



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 13, 2024 – 02:34 AM EDT

PDB ID : 3WMW  
Title : GalE-like L-Threonine dehydrogenase from Cupriavidus necator (apo form)  
Authors : Nakano, S.; Okazaki, S.; Tokiwa, H.; Asano, Y.  
Deposited on : 2013-11-29  
Resolution : 2.25 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

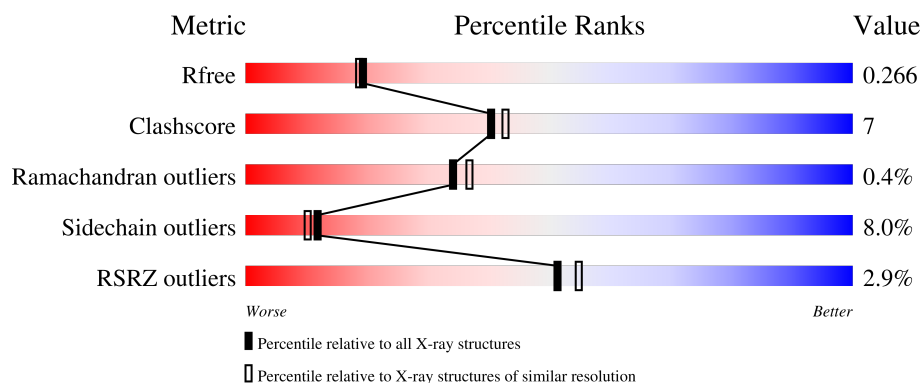
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	358	 2% 65% 11% • 23%
1	B	358	 3% 61% 15% • 22%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4402 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 NAD dependent epimerase/dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	0	0
			2147	1368	367	401	11			
1	B	278	Total	C	N	O	S	0	0	0
			2137	1364	366	396	11			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q0K312
A	-18	GLY	-	expression tag	UNP Q0K312
A	-17	SER	-	expression tag	UNP Q0K312
A	-16	SER	-	expression tag	UNP Q0K312
A	-15	HIS	-	expression tag	UNP Q0K312
A	-14	HIS	-	expression tag	UNP Q0K312
A	-13	HIS	-	expression tag	UNP Q0K312
A	-12	HIS	-	expression tag	UNP Q0K312
A	-11	HIS	-	expression tag	UNP Q0K312
A	-10	HIS	-	expression tag	UNP Q0K312
A	-9	SER	-	expression tag	UNP Q0K312
A	-8	SER	-	expression tag	UNP Q0K312
A	-7	GLY	-	expression tag	UNP Q0K312
A	-6	LEU	-	expression tag	UNP Q0K312
A	-5	VAL	-	expression tag	UNP Q0K312
A	-4	PRO	-	expression tag	UNP Q0K312
A	-3	ARG	-	expression tag	UNP Q0K312
A	-2	GLY	-	expression tag	UNP Q0K312
A	-1	SER	-	expression tag	UNP Q0K312
A	0	HIS	-	expression tag	UNP Q0K312
A	319	ASP	-	expression tag	UNP Q0K312
A	320	PRO	-	expression tag	UNP Q0K312
A	321	ALA	-	expression tag	UNP Q0K312
A	322	ALA	-	expression tag	UNP Q0K312
A	323	ASN	-	expression tag	UNP Q0K312

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Chain	Residue	Modelled	Actual	Comment	Reference
A	324	LYS	-	expression tag	UNP Q0K312
A	325	ALA	-	expression tag	UNP Q0K312
A	326	ARG	-	expression tag	UNP Q0K312
A	327	LYS	-	expression tag	UNP Q0K312
A	328	GLU	-	expression tag	UNP Q0K312
A	329	ALA	-	expression tag	UNP Q0K312
A	330	GLU	-	expression tag	UNP Q0K312
A	331	LEU	-	expression tag	UNP Q0K312
A	332	ALA	-	expression tag	UNP Q0K312
A	333	ALA	-	expression tag	UNP Q0K312
A	334	ALA	-	expression tag	UNP Q0K312
A	335	THR	-	expression tag	UNP Q0K312
A	336	ALA	-	expression tag	UNP Q0K312
A	337	GLU	-	expression tag	UNP Q0K312
A	338	GLN	-	expression tag	UNP Q0K312
B	-19	MET	-	expression tag	UNP Q0K312
B	-18	GLY	-	expression tag	UNP Q0K312
B	-17	SER	-	expression tag	UNP Q0K312
B	-16	SER	-	expression tag	UNP Q0K312
B	-15	HIS	-	expression tag	UNP Q0K312
B	-14	HIS	-	expression tag	UNP Q0K312
B	-13	HIS	-	expression tag	UNP Q0K312
B	-12	HIS	-	expression tag	UNP Q0K312
B	-11	HIS	-	expression tag	UNP Q0K312
B	-10	HIS	-	expression tag	UNP Q0K312
B	-9	SER	-	expression tag	UNP Q0K312
B	-8	SER	-	expression tag	UNP Q0K312
B	-7	GLY	-	expression tag	UNP Q0K312
B	-6	LEU	-	expression tag	UNP Q0K312
B	-5	VAL	-	expression tag	UNP Q0K312
B	-4	PRO	-	expression tag	UNP Q0K312
B	-3	ARG	-	expression tag	UNP Q0K312
B	-2	GLY	-	expression tag	UNP Q0K312
B	-1	SER	-	expression tag	UNP Q0K312
B	0	HIS	-	expression tag	UNP Q0K312
B	319	ASP	-	expression tag	UNP Q0K312
B	320	PRO	-	expression tag	UNP Q0K312
B	321	ALA	-	expression tag	UNP Q0K312
B	322	ALA	-	expression tag	UNP Q0K312
B	323	ASN	-	expression tag	UNP Q0K312
B	324	LYS	-	expression tag	UNP Q0K312
B	325	ALA	-	expression tag	UNP Q0K312

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Chain	Residue	Modelled	Actual	Comment	Reference
B	326	ARG	-	expression tag	UNP Q0K312
B	327	LYS	-	expression tag	UNP Q0K312
B	328	GLU	-	expression tag	UNP Q0K312
B	329	ALA	-	expression tag	UNP Q0K312
B	330	GLU	-	expression tag	UNP Q0K312
B	331	LEU	-	expression tag	UNP Q0K312
B	332	ALA	-	expression tag	UNP Q0K312
B	333	ALA	-	expression tag	UNP Q0K312
B	334	ALA	-	expression tag	UNP Q0K312
B	335	THR	-	expression tag	UNP Q0K312
B	336	ALA	-	expression tag	UNP Q0K312
B	337	GLU	-	expression tag	UNP Q0K312
B	338	GLN	-	expression tag	UNP Q0K312

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Ca 2 2	0	0
2	B	2	Total Ca 2 2	0	0

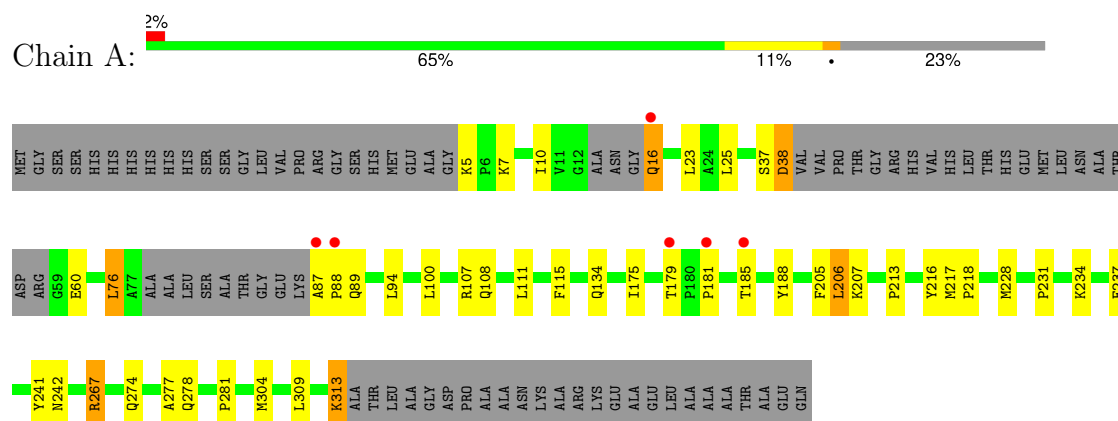
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	64	Total O 64 64	0	0
3	B	50	Total O 50 50	0	0

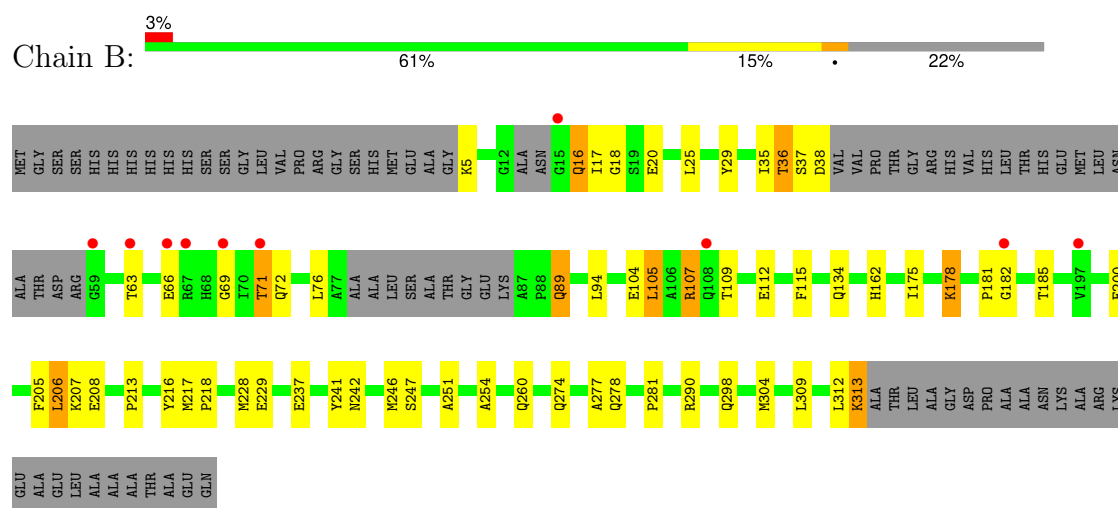
### 3 Residue-property plots [i](#)

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: NAD dependent epimerase/dehydratase



- Molecule 1: NAD dependent epimerase/dehydratase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.01Å 83.49Å 106.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 2.25 48.81 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.80-2.25) 99.6 (48.81-2.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.91 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.227 , 0.264 0.231 , 0.266	Depositor DCC
$R_{free}$ test set	1575 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4402	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.66 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.7125e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: CA

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	0.47	0/2200	0.59	0/2995
1	B	0.44	0/2190	0.60	0/2979
All	All	0.45	0/4390	0.60	0/5974

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	5	LYS	Peptide
1	B	69	GLY	Peptide

### 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	2147	0	2105	26	0
1	B	2137	0	2089	36	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	64	0	0	0	0
3	B	50	0	0	2	0
All	All	4402	0	4194	61	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 61 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:267:ARG:HG3	1:A:267:ARG:HH11	1.30	0.96
1:B:71:THR:HG22	1:B:72:GLN:HG3	1.54	0.88
1:B:107:ARG:HH11	1:B:107:ARG:HG2	1.36	0.87
1:B:107:ARG:HH11	1:B:107:ARG:CG	1.96	0.78
1:B:104:GLU:OE2	1:B:107:ARG:NH1	2.20	0.75

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	269/358 (75%)	261 (97%)	7 (3%)	1 (0%)	34	37
1	B	270/358 (75%)	255 (94%)	14 (5%)	1 (0%)	34	37
All	All	539/716 (75%)	516 (96%)	21 (4%)	2 (0%)	34	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	PRO
1	B	200	GLU

### 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	221/278 (80%)	205 (93%)	16 (7%)	14	12
1	B	217/278 (78%)	198 (91%)	19 (9%)	10	8
All	All	438/556 (79%)	403 (92%)	35 (8%)	12	10

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	206	LEU
1	B	246	MET
1	B	298	GLN
1	A	206	LEU
1	A	111	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	33	ASN
1	B	68	HIS
1	B	278	GLN
1	B	159	HIS
1	B	274	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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, 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	277/358 (77%)	0.07	6 (2%) 62 65	16, 29, 66, 108	0
1	B	278/358 (77%)	0.21	10 (3%) 42 44	18, 34, 79, 99	0
All	All	555/716 (77%)	0.14	16 (2%) 51 55	16, 31, 73, 108	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	87	ALA	8.9
1	B	67	ARG	5.2
1	B	63	THR	3.1
1	A	16	GLN	3.0
1	B	108	GLN	2.8

### 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 monosaccharides 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	CA	B	401	1/1	0.79	0.13	37,37,37,37	0
2	CA	A	401	1/1	0.81	0.14	42,42,42,42	0
2	CA	A	402	1/1	0.99	0.10	31,31,31,31	0
2	CA	B	402	1/1	0.99	0.10	33,33,33,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.