



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:19 PM UTC

PDB ID : 2DTX / pdb\_00002dtx  
Title : Structure of Thermoplasma acidophilum aldohexose dehydrogenase (AldT) in complex with D-mannose  
Authors : Yasutake, Y.; Nishiya, Y.; Tamura, N.; Tamura, T.  
Deposited on : 2006-07-18  
Resolution : 1.60 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

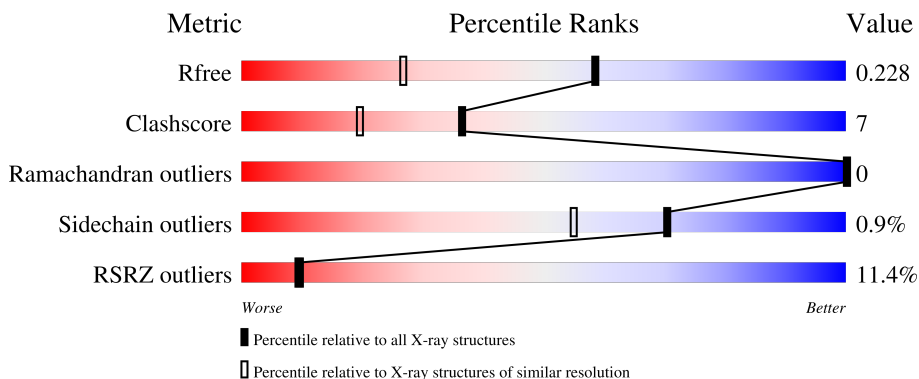
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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))
$R_{free}$	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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  $\geq 3$ , 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	264	
1	B	264	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4356 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.

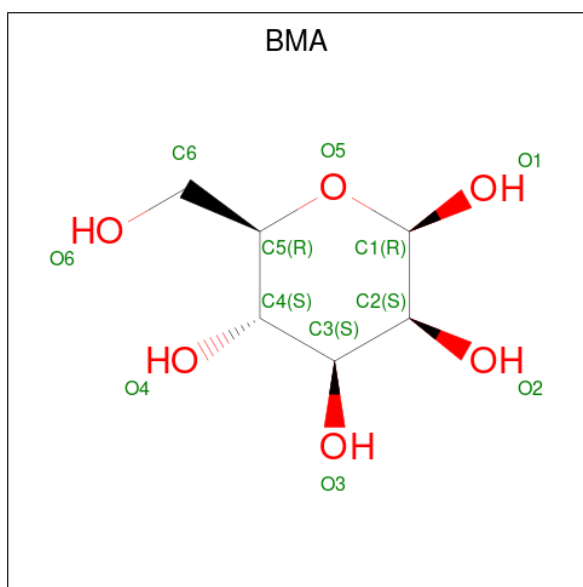
- Molecule 1 is a protein called Glucose 1-dehydrogenase related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	255	1964	1241	335	378	10	0	2	0
1	B	255	1981	1250	340	381	10	0	4	0

There are 20 discrepancies between the modelled and reference sequences:

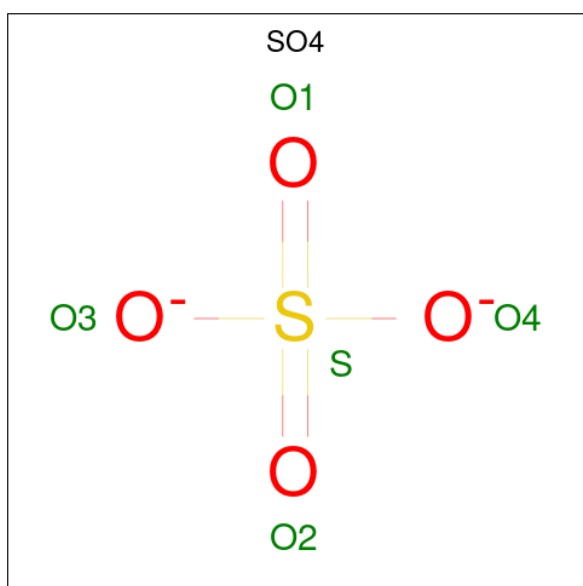
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q9HK51
A	1	GLY	-	expression tag	UNP Q9HK51
A	256	LEU	-	expression tag	UNP Q9HK51
A	257	GLU	-	expression tag	UNP Q9HK51
A	258	HIS	-	expression tag	UNP Q9HK51
A	259	HIS	-	expression tag	UNP Q9HK51
A	260	HIS	-	expression tag	UNP Q9HK51
A	261	HIS	-	expression tag	UNP Q9HK51
A	262	HIS	-	expression tag	UNP Q9HK51
A	263	HIS	-	expression tag	UNP Q9HK51
B	0	MET	-	expression tag	UNP Q9HK51
B	1	GLY	-	expression tag	UNP Q9HK51
B	256	LEU	-	expression tag	UNP Q9HK51
B	257	GLU	-	expression tag	UNP Q9HK51
B	258	HIS	-	expression tag	UNP Q9HK51
B	259	HIS	-	expression tag	UNP Q9HK51
B	260	HIS	-	expression tag	UNP Q9HK51
B	261	HIS	-	expression tag	UNP Q9HK51
B	262	HIS	-	expression tag	UNP Q9HK51
B	263	HIS	-	expression tag	UNP Q9HK51

- Molecule 2 is beta-D-mannopyranose (CCD ID: BMA) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 10 6 4	0	0
2	B	1	Total C O 10 6 4	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	203	Total 203	O 203	0	0
4	B	178	Total 178	O 178	0	0



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.88Å 81.88Å 138.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 1.60 40.00 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-1.60) 99.8 (40.00-1.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.63 (at 1.60Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.198 , 0.221 0.204 , 0.228	Depositor DCC
$R_{free}$ test set	3604 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.9	Xtrriage
Anisotropy	0.400	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 38.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4356	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: BMA, 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	0.50	1/2002 (0.0%)	0.92	6/2712 (0.2%)
1	B	0.47	0/2019	0.93	5/2734 (0.2%)
All	All	0.48	1/4021 (0.0%)	0.92	11/5446 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	ILE	CA-CB	6.10	1.57	1.54

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	135	ALA	N-CA-C	-8.37	103.06	113.18
1	A	138	ILE	N-CA-C	7.58	119.72	108.96
1	A	135	ALA	N-CA-C	-7.36	104.28	113.18
1	B	138	ILE	N-CA-C	6.86	118.70	108.96
1	B	34	VAL	N-CA-C	5.75	116.22	108.17

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	1964	0	1967	25	0
1	B	1981	0	1983	31	0
2	A	10	0	7	2	0
2	B	10	0	7	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	203	0	0	7	0
4	B	178	0	0	5	0
All	All	4356	0	3964	57	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.

The worst 5 of 57 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)
2:B:302:BMA:C1	4:B:772:HOH:O	1.89	1.19
2:A:301:BMA:C1	4:A:771:HOH:O	1.95	1.13
2:B:302:BMA:C3	4:B:774:HOH:O	2.24	0.84
1:B:46:LYS:HD3	1:B:46:LYS:H	1.43	0.83
1:B:194:PRO:HG2	1:B:195:MET:HE1	1.64	0.80

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	255/264 (97%)	246 (96%)	9 (4%)	0	100	100
1	B	257/264 (97%)	247 (96%)	10 (4%)	0	100	100
All	All	512/528 (97%)	493 (96%)	19 (4%)	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	215/222 (97%)	214 (100%)	1 (0%)	81	70
1	B	217/222 (98%)	214 (99%)	3 (1%)	59	38
All	All	432/444 (97%)	428 (99%)	4 (1%)	70	55

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	217	GLN
1	B	44	GLU
1	B	46	LYS
1	B	217	GLN

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	40	HIS
1	A	66	HIS
1	B	40	HIS
1	B	66	HIS
1	B	217	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](#)

4 ligands are 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
3	SO4	A	351	-	4,4,4	0.43	0	6,6,6	0.29	0
3	SO4	B	352	-	4,4,4	0.47	0	6,6,6	0.13	0
2	BMA	B	302	-	10,10,12	3.07	1 (10%)	13,13,17	2.31	4 (30%)
2	BMA	A	301	-	10,10,12	3.07	1 (10%)	13,13,17	2.31	4 (30%)

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	BMA	B	302	-	-	2/2/15/22	0/1/1/1
2	BMA	A	301	-	-	2/2/15/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	302	BMA	O2-C2	-9.30	1.16	1.43
2	A	301	BMA	O2-C2	-9.29	1.16	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	BMA	O2-C2-C1	5.15	120.23	110.39
2	B	302	BMA	O2-C2-C1	5.14	120.22	110.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	BMA	C3-C4-C5	-3.94	105.74	110.76
2	B	302	BMA	C3-C4-C5	-3.92	105.76	110.76
2	B	302	BMA	O5-C1-C2	-3.74	106.12	110.59

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	BMA	O5-C5-C6-O6
2	B	302	BMA	O5-C5-C6-O6
2	B	302	BMA	C4-C5-C6-O6
2	A	301	BMA	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	302	BMA	2	0
2	A	301	BMA	2	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	255/264 (96%)	0.22	18 (7%) 22 22	6, 16, 35, 50	2 (0%)
1	B	255/264 (96%)	0.61	40 (15%) 5 4	6, 19, 39, 52	4 (1%)
All	All	510/528 (96%)	0.42	58 (11%) 10 9	6, 17, 37, 52	6 (1%)

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	195	MET	5.6
1	B	166	LEU	5.4
1	B	82	GLY	5.1
1	B	194	PRO	4.6
1	A	191	GLY	4.5

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	BMA	A	301	10/12	0.81	0.16	28,33,36,37	10
2	BMA	B	302	10/12	0.84	0.15	27,32,36,36	0
3	SO4	B	352	5/5	0.87	0.16	26,28,32,32	0
3	SO4	A	351	5/5	0.90	0.15	23,27,30,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.