wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 11:57 PM EST

PDB ID	:	4LRT
Title	:	Crystal and solution structures of the bifunctional enzyme (Aldolase/Aldehyde dehydrogenase) from Thermomonospora curvata, reveal a cofactor-binding domain motion during NAD+ and CoA accommodation whithin the shared cofactor-binding site
Authors	:	Fischer, B.; Branlant, G.; Talfournier, F.; Gruez, A.
Deposited on	:	2013-07-20
Resolution	:	1.50 Å(reported)

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

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

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

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

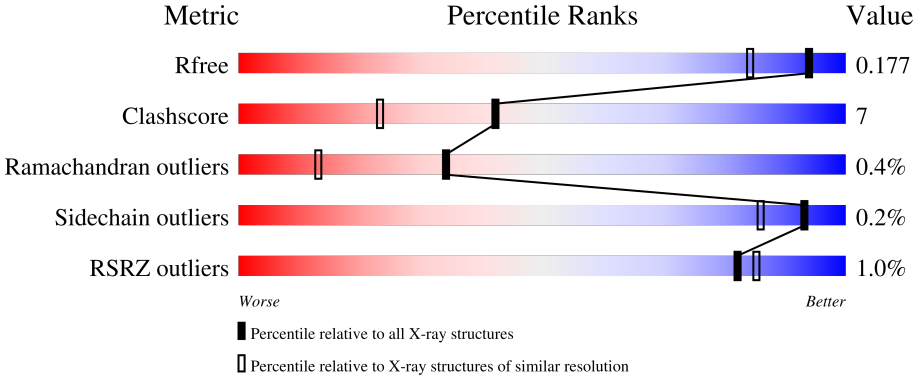
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.50 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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	355	.% 85% 9% 6%
1	C	355	88% 6% 6%
2	B	323	.% 79% 13% 9%
2	D	323	2% 80% 10% • 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	GOL	C	403	-	-	X	-

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 12212 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 4-hydroxy-2-oxovalerate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	2819	1737	520	551	11	0	38	0
1	C	335	2747	1700	507	530	10	0	29	0

- Molecule 2 is a protein called Acetaldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	295	2625	1650	459	499	17	0	47	0
2	D	293	2515	1581	440	477	17	0	43	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP D1A3K7
B	2	GLY	-	expression tag	UNP D1A3K7
B	3	SER	-	expression tag	UNP D1A3K7
B	4	SER	-	expression tag	UNP D1A3K7
B	5	HIS	-	expression tag	UNP D1A3K7
B	6	HIS	-	expression tag	UNP D1A3K7
B	7	HIS	-	expression tag	UNP D1A3K7
B	8	HIS	-	expression tag	UNP D1A3K7
B	9	HIS	-	expression tag	UNP D1A3K7
B	10	HIS	-	expression tag	UNP D1A3K7
B	11	SER	-	expression tag	UNP D1A3K7
B	12	SER	-	expression tag	UNP D1A3K7
B	13	GLY	-	expression tag	UNP D1A3K7
B	14	LEU	-	expression tag	UNP D1A3K7
B	15	VAL	-	expression tag	UNP D1A3K7
B	16	PRO	-	expression tag	UNP D1A3K7

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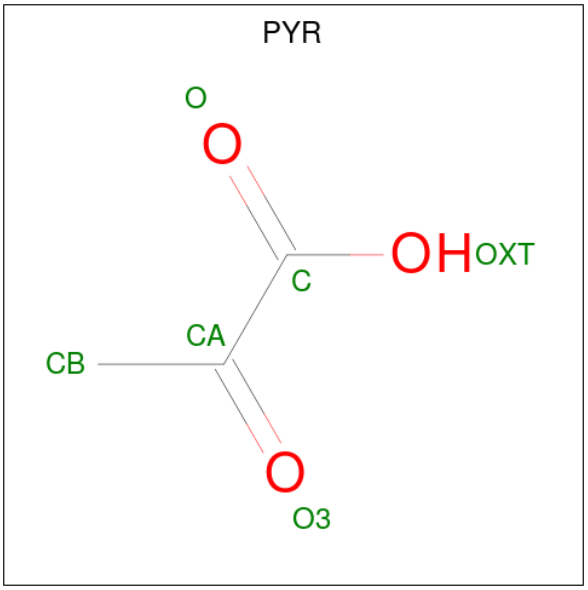
Chain	Residue	Modelled	Actual	Comment	Reference
B	17	ARG	-	expression tag	UNP D1A3K7
B	18	GLY	-	expression tag	UNP D1A3K7
B	19	SER	-	expression tag	UNP D1A3K7
B	20	HIS	-	expression tag	UNP D1A3K7
D	1	MET	-	initiating methionine	UNP D1A3K7
D	2	GLY	-	expression tag	UNP D1A3K7
D	3	SER	-	expression tag	UNP D1A3K7
D	4	SER	-	expression tag	UNP D1A3K7
D	5	HIS	-	expression tag	UNP D1A3K7
D	6	HIS	-	expression tag	UNP D1A3K7
D	7	HIS	-	expression tag	UNP D1A3K7
D	8	HIS	-	expression tag	UNP D1A3K7
D	9	HIS	-	expression tag	UNP D1A3K7
D	10	HIS	-	expression tag	UNP D1A3K7
D	11	SER	-	expression tag	UNP D1A3K7
D	12	SER	-	expression tag	UNP D1A3K7
D	13	GLY	-	expression tag	UNP D1A3K7
D	14	LEU	-	expression tag	UNP D1A3K7
D	15	VAL	-	expression tag	UNP D1A3K7
D	16	PRO	-	expression tag	UNP D1A3K7
D	17	ARG	-	expression tag	UNP D1A3K7
D	18	GLY	-	expression tag	UNP D1A3K7
D	19	SER	-	expression tag	UNP D1A3K7
D	20	HIS	-	expression tag	UNP D1A3K7

- Molecule 3 is PYRUVIC ACID (three-letter code: PYR) (formula: $C_3H_4O_3$).



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

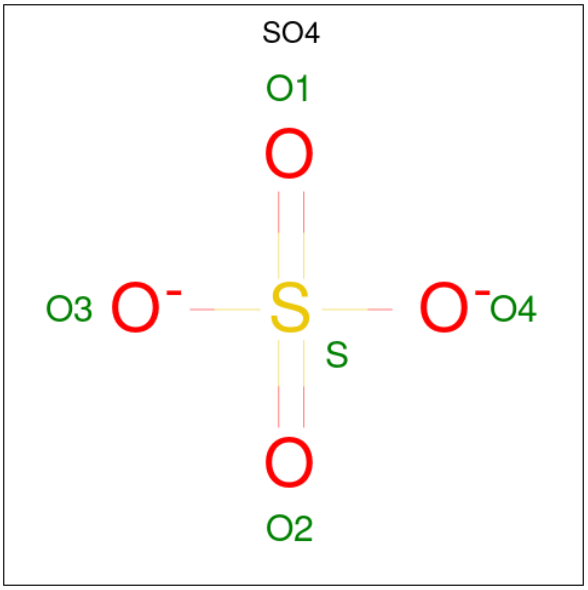
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
4	A	1	1	1	0	0
			Total	Na		
4	B	2	2	2	0	0
			Total	Na		
4	D	1	1	1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

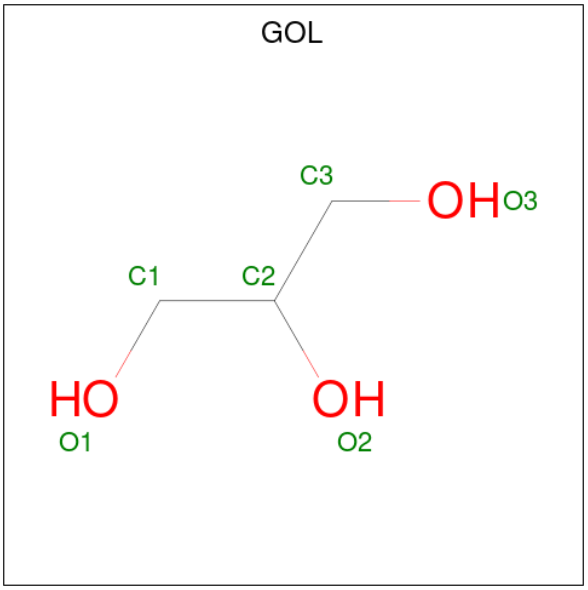
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
5	A	1	1	1	0	0
			Total	Mg		
5	C	1	1	1	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



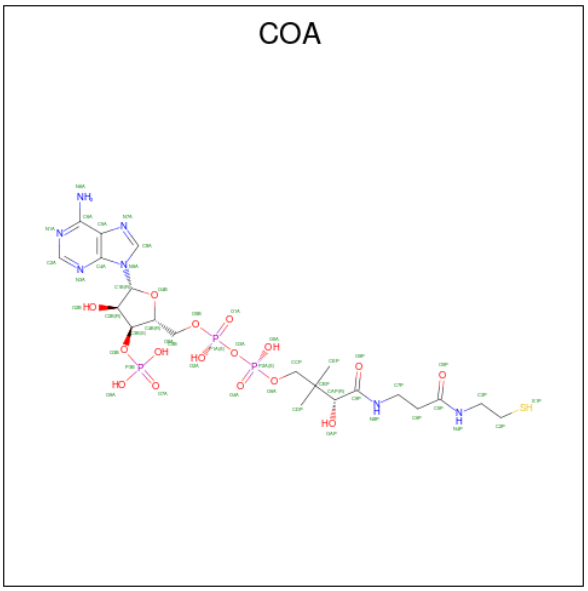
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
6	B	1	5	4	1	0	0
			Total	O	S		
6	D	1	5	4	1	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 8 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



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

- Molecule 9 is water.

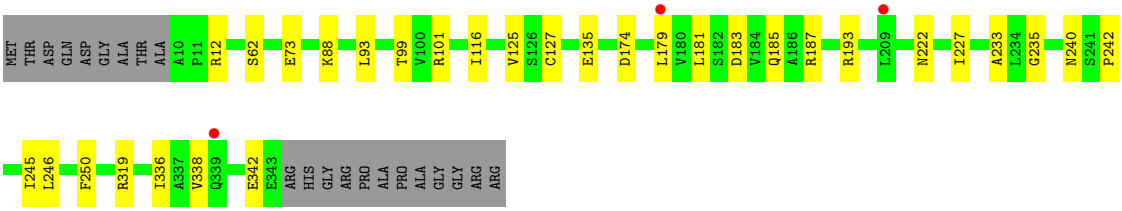
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	360	360	360	0	0
			Total	O		
9	B	309	309	309	0	0
			Total	O		
9	C	371	371	371	0	0
			Total	O		
9	D	324	324	324	0	0

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: 4-hydroxy-2-oxovalerate aldolase

Chain A:

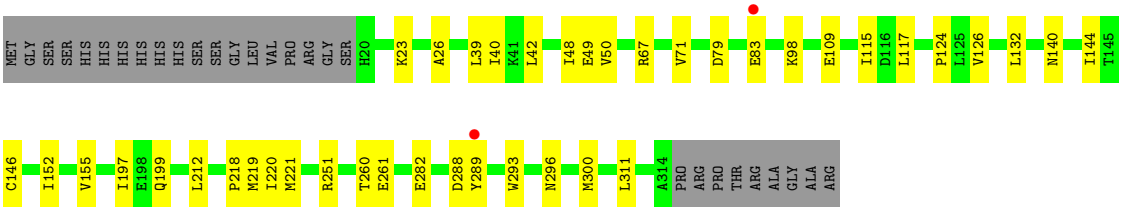


• Molecule 1: 4-hydroxy-2-oxovalerate aldolase

Chain C:

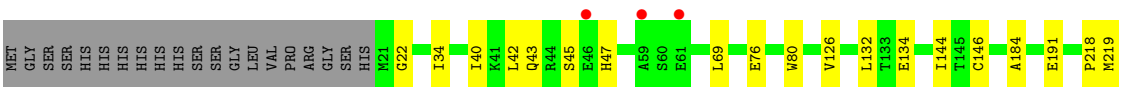
• Molecule 2: Acetaldehyde dehydrogenase

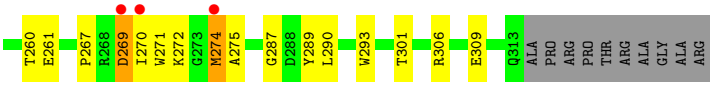
Chain B:



• Molecule 2: Acetaldehyde dehydrogenase

Chain D:




T260
E261
P267
R268
D269
I270
W271
K272
G273
M274
A275
G287
D288
Y289
L290
W293
T301
R306
E309
Q313
ALA
PRO
ARG
PRO
THR
ARG
ALA
GLY
ALA
ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	94.50Å 116.70Å 131.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.45 – 1.50 46.45 – 1.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.45-1.50) 90.0 (46.45-1.50)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.07 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.151 , 0.170 0.158 , 0.177	Depositor DCC
R_{free} test set	10429 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	17.1	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 42.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	12212	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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, NA, PYR, GOL, SO4, MG

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	0.56	3/2859 (0.1%)	0.63	0/3880
1	C	0.52	0/2788	0.64	0/3780
2	B	0.48	0/2671	0.61	0/3638
2	D	0.50	0/2564	0.66	0/3495
All	All	0.52	3/10882 (0.0%)	0.64	0/14793

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
2	D	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	127[A]	CYS	CB-SG	5.06	1.90	1.82
1	A	127[B]	CYS	CB-SG	5.06	1.90	1.82
1	A	127[C]	CYS	CB-SG	5.06	1.90	1.82

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	22[B]	GLY	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2819	0	2714	36	0
1	C	2747	0	2670	34	0
2	B	2625	0	2621	54	0
2	D	2515	0	2507	37	0
3	A	6	0	0	0	0
3	C	6	0	0	0	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	B	5	0	0	0	0
6	D	5	0	0	0	0
7	B	6	0	8	0	0
7	C	12	0	16	6	0
8	B	48	0	31	2	0
8	D	48	0	31	1	0
9	A	360	0	0	10	0
9	B	309	0	0	8	0
9	C	371	0	0	6	0
9	D	324	0	0	6	0
All	All	12212	0	10598	149	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 7.

The worst 5 of 149 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)
2:B:152[B]:ILE:CD1	2:B:197[B]:ILE:HD13	1.37	1.49
1:C:68[B]:PHE:CD2	2:D:271[B]:TRP:HA	1.53	1.41
2:B:152[B]:ILE:HD13	2:B:197[B]:ILE:CD1	1.69	1.22
2:D:146[B]:CYS:SG	9:D:819:HOH:O	2.05	1.09
2:B:152[B]:ILE:CD1	2:B:197[B]:ILE:CD1	2.25	1.06

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	373/355 (105%)	368 (99%)	4 (1%)	1 (0%)	41	18
1	C	363/355 (102%)	358 (99%)	4 (1%)	1 (0%)	41	18
2	B	345/323 (107%)	337 (98%)	5 (1%)	3 (1%)	17	3
2	D	332/323 (103%)	322 (97%)	9 (3%)	1 (0%)	41	18
All	All	1413/1356 (104%)	1385 (98%)	22 (2%)	6 (0%)	34	13

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	LEU
2	B	144	ILE
2	D	144	ILE
2	B	288[A]	ASP
2	B	288[B]	ASP

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	285/257 (111%)	285 (100%)	0	100	100
1	C	276/257 (107%)	276 (100%)	0	100	100
2	B	274/245 (112%)	274 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	D	261/245 (106%)	258 (99%)	3 (1%)	73 53
All	All	1096/1004 (109%)	1093 (100%)	3 (0%)	93 85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	269[A]	ASP
2	D	274[A]	MET
2	D	274[B]	MET

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

Mol	Chain	Res	Type
2	D	263	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)

Of 15 ligands modelled in this entry, 6 are monoatomic - leaving 9 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	$\#\|Z\| > 2$
8	COA	B	405	2	41,50,50	0.94	3 (7%)	52,75,75	1.31	4 (7%)
8	COA	D	403	2	41,50,50	1.07	4 (9%)	52,75,75	2.09	11 (21%)
7	GOL	B	404	-	5,5,5	0.36	0	5,5,5	0.30	0
7	GOL	C	402	-	5,5,5	0.23	0	5,5,5	0.43	0
6	SO4	B	401	-	4,4,4	0.17	0	6,6,6	0.33	0
7	GOL	C	403	-	5,5,5	0.34	0	5,5,5	0.47	0
3	PYR	C	401	5	5,5,5	2.64	3 (60%)	3,6,6	1.30	0
6	SO4	D	401	-	4,4,4	0.27	0	6,6,6	0.52	0
3	PYR	A	401	5	5,5,5	2.68	3 (60%)	3,6,6	1.30	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
8	COA	B	405	2	-	3/44/64/64	0/3/3/3
8	COA	D	403	2	-	6/44/64/64	0/3/3/3
7	GOL	B	404	-	-	4/4/4/4	-
7	GOL	C	402	-	-	4/4/4/4	-
7	GOL	C	403	-	-	2/4/4/4	-
3	PYR	C	401	5	-	0/4/4/4	-
3	PYR	A	401	5	-	0/4/4/4	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	PYR	CA-C	-4.23	1.39	1.54
3	C	401	PYR	CA-C	-4.17	1.39	1.54
3	A	401	PYR	O3-CA	3.40	1.30	1.23
3	C	401	PYR	O3-CA	3.36	1.30	1.23
8	D	403	COA	CDP-CBP	-2.81	1.47	1.53

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	D	403	COA	CDP-CBP-CCP	7.31	120.16	108.23
8	D	403	COA	CDP-CBP-CAP	-6.98	96.71	108.82
8	D	403	COA	CEP-CBP-CCP	5.27	116.83	108.23
8	D	403	COA	CEP-CBP-CAP	4.27	116.23	108.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	B	405	COA	N3A-C2A-N1A	-3.77	122.78	128.68

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	404	GOL	C1-C2-C3-O3
7	B	404	GOL	O2-C2-C3-O3
7	C	402	GOL	O1-C1-C2-C3
8	B	405	COA	C3B-O3B-P3B-O7A
8	D	403	COA	C3B-O3B-P3B-O7A

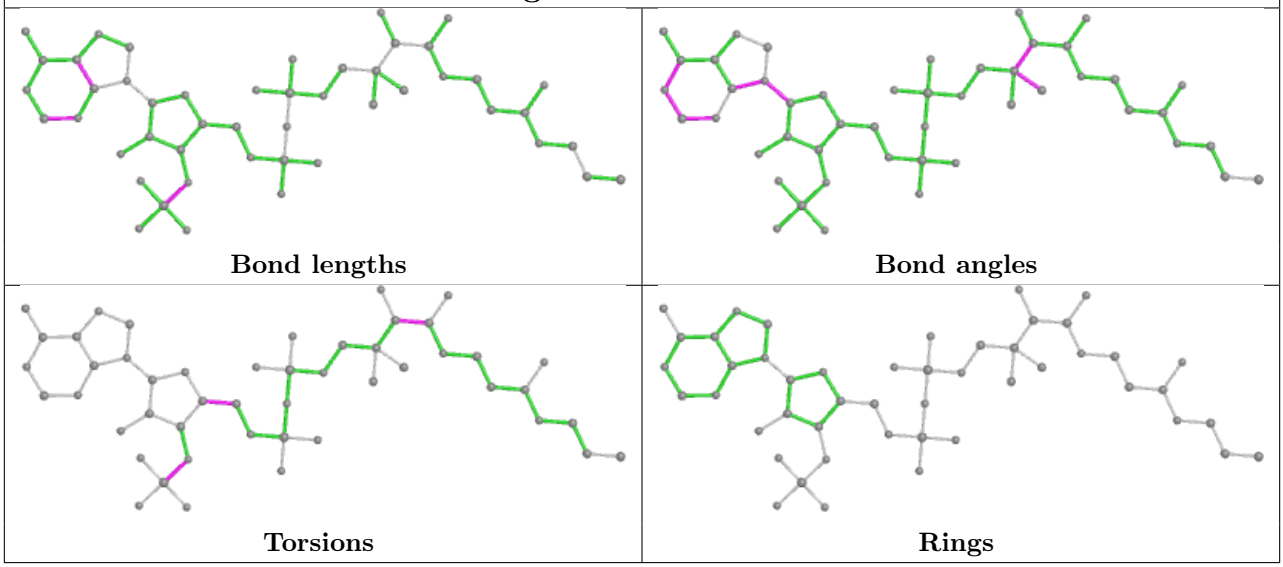
There are no ring outliers.

4 monomers are involved in 9 short contacts:

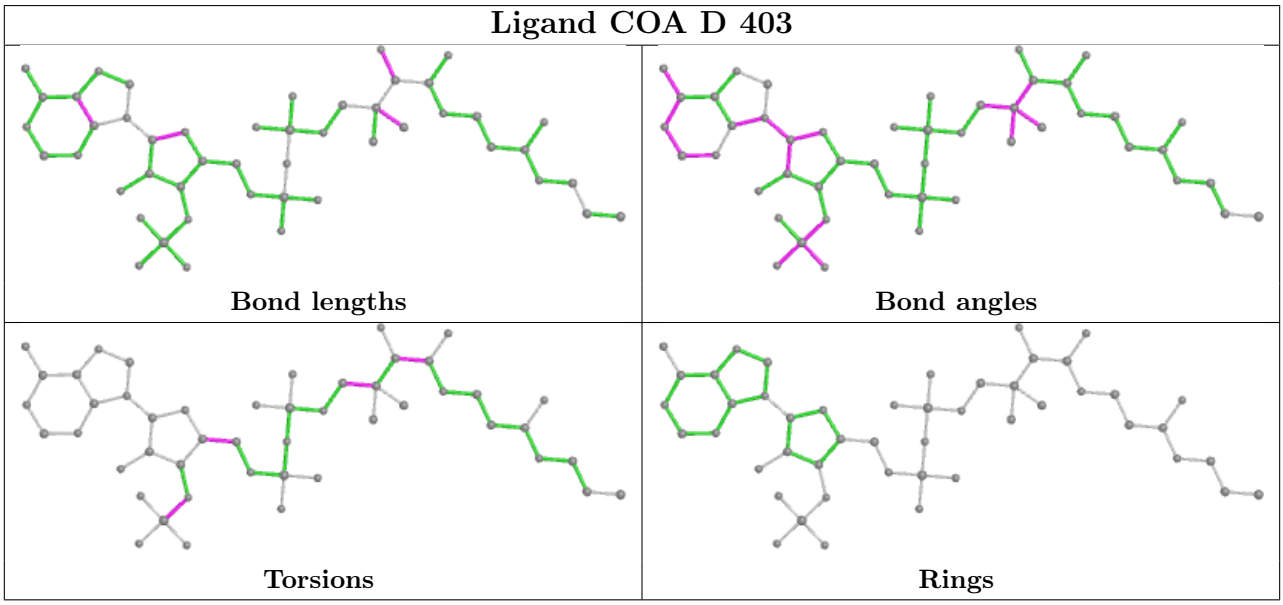
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	405	COA	2	0
8	D	403	COA	1	0
7	C	402	GOL	2	0
7	C	403	GOL	4	0

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 B 405



Ligand COA D 403



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	334/355 (94%)	-0.10	3 (0%)	84	87	12, 17, 25, 38	13 (3%)
1	C	335/355 (94%)	-0.19	1 (0%)	94	95	11, 16, 23, 33	13 (3%)
2	B	295/323 (91%)	-0.19	2 (0%)	87	90	12, 20, 29, 34	12 (4%)
2	D	293/323 (90%)	-0.22	6 (2%)	65	70	11, 16, 30, 41	8 (2%)
All	All	1257/1356 (92%)	-0.17	12 (0%)	82	85	11, 17, 28, 41	46 (3%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	270[A]	ILE	8.0
2	D	269[A]	ASP	7.0
2	D	59	ALA	3.6
1	C	345	HIS	3.0
2	D	61	GLU	2.9

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)

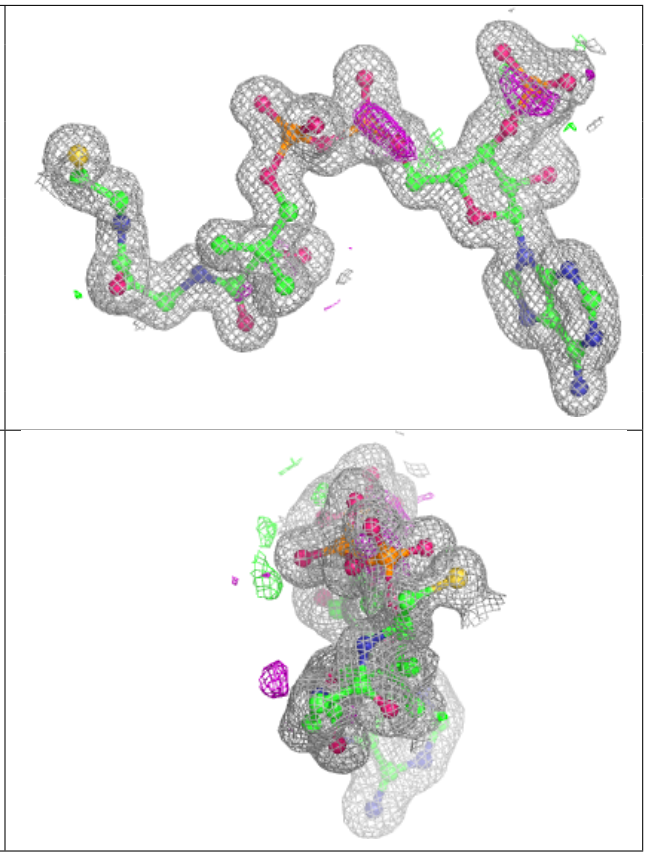
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

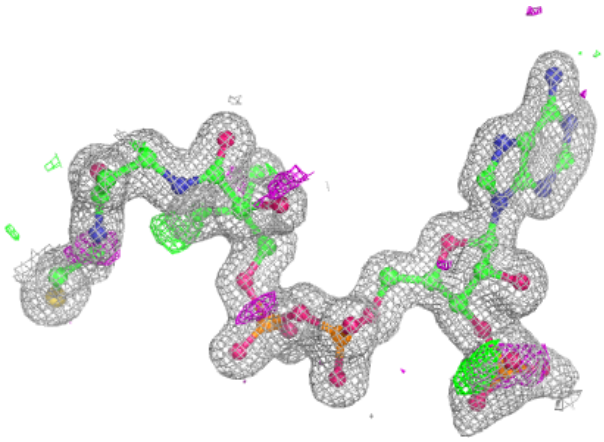
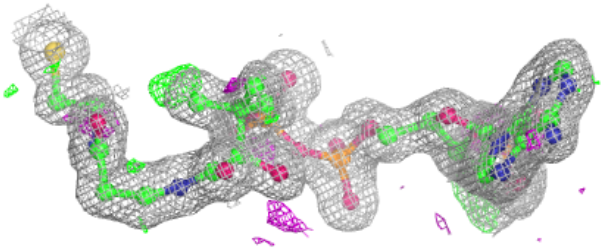
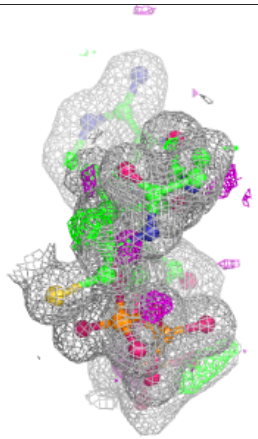
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	GOL	C	402	6/6	0.75	0.28	30,36,37,38	6
7	GOL	B	404	6/6	0.82	0.20	25,29,30,30	6
7	GOL	C	403	6/6	0.83	0.17	25,31,32,39	0
6	SO4	D	401	5/5	0.89	0.14	23,26,28,29	5
3	PYR	A	401	6/6	0.93	0.20	13,18,21,25	6
3	PYR	C	401	6/6	0.93	0.20	15,17,18,22	6
6	SO4	B	401	5/5	0.95	0.09	19,21,23,23	5
4	NA	B	402	1/1	0.96	0.12	31,31,31,31	0
8	COA	B	405	48/48	0.97	0.07	13,17,25,28	5
8	COA	D	403	48/48	0.97	0.07	11,17,31,33	1
4	NA	B	403	1/1	0.99	0.11	16,16,16,16	0
4	NA	A	402	1/1	0.99	0.11	24,24,24,24	0
5	MG	A	403	1/1	1.00	0.17	9,9,9,9	0
5	MG	C	404	1/1	1.00	0.18	8,8,8,8	0
4	NA	D	402	1/1	1.00	0.06	15,15,15,15	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 B 405:

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 403: $2mF_o$-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.