wwPDB X-ray Structure Validation Summary Report (i)

May 16, 2020 – 06:56 pm BST

PDB ID	:	8LDH
Title	:	REFINED CRYSTAL STRUCTURE OF DOGFISH M4 APO-LACTATE DEHYDROGENASE
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Deposited on	:	1988-01-04
Resolution	:	2.80 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 (i)) were used in the production of this report:

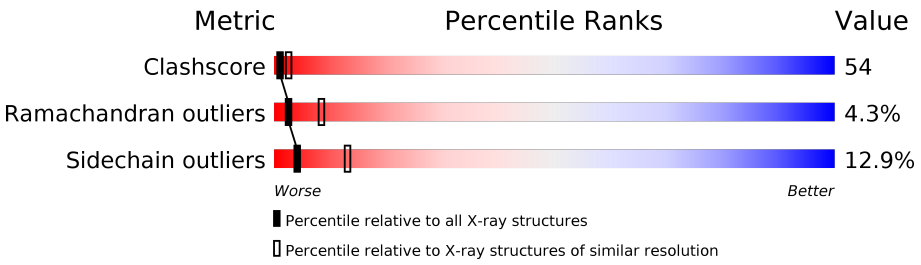
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	330	31% 52% 14% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2852 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.

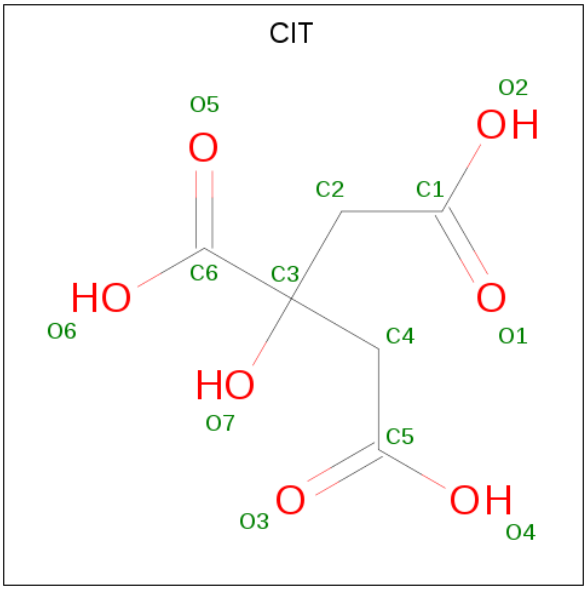
- Molecule 1 is a protein called M4 APO-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	330	2545	1620	439	468	18	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	ASN	TRP	CONFLICT	UNP P00341
A	206	VAL	ASN	CONFLICT	UNP P00341
A	208	SER	LEU	CONFLICT	UNP P00341
A	209	ILE	LYS	CONFLICT	UNP P00341
A	210	LYS	GLU	CONFLICT	UNP P00341
A	214	LEU	GLU	CONFLICT	UNP P00341
A	215	ASP	LEU	CONFLICT	UNP P00341
A	308	ASN	ASP	CONFLICT	UNP P00341

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	13	6	7	0	0
			Total	C	O		
2	A	1	13	6	7	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	281	281	281	0	0

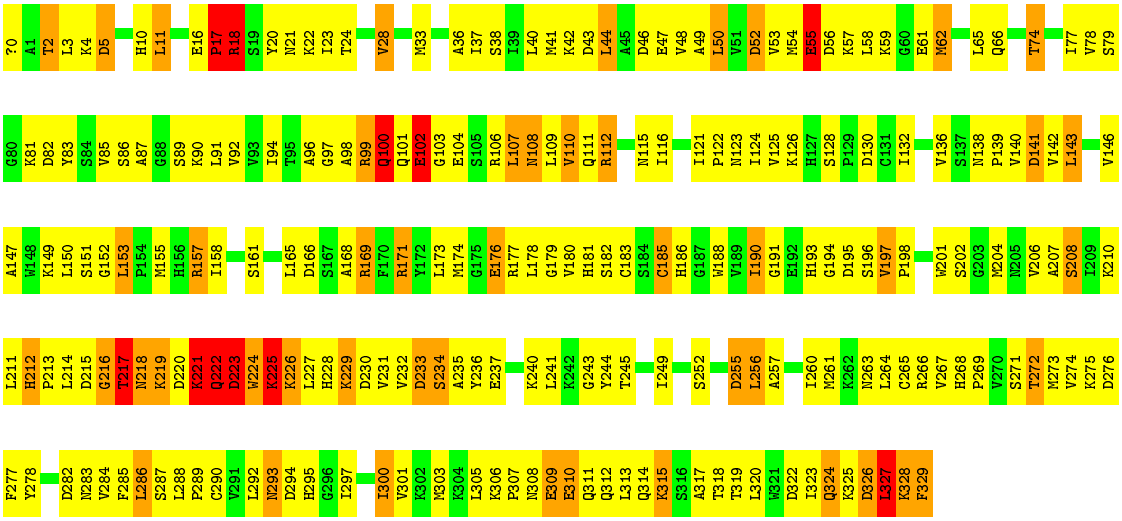
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

- Molecule 1: M4 APO-LACTATE DEHYDROGENASE

Chain A: 31% 52% 14% •



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	F 4 2 2	Depositor
Cell constants a, b, c, α, β, γ	146.80Å 146.80Å 155.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.191 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2852	wwPDB-VP
Average B, all atoms ($Å^2$)	13.0	wwPDB-VP

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: ACE, CIT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	1.14	7/2590 (0.3%)	1.96	71/3502 (2.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	PRO	C-N	-8.76	1.13	1.34
1	A	18	ARG	C-N	-7.09	1.17	1.34
1	A	309	GLU	CD-OE1	-6.88	1.18	1.25
1	A	18	ARG	CA-CB	6.02	1.67	1.53
1	A	328	LYS	N-CA	-5.99	1.34	1.46

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	18	ARG	NE-CZ-NH1	29.32	134.96	120.30
1	A	18	ARG	NE-CZ-NH2	-23.73	108.43	120.30
1	A	327	LEU	C-N-CA	19.51	170.48	121.70
1	A	157	ARG	NE-CZ-NH2	12.04	126.32	120.30
1	A	171	ARG	NE-CZ-NH2	-10.89	114.86	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	PRO	Mainchain
1	A	18	ARG	Sidechain

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	2545	0	2610	279	76
2	A	26	0	10	5	0
3	A	281	0	0	40	19
All	All	2852	0	2620	279	77

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 54.

The worst 5 of 279 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:273:MET:CE	1:A:275:LYS:HB2	1.75	1.16
1:A:197:VAL:HG23	1:A:228:HIS:HE1	1.13	1.12
1:A:17:PRO:HA	1:A:18:ARG:HD3	1.32	1.11
1:A:100:GLN:HB2	1:A:109:LEU:HD22	1.35	1.04
1:A:273:MET:HE3	1:A:275:LYS:HB2	1.37	1.04

The worst 5 of 77 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:LEU:CD2	1:A:329:PHE:CD2[32_555]	0.39	1.81
1:A:107:LEU:CG	1:A:329:PHE:CG[32_555]	0.73	1.47
1:A:104:GLU:CG	1:A:112:ARG:CG[32_555]	0.78	1.42
1:A:103:GLY:O	1:A:112:ARG:O[32_555]	0.78	1.42
1:A:101:GLN:CG	3:A:426:HOH:O[32_555]	0.79	1.41

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	328/330 (99%)	293 (89%)	21 (6%)	14 (4%)	2 8

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	SER
1	A	217	THR
1	A	218	ASN
1	A	221	LYS
1	A	222	GLN

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	286/286 (100%)	249 (87%)	37 (13%)	4 13

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	155	MET
1	A	190	ILE
1	A	311	GLN
1	A	169	ARG
1	A	176	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
1	A	181	HIS
1	A	295	HIS
1	A	127	HIS
1	A	293	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	CIT	A	331	-	3,12,12	2.80	2 (66%)	3,17,17	7.06	2 (66%)
2	CIT	A	330	-	3,12,12	3.75	2 (66%)	3,17,17	6.80	3 (100%)

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	CIT	A	331	-	-	2/6/16/16	-
2	CIT	A	330	-	-	3/6/16/16	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	330	CIT	C4-C3	-5.15	1.47	1.54
2	A	331	CIT	C4-C3	-3.81	1.49	1.54
2	A	330	CIT	O7-C3	-3.69	1.37	1.43
2	A	331	CIT	O7-C3	2.51	1.47	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	331	CIT	C3-C2-C1	10.89	132.42	114.98
2	A	330	CIT	C3-C4-C5	9.73	130.57	114.98
2	A	330	CIT	C3-C2-C1	6.06	124.69	114.98
2	A	331	CIT	C3-C4-C5	5.22	123.34	114.98
2	A	330	CIT	C4-C3-C2	2.67	116.47	109.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	331	CIT	C6-C3-C4-C5
2	A	330	CIT	C1-C2-C3-O7
2	A	330	CIT	C1-C2-C3-C6
2	A	330	CIT	C1-C2-C3-C4
2	A	331	CIT	O7-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	331	CIT	1	0
2	A	330	CIT	4	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	18:ARG	C	19:SER	N	1.17
1	A	17:PRO	C	18:ARG	N	1.13

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.