wwPDB X-ray Structure Validation Summary Report (i)

Oct 10, 2023 – 10:21 AM EDT

PDB ID	:	7LDU
Title	:	Zoogloea ramigera biosynthetic thiolase Q183Y/Y218E/delH221 mutant
Authors	:	Marshall, A.C.; Bruning, J.B.
Deposited on	:	2021-01-14
Resolution	:	2.85 Å(reported)

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

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

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

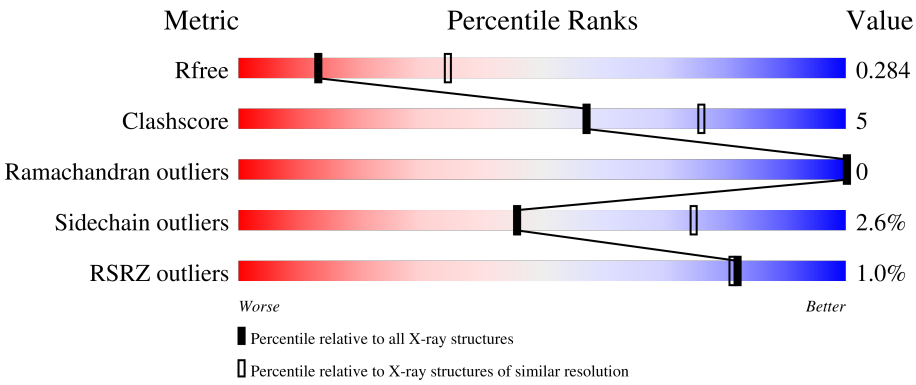
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	398	85% 12% • •
1	B	398	86% 11% • •
1	C	398	85% 12% • •
1	D	398	4% 85% 12% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11586 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 Acetyl-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	389	2802	1740	502	539	21	0	0	0
1	B	389	2803	1741	502	539	21	0	0	0
1	C	389	2795	1735	500	539	21	0	0	0
1	D	389	2765	1719	496	529	21	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P07097
A	-5	HIS	-	expression tag	UNP P07097
A	-4	HIS	-	expression tag	UNP P07097
A	-3	HIS	-	expression tag	UNP P07097
A	-2	HIS	-	expression tag	UNP P07097
A	-1	HIS	-	expression tag	UNP P07097
A	0	HIS	-	expression tag	UNP P07097
A	11	ALA	-	insertion	UNP P07097
A	129	ARG	ALA	conflict	UNP P07097
A	183	TYR	GLN	engineered mutation	UNP P07097
A	218	GLU	TYR	engineered mutation	UNP P07097
A	?	-	HIS	deletion	UNP P07097
B	-6	MET	-	initiating methionine	UNP P07097
B	-5	HIS	-	expression tag	UNP P07097
B	-4	HIS	-	expression tag	UNP P07097
B	-3	HIS	-	expression tag	UNP P07097
B	-2	HIS	-	expression tag	UNP P07097
B	-1	HIS	-	expression tag	UNP P07097
B	0	HIS	-	expression tag	UNP P07097
B	11	ALA	-	insertion	UNP P07097
B	129	ARG	ALA	conflict	UNP P07097

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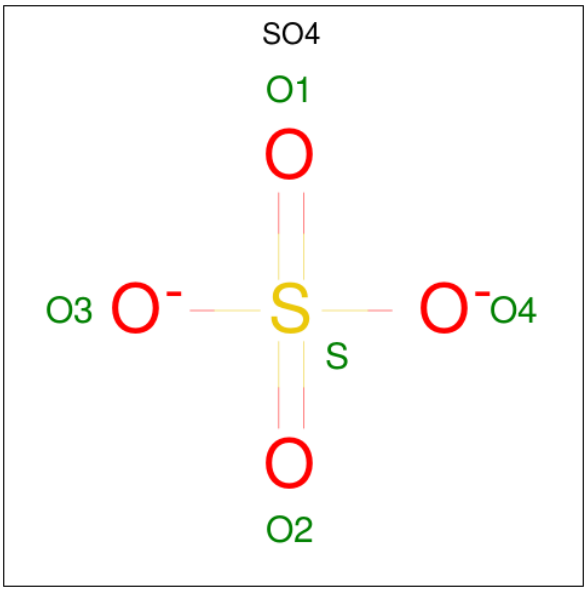
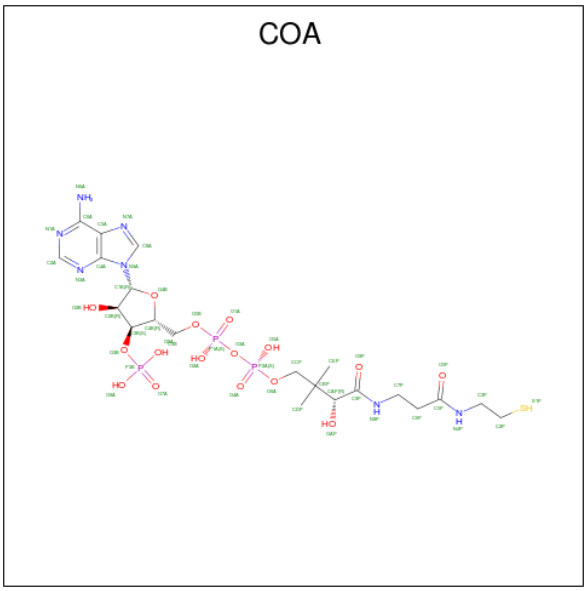
Chain	Residue	Modelled	Actual	Comment	Reference
B	183	TYR	GLN	engineered mutation	UNP P07097
B	218	GLU	TYR	engineered mutation	UNP P07097
B	?	-	HIS	deletion	UNP P07097
C	-6	MET	-	initiating methionine	UNP P07097
C	-5	HIS	-	expression tag	UNP P07097
C	-4	HIS	-	expression tag	UNP P07097
C	-3	HIS	-	expression tag	UNP P07097
C	-2	HIS	-	expression tag	UNP P07097
C	-1	HIS	-	expression tag	UNP P07097
C	0	HIS	-	expression tag	UNP P07097
C	11	ALA	-	insertion	UNP P07097
C	129	ARG	ALA	conflict	UNP P07097
C	183	TYR	GLN	engineered mutation	UNP P07097
C	218	GLU	TYR	engineered mutation	UNP P07097
C	?	-	HIS	deletion	UNP P07097
D	-6	MET	-	initiating methionine	UNP P07097
D	-5	HIS	-	expression tag	UNP P07097
D	-4	HIS	-	expression tag	UNP P07097
D	-3	HIS	-	expression tag	UNP P07097
D	-2	HIS	-	expression tag	UNP P07097
D	-1	HIS	-	expression tag	UNP P07097
D	0	HIS	-	expression tag	UNP P07097
D	11	ALA	-	insertion	UNP P07097
D	129	ARG	ALA	conflict	UNP P07097
D	183	TYR	GLN	engineered mutation	UNP P07097
D	218	GLU	TYR	engineered mutation	UNP P07097
D	?	-	HIS	deletion	UNP P07097

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	A	1	5	4	1		0	0
2	A	1	5	4	1		0	0
2	A	1	5	4	1		0	0
2	A	1	5	4	1		0	0
2	A	1	5	4	1		0	0
2	B	1	5	4	1		0	0
2	B	1	5	4	1		0	0
2	B	1	5	4	1		0	0

- Molecule 3 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	N	O	P	S		
3	A	1	48	21	7	16	3	1	0	0
3	B	1	48	21	7	16	3	1	0	0
3	C	1	48	21	7	16	3	1	0	0
3	D	1	48	21	7	16	3	1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	1	1	1	0	0
4	B	1	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	58	58	58	0	0
5	B	57	57	57	0	0
5	C	42	42	42	0	0

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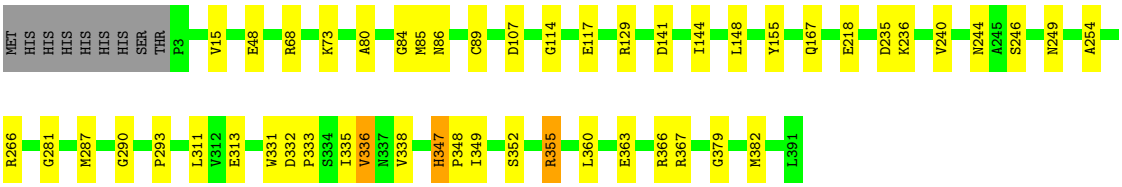
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	D	30	30	30	0	0

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.

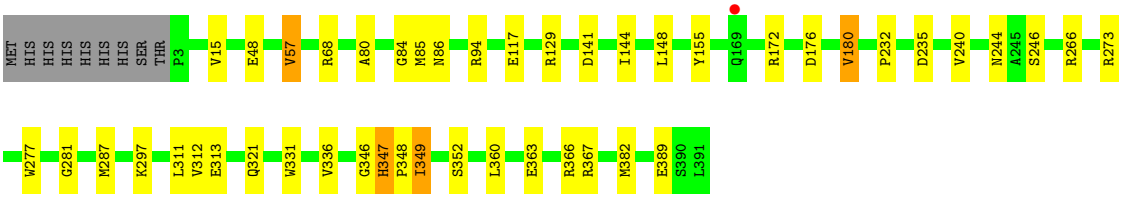
• Molecule 1: Acetyl-CoA acetyltransferase

Chain A:



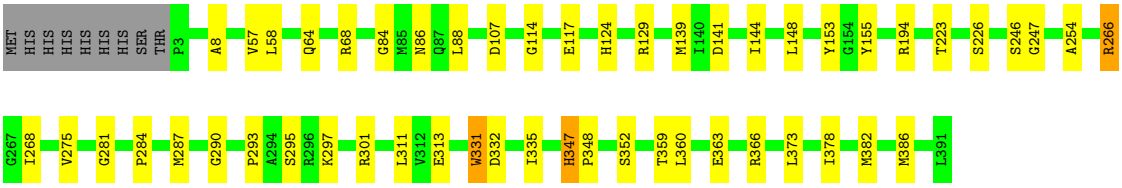
• Molecule 1: Acetyl-CoA acetyltransferase

Chain B:



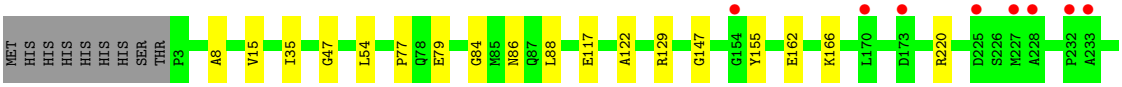
• Molecule 1: Acetyl-CoA acetyltransferase

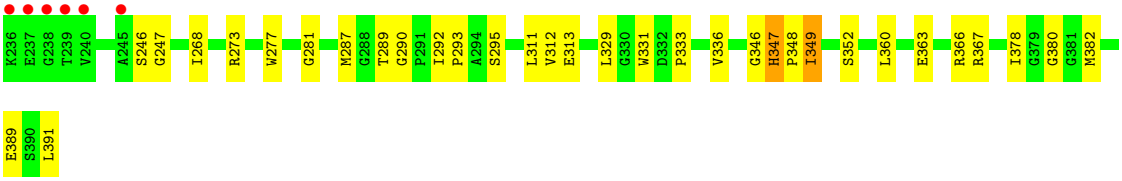
Chain C:



• Molecule 1: Acetyl-CoA acetyltransferase

Chain D:




K236
E237
G238
T239
V240
A245
S246
G247
I268
R273
W277
G281
M287
G288
T289
G290
P291
I292
P293
A294
S295
L311
V312
E313
L329
G330
W331
D332
P333
V336
G346
H347
P348
I349
S352
L360
E363
R366
R367
I378
G379
G380
G381
M382
E389
S390
L391

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	83.85Å 79.15Å 150.96Å 90.00° 94.00° 90.00°	Depositor
Resolution (Å)	46.79 – 2.85 46.79 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.79-2.85) 81.4 (46.79-2.85)	Depositor EDS
R_{merge}	0.58	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.24 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.240 , 0.282 0.241 , 0.284	Depositor DCC
R_{free} test set	2303 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	22.0	Xtriage
Anisotropy	0.818	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 25.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	11586	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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: SO4, COA, SCY, CL

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	0.24	0/2833	0.43	0/3827
1	B	0.25	0/2834	0.43	0/3827
1	C	0.25	0/2826	0.44	0/3819
1	D	0.24	0/2795	0.44	0/3778
All	All	0.25	0/11288	0.43	0/15251

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2802	0	2786	28	0
1	B	2803	0	2798	26	0
1	C	2795	0	2776	35	0
1	D	2765	0	2736	34	0
2	A	25	0	0	1	0
2	B	15	0	0	1	0
3	A	48	0	32	0	0
3	B	48	0	32	0	0
3	C	48	0	32	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	48	0	32	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	58	0	0	0	0
5	B	57	0	0	0	0
5	C	42	0	0	0	0
5	D	30	0	0	0	0
All	All	11586	0	11224	110	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 110 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:C:311:LEU:HD21	1:C:363:GLU:HG3	1.57	0.85
1:D:247:GLY:HA2	3:D:401:COA:H131	1.67	0.76
1:C:57:VAL:HG23	1:C:58:LEU:HG	1.66	0.75
1:B:363:GLU:OE2	1:B:366:ARG:NH2	2.27	0.68
1:C:266:ARG:HB3	1:C:268:ILE:HG13	1.77	0.67

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	386/398 (97%)	375 (97%)	11 (3%)	0	100	100
1	B	386/398 (97%)	374 (97%)	12 (3%)	0	100	100
1	C	386/398 (97%)	375 (97%)	11 (3%)	0	100	100
1	D	386/398 (97%)	373 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1544/1592 (97%)	1497 (97%)	47 (3%)	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	271/284 (95%)	264 (97%)	7 (3%)	46	75
1	B	273/284 (96%)	263 (96%)	10 (4%)	34	65
1	C	271/284 (95%)	265 (98%)	6 (2%)	52	79
1	D	262/284 (92%)	257 (98%)	5 (2%)	57	81
All	All	1077/1136 (95%)	1049 (97%)	28 (3%)	46	75

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	331	TRP
1	D	349	ILE
1	C	155	TYR
1	D	287	MET
1	B	349	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	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)

4 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	SCY	B	89	1	7,8,9	0.92	0	3,9,11	0.83	0
1	SCY	C	89	1	7,8,9	0.91	0	3,9,11	0.83	0
1	SCY	A	89	1	7,8,9	0.93	0	3,9,11	0.81	0
1	SCY	D	89	1	7,8,9	0.91	0	3,9,11	0.84	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
1	SCY	B	89	1	-	0/5/7/9	-
1	SCY	C	89	1	-	0/5/7/9	-
1	SCY	A	89	1	-	0/5/7/9	-
1	SCY	D	89	1	-	0/5/7/9	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	89	SCY	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SO4	A	405	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	402	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	401	-	4,4,4	0.14	0	6,6,6	0.06	0
2	SO4	B	402	-	4,4,4	0.15	0	6,6,6	0.05	0
2	SO4	B	403	-	4,4,4	0.15	0	6,6,6	0.04	0
3	COA	C	401	-	41,50,50	1.08	2 (4%)	52,75,75	1.55	7 (13%)
2	SO4	B	401	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	406	-	4,4,4	0.14	0	6,6,6	0.05	0
3	COA	B	404	-	41,50,50	1.11	3 (7%)	52,75,75	1.54	9 (17%)
2	SO4	A	403	-	4,4,4	0.14	0	6,6,6	0.04	0
3	COA	A	404	-	41,50,50	1.05	2 (4%)	52,75,75	1.54	7 (13%)
3	COA	D	401	-	41,50,50	1.10	3 (7%)	52,75,75	1.60	10 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	COA	A	404	-	-	14/44/64/64	0/3/3/3
3	COA	C	401	-	-	18/44/64/64	0/3/3/3
3	COA	D	401	-	-	18/44/64/64	0/3/3/3
3	COA	B	404	-	-	10/44/64/64	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)
3	B	404	COA	O4B-C1B	3.66	1.46	1.41
3	D	401	COA	O4B-C1B	3.49	1.46	1.41
3	A	404	COA	O4B-C1B	3.43	1.45	1.41
3	C	401	COA	O4B-C1B	3.22	1.45	1.41
3	C	401	COA	C8A-N7A	-2.46	1.30	1.34

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	401	COA	P2A-O3A-P1A	-6.01	112.20	132.83
3	B	404	COA	P2A-O3A-P1A	-5.87	112.67	132.83
3	A	404	COA	P2A-O3A-P1A	-5.83	112.83	132.83
3	C	401	COA	P2A-O3A-P1A	-5.37	114.40	132.83
3	D	401	COA	N3A-C2A-N1A	-4.26	122.02	128.68

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	COA	C3B-C4B-C5B-O5B
3	A	404	COA	O4B-C4B-C5B-O5B
3	A	404	COA	C5B-O5B-P1A-O2A
3	A	404	COA	CCP-O6A-P2A-O3A
3	A	404	COA	CAP-CBP-CCP-O6A

There are no ring outliers.

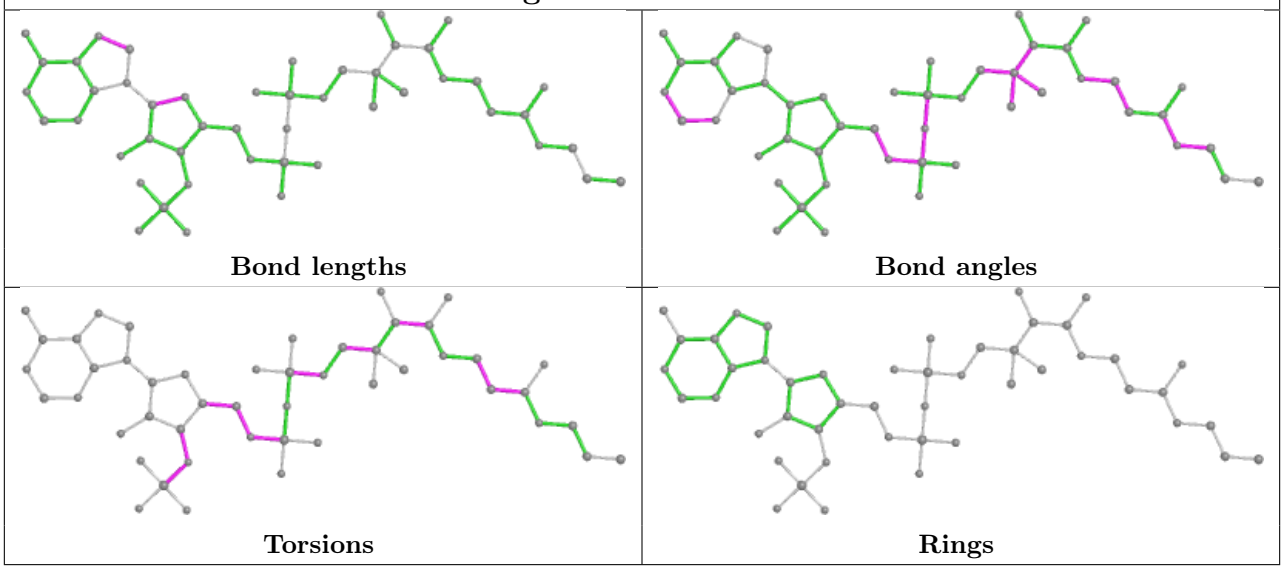
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	COA	2	0
2	B	401	SO4	1	0
2	A	406	SO4	1	0
3	D	401	COA	3	0

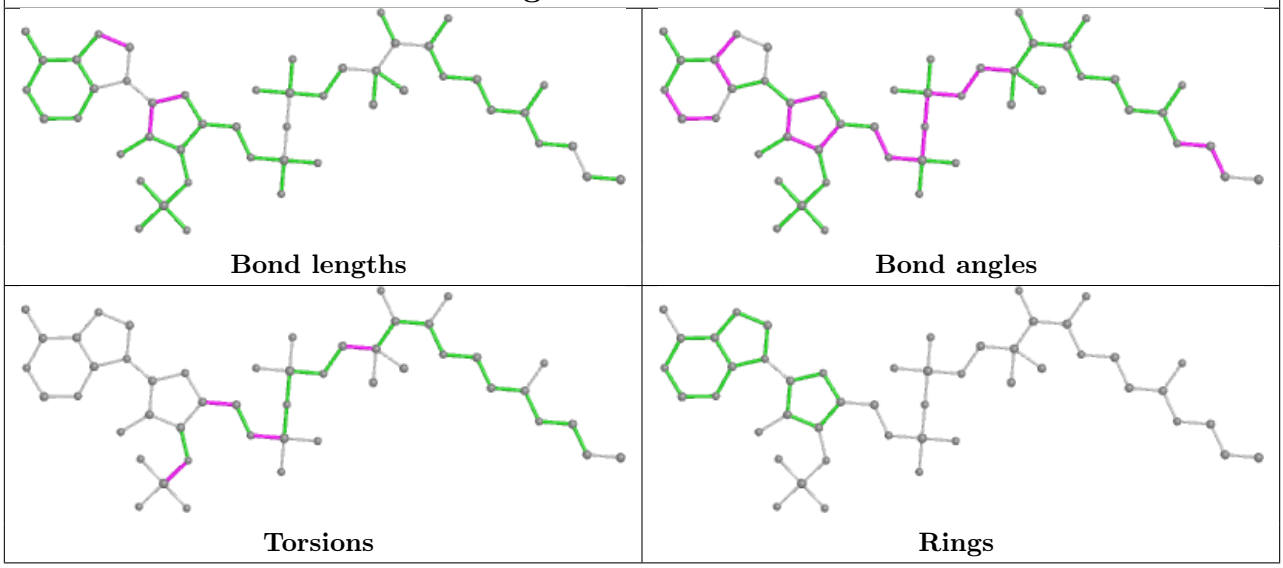
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

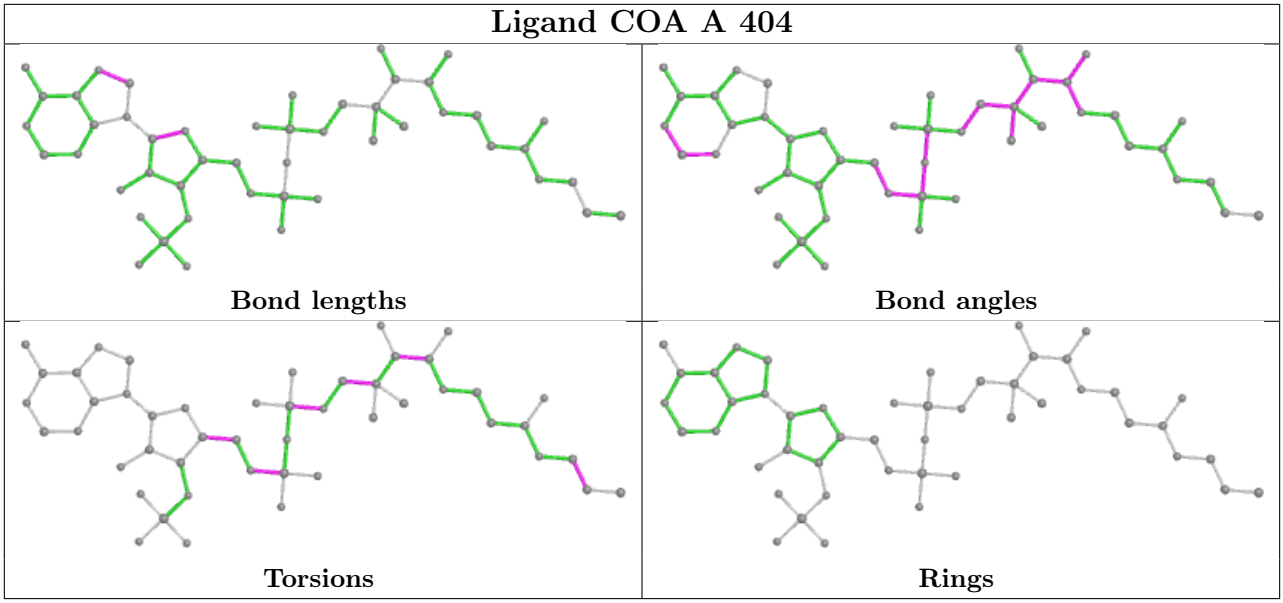
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

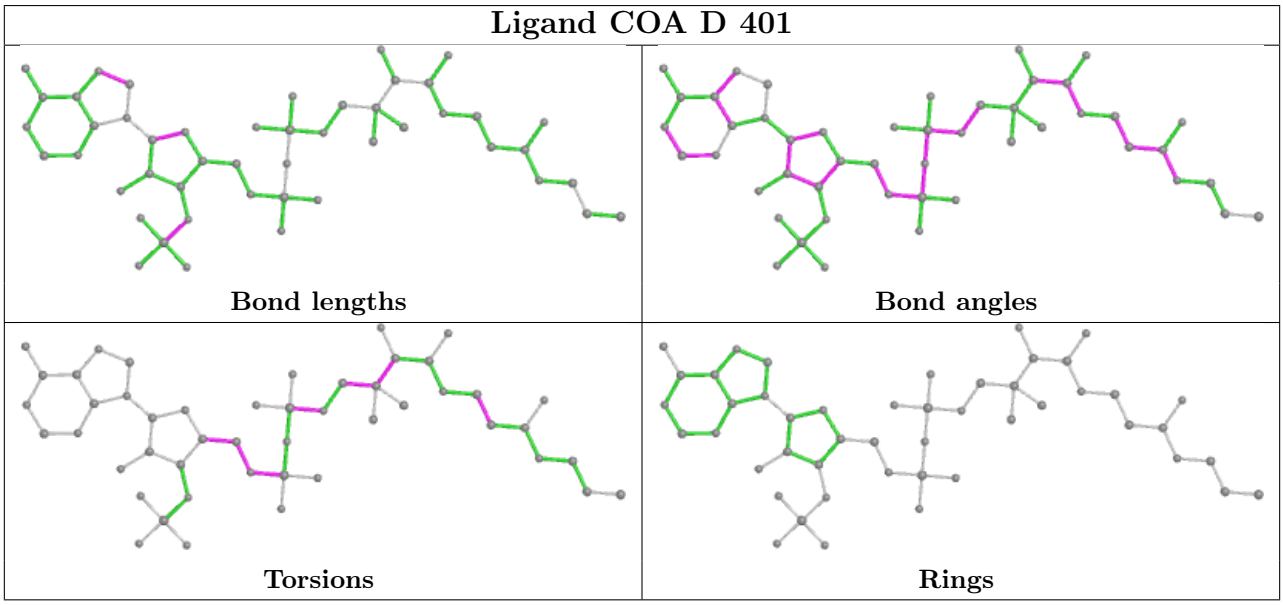
Ligand COA C 401



Ligand COA B 404







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	388/398 (97%)	-0.75	0 100 100	15, 33, 66, 128	0
1	B	388/398 (97%)	-0.73	1 (0%) 94 94	16, 33, 70, 122	0
1	C	388/398 (97%)	-0.50	0 100 100	28, 53, 90, 126	0
1	D	388/398 (97%)	-0.14	14 (3%) 42 37	30, 61, 122, 158	0
All	All	1552/1592 (97%)	-0.53	15 (0%) 82 81	15, 44, 98, 158	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	228	ALA	4.7
1	D	232	PRO	3.9
1	D	233	ALA	3.4
1	D	238	GLY	3.3
1	D	173	ASP	3.2

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	SCY	D	89	9/10	0.98	0.12	49,57,63,63	0
1	SCY	B	89	9/10	0.99	0.12	35,39,53,55	0
1	SCY	C	89	9/10	0.99	0.12	46,52,57,59	0
1	SCY	A	89	9/10	0.99	0.11	23,28,34,37	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

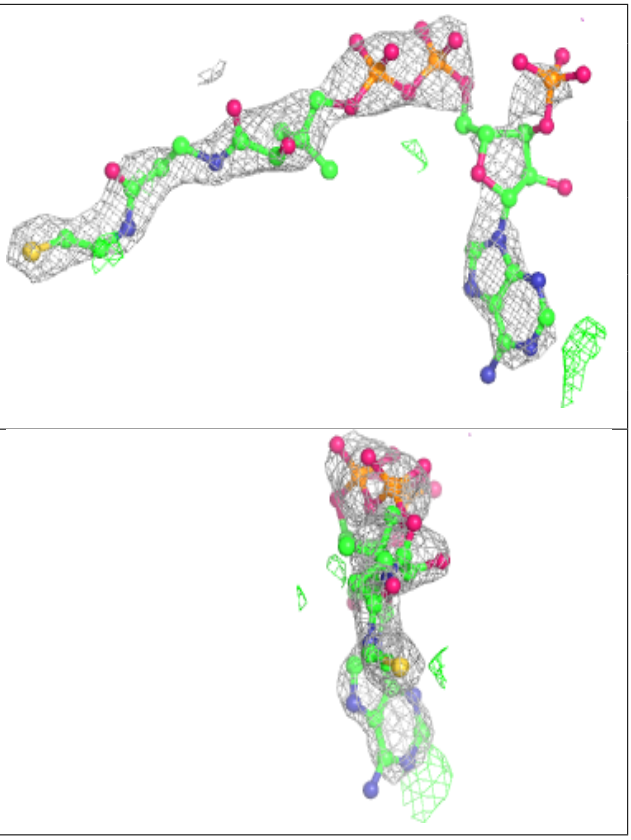
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

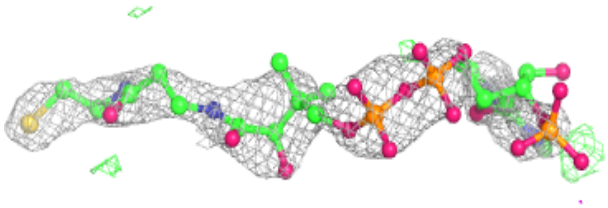
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	COA	D	401	48/48	0.90	0.29	68,106,114,120	48
3	COA	C	401	48/48	0.96	0.15	57,80,93,97	0
3	COA	B	404	48/48	0.96	0.17	36,64,83,90	48
3	COA	A	404	48/48	0.97	0.15	29,44,65,73	48
2	SO4	A	403	5/5	0.97	0.23	75,77,79,82	0
2	SO4	A	406	5/5	0.97	0.09	75,78,82,84	0
2	SO4	B	403	5/5	0.97	0.22	71,75,79,83	0
2	SO4	A	402	5/5	0.98	0.10	57,60,65,67	0
2	SO4	B	401	5/5	0.98	0.12	74,77,84,90	0
2	SO4	B	402	5/5	0.98	0.10	49,49,57,73	0
2	SO4	A	405	5/5	0.98	0.07	82,82,88,88	0
2	SO4	A	401	5/5	0.99	0.10	45,48,59,63	0
4	CL	A	407	1/1	0.99	0.04	44,44,44,44	0
4	CL	B	405	1/1	0.99	0.04	35,35,35,35	0

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

Electron density around COA D 401:

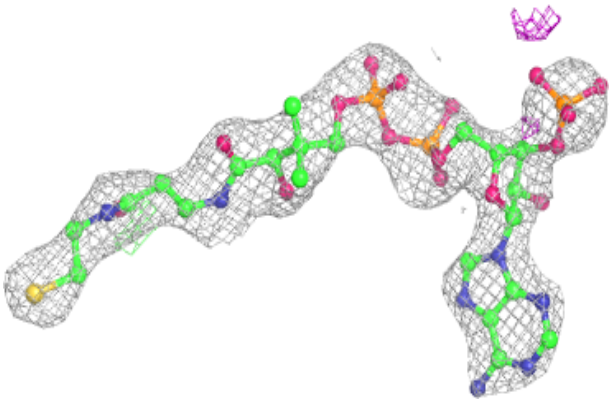
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

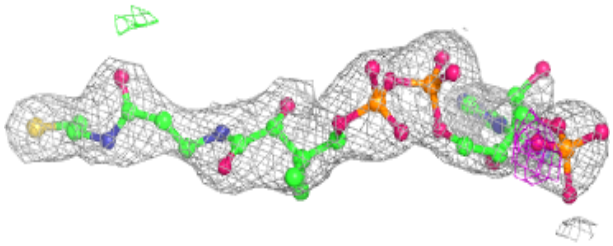


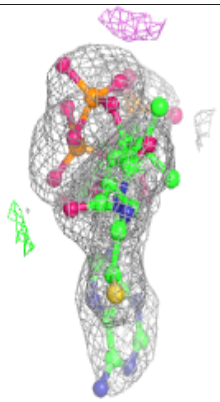


Electron density around COA C 401:

$2mF_o$-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 404:

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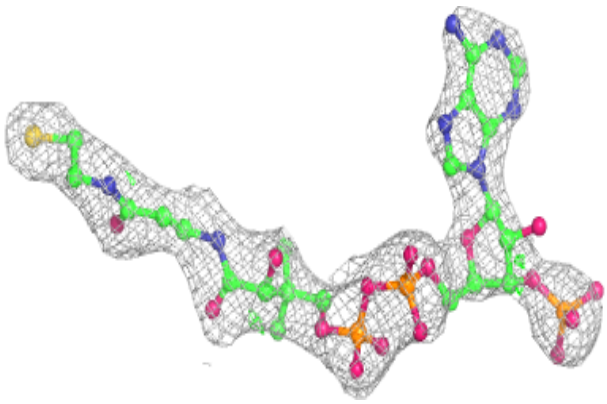
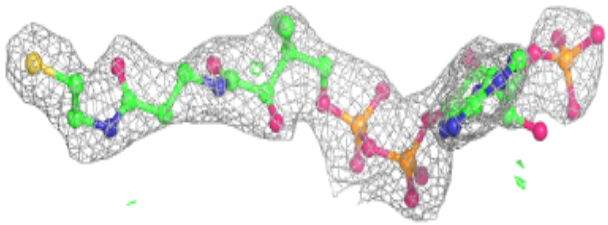
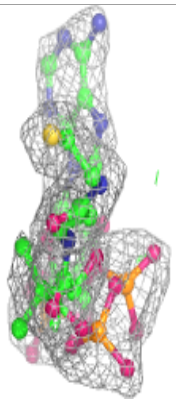
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

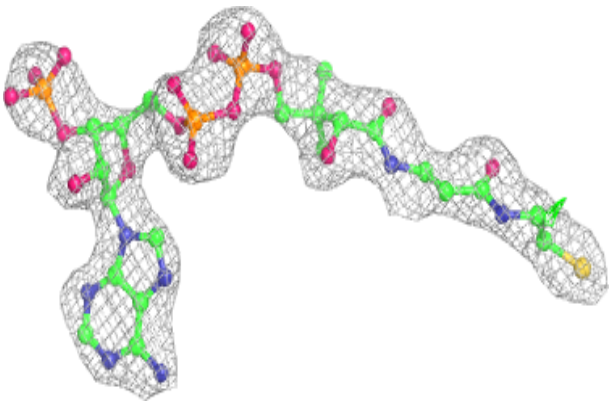


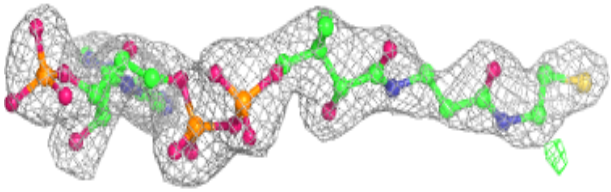


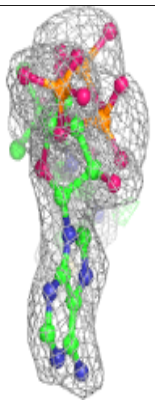


Electron density around COA A 404:

$2mF_o$-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.