



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:04 am GMT

PDB ID : 1XAB
Title : 3-ISOPROPYLMALATE DEHYDROGENASE, LOW TEMPERATURE
(150K) STRUCTURE
Authors : Nagata, C.; Moriyama, H.; Tanaka, N.
Deposited on : 1995-11-09
Resolution : 2.10 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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

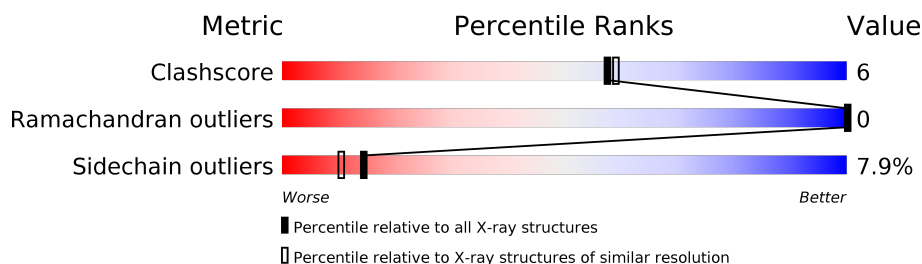
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	345	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4040 atoms, of which 1146 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 3-ISOPROPYLMALATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	345	Total	C	H	N	O	S	0	0	0
			3143	1654	548	452	483	6			

- Molecule 2 is water.

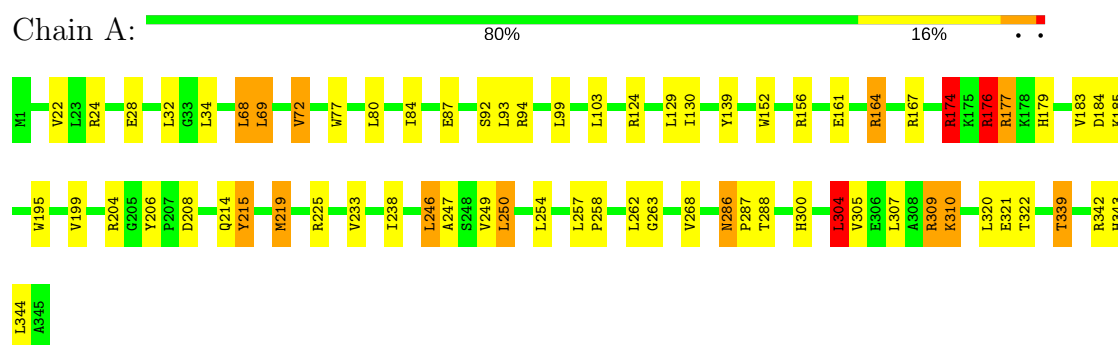
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	299	Total	H	O	0	0
			897	598	299		

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 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.

Note EDS was not executed.

• Molecule 1: 3-ISOPROPYLMALATE DEHYDROGENASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	76.90Å 76.90Å 156.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.10)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.158 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4040	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

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	0.83	0/2650	1.54	40/3596 (1.1%)

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	ARG	NE-CZ-NH2	-12.86	113.87	120.30
1	A	174	ARG	NE-CZ-NH1	11.49	126.04	120.30
1	A	177	ARG	NE-CZ-NH2	-10.95	114.82	120.30
1	A	24	ARG	NE-CZ-NH2	-10.90	114.85	120.30
1	A	176	ARG	NE-CZ-NH2	-10.59	115.01	120.30
1	A	94	ARG	NE-CZ-NH2	-10.24	115.18	120.30
1	A	177	ARG	NE-CZ-NH1	9.20	124.90	120.30
1	A	225	ARG	NE-CZ-NH2	-8.71	115.95	120.30
1	A	152	TRP	CD1-CG-CD2	8.36	112.98	106.30
1	A	77	TRP	CD1-CG-CD2	8.21	112.87	106.30
1	A	225	ARG	NE-CZ-NH1	7.76	124.18	120.30
1	A	152	TRP	CE2-CD2-CG	-7.55	101.26	107.30
1	A	215	TYR	CB-CG-CD2	-7.50	116.50	121.00
1	A	94	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	A	24	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	A	77	TRP	CE2-CD2-CG	-7.14	101.58	107.30
1	A	309	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	A	167	ARG	NE-CZ-NH2	-6.82	116.89	120.30
1	A	124	ARG	NE-CZ-NH2	-6.74	116.93	120.30
1	A	152	TRP	CG-CD2-CE3	6.74	139.96	133.90
1	A	152	TRP	CB-CG-CD1	-6.47	118.59	127.00
1	A	195	TRP	CE2-CD2-CG	-6.34	102.23	107.30
1	A	124	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	A	176	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	A	195	TRP	CD1-CG-CD2	6.08	111.17	106.30
1	A	152	TRP	CG-CD1-NE1	-5.81	104.29	110.10
1	A	156	ARG	NE-CZ-NH2	-5.79	117.41	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	TRP	CG-CD2-CE3	5.74	139.07	133.90
1	A	215	TYR	CG-CD2-CE2	-5.71	116.74	121.30
1	A	77	TRP	CG-CD1-NE1	-5.49	104.61	110.10
1	A	204	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	A	304	LEU	CA-CB-CG	5.43	127.79	115.30
1	A	156	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	72	VAL	CA-CB-CG2	-5.32	102.93	110.90
1	A	72	VAL	N-CA-CB	-5.29	99.86	111.50
1	A	77	TRP	CB-CG-CD1	-5.25	120.18	127.00
1	A	219	MET	CG-SD-CE	-5.11	92.03	100.20
1	A	68	LEU	N-CA-C	-5.06	97.35	111.00
1	A	310	LYS	CB-CG-CD	-5.05	98.46	111.60
1	A	199	VAL	CG1-CB-CG2	-5.00	102.90	110.90

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	2595	548	2633	29	2
2	A	299	598	0	2	3
All	All	2894	1146	2633	29	3

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 6.

All (29) 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:161:GLU:HA	1:A:164:ARG:HD3	1.75	0.68
1:A:247:ALA:HA	1:A:250:LEU:HD22	1.83	0.61
1:A:183:VAL:HG21	1:A:219:MET:HG2	1.85	0.59
1:A:322:THR:OG1	1:A:339:THR:HG21	2.03	0.58
1:A:286:ASN:HD22	1:A:287:PRO:HD2	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:LEU:HA	1:A:263:GLY:HA3	1.88	0.56
1:A:339:THR:HB	1:A:342:ARG:NH1	2.22	0.54
1:A:103:LEU:HB3	1:A:129:LEU:HD11	1.90	0.53
1:A:130:ILE:HD13	1:A:233:VAL:HB	1.92	0.52
1:A:174:ARG:HD3	1:A:208:ASP:OD2	2.09	0.51
1:A:177:ARG:O	1:A:179:HIS:HD2	1.94	0.50
1:A:310:LYS:HE3	1:A:344:LEU:HD12	1.96	0.48
1:A:184:ASP:O	1:A:215:TYR:HA	2.14	0.47
1:A:339:THR:O	1:A:343:HIS:HD2	1.97	0.47
1:A:80:LEU:HD13	1:A:84:ILE:HD12	1.97	0.47
1:A:139:TYR:OH	1:A:238:ILE:HG13	2.16	0.46
1:A:300:HIS:HE1	2:A:514:HOH:O	1.99	0.46
1:A:22:VAL:HG13	1:A:344:LEU:HD21	1.98	0.45
1:A:176:ARG:HB2	1:A:177:ARG:H	1.68	0.45
1:A:183:VAL:HA	1:A:214:GLN:O	2.17	0.44
1:A:310:LYS:HE2	2:A:782:HOH:O	2.17	0.44
1:A:339:THR:HB	1:A:342:ARG:HH12	1.83	0.43
1:A:246:LEU:O	1:A:249:VAL:HG22	2.18	0.43
1:A:286:ASN:ND2	1:A:288:THR:H	2.17	0.43
1:A:69:LEU:HD12	1:A:268:VAL:HG11	2.01	0.43
1:A:305:VAL:O	1:A:309:ARG:HG2	2.19	0.42
1:A:304:LEU:HG	1:A:307:LEU:HD12	2.01	0.42
1:A:321:GLU:HG2	1:A:322:THR:HG23	2.01	0.41
1:A:257:LEU:HA	1:A:258:PRO:HD2	1.98	0.41

All (3) 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:174:ARG:HH22	2:A:536:HOH:H1[4_545]	1.04	0.56
2:A:467:HOH:H2	2:A:531:HOH:H1[4_545]	1.18	0.42
1:A:206:TYR:HH	2:A:537:HOH:H1[4_545]	1.31	0.29

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	343/345 (99%)	334 (97%)	9 (3%)	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	266/266 (100%)	245 (92%)	21 (8%)	14	10

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLU
1	A	32	LEU
1	A	34	LEU
1	A	68	LEU
1	A	69	LEU
1	A	72	VAL
1	A	87	GLU
1	A	92	SER
1	A	93	LEU
1	A	164	ARG
1	A	174	ARG
1	A	176	ARG
1	A	185	LYS
1	A	246	LEU
1	A	250	LEU
1	A	254	LEU
1	A	262	LEU
1	A	286	ASN
1	A	304	LEU
1	A	320	LEU
1	A	339	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	153	ASN
1	A	179	HIS
1	A	286	ASN
1	A	343	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 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.