	39/40 (98%)	38 (97%)	1 (3%)	46 63
12	Y	39/40 (98%)	36 (92%)	3 (8%)	13 16
13	M	37/38 (97%)	30 (81%)	7 (19%)	1 1
13	Z	37/38 (97%)	32 (86%)	5 (14%)	4 4
All	All	3040/3082 (99%)	2918 (96%)	122 (4%)	31 44

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	38	ARG
9	V	29	LEU
2	O	61	VAL
9	V	10	ARG
13	Z	34	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
4	Q	101	HIS
4	Q	109	HIS
7	T	76	ASN
7	G	8	HIS
5	E	94	ASN

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	$\#\|Z\| > 2$
2	FME	B	1	2	8,9,10	1.51	1 (12%)	7,9,11	7.06	5 (71%)
9	SAC	I	1	9	7,8,9	2.61	2 (28%)	8,9,11	1.92	3 (37%)
1	FME	N	1	1	8,9,10	0.88	0	7,9,11	5.71	1 (14%)
1	FME	A	1	1	8,9,10	0.88	0	7,9,11	5.01	3 (42%)
9	SAC	V	1	9	7,8,9	2.51	2 (28%)	8,9,11	4.36	3 (37%)
7	TPO	T	11	7	8,10,11	1.99	2 (25%)	10,14,16	1.27	2 (20%)
7	TPO	G	11	7	8,10,11	2.22	2 (25%)	10,14,16	1.29	1 (10%)
2	FME	O	1	2	8,9,10	0.92	0	7,9,11	6.06	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
2	FME	B	1	2	-	1/7/9/11	-
9	SAC	I	1	9	-	3/7/8/10	-
1	FME	N	1	1	-	4/7/9/11	-
1	FME	A	1	1	-	4/7/9/11	-
9	SAC	V	1	9	-	1/7/8/10	-
7	TPO	T	11	7	-	3/9/11/13	-
7	TPO	G	11	7	-	4/9/11/13	-
2	FME	O	1	2	-	1/7/9/11	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	1	SAC	OAC-C1A	5.47	1.35	1.23
9	V	1	SAC	CA-N	4.63	1.52	1.46
9	V	1	SAC	OAC-C1A	4.52	1.33	1.23
7	G	11	TPO	P-OG1	3.85	1.66	1.59
9	I	1	SAC	CA-N	3.72	1.51	1.46

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	FME	CA-N-CN	-17.00	96.68	122.82
2	O	1	FME	CA-N-CN	-14.97	99.80	122.82
1	N	1	FME	CA-N-CN	-14.72	100.18	122.82
1	A	1	FME	CA-N-CN	-12.61	103.43	122.82
9	V	1	SAC	CB-CA-N	-7.50	93.72	110.55

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.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	FME	2	0
7	T	11	TPO	2	0
7	G	11	TPO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 52 ligands modelled in this entry, 8 are monoatomic and 2 are unknown - leaving 42 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
19	PGV	P	1268	-	50,50,50	1.18	2 (4%)	53,56,56	1.31	5 (9%)
25	CDL	C	270	-	99,99,99	1.36	13 (13%)	105,111,111	1.30	13 (12%)
14	HEA	A	516	1	57,67,67	1.57	10 (17%)	61,103,103	2.03	23 (37%)
27	DMU	M	526	-	34,34,34	0.86	1 (2%)	45,45,45	2.45	17 (37%)
22	CHD	P	1525	-	32,32,32	0.94	1 (3%)	51,51,51	1.41	7 (13%)
24	PEK	C	265	-	52,52,52	1.21	2 (3%)	55,57,57	1.13	4 (7%)
22	CHD	C	271	-	32,32,32	0.62	0	51,51,51	2.05	18 (35%)
21	PSC	B	229	-	51,51,51	1.18	3 (5%)	57,59,59	1.04	3 (5%)
21	PSC	O	1229	-	51,51,51	1.16	3 (5%)	57,59,59	0.97	2 (3%)
22	CHD	P	1271	-	32,32,32	0.62	0	51,51,51	2.07	16 (31%)
18	TGL	A	521	-	62,62,62	1.27	6 (9%)	65,65,65	1.74	14 (21%)
24	PEK	G	264	-	52,52,52	1.00	4 (7%)	55,57,57	1.51	9 (16%)
19	PGV	P	1267	-	50,50,50	0.77	1 (2%)	53,56,56	1.13	5 (9%)
24	PEK	T	1264	-	52,52,52	0.98	4 (7%)	55,57,57	1.39	9 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CHD	C	525	-	32,32,32	0.81	0	51,51,51	0.99	2 (3%)
25	CDL	T	1269	-	99,99,99	1.36	12 (12%)	105,111,111	1.26	7 (6%)
18	TGL	N	1522	-	62,62,62	1.51	7 (11%)	65,65,65	1.57	15 (23%)
14	HEA	N	515	1	57,67,67	1.66	9 (15%)	61,103,103	3.08	31 (50%)
24	PEK	T	263	-	52,52,52	1.22	3 (5%)	55,57,57	1.13	5 (9%)
14	HEA	N	516	1	57,67,67	1.41	8 (14%)	61,103,103	1.86	21 (34%)
18	TGL	Q	1523	-	62,62,62	1.32	6 (9%)	65,65,65	1.40	12 (18%)
19	PGV	N	1266	-	50,50,50	0.85	2 (4%)	53,56,56	1.24	5 (9%)
20	CUA	B	228	2	0,1,1	-	-	-		
24	PEK	T	1265	-	52,52,52	1.26	3 (5%)	55,57,57	1.13	5 (9%)
20	CUA	O	228	2	0,1,1	-	-	-		
19	PGV	C	268	-	50,50,50	1.20	2 (4%)	53,56,56	1.28	4 (7%)
25	CDL	P	1270	-	99,99,99	1.37	12 (12%)	105,111,111	1.36	13 (12%)
27	DMU	Z	1526	-	34,34,34	0.85	1 (2%)	45,45,45	2.50	16 (35%)
18	TGL	D	523	-	62,62,62	1.29	6 (9%)	65,65,65	1.56	10 (15%)
18	TGL	N	1521	-	62,62,62	1.23	6 (9%)	65,65,65	1.50	10 (15%)
14	HEA	A	515	1	57,67,67	1.59	11 (19%)	61,103,103	2.39	15 (24%)
19	PGV	A	522	-	50,50,50	0.81	2 (4%)	53,56,56	1.14	2 (3%)
19	PGV	C	267	-	50,50,50	0.81	2 (4%)	53,56,56	1.12	5 (9%)
24	PEK	G	1263	-	52,52,52	1.19	2 (3%)	55,57,57	1.19	6 (10%)
18	TGL	L	522	-	62,62,62	1.36	7 (11%)	65,65,65	1.54	12 (18%)
22	CHD	J	60	-	32,32,32	0.81	0	51,51,51	2.86	22 (43%)
25	CDL	G	269	-	99,99,99	1.38	12 (12%)	105,111,111	1.31	9 (8%)
19	PGV	N	1524	-	50,50,50	1.03	2 (4%)	53,56,56	1.15	4 (7%)
22	CHD	W	1059	-	32,32,32	0.84	0	51,51,51	3.09	21 (41%)
22	CHD	B	1085	-	32,32,32	1.13	4 (12%)	51,51,51	1.47	9 (17%)
19	PGV	A	524	-	50,50,50	1.18	2 (4%)	53,56,56	1.04	5 (9%)
22	CHD	G	229	-	32,32,32	0.89	0	51,51,51	1.55	10 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	PGV	P	1268	-	-	33/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	CDL	C	270	-	-	68/110/110/110	-
27	DMU	M	526	-	2/2/10/10	8/19/59/59	0/2/2/2
14	HEA	A	516	1	-	5/32/76/76	-
22	CHD	P	1525	-	-	1/9/74/74	0/4/4/4
24	PEK	C	265	-	-	23/56/56/56	-
22	CHD	C	271	-	-	6/9/74/74	0/4/4/4
21	PSC	B	229	-	-	35/55/55/55	-
21	PSC	O	1229	-	-	37/55/55/55	-
22	CHD	P	1271	-	-	6/9/74/74	0/4/4/4
18	TGL	A	521	-	-	35/65/65/65	-
24	PEK	G	264	-	-	25/56/56/56	-
19	PGV	P	1267	-	-	14/55/55/55	-
24	PEK	T	1264	-	-	24/56/56/56	-
22	CHD	C	525	-	-	2/9/74/74	0/4/4/4
25	CDL	T	1269	-	-	51/110/110/110	-
18	TGL	N	1522	-	-	34/65/65/65	-
14	HEA	N	515	1	-	6/32/76/76	-
24	PEK	T	263	-	-	34/56/56/56	-
14	HEA	N	516	1	-	6/32/76/76	-
18	TGL	Q	1523	-	-	36/65/65/65	-
19	PGV	N	1266	-	-	15/55/55/55	-
24	PEK	T	1265	-	-	32/56/56/56	-
19	PGV	C	268	-	-	35/55/55/55	-
25	CDL	P	1270	-	-	68/110/110/110	-
27	DMU	Z	1526	-	4/4/10/10	9/19/59/59	0/2/2/2
18	TGL	D	523	-	-	37/65/65/65	-
18	TGL	N	1521	-	-	31/65/65/65	-
14	HEA	A	515	1	-	5/32/76/76	-
19	PGV	A	522	-	-	14/55/55/55	-
19	PGV	C	267	-	-	17/55/55/55	-
24	PEK	G	1263	-	-	32/56/56/56	-
18	TGL	L	522	-	-	39/65/65/65	-
22	CHD	J	60	-	-	6/9/74/74	0/4/4/4
25	CDL	G	269	-	-	67/110/110/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	PGV	N	1524	-	-	41/55/55/55	-
22	CHD	W	1059	-	-	8/9/74/74	0/4/4/4
22	CHD	B	1085	-	-	2/9/74/74	0/4/4/4
19	PGV	A	524	-	-	33/55/55/55	-
22	CHD	G	229	-	-	2/9/74/74	0/4/4/4

The worst 5 of 171 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	N	1522	TGL	OG2-CB1	6.24	1.51	1.34
18	N	1522	TGL	OG1-CA1	6.15	1.51	1.33
14	N	515	HEA	CHC-C4B	5.95	1.50	1.35
18	L	522	TGL	OG2-CB1	5.82	1.50	1.34
24	T	263	PEK	O03-C21	5.77	1.50	1.33

The worst 5 of 421 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
14	N	515	HEA	C17-C18-C19	-10.39	102.64	127.66
14	A	515	HEA	C17-C18-C19	-10.22	103.05	127.66
14	N	515	HEA	C17-C16-C15	8.77	141.84	112.98
14	A	515	HEA	C17-C16-C15	8.00	139.29	112.98
14	N	515	HEA	C3D-C4D-ND	7.86	117.97	110.36

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
27	M	526	DMU	C2
27	M	526	DMU	C5
27	Z	1526	DMU	C3
27	Z	1526	DMU	C5
27	Z	1526	DMU	C2

5 of 982 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	Q	1523	TGL	OC1-CC1-OG3-CG3
19	A	524	PGV	C04-O12-P-O13
19	A	524	PGV	C04-O12-P-O14
19	A	524	PGV	C02-C03-O11-P
19	A	524	PGV	O02-C1-O01-C02

There are no ring outliers.

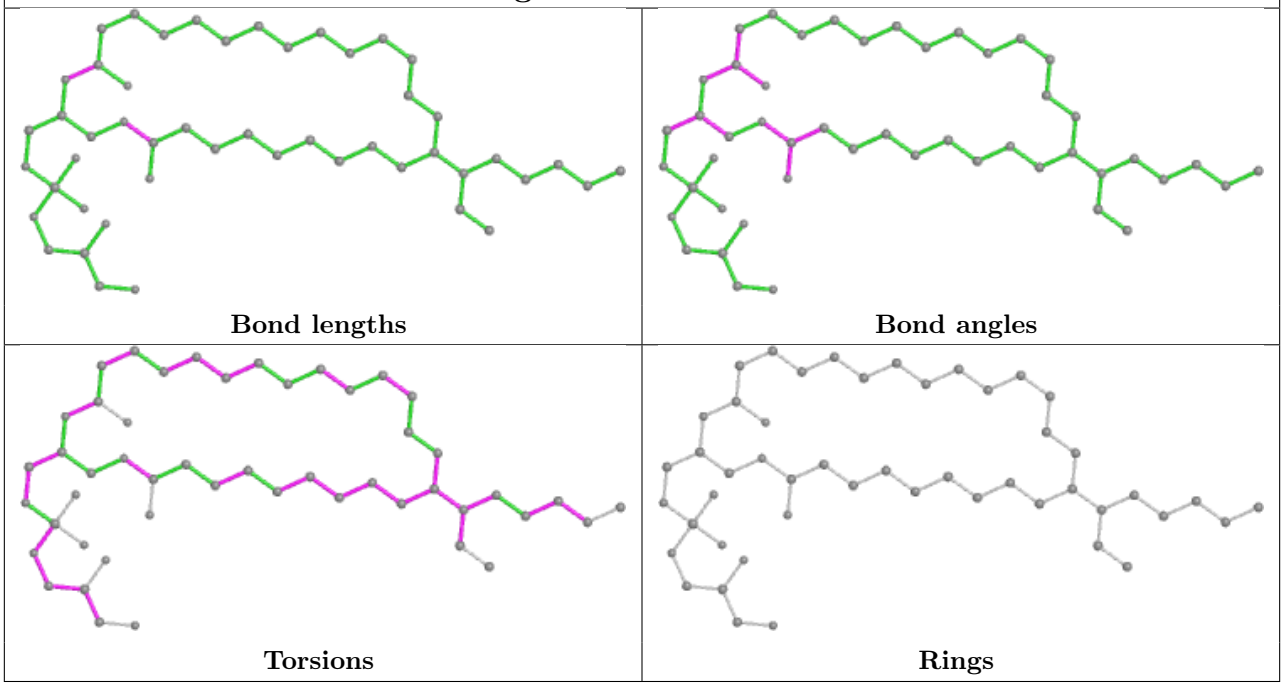
35 monomers are involved in 238 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	P	1268	PGV	4	0
25	C	270	CDL	17	0
14	A	516	HEA	1	0
24	C	265	PEK	5	0
22	C	271	CHD	3	0
21	B	229	PSC	13	0
21	O	1229	PSC	17	0
22	P	1271	CHD	1	0
18	A	521	TGL	6	0
24	G	264	PEK	4	0
19	P	1267	PGV	2	0
24	T	1264	PEK	6	0
25	T	1269	CDL	22	0
18	N	1522	TGL	12	0
14	N	515	HEA	6	0
24	T	263	PEK	9	0
14	N	516	HEA	3	0
18	Q	1523	TGL	4	0
19	N	1266	PGV	2	0
24	T	1265	PEK	6	0
19	C	268	PGV	3	0
25	P	1270	CDL	14	0
18	D	523	TGL	6	0
18	N	1521	TGL	9	0
14	A	515	HEA	5	0
19	A	522	PGV	1	0
19	C	267	PGV	5	0
24	G	1263	PEK	8	0
18	L	522	TGL	15	0
22	J	60	CHD	3	0
25	G	269	CDL	18	0
19	N	1524	PGV	8	0
22	W	1059	CHD	3	0
22	B	1085	CHD	1	0
19	A	524	PGV	9	0

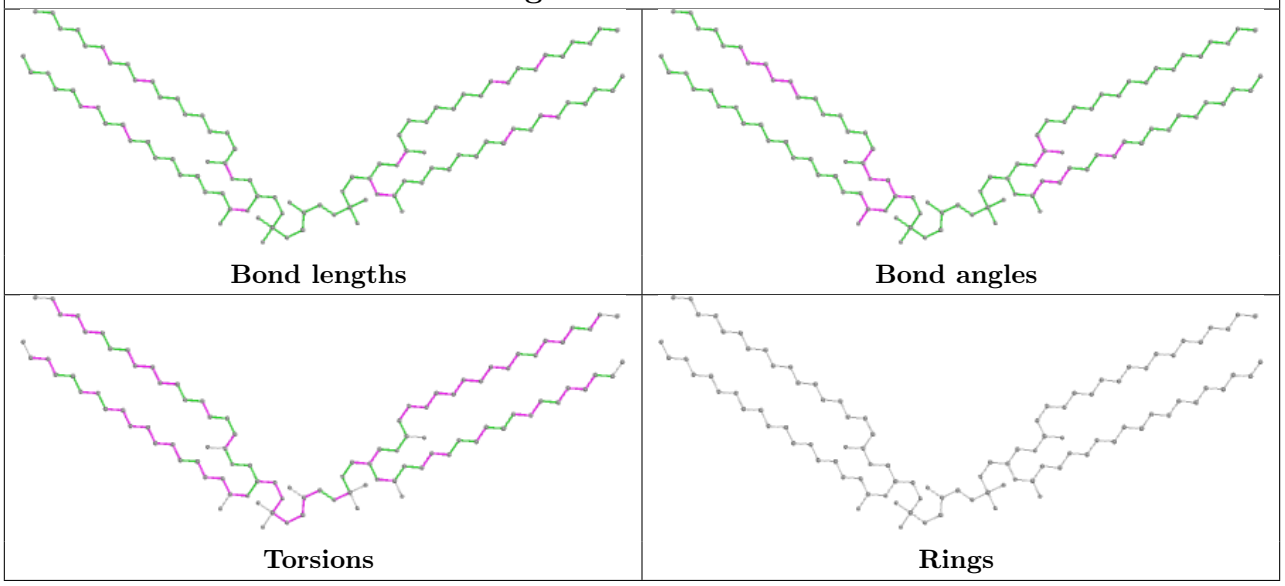
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

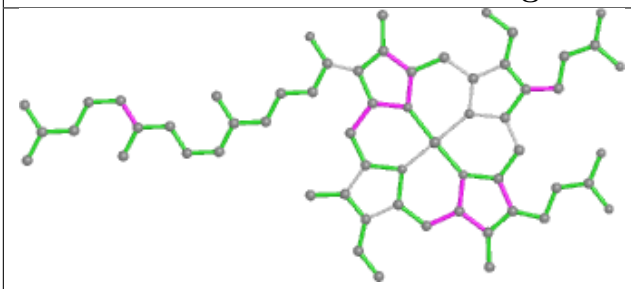
Ligand PGV P 1268



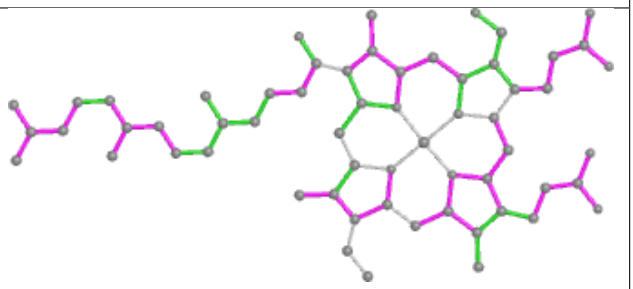
Ligand CDL C 270



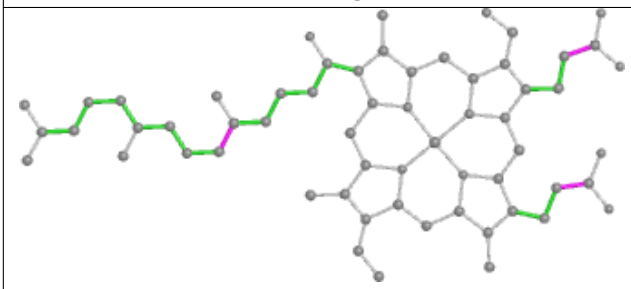
Ligand HEA A 516



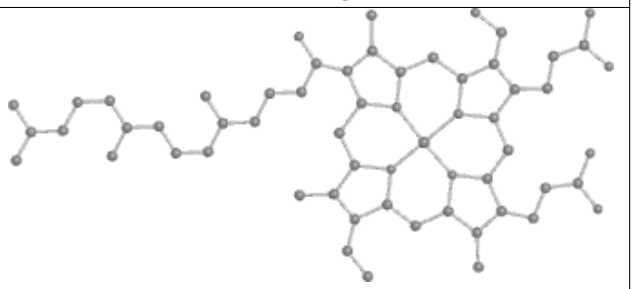
Bond lengths



Bond angles

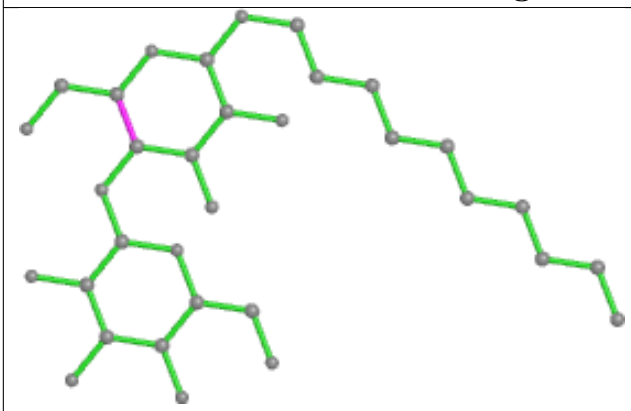


Torsions

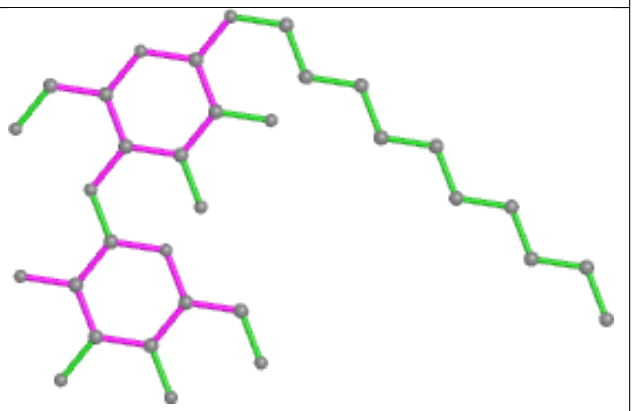


Rings

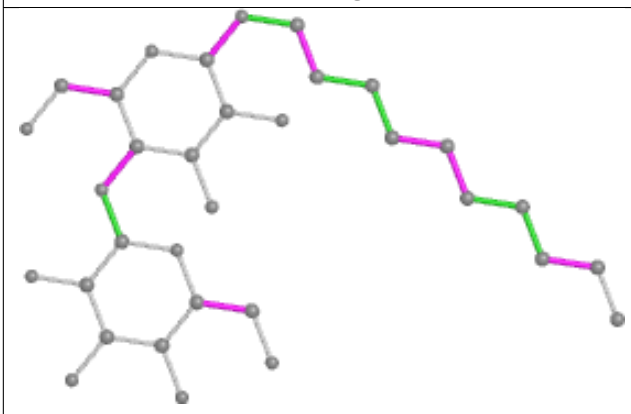
Ligand DMU M 526



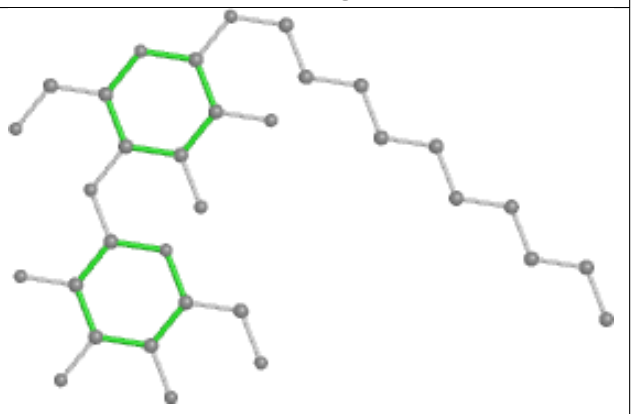
Bond lengths



Bond angles

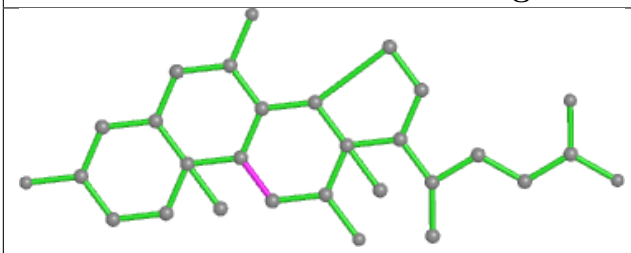


Torsions

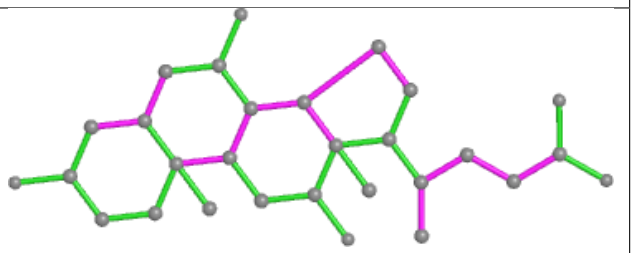


Rings

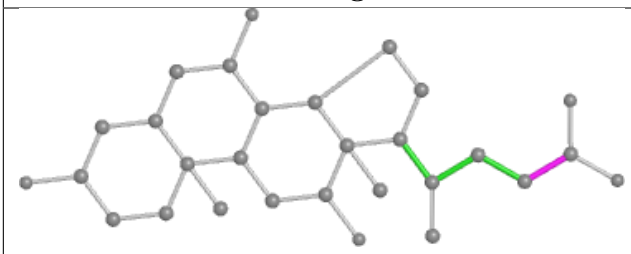
Ligand CHD P 1525



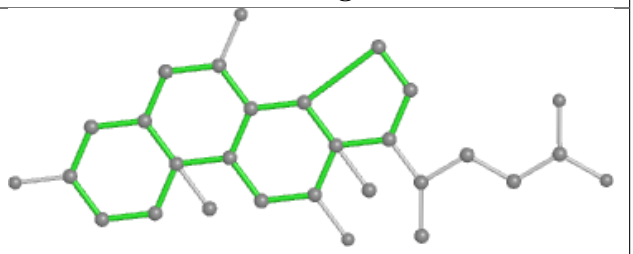
Bond lengths



Bond angles

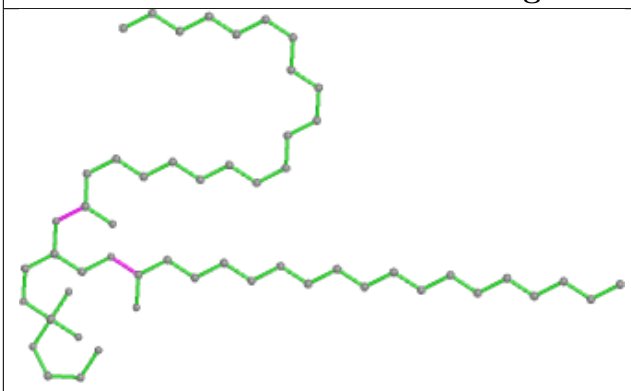


Torsions

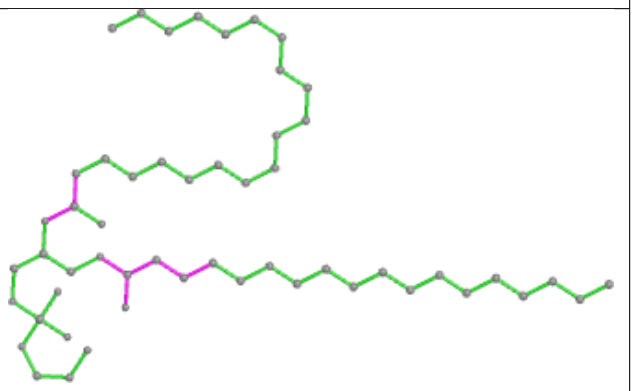


Rings

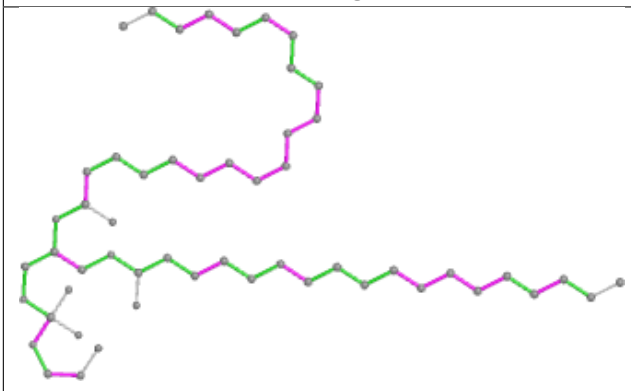
Ligand PEK C 265



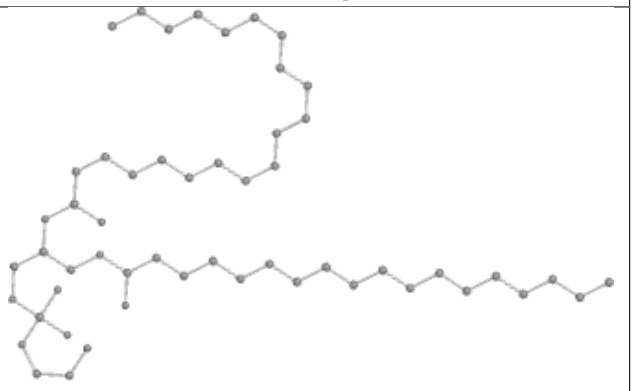
Bond lengths



Bond angles

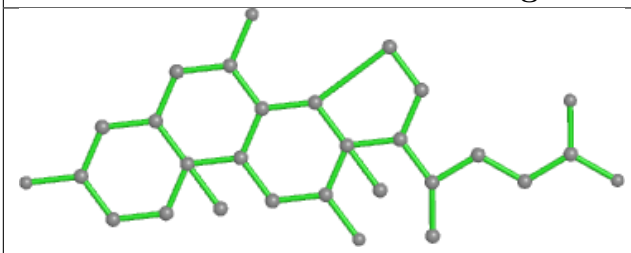


Torsions

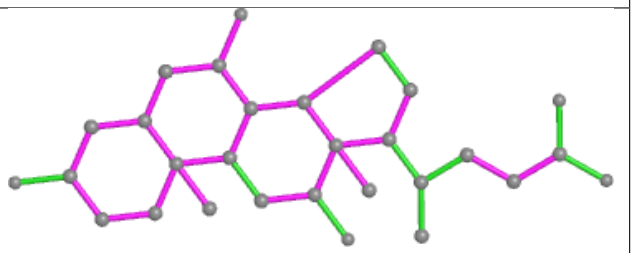


Rings

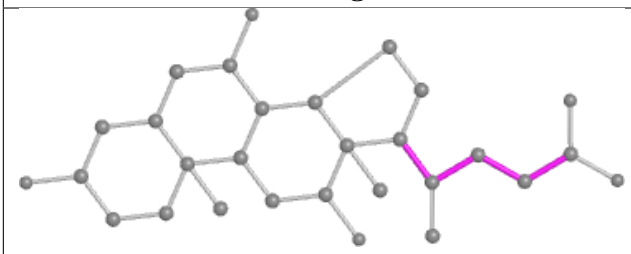
Ligand CHD C 271



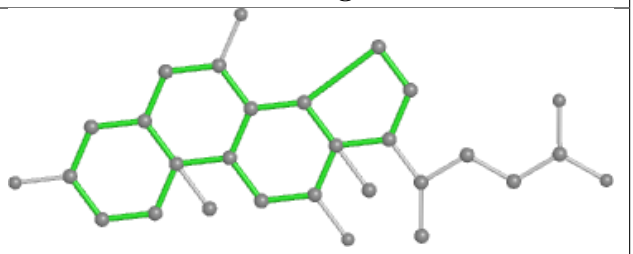
Bond lengths



Bond angles

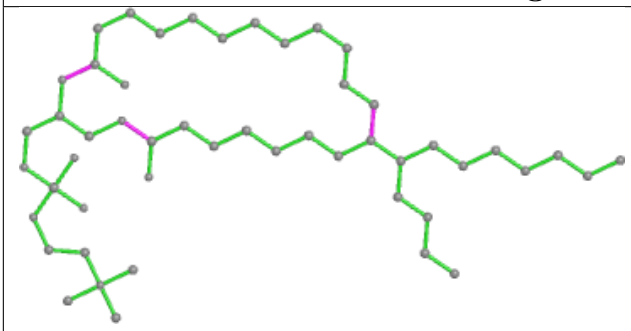


Torsions

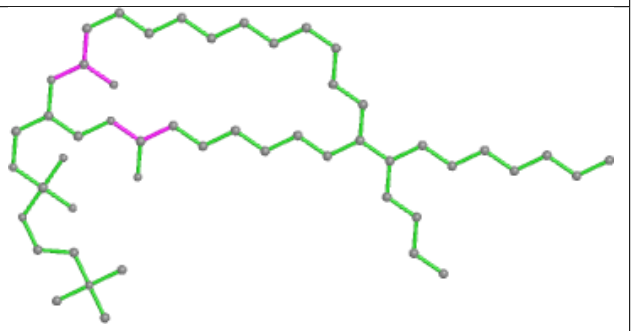


Rings

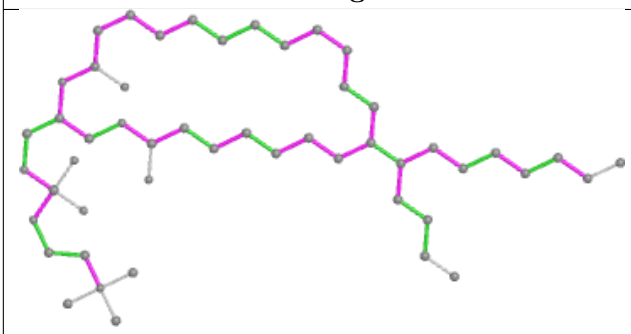
Ligand PSC B 229



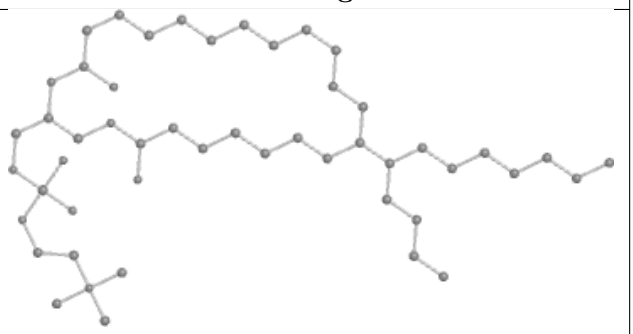
Bond lengths



Bond angles

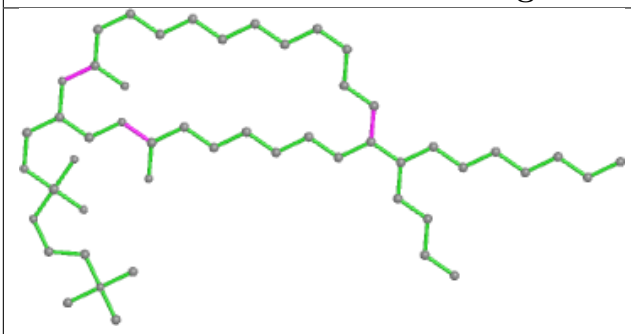


Torsions

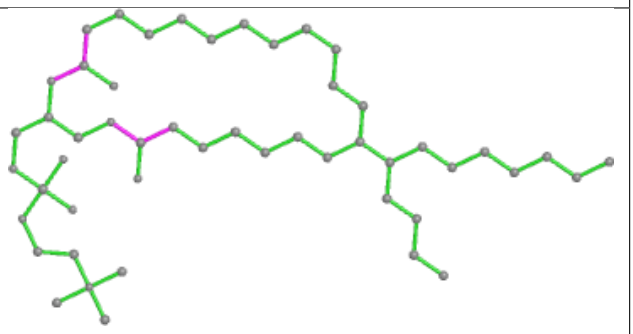


Rings

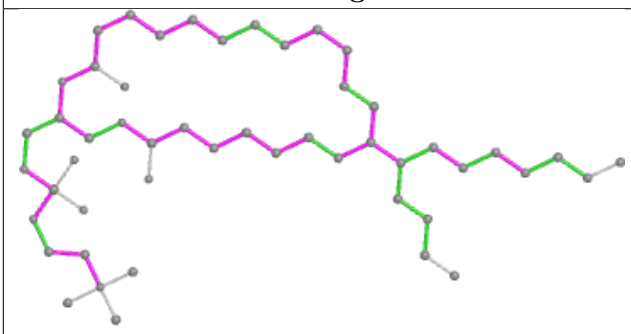
Ligand PSC O 1229



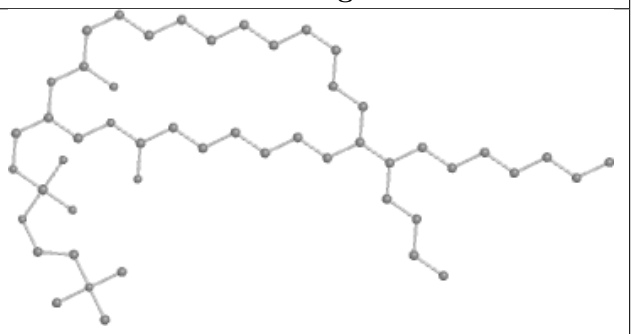
Bond lengths



Bond angles

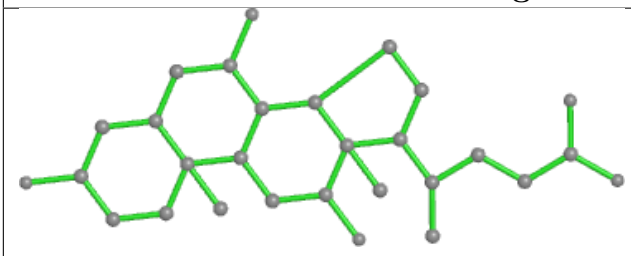


Torsions

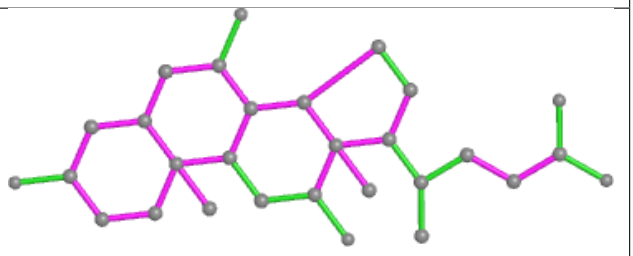


Rings

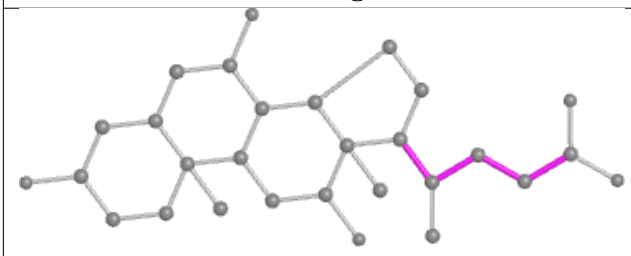
Ligand CHD P 1271



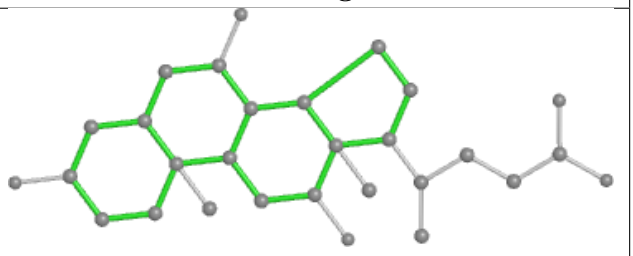
Bond lengths



Bond angles

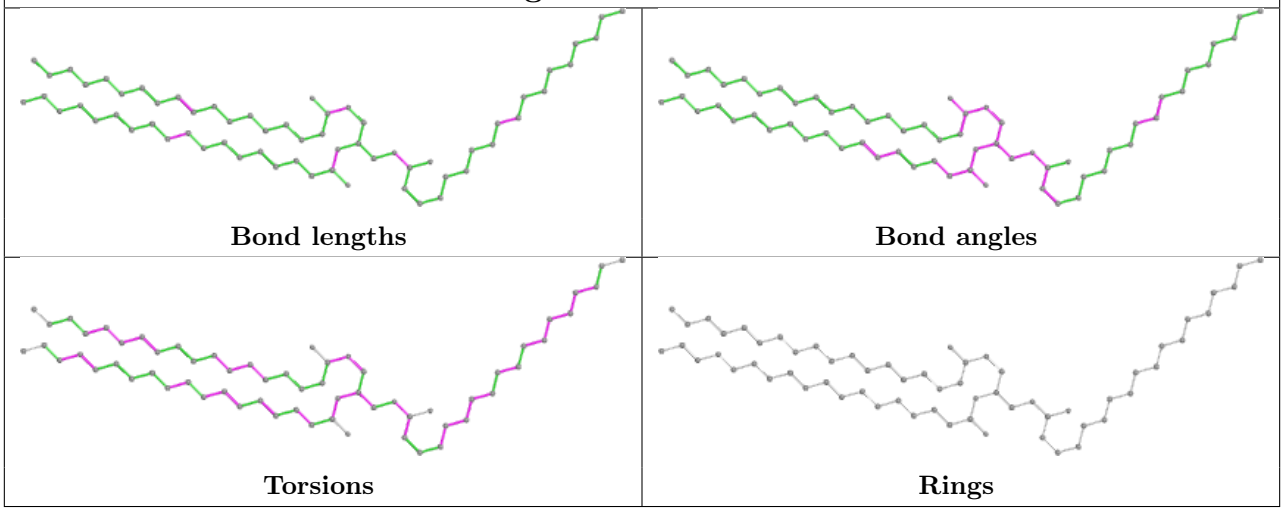


Torsions

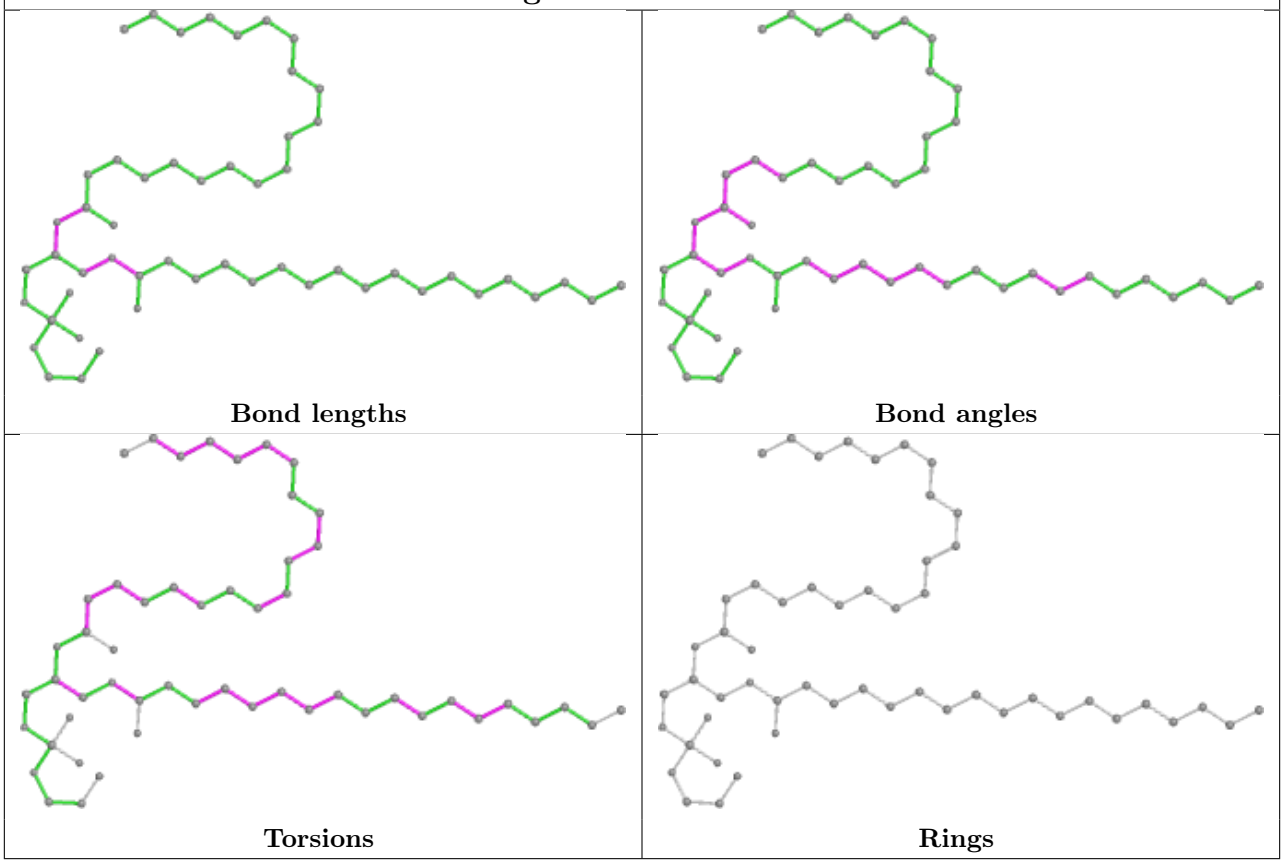


Rings

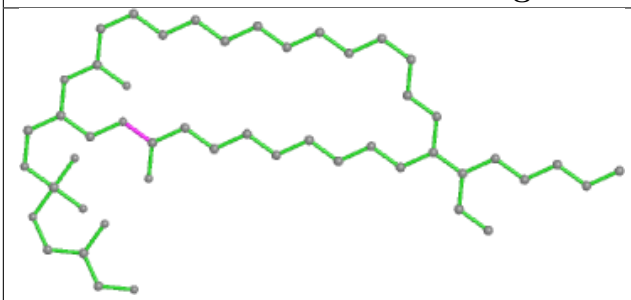
Ligand TGL A 521



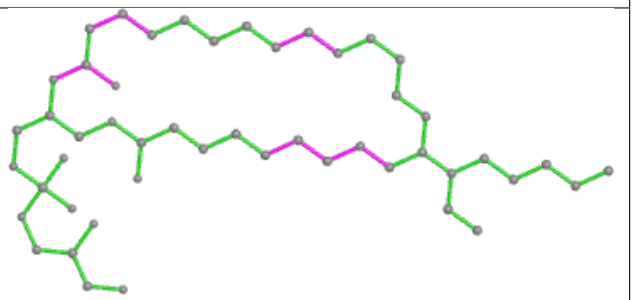
Ligand PEK G 264



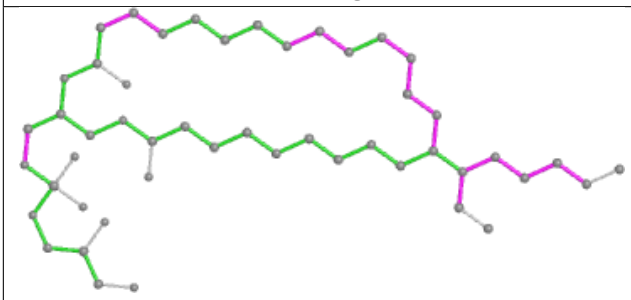
Ligand PGV P 1267



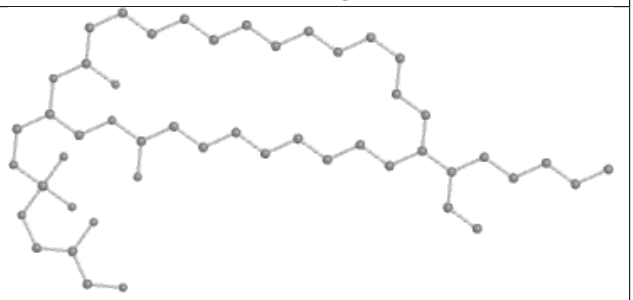
Bond lengths



Bond angles

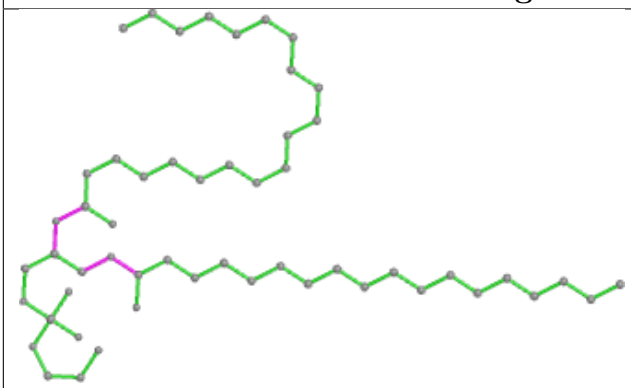


Torsions

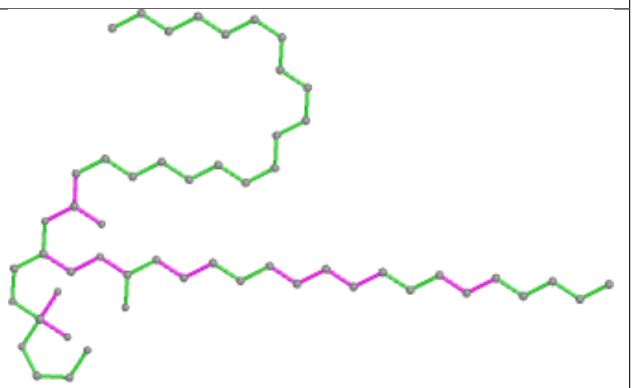


Rings

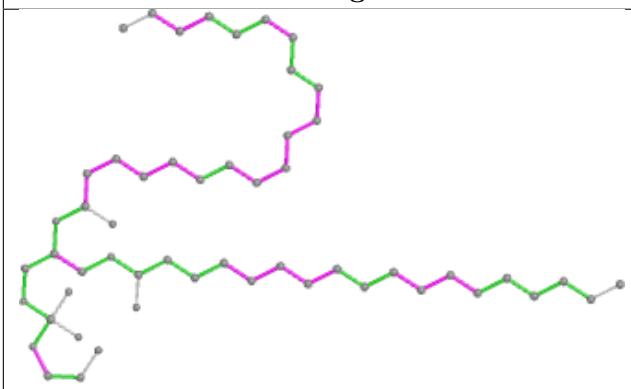
Ligand PEK T 1264



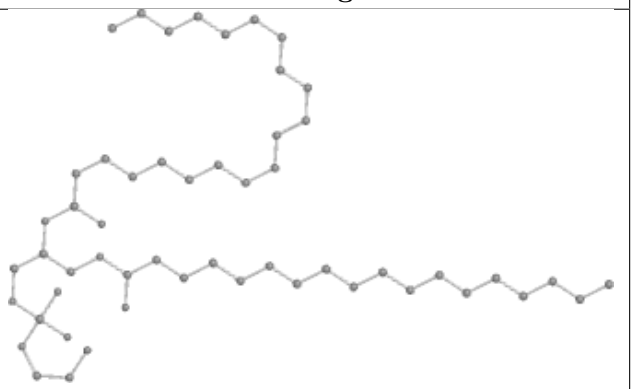
Bond lengths



Bond angles

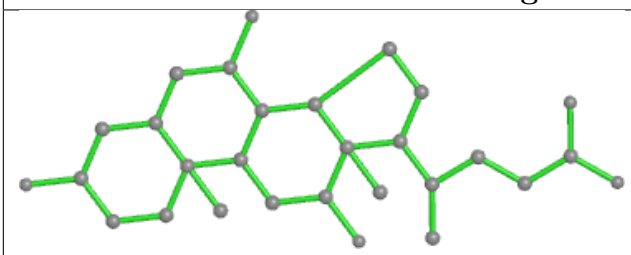


Torsions

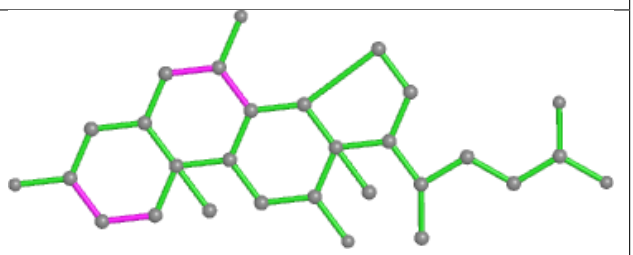


Rings

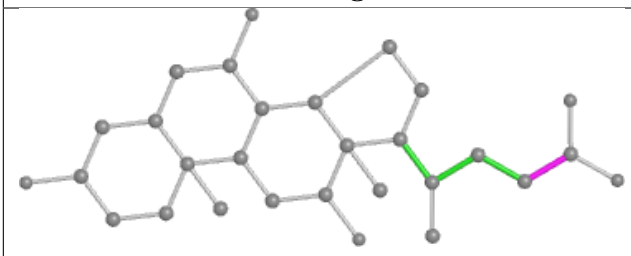
Ligand CHD C 525



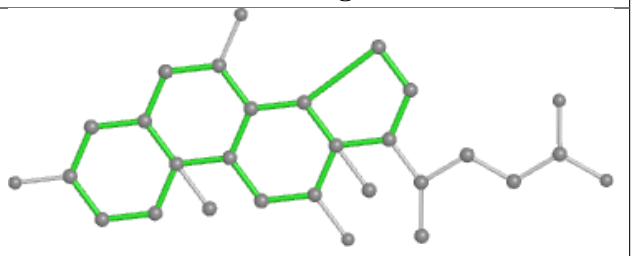
Bond lengths



Bond angles

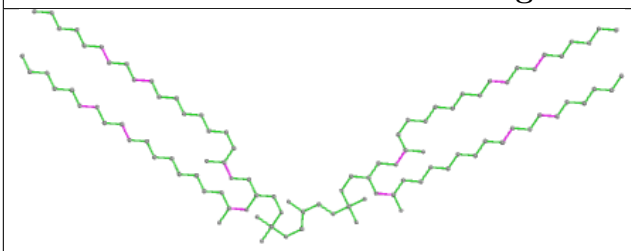


Torsions

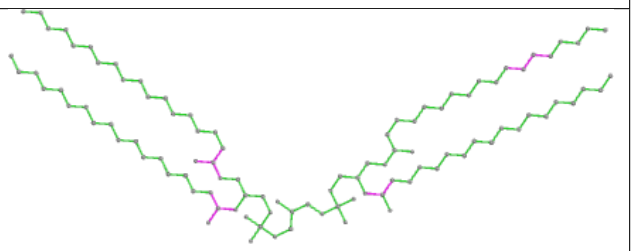


Rings

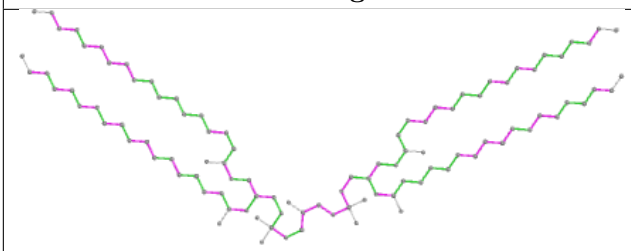
Ligand CDL T 1269



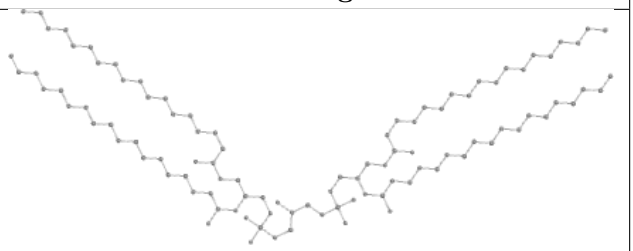
Bond lengths



Bond angles

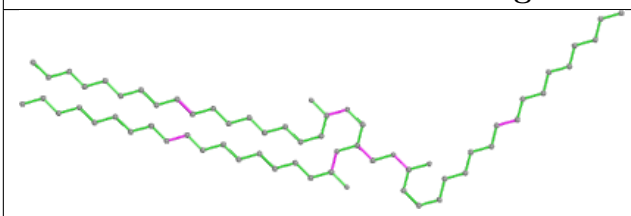


Torsions

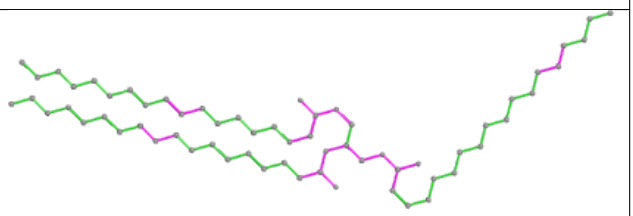


Rings

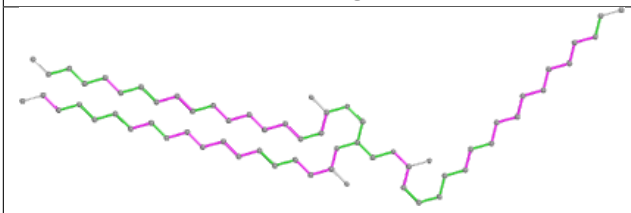
Ligand TGL N 1522



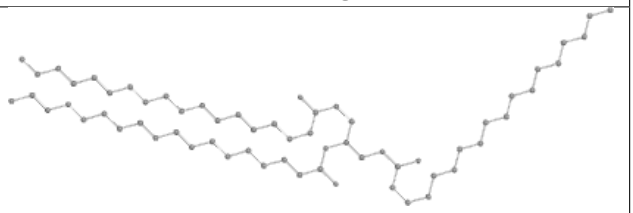
Bond lengths



Bond angles

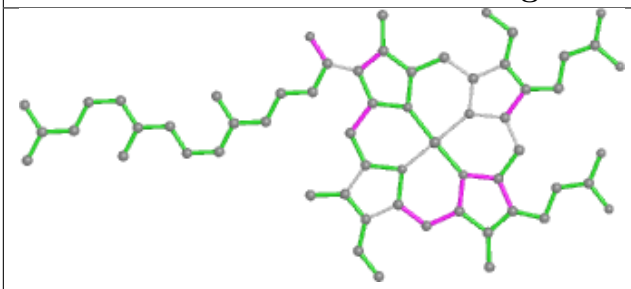


Torsions

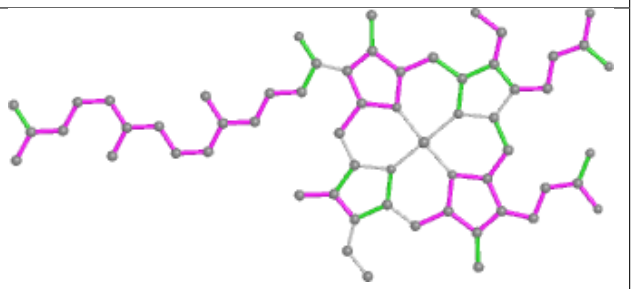


Rings

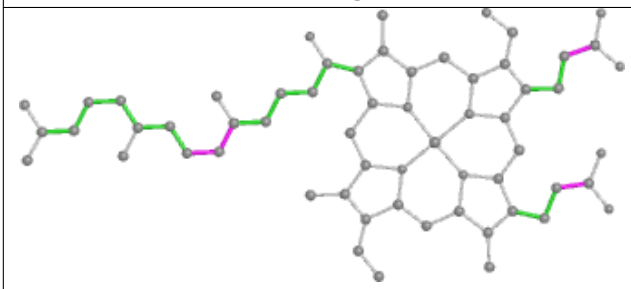
Ligand HEA N 515



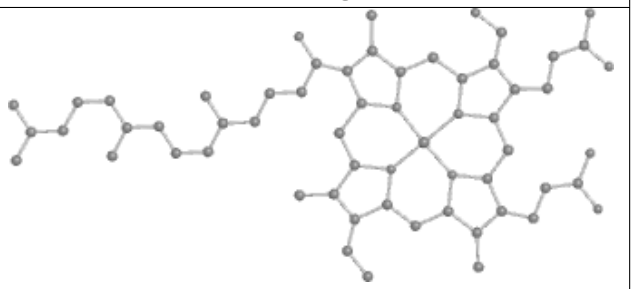
Bond lengths



Bond angles

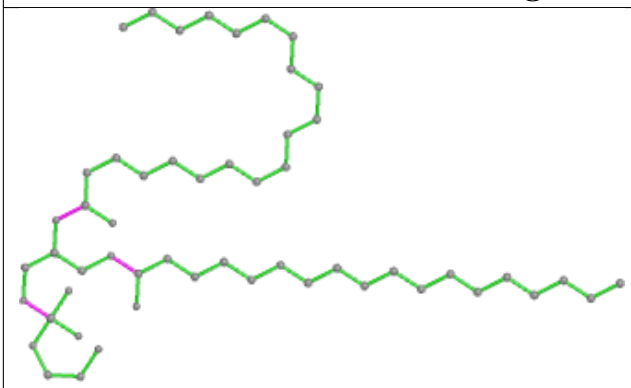


Torsions

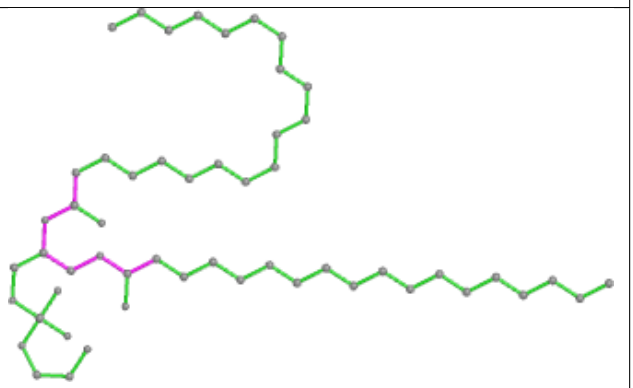


Rings

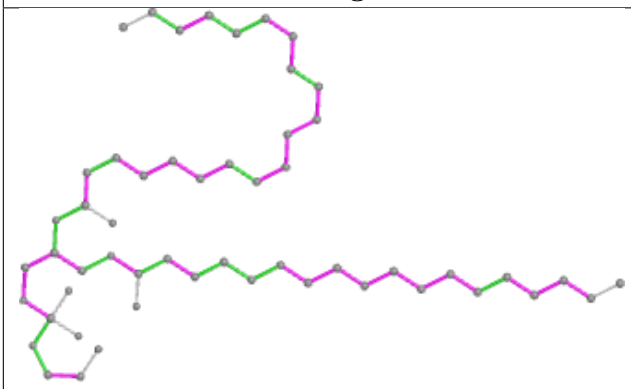
Ligand PEK T 263



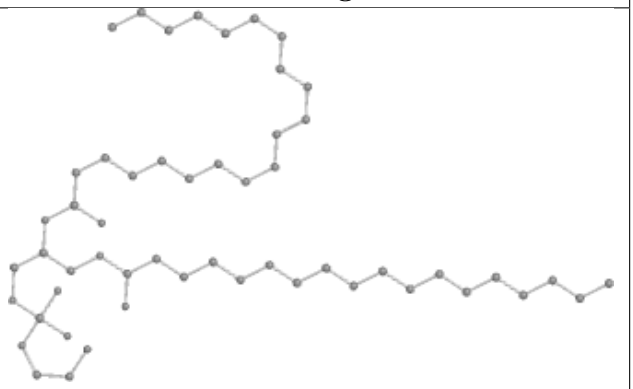
Bond lengths



Bond angles

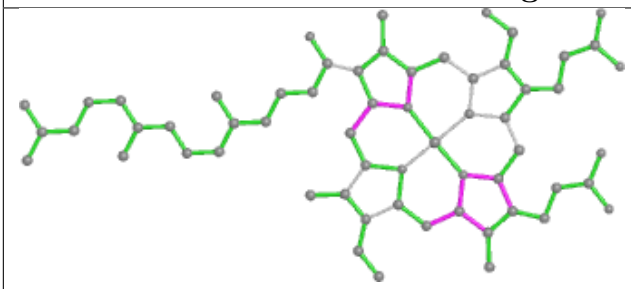


Torsions

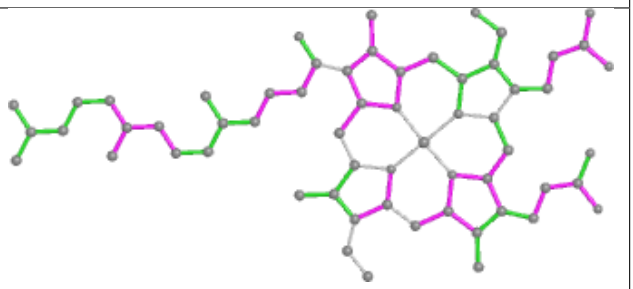


Rings

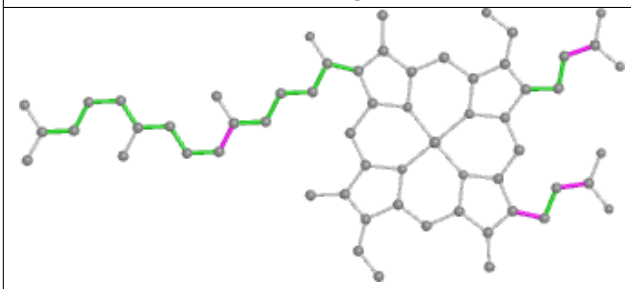
Ligand HEA N 516



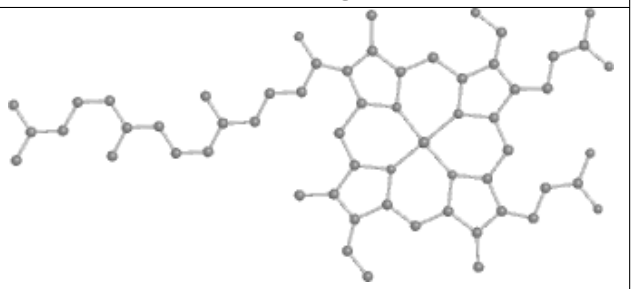
Bond lengths



Bond angles

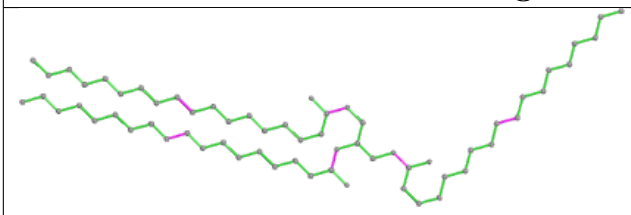


Torsions

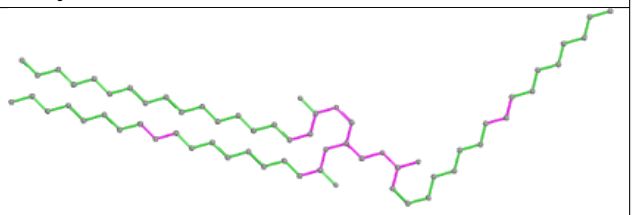


Rings

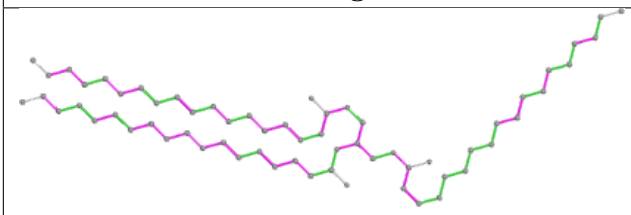
Ligand TGL Q 1523



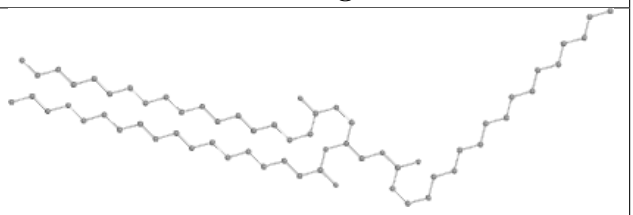
Bond lengths



Bond angles

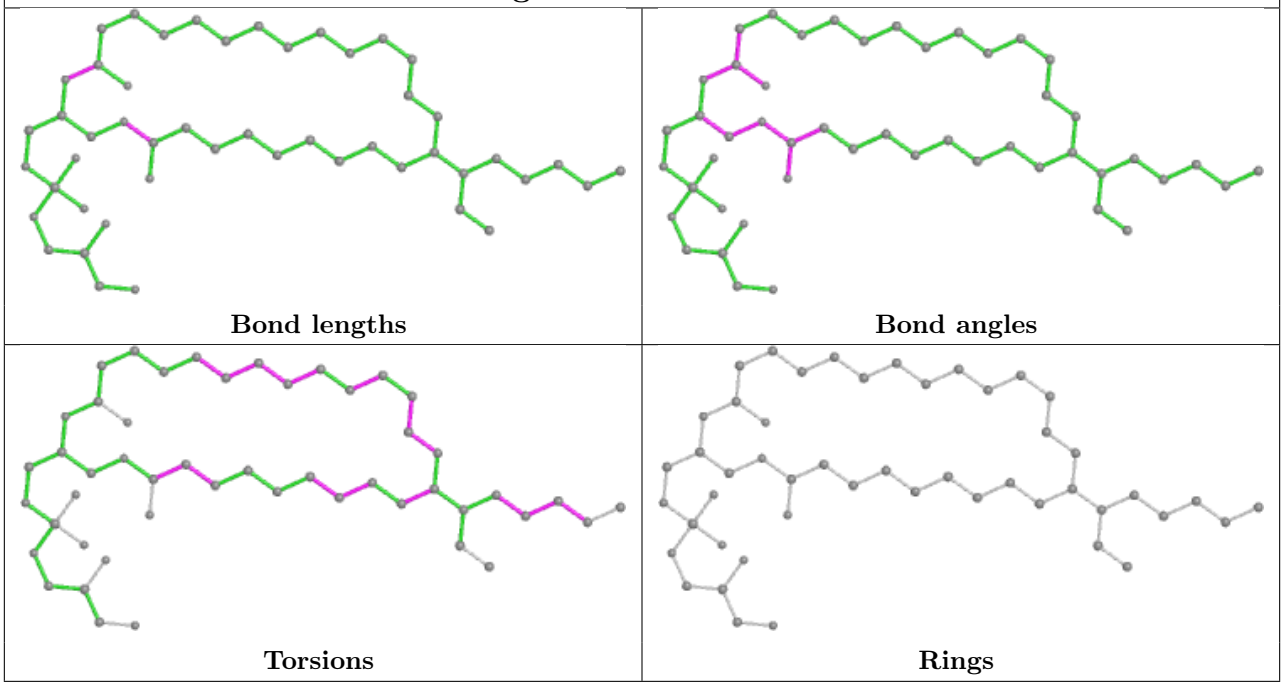


Torsions

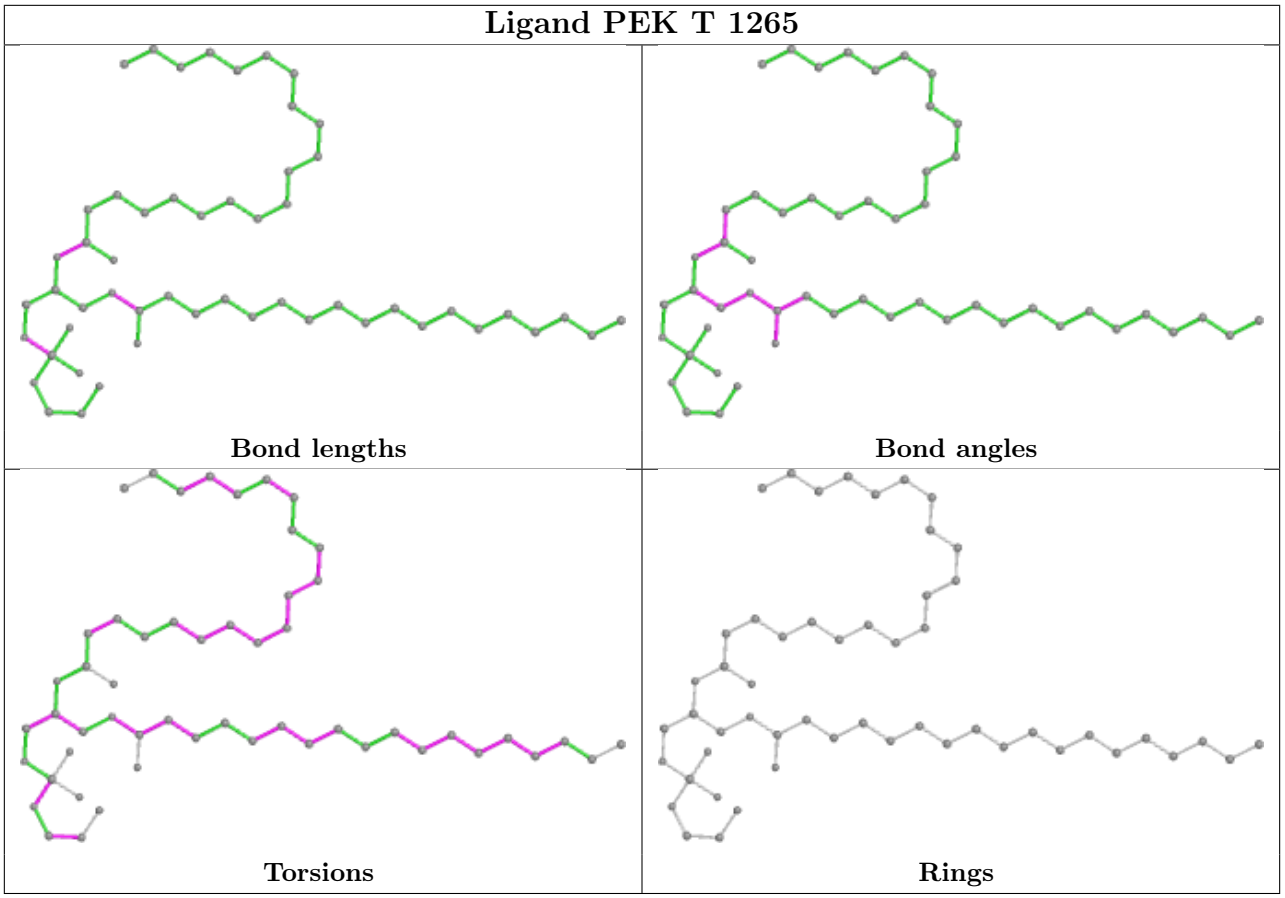


Rings

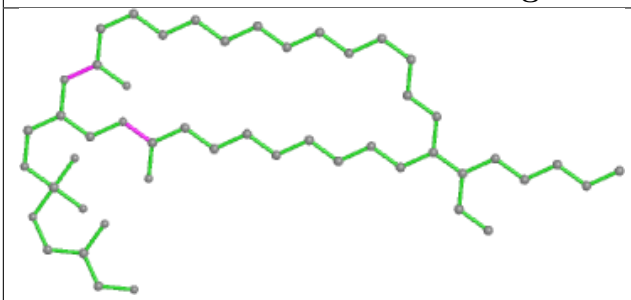
Ligand PGV N 1266



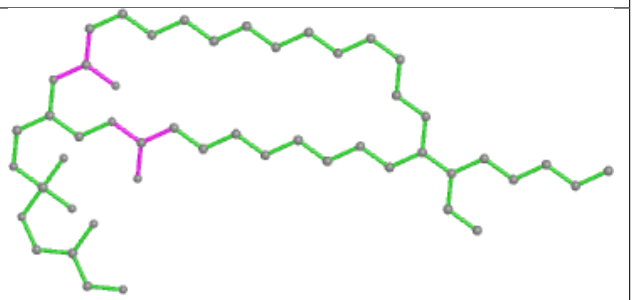
Ligand PEK T 1265



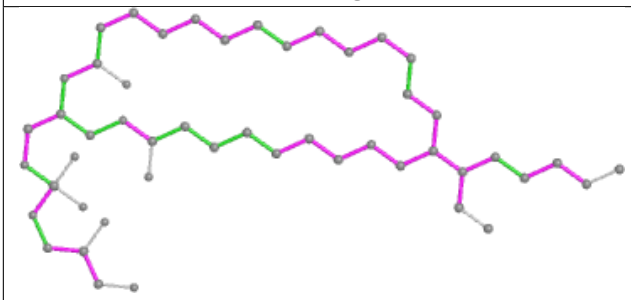
Ligand PGV C 268



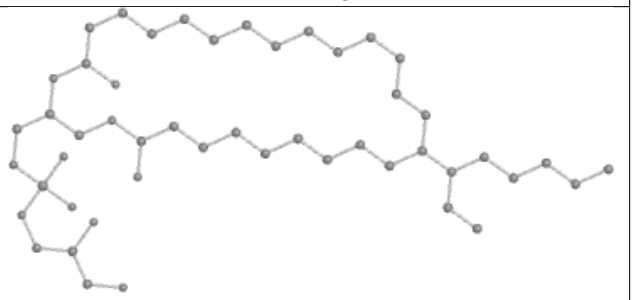
Bond lengths



Bond angles

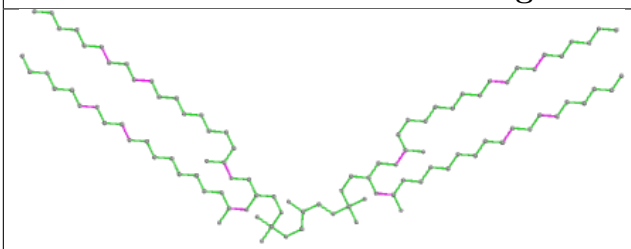


Torsions

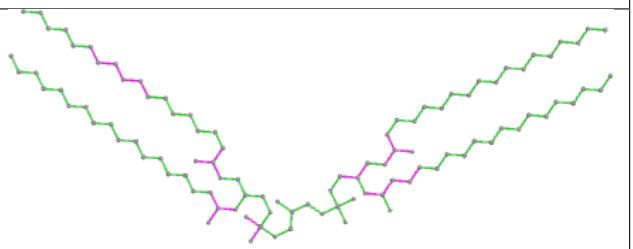


Rings

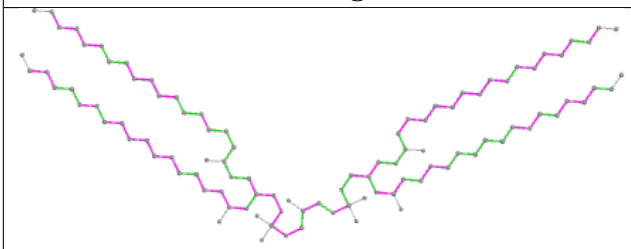
Ligand CDL P 1270



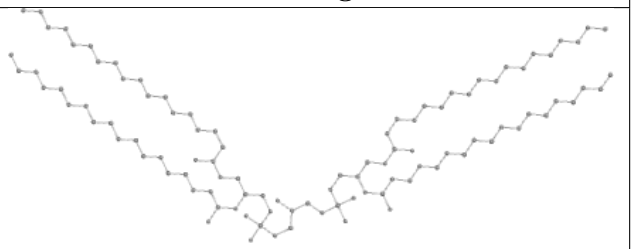
Bond lengths



Bond angles

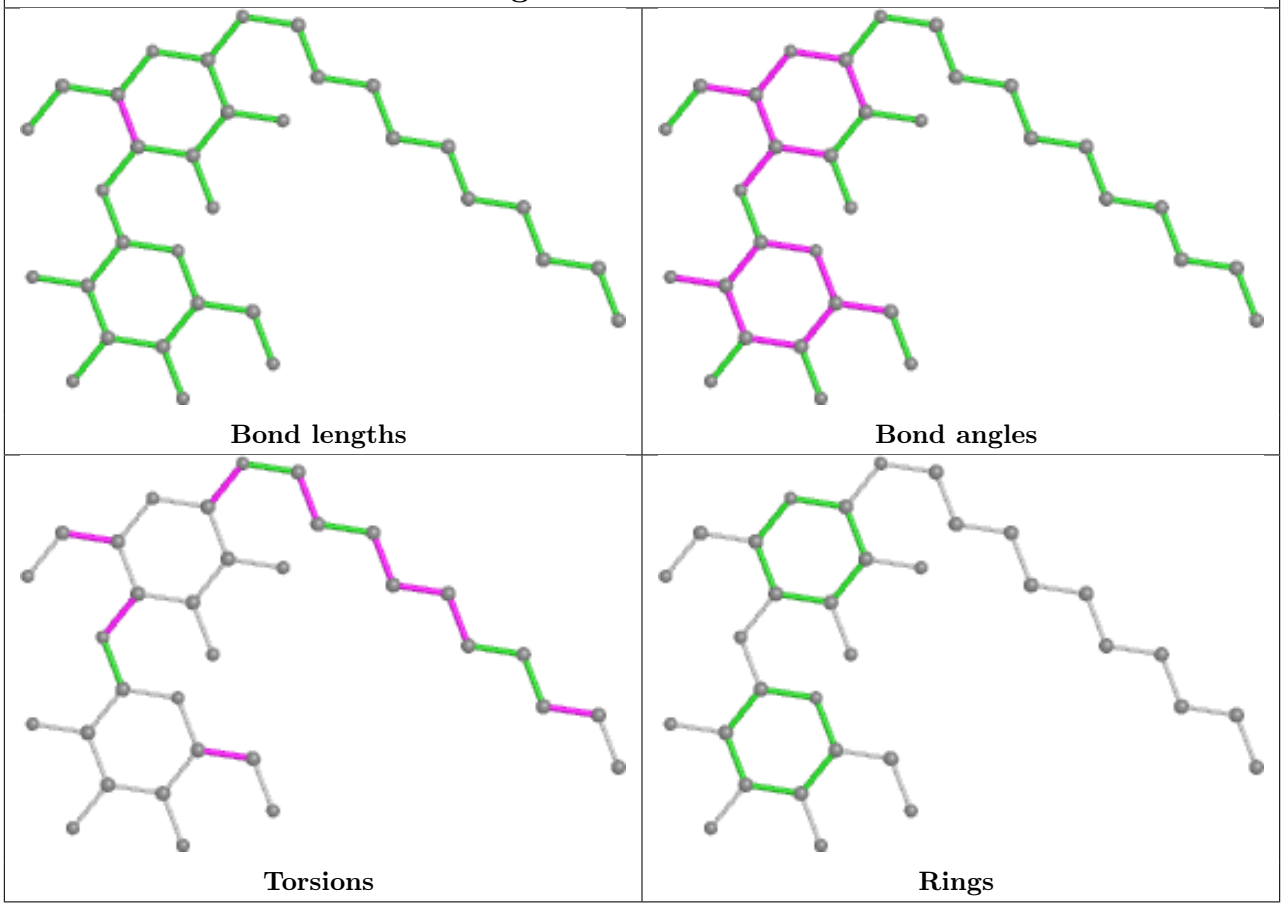


Torsions

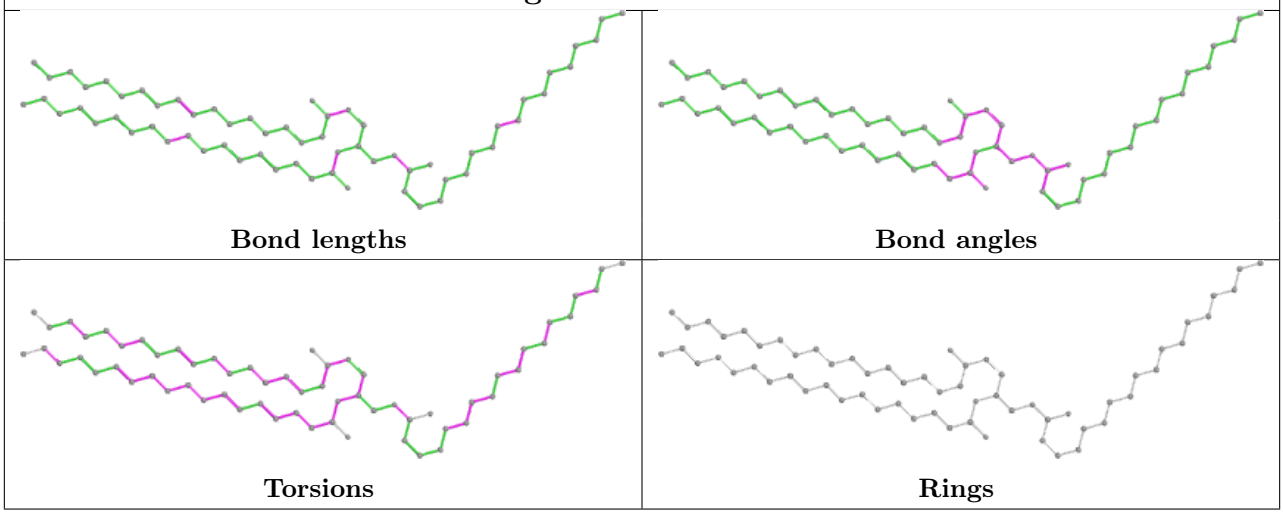


Rings

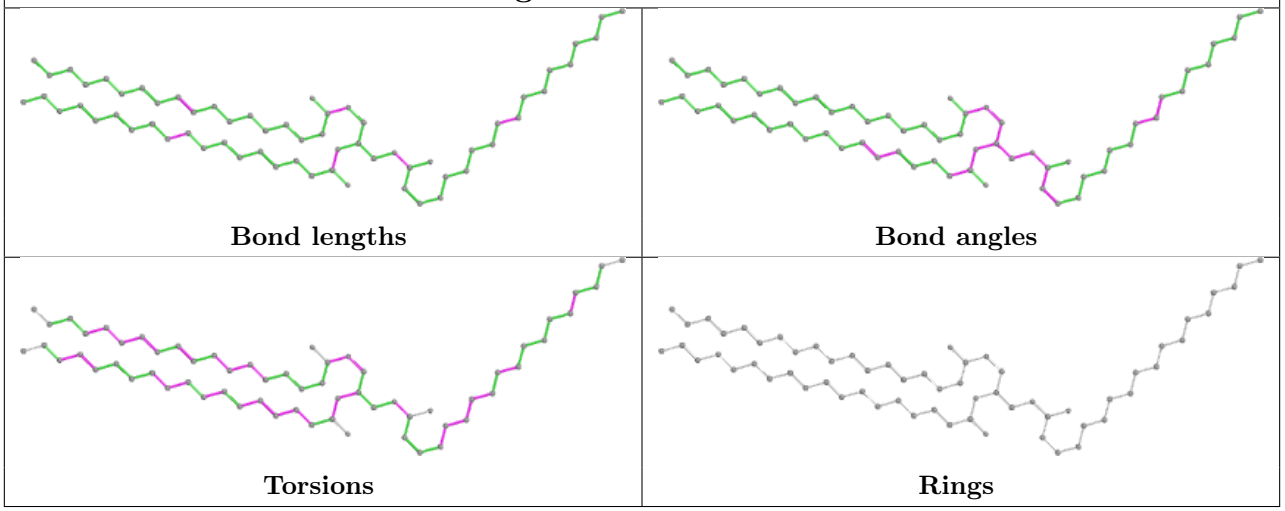
Ligand DMU Z 1526



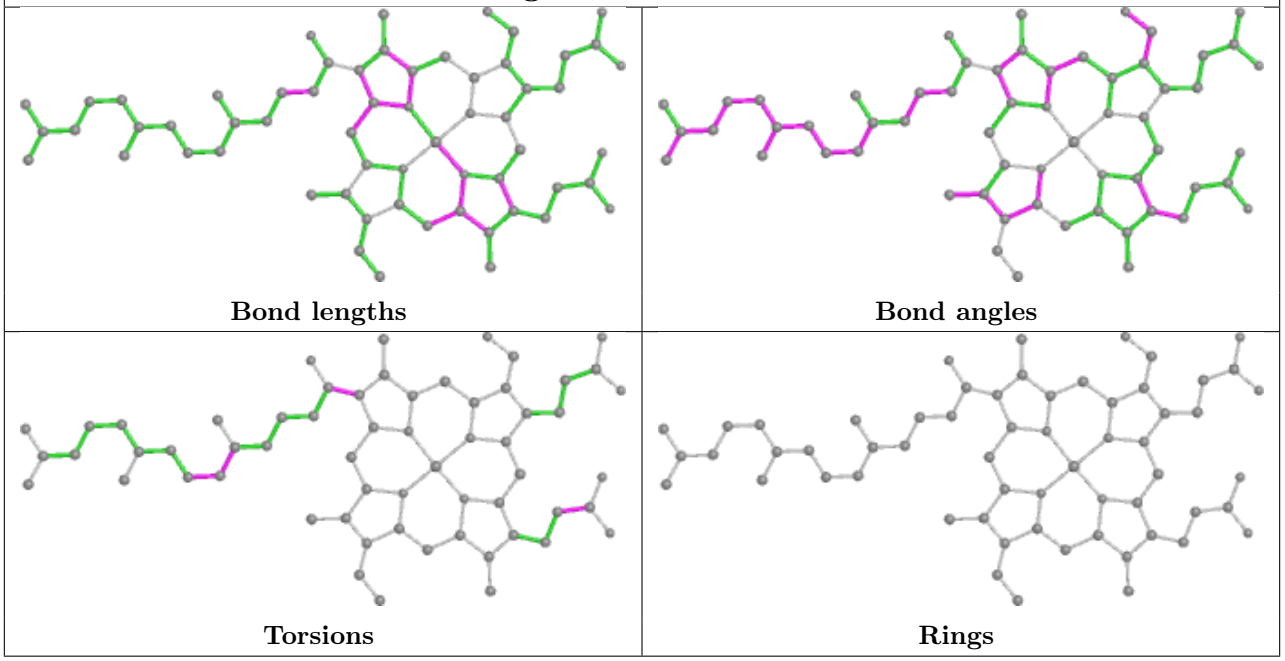
Ligand TGL D 523



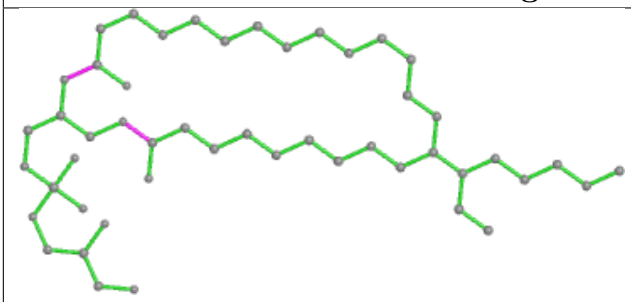
Ligand TGL N 1521



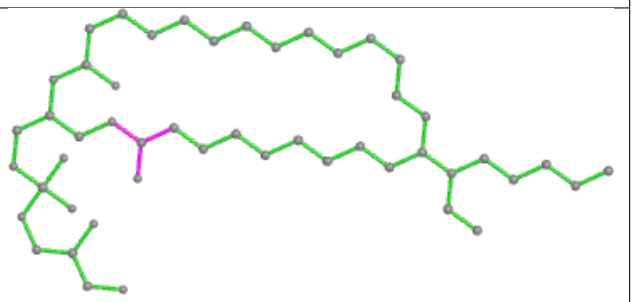
Ligand HEA A 515



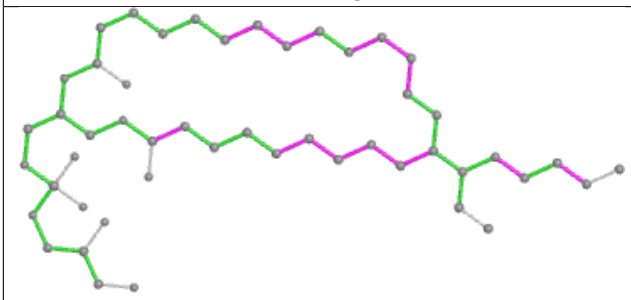
Ligand PGV A 522



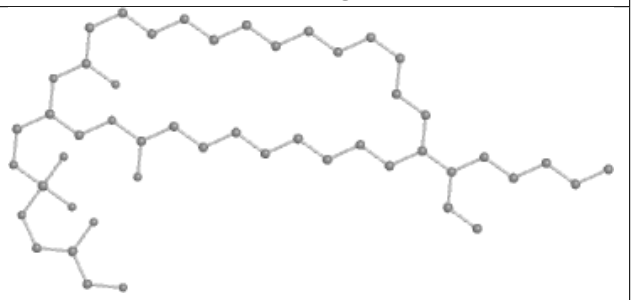
Bond lengths



Bond angles

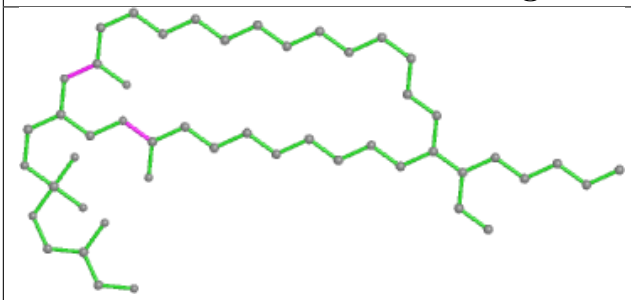


Torsions

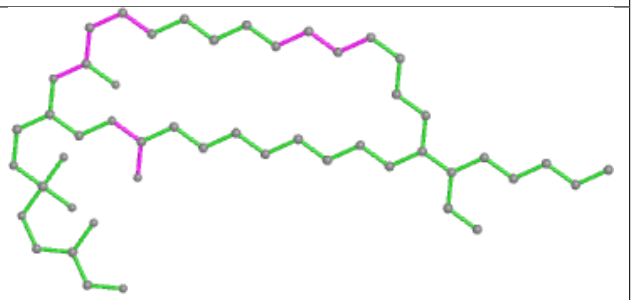


Rings

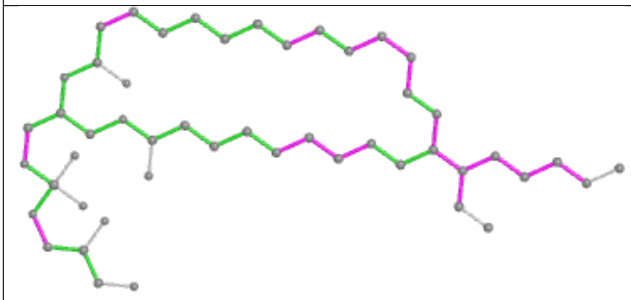
Ligand PGV C 267



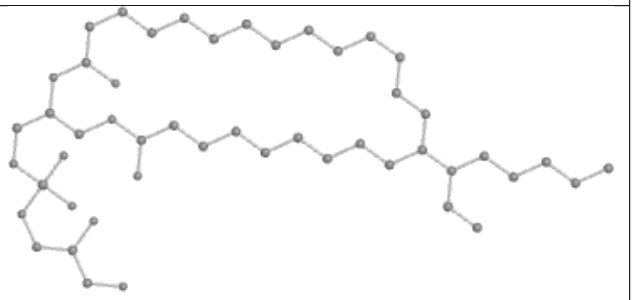
Bond lengths



Bond angles

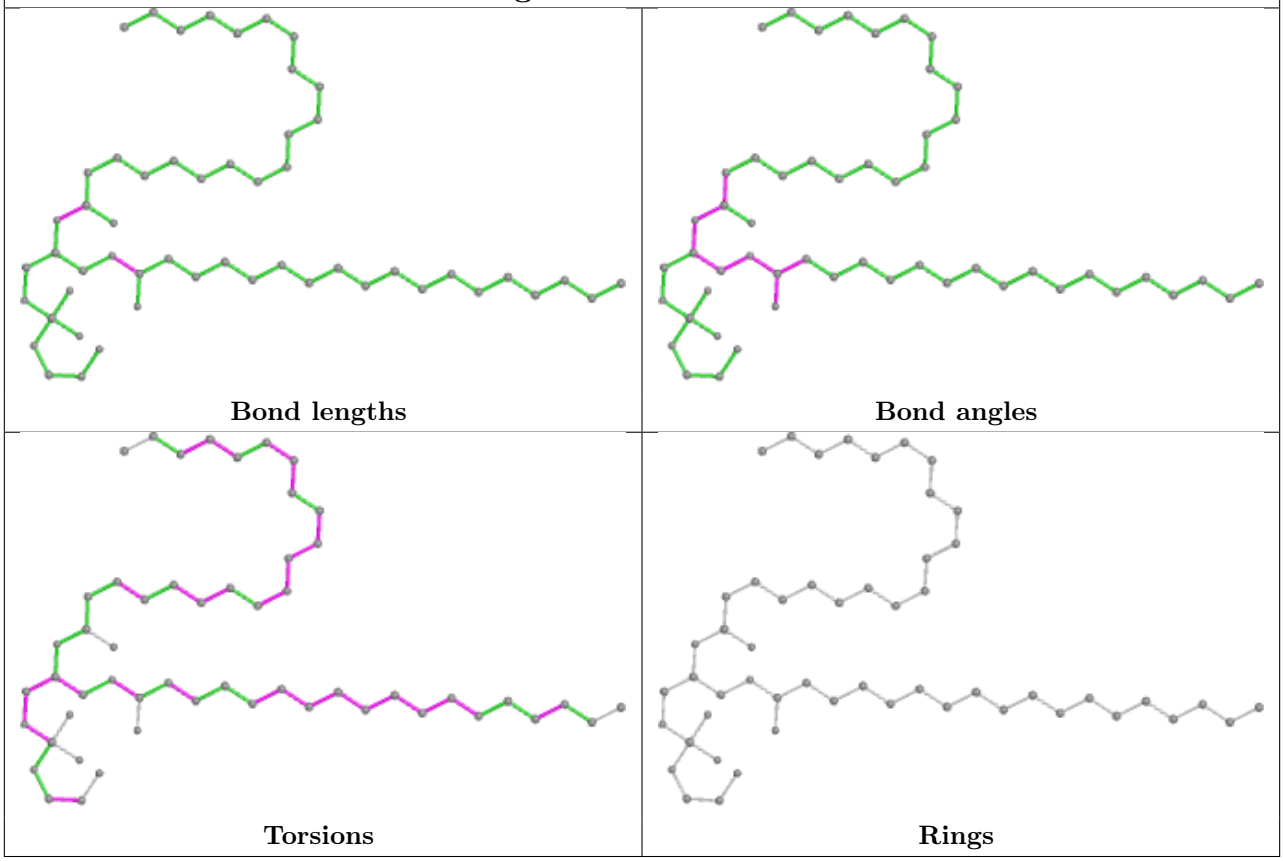


Torsions

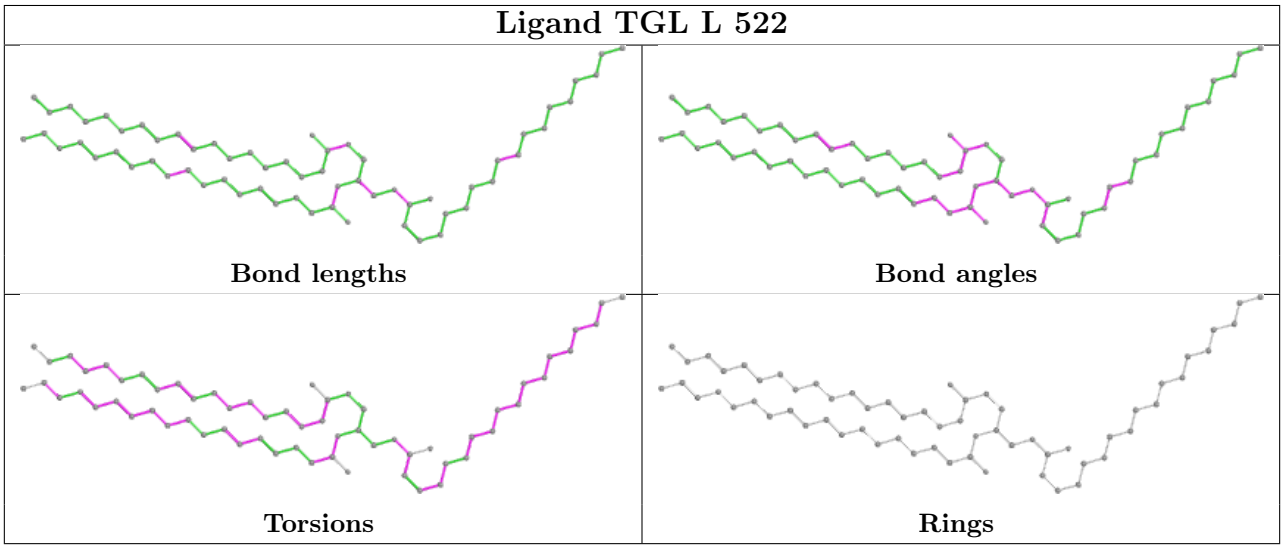


Rings

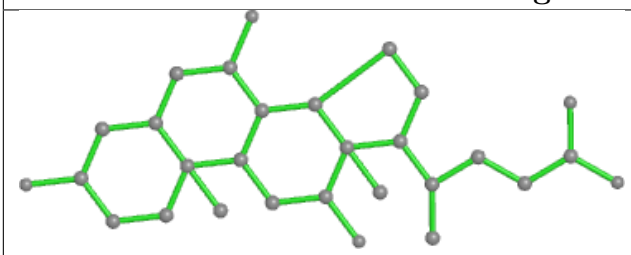
Ligand PEK G 1263



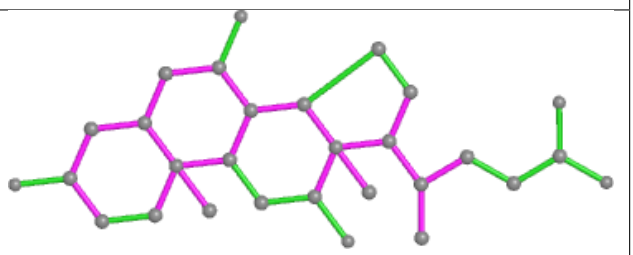
Ligand TGL L 522



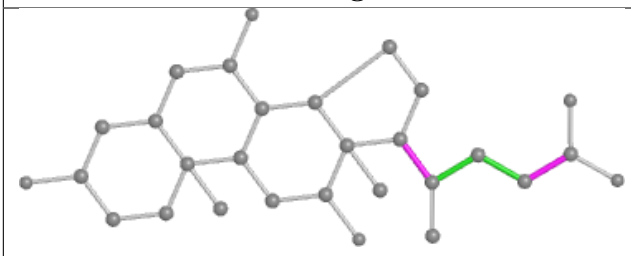
Ligand CHD J 60



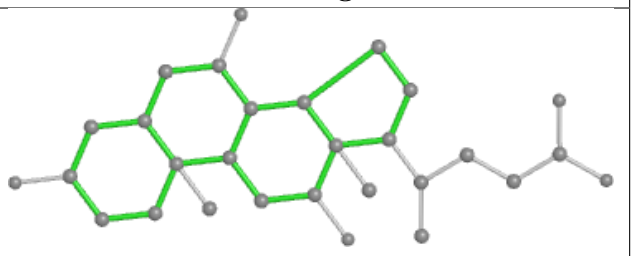
Bond lengths



Bond angles

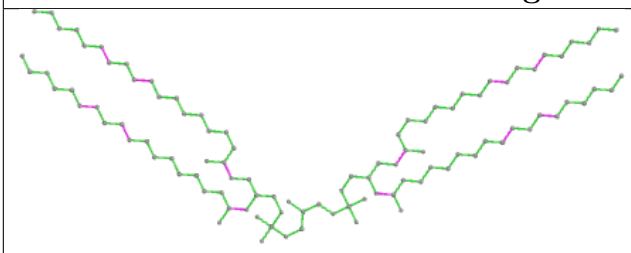


Torsions

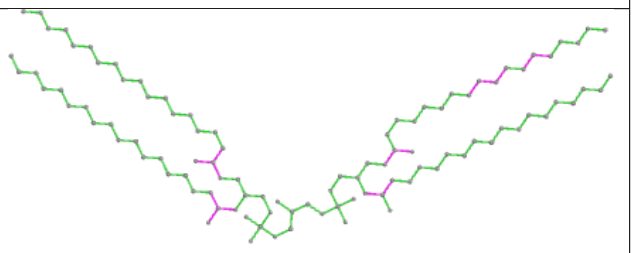


Rings

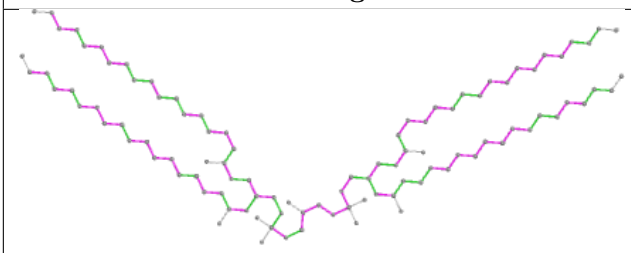
Ligand CDL G 269



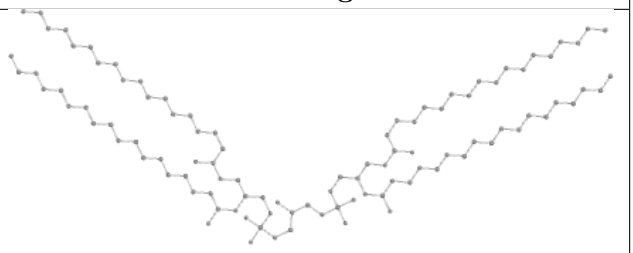
Bond lengths



Bond angles

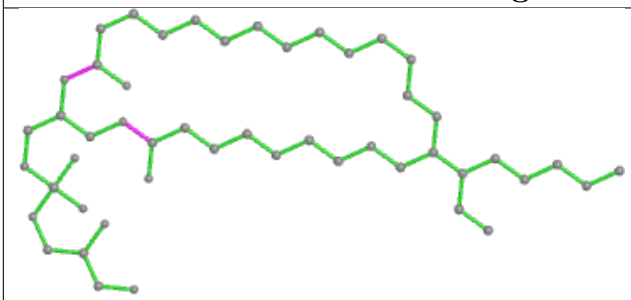


Torsions

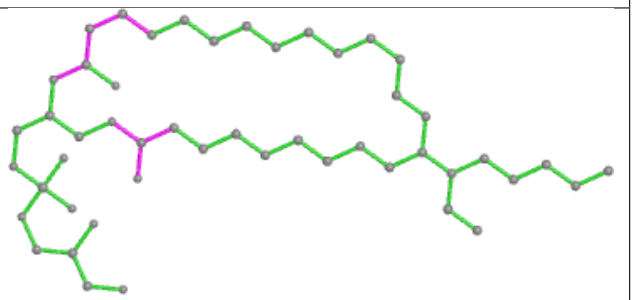


Rings

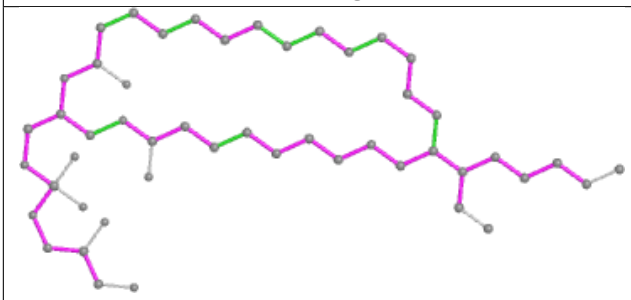
Ligand PGV N 1524



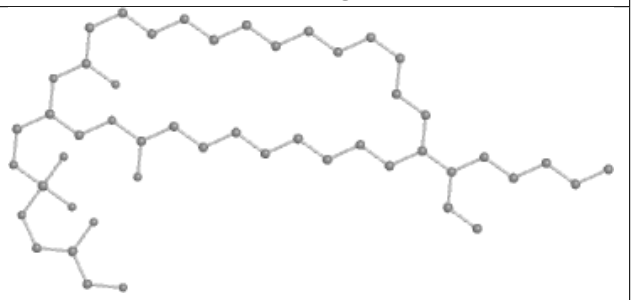
Bond lengths



Bond angles

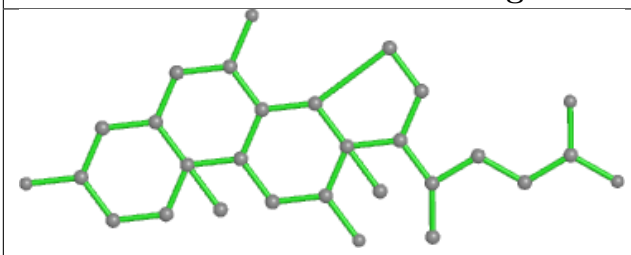


Torsions

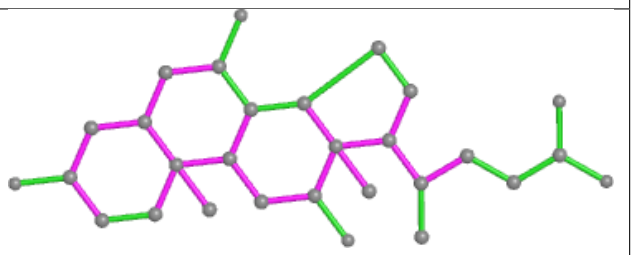


Rings

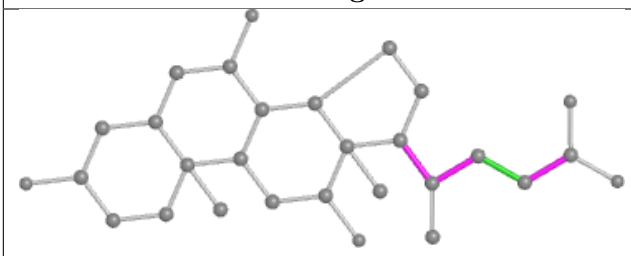
Ligand CHD W 1059



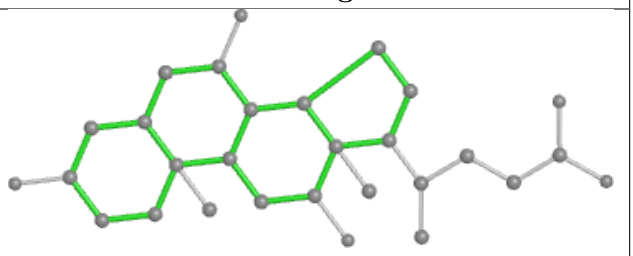
Bond lengths



Bond angles

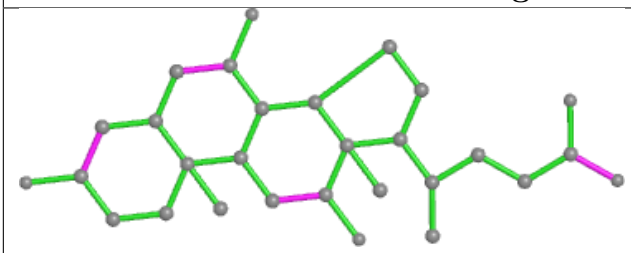


Torsions

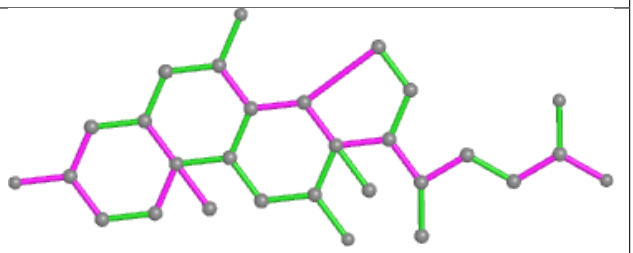


Rings

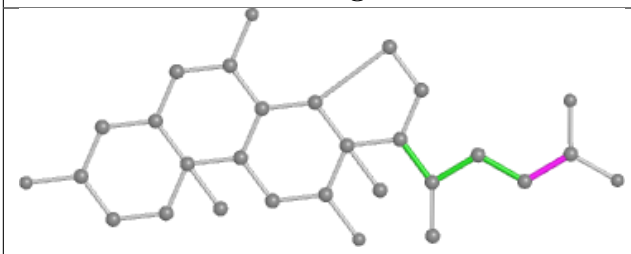
Ligand CHD B 1085



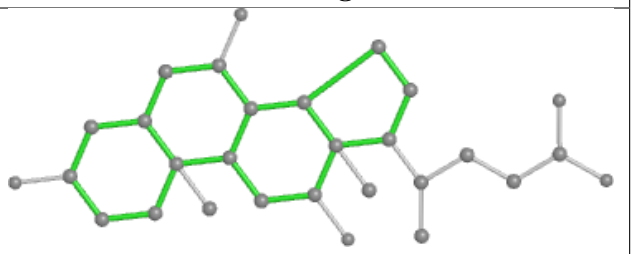
Bond lengths



Bond angles

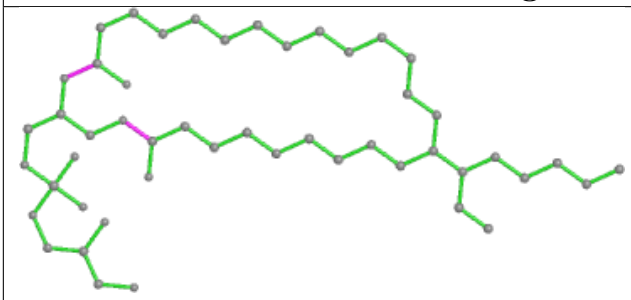


Torsions

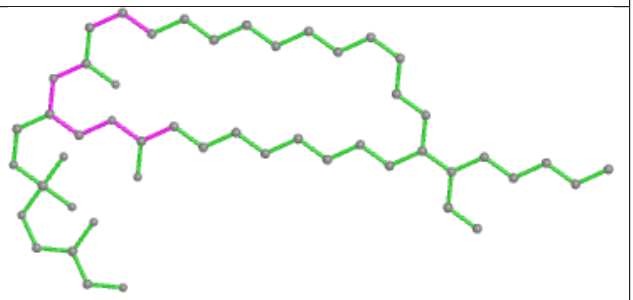


Rings

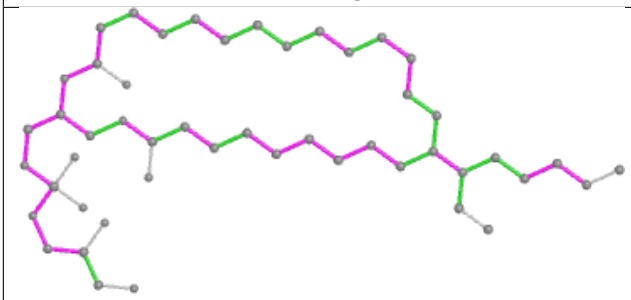
Ligand PGV A 524



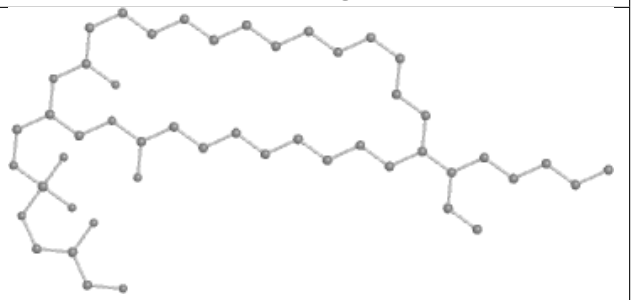
Bond lengths



Bond angles

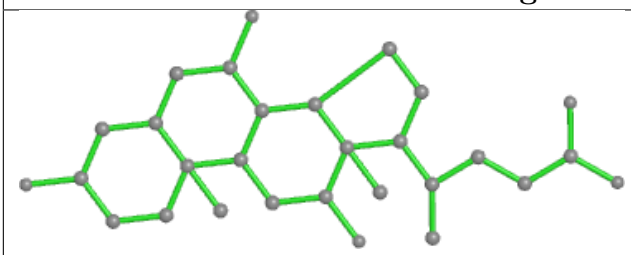


Torsions

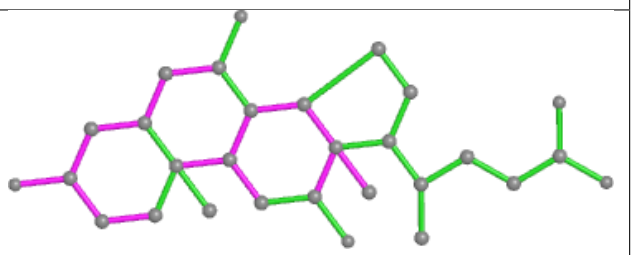


Rings

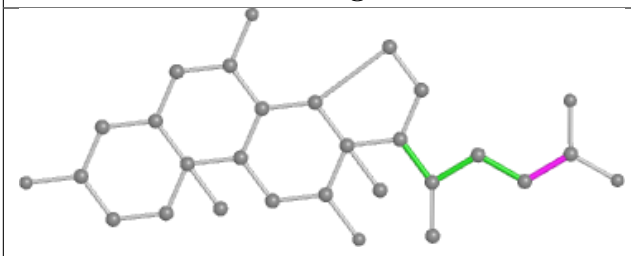
Ligand CHD G 229



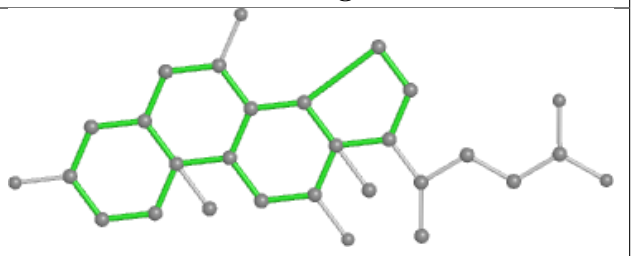
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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%)	-0.01	0 100 100	15, 20, 27, 56	0
1	N	513/514 (99%)	-0.10	1 (0%) 95 96	17, 22, 29, 55	0
2	B	226/227 (99%)	-0.09	1 (0%) 92 95	14, 24, 51, 74	0
2	O	226/227 (99%)	0.01	8 (3%) 44 51	19, 27, 54, 72	0
3	C	259/261 (99%)	-0.01	1 (0%) 92 95	16, 22, 33, 52	0
3	P	259/261 (99%)	-0.05	1 (0%) 92 95	17, 23, 36, 55	0
4	D	144/147 (97%)	-0.32	0 100 100	17, 25, 44, 70	0
4	Q	144/147 (97%)	0.72	14 (9%) 7 10	24, 35, 59, 101	0
5	E	105/109 (96%)	-0.33	2 (1%) 66 73	16, 23, 51, 89	0
5	R	105/109 (96%)	0.13	4 (3%) 40 47	20, 27, 60, 91	0
6	F	98/98 (100%)	0.32	7 (7%) 16 21	18, 28, 75, 110	0
6	S	98/98 (100%)	0.54	8 (8%) 11 15	16, 26, 79, 108	0
7	G	83/85 (97%)	0.77	18 (21%) 0 1	16, 28, 95, 99	0
7	T	83/85 (97%)	0.93	18 (21%) 0 1	18, 29, 96, 100	0
8	H	79/85 (92%)	0.43	10 (12%) 3 5	20, 31, 79, 104	0
8	U	79/85 (92%)	0.54	9 (11%) 5 7	22, 32, 80, 105	0
9	I	72/73 (98%)	0.14	2 (2%) 53 60	19, 34, 58, 67	0
9	V	72/73 (98%)	0.27	6 (8%) 11 15	20, 39, 59, 83	0
10	J	58/59 (98%)	0.18	3 (5%) 27 34	22, 31, 60, 94	0
10	W	58/59 (98%)	0.21	3 (5%) 27 34	21, 32, 65, 99	0
11	K	49/56 (87%)	-0.16	0 100 100	23, 30, 40, 54	0
11	X	49/56 (87%)	0.23	2 (4%) 37 44	28, 36, 51, 66	0
12	L	46/47 (97%)	-0.02	1 (2%) 62 69	19, 26, 50, 74	0
12	Y	46/47 (97%)	0.04	1 (2%) 62 69	21, 28, 54, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	M	43/46 (93%)	-0.04	1 (2%) 60 67	18, 24, 67, 94	0
13	Z	43/46 (93%)	0.28	5 (11%) 4 6	25, 31, 77, 98	0
All	All	3550/3614 (98%)	0.09	126 (3%) 44 51	14, 24, 55, 110	0

The worst 5 of 126 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	S	97	ALA	23.7
4	Q	5	VAL	22.0
4	Q	4	SER	17.7
4	Q	6	VAL	17.7
6	F	97	ALA	10.6

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	G	11	11/12	0.44	0.36	63,71,87,88	0
9	SAC	V	1	9/10	0.48	0.58	88,90,91,91	0
7	TPO	T	11	11/12	0.52	0.36	66,73,89,89	0
9	SAC	I	1	9/10	0.56	0.44	76,79,82,83	0
1	FME	A	1	10/11	0.89	0.17	36,39,58,66	0
1	FME	N	1	10/11	0.94	0.21	37,41,58,60	0
2	FME	B	1	10/11	0.95	0.17	23,24,33,45	0
2	FME	O	1	10/11	0.97	0.20	25,26,33,38	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	PEK	T	263	53/53	0.47	0.42	51,91,109,111	0
22	CHD	W	1059	29/29	0.48	0.42	95,105,107,107	0
22	CHD	J	60	29/29	0.52	0.41	99,107,110,111	0
24	PEK	C	265	53/53	0.53	0.32	43,91,99,100	0
23	UNX	P	262	1/1	0.54	0.28	44,44,44,44	0
24	PEK	T	1265	53/53	0.54	0.34	42,90,101,102	0
25	CDL	T	1269	100/100	0.56	0.36	56,86,108,109	0
24	PEK	G	1263	53/53	0.58	0.36	55,94,110,110	0
19	PGV	P	1268	51/51	0.59	0.34	77,90,102,103	0
25	CDL	G	269	100/100	0.61	0.36	65,85,106,111	0
19	PGV	C	268	51/51	0.61	0.32	63,88,101,102	0
18	TGL	Q	1523	63/63	0.64	0.28	49,74,91,92	0
23	UNX	C	262	1/1	0.64	0.42	43,43,43,43	0
18	TGL	N	1522	63/63	0.64	0.32	47,71,84,86	0
21	PSC	O	1229	52/52	0.65	0.35	40,85,110,113	0
21	PSC	B	229	52/52	0.67	0.33	48,92,113,115	0
19	PGV	N	1524	51/51	0.70	0.34	43,69,102,102	0
25	CDL	P	1270	100/100	0.73	0.36	45,85,107,109	0
19	PGV	A	524	51/51	0.74	0.30	34,69,94,96	0
22	CHD	P	1271	29/29	0.74	0.24	82,90,91,91	0
18	TGL	L	522	63/63	0.74	0.30	38,62,80,83	0
25	CDL	C	270	100/100	0.75	0.36	42,84,106,108	0
18	TGL	D	523	63/63	0.75	0.26	50,69,91,91	0
22	CHD	C	271	29/29	0.76	0.26	79,89,90,91	0
18	TGL	N	1521	63/63	0.79	0.27	48,73,88,91	0
16	MG	N	518	1/1	0.81	0.13	23,23,23,23	0
18	TGL	A	521	63/63	0.82	0.25	50,70,88,92	0
27	DMU	Z	1526	33/33	0.92	0.18	37,45,57,57	0
27	DMU	M	526	33/33	0.93	0.13	34,40,51,52	0
16	MG	A	518	1/1	0.93	0.10	21,21,21,21	0
24	PEK	T	1264	53/53	0.94	0.16	19,44,71,73	0
14	HEA	N	515	60/60	0.95	0.19	20,33,50,53	0
24	PEK	G	264	53/53	0.95	0.18	17,41,71,72	0
22	CHD	P	1525	29/29	0.95	0.11	24,28,31,33	0
22	CHD	C	525	29/29	0.96	0.13	24,29,32,33	0
19	PGV	C	267	51/51	0.96	0.18	17,29,64,69	0
20	CUA	O	228	2/2	0.97	0.12	22,22,22,22	0
17	NA	N	519	1/1	0.97	0.07	24,24,24,24	0
19	PGV	N	1266	51/51	0.97	0.17	19,38,57,59	0
22	CHD	B	1085	29/29	0.97	0.11	12,15,23,33	0
19	PGV	P	1267	51/51	0.97	0.18	19,29,65,69	0
19	PGV	A	522	51/51	0.97	0.17	19,32,54,56	0

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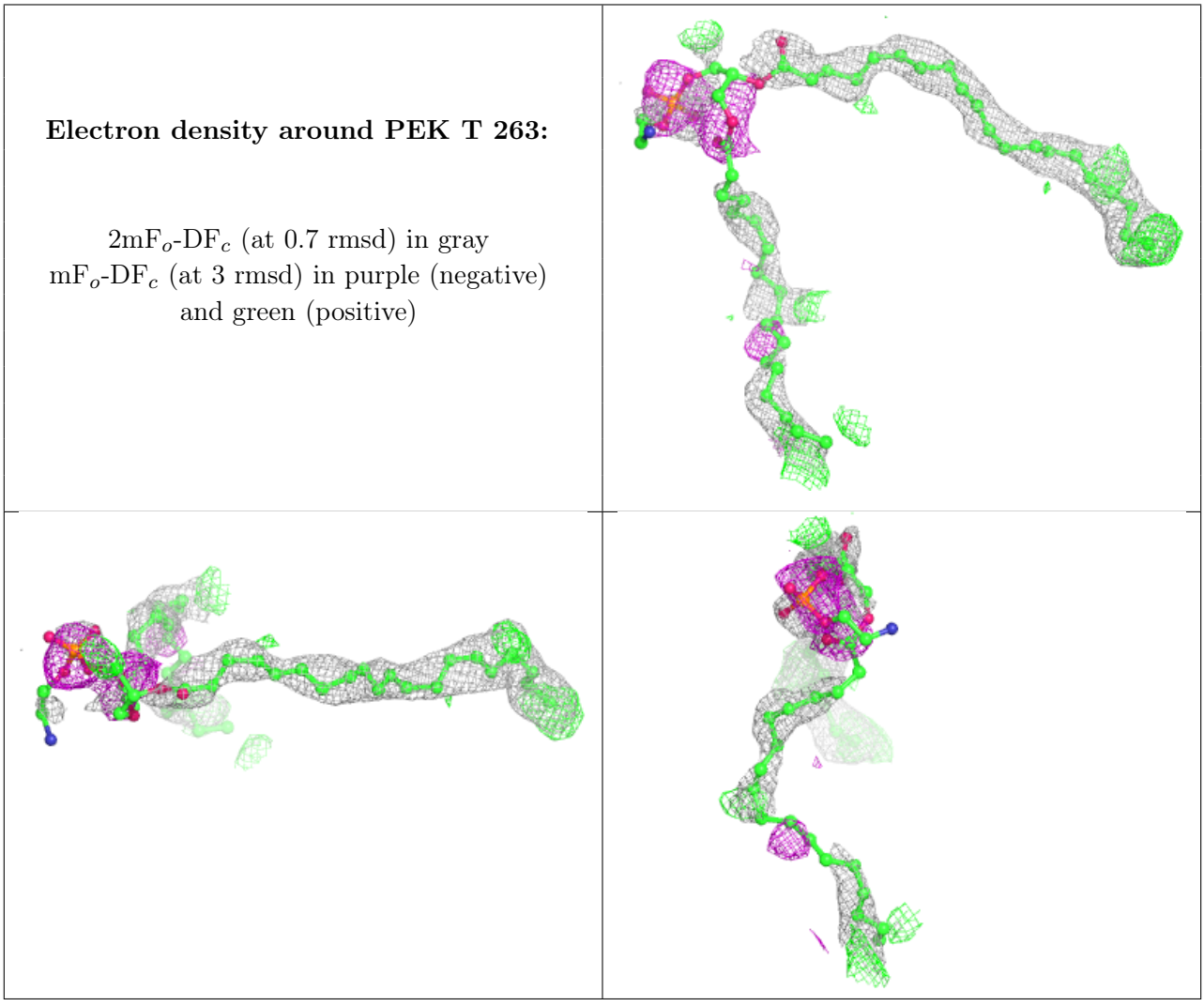
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
14	HEA	N	516	60/60	0.98	0.14	15,19,26,30	0
22	CHD	G	229	29/29	0.98	0.10	10,16,19,25	0
14	HEA	A	516	60/60	0.98	0.14	11,18,24,26	0
14	HEA	A	515	60/60	0.98	0.16	14,19,41,50	0
17	NA	A	519	1/1	0.98	0.08	22,22,22,22	0
15	CU	N	517	1/1	0.99	0.20	23,23,23,23	0
26	ZN	F	99	1/1	0.99	0.15	23,23,23,23	0
26	ZN	S	99	1/1	0.99	0.14	23,23,23,23	0
20	CUA	B	228	2/2	0.99	0.14	18,18,18,18	0
15	CU	A	517	1/1	0.99	0.19	20,20,20,20	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.

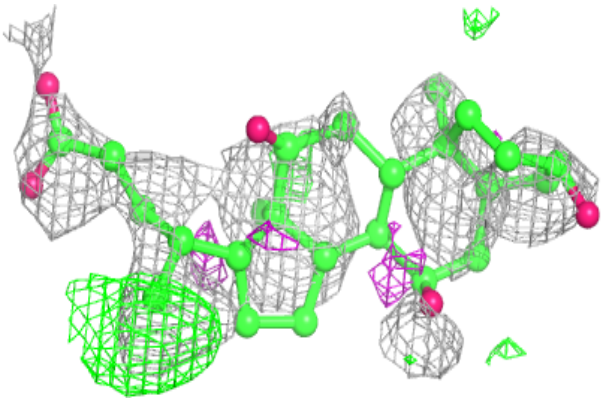
Electron density around PEK T 263:

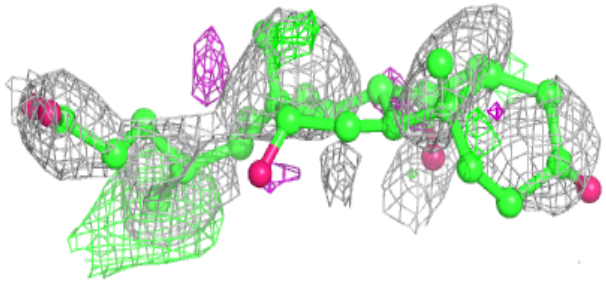
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

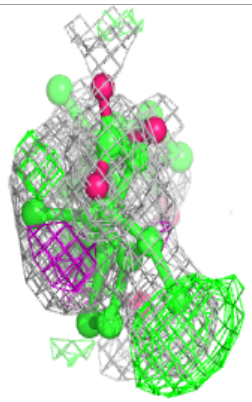


Electron density around CHD W 1059:

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

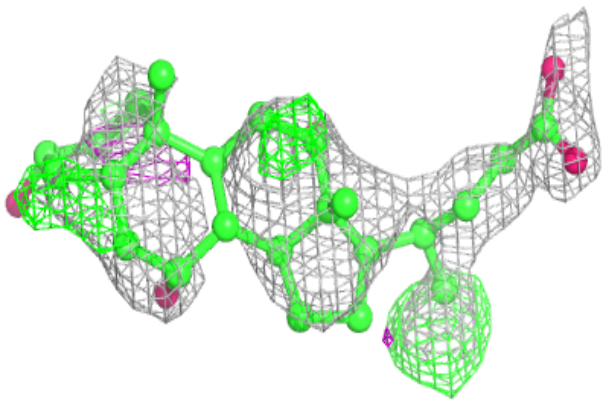


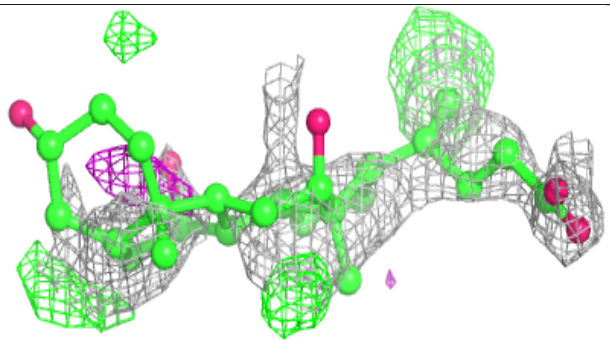


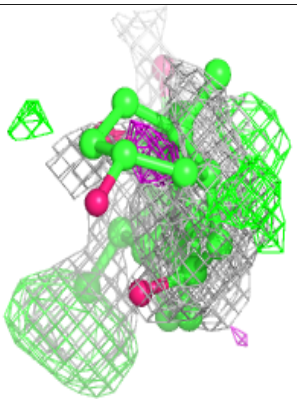


Electron density around CHD J 60:

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

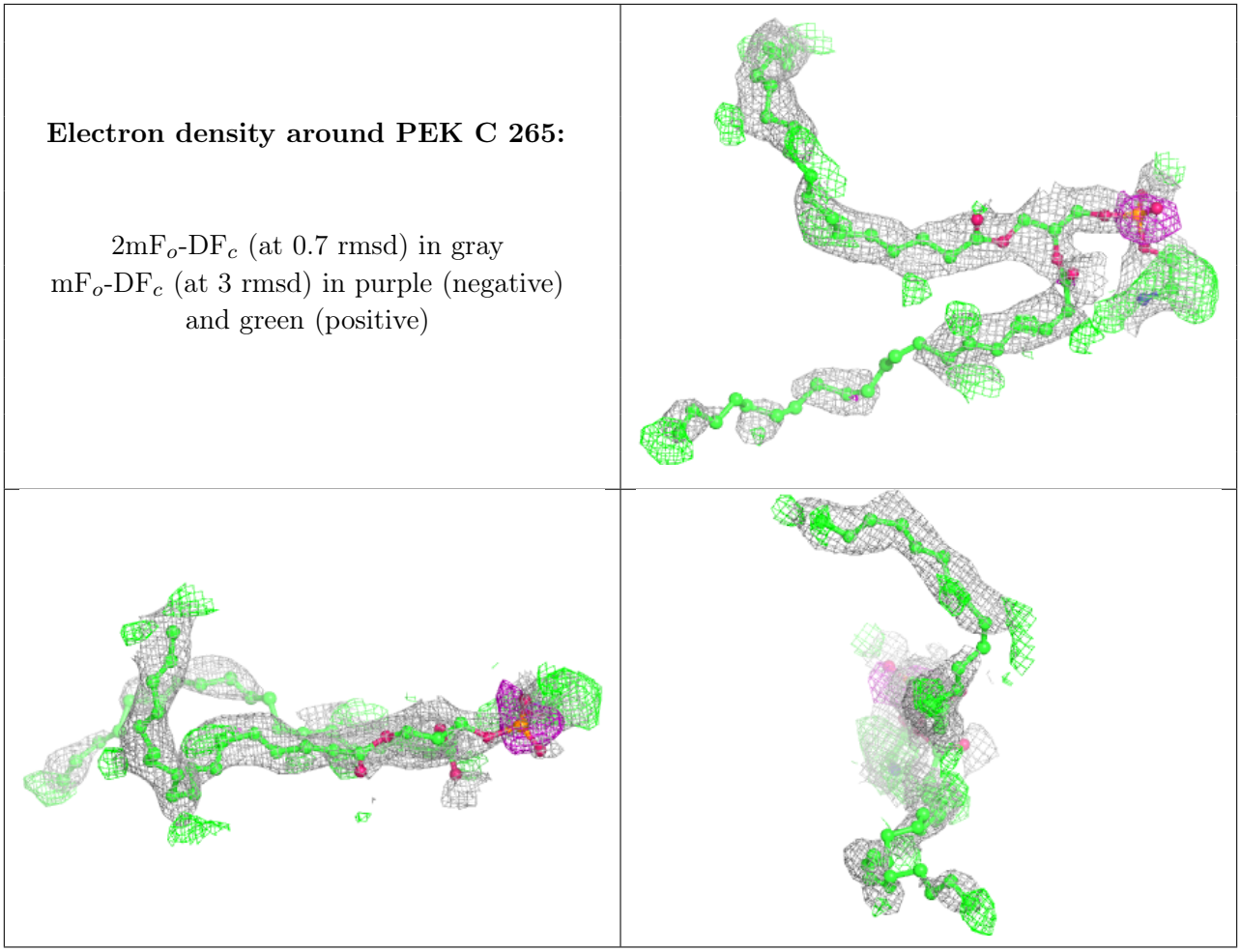






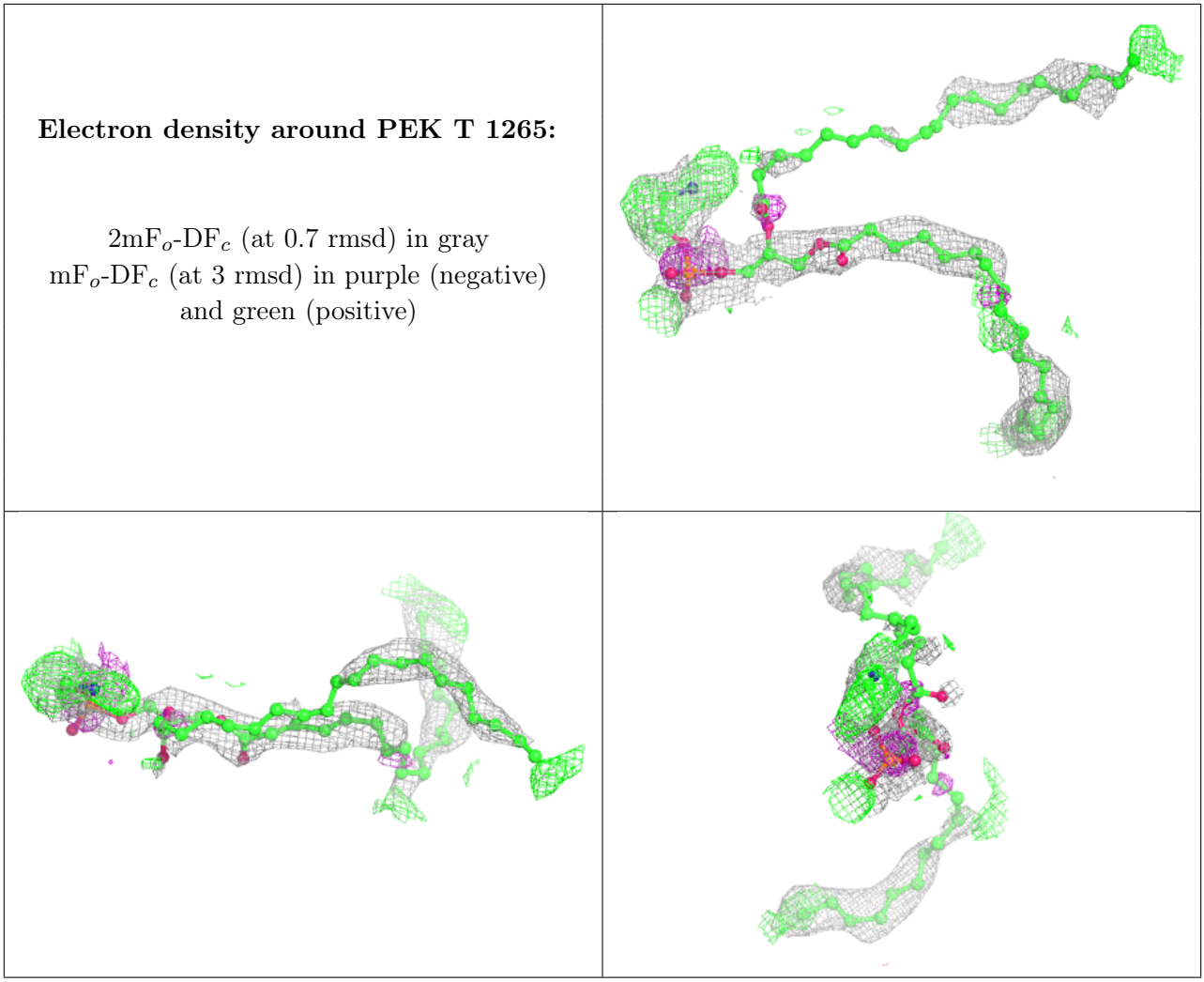
Electron density around PEK C 265:

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



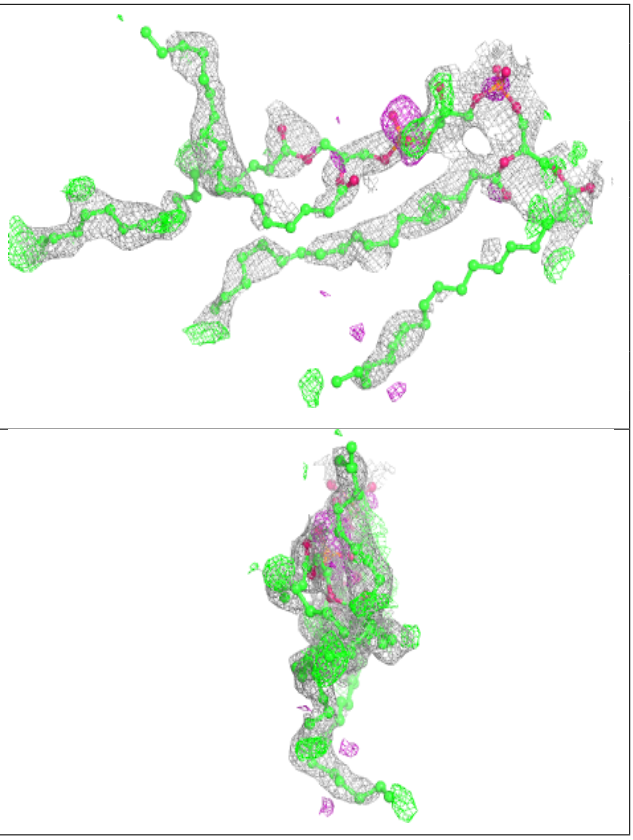
Electron density around PEK T 1265:

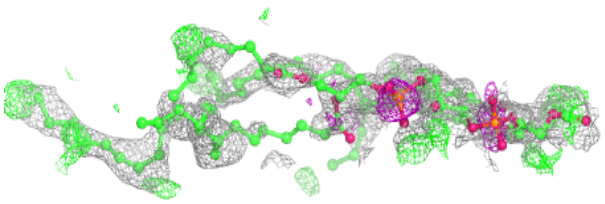
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around CDL T 1269:

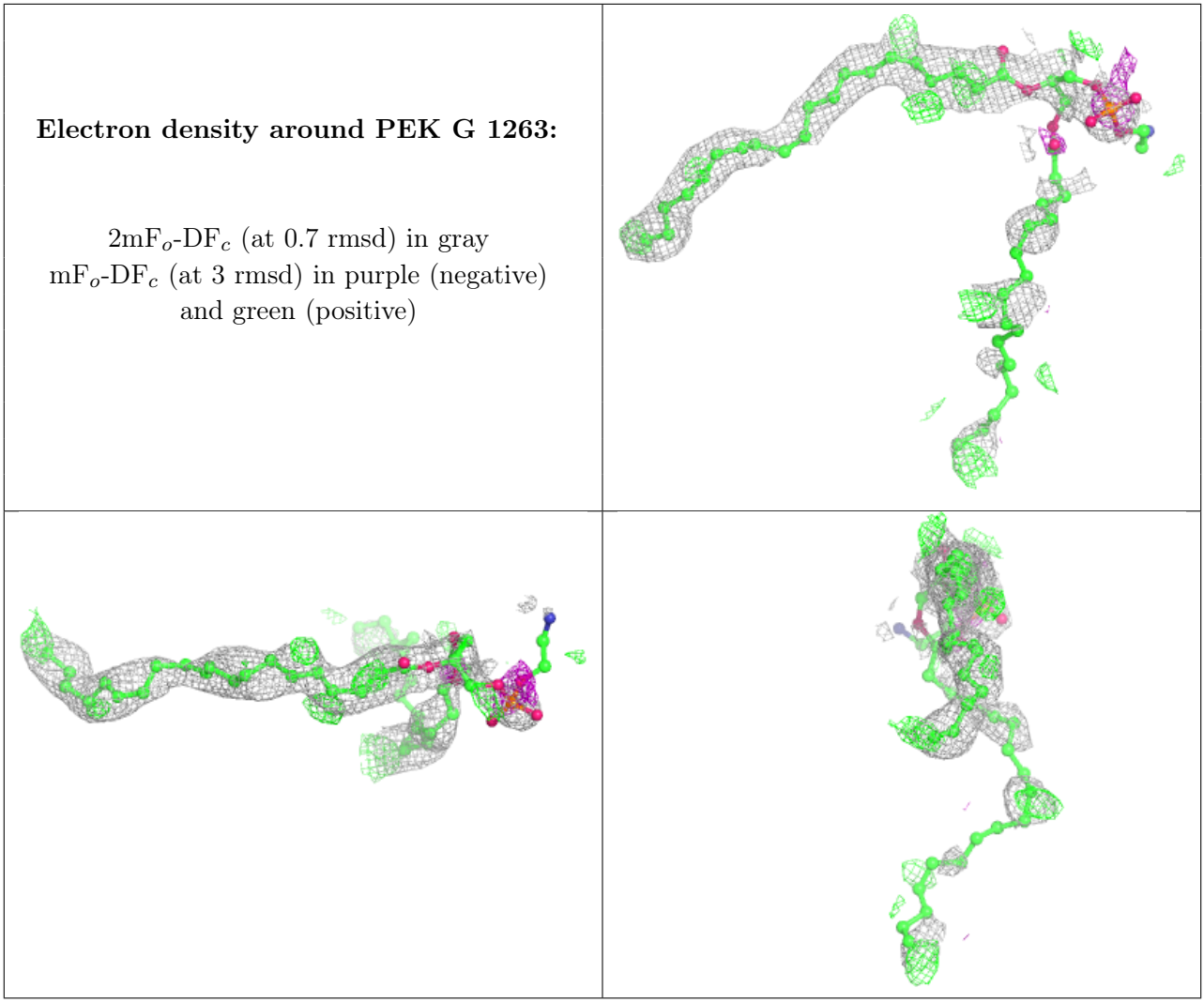
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





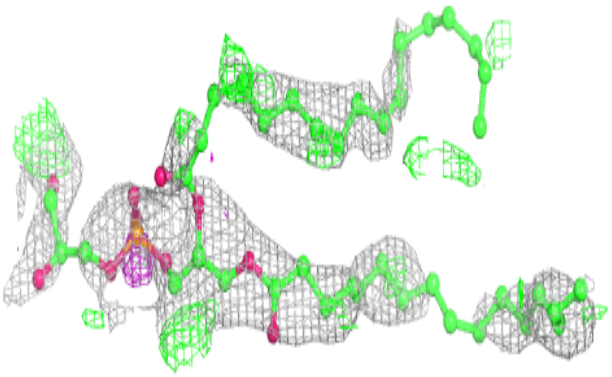
Electron density around PEK G 1263:

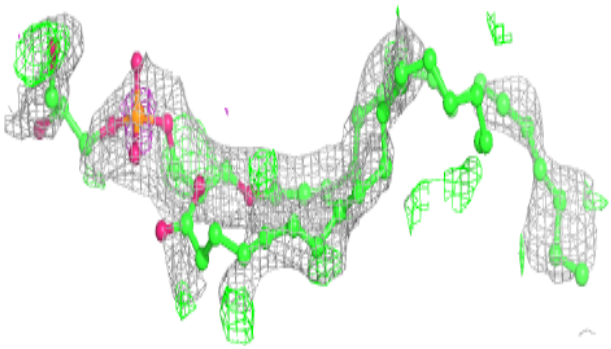
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

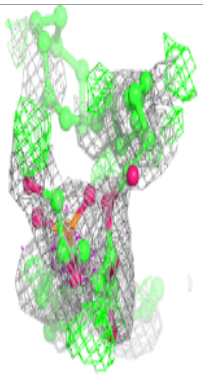


Electron density around PGV P 1268:

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

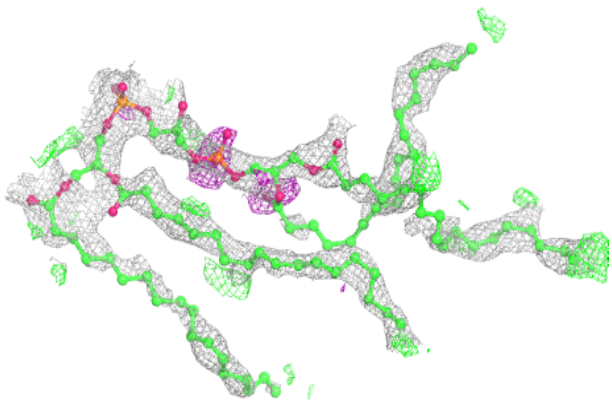


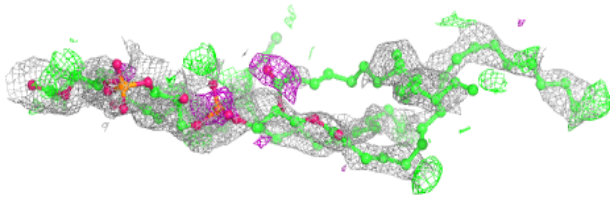


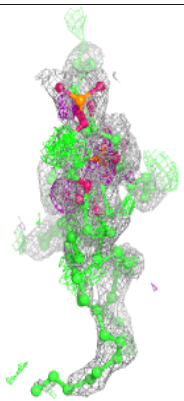


Electron density around CDL G 269:

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

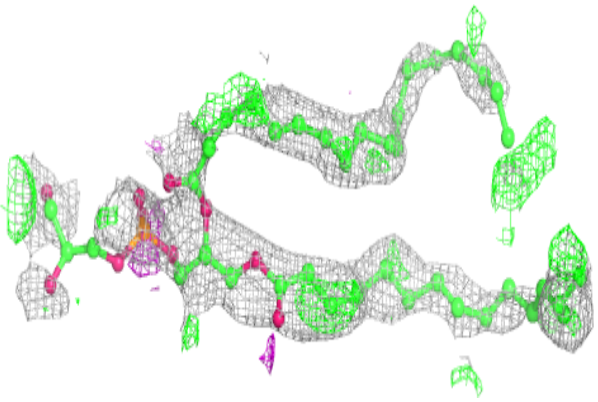


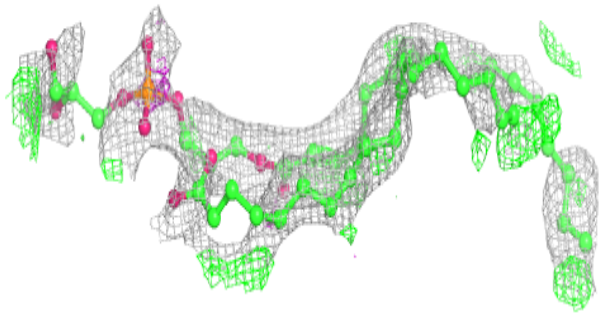


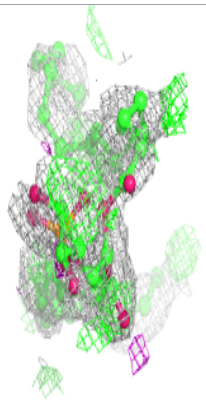


Electron density around PGV C 268:

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

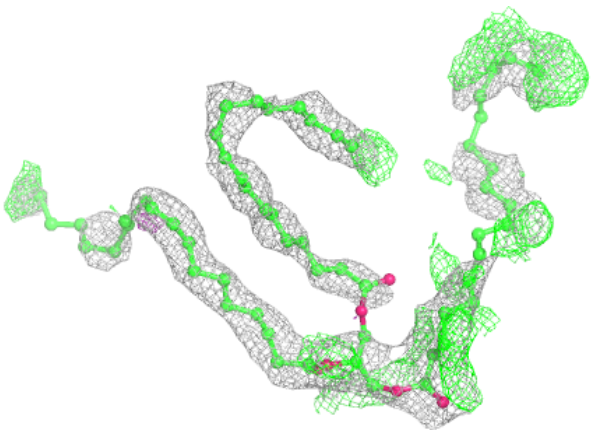


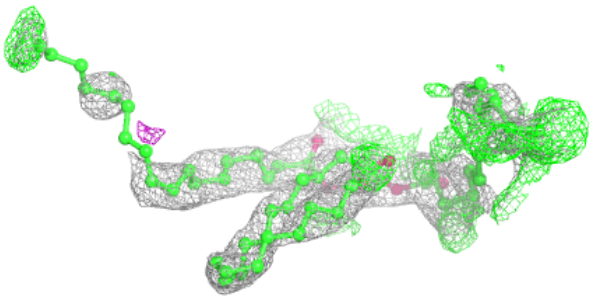


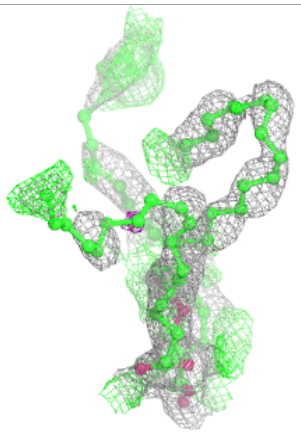


Electron density around TGL Q 1523:

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

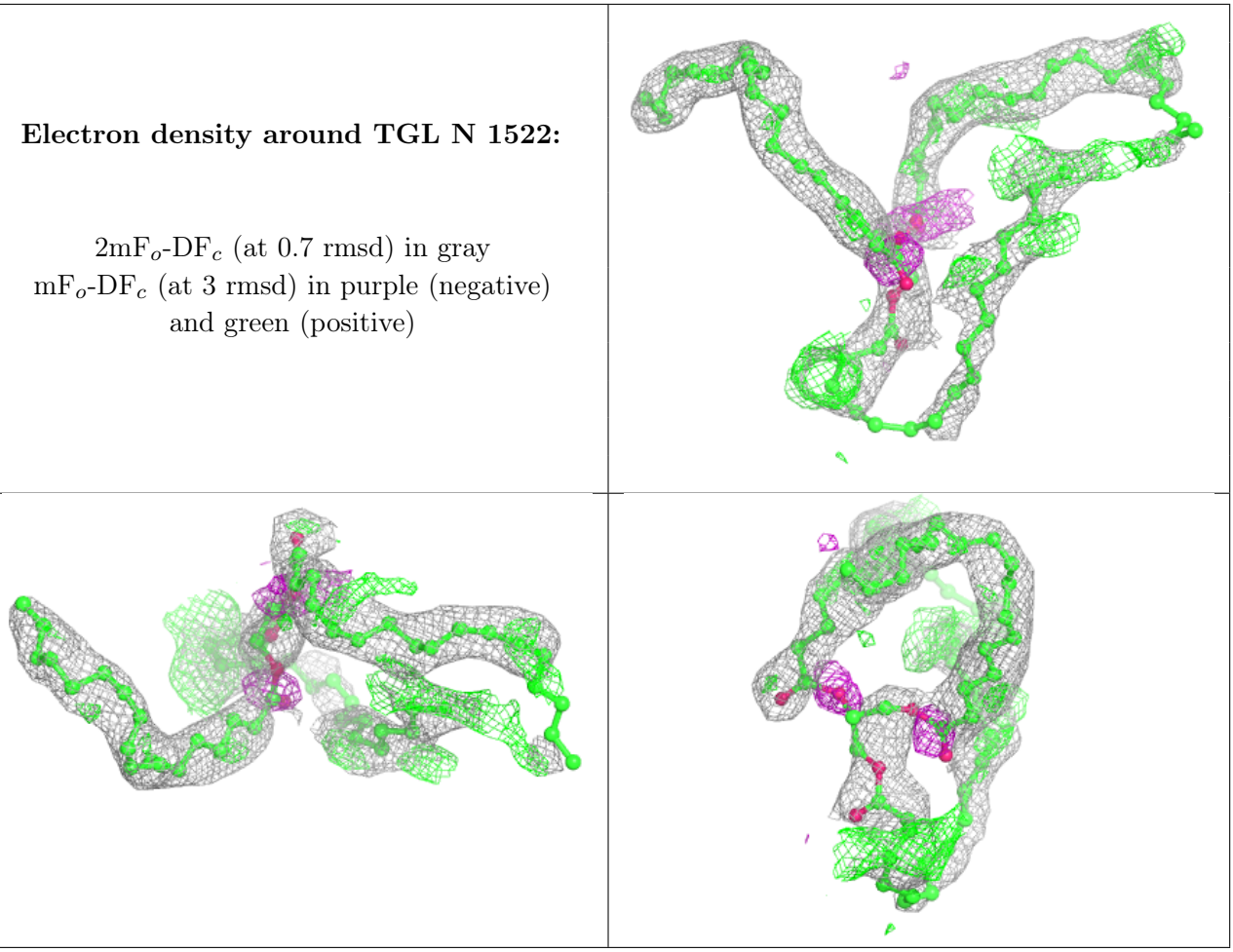






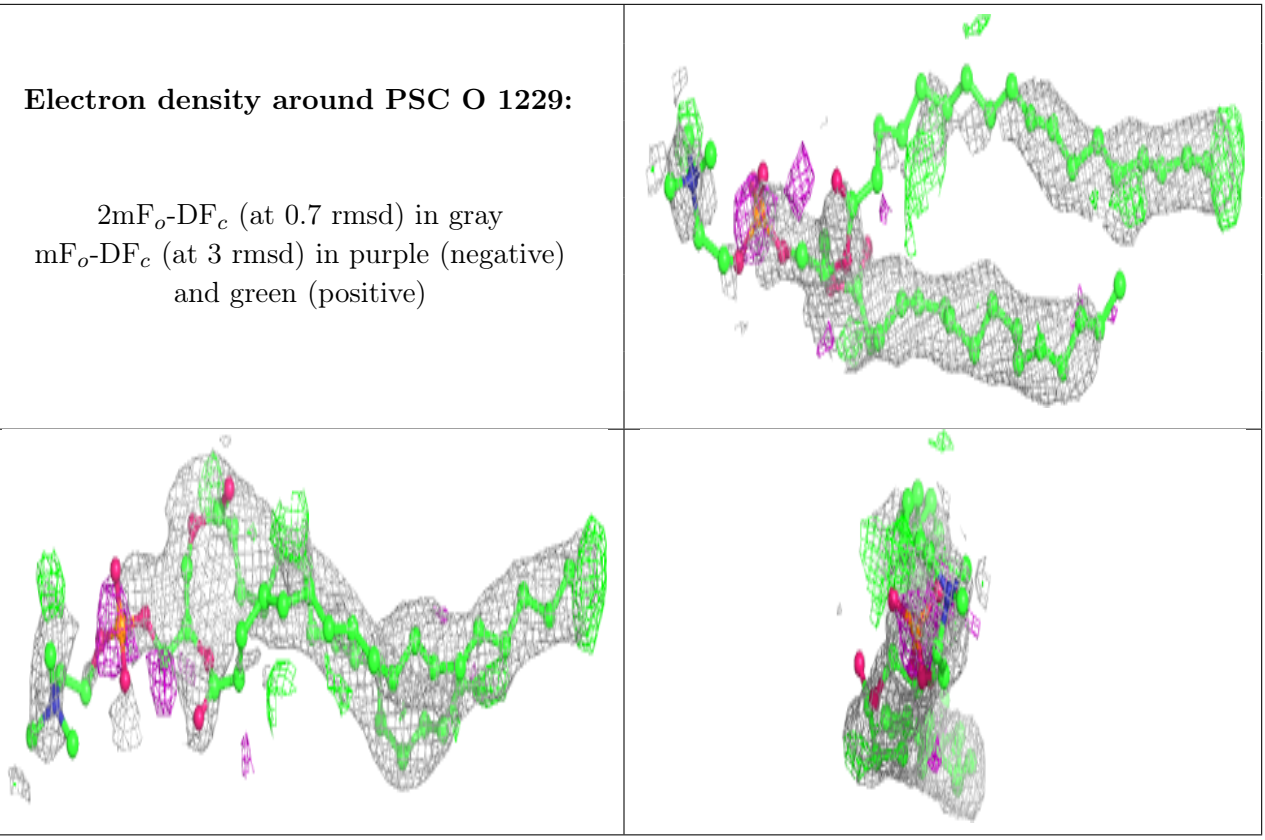
Electron density around TGL N 1522:

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



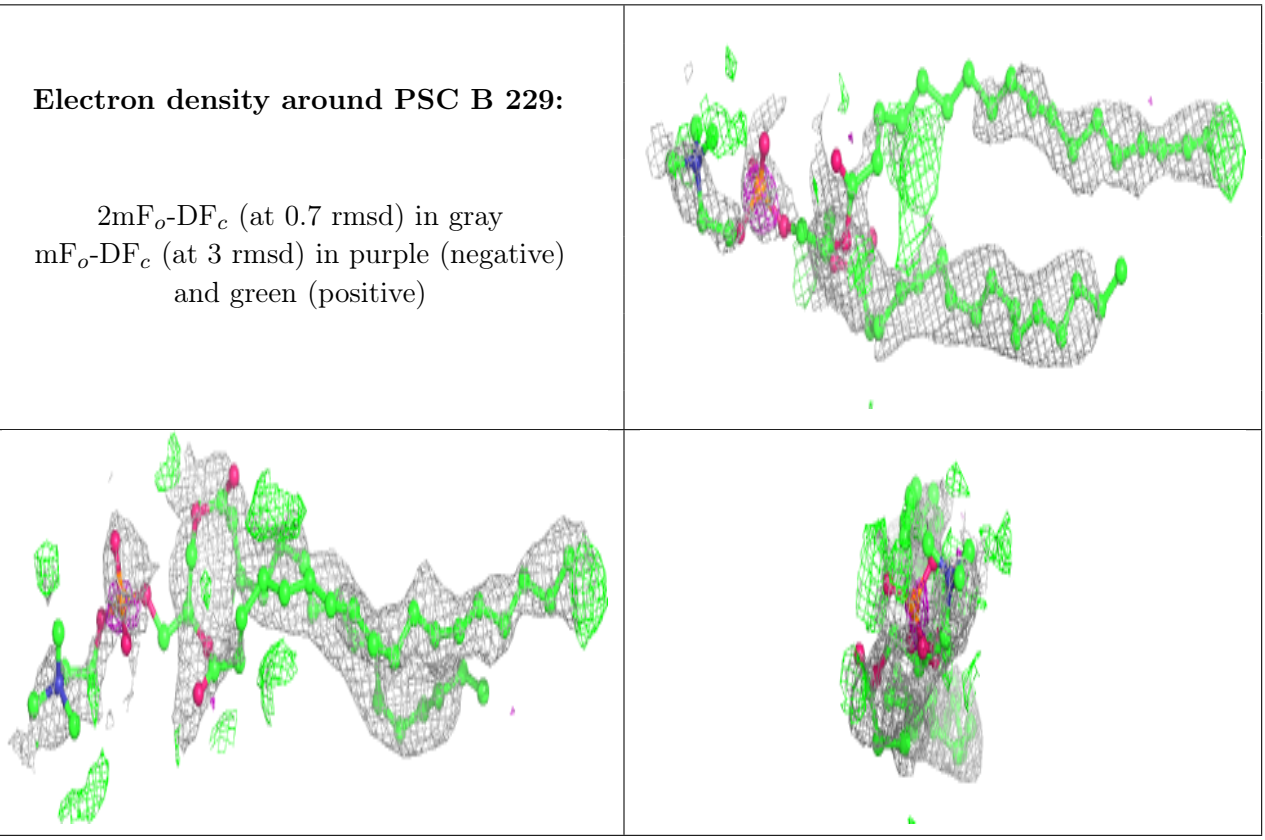
Electron density around PSC O 1229:

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



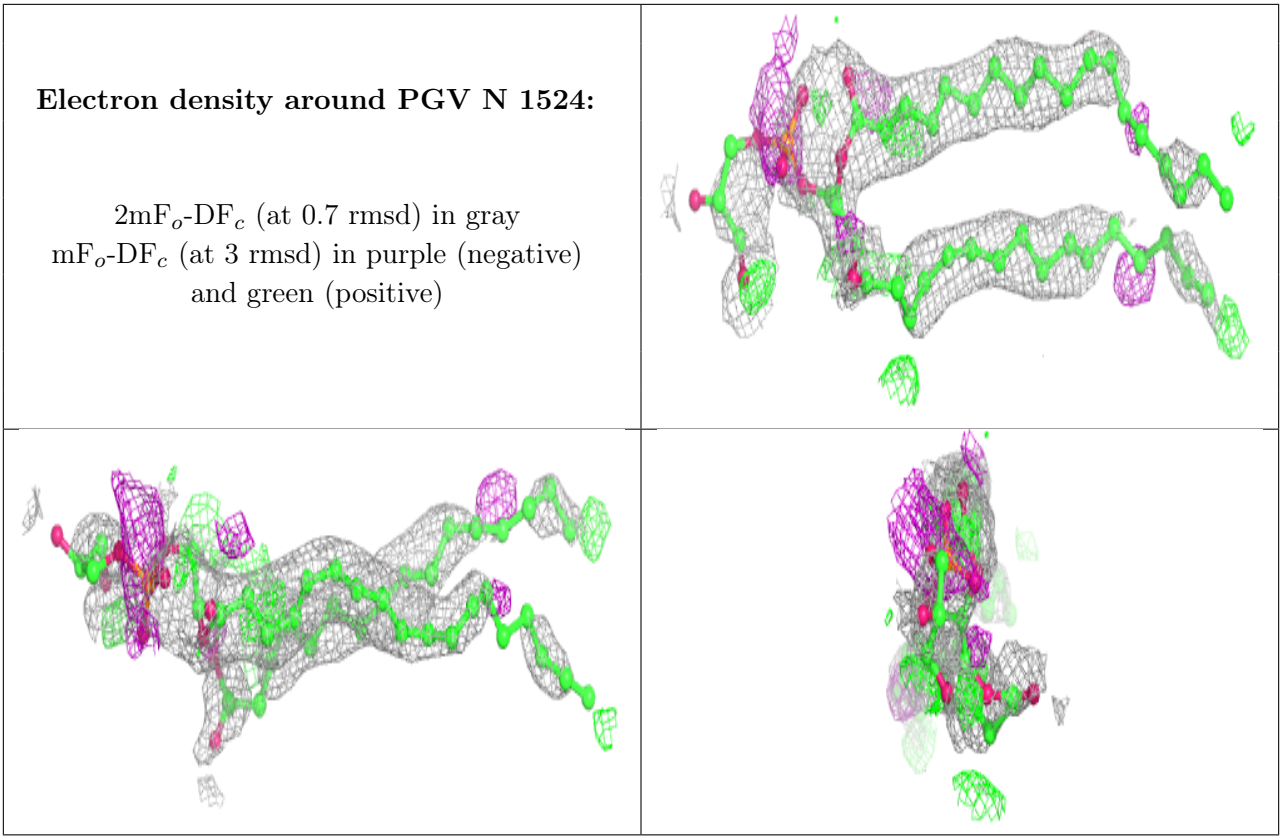
Electron density around PSC B 229:

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



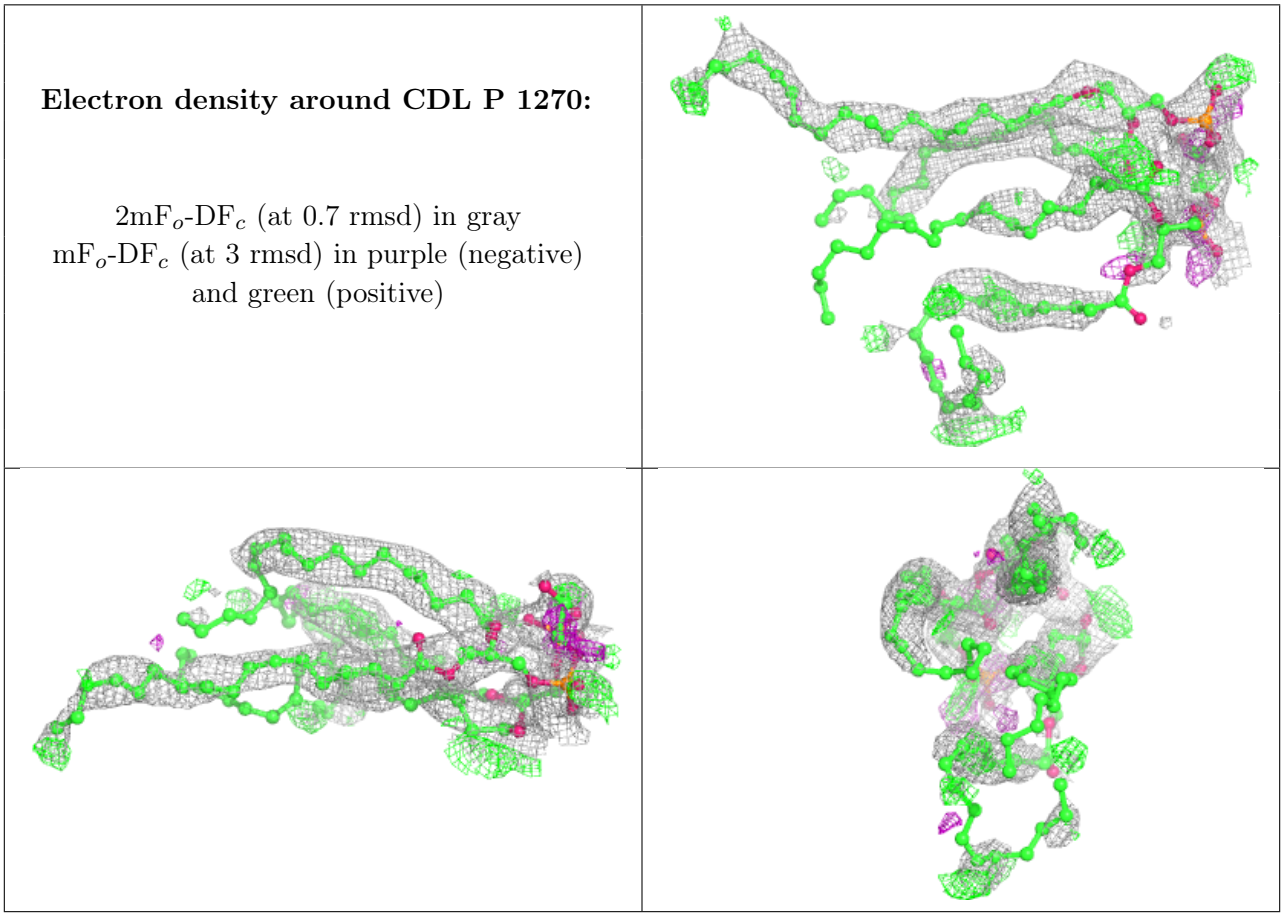
Electron density around PGV N 1524:

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



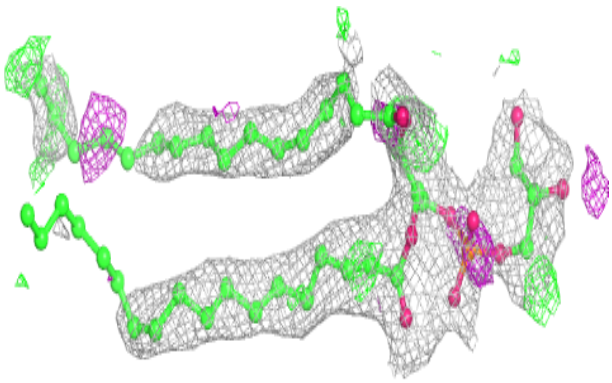
Electron density around CDL P 1270:

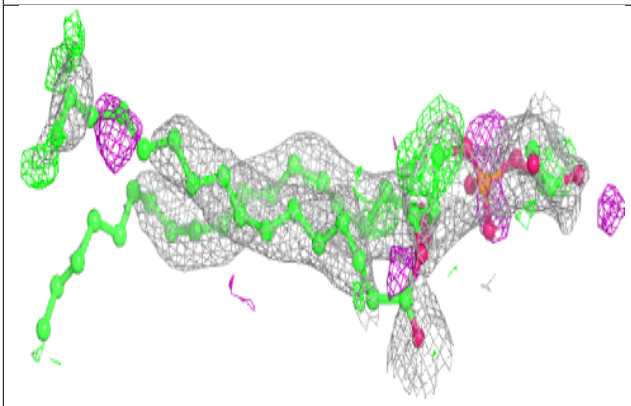
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

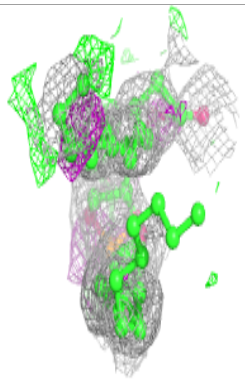


Electron density around PGV A 524:

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

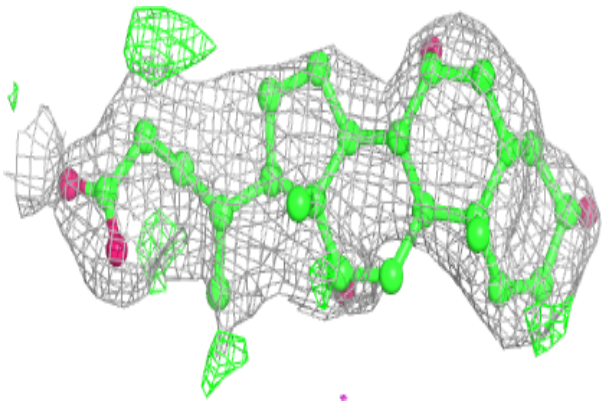


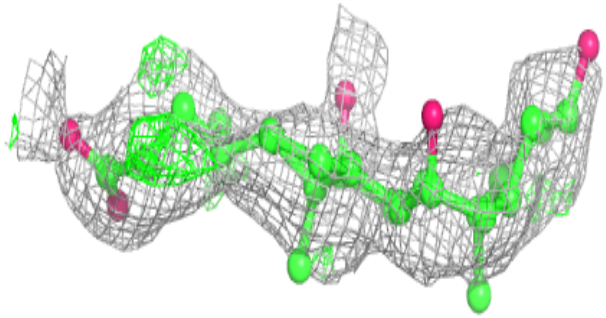


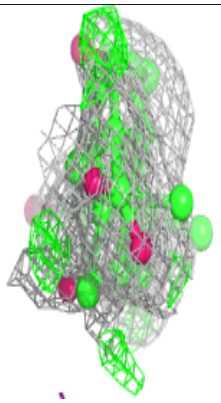


Electron density around CHD P 1271:

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

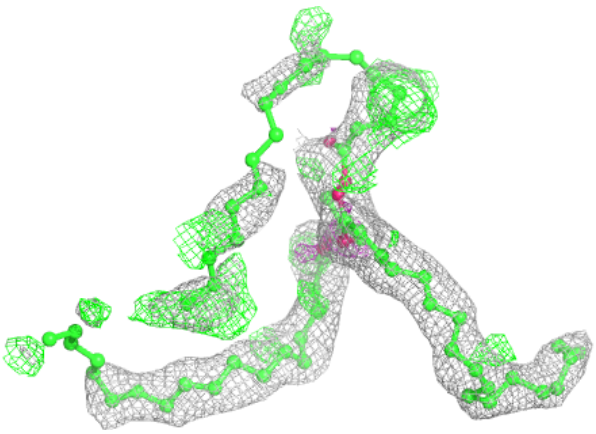


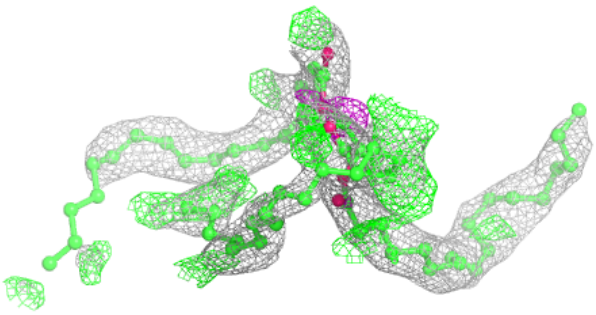




Electron density around TGL L 522:

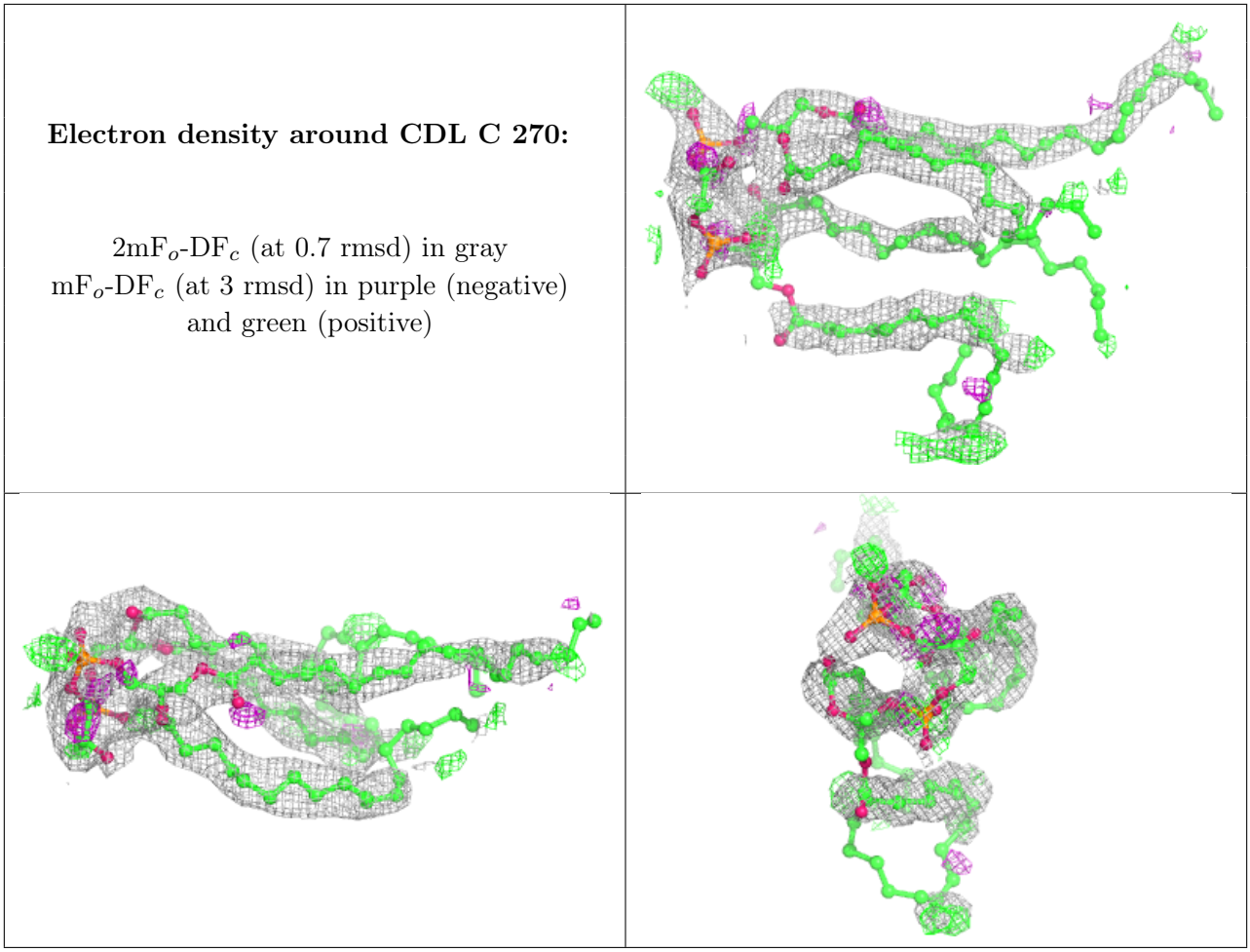
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





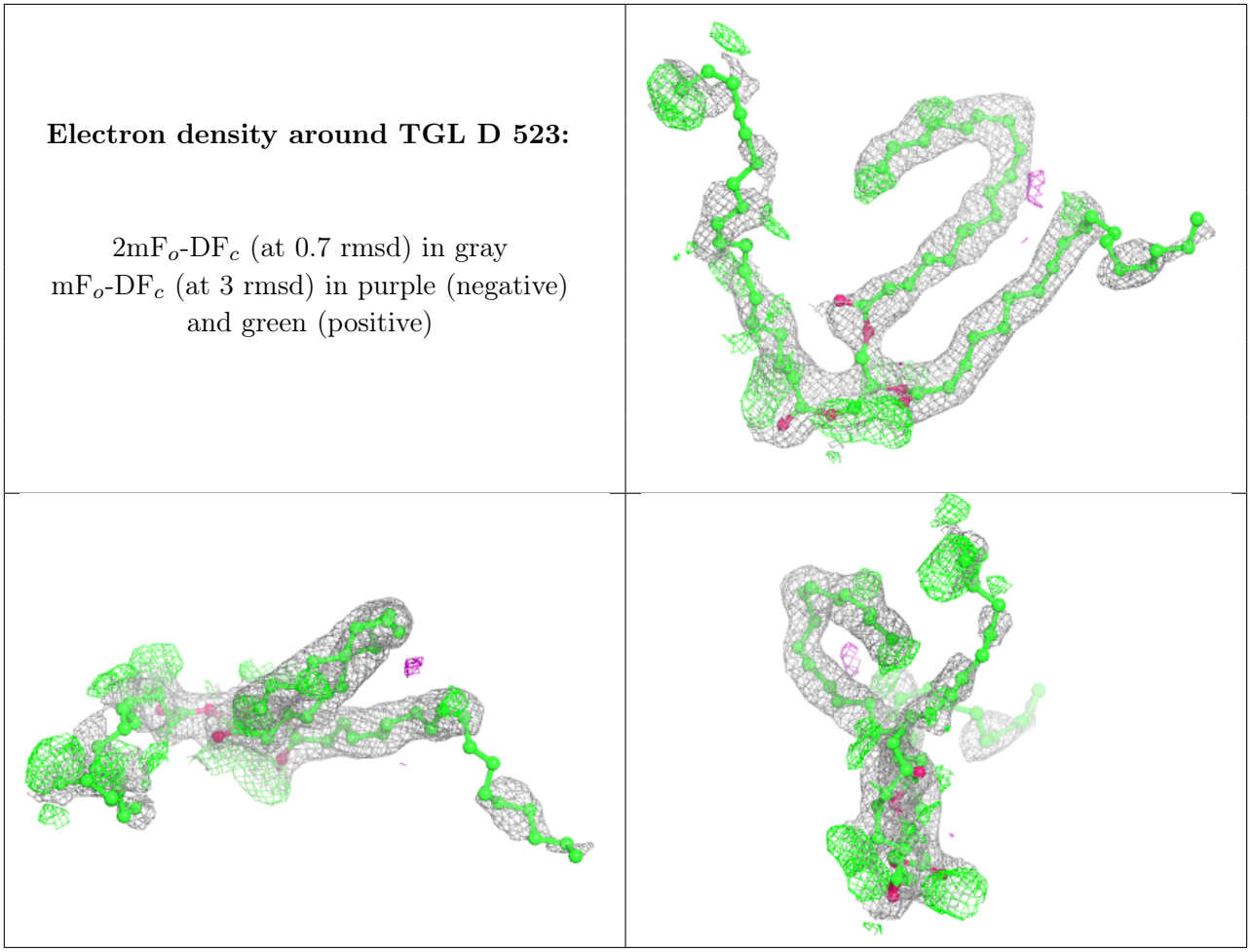
Electron density around CDL C 270:

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



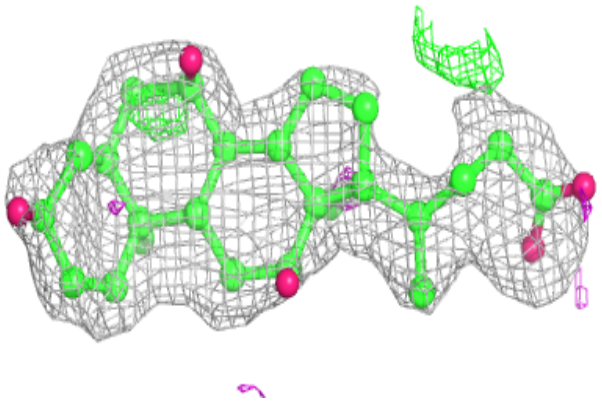
Electron density around TGL D 523:

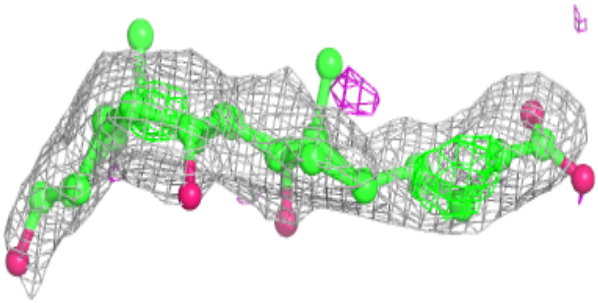
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

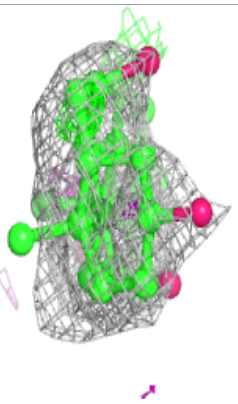


Electron density around CHD C 271:

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

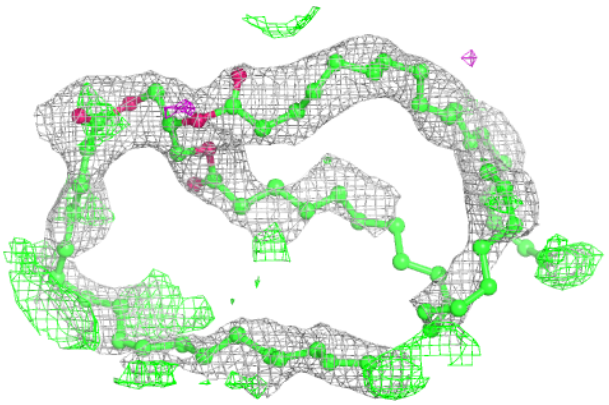


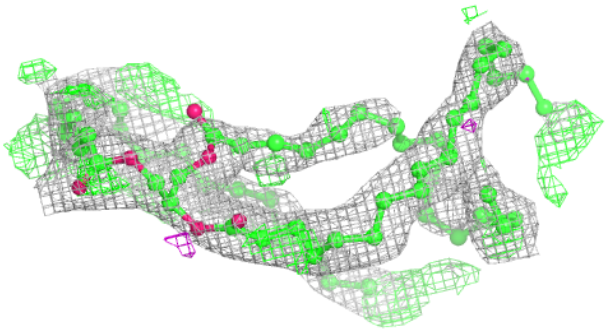


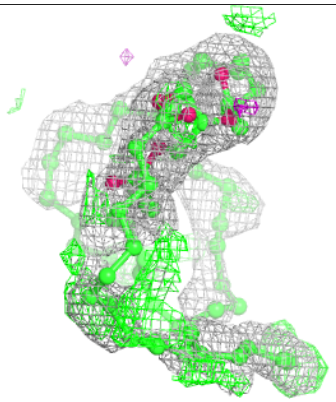


Electron density around TGL N 1521:

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

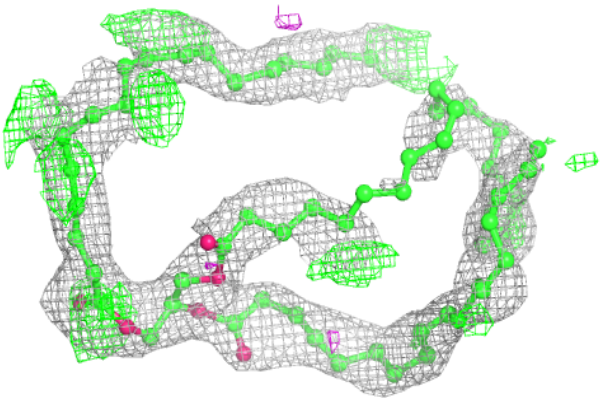


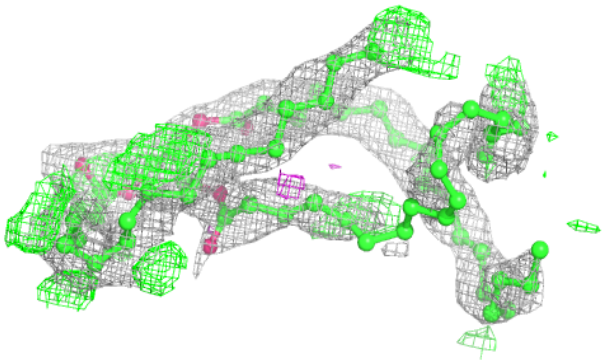


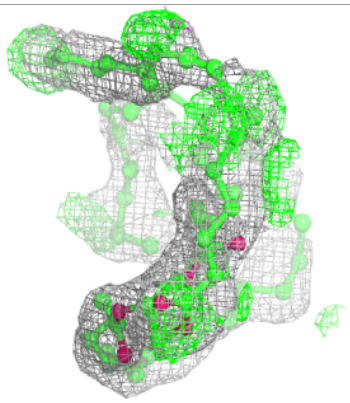


Electron density around TGL A 521:

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

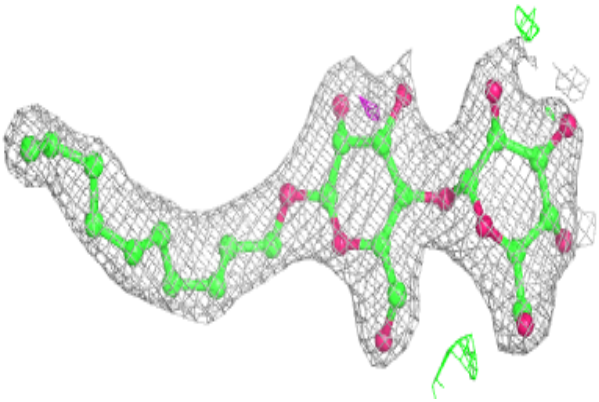


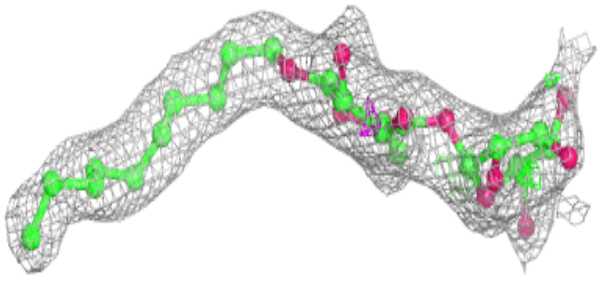


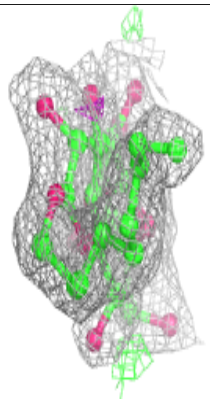


Electron density around DMU Z 1526:

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

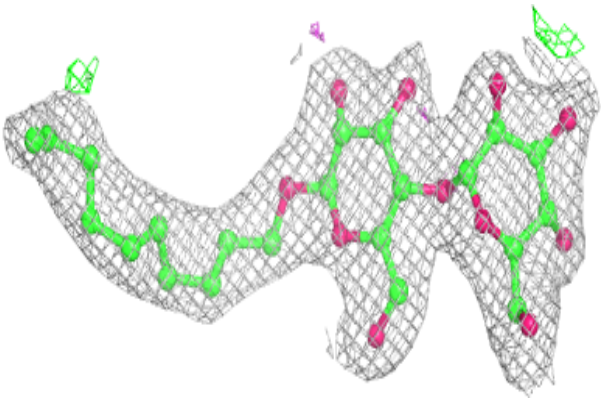


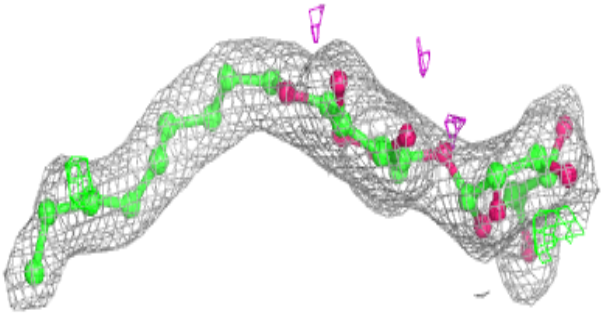


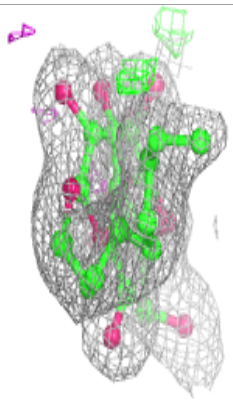


Electron density around DMU M 526:

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

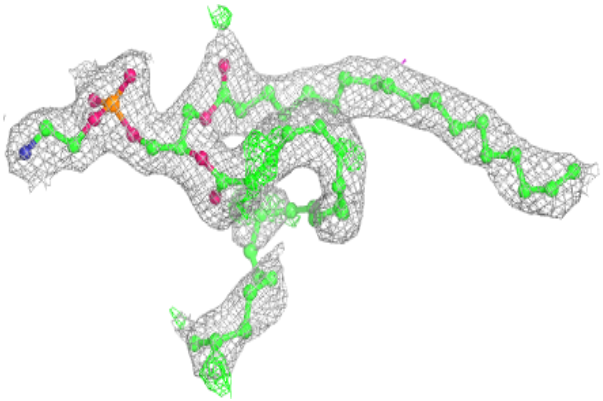


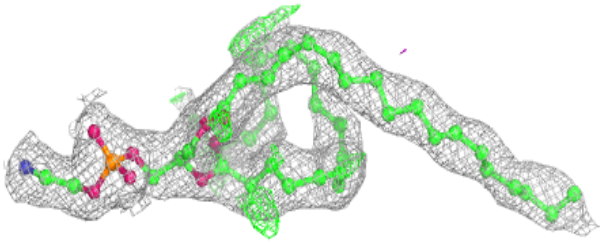


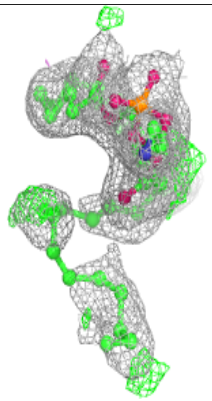


Electron density around PEK T 1264:

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

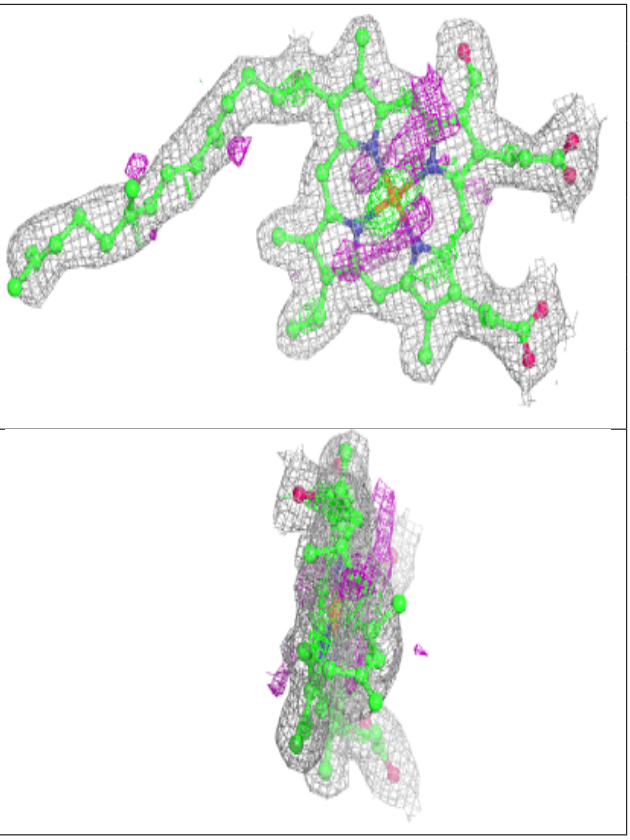






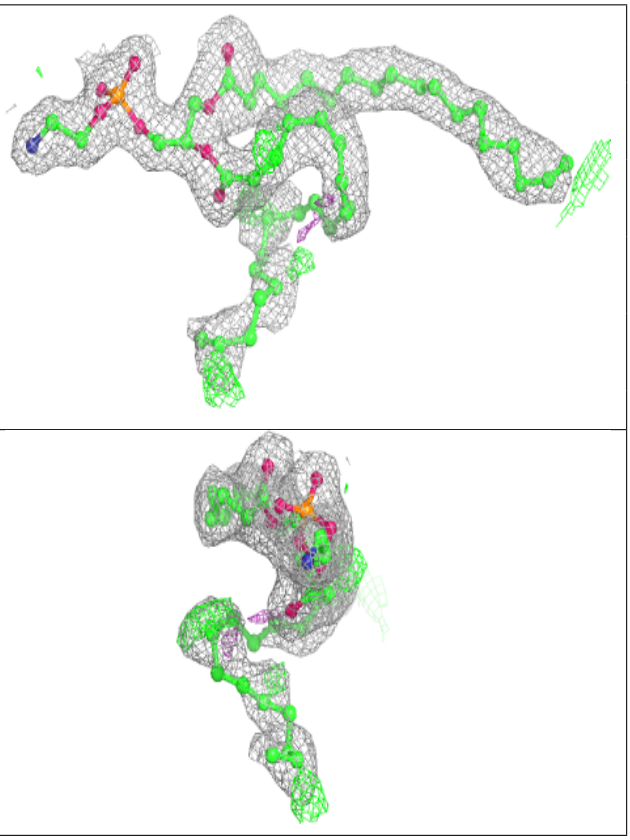
Electron density around HEA N 515:

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



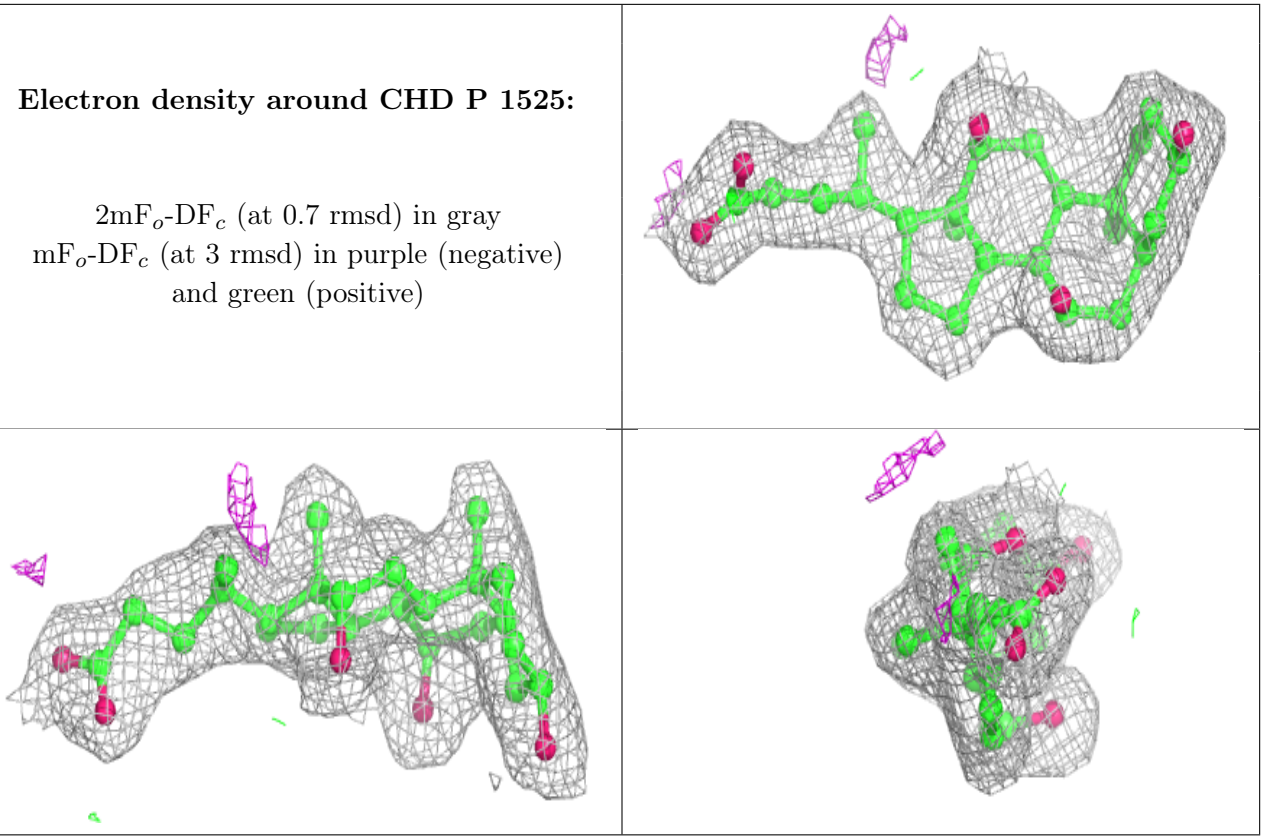
Electron density around PEK G 264:

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



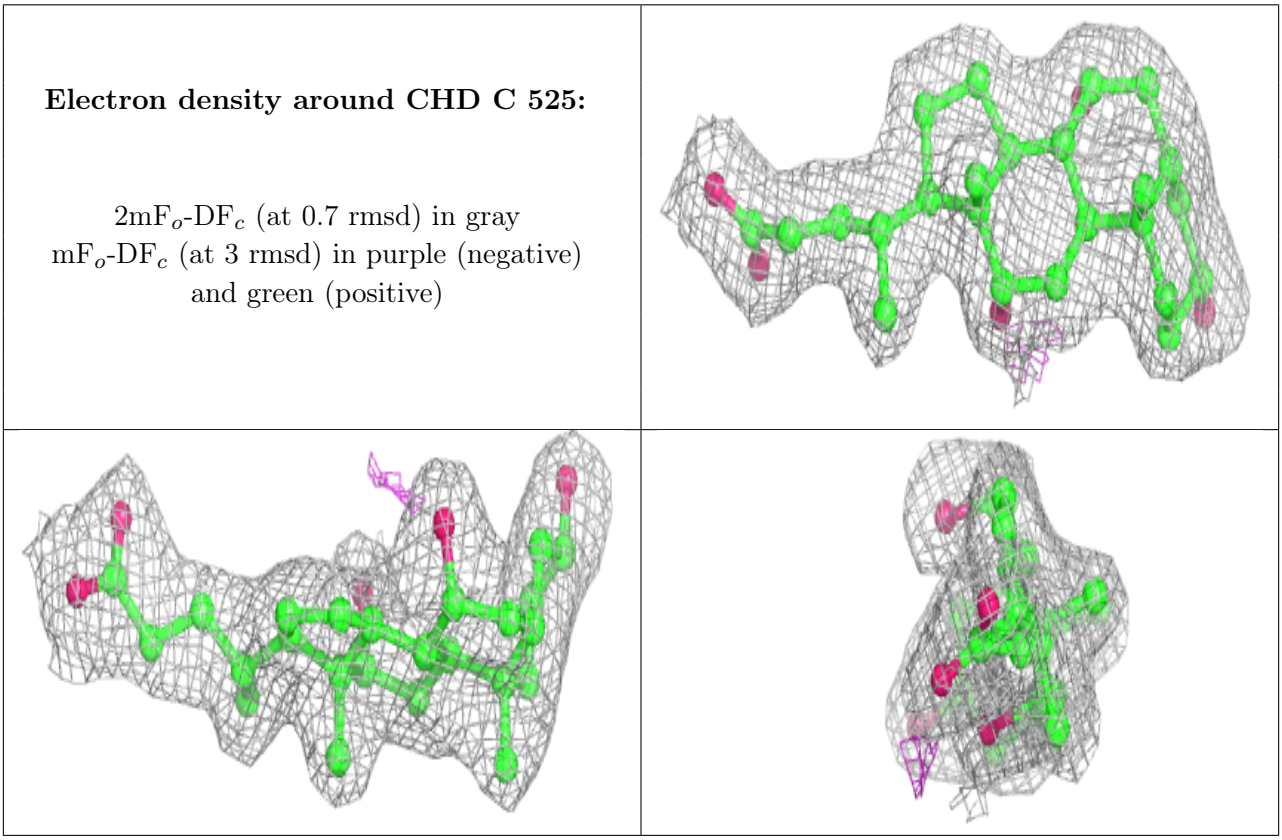
Electron density around CHD P 1525:

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



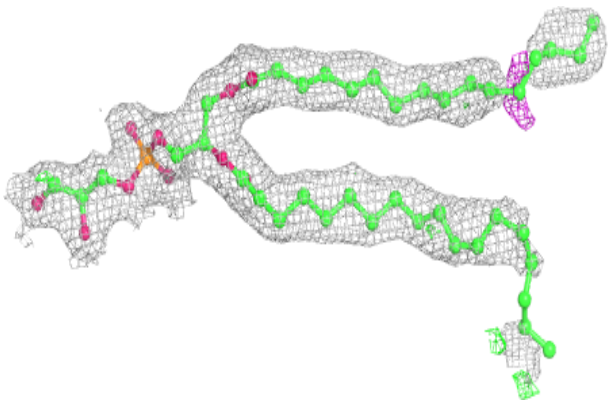
Electron density around CHD C 525:

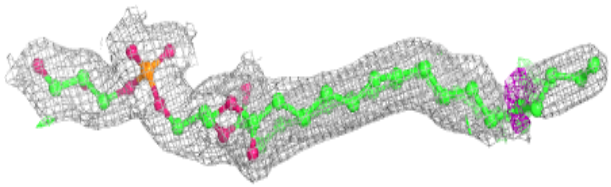
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

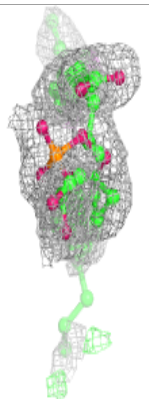


Electron density around PGV C 267:

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

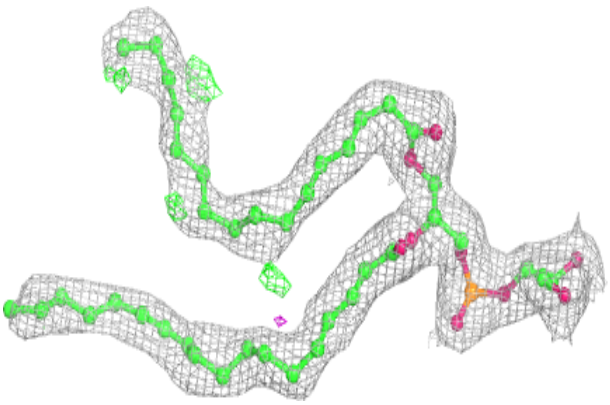


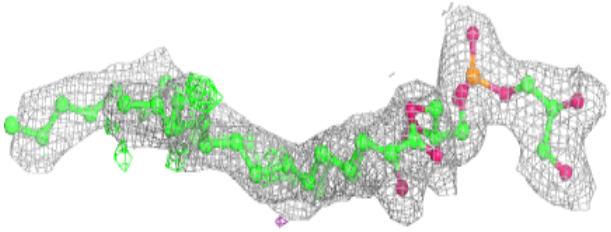


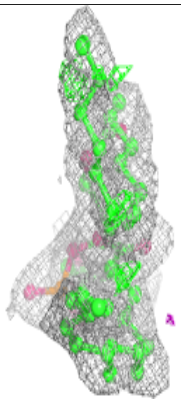


Electron density around PGV N 1266:

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

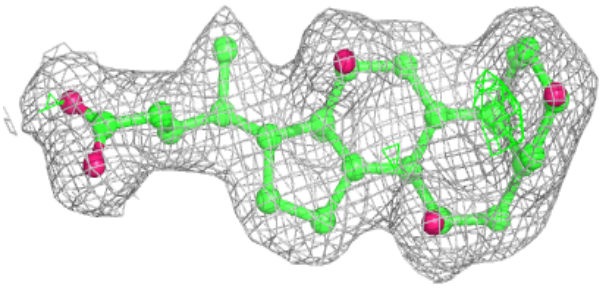


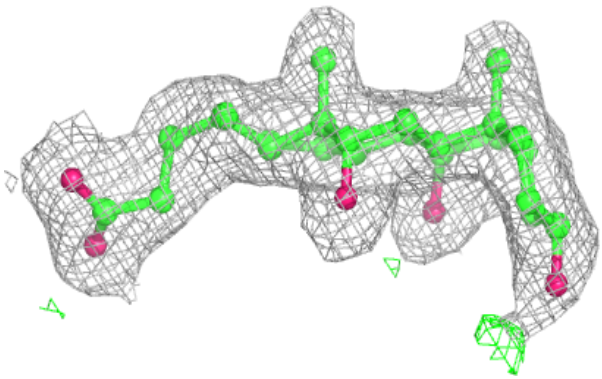


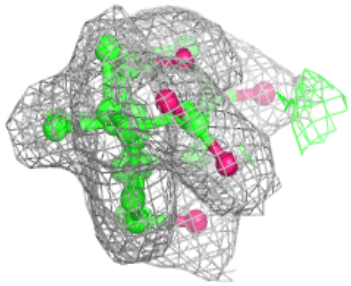


Electron density around CHD B 1085:

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

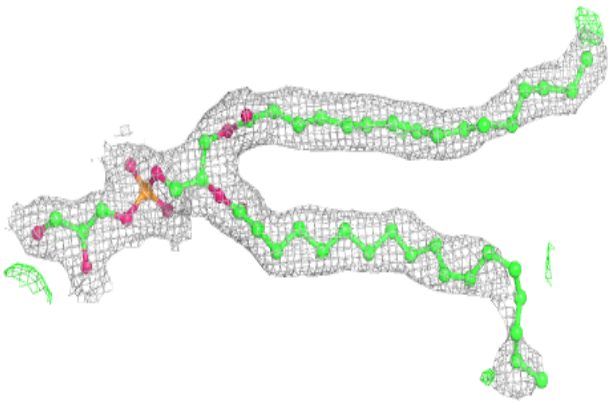


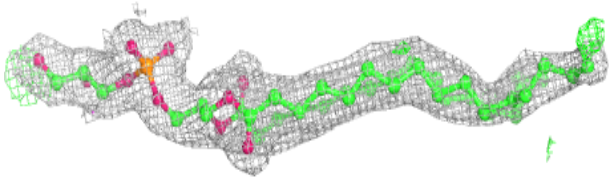


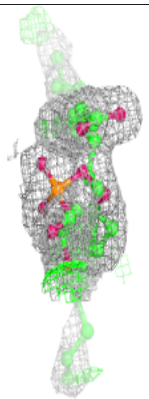


Electron density around PGV P 1267:

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

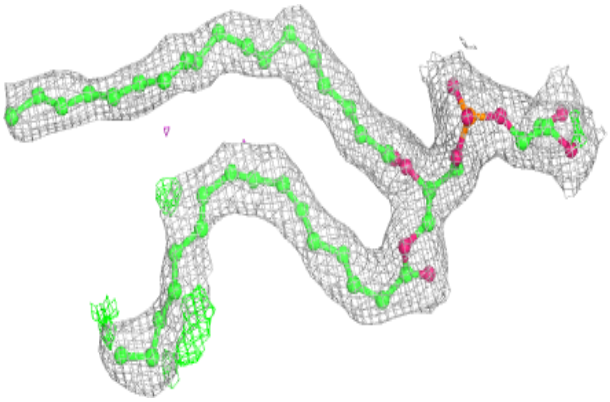


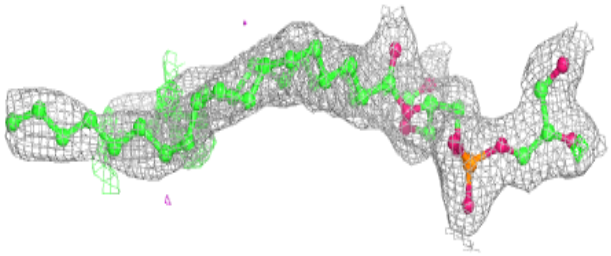


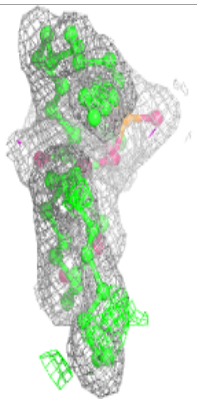


Electron density around PGV A 522:

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

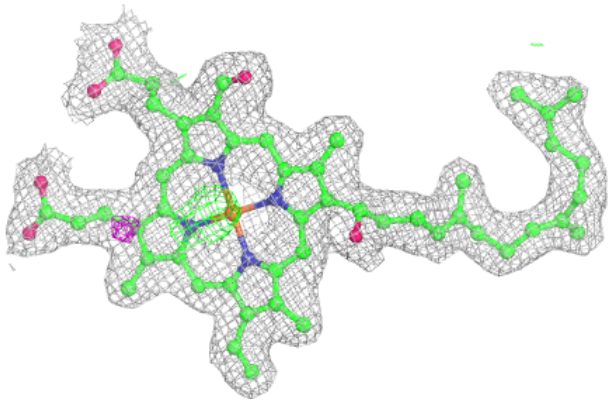


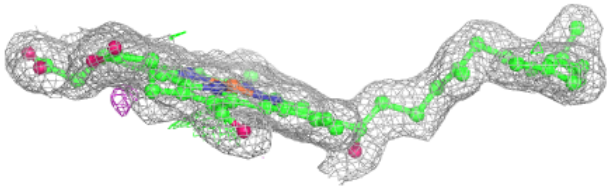


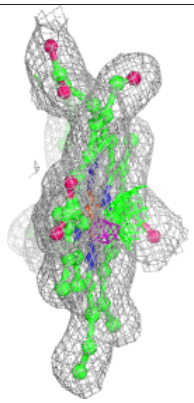


Electron density around HEA N 516:

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

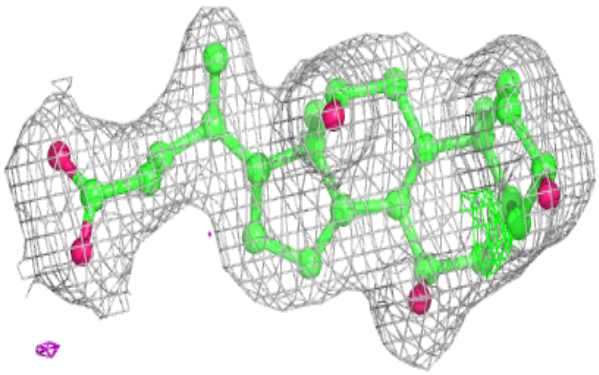


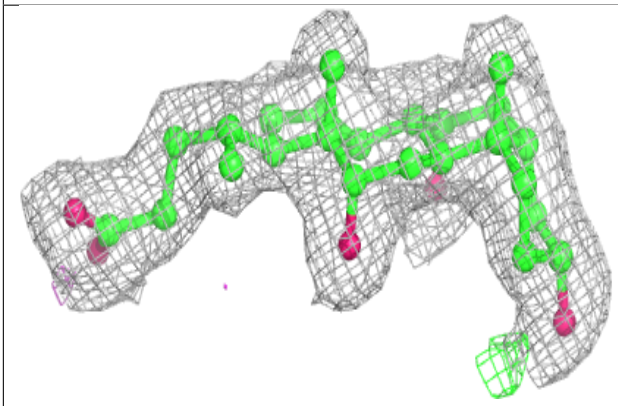


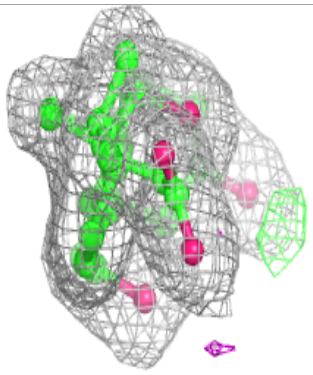


Electron density around CHD G 229:

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

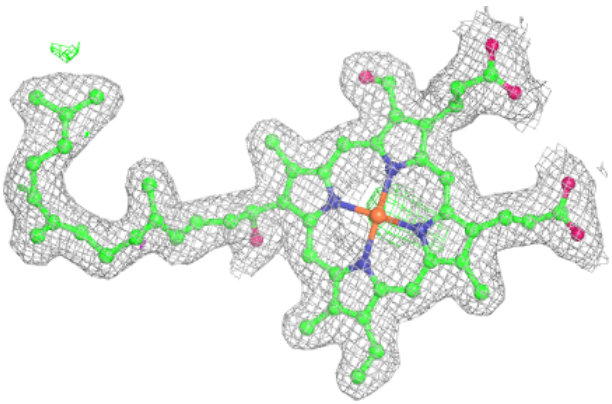


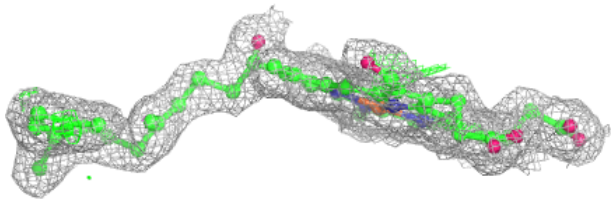


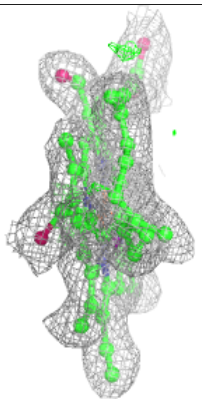


Electron density around HEA A 516:

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

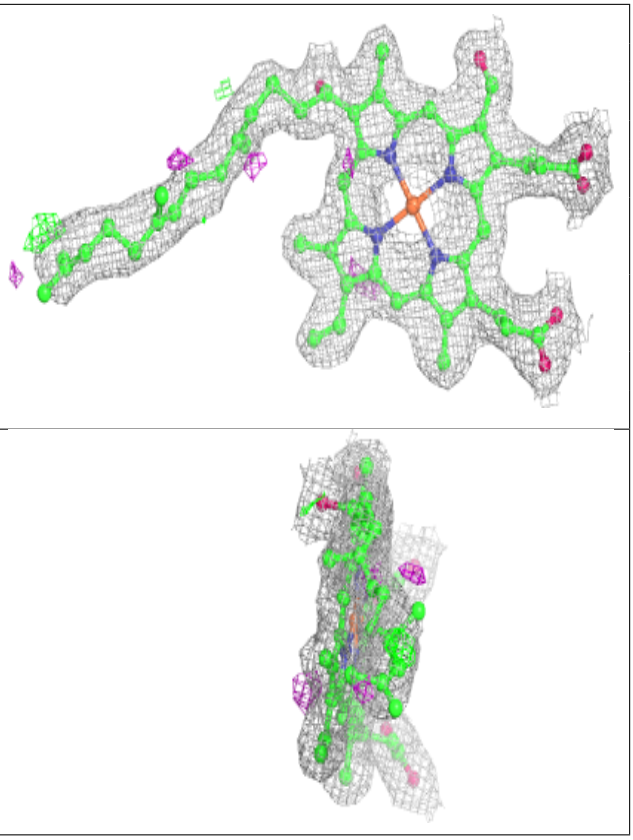






Electron density around HEA A 515:

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



6.5 Other polymers (i)

There are no such residues in this entry.