wwPDB X-ray Structure Validation Summary Report (i)

Apr 21, 2024 – 08:40 am BST

PDB ID	:	6HXL
Title	:	Structure of the citryl-CoA lyase core module of human ATP citrate lyase in complex with citrate and CoASH (space group P21)
Authors	:	Verstraete, K.; Verschueren, K.
Deposited on	:	2018-10-17
Resolution	:	1.35 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:

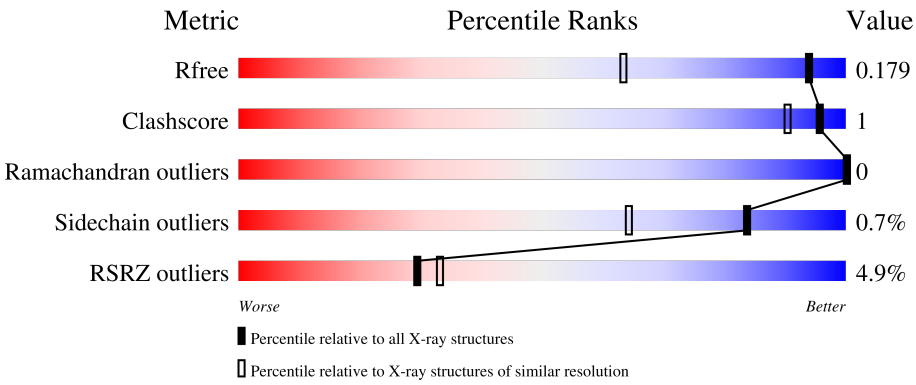
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.35 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	1509 (1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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	270	% 94%
1	B	270	3% 93%
1	C	270	4% 95%
1	D	270	4% 96%
1	E	270	11% 93%

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Mol	Chain	Length	Quality of chain
1	F	270	5% 93%
1	G	270	3% 94%
1	H	270	5% 94%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 36317 atoms, of which 17356 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 ATP-citrate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	263	4295	1361	2166	362	383	23	1	17	0
1	B	261	4174	1329	2102	349	375	19	0	10	0
1	C	262	4211	1335	2122	355	379	20	7	11	0
1	D	262	4154	1319	2095	348	372	20	0	7	0
1	E	261	4203	1334	2121	351	376	21	0	12	0
1	F	263	4306	1367	2176	358	381	24	0	19	0
1	G	262	4241	1345	2138	357	379	22	0	14	0
1	H	264	4235	1347	2129	355	379	25	0	12	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	832	GLY	-	expression tag	UNP P53396
A	833	SER	-	expression tag	UNP P53396
A	834	HIS	-	expression tag	UNP P53396
A	835	MET	-	expression tag	UNP P53396
B	832	GLY	-	expression tag	UNP P53396
B	833	SER	-	expression tag	UNP P53396
B	834	HIS	-	expression tag	UNP P53396
B	835	MET	-	expression tag	UNP P53396
C	832	GLY	-	expression tag	UNP P53396
C	833	SER	-	expression tag	UNP P53396
C	834	HIS	-	expression tag	UNP P53396
C	835	MET	-	expression tag	UNP P53396
D	832	GLY	-	expression tag	UNP P53396

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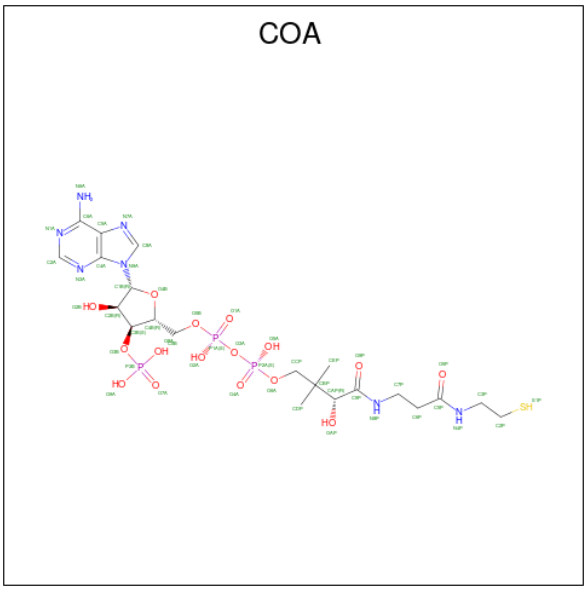
Chain	Residue	Modelled	Actual	Comment	Reference
D	833	SER	-	expression tag	UNP P53396
D	834	HIS	-	expression tag	UNP P53396
D	835	MET	-	expression tag	UNP P53396
E	832	GLY	-	expression tag	UNP P53396
E	833	SER	-	expression tag	UNP P53396
E	834	HIS	-	expression tag	UNP P53396
E	835	MET	-	expression tag	UNP P53396
F	832	GLY	-	expression tag	UNP P53396
F	833	SER	-	expression tag	UNP P53396
F	834	HIS	-	expression tag	UNP P53396
F	835	MET	-	expression tag	UNP P53396
G	832	GLY	-	expression tag	UNP P53396
G	833	SER	-	expression tag	UNP P53396
G	834	HIS	-	expression tag	UNP P53396
G	835	MET	-	expression tag	UNP P53396
H	832	GLY	-	expression tag	UNP P53396
H	833	SER	-	expression tag	UNP P53396
H	834	HIS	-	expression tag	UNP P53396
H	835	MET	-	expression tag	UNP P53396

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
2	A	1	80	21	32	7	16	3	1	0	1

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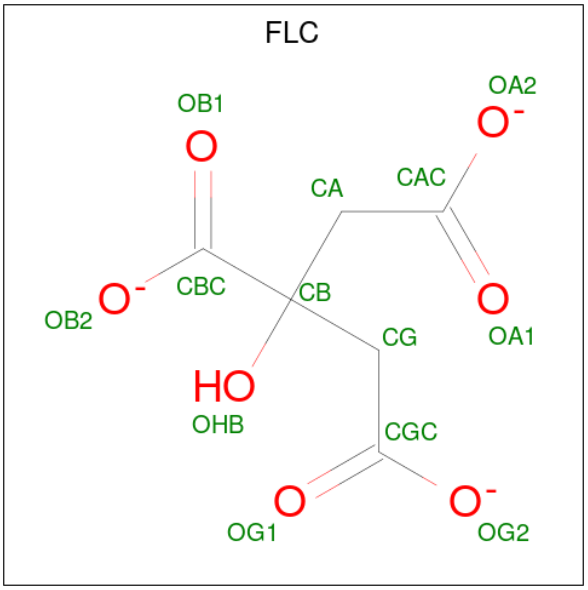
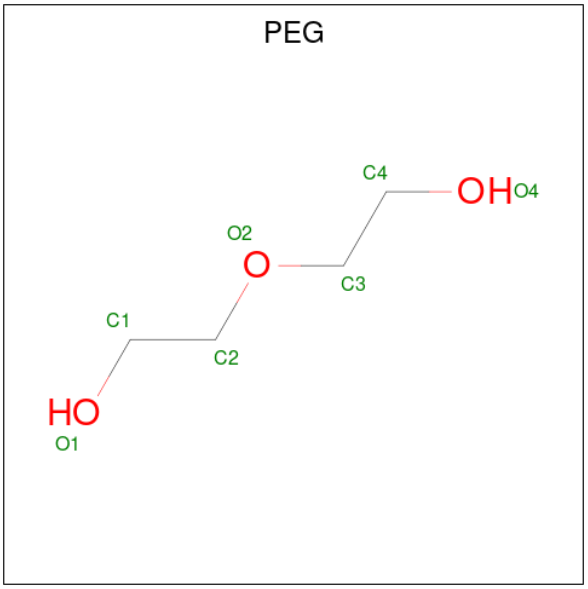
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
2	B	1	80	21	32	7	16	3	1	0	1
2	C	1	80	21	32	7	16	3	1	0	1
2	D	1	80	21	32	7	16	3	1	0	0
2	E	1	80	21	32	7	16	3	1	0	1
2	G	1	80	21	32	7	16	3	1	0	1
2	H	1	80	21	32	7	16	3	1	0	0

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$) (labeled as "Ligand of Interest" by depositor).



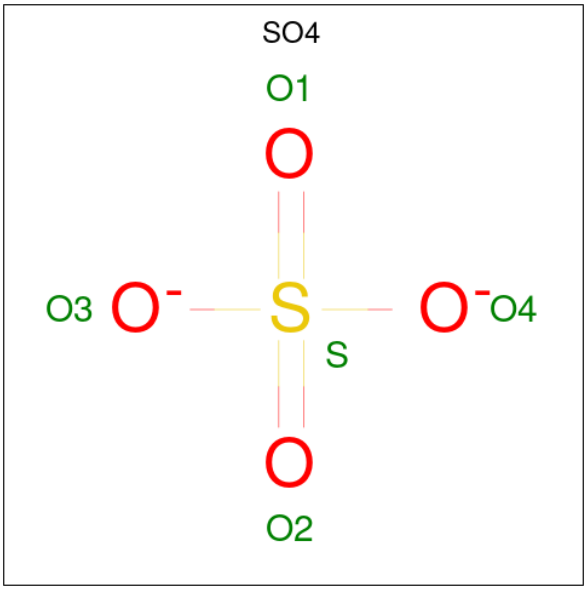
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	18	6	5	7	0	1
3	B	1	18	6	5	7	0	1
3	C	1	18	6	5	7	0	1
3	E	1	18	6	5	7	0	1
3	G	1	18	6	5	7	0	1

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).



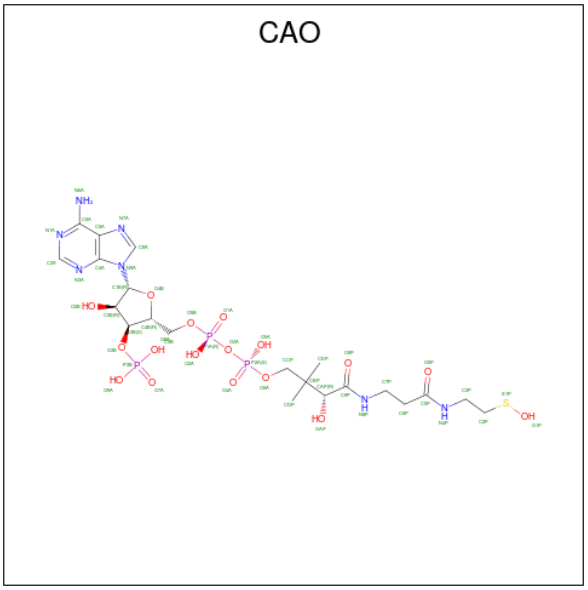
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	B	1	17	4	10	3	0	0
			Total	C	H	O		
4	E	1	17	4	10	3	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S) (labeled as "Ligand of Interest" by depositor).



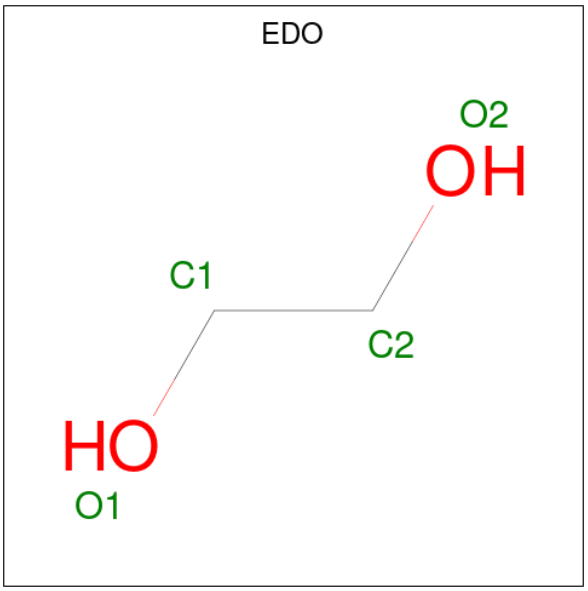
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
5	D	1	5	4	1	0	0
			Total	O	S		
5	D	1	5	4	1	0	0

- Molecule 6 is OXIDIZED COENZYME A (three-letter code: CAO) (formula: $C_{21}H_{36}N_7O_{17}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
6	F	1	81	21	32	7	17	3	1	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
7	H	1	10	2	6	2	0	0

- Molecule 8 is water.

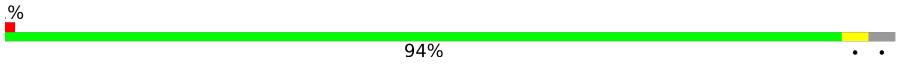
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	224	224	224	0	1
8	B	217	217	217	0	1
8	C	237	237	237	0	1
8	D	219	219	219	0	0
8	E	170	170	170	0	1
8	F	209	209	209	0	0
8	G	227	227	227	0	2
8	H	210	210	210	0	0

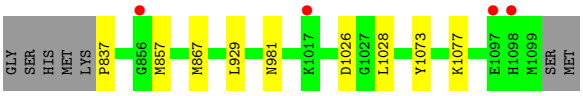
3 Residue-property plots (i)

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: ATP-citrate synthase

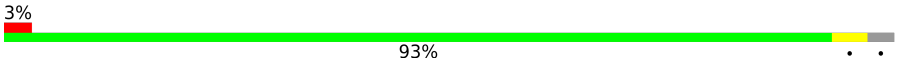
Chain A:

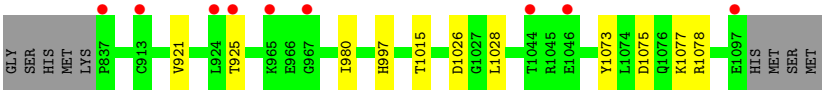




• Molecule 1: ATP-citrate synthase

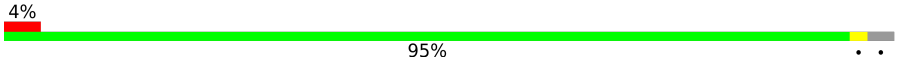
Chain B:

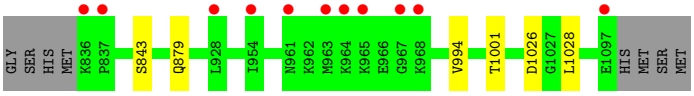




• Molecule 1: ATP-citrate synthase

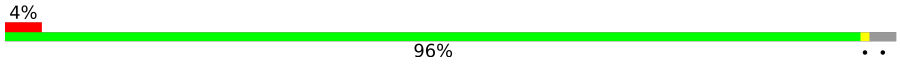
Chain C:

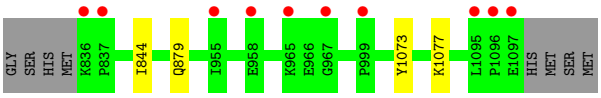




• Molecule 1: ATP-citrate synthase

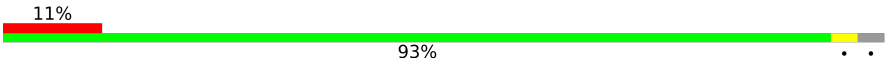
Chain D:

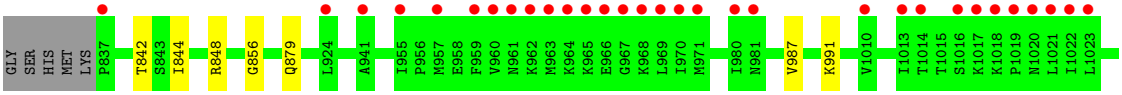


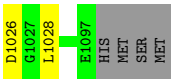


• Molecule 1: ATP-citrate synthase

Chain E:

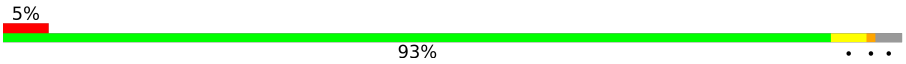


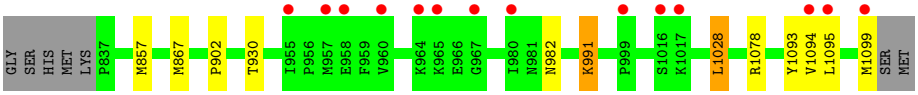




- Molecule 1: ATP-citrate synthase

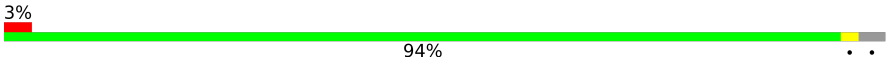
Chain F:

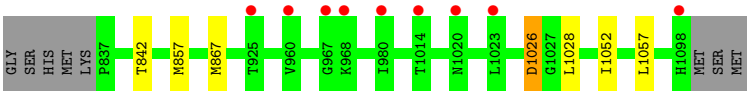




- Molecule 1: ATP-citrate synthase

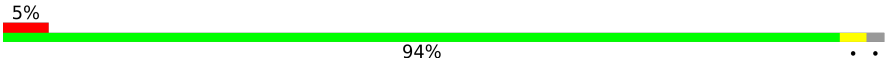
Chain G:

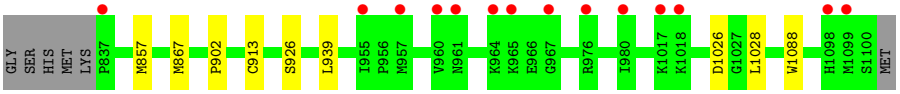




- Molecule 1: ATP-citrate synthase

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	67.71Å 147.90Å 113.69Å 90.00° 105.28° 90.00°	Depositor
Resolution (Å)	47.85 – 1.35 47.85 – 1.35	Depositor EDS
% Data completeness (in resolution range)	97.5 (47.85-1.35) 97.5 (47.85-1.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.11 (at 1.35Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.156 , 0.174 0.161 , 0.179	Depositor DCC
R_{free} test set	23068 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	13.1	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 47.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	36317	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.44% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: COA, PEG, FLC, EDO, SO4, CAO

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	0.49	0/2208	0.64	0/2970
1	B	0.50	0/2139	0.64	0/2881
1	C	0.51	0/2158	0.64	0/2904
1	D	0.47	0/2120	0.62	0/2853
1	E	0.50	0/2152	0.63	0/2896
1	F	0.49	0/2200	0.62	0/2961
1	G	0.51	0/2185	0.64	0/2939
1	H	0.49	0/2175	0.61	0/2924
All	All	0.50	0/17337	0.63	0/23328

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	1093	TYR	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2129	2166	2117	4	0
1	B	2072	2102	2091	7	0
1	C	2089	2122	2081	4	0
1	D	2059	2095	2073	2	0
1	E	2082	2121	2081	9	0
1	F	2130	2176	2141	10	0
1	G	2103	2138	2086	4	0
1	H	2106	2129	2108	6	0
2	A	48	32	32	0	0
2	B	48	32	32	0	0
2	C	48	32	32	0	0
2	D	48	32	32	0	0
2	E	48	32	32	0	0
2	G	48	32	32	0	0
2	H	48	32	32	0	0
3	A	13	5	5	0	0
3	B	13	5	5	0	0
3	C	13	5	5	0	0
3	E	13	5	5	0	0
3	G	13	5	5	1	0
4	B	7	10	10	0	0
4	E	7	10	10	1	0
5	D	10	0	0	0	0
6	F	49	32	32	0	0
7	H	4	6	6	0	0
8	A	224	0	0	0	0
8	B	217	0	0	1	0
8	C	237	0	0	1	0
8	D	219	0	0	0	0
8	E	170	0	0	0	0
8	F	209	0	0	1	0
8	G	227	0	0	0	0
8	H	210	0	0	1	0
All	All	18961	17356	17085	39	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 1.

The worst 5 of 39 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:856:GLY:HA2	8:H:1330:HOH:O	1.64	0.96
1:A:857[B]:MET:SD	1:A:867[B]:MET:SD	2.79	0.79
1:G:857[B]:MET:SD	1:G:867[B]:MET:SD	2.80	0.78
1:B:921:VAL:O	1:B:925[B]:THR:HG22	1.85	0.77
1:E:987:VAL:HG13	1:E:1028[A]:LEU:HD12	1.67	0.75

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	278/270 (103%)	275 (99%)	3 (1%)	0	100	100
1	B	269/270 (100%)	265 (98%)	4 (2%)	0	100	100
1	C	271/270 (100%)	266 (98%)	5 (2%)	0	100	100
1	D	267/270 (99%)	263 (98%)	4 (2%)	0	100	100
1	E	271/270 (100%)	267 (98%)	4 (2%)	0	100	100
1	F	277/270 (103%)	272 (98%)	5 (2%)	0	100	100
1	G	274/270 (102%)	269 (98%)	5 (2%)	0	100	100
1	H	274/270 (102%)	270 (98%)	4 (2%)	0	100	100
All	All	2181/2160 (101%)	2147 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	233/226 (103%)	230 (99%)	3 (1%)	69	37
1	B	227/226 (100%)	224 (99%)	3 (1%)	69	37
1	C	228/226 (101%)	226 (99%)	2 (1%)	78	53
1	D	223/226 (99%)	223 (100%)	0	100	100
1	E	227/226 (100%)	226 (100%)	1 (0%)	91	81
1	F	233/226 (103%)	230 (99%)	3 (1%)	69	37
1	G	230/226 (102%)	228 (99%)	2 (1%)	78	53
1	H	230/226 (102%)	229 (100%)	1 (0%)	91	81
All	All	1831/1808 (101%)	1816 (99%)	15 (1%)	84	59

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1028	LEU
1	G	1028	LEU
1	E	1026	ASP
1	H	1028	LEU
1	F	1028[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	879	GLN
1	G	879	GLN
1	D	981	ASN
1	D	879	GLN
1	F	888	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

18 ligands 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	$\#\|Z\| > 2$
3	FLC	G	1201[A]	-	12,12,12	1.01	0	17,17,17	2.59	6 (35%)
2	COA	B	1201[A]	-	41,50,50	0.81	1 (2%)	52,75,75	1.34	6 (11%)
7	EDO	H	1202	-	3,3,3	0.39	0	2,2,2	0.37	0
2	COA	A	1200[A]	-	41,50,50	0.76	1 (2%)	52,75,75	1.14	3 (5%)
3	FLC	C	1201[A]	-	12,12,12	0.97	0	17,17,17	2.34	4 (23%)
4	PEG	B	1203	-	6,6,6	0.24	0	5,5,5	0.09	0
2	COA	D	1201	-	41,50,50	0.86	2 (4%)	52,75,75	1.23	5 (9%)
2	COA	C	1200[A]	-	41,50,50	0.81	1 (2%)	52,75,75	1.17	2 (3%)
6	CAO	F	1200	-	41,51,51	0.62	0	53,76,76	0.67	1 (1%)
2	COA	H	1201	-	41,50,50	0.84	2 (4%)	52,75,75	1.20	6 (11%)
3	FLC	E	1202[A]	-	12,12,12	1.03	0	17,17,17	2.42	5 (29%)
2	COA	G	1200[A]	-	41,50,50	0.78	1 (2%)	52,75,75	1.08	2 (3%)
4	PEG	E	1203	-	6,6,6	0.18	0	5,5,5	0.33	0
5	SO4	D	1202	-	4,4,4	0.54	0	6,6,6	0.44	0
5	SO4	D	1203	-	4,4,4	0.39	0	6,6,6	0.68	0
3	FLC	B	1202[A]	-	12,12,12	0.98	0	17,17,17	2.38	5 (29%)
3	FLC	A	1201[A]	-	12,12,12	0.93	0	17,17,17	2.70	7 (41%)
2	COA	E	1201[A]	-	41,50,50	0.83	2 (4%)	52,75,75	1.11	4 (7%)

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
3	FLC	G	1201[A]	-	-	7/16/16/16	-
2	COA	B	1201[A]	-	-	2/44/64/64	0/3/3/3
7	EDO	H	1202	-	-	0/1/1/1	-
2	COA	A	1200[A]	-	-	2/44/64/64	0/3/3/3
3	FLC	C	1201[A]	-	-	9/16/16/16	-
4	PEG	B	1203	-	-	0/4/4/4	-
2	COA	D	1201	-	-	1/44/64/64	0/3/3/3
2	COA	C	1200[A]	-	-	2/44/64/64	0/3/3/3
2	COA	H	1201	-	-	3/44/64/64	0/3/3/3
3	FLC	E	1202[A]	-	-	6/16/16/16	-
2	COA	G	1200[A]	-	-	3/44/64/64	0/3/3/3
4	PEG	E	1203	-	-	3/4/4/4	-
6	CAO	F	1200	-	-	1/44/65/65	0/3/3/3
3	FLC	B	1202[A]	-	-	8/16/16/16	-
3	FLC	A	1201[A]	-	-	8/16/16/16	-
2	COA	E	1201[A]	-	-	2/44/64/64	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1201[A]	COA	C2A-N3A	2.69	1.36	1.32
2	D	1201	COA	C5A-C4A	2.55	1.47	1.40
2	H	1201	COA	C5A-C4A	2.44	1.47	1.40
2	C	1200[A]	COA	C2A-N3A	2.39	1.35	1.32
2	G	1200[A]	COA	C2A-N3A	2.37	1.35	1.32

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1201[A]	FLC	OB1-CBC-CB	-6.42	113.16	122.25
3	C	1201[A]	FLC	CG-CB-CBC	-6.40	96.36	110.11
3	A	1201[A]	FLC	CG-CB-CBC	-6.29	96.60	110.11
3	G	1201[A]	FLC	CG-CB-CBC	-6.21	96.76	110.11
3	G	1201[A]	FLC	OB1-CBC-CB	-6.03	113.71	122.25

There are no chirality outliers.

5 of 57 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1200[A]	COA	CCP-O6A-P2A-O3A
2	E	1201[A]	COA	CCP-O6A-P2A-O3A
3	A	1201[A]	FLC	CA-CB-CBC-OB2
3	A	1201[A]	FLC	CA-CB-CG-CGC
3	A	1201[A]	FLC	CBC-CB-CG-CGC

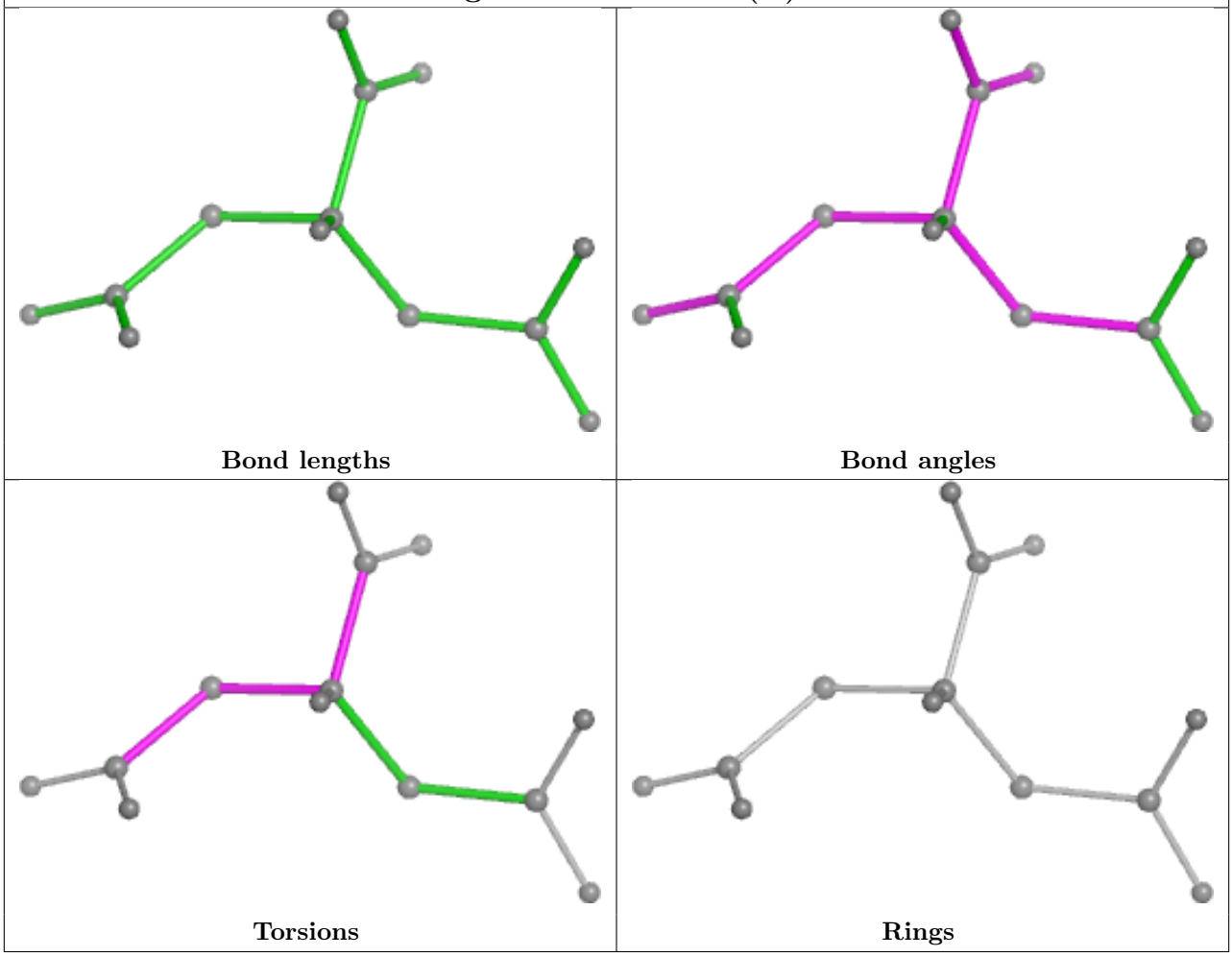
There are no ring outliers.

2 monomers are involved in 2 short contacts:

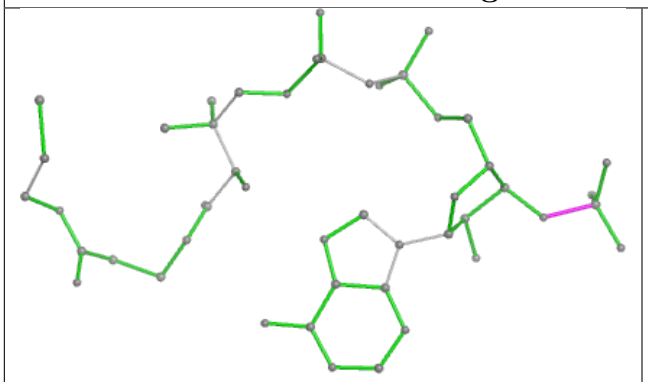
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	1201[A]	FLC	1	0
4	E	1203	PEG	1	0

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

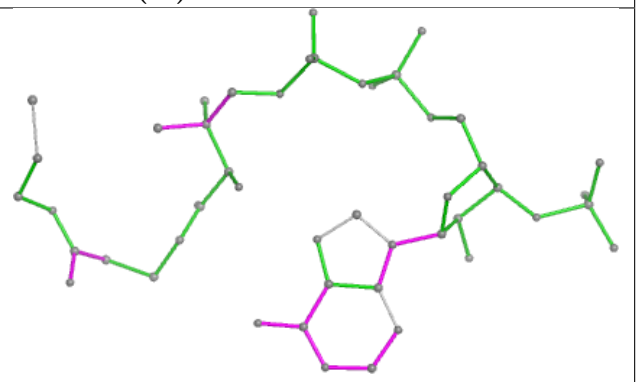
Ligand FLC G 1201 (A)



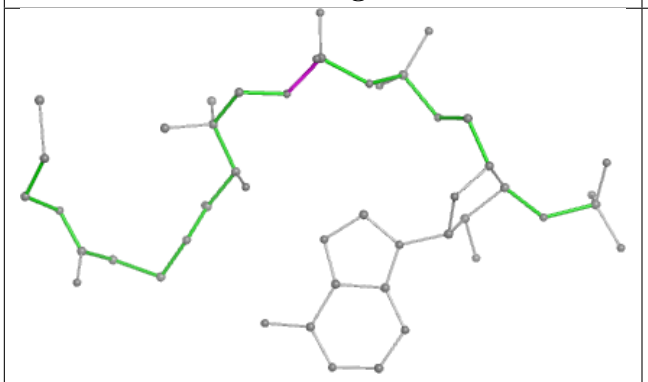
Ligand COA B 1201 (A)



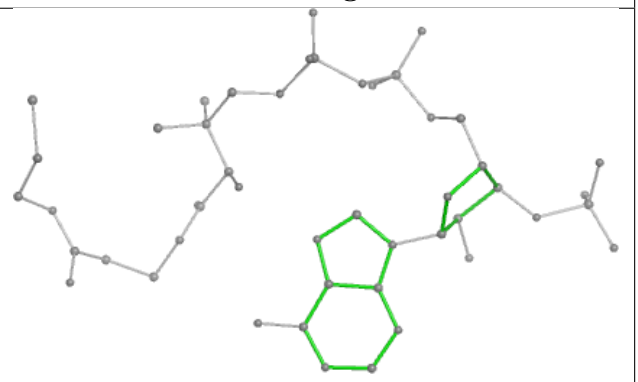
Bond lengths



Bond angles

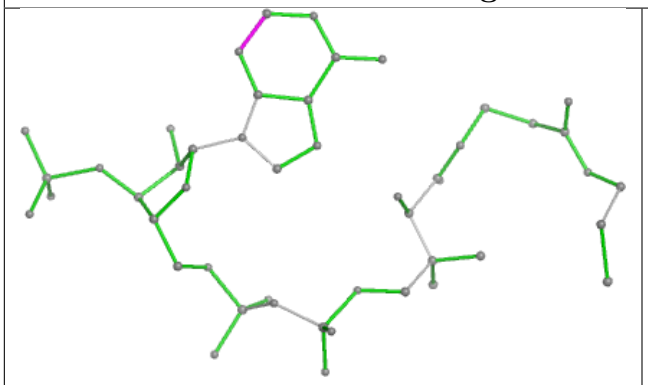


Torsions



Rings

Ligand COA A 1200 (A)



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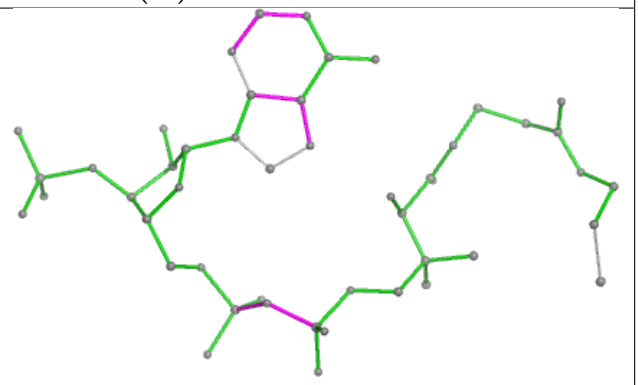

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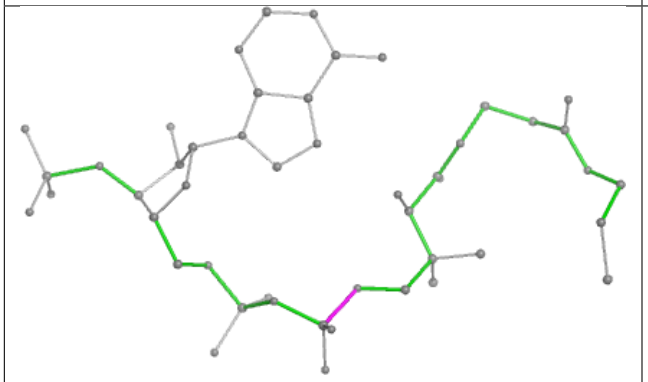

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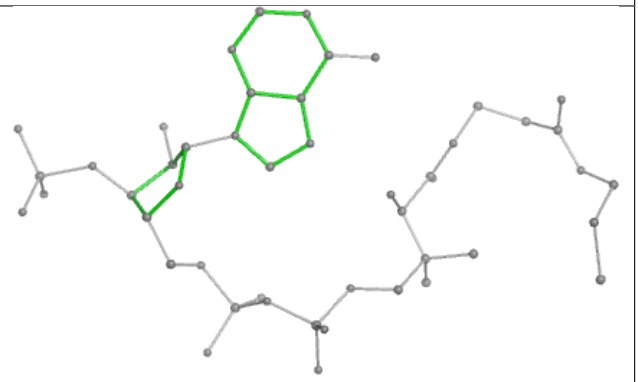

Rings

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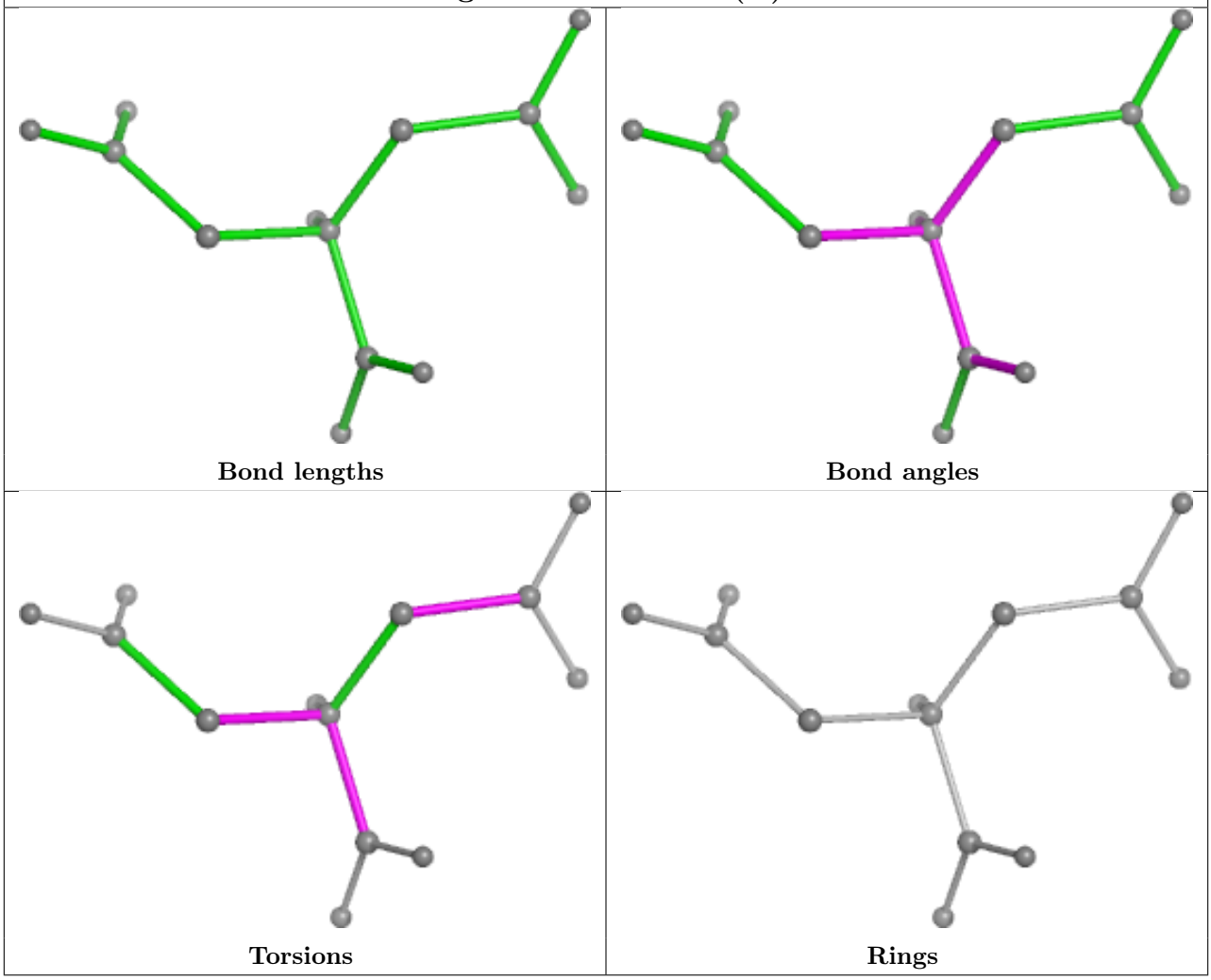
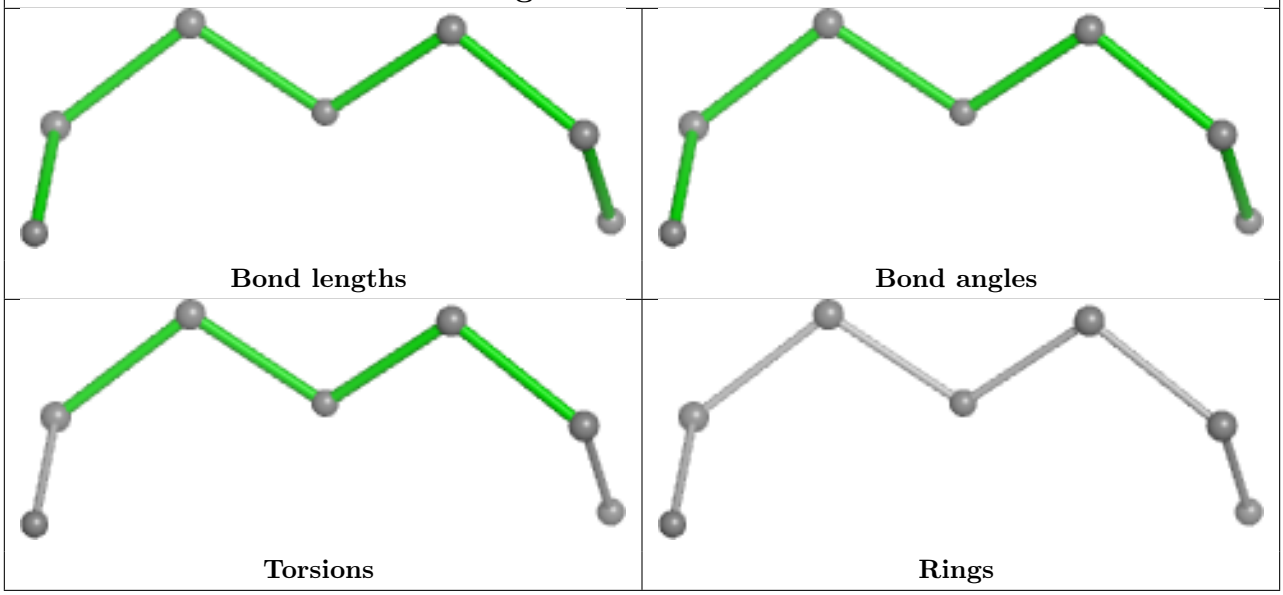
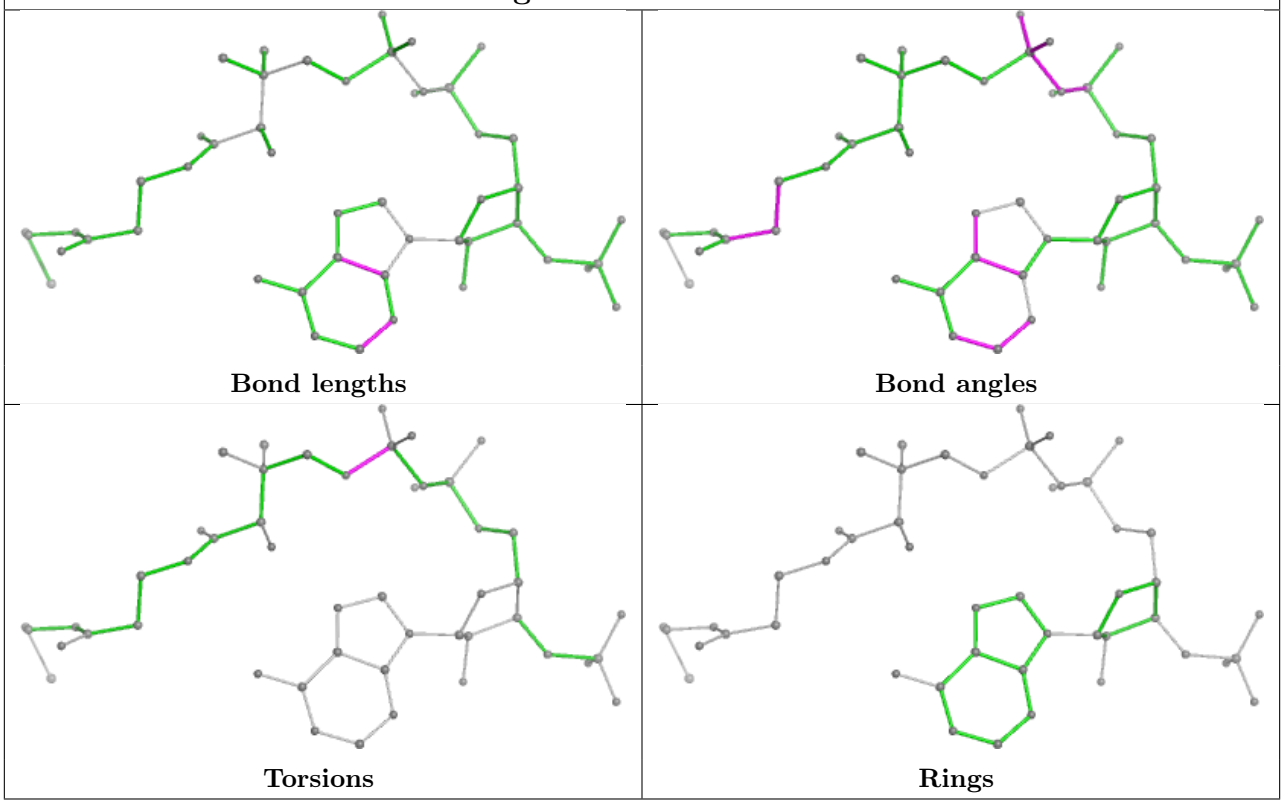


Ligand PEG B 1203



Ligand COA D 1201



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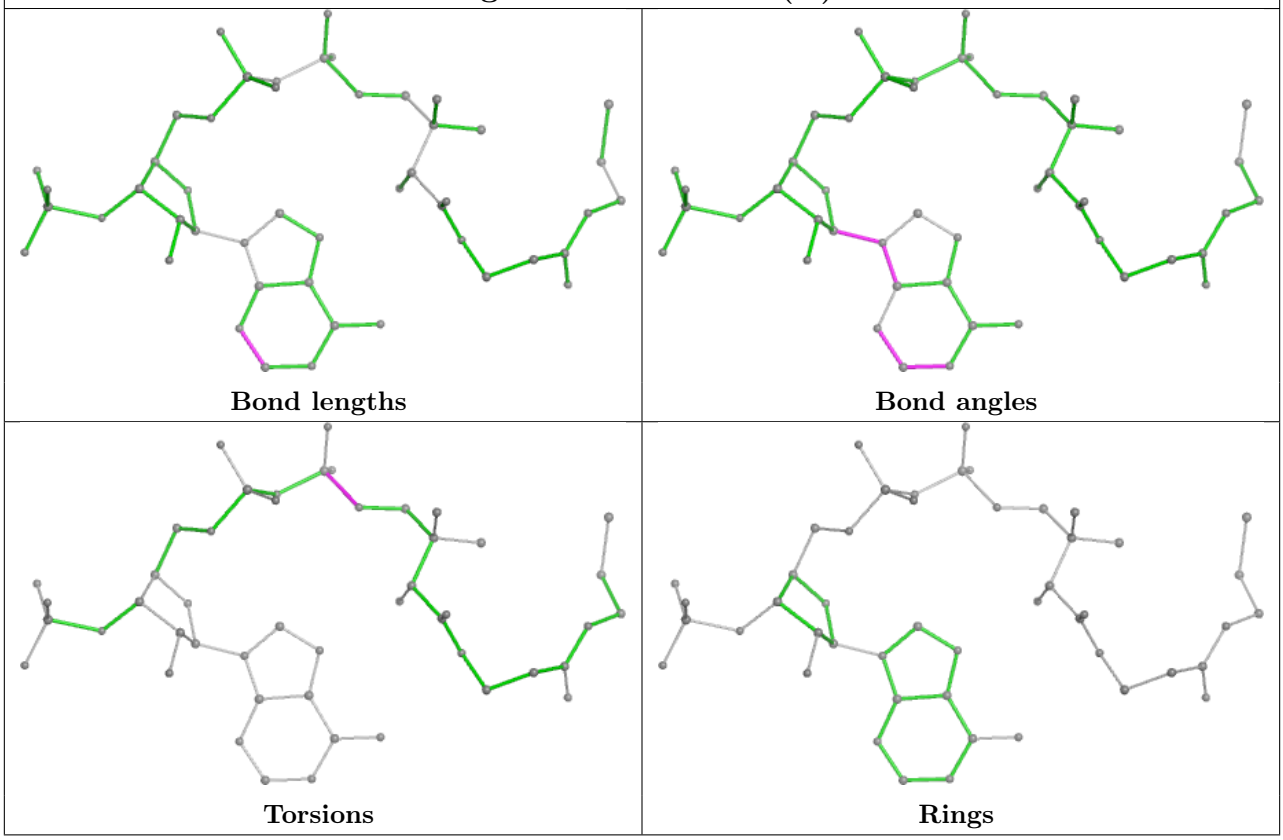
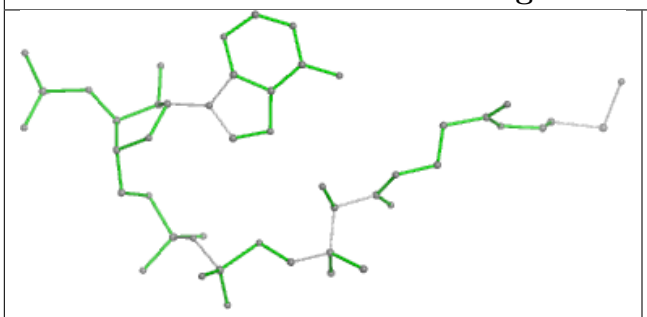
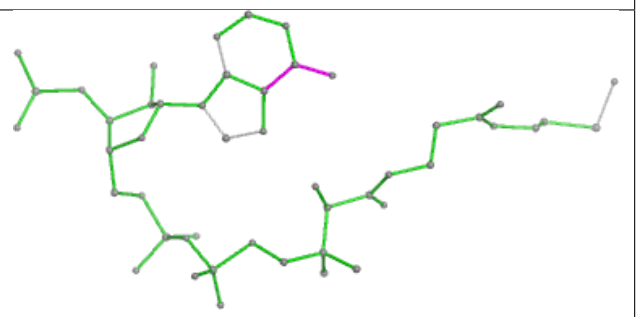


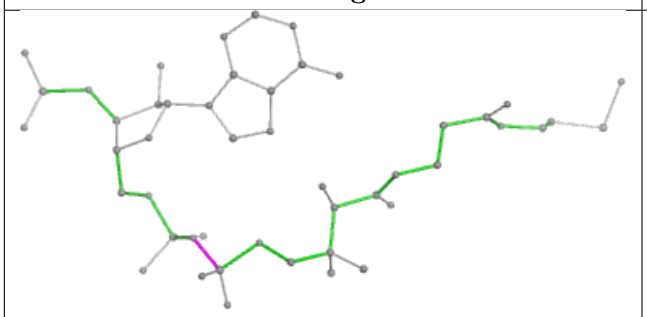
Ligand CAO F 1200



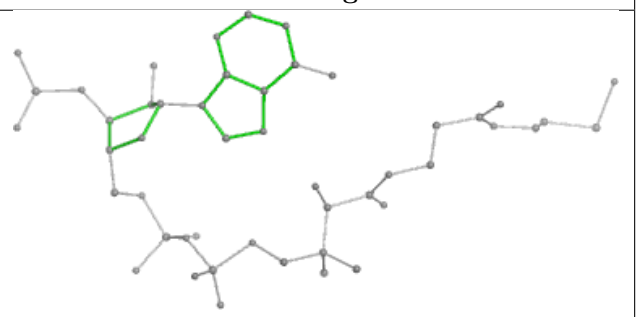
Bond lengths



Bond angles

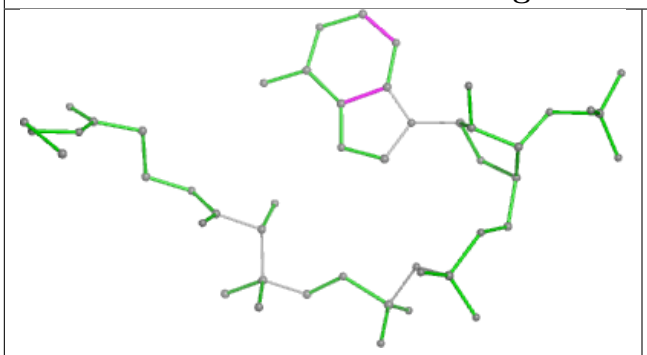


Torsions

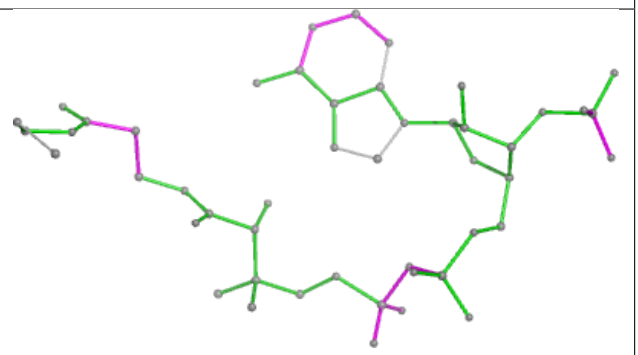


Rings

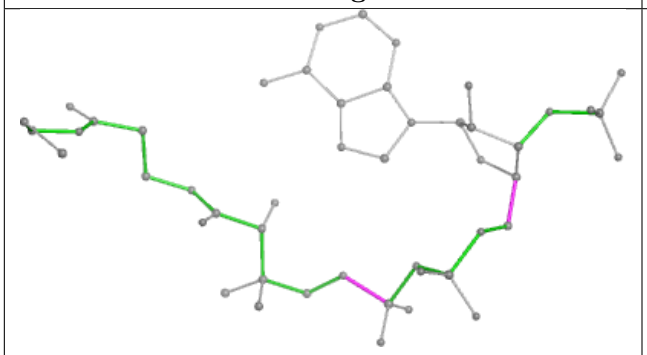
Ligand COA H 1201



Bond lengths



Bond angles



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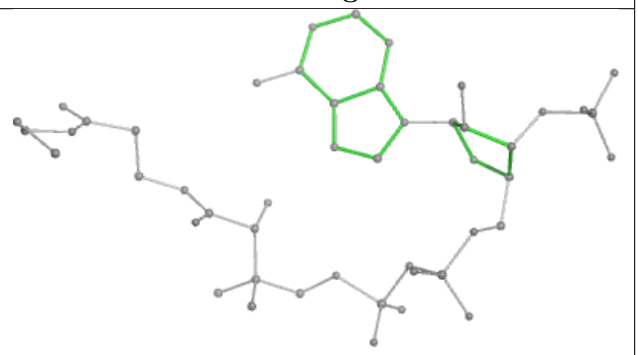
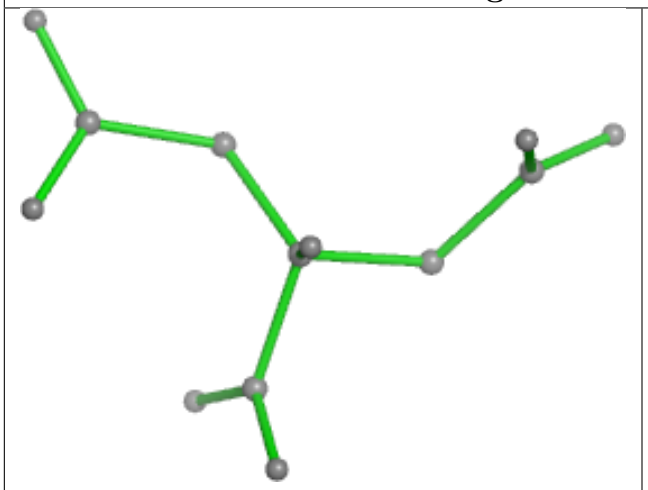
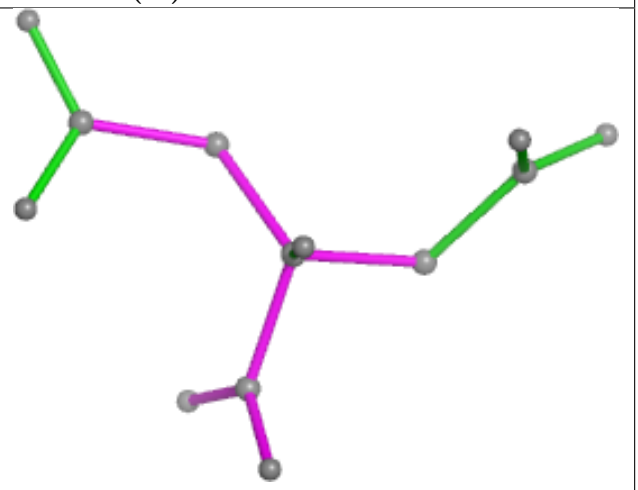


Rings

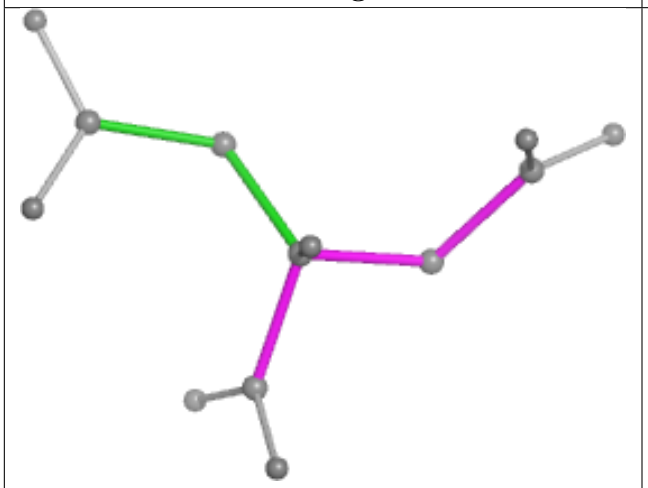
Ligand FLC E 1202 (A)



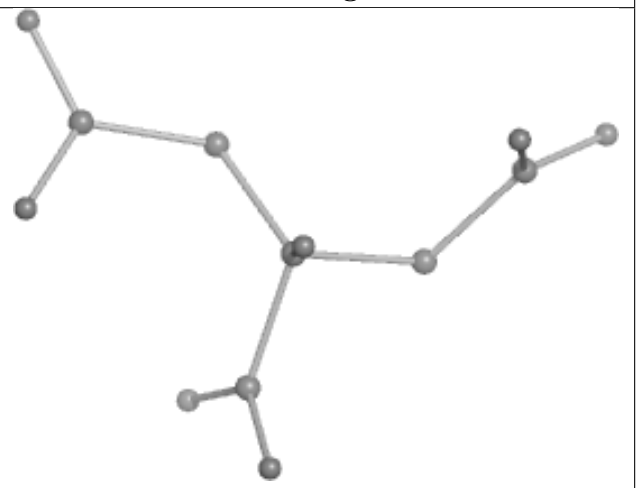
Bond lengths



Bond angles

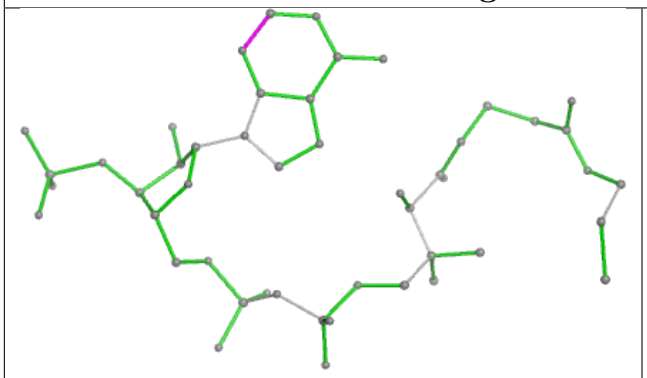


Torsions

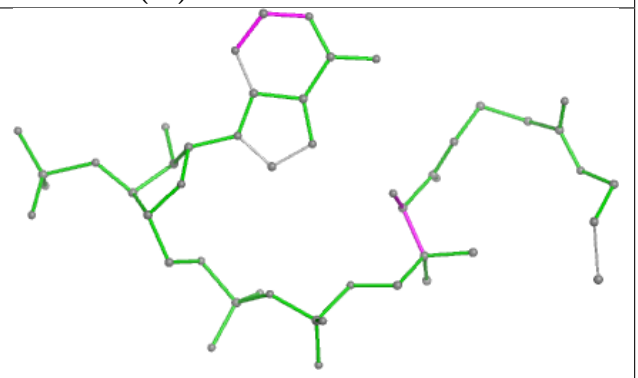


Rings

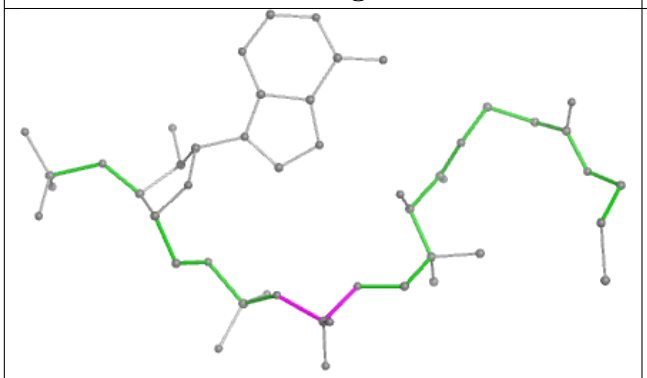
Ligand COA G 1200 (A)



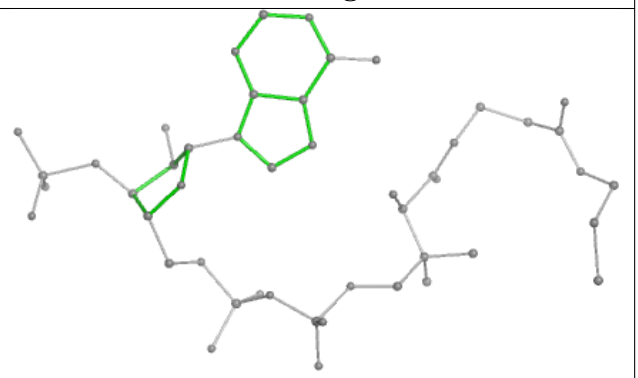
Bond lengths



Bond angles

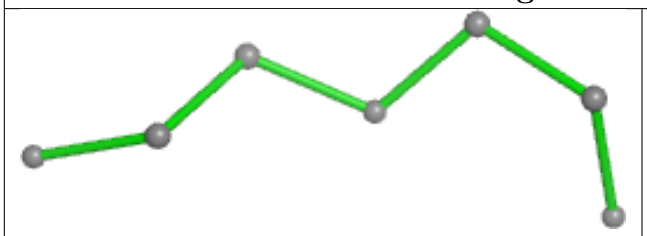


Torsions

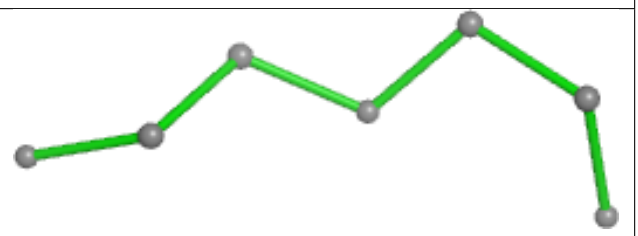


Rings

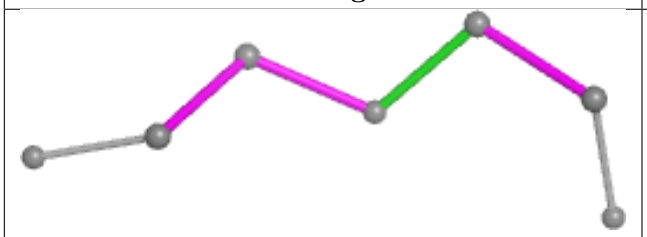
Ligand PEG E 1203



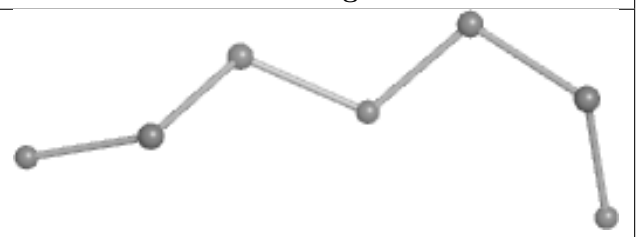
Bond lengths



Bond angles

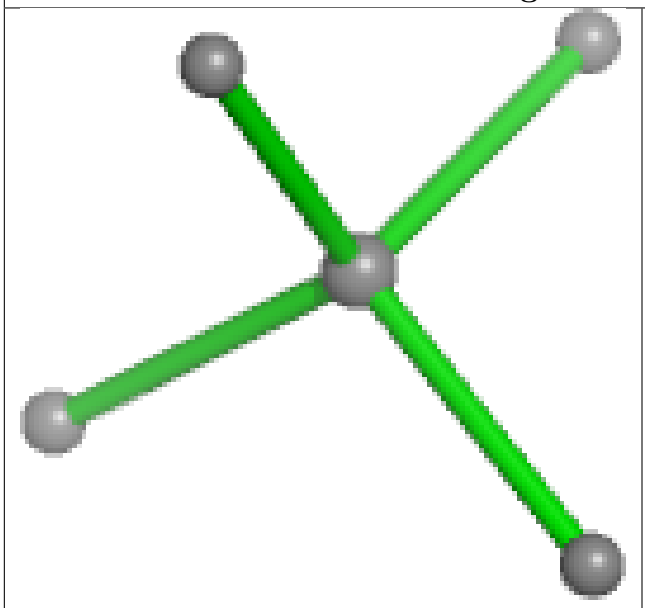


Torsions

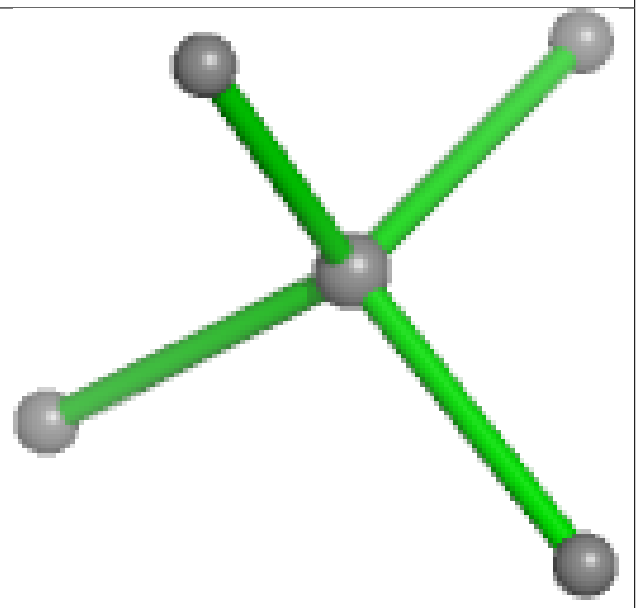


Rings

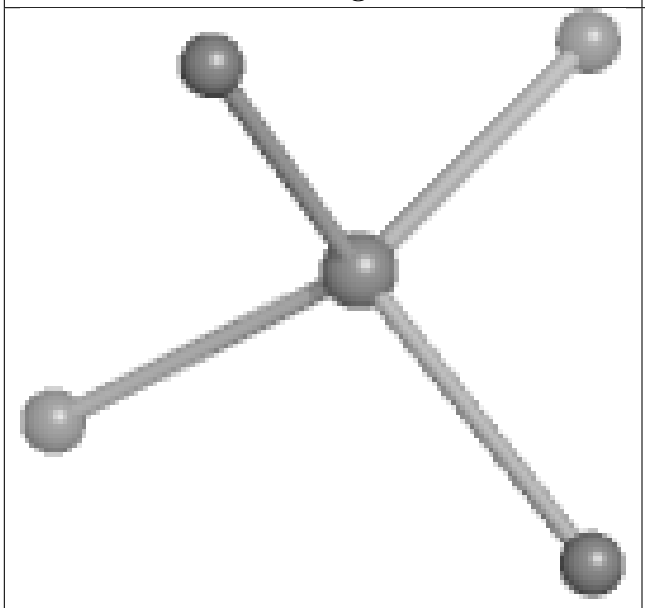
Ligand SO4 D 1202



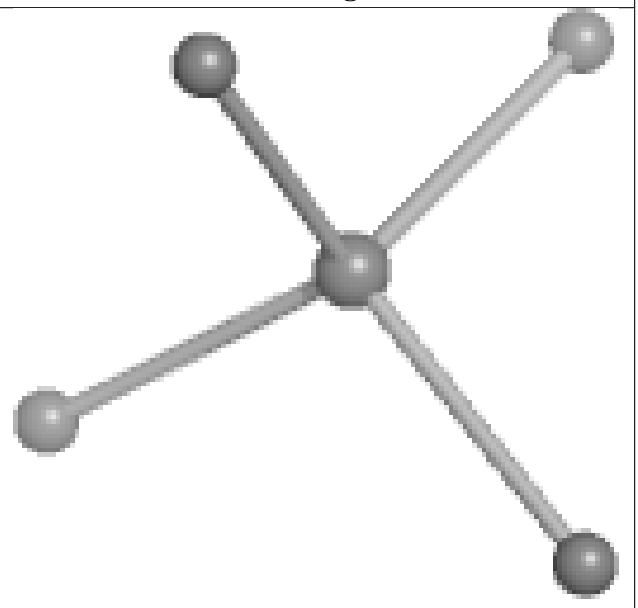
Bond lengths



Bond angles

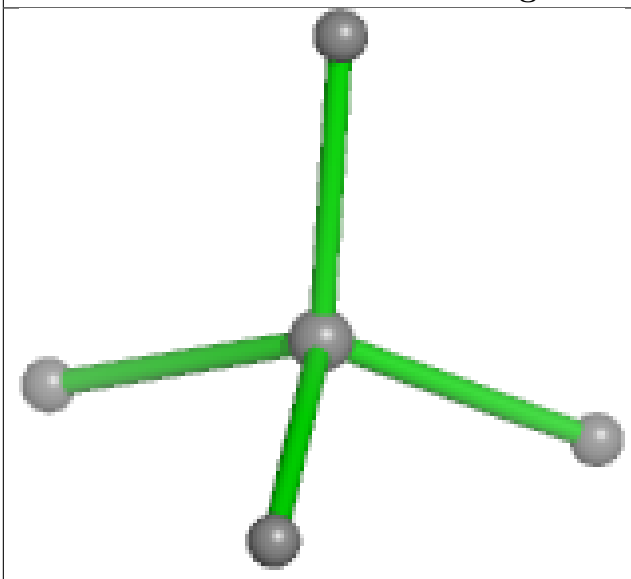


Torsions

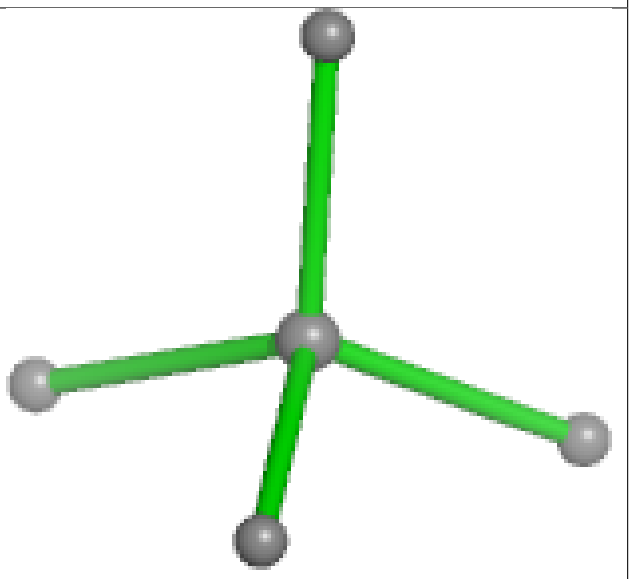


Rings

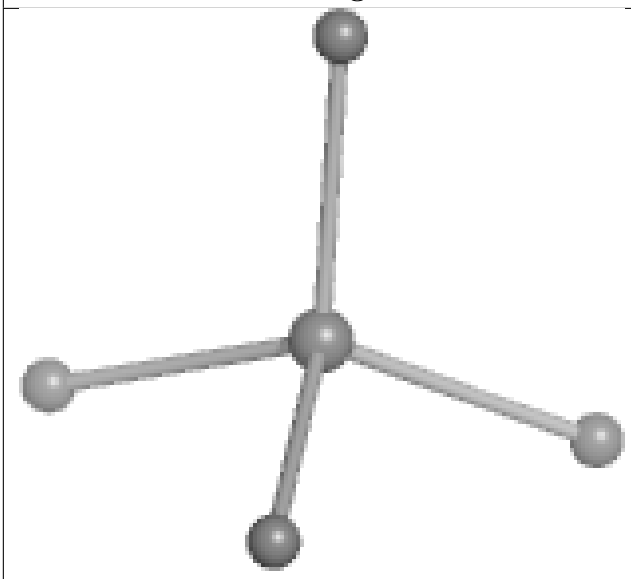
Ligand SO4 D 1203



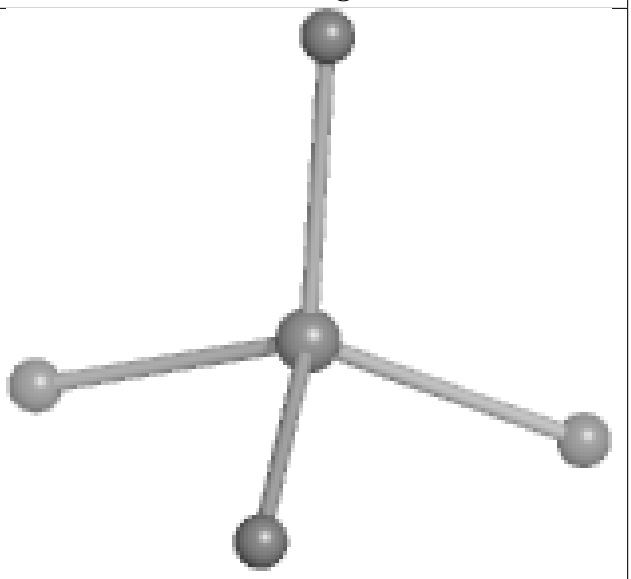
Bond lengths



Bond angles

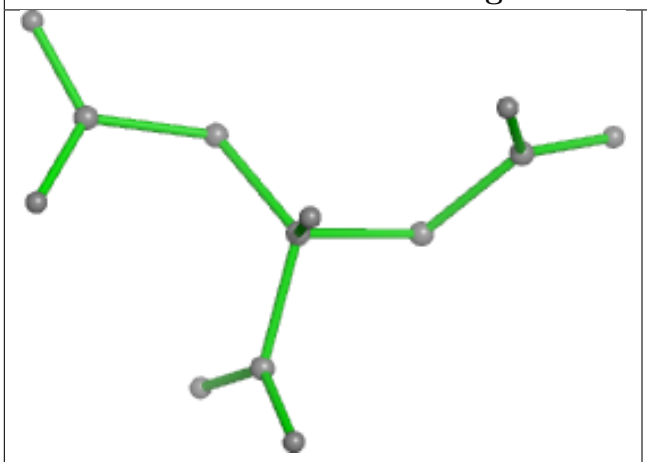


Torsions

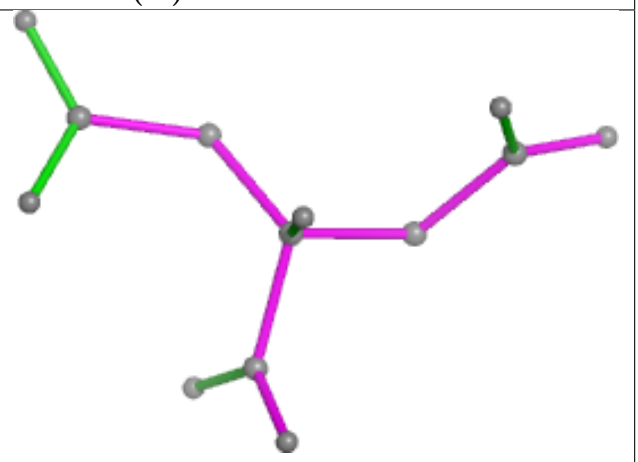


Rings

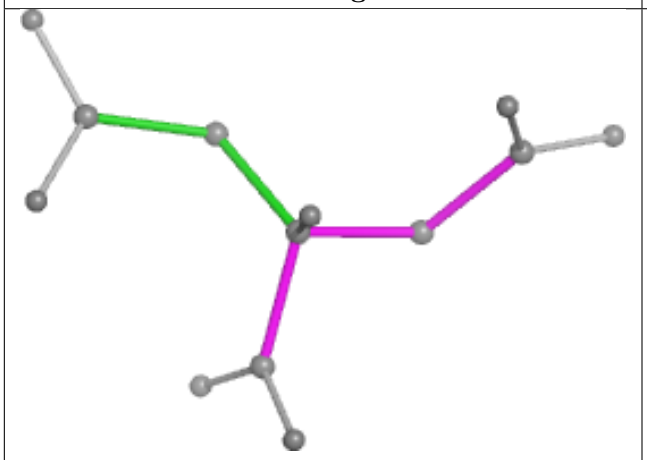
Ligand FLC B 1202 (A)



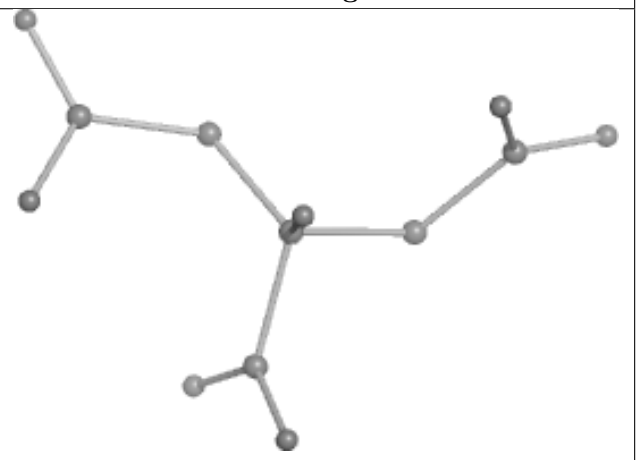
Bond lengths



Bond angles

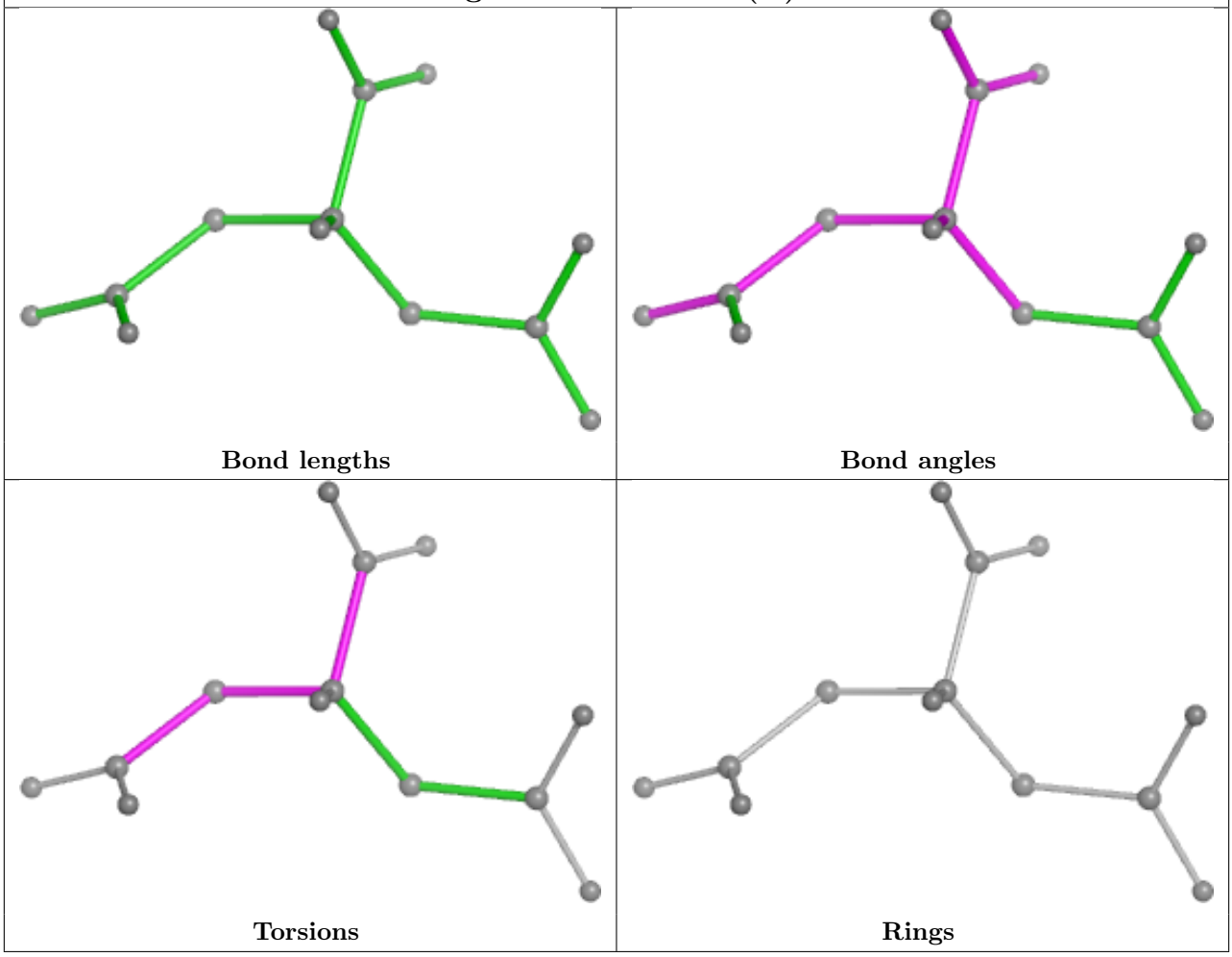


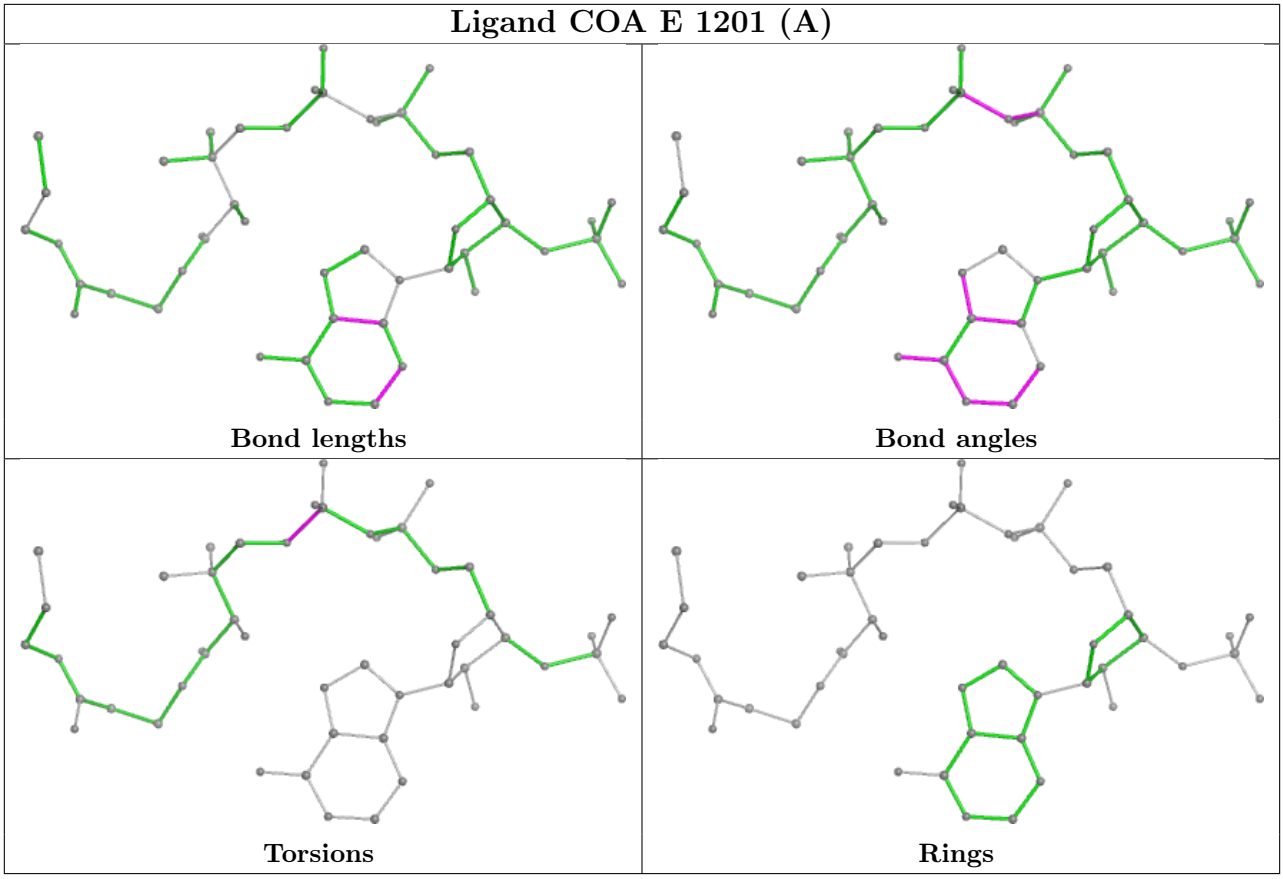
Torsions



Rings

Ligand FLC A 1201 (A)





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	263/270 (97%)	-0.10	4 (1%)	73	78	9, 15, 36, 51	0
1	B	261/270 (96%)	-0.08	9 (3%)	45	51	8, 15, 34, 60	0
1	C	262/270 (97%)	0.03	11 (4%)	36	41	9, 16, 37, 62	0
1	D	262/270 (97%)	-0.11	10 (3%)	40	45	9, 17, 43, 81	0
1	E	261/270 (96%)	0.48	31 (11%)	4	4	9, 18, 43, 66	0
1	F	263/270 (97%)	0.06	14 (5%)	26	29	9, 16, 37, 65	3 (1%)
1	G	262/270 (97%)	0.14	9 (3%)	45	51	8, 16, 35, 55	0
1	H	264/270 (97%)	-0.01	14 (5%)	26	29	9, 16, 38, 67	0
All	All	2098/2160 (97%)	0.05	102 (4%)	29	33	8, 16, 39, 81	3 (0%)

The worst 5 of 102 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	967	GLY	6.7
1	C	965	LYS	6.5
1	E	1013	ILE	6.1
1	C	836	LYS	5.7
1	E	980	ILE	5.4

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

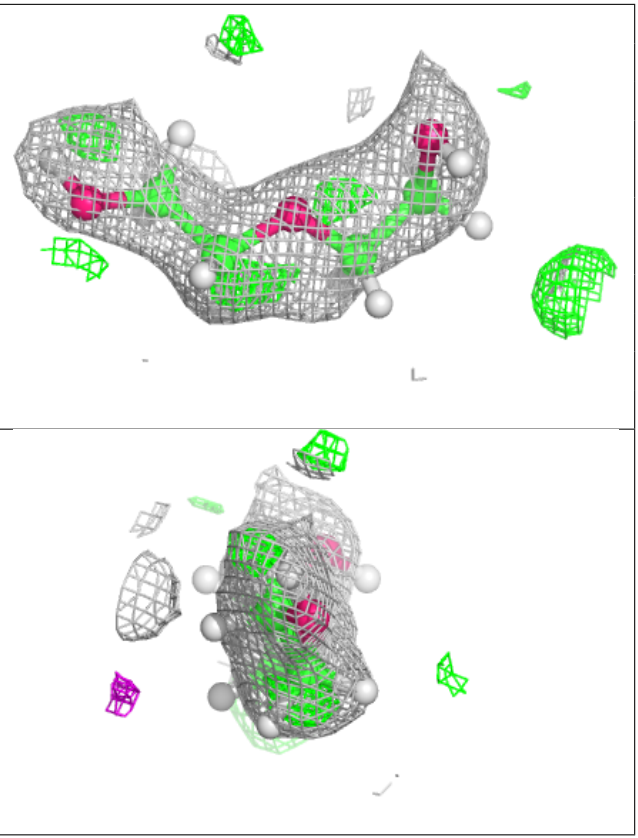
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

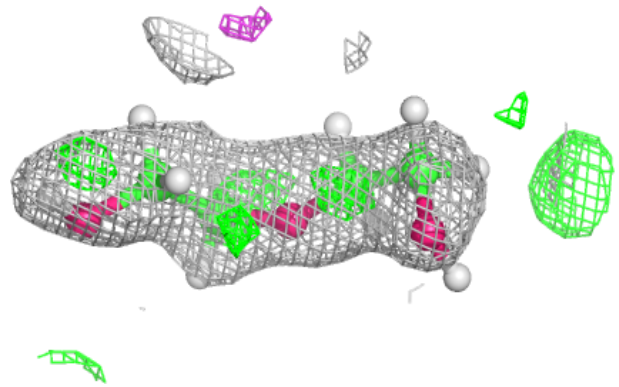
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	PEG	E	1203	7/7	0.81	0.15	39,42,46,46	0
4	PEG	B	1203	7/7	0.82	0.15	30,34,48,48	0
2	COA	H	1201	48/48	0.86	0.19	21,29,52,58	0
6	CAO	F	1200	49/49	0.88	0.13	9,28,47,54	0
2	COA	D	1201	48/48	0.89	0.12	19,29,49,56	0
2	COA	E	1201[A]	48/48	0.89	0.20	12,25,50,57	2
2	COA	C	1200[A]	48/48	0.91	0.10	13,23,42,47	2
7	EDO	H	1202	4/4	0.92	0.06	32,34,37,37	0
5	SO4	D	1202	5/5	0.93	0.15	22,30,34,37	0
3	FLC	G	1201[A]	13/13	0.94	0.08	12,17,23,24	0
2	COA	G	1200[A]	48/48	0.94	0.13	11,18,36,45	2
3	FLC	E	1202[A]	13/13	0.94	0.08	15,20,29,29	0
3	FLC	A	1201[A]	13/13	0.95	0.08	12,16,26,26	0
2	COA	A	1200[A]	48/48	0.95	0.09	12,18,38,46	2
3	FLC	C	1201[A]	13/13	0.96	0.08	13,16,24,26	0
2	COA	B	1201[A]	48/48	0.97	0.10	6,11,20,29	80
3	FLC	B	1202[A]	13/13	0.97	0.07	10,14,19,20	0
5	SO4	D	1203	5/5	0.99	0.08	13,13,16,20	5

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 PEG E 1203:

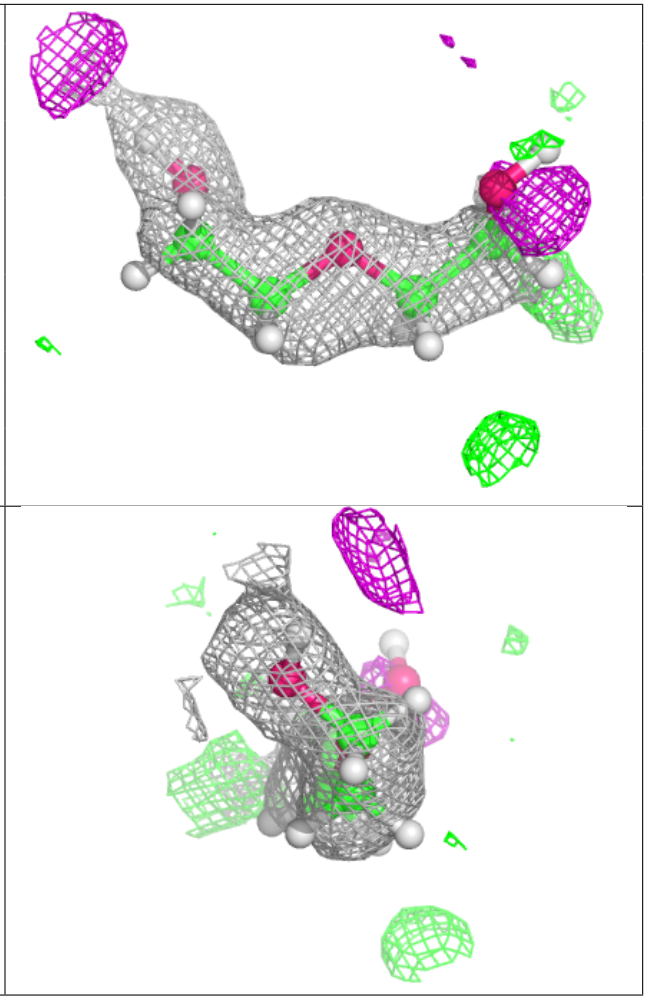
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





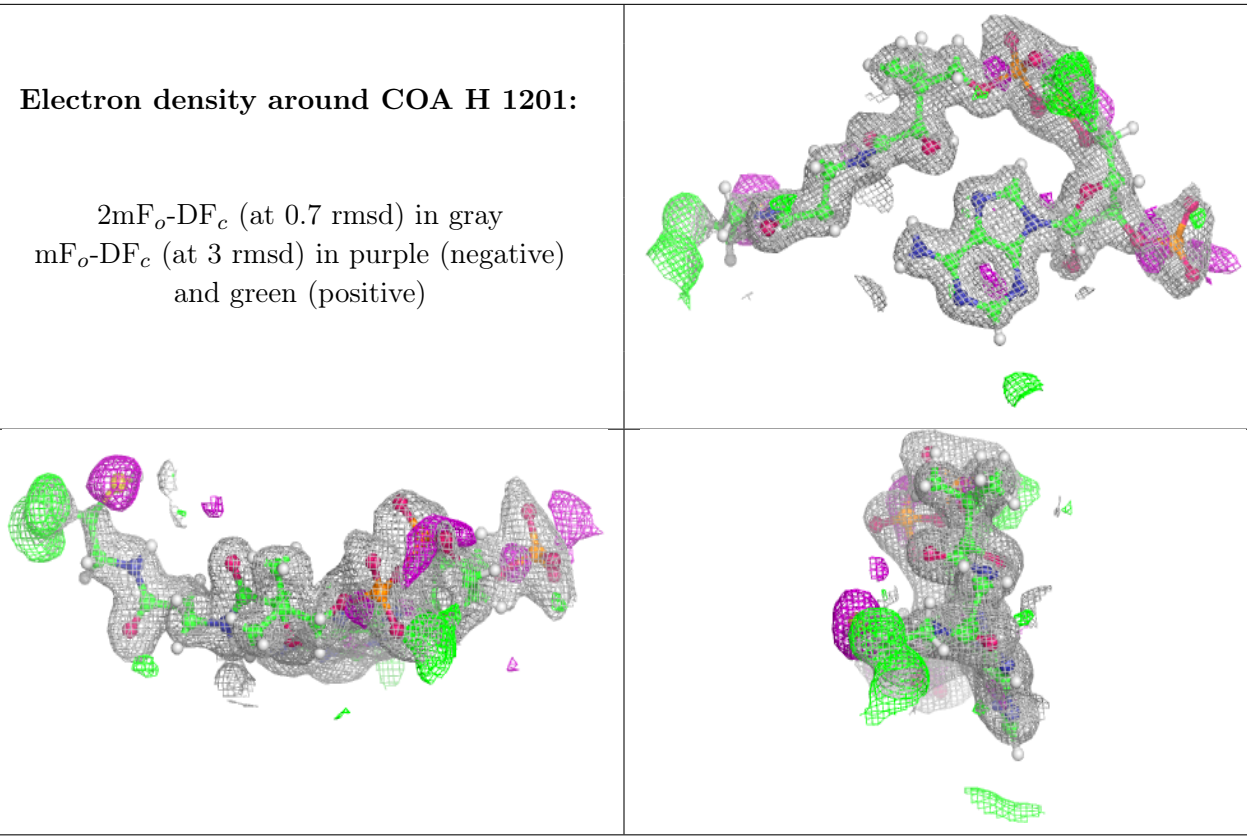
Electron density around PEG B 1203:

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



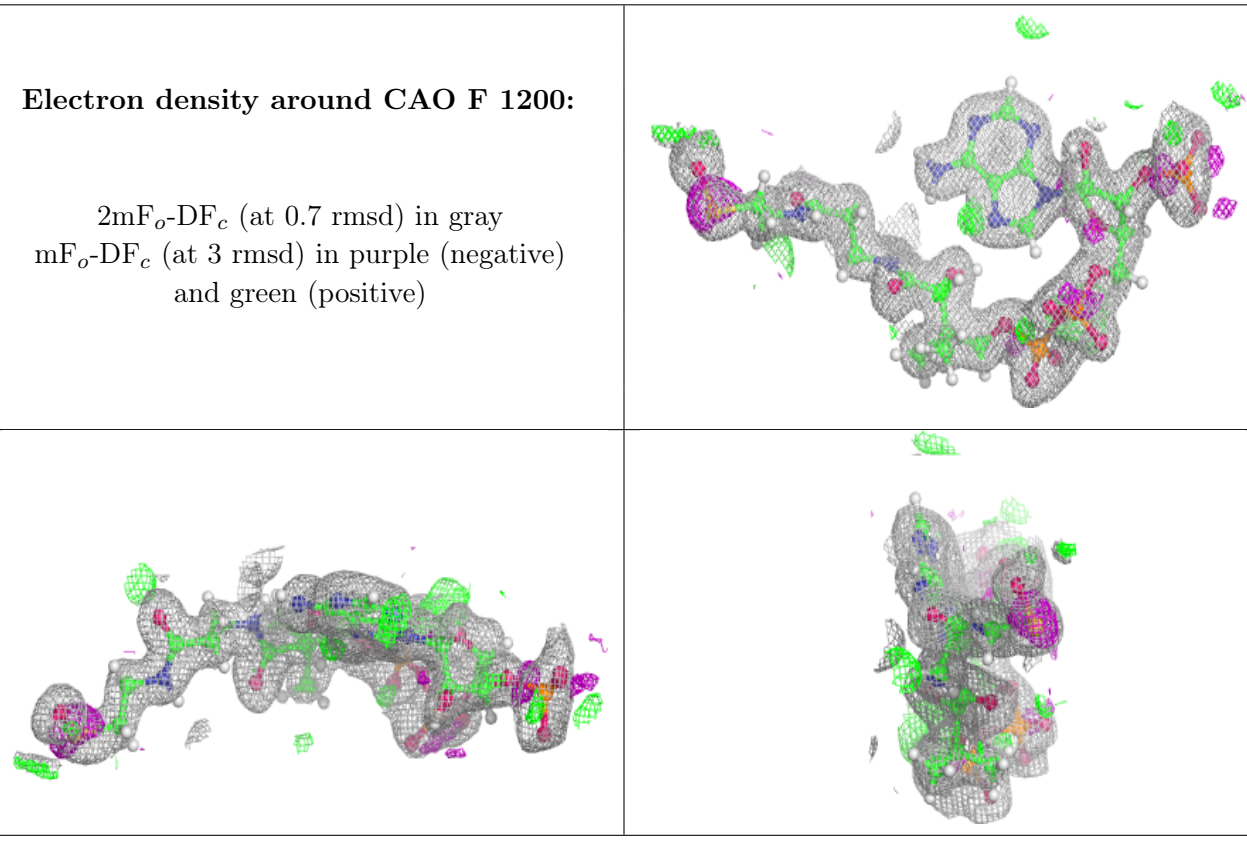
Electron density around COA H 1201:

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



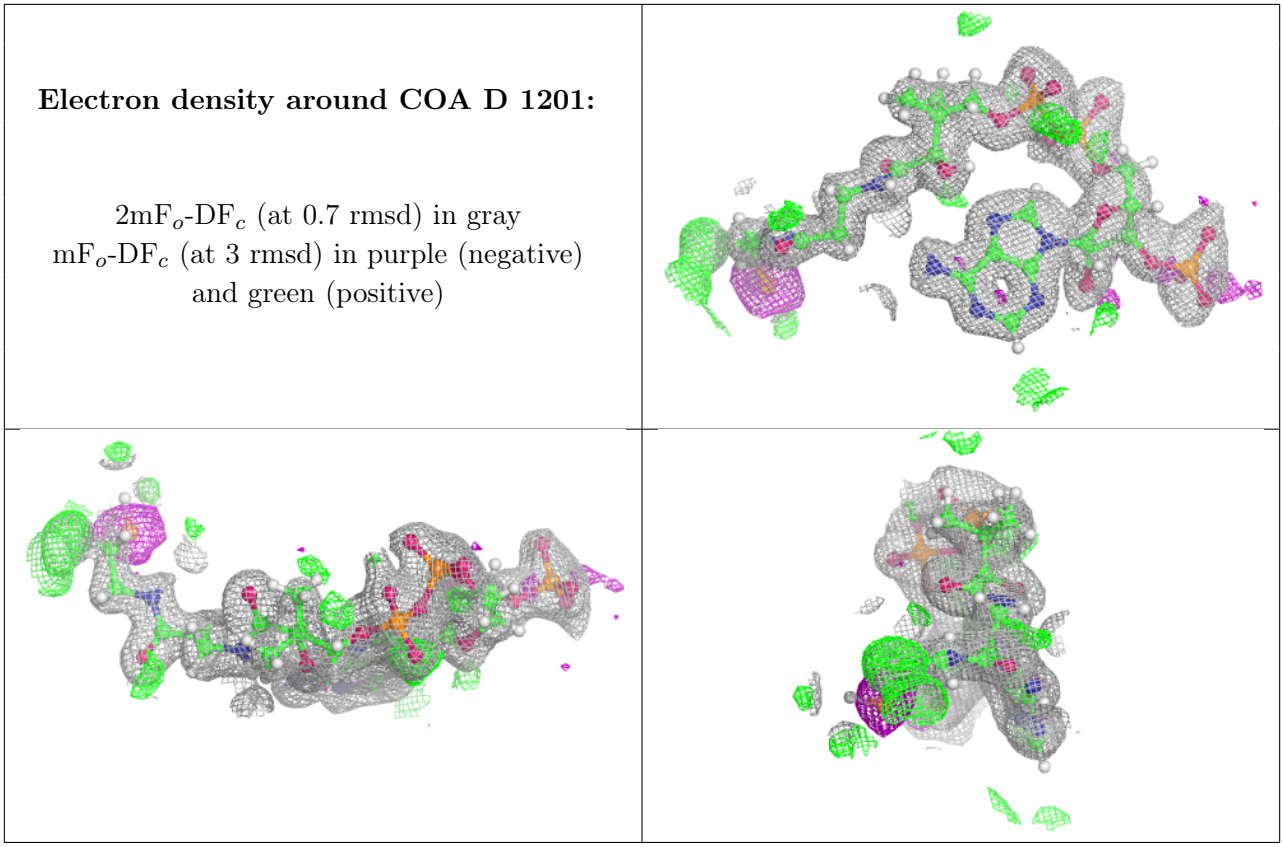
Electron density around CAO F 1200:

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



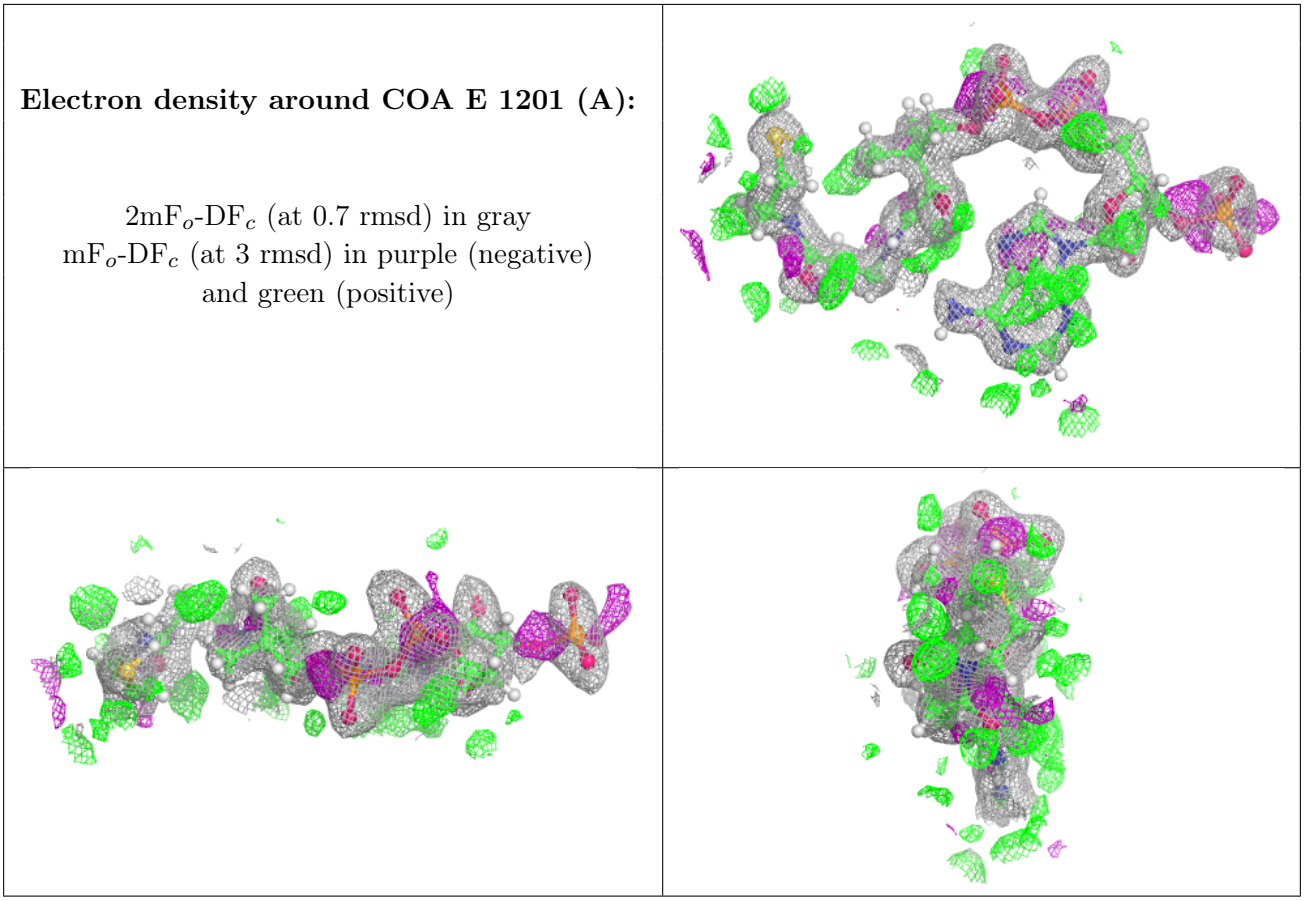
Electron density around COA D 1201:

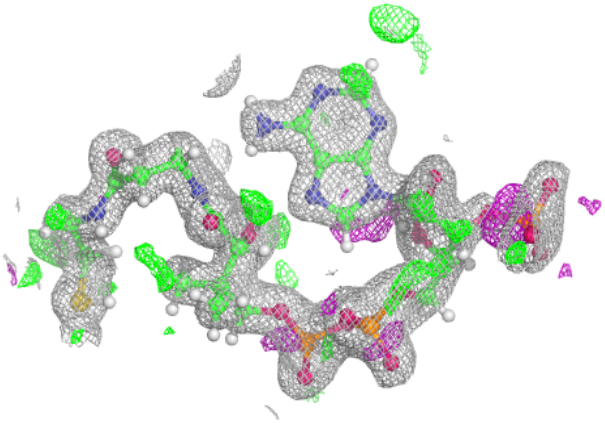
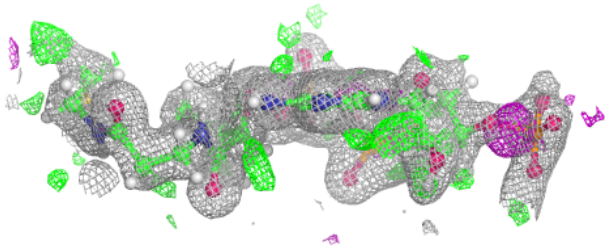
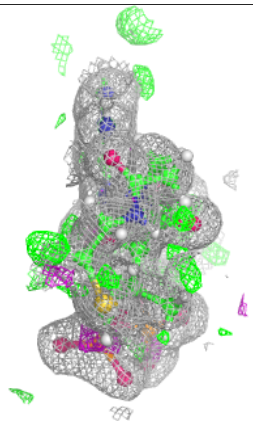
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around COA E 1201 (A):

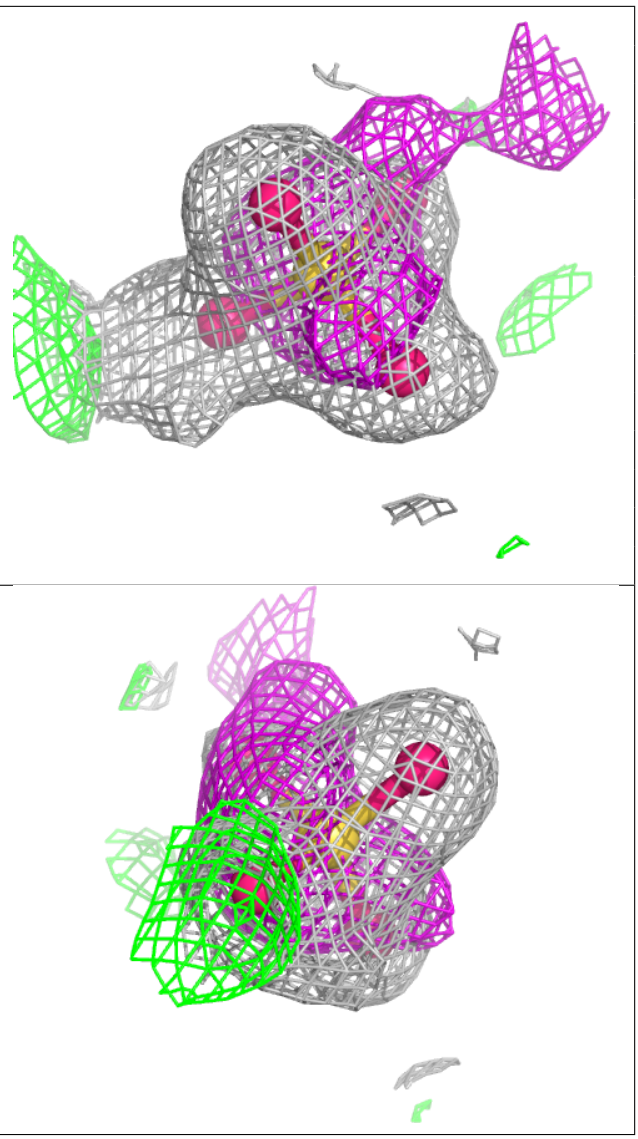
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around COA C 1200 (A): $2mF_o$-DF_c (at 0.7 rmsd) in gray mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)	
	

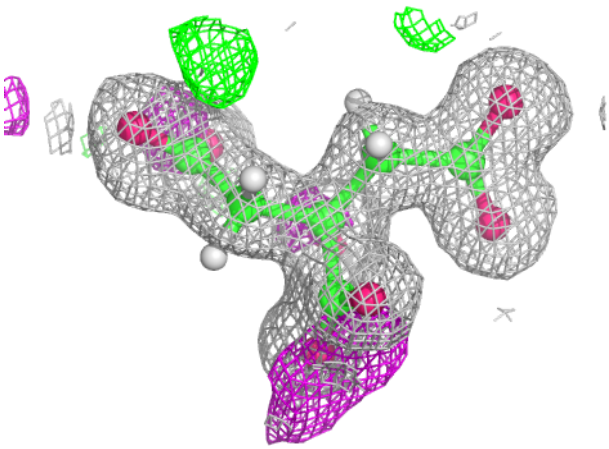
Electron density around SO4 D 1202:

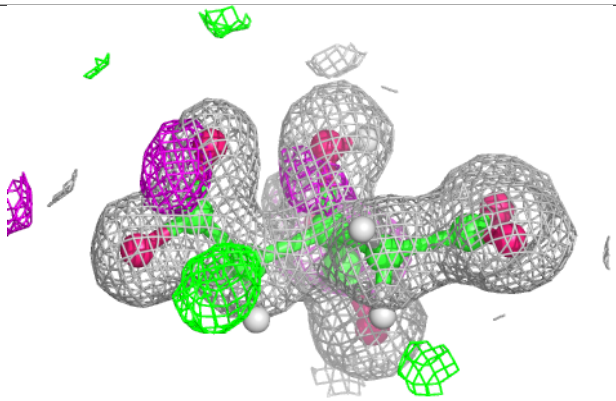
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

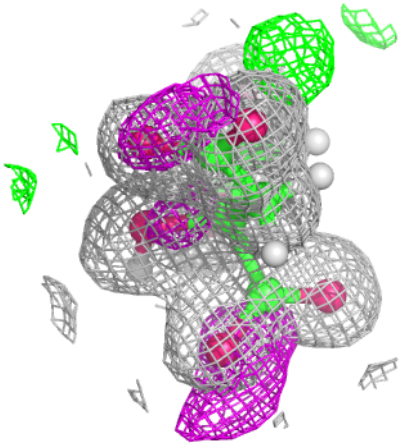


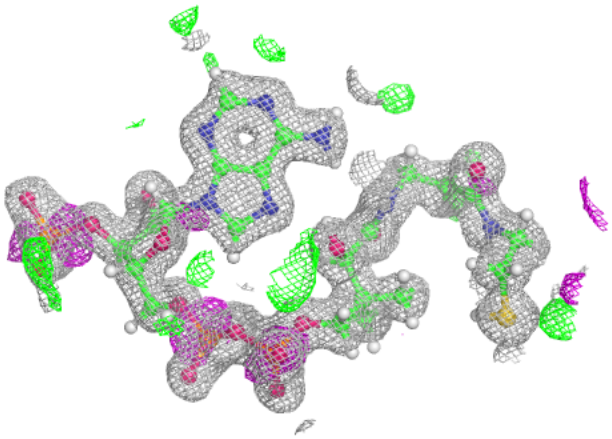
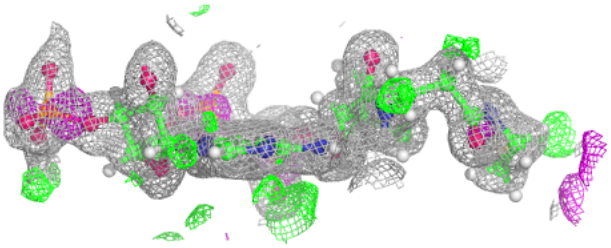
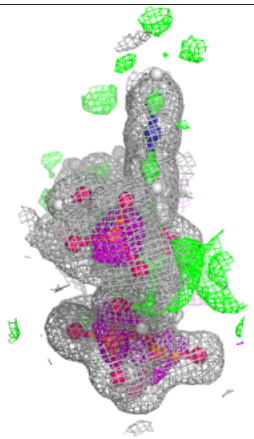
Electron density around FLC G 1201 (A):

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



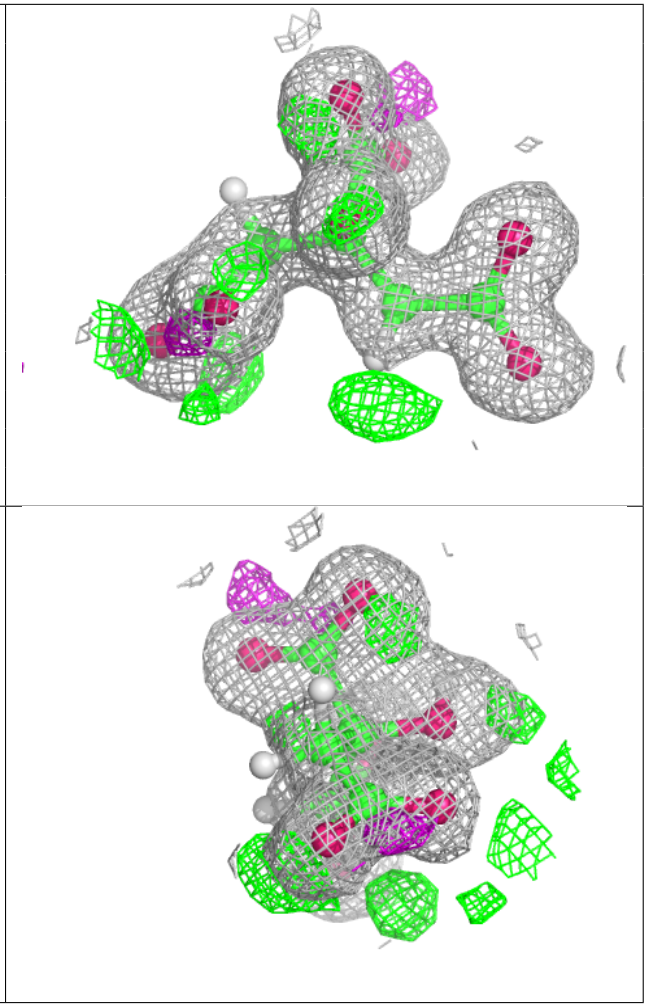




Electron density around COA G 1200 (A): $2mF_o$-DF_c (at 0.7 rmsd) in gray mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)	
	

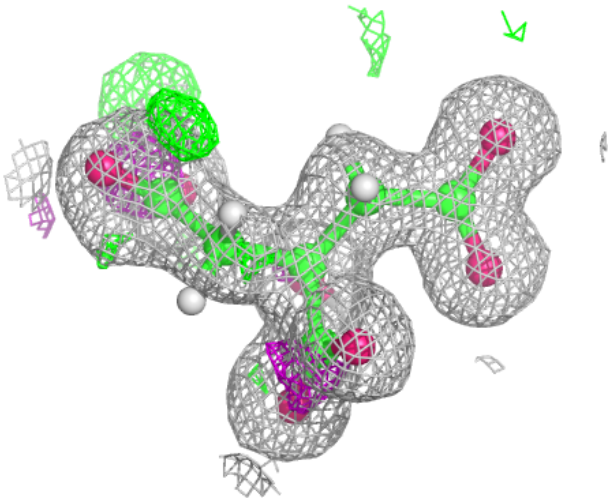
Electron density around FLC E 1202 (A):

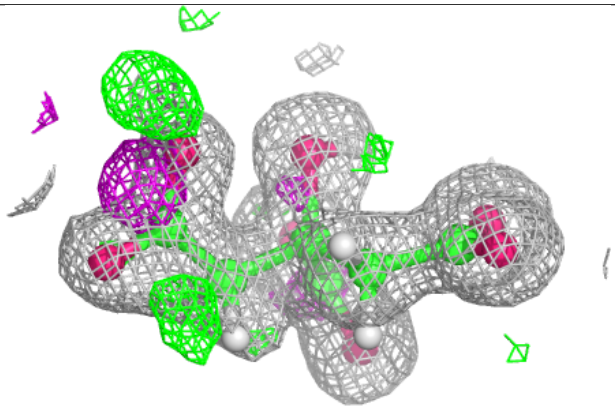
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

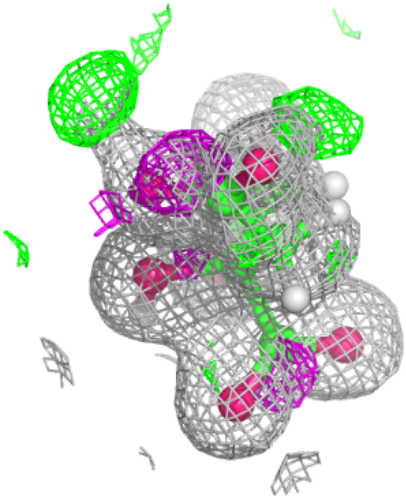


Electron density around FLC A 1201 (A):

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

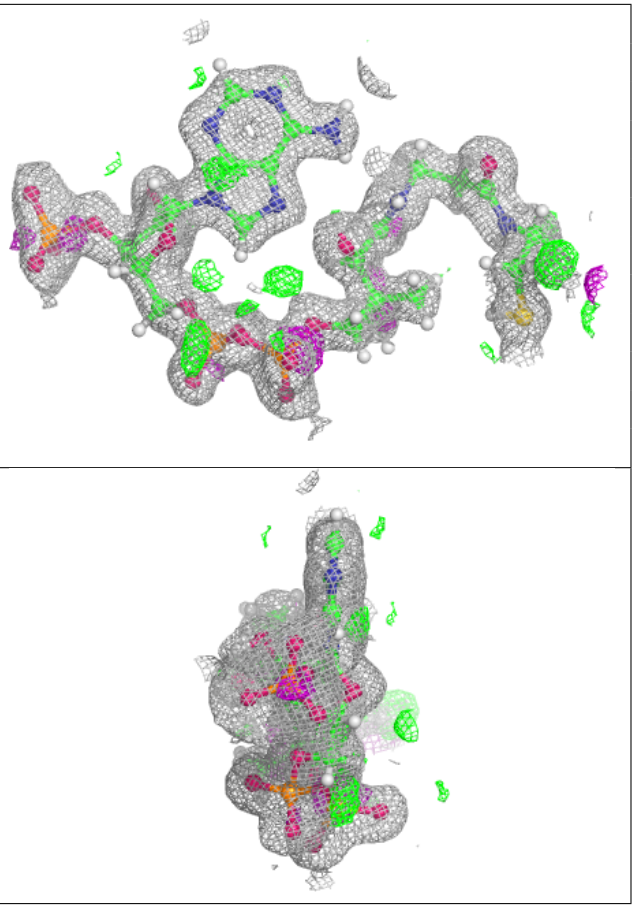






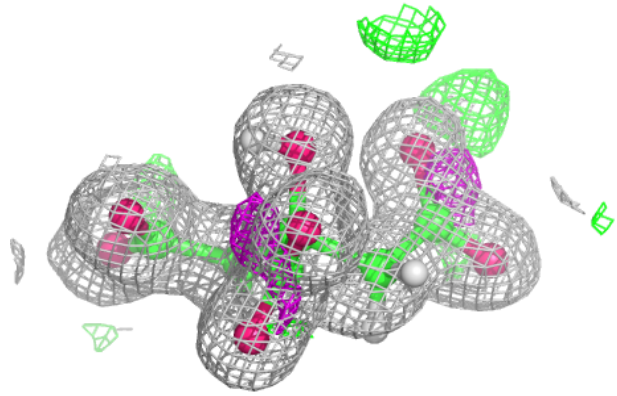
Electron density around COA A 1200 (A):

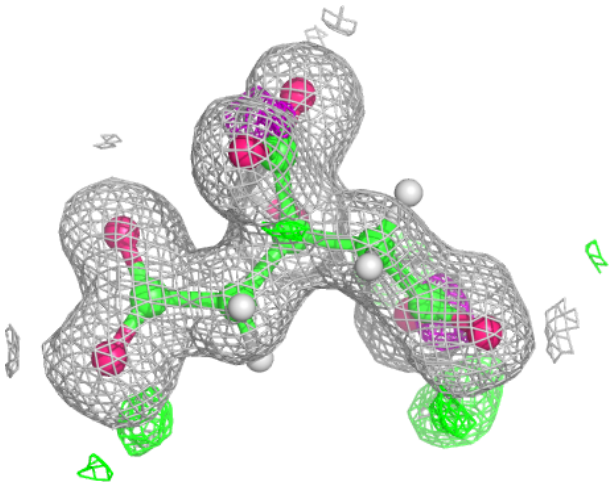
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

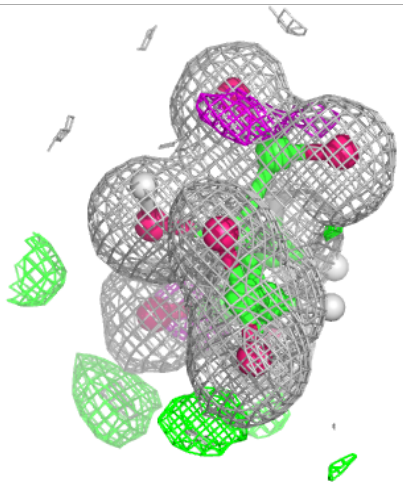


Electron density around FLC C 1201 (A):

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

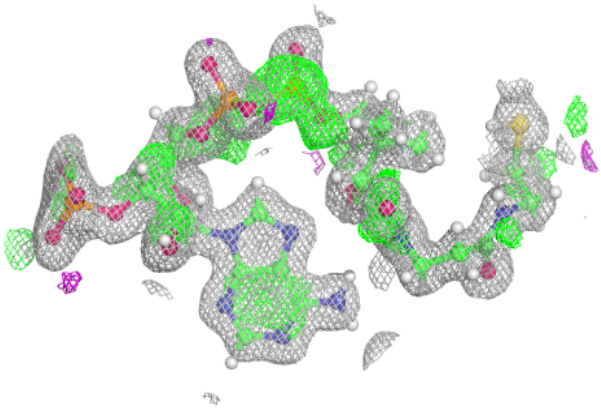


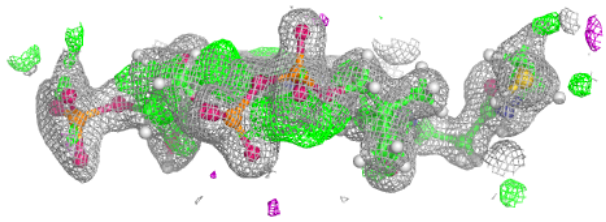


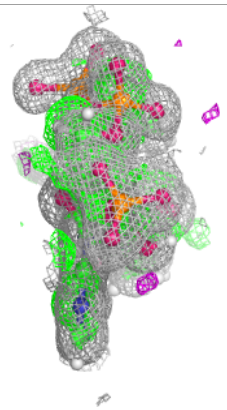


Electron density around COA B 1201 (A):

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

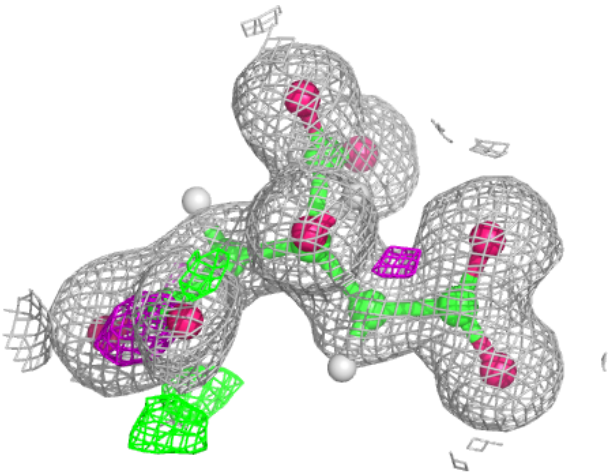


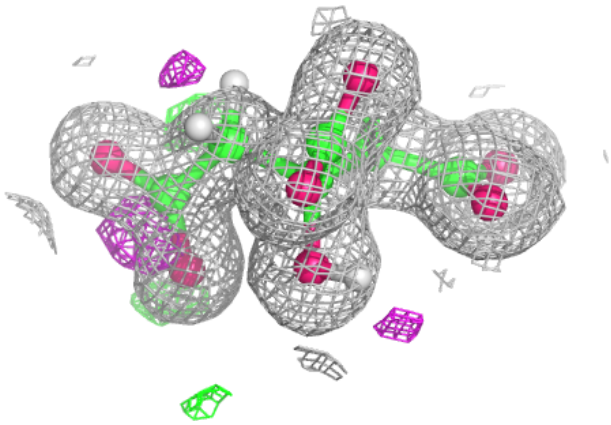


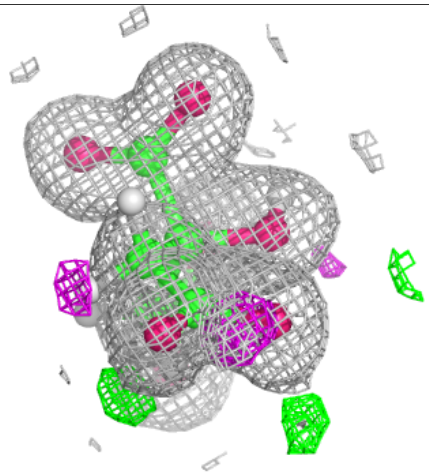


Electron density around FLC B 1202 (A):

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

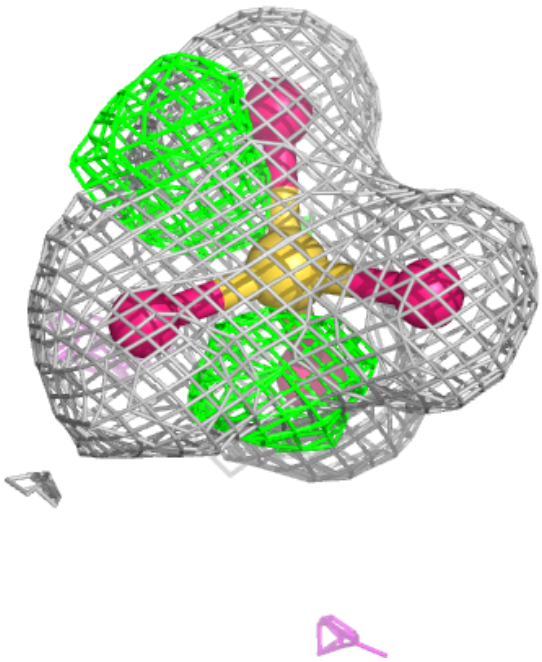


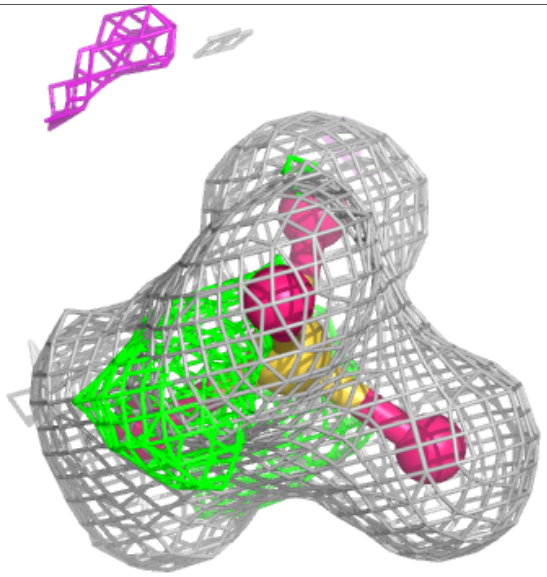


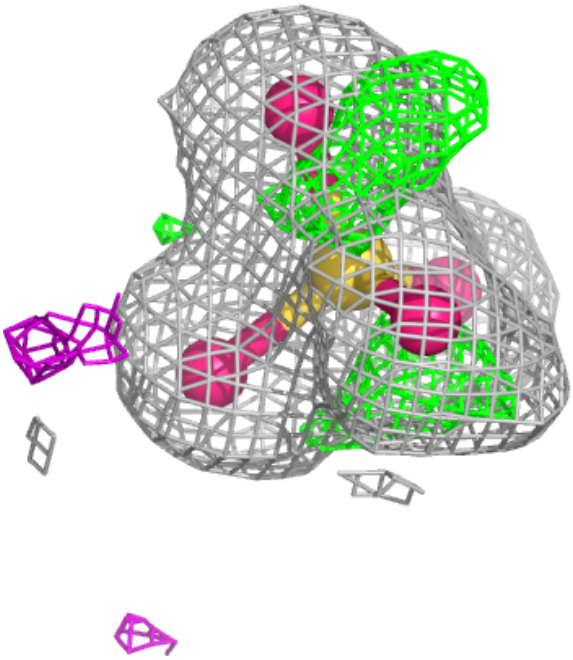


Electron density around SO4 D 1203:

$2mF_o$-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.