



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 03:05 am GMT

PDB ID : 4Z0M  
Title : EchA5 Mycobacterium tuberculosis  
Authors : Chaudhary, S.; Gokhale, R.S.  
Deposited on : 2015-03-26  
Resolution : 1.97 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

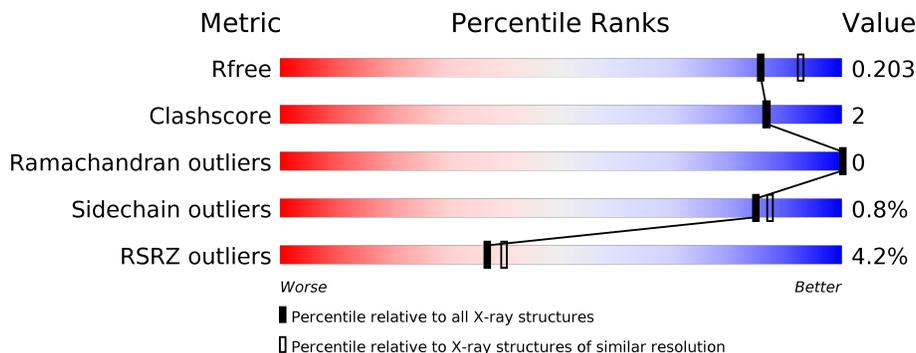
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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))
$R_{free}$	100719	9293 (2.00-1.96)
Clashscore	112137	10621 (2.00-1.96)
Ramachandran outliers	110173	10502 (2.00-1.96)
Sidechain outliers	110143	10501 (2.00-1.96)
RSRZ outliers	101464	9395 (2.00-1.96)

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  $\geq 3$ , 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	269	 3% 81% 8% • 10%
1	B	269	 5% 81% 7% • 11%
1	C	269	 3% 77% 8% • 14%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5621 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	241	Total 1731	C 1085	N 319	O 316	S 11	0	0	0
1	B	239	Total 1702	C 1069	N 314	O 308	S 11	0	0	0
1	C	230	Total 1640	C 1037	N 298	O 294	S 11	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	264	HIS	-	expression tag	UNP I6Y4E8
A	265	HIS	-	expression tag	UNP I6Y4E8
A	266	HIS	-	expression tag	UNP I6Y4E8
A	267	HIS	-	expression tag	UNP I6Y4E8
A	268	HIS	-	expression tag	UNP I6Y4E8
A	269	HIS	-	expression tag	UNP I6Y4E8
B	264	HIS	-	expression tag	UNP I6Y4E8
B	265	HIS	-	expression tag	UNP I6Y4E8
B	266	HIS	-	expression tag	UNP I6Y4E8
B	267	HIS	-	expression tag	UNP I6Y4E8
B	268	HIS	-	expression tag	UNP I6Y4E8
B	269	HIS	-	expression tag	UNP I6Y4E8
C	264	HIS	-	expression tag	UNP I6Y4E8
C	265	HIS	-	expression tag	UNP I6Y4E8
C	266	HIS	-	expression tag	UNP I6Y4E8
C	267	HIS	-	expression tag	UNP I6Y4E8
C	268	HIS	-	expression tag	UNP I6Y4E8
C	269	HIS	-	expression tag	UNP I6Y4E8

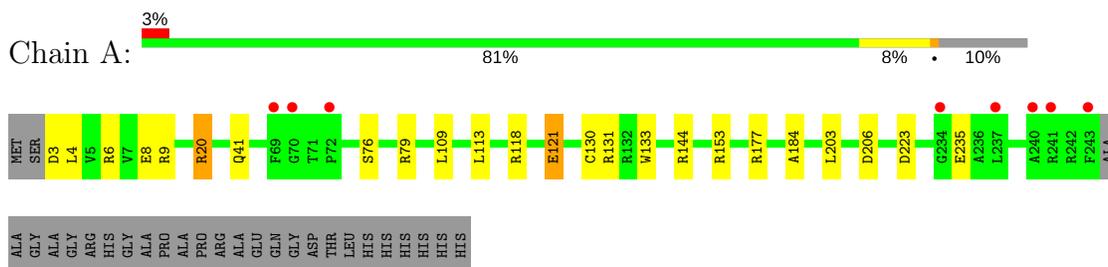
- Molecule 2 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	A	195	Total 195	O 195	0	0
2	B	202	Total 202	O 202	0	0
2	C	151	Total 151	O 151	0	0

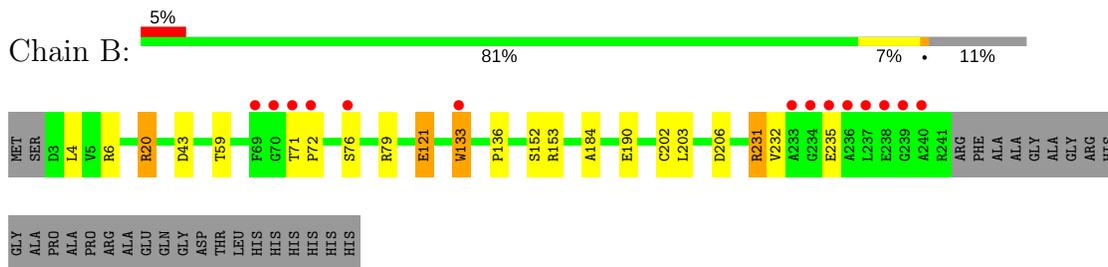
### 3 Residue-property plots [i](#)

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.

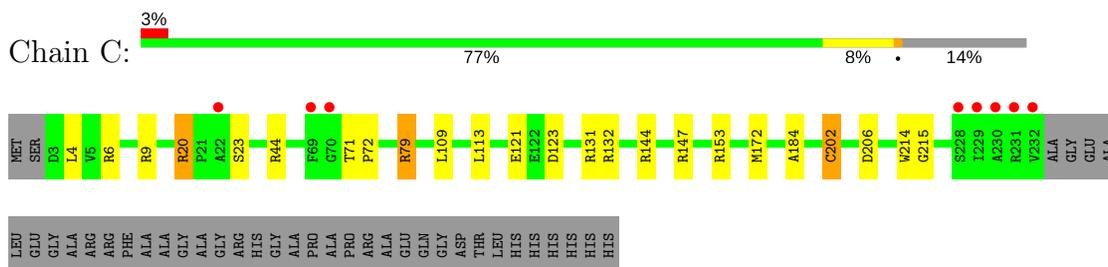
- Molecule 1: Enoyl-CoA hydratase



- Molecule 1: Enoyl-CoA hydratase



- Molecule 1: Enoyl-CoA hydratase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.71Å 136.71Å 125.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.53 – 1.97 37.65 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.53-1.97) 99.3 (37.65-1.97)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 1.97Å)	Xtrriage
Refinement program	REFMAC 5.8.0103	Depositor
R, $R_{free}$	0.168 , 0.195 0.177 , 0.203	Depositor DCC
$R_{free}$ test set	4759 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.1	Xtrriage
Anisotropy	0.287	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 58.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5621	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% of the height of the origin peak. No significant pseudotranslation is detected.*

<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](#)

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	1.23	3/1761 (0.2%)	1.10	12/2390 (0.5%)
1	B	1.24	5/1732 (0.3%)	1.27	12/2351 (0.5%)
1	C	1.20	3/1671 (0.2%)	1.16	18/2269 (0.8%)
All	All	1.22	11/5164 (0.2%)	1.18	42/7010 (0.6%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	215	GLY	N-CA	7.89	1.57	1.46
1	B	121	GLU	CD-OE2	7.76	1.34	1.25
1	B	202	CYS	CB-SG	-7.17	1.70	1.82
1	A	206	ASP	CB-CG	6.90	1.66	1.51
1	C	202	CYS	CB-SG	-6.86	1.70	1.82

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	231	ARG	NE-CZ-NH1	-17.48	111.56	120.30
1	B	231	ARG	NE-CZ-NH2	15.05	127.82	120.30
1	B	79	ARG	NE-CZ-NH1	12.15	126.38	120.30
1	B	20	ARG	NE-CZ-NH2	-10.99	114.80	120.30
1	B	20	ARG	NE-CZ-NH1	10.82	125.71	120.30

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	1731	0	1713	9	0
1	B	1702	0	1688	11	0
1	C	1640	0	1616	7	1
2	A	195	0	0	3	0
2	B	202	0	0	4	1
2	C	151	0	0	1	0
All	All	5621	0	5017	25	1

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 2.

The worst 5 of 25 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:B:4:LEU:HD22	1:B:20:ARG:HD3	1.75	0.68
1:A:4:LEU:HD22	1:A:20:ARG:HD3	1.79	0.64
1:C:4:LEU:HD22	1:C:20:ARG:HD3	1.80	0.63
1:C:121:GLU:HG3	1:C:184:ALA:HB2	1.82	0.62
1:A:41:GLN:HG2	2:A:395:HOH:O	1.98	0.62

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:ARG:CG	2:B:483:HOH:O[2_565]	2.18	0.02

## 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	239/269 (89%)	232 (97%)	7 (3%)	0	100	100
1	B	237/269 (88%)	230 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	228/269 (85%)	222 (97%)	6 (3%)	0	100	100
All	All	704/807 (87%)	684 (97%)	20 (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	163/192 (85%)	161 (99%)	2 (1%)	75	78
1	B	159/192 (83%)	158 (99%)	1 (1%)	89	91
1	C	151/192 (79%)	150 (99%)	1 (1%)	87	89
All	All	473/576 (82%)	469 (99%)	4 (1%)	85	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
1	A	76	SER
1	B	76	SER
1	C	23	SER

Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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	241/269 (89%)	-0.26	8 (3%) 47 50	18, 27, 49, 67	0
1	B	239/269 (88%)	-0.08	14 (5%) 23 26	20, 29, 57, 82	0
1	C	230/269 (85%)	-0.18	8 (3%) 44 48	19, 33, 53, 85	0
All	All	710/807 (87%)	-0.17	30 (4%) 37 40	18, 30, 54, 85	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	234	GLY	5.8
1	B	240	ALA	5.6
1	B	237	LEU	5.5
1	C	232	VAL	5.1
1	B	72	PRO	4.3

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.