



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 10, 2017 – 05:51 PM EST

PDB ID : 5M1B  
Title : Crystal structure of C-terminally tagged apo-UbiD from E. coli  
Authors : White, M.; Leys, D.  
Deposited on : 2016-10-07  
Resolution : 3.15 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.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : unknown  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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-20028442

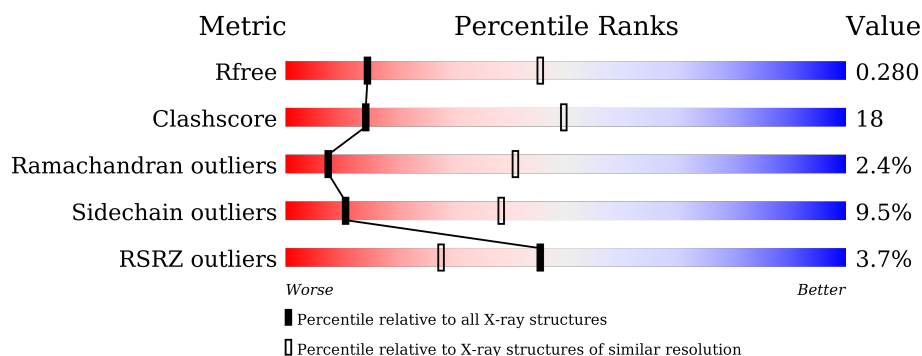
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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))
$R_{free}$	91344	1112 (3.20-3.12)
Clashscore	102246	1249 (3.20-3.12)
Ramachandran outliers	100387	1222 (3.20-3.12)
Sidechain outliers	100360	1221 (3.20-3.12)
RSRZ outliers	91569	1117 (3.20-3.12)

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	505	<div> <div>2%</div> <div>57%</div> <div>26%</div> <div>•</div> <div>13%</div> </div>
1	B	505	<div> <div>6%</div> <div>49%</div> <div>36%</div> <div>6%</div> <div>9%</div> </div>
1	C	505	<div> <div>%</div> <div>53%</div> <div>32%</div> <div>•</div> <div>11%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10593 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 3-octaprenyl-4-hydroxybenzoate carboxy-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	440	Total	C	N	O	S	0	0	0
			3451	2205	588	641	17			
1	B	461	Total	C	N	O	S	0	0	0
			3625	2318	617	673	17			
1	C	448	Total	C	N	O	S	0	0	0
			3517	2252	596	652	17			

There are 24 discrepancies between the modelled and reference sequences:

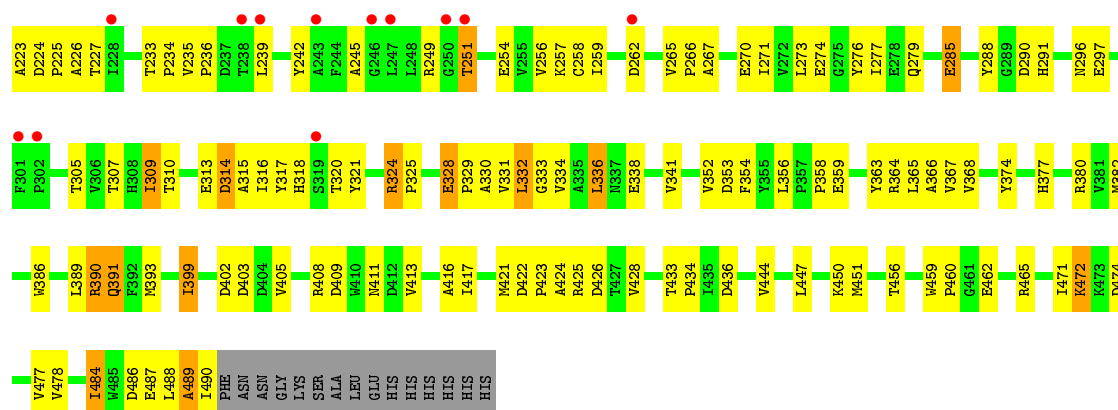
Chain	Residue	Modelled	Actual	Comment	Reference
A	498	LEU	-	expression tag	UNP P0AAB5
A	499	GLU	-	expression tag	UNP P0AAB5
A	500	HIS	-	expression tag	UNP P0AAB5
A	501	HIS	-	expression tag	UNP P0AAB5
A	502	HIS	-	expression tag	UNP P0AAB5
A	503	HIS	-	expression tag	UNP P0AAB5
A	504	HIS	-	expression tag	UNP P0AAB5
A	505	HIS	-	expression tag	UNP P0AAB5
B	498	LEU	-	expression tag	UNP P0AAB5
B	499	GLU	-	expression tag	UNP P0AAB5
B	500	HIS	-	expression tag	UNP P0AAB5
B	501	HIS	-	expression tag	UNP P0AAB5
B	502	HIS	-	expression tag	UNP P0AAB5
B	503	HIS	-	expression tag	UNP P0AAB5
B	504	HIS	-	expression tag	UNP P0AAB5
B	505	HIS	-	expression tag	UNP P0AAB5
C	498	LEU	-	expression tag	UNP P0AAB5
C	499	GLU	-	expression tag	UNP P0AAB5
C	500	HIS	-	expression tag	UNP P0AAB5
C	501	HIS	-	expression tag	UNP P0AAB5
C	502	HIS	-	expression tag	UNP P0AAB5
C	503	HIS	-	expression tag	UNP P0AAB5
C	504	HIS	-	expression tag	UNP P0AAB5

*Continued on next page...*

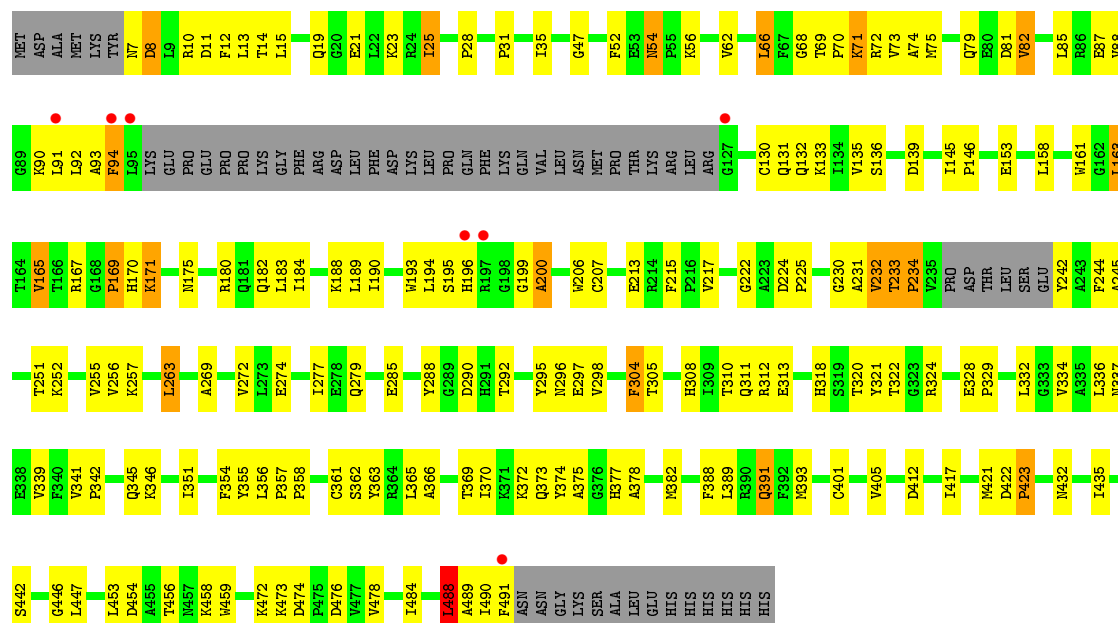
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	505	HIS	-	expression tag	UNP P0AAB5





● Molecule 1: 3-octaprenyl-4-hydroxybenzoate carboxy-lyase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	210.19Å 210.19Å 109.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.90 – 3.15 29.89 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.90-3.15) 100.0 (29.89-3.15)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.23 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.221 , 0.277 0.221 , 0.280	Depositor DCC
$R_{free}$ test set	2151 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.2	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 55.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	10593	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.91% 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](#)

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	0.54	0/3534	0.78	0/4812
1	B	0.55	0/3717	0.78	4/5065 (0.1%)
1	C	0.52	0/3606	0.77	2/4914 (0.0%)
All	All	0.54	0/10857	0.78	6/14791 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	C	488	LEU	CA-CB-CG	6.82	130.98	115.30
1	B	336	LEU	CA-CB-CG	5.96	129.01	115.30
1	C	66	LEU	CA-CB-CG	5.74	128.50	115.30
1	B	399	ILE	N-CA-C	-5.43	96.34	111.00
1	B	50	LEU	CA-CB-CG	5.37	127.64	115.30

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	3451	0	3425	125	0
1	B	3625	0	3594	153	0
1	C	3517	0	3475	122	0
All	All	10593	0	10494	382	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 382 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:90:LYS:HD2	1:A:339:VAL:HG13	1.27	1.12
1:A:25:ILE:HD12	1:A:52:PHE:CD1	1.87	1.08
1:C:93:ALA:HB3	1:C:346:LYS:NZ	1.70	1.06
1:C:135:VAL:HG13	1:C:139:ASP:HB3	1.43	0.98
1:A:27:LEU:HD23	1:A:28:PRO:HD2	1.49	0.95

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	432/505 (86%)	381 (88%)	40 (9%)	11 (2%)	7	39
1	B	457/505 (90%)	397 (87%)	49 (11%)	11 (2%)	7	41
1	C	442/505 (88%)	401 (91%)	31 (7%)	10 (2%)	8	42
All	All	1331/1515 (88%)	1179 (89%)	120 (9%)	32 (2%)	7	41

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	VAL
1	A	232	VAL
1	A	489	ALA
1	B	195	SER
1	B	489	ALA

### 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	371/430 (86%)	341 (92%)	30 (8%)	15	49
1	B	390/430 (91%)	345 (88%)	45 (12%)	7	29
1	C	377/430 (88%)	344 (91%)	33 (9%)	12	43
All	All	1138/1290 (88%)	1030 (90%)	108 (10%)	11	38

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	161	TRP
1	B	279	GLN
1	C	298	VAL
1	B	175	ASN
1	B	192	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	196	HIS
1	B	296	ASN
1	C	337	ASN
1	B	170	HIS
1	C	347	GLN

### 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	440/505 (87%)	-0.32	12 (2%) 58 42	29, 75, 144, 182	0
1	B	461/505 (91%)	0.12	31 (6%) 21 11	26, 115, 166, 244	2 (0%)
1	C	448/505 (88%)	-0.37	7 (1%) 74 61	31, 76, 135, 174	0
All	All	1349/1515 (89%)	-0.19	50 (3%) 45 28	26, 84, 153, 244	2 (0%)

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	ALA	6.6
1	C	95	LEU	5.7
1	B	238	THR	4.3
1	B	26	THR	4.1
1	C	491	PHE	3.9

### 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.