



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:06 PM UTC

PDB ID : 2CMD / pdb_00002cmd
Title : THE CRYSTAL STRUCTURE OF E.COLI MALATE DEHYDROGENASE: A COMPLEX OF THE APOENZYME AND CITRATE AT 1.87 ANGSTROMS RESOLUTION
Authors : Hall, M.D.; Banaszak, L.J.
Deposited on : 1992-09-23
Resolution : 1.87 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)	:	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

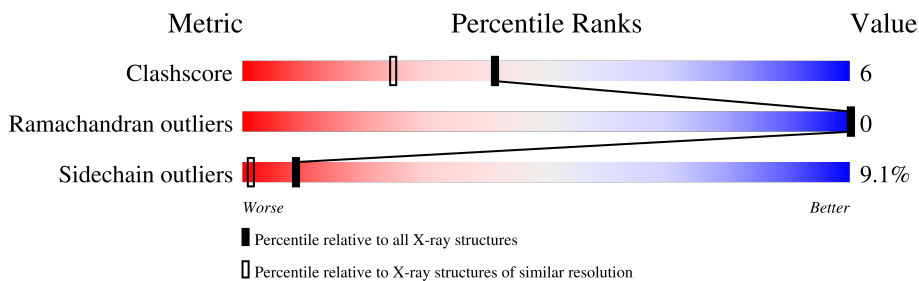
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 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	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)

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	312	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3079 atoms, of which 694 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.

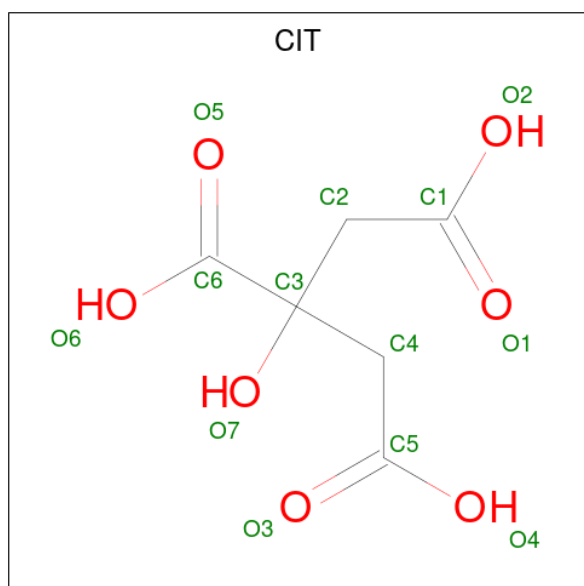
- Molecule 1 is a protein called MALATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	312	Total	C	H	N	O	S		0	0	0
			2782	1441	504	390	440	7				

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	80	ARG	ALA	conflict	UNP P61889
A	307	GLN	GLU	conflict	UNP P61889

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			15	6	2	7		

- Molecule 3 is water.


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	94	Total	H	O	0	0
			282	188	94		

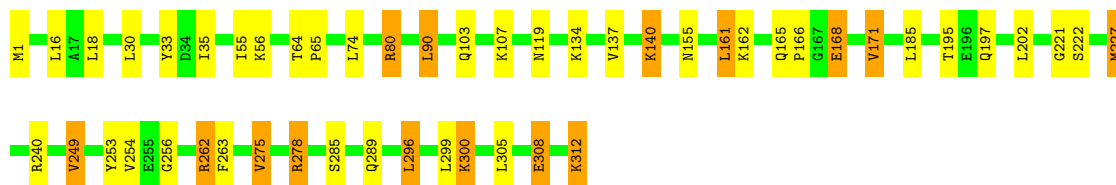
3 Residue-property plots

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: MALATE DEHYDROGENASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.95Å 42.90Å 84.05Å 90.00° 130.21° 90.00°	Depositor
Resolution (Å)	8.00 – 1.87	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-1.87)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.188 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3079	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CIT

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	0.76	1/2306 (0.0%)	0.92	1/3121 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	227	MET	SD-CE	-5.86	1.65	1.79

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	VAL	N-CA-C	5.48	115.79	108.11

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	ARG	Sidechain
1	A	253	TYR	Sidechain
1	A	262	ARG	Sidechain
1	A	275	VAL	Mainchain
1	A	278	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	33	TYR	Sidechain
1	A	80	ARG	Sidechain

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	2278	504	2367	30	0
2	A	13	2	5	0	0
3	A	94	188	0	1	0
All	All	2385	694	2372	30	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 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:80:ARG:HD3	1:A:222:SER:H	1.48	0.79
1:A:80:ARG:CD	1:A:222:SER:H	2.01	0.73
1:A:262:ARG:HD3	1:A:263:PHE:CE2	2.30	0.66
1:A:140:LYS:H	1:A:140:LYS:HD2	1.60	0.65
1:A:195:THR:OG1	1:A:197:GLN:HG2	1.96	0.65
1:A:308:GLU:O	1:A:312:LYS:HG3	1.98	0.63
1:A:140:LYS:H	1:A:140:LYS:CD	2.15	0.59
1:A:161:LEU:HD13	1:A:162:LYS:HE2	1.84	0.58
1:A:305:LEU:HD12	1:A:308:GLU:OE1	2.05	0.57
1:A:285:SER:O	1:A:289:GLN:HG3	2.05	0.55
1:A:140:LYS:HD2	1:A:140:LYS:N	2.22	0.54
1:A:155:ASN:HD21	1:A:171:VAL:H	1.56	0.54
1:A:80:ARG:HD3	1:A:222:SER:OG	2.09	0.53
1:A:30:LEU:HD23	1:A:55:ILE:HD12	1.90	0.53
1:A:161:LEU:HD12	1:A:202:LEU:HD11	1.90	0.53
1:A:168:GLU:O	1:A:168:GLU:HG2	2.09	0.51
1:A:300:LYS:HB3	1:A:300:LYS:HE2	1.50	0.48
1:A:64:THR:HB	1:A:65:PRO:HD3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:LEU:O	1:A:300:LYS:HG2	2.14	0.47
1:A:90:LEU:HD23	1:A:119:ASN:HB3	1.98	0.46
1:A:155:ASN:HD22	1:A:171:VAL:HG13	1.79	0.45
1:A:80:ARG:HD2	1:A:221:GLY:CA	2.47	0.45
1:A:197:GLN:HG3	3:A:349:HOH:O	2.17	0.43
1:A:80:ARG:NH2	1:A:221:GLY:HA3	2.33	0.43
1:A:103:GLN:O	1:A:107:LYS:HG2	2.18	0.43
1:A:140:LYS:CD	1:A:140:LYS:N	2.82	0.42
1:A:256:GLY:HA2	1:A:278:ARG:HE	1.83	0.42
1:A:227:MET:O	1:A:227:MET:HE3	2.20	0.41
1:A:165:GLN:HA	1:A:166:PRO:HD3	1.94	0.41
1:A:300:LYS:HG2	1:A:300:LYS:H	1.70	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	310/312 (99%)	307 (99%)	3 (1%)	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	242/242 (100%)	220 (91%)	22 (9%)	9 1

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	16	LEU
1	A	18	LEU
1	A	35	ILE
1	A	56	LYS
1	A	74	LEU
1	A	90	LEU
1	A	134	LYS
1	A	137	VAL
1	A	140	LYS
1	A	161	LEU
1	A	168	GLU
1	A	171	VAL
1	A	185	LEU
1	A	249	VAL
1	A	254	VAL
1	A	275	VAL
1	A	296	LEU
1	A	299	LEU
1	A	300	LYS
1	A	308	GLU
1	A	312	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	103	GLN
1	A	155	ASN
1	A	207	GLN
1	A	208	ASN
1	A	243	GLN
1	A	259	GLN
1	A	266	GLN
1	A	289	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 ⓘ

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	CIT	A	313	-	12,12,12	1.59	2 (16%)	17,17,17	1.10	1 (5%)

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
2	CIT	A	313	-	-	0/16/16/16	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	313	CIT	C4-C3	-3.33	1.49	1.54
2	A	313	CIT	C2-C3	2.30	1.56	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	313	CIT	O2-C1-O1	-2.12	117.87	123.33

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

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.