



wwPDB X-ray Structure Validation Summary Report

Aug 31, 2023 – 12:34 PM EDT

PDB ID : 2LDX
Title : CHARACTERIZATION OF THE ANTIGENIC SITES ON THE REFINED
3-ANGSTROMS RESOLUTION STRUCTURE OF MOUSE TESTICULAR
LACTATE DEHYDROGENASE C4
Authors : Griffith, J.P.; Rossmann, M.G.
Deposited on : 1987-11-25
Resolution : 2.96 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  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](#) ) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
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

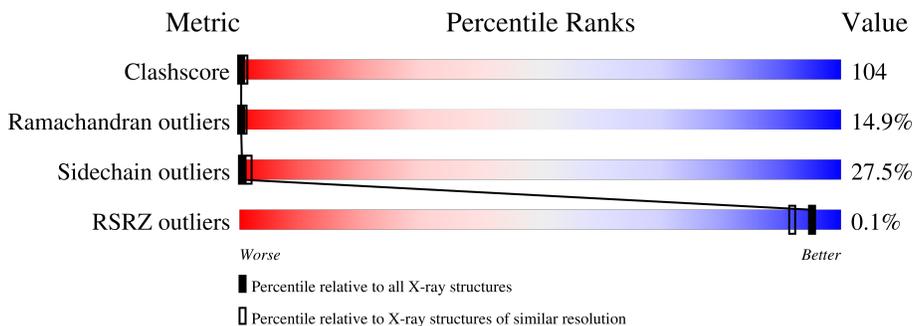
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 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))
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 $\leq 5\%$. 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	331	
1	B	331	
1	C	331	
1	D	331	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10091 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 APO-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	331	2515	1603	432	468	12	0	0	0
1	B	331	2515	1603	432	468	12	0	0	0
1	C	331	2515	1603	432	468	12	0	0	0
1	D	331	2515	1603	432	468	12	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	ASP	ASN	conflict	UNP P00342
A	55	ASP	ASN	conflict	UNP P00342
A	65	GLN	LEU	conflict	UNP P00342
A	103	GLN	GLU	conflict	UNP P00342
A	123	VAL	ILE	conflict	UNP P00342
A	124	ILE	VAL	conflict	UNP P00342
A	134	VAL	ILE	conflict	UNP P00342
A	221	LYS	SER	conflict	UNP P00342
A	222	ASN	ASP	conflict	UNP P00342
A	224	GLN	GLU	conflict	UNP P00342
A	242	ASP	ASN	conflict	UNP P00342
A	296	GLU	GLN	conflict	UNP P00342
A	328	ASN	ASP	conflict	UNP P00342
A	330	GLU	GLN	conflict	UNP P00342
B	29	ASP	ASN	conflict	UNP P00342
B	55	ASP	ASN	conflict	UNP P00342
B	65	GLN	LEU	conflict	UNP P00342
B	103	GLN	GLU	conflict	UNP P00342
B	123	VAL	ILE	conflict	UNP P00342
B	124	ILE	VAL	conflict	UNP P00342
B	134	VAL	ILE	conflict	UNP P00342

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Chain	Residue	Modelled	Actual	Comment	Reference
B	221	LYS	SER	conflict	UNP P00342
B	222	ASN	ASP	conflict	UNP P00342
B	224	GLN	GLU	conflict	UNP P00342
B	242	ASP	ASN	conflict	UNP P00342
B	296	GLU	GLN	conflict	UNP P00342
B	328	ASN	ASP	conflict	UNP P00342
B	330	GLU	GLN	conflict	UNP P00342
C	29	ASP	ASN	conflict	UNP P00342
C	55	ASP	ASN	conflict	UNP P00342
C	65	GLN	LEU	conflict	UNP P00342
C	103	GLN	GLU	conflict	UNP P00342
C	123	VAL	ILE	conflict	UNP P00342
C	124	ILE	VAL	conflict	UNP P00342
C	134	VAL	ILE	conflict	UNP P00342
C	221	LYS	SER	conflict	UNP P00342
C	222	ASN	ASP	conflict	UNP P00342
C	224	GLN	GLU	conflict	UNP P00342
C	242	ASP	ASN	conflict	UNP P00342
C	296	GLU	GLN	conflict	UNP P00342
C	328	ASN	ASP	conflict	UNP P00342
C	330	GLU	GLN	conflict	UNP P00342
D	29	ASP	ASN	conflict	UNP P00342
D	55	ASP	ASN	conflict	UNP P00342
D	65	GLN	LEU	conflict	UNP P00342
D	103	GLN	GLU	conflict	UNP P00342
D	123	VAL	ILE	conflict	UNP P00342
D	124	ILE	VAL	conflict	UNP P00342
D	134	VAL	ILE	conflict	UNP P00342
D	221	LYS	SER	conflict	UNP P00342
D	222	ASN	ASP	conflict	UNP P00342
D	224	GLN	GLU	conflict	UNP P00342
D	242	ASP	ASN	conflict	UNP P00342
D	296	GLU	GLN	conflict	UNP P00342
D	328	ASN	ASP	conflict	UNP P00342
D	330	GLU	GLN	conflict	UNP P00342

- Molecule 2 is water.

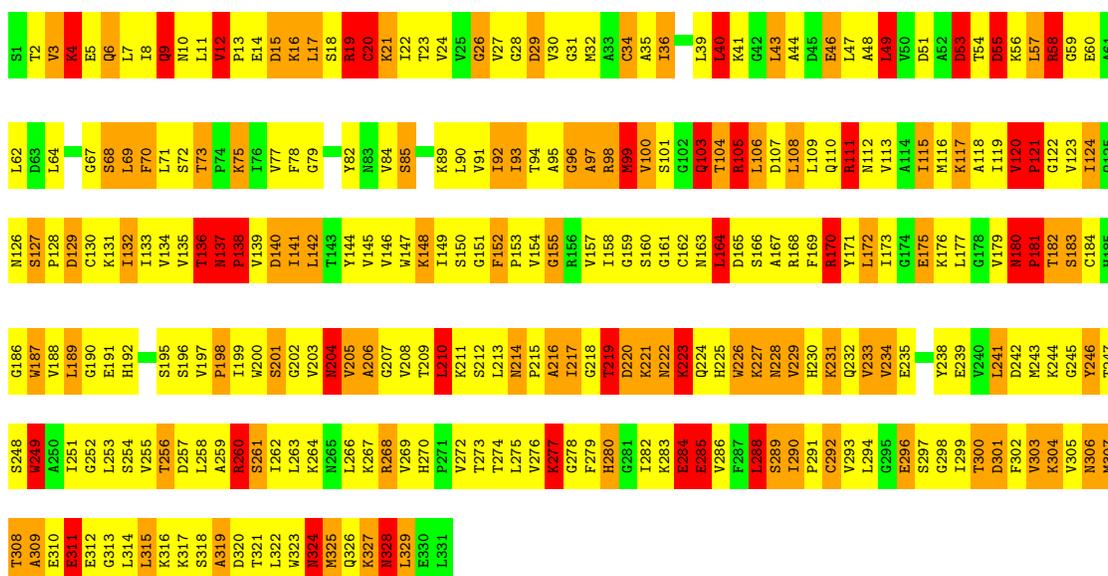
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	29	Total O 29 29	0	0
2	D	2	Total O 2 2	0	0

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.

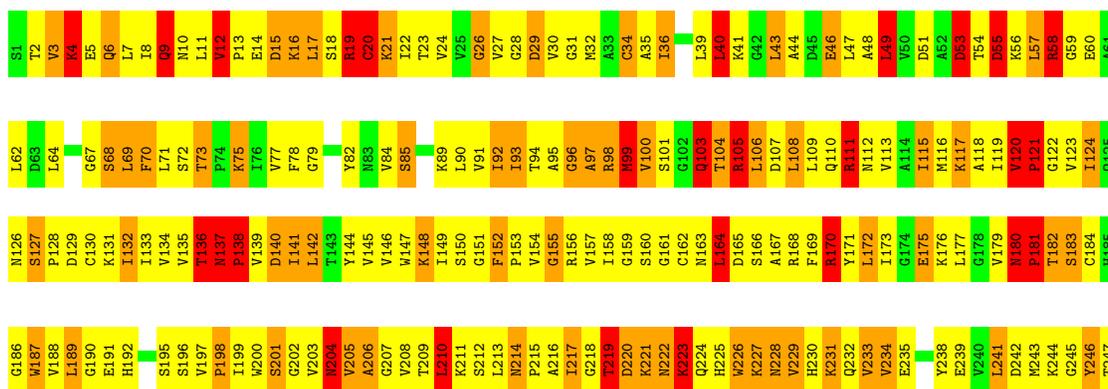
• Molecule 1: APO-LACTATE DEHYDROGENASE

Chain A: 



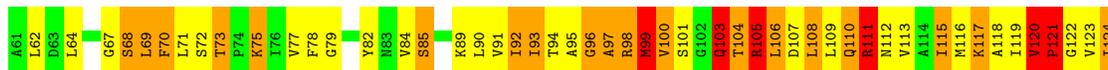
• Molecule 1: APO-LACTATE DEHYDROGENASE

Chain B: 

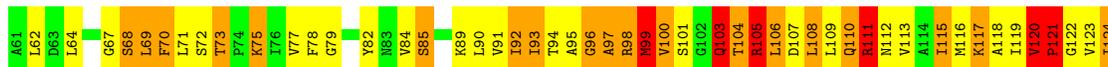




● Molecule 1: APO-LACTATE DEHYDROGENASE



● Molecule 1: APO-LACTATE DEHYDROGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	84.80Å 76.60Å 63.90Å 109.70° 89.50° 96.50°	Depositor
Resolution (Å)	10.00 – 2.96 10.00 – 2.91	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.96) 62.3 (10.00-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	306.79 (at 2.89Å)	Xtrriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.256 , (Not available) 0.261 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	44.1	Xtrriage
Anisotropy	0.259	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 11.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	10091	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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

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	1.06	3/2556 (0.1%)	1.96	68/3465 (2.0%)
1	B	1.06	3/2556 (0.1%)	1.96	68/3465 (2.0%)
1	C	1.06	3/2556 (0.1%)	1.96	67/3465 (1.9%)
1	D	1.06	3/2556 (0.1%)	1.96	68/3465 (2.0%)
All	All	1.06	12/10224 (0.1%)	1.96	271/13860 (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	3
1	B	0	3
1	C	0	3
1	D	0	3
All	All	0	12

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	58	ARG	CZ-NH1	6.12	1.41	1.33
1	B	58	ARG	CZ-NH1	6.06	1.41	1.33
1	A	58	ARG	CZ-NH1	6.04	1.41	1.33
1	C	58	ARG	CZ-NH1	6.03	1.40	1.33
1	D	34	CYS	CB-SG	-5.67	1.72	1.81

The worst 5 of 271 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ARG	CD-NE-CZ	21.41	153.58	123.60
1	D	58	ARG	CD-NE-CZ	21.38	153.54	123.60
1	C	58	ARG	CD-NE-CZ	21.38	153.53	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	58	ARG	CD-NE-CZ	21.36	153.51	123.60
1	D	170	ARG	NE-CZ-NH1	20.61	130.61	120.30

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	136	THR	Mainchain
1	A	181	PRO	Mainchain
1	A	311	GLU	Mainchain
1	B	136	THR	Mainchain
1	B	181	PRO	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2515	0	2611	672	0
1	B	2515	0	2611	668	0
1	C	2515	0	2611	671	39
1	D	2515	0	2611	679	35
2	A	29	0	0	1	4
2	D	2	0	0	3	0
All	All	10091	0	10444	2129	39

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 104.

The worst 5 of 2129 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:212:SER:HB2	1:D:208:VAL:CG1	1.20	1.63
1:A:208:VAL:CG1	1:B:212:SER:HB2	1.20	1.61
1:C:208:VAL:CG1	1:D:212:SER:HB2	1.20	1.60
1:A:212:SER:HB2	1:B:208:VAL:CG1	1.20	1.60
1:A:210:LEU:CB	1:B:202:GLY:HA3	1.59	1.32

The worst 5 of 39 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:C:111:ARG:CA	1:D:330:GLU:CD[1_566]	0.93	1.27
1:C:330:GLU:CD	1:D:111:ARG:CA[1_566]	0.93	1.27
1:C:111:ARG:CB	1:D:330:GLU:OE2[1_566]	0.97	1.23
1:C:330:GLU:OE2	1:D:111:ARG:CB[1_566]	0.97	1.23
1:C:126:ASN:CA	2:A:345:HOH:O[1_556]	1.06	1.14

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	329/331 (99%)	206 (63%)	74 (22%)	49 (15%)	0	1
1	B	329/331 (99%)	206 (63%)	74 (22%)	49 (15%)	0	1
1	C	329/331 (99%)	205 (62%)	75 (23%)	49 (15%)	0	1
1	D	329/331 (99%)	205 (62%)	75 (23%)	49 (15%)	0	1
All	All	1316/1324 (99%)	822 (62%)	298 (23%)	196 (15%)	0	1

5 of 196 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	29	ASP
1	A	54	THR
1	A	69	LEU
1	A	70	PHE

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	282/282 (100%)	205 (73%)	77 (27%)	0	1
1	B	282/282 (100%)	205 (73%)	77 (27%)	0	1
1	C	282/282 (100%)	204 (72%)	78 (28%)	0	1
1	D	282/282 (100%)	204 (72%)	78 (28%)	0	1
All	All	1128/1128 (100%)	818 (72%)	310 (28%)	0	1

5 of 310 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	328	ASN
1	D	231	LYS
1	D	14	GLU
1	D	111	ARG
1	D	300	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	270	HIS
1	D	65	GLN
1	C	306	ASN
1	D	6	GLN
1	D	185	HIS

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](#)

There are no ligands in this entry.

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	331/331 (100%)	-0.59	0 100 100	2, 15, 33, 45	0
1	B	331/331 (100%)	-0.58	0 100 100	2, 15, 33, 45	0
1	C	331/331 (100%)	-0.56	0 100 100	2, 15, 33, 45	0
1	D	331/331 (100%)	-0.52	1 (0%) 94 87	2, 15, 33, 45	0
All	All	1324/1324 (100%)	-0.56	1 (0%) 95 92	2, 15, 33, 45	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	13	PRO	4.6

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.