



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 06:46 pm GMT

PDB ID : 3D5T
Title : Crystal structure of malate dehydrogenase from Burkholderia pseudomallei
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2008-05-16
Resolution : 2.51 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

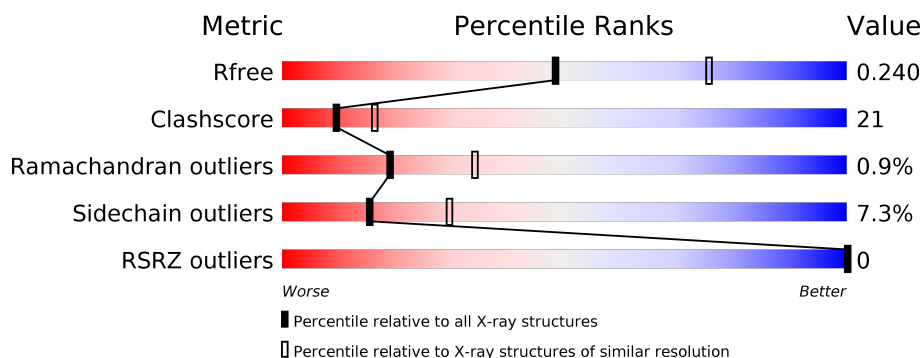
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	111664	4155 (2.50-2.50)
Clashscore	122126	4827 (2.50-2.50)
Ramachandran outliers	120053	4735 (2.50-2.50)
Sidechain outliers	120020	4737 (2.50-2.50)
RSRZ outliers	108989	4058 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	331	
1	B	331	
1	C	331	
1	D	331	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10008 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 Malate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2376	1504	413	450	9			
1	B	321	Total	C	N	O	S	0	0	0
			2395	1515	417	454	9			
1	C	323	Total	C	N	O	S	0	0	0
			2418	1531	422	456	9			
1	D	321	Total	C	N	O	S	0	0	0
			2390	1514	412	455	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP Q3JKE9
A	-2	PRO	-	EXPRESSION TAG	UNP Q3JKE9
A	-1	GLY	-	EXPRESSION TAG	UNP Q3JKE9
A	0	SER	-	EXPRESSION TAG	UNP Q3JKE9
B	-3	GLY	-	EXPRESSION TAG	UNP Q3JKE9
B	-2	PRO	-	EXPRESSION TAG	UNP Q3JKE9
B	-1	GLY	-	EXPRESSION TAG	UNP Q3JKE9
B	0	SER	-	EXPRESSION TAG	UNP Q3JKE9
C	-3	GLY	-	EXPRESSION TAG	UNP Q3JKE9
C	-2	PRO	-	EXPRESSION TAG	UNP Q3JKE9
C	-1	GLY	-	EXPRESSION TAG	UNP Q3JKE9
C	0	SER	-	EXPRESSION TAG	UNP Q3JKE9
D	-3	GLY	-	EXPRESSION TAG	UNP Q3JKE9
D	-2	PRO	-	EXPRESSION TAG	UNP Q3JKE9
D	-1	GLY	-	EXPRESSION TAG	UNP Q3JKE9
D	0	SER	-	EXPRESSION TAG	UNP Q3JKE9

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Na	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		

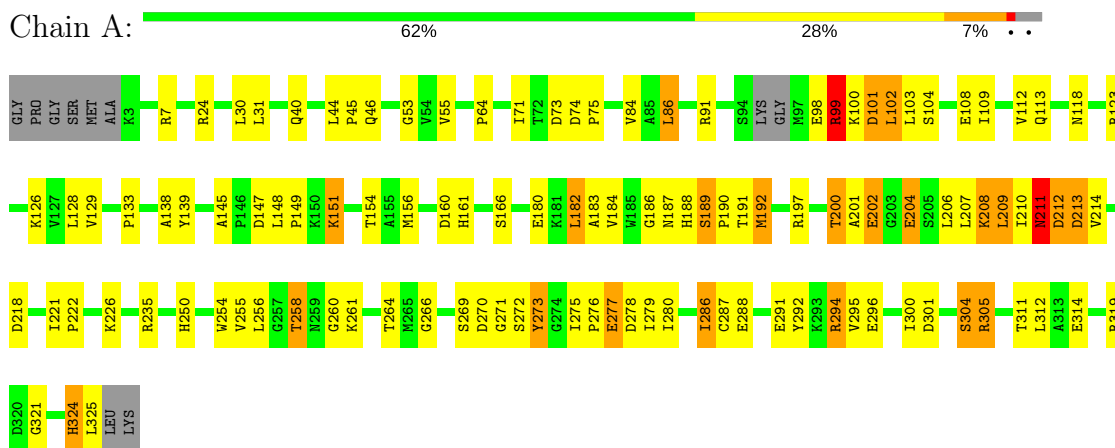
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	78	Total	O	0	0
			78	78		
4	B	131	Total	O	0	0
			131	131		
4	C	84	Total	O	0	0
			84	84		
4	D	134	Total	O	0	0
			134	134		

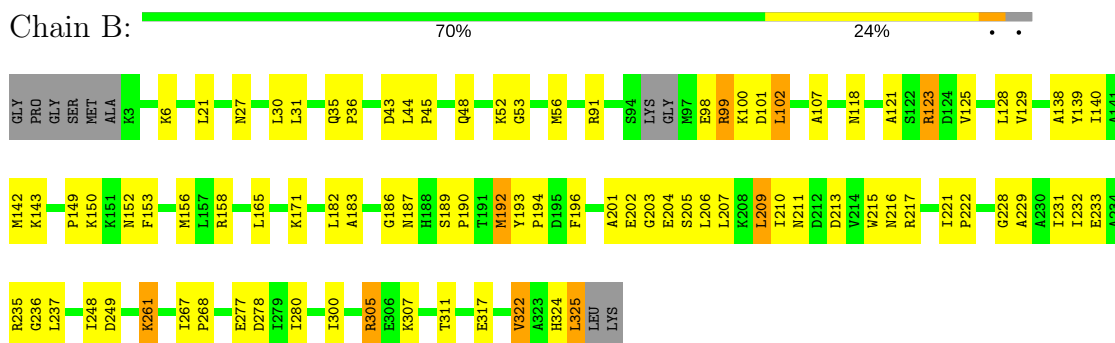
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

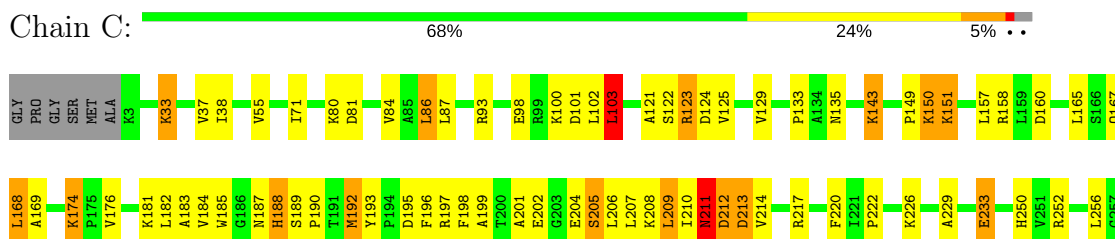
• Molecule 1: Malate dehydrogenase

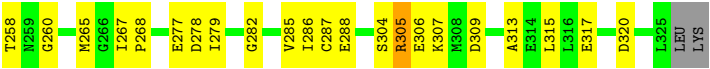


• Molecule 1: Malate dehydrogenase

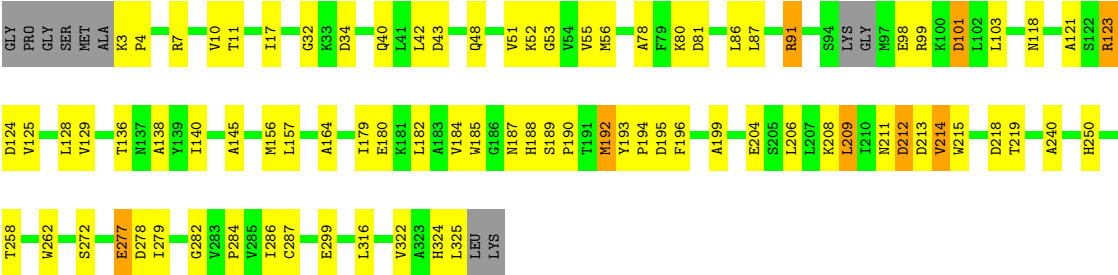


• Molecule 1: Malate dehydrogenase





● Molecule 1: Malate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.39Å 79.61Å 288.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.62 – 2.51 47.60 – 2.51	Depositor EDS
% Data completeness (in resolution range)	89.1 (47.62-2.51) 89.1 (47.60-2.51)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.51Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.178 , 0.241 0.178 , 0.240	Depositor DCC
R_{free} test set	2181 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10008	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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 33.81 % 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 7.5381e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NA, MG

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	0.83	0/2417	0.88	0/3290
1	B	0.88	1/2436 (0.0%)	0.91	0/3312
1	C	0.94	1/2459 (0.0%)	0.90	2/3337 (0.1%)
1	D	0.91	1/2431 (0.0%)	0.90	2/3305 (0.1%)
All	All	0.89	3/9743 (0.0%)	0.90	4/13244 (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	C	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	233	GLU	CG-CD	6.77	1.62	1.51
1	B	322	VAL	CB-CG1	-5.14	1.42	1.52
1	D	299	GLU	CG-CD	5.10	1.59	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	320	ASP	CB-CG-OD1	6.73	124.35	118.30
1	C	103	LEU	CA-CB-CG	5.47	127.88	115.30
1	D	195	ASP	CB-CG-OD1	5.25	123.03	118.30
1	D	195	ASP	CB-CG-OD2	-5.11	113.70	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	288	GLU	Peptide

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	2376	0	2369	144	0
1	B	2395	0	2401	90	0
1	C	2418	0	2447	94	0
1	D	2390	0	2397	74	0
2	B	1	0	0	0	0
3	B	1	0	0	0	0
4	A	78	0	0	6	0
4	B	131	0	0	4	0
4	C	84	0	0	3	0
4	D	134	0	0	7	0
All	All	10008	0	9614	400	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 21.

The worst 5 of 400 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:260:GLY:CA	1:A:286:ILE:HD11	1.29	1.62
1:A:260:GLY:HA2	1:A:286:ILE:CD1	1.36	1.50
1:B:192:MET:CE	1:B:194:PRO:HD3	1.47	1.40
1:B:324:HIS:CD2	1:B:325:LEU:HD21	1.65	1.32
1:A:182:LEU:HD13	1:A:183:ALA:N	1.42	1.30

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	317/331 (96%)	285 (90%)	26 (8%)	6 (2%)	9	15
1	B	317/331 (96%)	304 (96%)	13 (4%)	0	100	100
1	C	319/331 (96%)	295 (92%)	20 (6%)	4 (1%)	13	23
1	D	317/331 (96%)	302 (95%)	14 (4%)	1 (0%)	43	64
All	All	1270/1324 (96%)	1186 (93%)	73 (6%)	11 (1%)	19	34

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	ARG
1	A	208	LYS
1	A	212	ASP
1	C	150	LYS
1	C	188	HIS

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	242/258 (94%)	218 (90%)	24 (10%)	8	16
1	B	246/258 (95%)	232 (94%)	14 (6%)	23	42
1	C	249/258 (96%)	230 (92%)	19 (8%)	14	28
1	D	246/258 (95%)	231 (94%)	15 (6%)	20	39
All	All	983/1032 (95%)	911 (93%)	72 (7%)	15	29

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	209	LEU
1	C	103	LEU
1	D	209	LEU
1	B	261	LYS
1	B	317	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	250	HIS
1	C	113	GLN
1	D	113	GLN
1	B	27	ASN
1	C	188	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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, 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	321/331 (96%)	-0.26	0 100 100	17, 39, 61, 75	0
1	B	321/331 (96%)	-0.54	0 100 100	15, 25, 46, 66	0
1	C	323/331 (97%)	-0.35	0 100 100	15, 33, 54, 64	0
1	D	321/331 (96%)	-0.49	0 100 100	16, 26, 46, 62	0
All	All	1286/1324 (97%)	-0.41	0 100 100	15, 30, 54, 75	0

There are no RSRZ outliers to report.

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 carbohydrates 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
3	MG	B	401	1/1	0.97	0.08	67,67,67,67	0
2	NA	B	402	1/1	0.99	0.05	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.