

wwPDB X-ray Structure Validation Summary Report (i)

Sep 16, 2021 – 02:02 pm BST

PDB ID : 701G

Title: Structure of Mycobacterium tuberculosis beta-oxidation trifunctional enzyme

alpha-E141A-H462A, beta-C92A mutant

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Deposited on : 2021-03-29

Resolution : 3.03 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

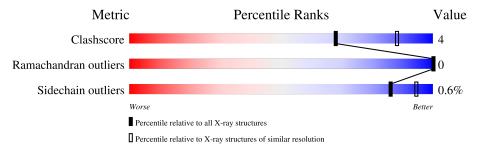
Validation Pipeline (wwPDB-VP) : 2.23.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 3.03 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	3096 (3.08-3.00)
Ramachandran outliers	138981	2986 (3.08-3.00)
Sidechain outliers	138945	2988 (3.08-3.00)

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 >=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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain			
1	D	403	88%	11%		
2	A	736	89%	10% •		



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8378 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 Putative acyltransferase Rv0859.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	D	402	Total 2959	C 1848	N 525	O 572	S 14	0	2	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	92	ALA	CYS	engineered mutation	UNP O53871

• Molecule 2 is a protein called 3-hydroxyacyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	A	727	Total 5385	C 3406	N 927	O 1031	S 21	0	1	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP O53872
A	-14	GLY	-	expression tag	UNP O53872
A	-13	SER	-	expression tag	UNP O53872
A	-12	SER	_	expression tag	UNP O53872
A	-11	HIS	-	expression tag	UNP O53872
A	-10	HIS	_	expression tag	UNP O53872
A	-9	HIS	_	expression tag	UNP O53872
A	-8	HIS	-	expression tag	UNP O53872
A	-7	HIS	_	expression tag	UNP O53872
A	-6	HIS	_	expression tag	UNP O53872
A	-5	SER	_	expression tag	UNP O53872
A	-4	GLN	_	expression tag	UNP O53872
A	-3	ASP	-	expression tag	UNP O53872
A	-2	PRO	-	expression tag	UNP O53872
A	-1	ASN	-	expression tag	UNP O53872

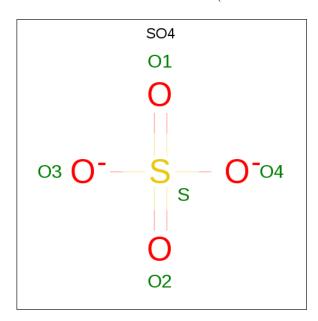
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Chain	Residue	Modelled	Actual	Comment	Reference
Α	0	SER	_	expression tag	UNP O53872
A	141	ALA	GLU	engineered mutation	UNP O53872
A	462	ALA	HIS	engineered mutation	UNP O53872

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	5	Total O 5 5	0	0
4	A	4	Total O 4 4	0	0

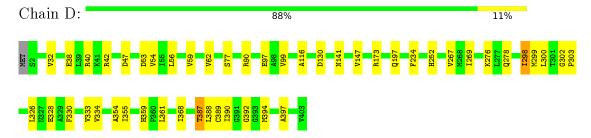


3 Residue-property plots (i)

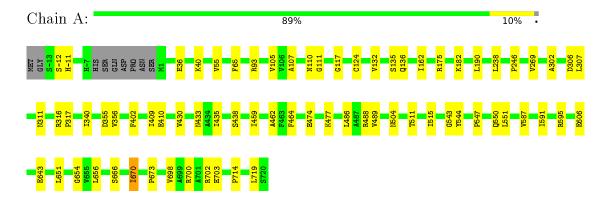
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

• Molecule 1: Putative acyltransferase Rv0859



• Molecule 2: 3-hydroxyacyl-CoA dehydrogenase





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	C 2 2 21	Depositor	
Cell constants	101.61Å 207.80Å 132.99Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	51.95 - 3.03	Depositor	
% Data completeness	99.8 (51.95-3.03)	Depositor	
(in resolution range)	,	Deposition	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	PHENIX 1.18.2_3874	Depositor	
R, R_{free}	0.226 , 0.275	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	8378	wwPDB-VP	
Average B, all atoms (Å ²)	97.0	wwPDB-VP	



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: 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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z >5	
1	D	0.24	0/3009	0.43	0/4076	
2	A	0.24	0/5488	0.40	0/7431	
All	All	0.24	0/8497	0.41	0/11507	

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	D	2959	0	2980	26	0
2	A	5385	0	5418	38	0
3	A	10	0	0	0	0
3	D	15	0	0	0	0
4	A	4	0	0	0	0
4	D	5	0	0	1	0
All	All	8378	0	8398	63	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.

The worst 5 of 63 close contacts within the same asymmetric unit are listed below, sorted by their



clash magnitude.

Atom-1	Atom-2	$egin{array}{l} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:D:299:MET:HG2	1:D:392:GLY:H	1.54	0.71
2:A:340:ILE:HG21	2:A:409:ILE:HG21	1.72	0.71
2:A:-12:SER:OG	2:A:-11:HIS:N	2.27	0.68
1:D:141:ASN:HB3	2:A:246:PRO:HG2	1.79	0.65
2:A:136:GLN:OE1	2:A:175:ARG:NH1	2.31	0.64

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	${f Analysed}$	Favoured	Allowed	Outliers	Perce	${f ntiles}$
1	D	402/403 (100%)	382 (95%)	20 (5%)	0	100	100
2	A	724/736~(98%)	689 (95%)	35 (5%)	0	100	100
All	All	$1126/1139 \ (99\%)$	1071 (95%)	55 (5%)	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	D	307/309 (99%)	304 (99%)	3 (1%)	76 91		
2	A	552/564 (98%)	550 (100%)	2 (0%)	91 96		

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
All	All	859/873 (98%)	854 (99%)	5 (1%)	86 94		

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	${f Res}$	Type
1	D	197	GLN
1	D	298	ILE
1	D	387	THR
2	A	433	ASN
2	A	670	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

5 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	Т	Clasin	Dog	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	m Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	D	502	_	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	D	503	_	4,4,4	0.14	0	6,6,6	0.04	0
3	SO4	A	802	_	4,4,4	0.14	0	6,6,6	0.04	0
3	SO4	D	501	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	A	801	-	4,4,4	0.14	0	6,6,6	0.06	0

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)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

