



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:56 PM UTC

PDB ID : 1EAF / pdb_00001eaf
Title : ATOMIC STRUCTURE OF THE CUBIC CORE OF THE PYRUVATE DE-HYDROGENASE MULTIENZYME COMPLEX
Authors : Mattevi, A.; Hol, W.G.J.
Deposited on : 1992-12-16
Resolution : 2.60 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

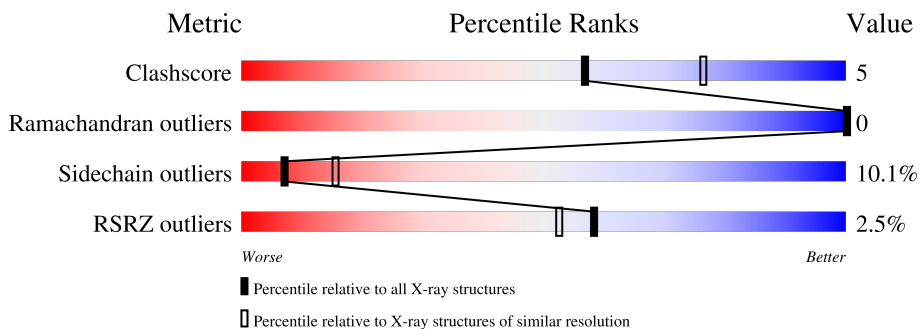
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 $\leq 5\%$. 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	243	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1967 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.

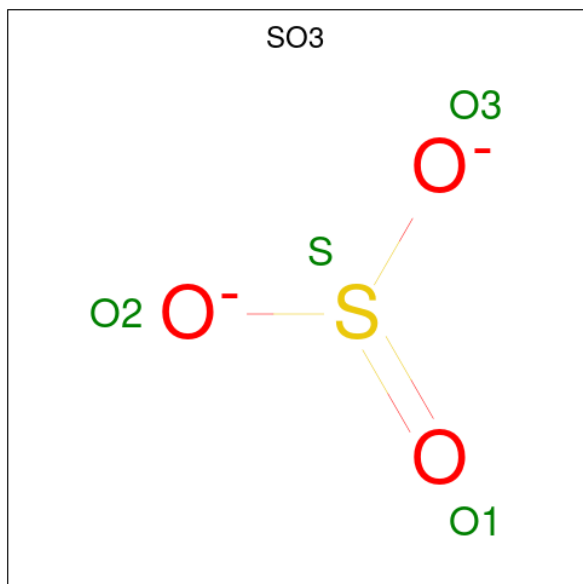
- Molecule 1 is a protein called DIHYDROLIPOYL-TRANSACETYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	243	1816	1171	311	327	7	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	458	LYS	GLU	conflict	UNP P10802

- Molecule 2 is SULFITE ION (CCD ID: SO3) (formula: O₃S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	4	3	1	0	0

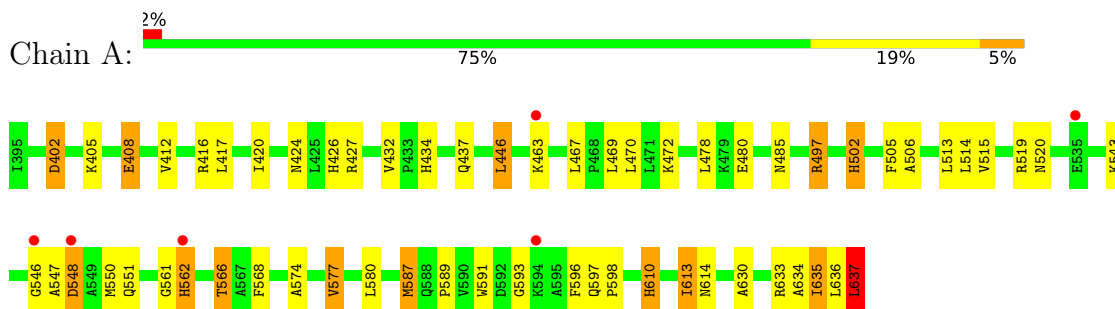
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	147	Total 147	O 147	0	0

3 Residue-property plots [i](#)

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 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: DIHYDROLIPOYL-TRANSACETYLASE



4 Data and refinement statistics

Property	Value	Source
Space group	F 4 3 2	Depositor
Cell constants a, b, c, α , β , γ	224.77Å 224.77Å 224.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60 10.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.60) 95.4 (10.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.63 (at 2.30Å)	Xtrriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.198 , (Not available) 0.184 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 109.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1967	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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: SO3

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	1.07	6/1853 (0.3%)	1.82	35/2523 (1.4%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	502	HIS	CD2-NE2	-7.08	1.30	1.37
1	A	426	HIS	CD2-NE2	-6.32	1.30	1.37
1	A	434	HIS	CD2-NE2	-5.76	1.31	1.37
1	A	562	HIS	CD2-NE2	-5.65	1.31	1.37
1	A	610	HIS	CD2-NE2	-5.36	1.31	1.37
1	A	515	VAL	CA-CB	5.21	1.60	1.54

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	577	VAL	N-CA-CB	-15.39	95.28	112.21
1	A	566	THR	N-CA-CB	-10.17	95.62	110.47
1	A	577	VAL	CB-CA-C	9.21	122.36	110.84
1	A	497	ARG	CA-CB-CG	-8.57	96.96	114.10
1	A	614	ASN	OD1-CG-ND2	-7.99	114.61	122.60
1	A	463	LYS	O-C-N	-7.64	114.25	123.19
1	A	637	LEU	CA-CB-CG	7.64	143.03	116.30
1	A	562	HIS	CB-CG-CD2	-7.55	121.39	131.20
1	A	610	HIS	CB-CG-CD2	-7.53	121.41	131.20
1	A	568	PHE	CA-CB-CG	7.08	120.88	113.80
1	A	597	GLN	OE1-CD-NE2	-6.88	115.72	122.60
1	A	405	LYS	CB-CG-CD	-6.82	95.61	111.30
1	A	587	MET	CG-SD-CE	-6.73	86.09	100.90
1	A	548	ASP	CA-CB-CG	6.72	119.32	112.60
1	A	566	THR	CB-CA-C	6.43	120.50	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	402	ASP	CA-CB-CG	6.34	118.94	112.60
1	A	635	ILE	CB-CG1-CD1	-6.30	100.56	113.80
1	A	610	HIS	CB-CG-ND1	6.11	131.87	122.70
1	A	546	GLY	CA-C-O	-6.09	116.04	121.64
1	A	408	GLU	CB-CG-CD	-5.94	102.50	112.60
1	A	426	HIS	CB-CG-CD2	-5.85	123.59	131.20
1	A	593	GLY	N-CA-C	-5.61	107.80	114.48
1	A	562	HIS	CB-CG-ND1	5.60	131.10	122.70
1	A	424	ASN	OD1-CG-ND2	-5.51	117.09	122.60
1	A	485	ASN	CB-CG-ND2	5.48	124.62	116.40
1	A	432	VAL	O-C-N	-5.43	117.95	121.37
1	A	505	PHE	CA-CB-CG	5.29	119.09	113.80
1	A	591	TRP	CG-CD1-NE1	-5.26	103.36	110.20
1	A	637	LEU	CD1-CG-CD2	-5.14	99.49	110.80
1	A	437	GLN	OE1-CD-NE2	-5.13	117.47	122.60
1	A	633	ARG	N-CA-C	-5.08	106.35	112.54
1	A	485	ASN	OD1-CG-ND2	-5.07	117.53	122.60
1	A	463	LYS	N-CA-C	-5.05	101.47	109.76
1	A	630	ALA	N-CA-C	-5.05	105.97	111.82
1	A	574	ALA	O-C-N	-5.01	116.14	121.30

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	1816	0	1866	17	3
2	A	4	0	0	0	0
3	A	147	0	0	3	1
All	All	1967	0	1866	17	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 5.

All (17) 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:502:HIS:HD2	1:A:520:ASN:H	1.40	0.68
1:A:562:HIS:HB2	3:A:748:HOH:O	1.96	0.65
1:A:562:HIS:H	1:A:562:HIS:CD2	2.20	0.60
1:A:561:GLY:HA3	3:A:721:HOH:O	2.02	0.59
1:A:514:LEU:HD22	1:A:550:MET:SD	2.42	0.58
1:A:502:HIS:CD2	1:A:520:ASN:H	2.23	0.54
1:A:446:LEU:HD21	1:A:469:LEU:HD22	1.89	0.53
1:A:416:ARG:O	1:A:420:ILE:HG12	2.10	0.52
1:A:587:MET:HE2	1:A:598:PRO:HB2	1.93	0.50
1:A:506:ALA:HB1	1:A:513:LEU:HD11	1.94	0.48
1:A:502:HIS:CG	1:A:519:ARG:HD3	2.49	0.47
1:A:480:GLU:HB2	3:A:754:HOH:O	2.15	0.46
1:A:634:ALA:O	1:A:637:LEU:HD23	2.17	0.45
1:A:547:ALA:HA	1:A:550:MET:HE3	1.99	0.44
1:A:589:PRO:HB2	1:A:596:PHE:HB3	2.00	0.43
1:A:610:HIS:HA	1:A:613:ILE:O	2.20	0.41
1:A:519:ARG:NH2	1:A:551:GLN:O	2.54	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:402:ASP:OD1	1:A:402:ASP:OD1[28_555]	0.70	1.50
1:A:402:ASP:CB	3:A:781:HOH:O[28_555]	1.89	0.31
1:A:402:ASP:CG	1:A:402:ASP:OD1[28_555]	1.91	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	241/243 (99%)	232 (96%)	9 (4%)	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	188/195 (96%)	169 (90%)	19 (10%)	7 15

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	408	GLU
1	A	412	VAL
1	A	417	LEU
1	A	427	ARG
1	A	446	LEU
1	A	467	LEU
1	A	470	LEU
1	A	472	LYS
1	A	478	LEU
1	A	497	ARG
1	A	543	LYS
1	A	548	ASP
1	A	566	THR
1	A	577	VAL
1	A	580	LEU
1	A	613	ILE
1	A	635	ILE
1	A	636	LEU
1	A	637	LEU

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

Mol	Chain	Res	Type
1	A	419	GLN
1	A	453	GLN
1	A	502	HIS
1	A	520	ASN
1	A	528	GLN

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 [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	SO3	A	785	-	1,3,3	6.80	1 (100%)	0,3,3	-	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	785	SO3	O1-S	6.80	1.73	1.44

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	243/243 (100%)	-0.52	6 (2%) 58 52	11, 27, 52, 61	1 (0%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	463	LYS	4.4
1	A	548	ASP	3.0
1	A	562	HIS	2.6
1	A	546	GLY	2.3
1	A	535	GLU	2.1
1	A	594	LYS	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 oligosaccharides 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	SO3	A	785	4/4	0.97	0.10	37,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.