



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:17 PM UTC

PDB ID : 4LGZ / pdb_00004lgz
Title : Structure of mouse 1-Pyrroline-5-Carboxylate Dehydrogenase (ALDH4A1)
complexed with acetate
Authors : Pemberton, T.A.; Tanner, J.J.
Deposited on : 2013-06-30
Resolution : 1.68 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	FAILED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

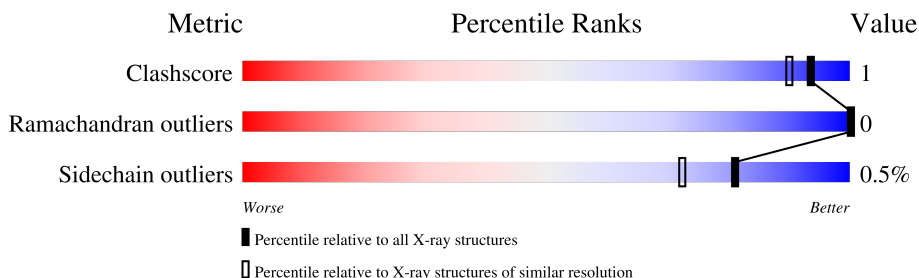
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.68 Å.

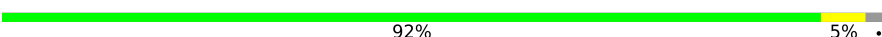
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1078 (1.68-1.68)
Ramachandran outliers	187476	1068 (1.68-1.68)
Sidechain outliers	187428	1067 (1.68-1.68)

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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	563	 91% 5%
1	B	563	 92% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8897 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 Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	533	Total	C	N	O	S	0	10	0
			4069	2607	685	759	18			
1	B	544	Total	C	N	O	S	0	3	0
			4120	2646	690	766	18			

There are 48 discrepancies between the modelled and reference sequences:

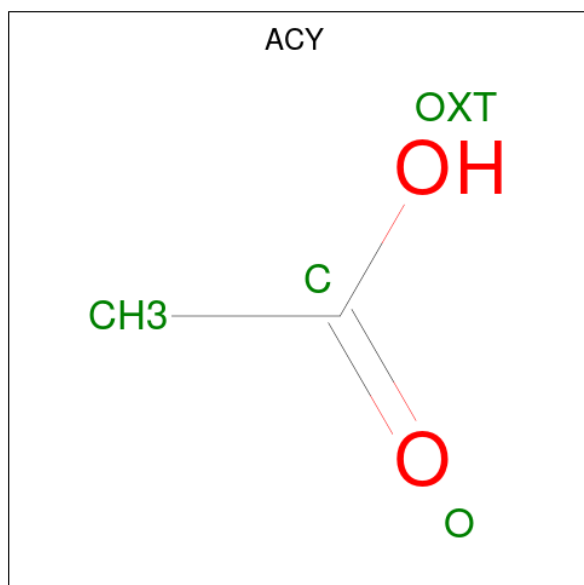
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q8CHT0
A	2	GLY	-	expression tag	UNP Q8CHT0
A	3	SER	-	expression tag	UNP Q8CHT0
A	4	SER	-	expression tag	UNP Q8CHT0
A	5	HIS	-	expression tag	UNP Q8CHT0
A	6	HIS	-	expression tag	UNP Q8CHT0
A	7	HIS	-	expression tag	UNP Q8CHT0
A	8	HIS	-	expression tag	UNP Q8CHT0
A	9	HIS	-	expression tag	UNP Q8CHT0
A	10	HIS	-	expression tag	UNP Q8CHT0
A	11	SER	-	expression tag	UNP Q8CHT0
A	12	SER	-	expression tag	UNP Q8CHT0
A	13	GLY	-	expression tag	UNP Q8CHT0
A	14	LEU	-	expression tag	UNP Q8CHT0
A	15	VAL	-	expression tag	UNP Q8CHT0
A	16	PRO	-	expression tag	UNP Q8CHT0
A	17	ARG	-	expression tag	UNP Q8CHT0
A	18	GLY	-	expression tag	UNP Q8CHT0
A	19	SER	-	expression tag	UNP Q8CHT0
A	20	HIS	-	expression tag	UNP Q8CHT0
A	21	MET	-	expression tag	UNP Q8CHT0
A	33	ALA	THR	conflict	UNP Q8CHT0
A	61	THR	MET	conflict	UNP Q8CHT0
A	468	LYS	GLN	conflict	UNP Q8CHT0
B	1	MET	-	initiating methionine	UNP Q8CHT0

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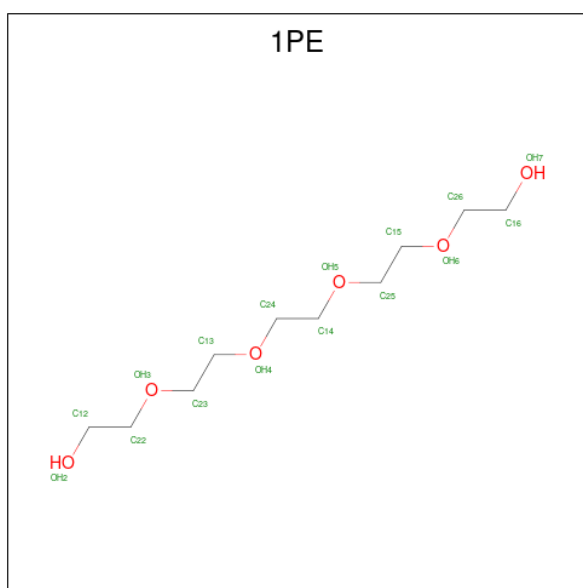
Chain	Residue	Modelled	Actual	Comment	Reference
B	2	GLY	-	expression tag	UNP Q8CHT0
B	3	SER	-	expression tag	UNP Q8CHT0
B	4	SER	-	expression tag	UNP Q8CHT0
B	5	HIS	-	expression tag	UNP Q8CHT0
B	6	HIS	-	expression tag	UNP Q8CHT0
B	7	HIS	-	expression tag	UNP Q8CHT0
B	8	HIS	-	expression tag	UNP Q8CHT0
B	9	HIS	-	expression tag	UNP Q8CHT0
B	10	HIS	-	expression tag	UNP Q8CHT0
B	11	SER	-	expression tag	UNP Q8CHT0
B	12	SER	-	expression tag	UNP Q8CHT0
B	13	GLY	-	expression tag	UNP Q8CHT0
B	14	LEU	-	expression tag	UNP Q8CHT0
B	15	VAL	-	expression tag	UNP Q8CHT0
B	16	PRO	-	expression tag	UNP Q8CHT0
B	17	ARG	-	expression tag	UNP Q8CHT0
B	18	GLY	-	expression tag	UNP Q8CHT0
B	19	SER	-	expression tag	UNP Q8CHT0
B	20	HIS	-	expression tag	UNP Q8CHT0
B	21	MET	-	expression tag	UNP Q8CHT0
B	33	ALA	THR	conflict	UNP Q8CHT0
B	61	THR	MET	conflict	UNP Q8CHT0
B	468	LYS	GLN	conflict	UNP Q8CHT0

- Molecule 2 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



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

- Molecule 3 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 16 10 6	0	0
3	B	1	Total C O 16 10 6	0	0

- Molecule 4 is water.

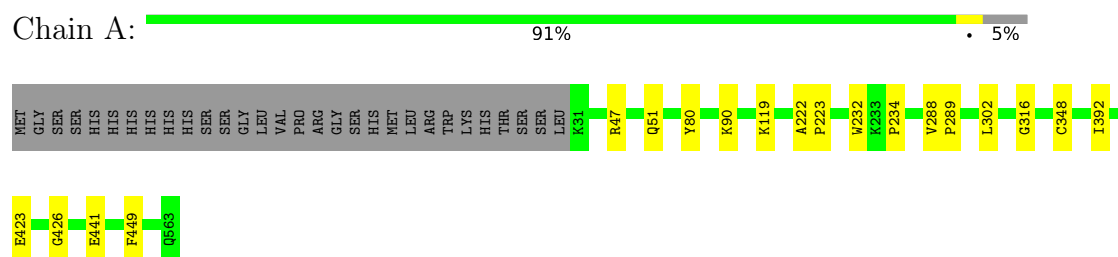
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	335	Total O 335 335	0	0
4	B	325	Total O 325 325	0	0

3 Residue-property plots [i](#)

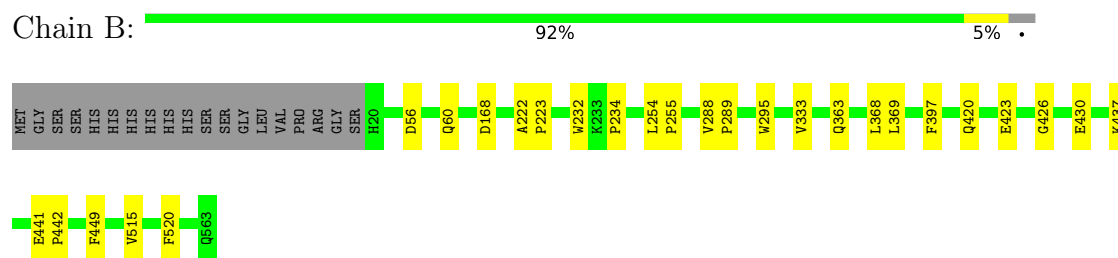
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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 failed to run properly.

- Molecule 1: Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial



- Molecule 1: Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.94Å 93.88Å 132.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.62 – 1.68	Depositor
% Data completeness (in resolution range)	98.4 (19.62-1.68)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 1.67Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.168 , 0.194	Depositor
Wilson B-factor (Å ²)	14.2	Xtriage
Anisotropy	0.236	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8897	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 1PE, ACY

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	0.40	0/4193	0.72	1/5708 (0.0%)
1	B	0.39	0/4235	0.72	0/5765
All	All	0.40	0/8428	0.72	1/11473 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	392	ILE	N-CA-C	5.79	116.57	110.72

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	4069	0	3926	9	0
1	B	4120	0	3968	15	0
2	A	8	0	6	0	0
2	B	8	0	6	1	0
3	A	16	0	22	0	0
3	B	16	0	22	0	0
4	A	335	0	0	1	0
4	B	325	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8897	0	7950	23	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 1.

All (23) 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:47:ARG:O	1:A:51:GLN:HG3	2.03	0.58
1:B:441:GLU:CD	1:B:442:PRO:HD2	2.32	0.54
1:B:222:ALA:HB3	1:B:223:PRO:HD3	1.91	0.52
1:B:437:LYS:N	1:B:437:LYS:HD2	2.25	0.52
1:B:420:GLN:HB2	1:B:430:GLU:CD	2.35	0.51
1:A:119:LYS:HE2	4:A:932:HOH:O	2.11	0.50
1:A:80:TYR:CD2	1:A:90:LYS:HD3	2.46	0.50
1:A:423:GLU:HA	1:A:426:GLY:O	2.11	0.49
1:B:288:VAL:HB	1:B:289:PRO:HD3	1.97	0.47
1:B:333:VAL:HG13	1:B:368:LEU:HD23	1.98	0.45
1:B:232:TRP:O	1:B:234:PRO:HD3	2.17	0.44
1:B:168:ASP:HB3	1:B:515:VAL:HB	1.99	0.44
1:A:316[B]:GLY:HA2	1:A:348[B]:CYS:HB2	1.99	0.44
1:B:423:GLU:HA	1:B:426:GLY:O	2.18	0.44
1:A:232:TRP:O	1:A:234:PRO:HD3	2.17	0.43
1:B:520:PHE:CZ	2:B:601:ACY:H2	2.52	0.43
1:A:288:VAL:HB	1:A:289:PRO:HD3	1.99	0.43
1:B:56:ASP:O	1:B:60:GLN:HG3	2.19	0.42
1:B:254:LEU:HA	1:B:255:PRO:HD3	1.94	0.42
1:B:397:PHE:CZ	1:B:423:GLU:HB3	2.55	0.41
1:A:302:LEU:HD11	1:B:295:TRP:CG	2.56	0.41
1:B:363:GLN:HG3	4:B:767:HOH:O	2.21	0.41
1:A:222:ALA:HB3	1:A:223:PRO:HD3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	541/563 (96%)	531 (98%)	10 (2%)	0	100	100
1	B	545/563 (97%)	533 (98%)	12 (2%)	0	100	100
All	All	1086/1126 (96%)	1064 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	413/461 (90%)	411 (100%)	2 (0%)	81	72
1	B	415/461 (90%)	413 (100%)	2 (0%)	81	72
All	All	828/922 (90%)	824 (100%)	4 (0%)	81	72

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	441	GLU
1	A	449	PHE
1	B	369	LEU
1	B	449	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	440	GLN
1	A	529	ASN
1	B	297	GLN
1	B	420	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

6 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	ACY	A	603	-	3,3,3	0.76	0	3,3,3	0.98	0
3	1PE	B	602	-	15,15,15	0.65	0	14,14,14	0.68	0
2	ACY	B	601	-	3,3,3	0.84	0	3,3,3	0.78	0
2	ACY	B	603	-	3,3,3	0.76	0	3,3,3	1.06	0
2	ACY	A	601	-	3,3,3	0.83	0	3,3,3	0.84	0
3	1PE	A	602	-	15,15,15	0.70	0	14,14,14	0.68	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
3	1PE	A	602	-	-	0/13/13/13	-
3	1PE	B	602	-	-	0/13/13/13	-

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
2	B	601	ACY	1	0

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

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.