



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 07:58 am BST

PDB ID : 3ROS
Title : Crystal structure of NAD-dependent aldehyde dehydrogenase from *Lactobacillus acidophilus*
Authors : Eswaramoorthy, S.; Almo, S.C.; Swaminathan, S.; New York Structural Genomics Research Consortium (NYSGRC)
Deposited on : 2011-04-26
Resolution : 1.88 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

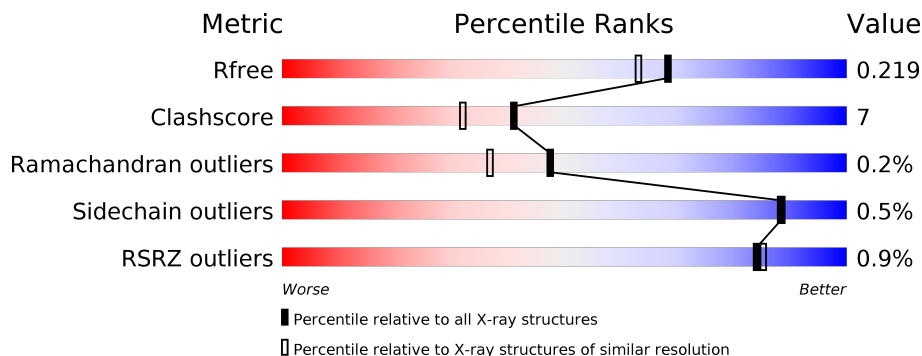
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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 $\leq 5\%$. 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	484	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3749 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.

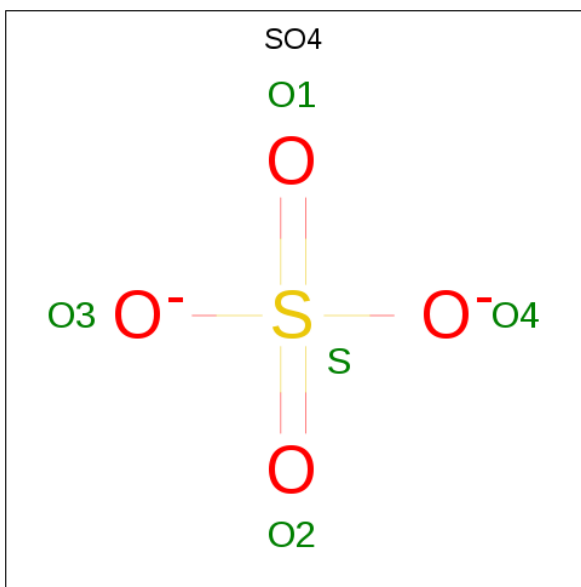
- Molecule 1 is a protein called NAD-dependent aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	459	3532	2230	596	693	4	9	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	EXPRESSION TAG	UNP Q5FIM9
A	0	VAL	-	EXPRESSION TAG	UNP Q5FIM9
A	461	ALA	-	EXPRESSION TAG	UNP Q5FIM9
A	462	GLU	-	EXPRESSION TAG	UNP Q5FIM9
A	463	ASN	-	EXPRESSION TAG	UNP Q5FIM9
A	464	LEU	-	EXPRESSION TAG	UNP Q5FIM9
A	465	TYR	-	EXPRESSION TAG	UNP Q5FIM9
A	466	PHE	-	EXPRESSION TAG	UNP Q5FIM9
A	467	GLN	-	EXPRESSION TAG	UNP Q5FIM9
A	468	SER	-	EXPRESSION TAG	UNP Q5FIM9
A	469	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	470	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	471	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	472	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	473	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	474	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	475	TRP	-	EXPRESSION TAG	UNP Q5FIM9
A	476	SER	-	EXPRESSION TAG	UNP Q5FIM9
A	477	HIS	-	EXPRESSION TAG	UNP Q5FIM9
A	478	PRO	-	EXPRESSION TAG	UNP Q5FIM9
A	479	GLN	-	EXPRESSION TAG	UNP Q5FIM9
A	480	PHE	-	EXPRESSION TAG	UNP Q5FIM9
A	481	GLU	-	EXPRESSION TAG	UNP Q5FIM9
A	482	LYS	-	EXPRESSION TAG	UNP Q5FIM9

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	212	212	212	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.00Å 45.73Å 96.38Å 90.00° 121.48° 90.00°	Depositor
Resolution (Å)	42.41 – 1.88 42.41 – 1.88	Depositor EDS
% Data completeness (in resolution range)	98.4 (42.41-1.88) 98.2 (42.41-1.88)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.61 (at 1.88Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.192 , 0.222 0.191 , 0.219	Depositor DCC
R_{free} test set	2011 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtrriage
Anisotropy	0.288	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3749	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.02% 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: SO4

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	0.30	0/3590	0.57	0/4849

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 [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	3532	0	3503	50	0
2	A	5	0	0	0	0
3	A	212	0	0	0	0
All	All	3749	0	3503	50	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.

All (50) 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:457:LYS:HE3	1:A:458:ASN:HD21	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:LYS:HE3	1:A:458:ASN:ND2	2.05	0.72
1:A:261:GLN:HE22	1:A:306:ASN:H	1.41	0.69
1:A:24:LYS:O	1:A:28:GLU:HG3	1.93	0.67
1:A:133:PHE:O	1:A:137:GLN:HG2	1.97	0.64
1:A:342:PHE:CE2	1:A:365:ILE:HD11	2.33	0.64
1:A:134:PRO:O	1:A:156:HIS:HE1	1.82	0.61
1:A:457:LYS:HG3	1:A:458:ASN:N	2.15	0.59
1:A:119:LYS:HG2	1:A:444:MSE:HE1	1.83	0.58
1:A:70:MSE:HG2	1:A:134:PRO:CG	2.34	0.58
1:A:142:PHE:HA	1:A:152:ILE:CD1	2.36	0.56
1:A:156:HIS:HD2	1:A:157:ALA:H	1.55	0.55
1:A:105:PRO:HB3	1:A:118:LEU:HD23	1.89	0.54
1:A:70:MSE:HG2	1:A:134:PRO:HG3	1.91	0.52
1:A:440:GLY:O	1:A:444:MSE:HG2	2.09	0.51
1:A:66:LEU:HD21	1:A:170:ILE:HD12	1.93	0.51
1:A:342:PHE:HE2	1:A:365:ILE:HD11	1.73	0.50
1:A:427:GLY:HA3	1:A:436:ARG:HD3	1.93	0.50
1:A:50:GLU:H	1:A:50:GLU:CD	2.14	0.50
1:A:131:TRP:O	1:A:134:PRO:HD3	2.11	0.50
1:A:156:HIS:CD2	1:A:157:ALA:H	2.30	0.50
1:A:79:SER:O	1:A:83:GLU:HG3	2.12	0.49
1:A:130:PRO:HD3	1:A:206:THR:O	2.13	0.49
1:A:160:VAL:N	1:A:161:PRO:CD	2.75	0.48
1:A:140:ARG:HG3	1:A:438:LEU:HG	1.96	0.48
1:A:267:LYS:HE2	1:A:360:GLU:HG3	1.95	0.48
1:A:206:THR:HA	1:A:229:GLU:O	2.13	0.48
1:A:70:MSE:HG2	1:A:134:PRO:HG2	1.96	0.48
1:A:140:ARG:NE	1:A:437:GLU:OE1	2.48	0.46
1:A:125:ILE:HD12	1:A:202:GLY:HA3	1.98	0.46
1:A:205:LEU:HD23	1:A:205:LEU:C	2.35	0.46
1:A:437:GLU:O	1:A:438:LEU:HB2	2.16	0.46
1:A:236:PHE:HB2	1:A:266:SER:HB3	1.98	0.44
1:A:46:ALA:O	1:A:50:GLU:OE1	2.35	0.44
1:A:205:LEU:HD23	1:A:206:THR:N	2.32	0.44
1:A:262:VAL:HG12	1:A:264:THR:H	1.82	0.44
1:A:315:GLU:HG2	1:A:342:PHE:HE1	1.82	0.43
1:A:7:VAL:HA	1:A:14:ALA:HA	2.01	0.42
1:A:126:MSE:SE	1:A:194:ILE:HG21	2.70	0.42
1:A:101:GLU:CD	1:A:101:GLU:H	2.22	0.42
1:A:11:THR:O	1:A:338:LYS:HE2	2.19	0.42
1:A:385:SER:HB3	1:A:431:LYS:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:THR:OG1	1:A:25:GLN:HG3	2.20	0.41
1:A:50:GLU:N	1:A:50:GLU:CD	2.73	0.41
1:A:155:LYS:HG3	1:A:186:PRO:HG2	2.02	0.41
1:A:311:LYS:O	1:A:315:GLU:HG3	2.19	0.41
1:A:20:ASN:HA	1:A:185:TYR:O	2.20	0.41
1:A:76:LYS:HE2	1:A:258:ASN:OD1	2.21	0.41
1:A:102:MSE:HE3	1:A:443:LEU:HD22	2.02	0.40
1:A:8:ASN:O	1:A:12:ASN:N	2.54	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	457/484 (94%)	441 (96%)	15 (3%)	1 (0%)	47 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	387	GLY

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	380/394 (96%)	378 (100%)	2 (0%)	88 88

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	362	PHE
1	A	411	MSE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	93	ASN
1	A	98	HIS
1	A	156	HIS
1	A	261	GLN
1	A	289	ASN
1	A	306	ASN
1	A	458	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](#)

1 ligand is 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	SO4	A	501	-	4,4,4	0.29	0	6,6,6	0.09	0

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.

No monomer is involved in short contacts.

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	449/484 (92%)	-0.18	4 (0%) 84 85	5, 12, 22, 30	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	336	ASP	3.7
1	A	440	GLY	2.5
1	A	188	TYR	2.3
1	A	338	LYS	2.2

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](#)

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
2	SO4	A	501	5/5	0.85	0.22	32,35,36,37	0

6.5 Other polymers

There are no such residues in this entry.