



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 04:49 am BST

PDB ID : 4FN7
Title : Apo Structure of the Mtb enoyl CoA isomerase (Rv0632c)
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Sacchettini, J.C.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2012-06-19
Resolution : 1.25 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 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

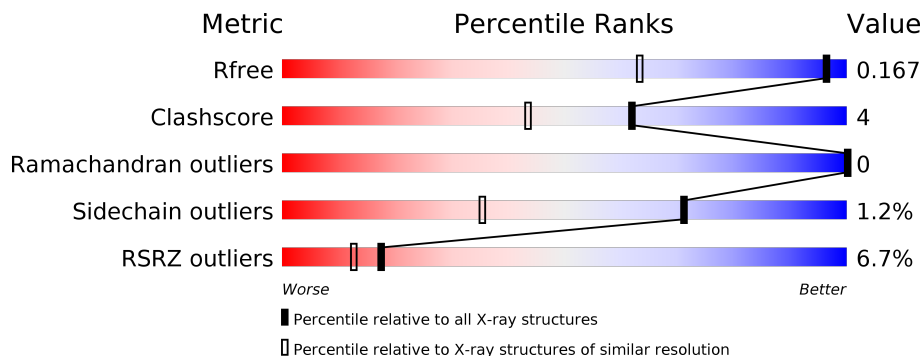
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.25 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	1023 (1.28-1.24)
Clashscore	141614	1060 (1.28-1.24)
Ramachandran outliers	138981	1029 (1.28-1.24)
Sidechain outliers	138945	1028 (1.28-1.24)
RSRZ outliers	127900	1004 (1.28-1.24)

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	231	 6% 92% 8%
1	B	231	 7% 90% 8%
1	C	231	 6% 93% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6185 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 Enoyl-CoA hydratase/isomerase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	231	1741	1100	304	326	11	0	8	0
1	B	226	1700	1075	297	317	11	0	6	0
1	C	230	1728	1091	304	322	11	0	7	0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

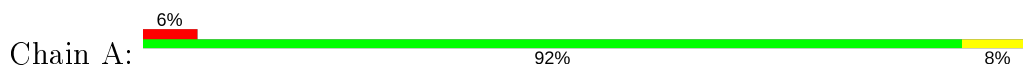
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	338	Total	O	0	0
			338	338		
3	B	327	Total	O	0	0
			327	327		
3	C	350	Total	O	0	0
			350	350		

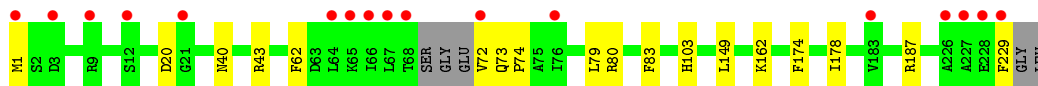
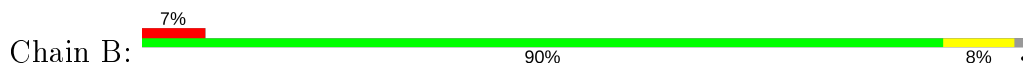
3 Residue-property plots [i](#)

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.

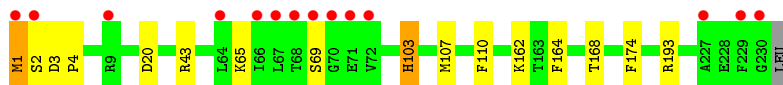
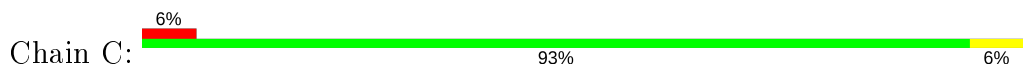
- Molecule 1: Enoyl-CoA hydratase/isomerase family protein



- Molecule 1: Enoyl-CoA hydratase/isomerase family protein



- Molecule 1: Enoyl-CoA hydratase/isomerase family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.13Å 68.68Å 75.57Å 90.00° 108.57° 90.00°	Depositor
Resolution (Å)	36.33 – 1.25 36.33 – 1.25	Depositor EDS
% Data completeness (in resolution range)	96.3 (36.33-1.25) 96.3 (36.33-1.25)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 1.25Å)	Xtrriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.149 , 0.183 0.130 , 0.167	Depositor DCC
R_{free} test set	8331 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	13.0	Xtrriage
Anisotropy	0.286	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	6185	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL

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	0.28	0/1792	0.49	0/2426
1	B	0.28	0/1743	0.49	0/2358
1	C	0.31	0/1778	0.51	0/2408
All	All	0.29	0/5313	0.50	0/7192

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

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	1741	0	1755	12	0
1	B	1700	0	1715	12	0
1	C	1728	0	1741	23	0
2	B	1	0	0	0	0
3	A	338	0	0	3	0
3	B	327	0	0	4	0
3	C	350	0	0	6	0
All	All	6185	0	5211	46	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 4.

All (46) 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:C:1[A]:MET:HE1	1:C:4:PRO:HB3	1.63	0.80
1:C:1[A]:MET:HB2	3:C:563:HOH:O	1.87	0.74
1:B:1:MET:HG2	1:B:20:ASP:HA	1.73	0.70
1:C:43:ARG:HD3	3:C:626:HOH:O	1.93	0.69
1:C:1[A]:MET:HE1	1:C:20:ASP:HA	1.75	0.68
1:A:57:VAL:HG12	1:A:103[B]:HIS:CE1	2.29	0.67
1:C:1[A]:MET:CE	1:C:4:PRO:HB3	2.27	0.65
1:C:1[A]:MET:CE	1:C:20:ASP:HA	2.28	0.64
1:A:1:MET:HE1	3:A:565:HOH:O	2.00	0.62
1:B:178:ILE:HD13	3:B:545:HOH:O	2.01	0.59
1:B:40[A]:ASN:OD1	1:B:43:ARG:NH2	2.36	0.58
1:B:80:ARG:HD2	3:B:708:HOH:O	2.04	0.58
1:C:1[A]:MET:HG2	1:C:2:SER:N	2.21	0.55
1:A:151:ARG:HD2	1:B:149:LEU:O	2.08	0.54
1:C:103[B]:HIS:CD2	3:C:385:HOH:O	2.61	0.52
1:B:79[A]:LEU:HD12	1:B:83:PHE:HE2	1.75	0.51
1:A:122:HIS:HD2	3:A:480:HOH:O	1.93	0.51
1:C:1[A]:MET:HE1	1:C:20:ASP:CB	2.41	0.51
1:C:193:ARG:HD2	3:C:578:HOH:O	2.10	0.50
1:A:146:LYS:NZ	3:A:614:HOH:O	2.45	0.50
1:C:1[A]:MET:SD	1:C:4:PRO:HA	2.52	0.49
1:C:1[A]:MET:HE1	1:C:20:ASP:CA	2.42	0.49
1:B:162[B]:LYS:HD2	3:B:483:HOH:O	2.16	0.46
1:C:162[A]:LYS:HD3	1:C:164:PHE:CZ	2.51	0.45
1:C:1[A]:MET:SD	1:C:3:ASP:C	2.95	0.45
1:B:62:PHE:CZ	1:B:79[A]:LEU:HD13	2.53	0.44
1:B:72:VAL:HG23	1:B:229:PHE:CE2	2.52	0.44
1:A:185:VAL:O	1:A:189[B]:GLU:HG3	2.18	0.44
1:C:168:THR:HB	3:C:601:HOH:O	2.18	0.43
1:C:65:LYS:O	1:C:69:SER:HB3	2.18	0.43
1:A:190:GLU:O	1:A:194[A]:GLU:HG3	2.19	0.43
1:C:1[B]:MET:HE2	3:C:547:HOH:O	2.19	0.43
1:A:107:MET:HA	1:A:110:PHE:CD2	2.54	0.43
1:C:1[A]:MET:HB3	1:C:1[A]:MET:HE2	1.48	0.43
1:C:107:MET:HA	1:C:110:PHE:CD2	2.55	0.42
1:A:146:LYS:HD3	3:B:722:HOH:O	2.19	0.42
1:B:73:GLN:HB3	1:B:74:PRO:HD3	2.02	0.41
1:A:26:LEU:HD13	1:A:107:MET:HG3	2.01	0.41
1:B:62:PHE:CE2	1:B:79[A]:LEU:HD13	2.56	0.41
1:A:118:ARG:O	1:A:175[B]:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ALA:HB2	1:A:46:VAL:HG11	2.03	0.40
1:B:187:ARG:HD2	1:B:187:ARG:HA	1.95	0.40

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	237/231 (103%)	229 (97%)	8 (3%)	0	100	100
1	B	228/231 (99%)	221 (97%)	7 (3%)	0	100	100
1	C	234/231 (101%)	227 (97%)	7 (3%)	0	100	100
All	All	699/693 (101%)	677 (97%)	22 (3%)	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	173/169 (102%)	172 (99%)	1 (1%)	86	62
1	B	168/169 (99%)	166 (99%)	2 (1%)	71	35
1	C	172/169 (102%)	167 (97%)	5 (3%)	42	7
All	All	513/507 (101%)	505 (98%)	8 (2%)	71	25

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	PHE
1	B	103	HIS
1	B	174	PHE
1	C	1[A]	MET
1	C	1[B]	MET
1	C	103[A]	HIS
1	C	103[B]	HIS
1	C	174	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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 [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

6.1 Protein, DNA and RNA chains

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	231/231 (100%)	0.46	15 (6%) 18 13	9, 13, 29, 41	0
1	B	226/231 (97%)	0.62	17 (7%) 14 10	9, 13, 31, 56	0
1	C	230/231 (99%)	0.57	14 (6%) 21 16	8, 11, 27, 44	0
All	All	687/693 (99%)	0.55	46 (6%) 17 13	8, 12, 31, 56	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	ALA	9.8
1	B	229	PHE	9.7
1	C	229	PHE	9.3
1	C	230	GLY	6.7
1	A	229	PHE	6.6
1	C	64	LEU	5.2
1	C	70	GLY	5.2
1	A	231	LEU	5.1
1	B	67	LEU	5.0
1	B	68	THR	4.8
1	A	230	GLY	4.8
1	B	72	VAL	4.7
1	B	64	LEU	4.3
1	C	69	SER	4.3
1	C	67	LEU	4.0
1	A	64	LEU	3.9
1	B	12	SER	3.8
1	B	228	GLU	3.8
1	B	226	ALA	3.8
1	C	68	THR	3.6
1	A	68	THR	3.5
1	C	1[A]	MET	3.5
1	B	1	MET	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	72	VAL	3.3
1	A	70	GLY	3.2
1	C	227	ALA	3.0
1	A	227	ALA	2.9
1	A	69	SER	2.8
1	B	21	GLY	2.8
1	B	9	ARG	2.7
1	A	226	ALA	2.6
1	A	1	MET	2.6
1	C	9	ARG	2.4
1	B	66	ILE	2.4
1	C	71	GLU	2.4
1	A	228	GLU	2.3
1	A	11	ASP	2.3
1	A	183	VAL	2.2
1	B	183	VAL	2.2
1	A	67	LEU	2.2
1	C	2	SER	2.2
1	B	76	ILE	2.1
1	B	3	ASP	2.1
1	B	65	LYS	2.1
1	C	66	ILE	2.0
1	A	201	HIS	2.0

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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
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2	CL	B	301	1/1	1.00	0.06	15,15,15,15	0
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6.5 Other polymers [i](#)

There are no such residues in this entry.