



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2017 – 11:36 AM EDT

PDB ID : 5NJI  
Title : Structure of the dehydratase domain of PpsC from Mycobacterium tuberculosis in complex with C12:1-CoA  
Authors : Gavalda, S.; Faille, A.; Mourey, L.; Pedelacq, J.D.  
Deposited on : 2017-03-28  
Resolution : 1.60 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  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029077  
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) : rb-20029077

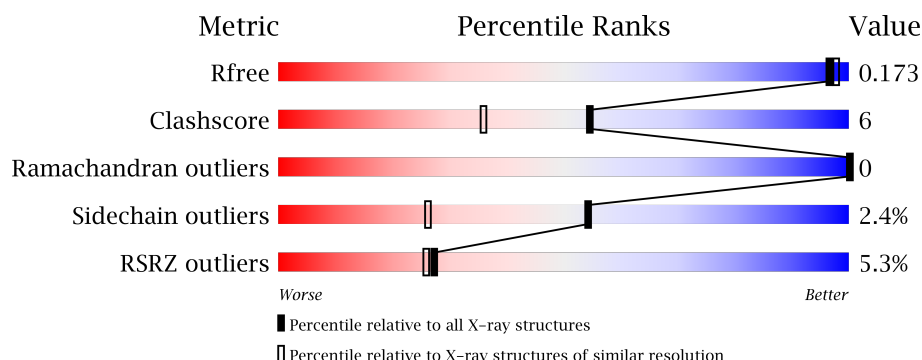
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	2696 (1.60-1.60)
Clashscore	112137	2967 (1.60-1.60)
Ramachandran outliers	110173	2887 (1.60-1.60)
Sidechain outliers	110143	2886 (1.60-1.60)
RSRZ outliers	101464	2714 (1.60-1.60)

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	322	<div> <div>4%</div> <div>75%</div> <div>6%</div> <div>17%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4551 atoms, of which 2119 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.

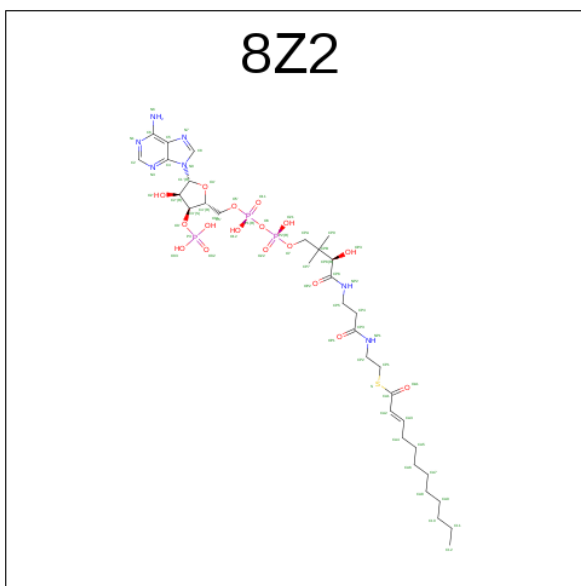
- Molecule 1 is a protein called Phthiocerol/phenolphthiocerol synthesis polyketide synthase type I PpsC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	266	Total	C	H	N	O	S	0	10	0
			4033	1269	2015	354	387	8			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	900	MET	-	initiating methionine	UNP Q7TXL8
A	901	GLY	-	expression tag	UNP Q7TXL8
A	902	SER	-	expression tag	UNP Q7TXL8
A	903	SER	-	expression tag	UNP Q7TXL8
A	904	HIS	-	expression tag	UNP Q7TXL8
A	905	HIS	-	expression tag	UNP Q7TXL8
A	906	HIS	-	expression tag	UNP Q7TXL8
A	907	HIS	-	expression tag	UNP Q7TXL8
A	908	HIS	-	expression tag	UNP Q7TXL8
A	909	HIS	-	expression tag	UNP Q7TXL8
A	910	SER	-	expression tag	UNP Q7TXL8
A	911	SER	-	expression tag	UNP Q7TXL8
A	912	GLY	-	expression tag	UNP Q7TXL8
A	913	LEU	-	expression tag	UNP Q7TXL8
A	914	VAL	-	expression tag	UNP Q7TXL8
A	915	PRO	-	expression tag	UNP Q7TXL8
A	916	ARG	-	expression tag	UNP Q7TXL8
A	917	GLY	-	expression tag	UNP Q7TXL8
A	918	SER	-	expression tag	UNP Q7TXL8
A	919	HIS	-	expression tag	UNP Q7TXL8
A	920	MET	-	expression tag	UNP Q7TXL8
A	959	PHE	HIS	engineered mutation	UNP Q7TXL8
A	1218	THR	-	expression tag	UNP Q7TXL8
A	1219	SER	-	expression tag	UNP Q7TXL8
A	1220	GLY	-	expression tag	UNP Q7TXL8
A	1221	SER	-	expression tag	UNP Q7TXL8

- Molecule 2 is {S}-[2-[3-[[[(2 {R})-4-[[[(2 {R}),3 {S}),4 {R}),5 {R}]-5-(6-aminopurin-9-yl)-4-oxidany-3-phosphonoxy-oxolan-2-yl]methoxy-oxidanyl-phosphoryl]oxy-oxidanyl-phosphoryl]oxy-3,3-dimethyl-2-oxidanyl-butanoyl]amino]propanoylamino]ethyl] ( {E})-dodec-2-enethioate (three-letter code: 8Z2) (formula: C<sub>33</sub>H<sub>56</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
2	A	1	226	66	104	14	34	6	2	0	1

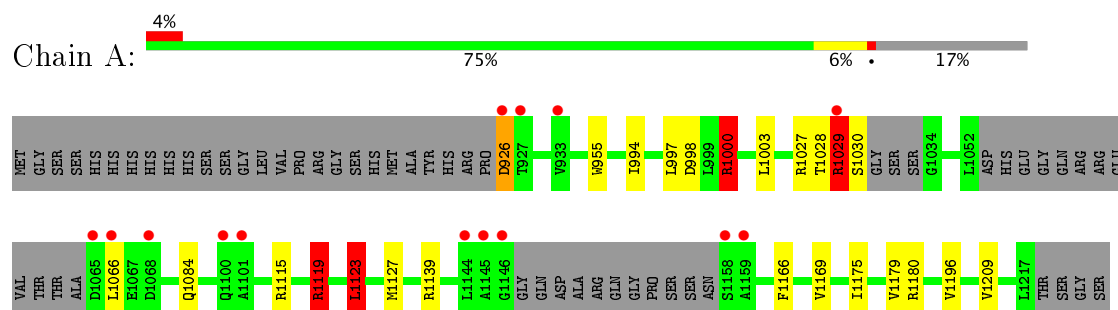
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	292	Total	O	0	0
			292	292		

### 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: Phthiocerol/phenolphthiocerol synthesis polyketide synthase type I PpsC



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.38Å 70.81Å 42.57Å 90.00° 104.87° 90.00°	Depositor
Resolution (Å)	36.33 – 1.60 41.15 – 1.50	Depositor EDS
% Data completeness (in resolution range)	98.5 (36.33-1.60) 98.7 (41.15-1.50)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 1.50Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, $R_{free}$	0.170 , 0.192 0.166 , 0.173	Depositor DCC
$R_{free}$ test set	1639 reflections (3.73%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.3	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 49.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4551	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.91% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 8Z2

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	0.89	15/2083 (0.7%)	0.86	9/2846 (0.3%)

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	A	0	1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1030[A]	SER	N-CA	7.50	1.61	1.46
1	A	1030[B]	SER	N-CA	7.50	1.61	1.46
1	A	1029	ARG	CZ-NH2	7.47	1.42	1.33
1	A	1127[A]	MET	CA-C	7.24	1.71	1.52
1	A	1127[B]	MET	CA-C	7.24	1.71	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1119	ARG	NE-CZ-NH1	11.37	125.98	120.30
1	A	1119	ARG	NE-CZ-NH2	-8.18	116.21	120.30
1	A	926	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	1000[A]	ARG	NE-CZ-NH1	-5.60	117.50	120.30
1	A	1000[B]	ARG	NE-CZ-NH1	-5.60	117.50	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1123[A]	LEU	Mainchain

## 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	2018	2015	1999	23	0
2	A	122	104	0	2	0
3	A	292	0	0	4	0
All	All	2432	2119	1999	25	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 6.

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)
2:A:1301[B]:8Z2:O4'	2:A:1301[B]:8Z2:C4'	1.64	1.41
1:A:1119:ARG:HD2	1:A:1119:ARG:H	1.30	0.95
1:A:1119:ARG:HD2	1:A:1119:ARG:N	1.98	0.77
1:A:1029:ARG:HG2	1:A:1029:ARG:HH11	1.65	0.61
1:A:1123[A]:LEU:HD12	1:A:1175:ILE:HD13	1.80	0.61

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	265/322 (82%)	260 (98%)	5 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	216/254 (85%)	210 (97%)	6 (3%)	49	21

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1000[B]	ARG
1	A	1119	ARG
1	A	1029	ARG
1	A	1000[A]	ARG
1	A	1084	GLN

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

### 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 ⓘ

2 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	8Z2	A	1301[A]	-	54,63,63	3.13	20 (37%)	61,89,89	3.16	24 (39%)
2	8Z2	A	1301[B]	-	54,63,63	2.23	17 (31%)	61,89,89	2.35	14 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	8Z2	A	1301[A]	-	-	0/57/78/78	0/3/3/3
2	8Z2	A	1301[B]	-	-	0/57/78/78	0/3/3/3

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301[A]	8Z2	C5-C4	-3.91	1.31	1.40
2	A	1301[B]	8Z2	C5-C4	-3.54	1.32	1.40
2	A	1301[B]	8Z2	O7-CPA	-3.27	1.33	1.43
2	A	1301[A]	8Z2	C2'-C1'	-3.16	1.48	1.53
2	A	1301[A]	8Z2	P3-O32	-2.88	1.40	1.50

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301[A]	8Z2	C1'-N9-C4	-13.73	102.91	126.64
2	A	1301[B]	8Z2	N3-C2-N1	-11.90	118.49	128.86
2	A	1301[A]	8Z2	N3-C2-N1	-11.50	118.84	128.86
2	A	1301[B]	8Z2	C4'-O4'-C1'	-7.80	101.47	109.77
2	A	1301[A]	8Z2	C2'-C3'-C4'	-5.75	92.95	103.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301[B]	8Z2	2	0

## 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	266/322 (82%)	0.00	14 (5%) 27 26	15, 23, 50, 86	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1066	LEU	7.6
1	A	1146	GLY	5.7
1	A	1145	ALA	4.5
1	A	1144	LEU	4.4
1	A	1100	GLN	3.8

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	8Z2	A	1301[B]	61/61	0.89	0.16	1.82	16,43,71,77	113

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	8Z2	A	1301[A]	61/61	0.89	0.16	1.81	16,43,67,73	113

## 6.5 Other polymers [i](#)

There are no such residues in this entry.