



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:54 PM UTC

PDB ID : 1XAB / pdb_00001xab
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

<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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
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

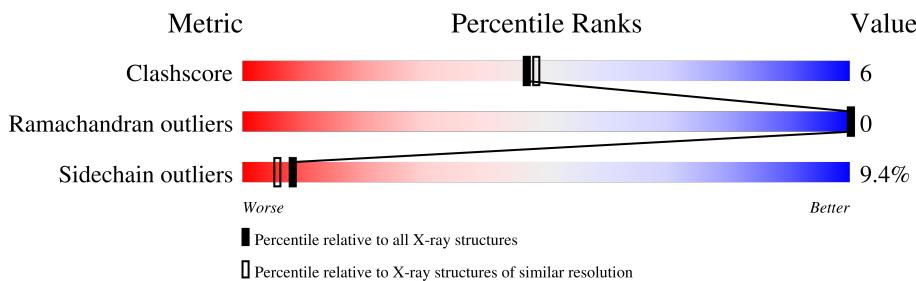
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (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 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 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.

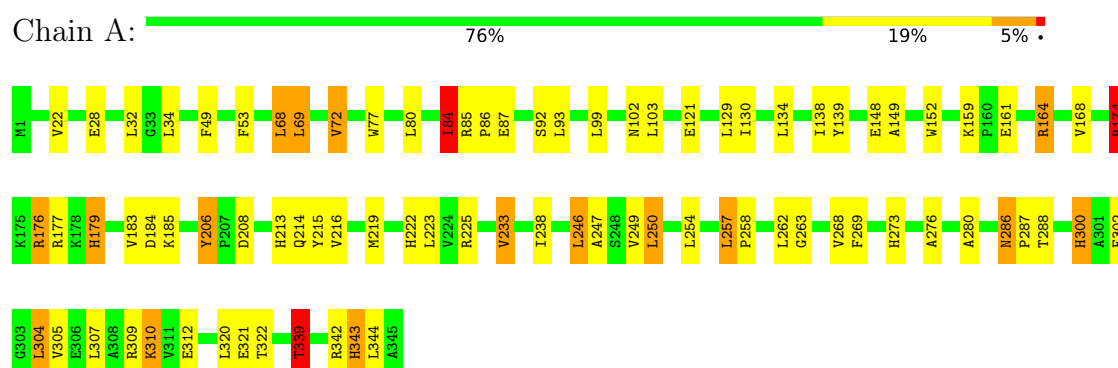
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	299	Total	H	O	0	0
			897	598	299		

3 Residue-property plots

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 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	1.03	10/2650 (0.4%)	1.71	39/3596 (1.1%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	343	HIS	CD2-NE2	-7.64	1.29	1.37
1	A	222	HIS	CD2-NE2	-7.22	1.29	1.37
1	A	213	HIS	CD2-NE2	-6.56	1.30	1.37
1	A	179	HIS	CD2-NE2	-6.40	1.30	1.37
1	A	343	HIS	CG-ND1	-6.07	1.31	1.38
1	A	179	HIS	CG-ND1	-5.91	1.31	1.38
1	A	273	HIS	CD2-NE2	-5.67	1.31	1.37
1	A	222	HIS	CG-ND1	-5.39	1.32	1.38
1	A	339	THR	CA-CB	5.30	1.62	1.53
1	A	222	HIS	CA-CB	-5.12	1.44	1.53

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	286	ASN	OD1-CG-ND2	-8.35	114.25	122.60
1	A	286	ASN	CB-CG-ND2	7.77	128.05	116.40
1	A	222	HIS	CB-CG-CD2	-7.70	121.19	131.20
1	A	273	HIS	CB-CG-CD2	-7.49	121.47	131.20
1	A	84	ILE	N-CA-C	7.25	119.10	112.29
1	A	49	PHE	CA-CB-CG	-7.24	106.56	113.80
1	A	269	PHE	CA-CB-CG	-6.77	107.03	113.80
1	A	85	ARG	CA-C-N	6.39	125.61	118.97
1	A	85	ARG	C-N-CA	6.39	125.61	118.97
1	A	216	VAL	N-CA-C	6.38	117.13	110.62
1	A	148	GLU	CB-CG-CD	6.29	123.29	112.60
1	A	152	TRP	CG-CD2-CE3	6.06	139.96	133.90
1	A	68	LEU	N-CA-C	-6.01	97.35	107.99
1	A	174	ARG	NE-CZ-NH2	-5.92	113.87	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	GLU	CB-CA-C	-5.90	101.62	110.88
1	A	72	VAL	N-CA-CB	-5.82	99.86	111.91
1	A	206	TYR	CA-C-N	5.80	125.48	119.56
1	A	206	TYR	C-N-CA	5.80	125.48	119.56
1	A	213	HIS	CB-CG-CD2	-5.73	123.75	131.20
1	A	233	VAL	O-C-N	-5.72	117.14	123.20
1	A	310	LYS	CB-CG-CD	-5.58	98.46	111.30
1	A	225	ARG	N-CA-C	5.57	118.54	111.69
1	A	138	ILE	N-CA-C	5.56	118.00	111.05
1	A	152	TRP	CB-CG-CD1	-5.54	118.59	126.90
1	A	280	ALA	O-C-N	-5.42	116.14	122.96
1	A	273	HIS	CB-CG-ND1	5.29	130.63	122.70
1	A	276	ALA	CA-C-N	5.27	125.33	119.32
1	A	276	ALA	C-N-CA	5.27	125.33	119.32
1	A	343	HIS	CB-CG-CD2	-5.19	124.45	131.20
1	A	77	TRP	CG-CD2-CE3	5.17	139.07	133.90
1	A	302	PHE	CA-CB-CG	-5.15	108.65	113.80
1	A	53	PHE	CA-CB-CG	5.12	118.92	113.80
1	A	159	LYS	CA-C-N	5.11	124.72	119.05
1	A	159	LYS	C-N-CA	5.11	124.72	119.05
1	A	149	ALA	N-CA-C	5.10	118.65	112.23
1	A	72	VAL	CB-CA-C	5.08	118.64	110.82
1	A	134	LEU	N-CA-C	5.07	120.45	113.97
1	A	257	LEU	N-CA-C	5.05	116.90	109.42
1	A	300	HIS	CB-CG-CD2	-5.03	124.66	131.20

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	2595	548	2633	30	2
2	A	299	598	0	2	3
All	All	2894	1146	2633	30	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 (30) 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:219:MET:HE3	1:A:223:LEU:HG	1.76	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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 [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	343/345 (99%)	334 (97%)	9 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	266/266 (100%)	241 (91%)	25 (9%)	8	6

All (25) 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

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Mol	Chain	Res	Type
1	A	84	ILE
1	A	86	PRO
1	A	87	GLU
1	A	92	SER
1	A	93	LEU
1	A	102	ASN
1	A	121	GLU
1	A	164	ARG
1	A	168	VAL
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	304	LEU
1	A	320	LEU
1	A	339	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	179	HIS
1	A	286	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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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.