



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 05:17 am BST

PDB ID : 4KS9
Title : Crystal Structure of Malonyl-CoA decarboxylase (Rmet_2797) from Cupriavidus metallidurans, Northeast Structural Genomics Consortium Target CrR76
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Deposited on : 2013-05-17
Resolution : 2.30 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	:	2.11
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)	:	2.11

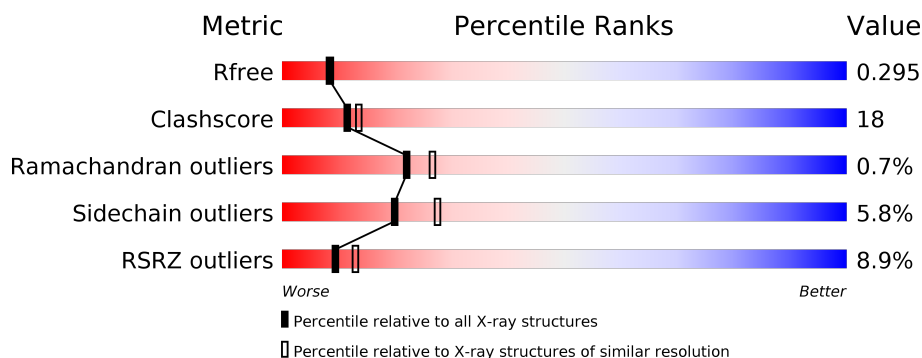
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	428	<div> <div>8%</div> <div> <div></div> <div>62%</div> <div>28%</div> <div>• 8%</div> </div> </div>
1	B	428	<div> <div>9%</div> <div> <div></div> <div>60%</div> <div>30%</div> <div>• 8%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6535 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 Malonyl-CoA decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			3118	1971	582	553	12			
1	B	395	Total	C	N	O	S	0	0	0
			3140	1985	585	558	12			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	474	ALA	-	EXPRESSION TAG	UNP Q1LJK6
A	475	ALA	-	EXPRESSION TAG	UNP Q1LJK6
A	476	ALA	-	EXPRESSION TAG	UNP Q1LJK6
A	477	LEU	-	EXPRESSION TAG	UNP Q1LJK6
A	478	GLU	-	EXPRESSION TAG	UNP Q1LJK6
A	479	HIS	-	EXPRESSION TAG	UNP Q1LJK6
A	480	HIS	-	EXPRESSION TAG	UNP Q1LJK6
A	481	HIS	-	EXPRESSION TAG	UNP Q1LJK6
A	482	HIS	-	EXPRESSION TAG	UNP Q1LJK6
A	483	HIS	-	EXPRESSION TAG	UNP Q1LJK6
A	484	HIS	-	EXPRESSION TAG	UNP Q1LJK6
B	474	ALA	-	EXPRESSION TAG	UNP Q1LJK6
B	475	ALA	-	EXPRESSION TAG	UNP Q1LJK6
B	476	ALA	-	EXPRESSION TAG	UNP Q1LJK6
B	477	LEU	-	EXPRESSION TAG	UNP Q1LJK6
B	478	GLU	-	EXPRESSION TAG	UNP Q1LJK6
B	479	HIS	-	EXPRESSION TAG	UNP Q1LJK6
B	480	HIS	-	EXPRESSION TAG	UNP Q1LJK6
B	481	HIS	-	EXPRESSION TAG	UNP Q1LJK6
B	482	HIS	-	EXPRESSION TAG	UNP Q1LJK6
B	483	HIS	-	EXPRESSION TAG	UNP Q1LJK6
B	484	HIS	-	EXPRESSION TAG	UNP Q1LJK6

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	127	Total 127	O 127	0	0
3	B	149	Total 149	O 149	0	0

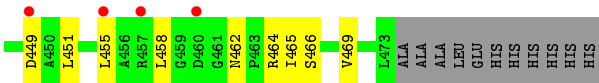
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

[illegible]

Chain B:

9% 60% 30% 8%

Label	Color	Value
S152	Red	0.09
S153	Red	0.09
C154	Green	0.60
G155	Yellow	0.30
F158	Red	0.09
L159	Green	0.60
I160	Green	0.60
Q161	Red	0.09
D162	Green	0.60
R163	Green	0.60
A164	Green	0.60
L167	Red	0.09
R171	Red	0.09
R172	Red	0.09
L176	Green	0.60
L177	Green	0.60
E181	Green	0.60
L198	Green	0.60
L210	Green	0.60
E211	Red	0.09
R212	Green	0.60
L213	Green	0.60
I214	Green	0.60
R215	Green	0.60
GLU	Green	0.60
ALA	Green	0.60
VAL	Green	0.60
HIS	Green	0.60
E221	Red	0.09
D222	Red	0.09
S223	Red	0.09
S224	Red	0.09
W225	Red	0.09
T226	Green	0.60
D227	Green	0.60
L228	Green	0.60
R229	Red	0.09
R230	Green	0.60
R231	Red	0.09
L232	Green	0.60
D233	Green	0.60
R236	Red	0.09
R237	Red	0.09
C238	Red	0.09
Y239	Green	0.60
A240	Green	0.60
F241	Green	0.60
F242	Green	0.60
H243	Green	0.60
P244	Green	0.60
R245	Green	0.60
L246	Green	0.60
P247	Green	0.60
R248	Green	0.60
L251	Green	0.60
L252	Green	0.60
F253	Green	0.60
V254	Red	0.09
D255	Green	0.60
V256	Green	0.60
V259	Green	0.60
P260	Green	0.60
E261	Green	0.60
V266	Green	0.60
L270	Green	0.60
ASP	Green	0.60
GLU	Green	0.60
ALA	Green	0.60
ALA	Green	0.60
PRO	Green	0.60
LEU	Green	0.60
GLU	Green	0.60
ASP	Green	0.60
L279	Red	0.09
R280	Red	0.09
R281	Red	0.09
W284	Green	0.60
A285	Green	0.60
I286	Red	0.09
S289	Green	0.60
N292	Green	0.60
G296	Green	0.60
L297	Green	0.60
V300	Green	0.60
L306	Green	0.60
L307	Green	0.60
Q315	Green	0.60
R316	Green	0.60
E317	Green	0.60
H318	Green	0.60
P319	Red	0.09
K320	Red	0.09
L321	Red	0.09
K322	Red	0.09
Q323	Green	0.60
F324	Green	0.60
A325	Green	0.60
H326	Green	0.60
W327	Green	0.60
W328	Green	0.60
K332	Red	0.09
M441	Green	0.60
V442	Green	0.60
N443	Green	0.60
W446	Green	0.60



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	191.01Å 69.39Å 74.36Å 90.00° 103.80° 90.00°	Depositor
Resolution (Å)	28.75 – 2.30 28.75 – 2.24	Depositor EDS
% Data completeness (in resolution range)	89.1 (28.75-2.30) 92.1 (28.75-2.24)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.24Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.239 , 0.286 0.250 , 0.295	Depositor DCC
R_{free} test set	4254 reflections (9.61%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6535	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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: 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	0.37	0/3182	0.58	0/4302
1	B	0.38	0/3204	0.58	0/4332
All	All	0.37	0/6386	0.58	0/8634

There are no bond length outliers.

There are no bond angle outliers.

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	3118	0	3107	110	0
1	B	3140	0	3132	110	0
2	B	1	0	0	0	0
3	A	127	0	0	6	0
3	B	149	0	0	5	0
All	All	6535	0	6239	220	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 18.

The worst 5 of 220 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:60:ALA:HB1	1:A:63:ARG:HH12	1.37	0.89
1:B:60:ALA:HB1	1:B:63:ARG:HH12	1.41	0.85
1:A:408:PRO:HA	1:A:411:ARG:HH12	1.42	0.84
1:B:247:PRO:O	1:B:248:ARG:HB2	1.78	0.83
1:B:408:PRO:HA	1:B:411:ARG:HH12	1.44	0.81

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	382/428 (89%)	361 (94%)	20 (5%)	1 (0%)	41	50
1	B	385/428 (90%)	360 (94%)	21 (6%)	4 (1%)	15	17
All	All	767/856 (90%)	721 (94%)	41 (5%)	5 (1%)	22	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	115	ASP
1	B	222	ILE
1	A	402	LYS
1	B	402	LYS
1	B	123	THR

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	317/342 (93%)	299 (94%)	18 (6%)	20	28
1	B	320/342 (94%)	301 (94%)	19 (6%)	19	27
All	All	637/684 (93%)	600 (94%)	37 (6%)	20	27

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	449	ASP
1	B	69	ARG
1	B	422	ARG
1	A	462	ASN
1	B	59	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	67	GLN
1	B	101	GLN
1	B	315	GLN
1	A	323	GLN
1	A	462	ASN

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 1 ligands modelled in this entry, 1 is 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

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 [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	392/428 (91%)	0.48	33 (8%) 11 15	23, 43, 70, 97	0
1	B	395/428 (92%)	0.59	37 (9%) 8 11	22, 43, 72, 91	0
All	All	787/856 (91%)	0.53	70 (8%) 9 13	22, 43, 71, 97	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	222	ILE	6.7
1	B	223	SER	6.4
1	B	116	ALA	6.3
1	B	125	SER	6.3
1	B	280	ARG	5.3

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(\AA^2)	Q<0.9
2	MG	B	501	1/1	0.97	0.11	29,29,29,29	0

6.5 Other polymers ⓘ

There are no such residues in this entry.