



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:16 PM GMT

PDB ID : 4OE6
Title : Crystal Structure of Yeast ALDH4A1
Authors : Tanner, J.J.
Deposited on : 2014-01-11
Resolution : 1.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

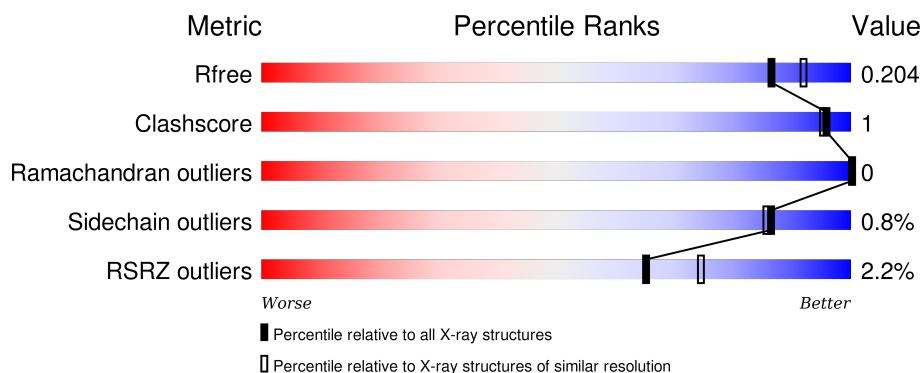
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

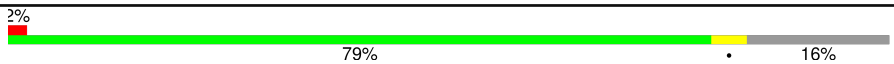
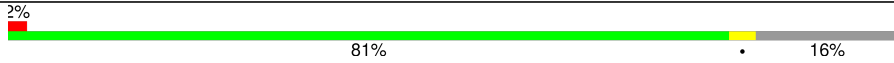
The reported resolution of this entry is 1.95 Å.

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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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. 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	580	
1	B	580	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7755 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	485	Total	C	N	O	S	0	0	0
			3767	2425	613	716	13			
1	B	486	Total	C	N	O	S	0	0	0
			3743	2411	606	713	13			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	EXPRESSION TAG	UNP P07275
A	3	ASP	-	EXPRESSION TAG	UNP P07275
A	4	HIS	-	EXPRESSION TAG	UNP P07275
A	5	HIS	-	EXPRESSION TAG	UNP P07275
A	6	HIS	-	EXPRESSION TAG	UNP P07275
A	7	HIS	-	EXPRESSION TAG	UNP P07275
A	8	HIS	-	EXPRESSION TAG	UNP P07275
A	9	HIS	-	EXPRESSION TAG	UNP P07275
A	10	HIS	-	EXPRESSION TAG	UNP P07275
A	11	HIS	-	EXPRESSION TAG	UNP P07275
A	12	ALA	-	EXPRESSION TAG	UNP P07275
A	13	SER	-	EXPRESSION TAG	UNP P07275
A	14	GLU	-	EXPRESSION TAG	UNP P07275
A	15	ASN	-	EXPRESSION TAG	UNP P07275
A	16	LEU	-	EXPRESSION TAG	UNP P07275
A	17	TYR	-	EXPRESSION TAG	UNP P07275
A	18	PHE	-	EXPRESSION TAG	UNP P07275
A	19	GLN	-	EXPRESSION TAG	UNP P07275
A	20	GLY	-	EXPRESSION TAG	UNP P07275
A	21	HIS	-	EXPRESSION TAG	UNP P07275
A	22	MET	-	EXPRESSION TAG	UNP P07275
A	576	GLU	-	EXPRESSION TAG	UNP P07275
A	577	LEU	-	EXPRESSION TAG	UNP P07275
A	578	GLY	-	EXPRESSION TAG	UNP P07275
A	579	SER	-	EXPRESSION TAG	UNP P07275

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Chain	Residue	Modelled	Actual	Comment	Reference
A	580	GLY	-	EXPRESSION TAG	UNP P07275
A	581	CYS	-	EXPRESSION TAG	UNP P07275
B	2	MET	-	EXPRESSION TAG	UNP P07275
B	3	ASP	-	EXPRESSION TAG	UNP P07275
B	4	HIS	-	EXPRESSION TAG	UNP P07275
B	5	HIS	-	EXPRESSION TAG	UNP P07275
B	6	HIS	-	EXPRESSION TAG	UNP P07275
B	7	HIS	-	EXPRESSION TAG	UNP P07275
B	8	HIS	-	EXPRESSION TAG	UNP P07275
B	9	HIS	-	EXPRESSION TAG	UNP P07275
B	10	HIS	-	EXPRESSION TAG	UNP P07275
B	11	HIS	-	EXPRESSION TAG	UNP P07275
B	12	ALA	-	EXPRESSION TAG	UNP P07275
B	13	SER	-	EXPRESSION TAG	UNP P07275
B	14	GLU	-	EXPRESSION TAG	UNP P07275
B	15	ASN	-	EXPRESSION TAG	UNP P07275
B	16	LEU	-	EXPRESSION TAG	UNP P07275
B	17	TYR	-	EXPRESSION TAG	UNP P07275
B	18	PHE	-	EXPRESSION TAG	UNP P07275
B	19	GLN	-	EXPRESSION TAG	UNP P07275
B	20	GLY	-	EXPRESSION TAG	UNP P07275
B	21	HIS	-	EXPRESSION TAG	UNP P07275
B	22	MET	-	EXPRESSION TAG	UNP P07275
B	576	GLU	-	EXPRESSION TAG	UNP P07275
B	577	LEU	-	EXPRESSION TAG	UNP P07275
B	578	GLY	-	EXPRESSION TAG	UNP P07275
B	579	SER	-	EXPRESSION TAG	UNP P07275
B	580	GLY	-	EXPRESSION TAG	UNP P07275
B	581	CYS	-	EXPRESSION TAG	UNP P07275

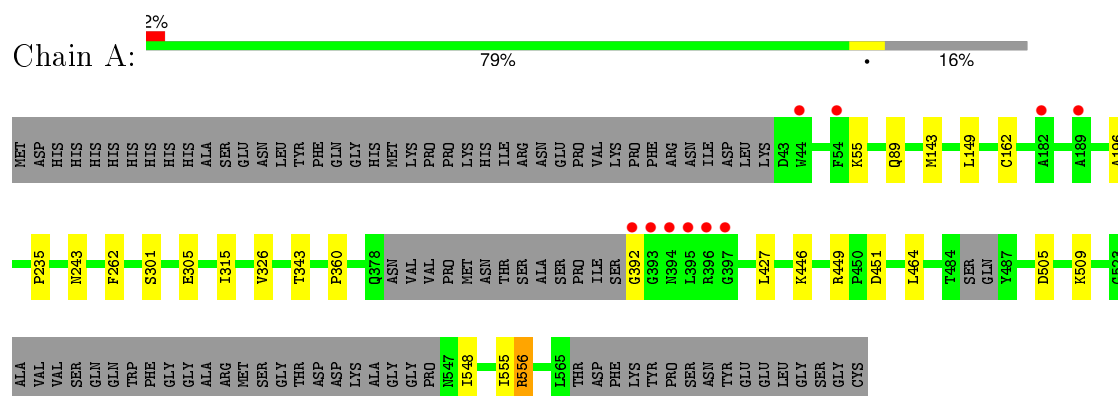
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	160	Total O 160 160	0	0
2	B	85	Total O 85 85	0	0

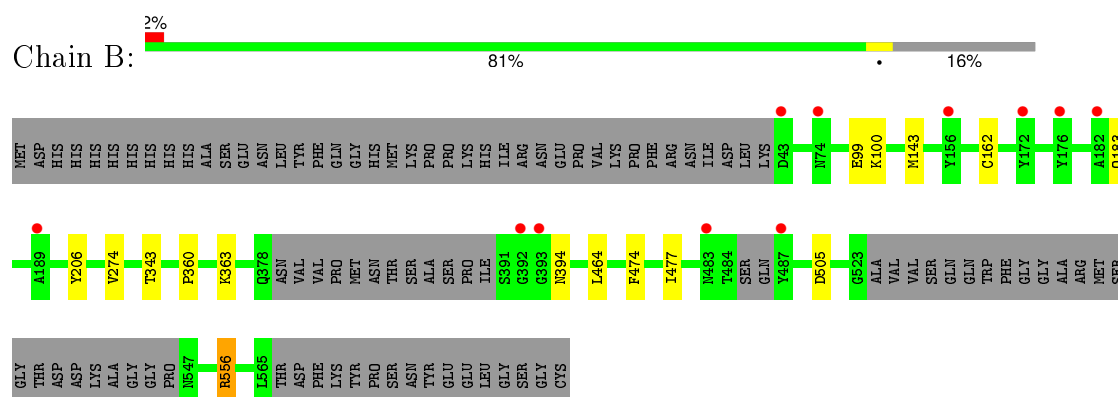
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	109.03Å 109.03Å 181.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.47 – 1.95 40.47 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.47-1.95) 99.8 (40.47-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.177 , 0.202 0.178 , 0.204	Depositor DCC
R_{free} test set	4431 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.1	EDS
Estimated twinning fraction	0.033 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 88280 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7755	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0/3854	0.53	0/5227
1	B	0.33	0/3829	0.48	0/5197
All	All	0.37	0/7683	0.50	0/10424

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

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	3767	0	3639	16	0
1	B	3743	0	3594	8	0
2	A	160	0	0	0	0
2	B	85	0	0	0	0
All	All	7755	0	7233	22	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 (22) 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:196:ALA:HB1	1:A:555:ILE:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:LYS:HG2	1:A:89:GLN:HE22	1.64	0.61
1:A:449:ARG:HG2	1:A:451:ASP:OD1	2.05	0.56
1:A:315:ILE:HG21	1:A:548:ILE:HD11	1.88	0.55
1:A:55:LYS:HA	1:A:89:GLN:NE2	2.22	0.54
1:B:343:THR:HG21	1:B:464:LEU:HB2	1.92	0.51
1:A:343:THR:HG21	1:A:464:LEU:HB2	1.92	0.50
1:B:360:PRO:HG2	1:B:363:LYS:HB2	1.97	0.47
1:A:55:LYS:HA	1:A:89:GLN:HE21	1.80	0.46
1:A:509:LYS:HB2	1:A:509:LYS:HE3	1.71	0.46
1:B:474:PHE:O	1:B:477:ILE:HG22	2.15	0.45
1:A:149:LEU:HD23	1:A:392:GLY:HA2	2.00	0.44
1:A:235:PRO:HG3	1:A:262:PHE:CE1	2.54	0.43
1:A:143:MET:HG3	1:A:162:CYS:SG	2.58	0.43
1:A:556:ARG:NH2	1:B:505:ASP:O	2.33	0.43
1:B:143:MET:HG3	1:B:162:CYS:SG	2.60	0.42
1:A:427:LEU:HD11	1:A:446:LYS:HB2	2.01	0.42
1:B:206:TYR:CG	1:B:274:VAL:HG11	2.55	0.41
1:A:505:ASP:O	1:B:556:ARG:NH2	2.47	0.41
1:A:301:SER:O	1:A:305:GLU:HB3	2.20	0.41
1:B:100:LYS:HA	1:B:100:LYS:HD2	1.85	0.41
1:A:326:VAL:O	1:A:360:PRO:HD3	2.21	0.40

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	477/580 (82%)	470 (98%)	7 (2%)	0	100	100
1	B	478/580 (82%)	470 (98%)	8 (2%)	0	100	100
All	All	955/1160 (82%)	940 (98%)	15 (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	392/492 (80%)	390 (100%)	2 (0%)	92	91
1	B	386/492 (78%)	382 (99%)	4 (1%)	82	80
All	All	778/984 (79%)	772 (99%)	6 (1%)	86	85

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	243	ASN
1	A	556	ARG
1	B	99	GLU
1	B	183	GLN
1	B	394	ASN
1	B	556	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates 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

6.1 Protein, DNA and RNA chains

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	485/580 (83%)	-0.12	10 (2%) 67 75	10, 21, 42, 62	0
1	B	486/580 (83%)	-0.00	11 (2%) 64 73	17, 30, 49, 60	0
All	All	971/1160 (83%)	-0.06	21 (2%) 65 74	10, 26, 47, 62	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	393	GLY	8.3
1	A	395	LEU	5.4
1	B	393	GLY	5.2
1	A	44	TRP	5.2
1	A	394	ASN	3.7
1	A	182	ALA	3.6
1	B	43	ASP	3.3
1	B	74	ASN	3.3
1	A	396	ARG	3.3
1	B	182	ALA	3.2
1	A	397	GLY	3.1
1	B	487	TYR	3.0
1	B	156	TYR	3.0
1	B	172	TYR	2.7
1	B	189	ALA	2.7
1	B	392	GLY	2.6
1	A	54	PHE	2.4
1	A	189	ALA	2.3
1	A	392	GLY	2.2
1	B	483	ASN	2.2
1	B	176	TYR	2.1

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 carbohydrates 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.