wwPDB X-ray Structure Validation Summary Report (i)

Aug 20, 2020 – 09:35 PM BST

PDB ID	:	6PCC
Title	:	Crystal structure of beta-ketoadipyl-CoA thiolase mutant (H356A) in complex hexanoyl coenzyme A
Authors	:	Sukritee, B.; Panjikar, S.
Deposited on	:	2019-06-17
Resolution	:	1.96 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 following versions of software and data (see references (1)) were used in the production of this report:

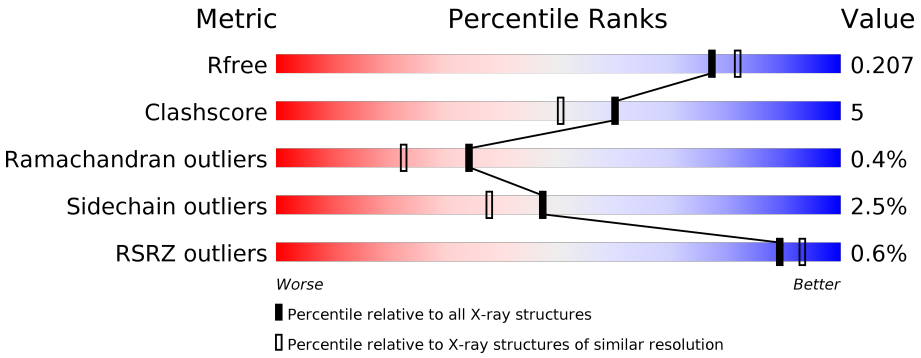
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 on 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	423	85% 9% • 5%
1	B	423	% 87% 7% 6%
1	C	423	87% 6% 6%
1	D	423	86% 9% 5%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	O8Y	A	1002	-	-	X	-
3	O8Y	B	502	-	-	X	-
3	O8Y	C	502	-	-	X	-
3	O8Y	D	502	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13336 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 Beta-ketoadipyl-CoA thiolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	3	0
			2972	1849	539	566	18			
1	B	398	Total	C	N	O	S	0	7	0
			2975	1849	539	567	20			
1	C	396	Total	C	N	O	S	0	5	0
			2934	1825	529	561	19			
1	D	402	Total	C	N	O	S	0	7	0
			2996	1863	543	572	18			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP Q88N39
A	-21	HIS	-	expression tag	UNP Q88N39
A	-20	HIS	-	expression tag	UNP Q88N39
A	-19	HIS	-	expression tag	UNP Q88N39
A	-18	HIS	-	expression tag	UNP Q88N39
A	-17	HIS	-	expression tag	UNP Q88N39
A	-16	HIS	-	expression tag	UNP Q88N39
A	-15	SER	-	expression tag	UNP Q88N39
A	-14	SER	-	expression tag	UNP Q88N39
A	-13	GLY	-	expression tag	UNP Q88N39
A	-12	VAL	-	expression tag	UNP Q88N39
A	-11	ASP	-	expression tag	UNP Q88N39
A	-10	LEU	-	expression tag	UNP Q88N39
A	-9	GLY	-	expression tag	UNP Q88N39
A	-8	THR	-	expression tag	UNP Q88N39
A	-7	GLU	-	expression tag	UNP Q88N39
A	-6	ASN	-	expression tag	UNP Q88N39
A	-5	LEU	-	expression tag	UNP Q88N39
A	-4	TYR	-	expression tag	UNP Q88N39
A	-3	HIS	-	expression tag	UNP Q88N39
A	-2	GLN	-	expression tag	UNP Q88N39

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q88N39
A	0	SER	-	expression tag	UNP Q88N39
A	356	ALA	HIS	engineered mutation	UNP Q88N39
B	-22	MET	-	initiating methionine	UNP Q88N39
B	-21	HIS	-	expression tag	UNP Q88N39
B	-20	HIS	-	expression tag	UNP Q88N39
B	-19	HIS	-	expression tag	UNP Q88N39
B	-18	HIS	-	expression tag	UNP Q88N39
B	-17	HIS	-	expression tag	UNP Q88N39
B	-16	HIS	-	expression tag	UNP Q88N39
B	-15	SER	-	expression tag	UNP Q88N39
B	-14	SER	-	expression tag	UNP Q88N39
B	-13	GLY	-	expression tag	UNP Q88N39
B	-12	VAL	-	expression tag	UNP Q88N39
B	-11	ASP	-	expression tag	UNP Q88N39
B	-10	LEU	-	expression tag	UNP Q88N39
B	-9	GLY	-	expression tag	UNP Q88N39
B	-8	THR	-	expression tag	UNP Q88N39
B	-7	GLU	-	expression tag	UNP Q88N39
B	-6	ASN	-	expression tag	UNP Q88N39
B	-5	LEU	-	expression tag	UNP Q88N39
B	-4	TYR	-	expression tag	UNP Q88N39
B	-3	HIS	-	expression tag	UNP Q88N39
B	-2	GLN	-	expression tag	UNP Q88N39
B	-1	GLY	-	expression tag	UNP Q88N39
B	0	SER	-	expression tag	UNP Q88N39
B	356	ALA	HIS	engineered mutation	UNP Q88N39
C	-22	MET	-	initiating methionine	UNP Q88N39
C	-21	HIS	-	expression tag	UNP Q88N39
C	-20	HIS	-	expression tag	UNP Q88N39
C	-19	HIS	-	expression tag	UNP Q88N39
C	-18	HIS	-	expression tag	UNP Q88N39
C	-17	HIS	-	expression tag	UNP Q88N39
C	-16	HIS	-	expression tag	UNP Q88N39
C	-15	SER	-	expression tag	UNP Q88N39
C	-14	SER	-	expression tag	UNP Q88N39
C	-13	GLY	-	expression tag	UNP Q88N39
C	-12	VAL	-	expression tag	UNP Q88N39
C	-11	ASP	-	expression tag	UNP Q88N39
C	-10	LEU	-	expression tag	UNP Q88N39
C	-9	GLY	-	expression tag	UNP Q88N39
C	-8	THR	-	expression tag	UNP Q88N39

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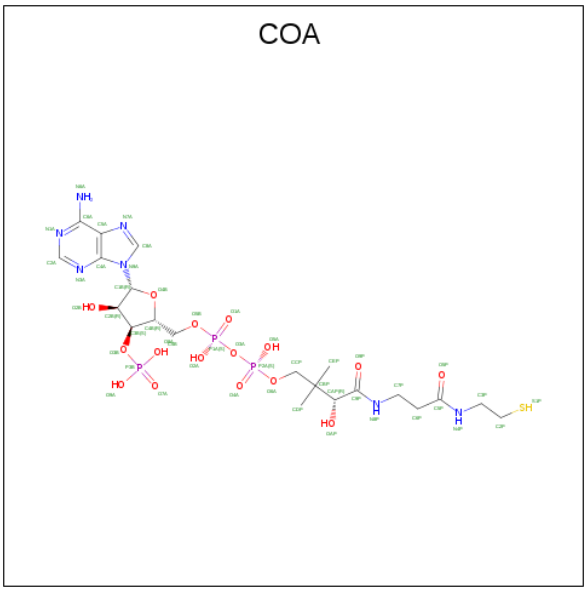
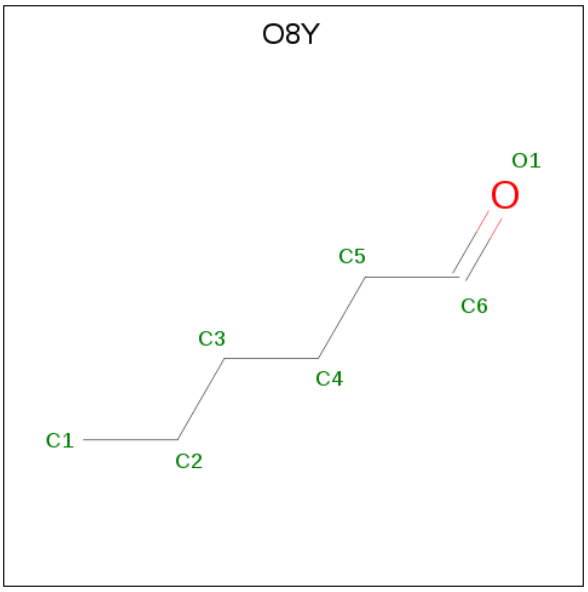
Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	GLU	-	expression tag	UNP Q88N39
C	-6	ASN	-	expression tag	UNP Q88N39
C	-5	LEU	-	expression tag	UNP Q88N39
C	-4	TYR	-	expression tag	UNP Q88N39
C	-3	HIS	-	expression tag	UNP Q88N39
C	-2	GLN	-	expression tag	UNP Q88N39
C	-1	GLY	-	expression tag	UNP Q88N39
C	0	SER	-	expression tag	UNP Q88N39
C	356	ALA	HIS	engineered mutation	UNP Q88N39
D	-22	MET	-	initiating methionine	UNP Q88N39
D	-21	HIS	-	expression tag	UNP Q88N39
D	-20	HIS	-	expression tag	UNP Q88N39
D	-19	HIS	-	expression tag	UNP Q88N39
D	-18	HIS	-	expression tag	UNP Q88N39
D	-17	HIS	-	expression tag	UNP Q88N39
D	-16	HIS	-	expression tag	UNP Q88N39
D	-15	SER	-	expression tag	UNP Q88N39
D	-14	SER	-	expression tag	UNP Q88N39
D	-13	GLY	-	expression tag	UNP Q88N39
D	-12	VAL	-	expression tag	UNP Q88N39
D	-11	ASP	-	expression tag	UNP Q88N39
D	-10	LEU	-	expression tag	UNP Q88N39
D	-9	GLY	-	expression tag	UNP Q88N39
D	-8	THR	-	expression tag	UNP Q88N39
D	-7	GLU	-	expression tag	UNP Q88N39
D	-6	ASN	-	expression tag	UNP Q88N39
D	-5	LEU	-	expression tag	UNP Q88N39
D	-4	TYR	-	expression tag	UNP Q88N39
D	-3	HIS	-	expression tag	UNP Q88N39
D	-2	GLN	-	expression tag	UNP Q88N39
D	-1	GLY	-	expression tag	UNP Q88N39
D	0	SER	-	expression tag	UNP Q88N39
D	356	ALA	HIS	engineered mutation	UNP Q88N39

- 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 author).



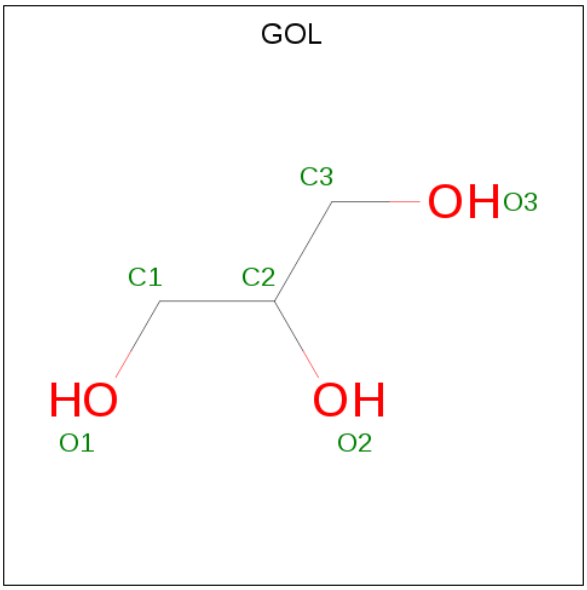
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is hexanal (three-letter code: O8Y) (formula: $C_6H_{12}O$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 6 1	0	0
3	B	1	Total C O 7 6 1	0	0
3	C	1	Total C O 7 6 1	0	0
3	D	1	Total C O 7 6 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	282	Total O 282 282	0	0

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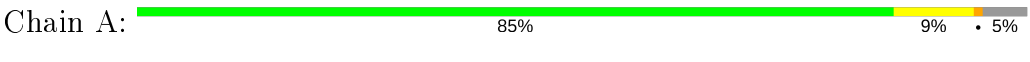
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	280	Total O 280 280	0	0
5	C	328	Total O 328 328	0	0
5	D	325	Total O 325 325	0	0

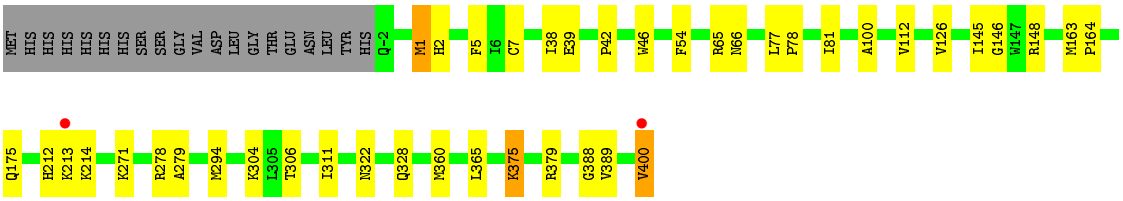
3 Residue-property plots (i)

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: Beta-ketoadipyl-CoA thiolase

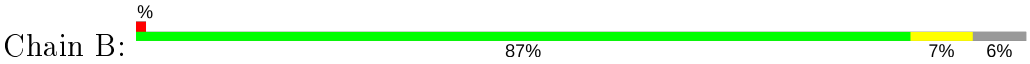
Chain A:

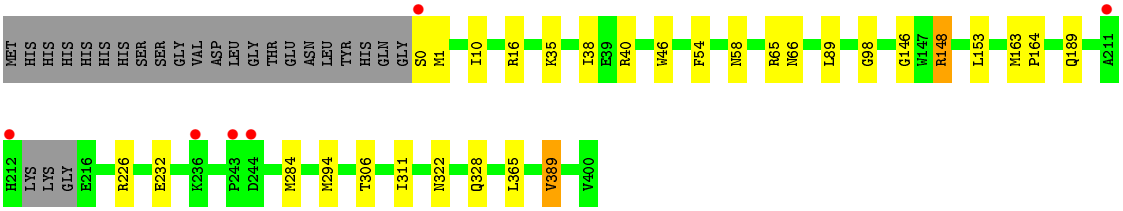




- Molecule 1: Beta-ketoadipyl-CoA thiolase

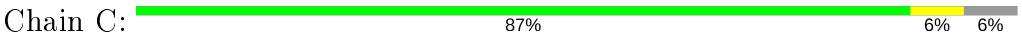
Chain B:

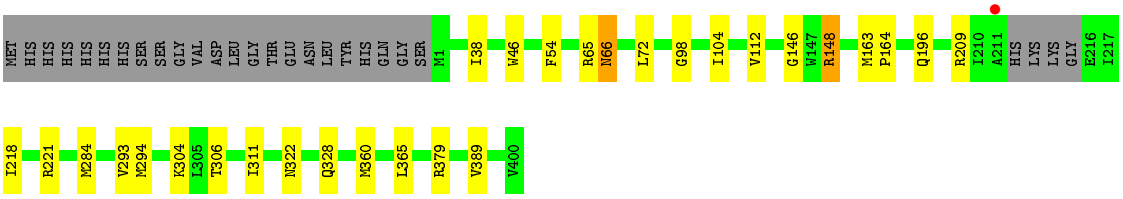




- Molecule 1: Beta-ketoadipyl-CoA thiolase

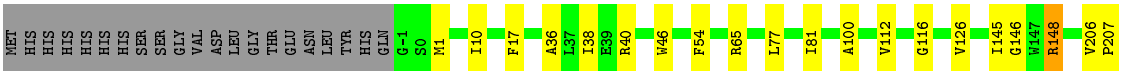
Chain C:





- Molecule 1: Beta-ketoadipyl-CoA thiolase

Chain D:




I218
V219
E220
P243
A249
V255
A265
A269
A279
M294
T306
I311
N322
Q328
G359
M360
L365
L370
V389
V400

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	111.39Å 116.40Å 127.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.94 – 1.96 19.94 – 1.96	Depositor EDS
% Data completeness (in resolution range)	95.3 (19.94-1.96) 95.4 (19.94-1.96)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 1.96Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.176 , 0.208 0.179 , 0.207	Depositor DCC
R_{free} test set	968 reflections (0.85%)	wwPDB-VP
Wilson B-factor (Å^2)	19.0	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.003 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13336	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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: COA, GOL, CSO, O8Y

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	0.42	0/3006	0.72	0/4066
1	B	0.41	0/3001	0.74	1/4060 (0.0%)
1	C	0.43	0/2959	0.74	0/4004
1	D	0.44	0/3030	0.74	0/4099
All	All	0.42	0/11996	0.73	1/16229 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	16	ARG	CG-CD-NE	-7.94	95.13	111.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2972	0	3005	38	0
1	B	2975	0	2996	23	0
1	C	2934	0	2960	24	0
1	D	2996	0	3022	30	0
2	A	48	0	31	0	0
2	B	48	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	48	0	31	0	0
2	D	48	0	31	2	0
3	A	7	0	0	5	0
3	B	7	0	0	10	0
3	C	7	0	0	9	0
3	D	7	0	0	9	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
4	D	6	0	8	0	0
5	A	282	0	0	4	0
5	B	280	0	0	3	0
5	C	328	0	0	4	0
5	D	325	0	0	0	0
All	All	13336	0	12139	112	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 112 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:MET:HE2	1:A:388:GLY:HA2	1.30	1.12
1:B:65[A]:ARG:HE	3:C:502:O8Y:C5	1.71	1.02
1:A:65[A]:ARG:HE	3:D:502:O8Y:C5	1.75	0.98
3:B:502:O8Y:C4	1:C:65[A]:ARG:HD2	2.00	0.91
1:A:65[B]:ARG:HD3	3:D:502:O8Y:C5	2.02	0.90

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	403/423 (95%)	386 (96%)	16 (4%)	1 (0%)	47	38
1	B	399/423 (94%)	383 (96%)	14 (4%)	2 (0%)	29	17
1	C	395/423 (93%)	373 (94%)	20 (5%)	2 (0%)	29	17
1	D	406/423 (96%)	391 (96%)	14 (3%)	1 (0%)	47	38
All	All	1603/1692 (95%)	1533 (96%)	64 (4%)	6 (0%)	34	22

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	66	ASN
1	B	389	VAL
1	C	66	ASN
1	C	389	VAL
1	D	389	VAL

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	300/315 (95%)	290 (97%)	10 (3%)	38	26
1	B	300/315 (95%)	292 (97%)	8 (3%)	44	34
1	C	296/315 (94%)	289 (98%)	7 (2%)	49	40
1	D	303/315 (96%)	298 (98%)	5 (2%)	60	55
All	All	1199/1260 (95%)	1169 (98%)	30 (2%)	47	38

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	54	PHE
1	B	294	MET
1	D	294	MET
1	B	232	GLU
1	B	328	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	212	HIS
1	B	66	ASN
1	C	137	ASN
1	A	181	GLN
1	B	189	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)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	CSO	B	386[B]	1	3,6,7	0.88	0	0,6,8	0.00	-
1	CSO	B	386[A]	1	3,6,7	0.78	0	0,6,8	0.00	-
1	CSO	C	386[B]	1	3,6,7	0.71	0	0,6,8	0.00	-
1	CSO	C	386[A]	1	3,6,7	0.69	0	0,6,8	0.00	-
1	CSO	A	386	1	3,6,7	0.66	0	0,6,8	0.00	-
1	CSO	D	386	1	3,6,7	0.76	0	0,6,8	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSO	B	386[B]	1	-	0/1/5/7	-
1	CSO	B	386[A]	1	-	0/1/5/7	-
1	CSO	C	386[B]	1	-	0/1/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSO	C	386[A]	1	-	0/1/5/7	-
1	CSO	A	386	1	-	0/1/5/7	-
1	CSO	D	386	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

12 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	$\#\|Z\| > 2$
2	COA	C	501	1	41,50,50	0.59	0	52,75,75	0.93	3 (5%)
4	GOL	A	1003	-	5,5,5	0.10	0	5,5,5	0.41	0
3	O8Y	C	502	-	6,6,6	0.75	0	5,5,5	0.66	0
3	O8Y	D	502	-	6,6,6	0.65	0	5,5,5	0.55	0
3	O8Y	B	502	-	6,6,6	0.61	0	5,5,5	0.30	0
2	COA	D	501	1	41,50,50	0.71	1 (2%)	52,75,75	0.92	3 (5%)
2	COA	B	501	1	41,50,50	0.61	0	52,75,75	0.79	1 (1%)
3	O8Y	A	1002	-	6,6,6	0.68	0	5,5,5	0.34	0
4	GOL	D	503	-	5,5,5	0.14	0	5,5,5	0.26	0
4	GOL	C	503	-	5,5,5	0.10	0	5,5,5	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	COA	A	1001	1	41,50,50	0.61	0	52,75,75	0.97	2 (3%)
4	GOL	B	503	-	5,5,5	0.13	0	5,5,5	0.32	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	COA	C	501	1	-	3/44/64/64	0/3/3/3
4	GOL	A	1003	-	-	0/4/4/4	-
3	O8Y	C	502	-	-	2/3/4/4	-
3	O8Y	D	502	-	-	1/3/4/4	-
3	O8Y	B	502	-	-	2/3/4/4	-
2	COA	D	501	1	-	6/44/64/64	0/3/3/3
2	COA	B	501	1	-	6/44/64/64	0/3/3/3
3	O8Y	A	1002	-	-	2/3/4/4	-
4	GOL	D	503	-	-	0/4/4/4	-
4	GOL	C	503	-	-	0/4/4/4	-
2	COA	A	1001	1	-	0/44/64/64	0/3/3/3
4	GOL	B	503	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	COA	P3B-O3B	2.66	1.64	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1001	COA	C5A-C6A-N6A	3.60	125.82	120.35
2	C	501	COA	O4B-C1B-C2B	-2.85	102.77	106.93
2	D	501	COA	C5A-C6A-N6A	2.64	124.37	120.35
2	C	501	COA	C5A-C6A-N6A	2.61	124.32	120.35
2	B	501	COA	C5A-C6A-N6A	2.48	124.12	120.35

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

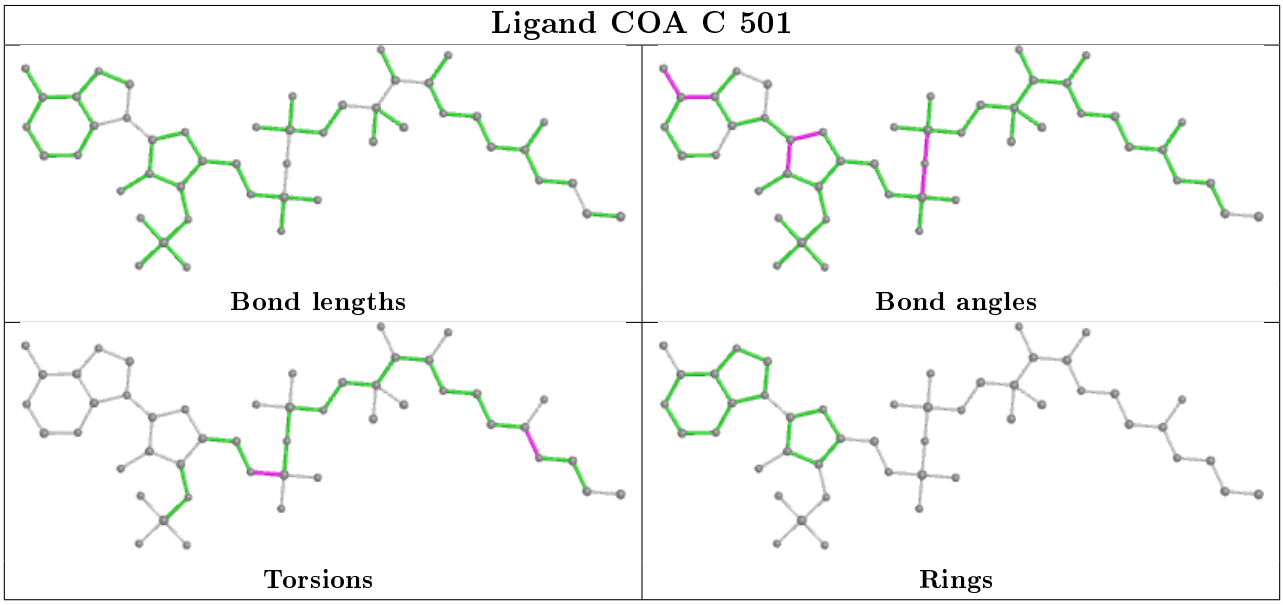
Mol	Chain	Res	Type	Atoms
2	C	501	COA	C5B-O5B-P1A-O1A
2	C	501	COA	C5B-O5B-P1A-O3A
3	C	502	O8Y	C3-C4-C5-C6
3	D	502	O8Y	C3-C4-C5-C6
3	B	502	O8Y	C3-C4-C5-C6

There are no ring outliers.

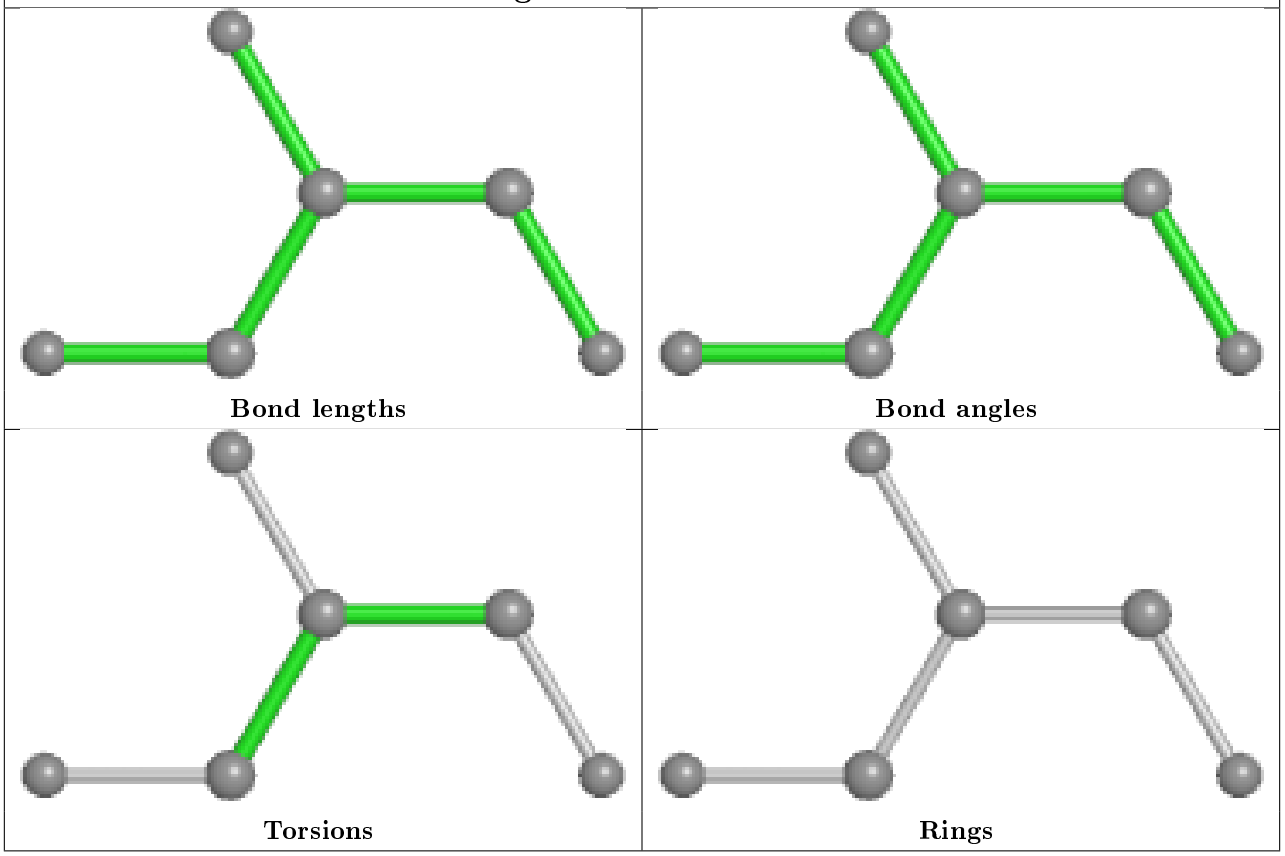
5 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	502	O8Y	9	0
3	D	502	O8Y	9	0
3	B	502	O8Y	10	0
2	D	501	COA	2	0
3	A	1002	O8Y	5	0

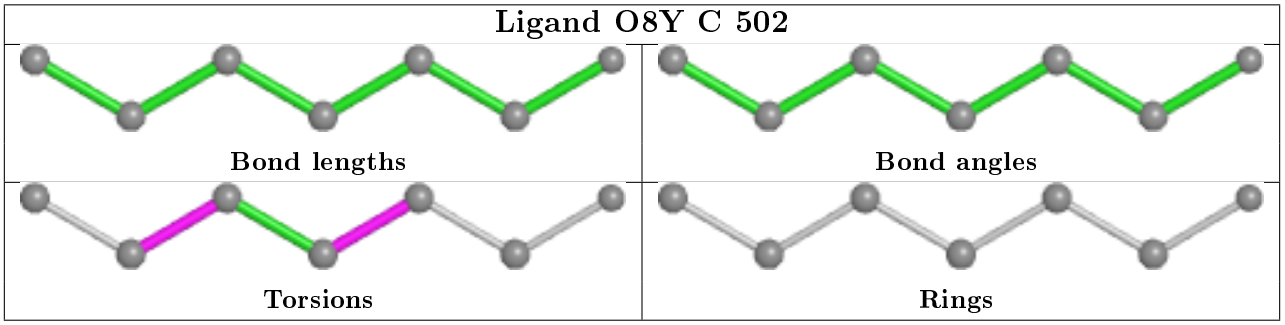
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



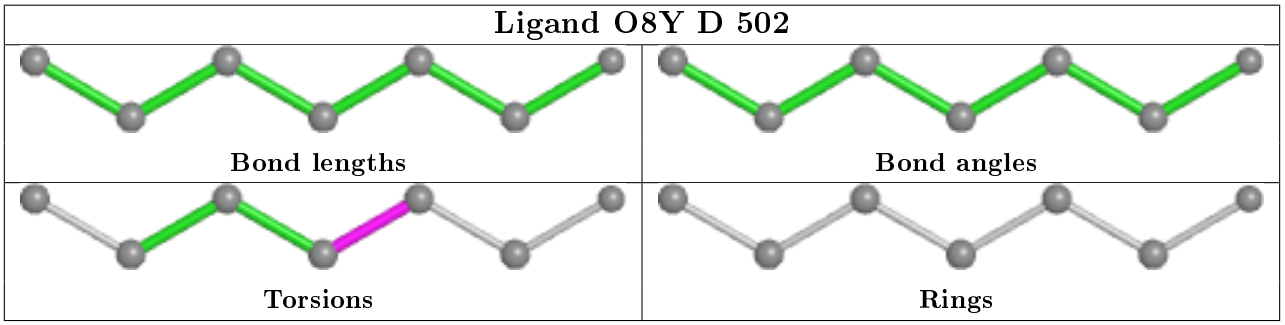
Ligand GOL A 1003



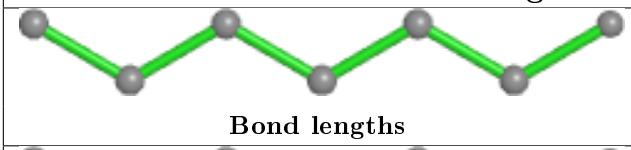
Ligand O8Y C 502



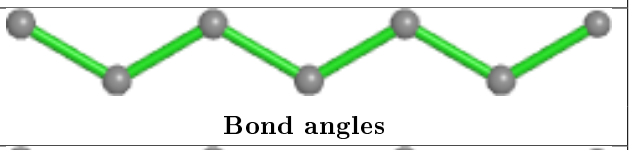
Ligand O8Y D 502



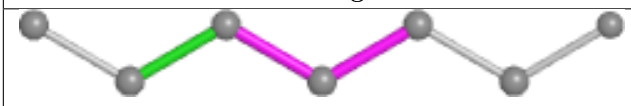
Ligand O8Y B 502



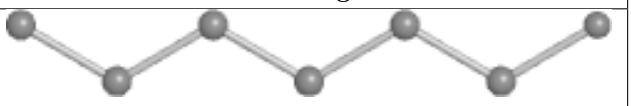
Bond lengths



Bond angles

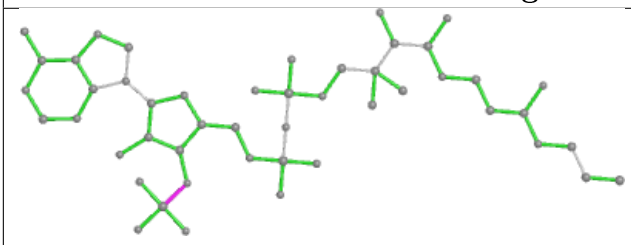


Torsions

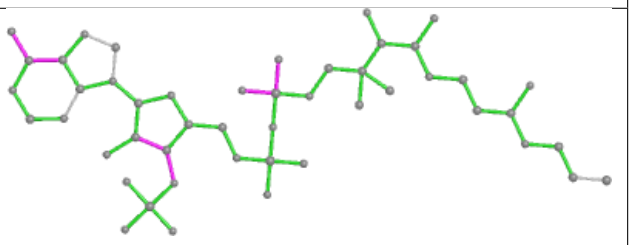


Rings

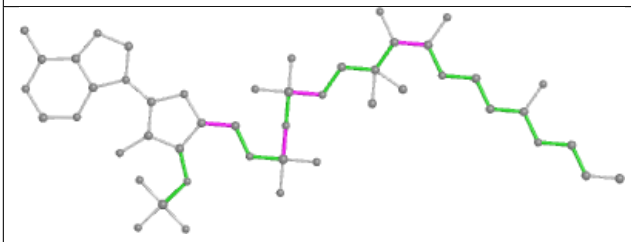
Ligand COA D 501



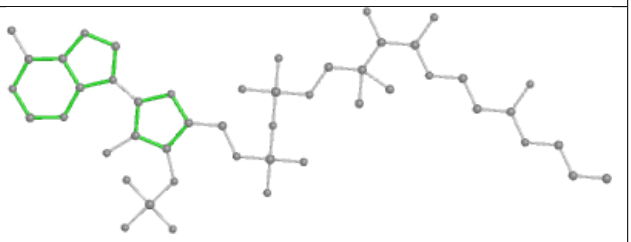
Bond lengths



Bond angles

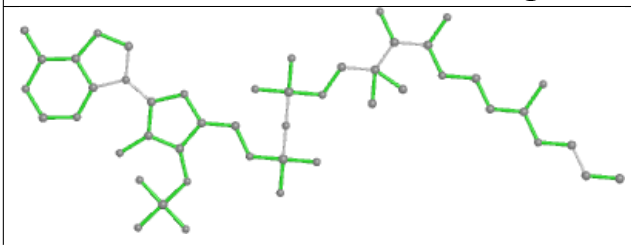


Torsions

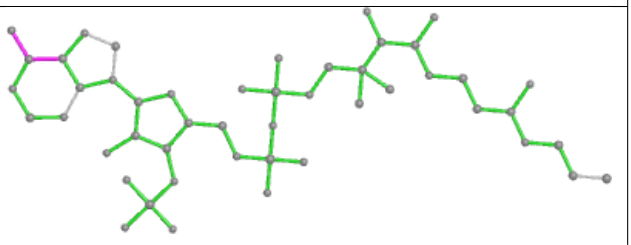


Rings

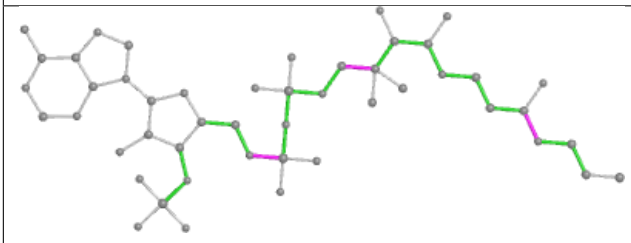
Ligand COA B 501



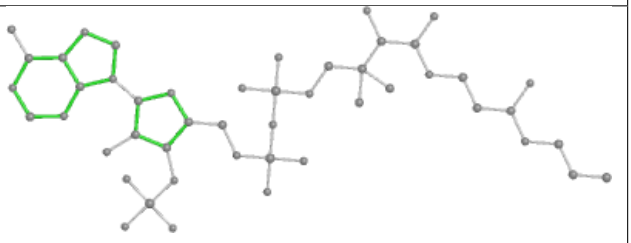
Bond lengths



Bond angles

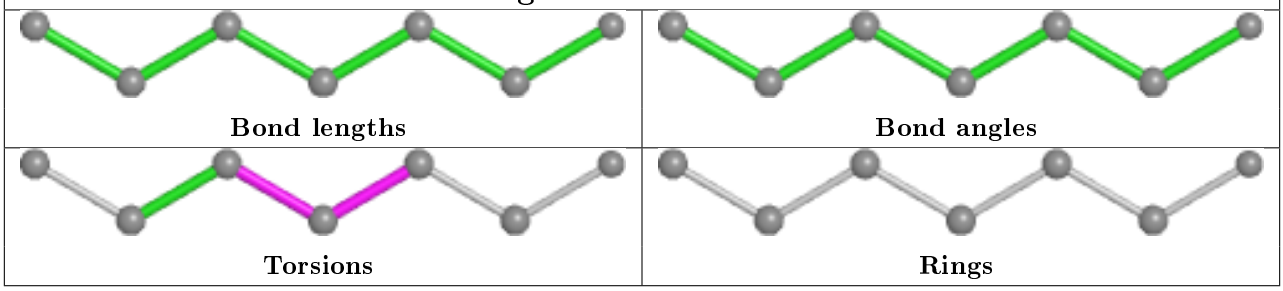


Torsions

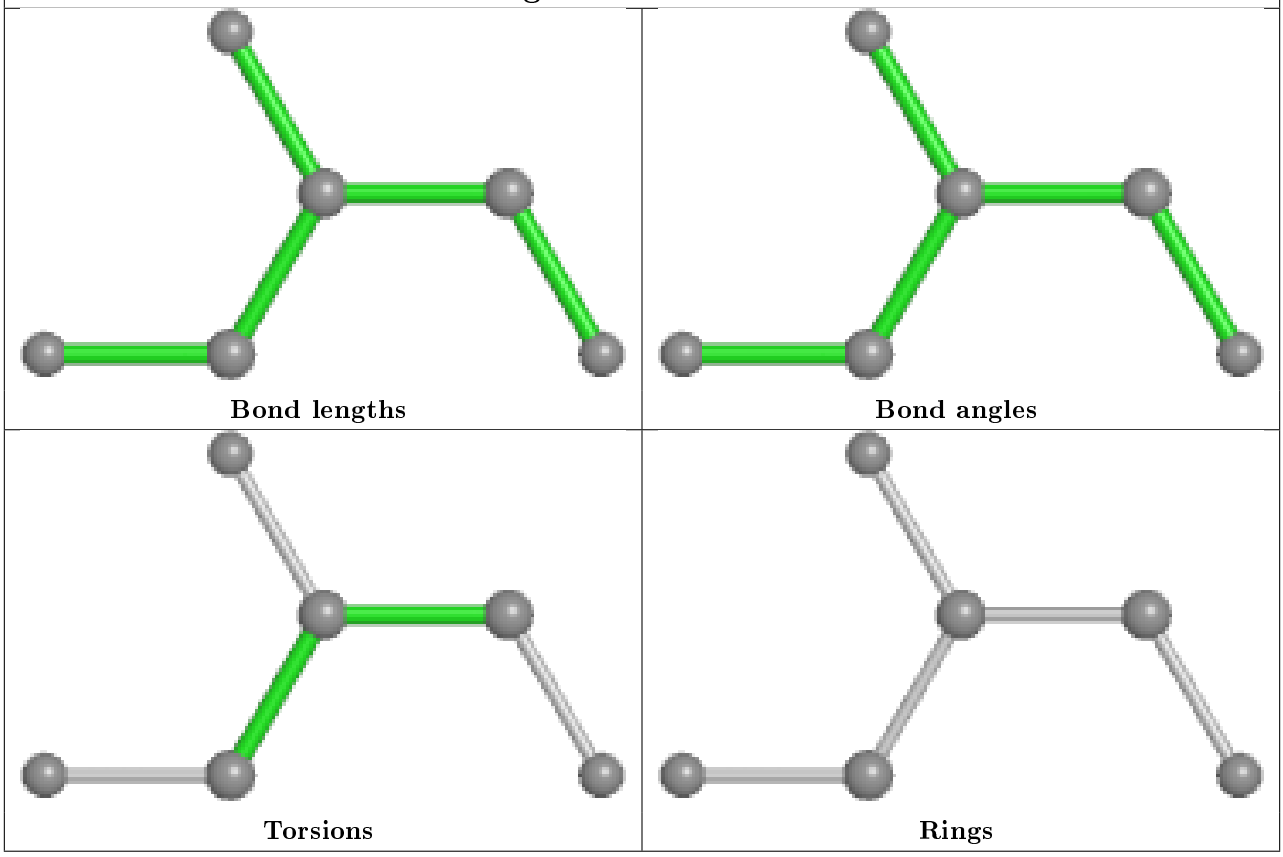


Rings

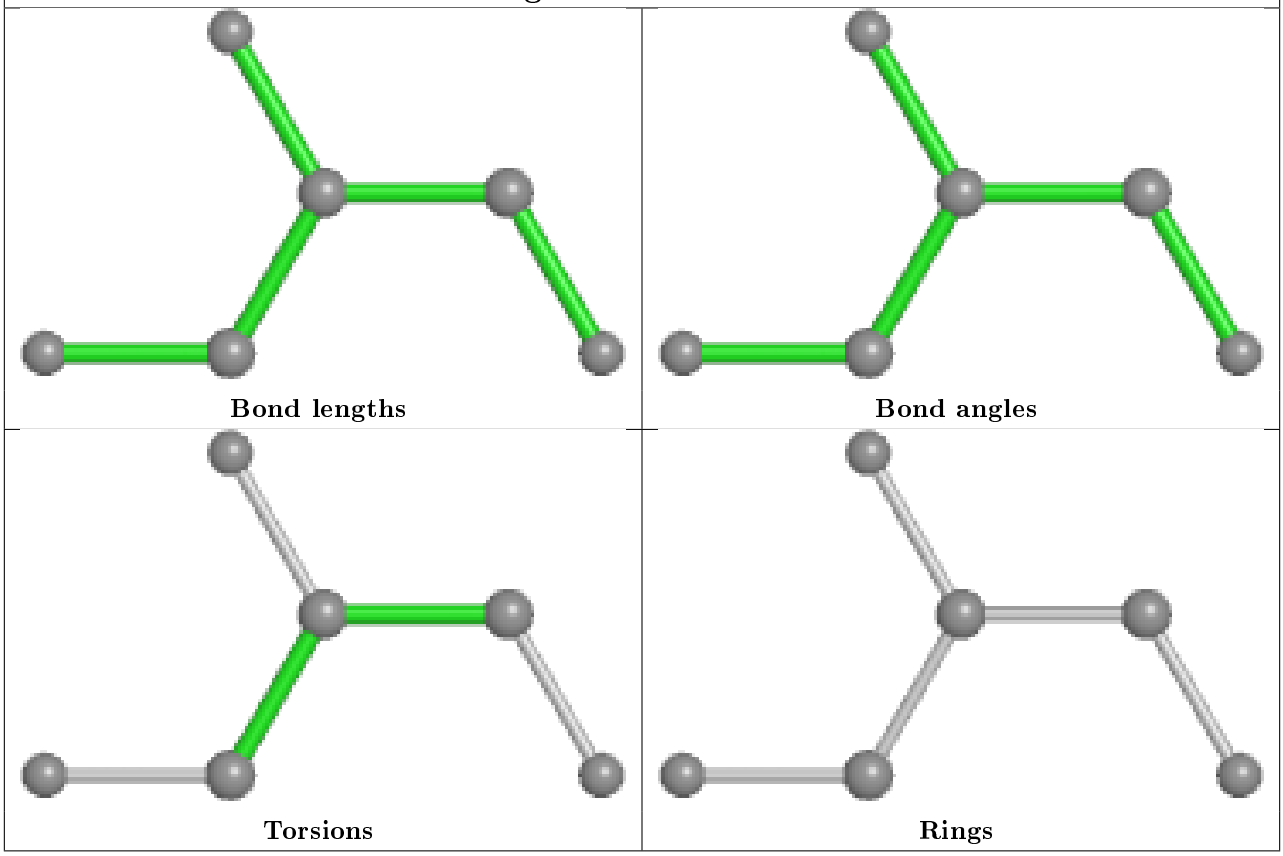
Ligand O8Y A 1002



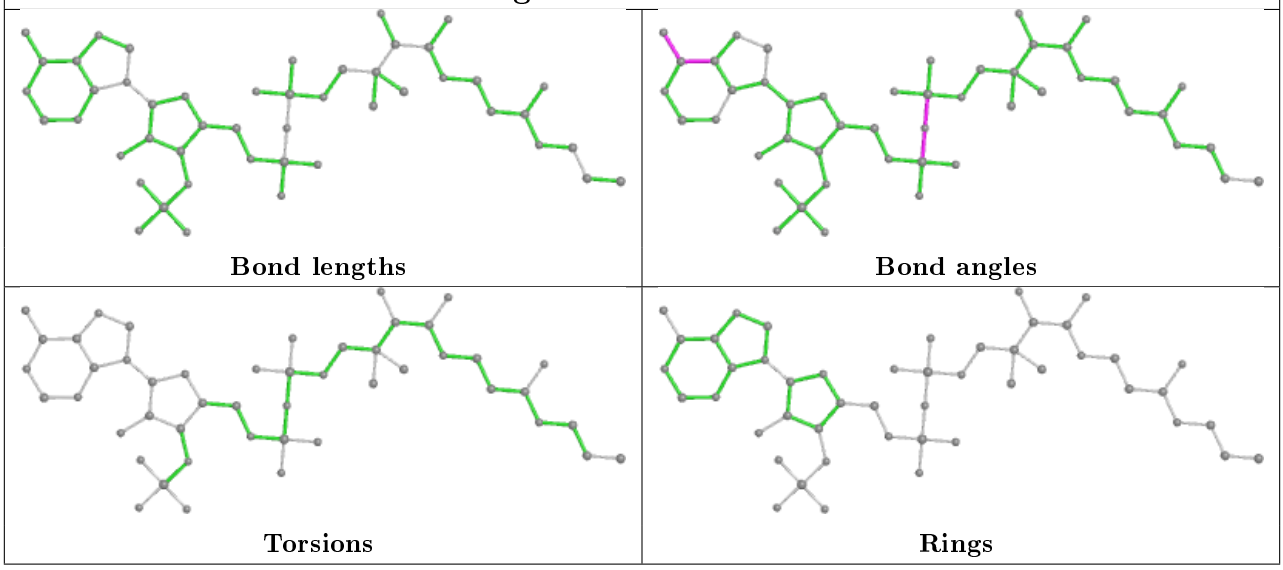
Ligand GOL D 503

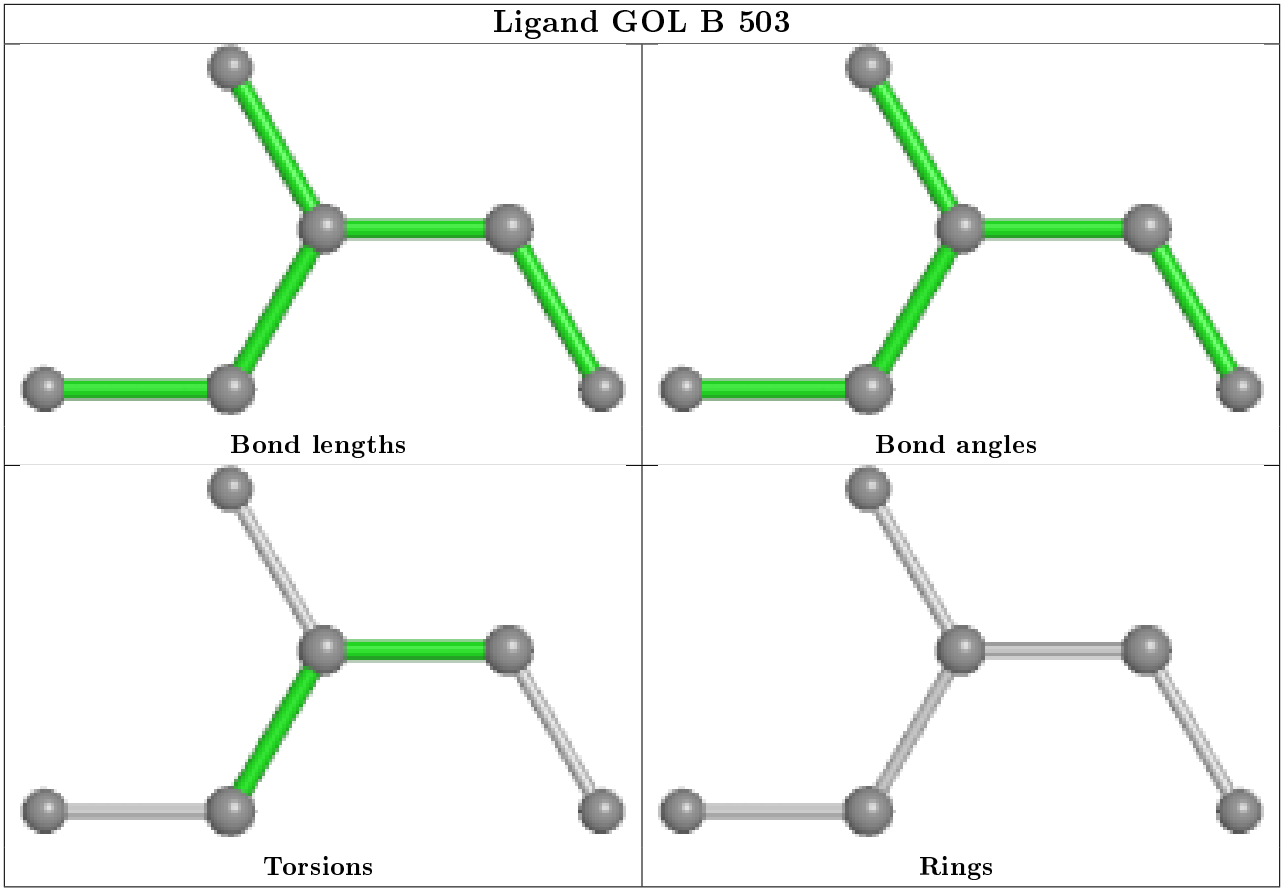


Ligand GOL C 503



Ligand COA A 1001





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	402/423 (95%)	-0.16	2 (0%)	91	94	12, 20, 35, 71	0
1	B	397/423 (93%)	-0.19	6 (1%)	73	81	11, 20, 37, 76	0
1	C	395/423 (93%)	-0.30	1 (0%)	94	96	11, 18, 32, 49	0
1	D	401/423 (94%)	-0.31	1 (0%)	95	97	12, 18, 29, 48	0
All	All	1595/1692 (94%)	-0.24	10 (0%)	89	93	11, 19, 34, 76	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	213	LYS	3.4
1	B	212	HIS	3.1
1	B	211	ALA	2.9
1	B	244	ASP	2.7
1	A	400	VAL	2.4

6.2 Non-standard residues in protein, DNA, RNA chains

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, 95^{th} 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
1	CSO	B	386[B]	7/8	0.98	0.07	20,20,21,24	7
1	CSO	B	386[A]	7/8	0.98	0.07	16,18,19,20	7
1	CSO	C	386[B]	7/8	0.98	0.09	15,15,15,16	7
1	CSO	C	386[A]	7/8	0.98	0.09	16,16,21,24	7
1	CSO	A	386	7/8	0.98	0.07	19,19,21,33	0
1	CSO	D	386	7/8	0.98	0.06	17,19,20,30	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

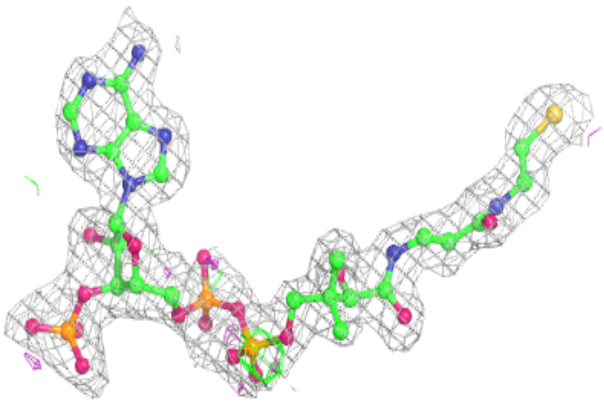
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

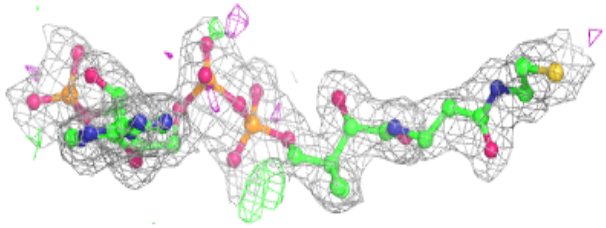
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	COA	D	501	48/48	0.88	0.15	22,30,57,69	1
2	COA	B	501	48/48	0.88	0.16	27,39,64,77	1
2	COA	C	501	48/48	0.90	0.16	22,32,52,57	1
2	COA	A	1001	48/48	0.90	0.14	22,28,62,76	1
3	O8Y	A	1002	7/7	0.91	0.17	16,18,23,27	3
3	O8Y	D	502	7/7	0.92	0.18	21,26,29,31	1
3	O8Y	B	502	7/7	0.93	0.14	17,20,23,24	2
4	GOL	B	503	6/6	0.94	0.11	24,26,26,29	0
4	GOL	A	1003	6/6	0.95	0.12	21,24,25,28	0
4	GOL	C	503	6/6	0.95	0.10	16,18,19,21	0
4	GOL	D	503	6/6	0.96	0.08	18,19,20,22	0
3	O8Y	C	502	7/7	0.96	0.12	17,20,22,25	2

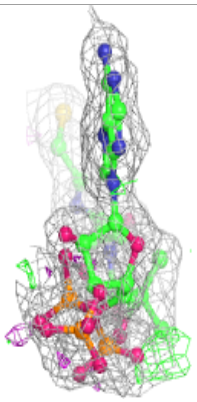
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around COA D 501:

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

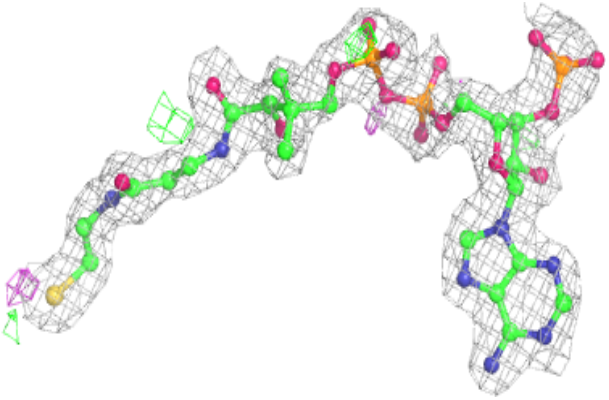


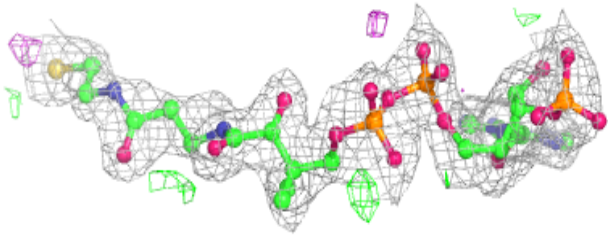


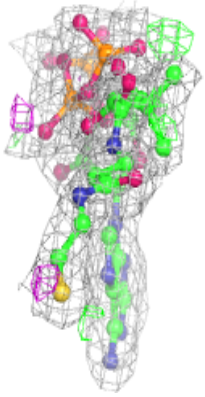


Electron density around COA B 501:

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

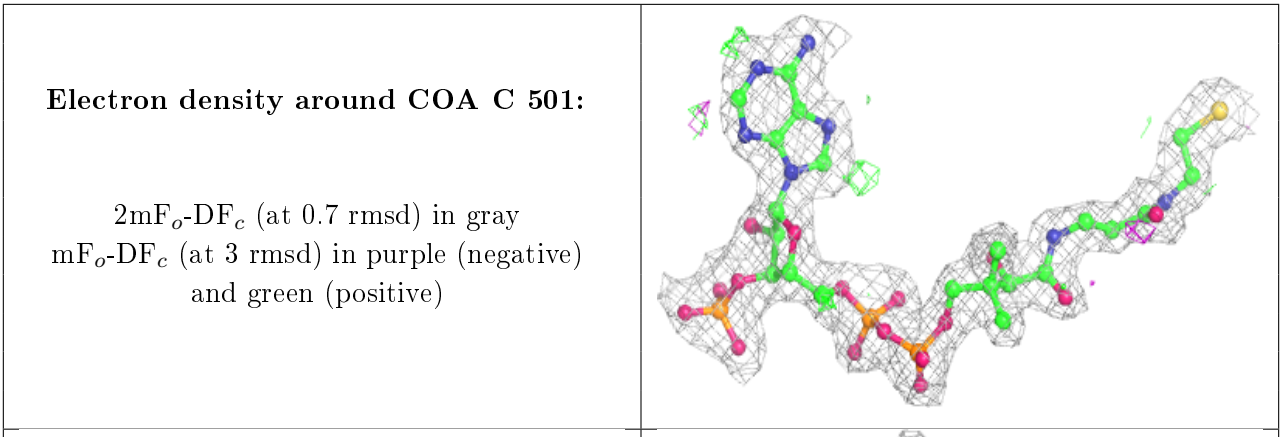






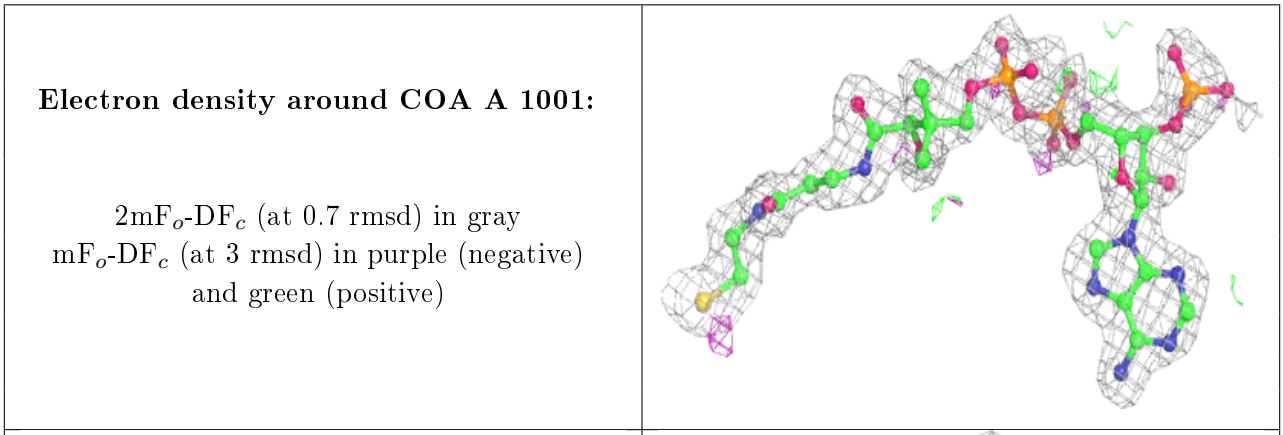
Electron density around COA C 501:

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



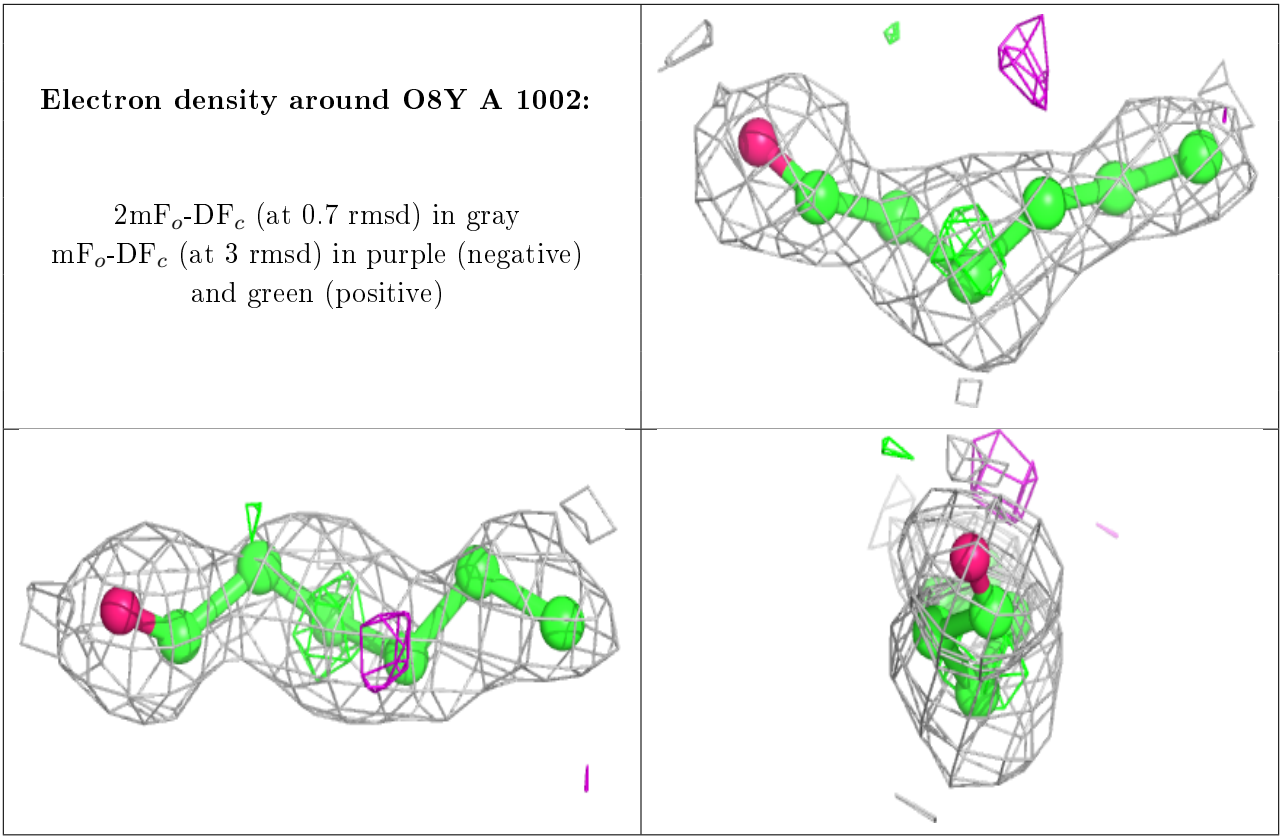
Electron density around COA A 1001:

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



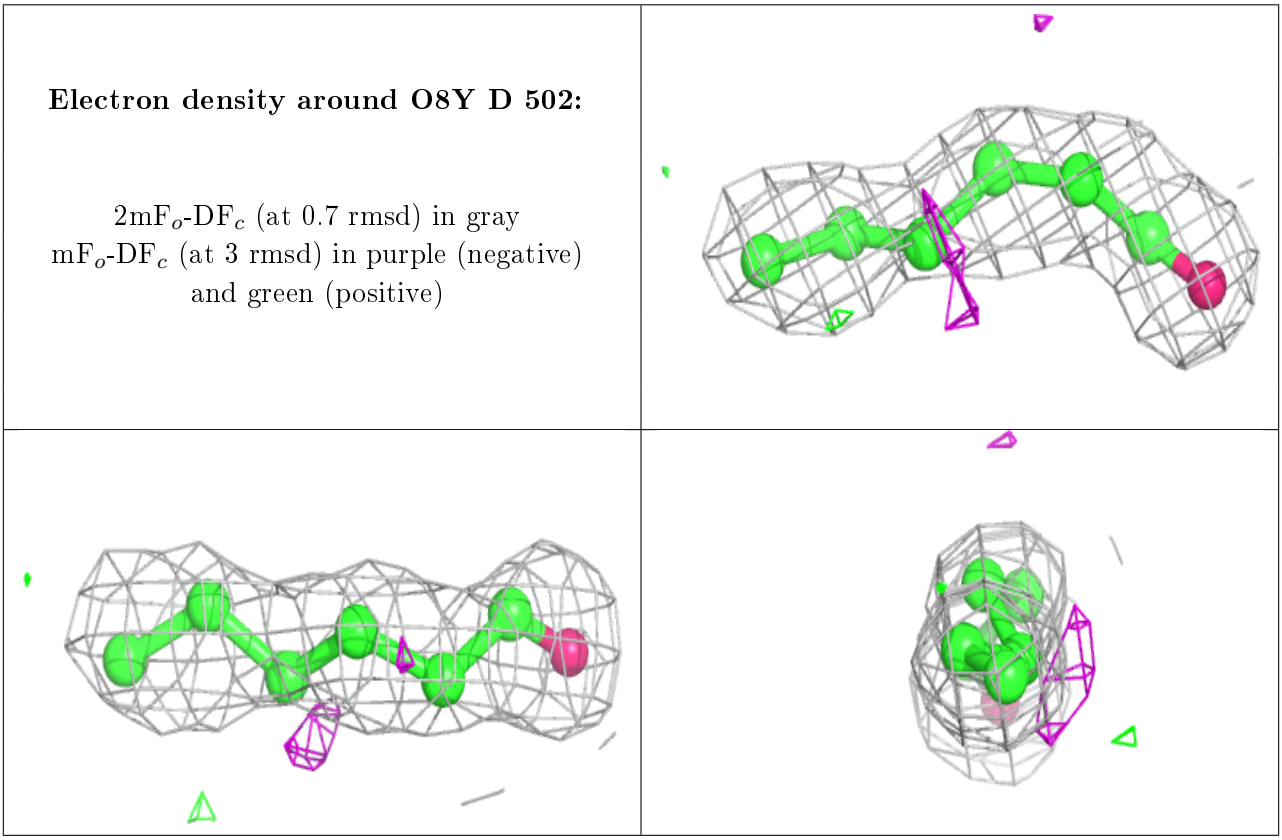
Electron density around O8Y A 1002:

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



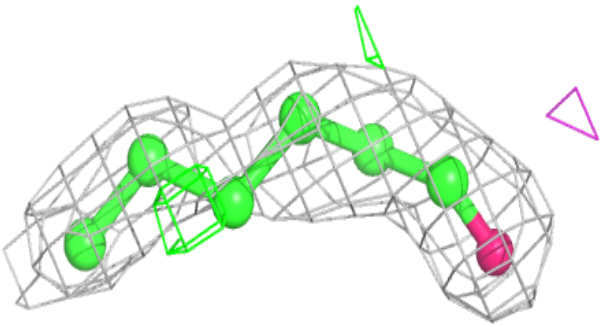
Electron density around O8Y D 502:

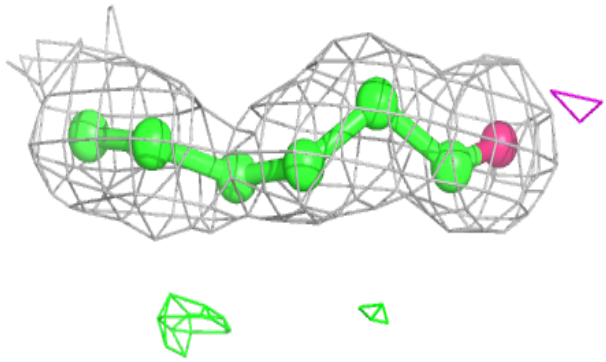
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

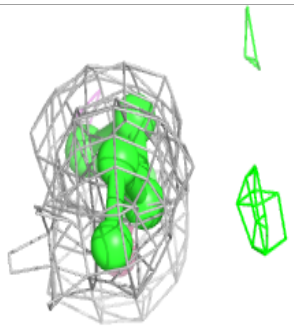


Electron density around O8Y B 502:

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

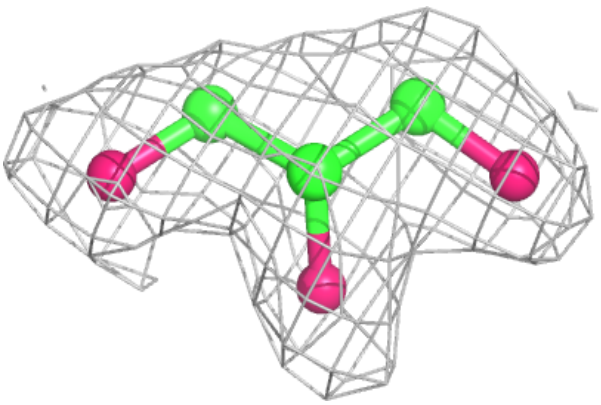


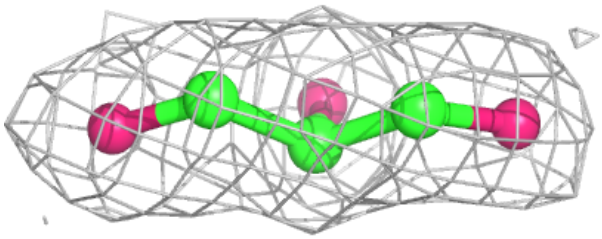


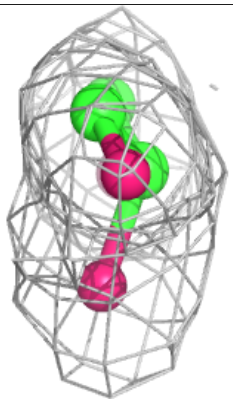


Electron density around GOL B 503:

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

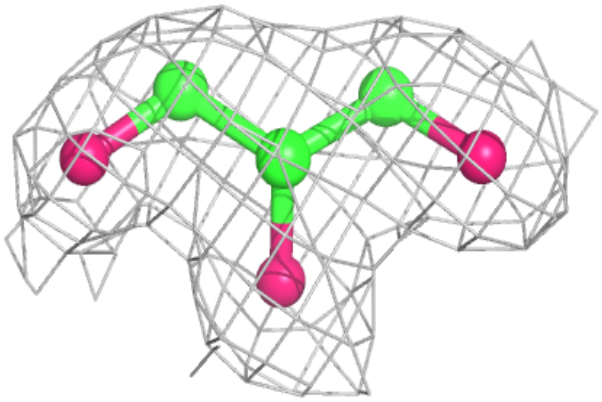


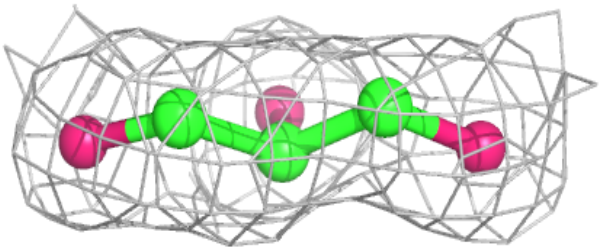


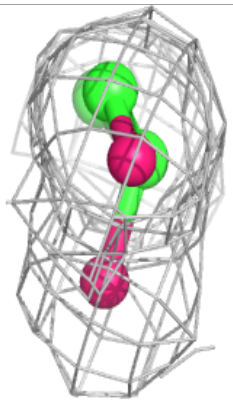


Electron density around GOL A 1003:

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

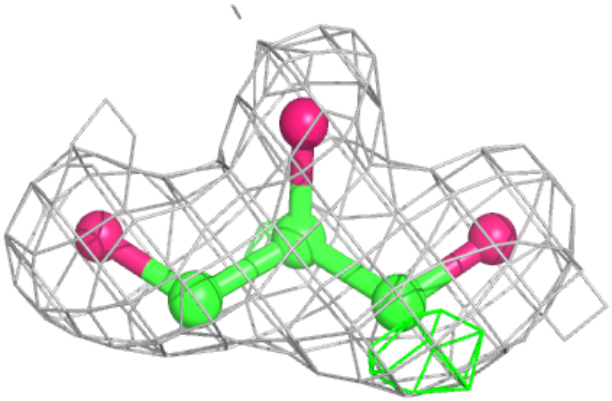


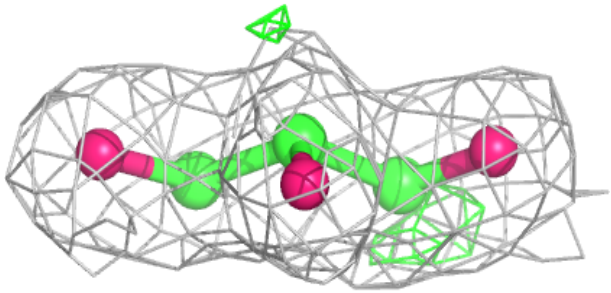


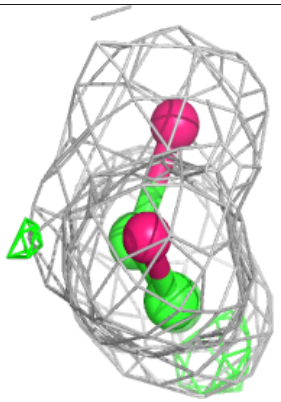


Electron density around GOL C 503:

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

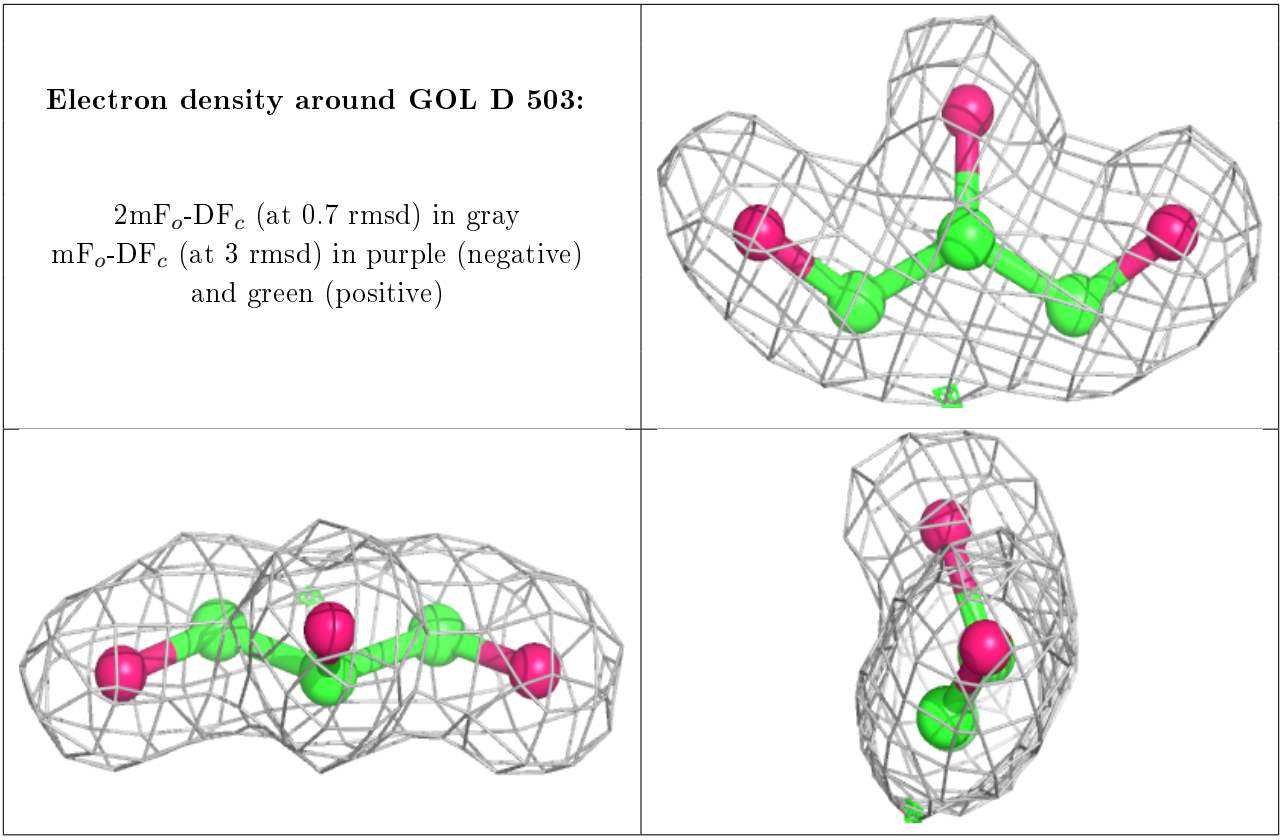






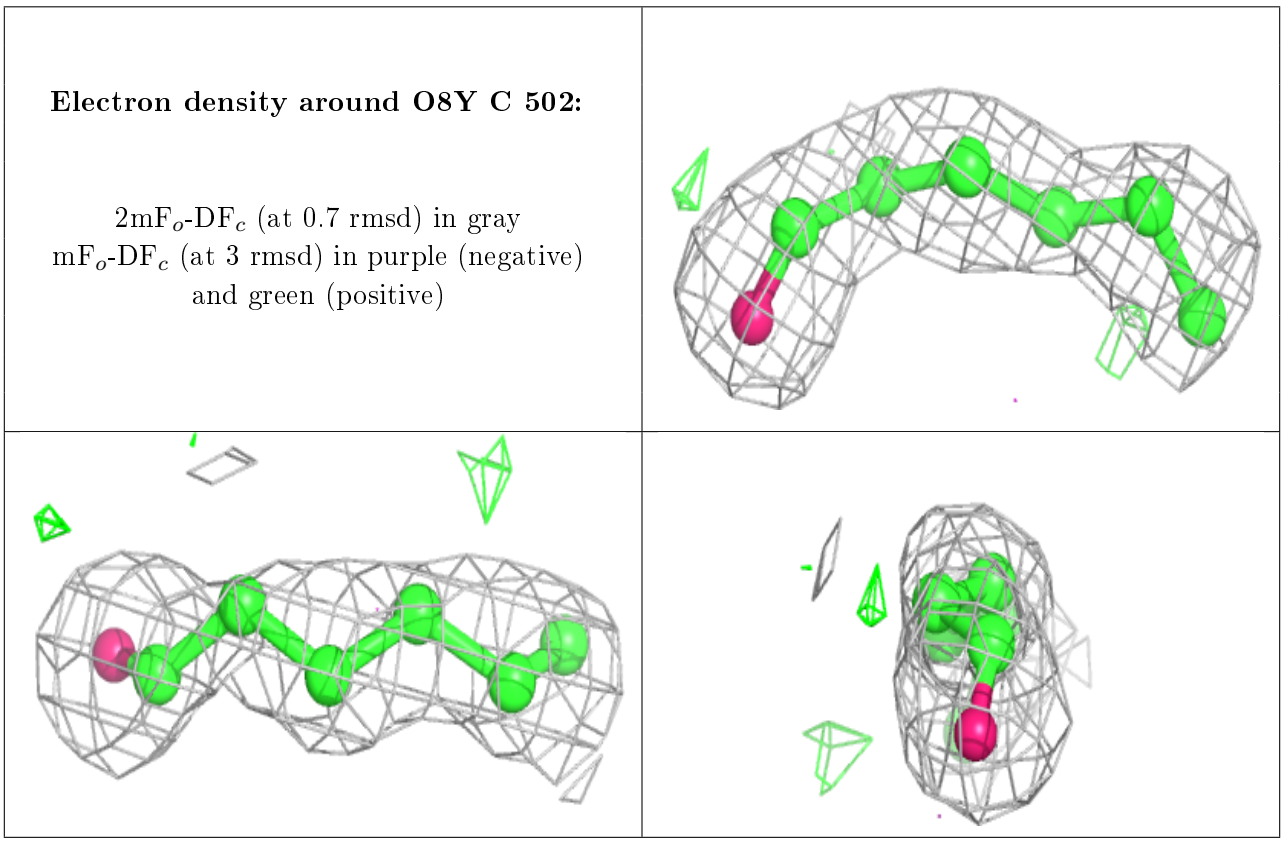
Electron density around GOL D 503:

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



Electron density around O8Y C 502:

$2mF_o$-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.