

# wwPDB X-ray Structure Validation Summary Report (i)

#### Oct 3, 2023 – 03:16 AM EDT

PDB ID	:	6OXD
Title	:	Structure of Mycobacterium tuberculosis methylmalonyl-CoA mutase with
		adenosyl cobalamin
Authors	:	Purchal, M.; Ruetz, M.; Banerjee, R.; Koutmos, M.
Deposited on		
Resolution	:	2.00 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
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)	:	2.35.1

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 21256 atoms, of which 9990 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 Methylmalonyl-CoA mutase large subunit.

Ν	/lol	Chain	Residues			Atom	ıs			ZeroOcc	AltConf	Trace
	1	А	736	Total 11127	$\begin{array}{c} \mathrm{C} \\ 3527 \end{array}$	Н 5528	N 996	O 1061	S 15	0	2	0

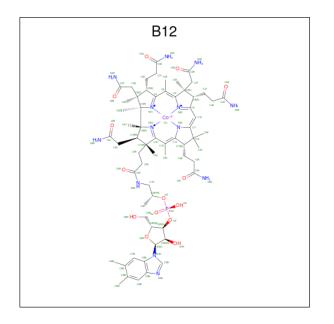
• Molecule 2 is a protein called Methylmalonyl-CoA mutase small subunit.

I	Mol	Chain	Residues			Atom	.s			ZeroOcc	AltConf	Trace
	2	В	590	Total 8746	C 2746	Н 4365	N 806	0 819	S 10	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Residue Modelled		Comment	Reference	
В	1	SER	-	expression tag	UNP A0A045IZR3	
В	2	VAL	MET	variant	UNP A0A045IZR3	

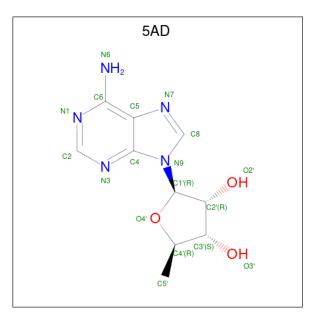
• Molecule 3 is COBALAMIN (three-letter code: B12) (formula:  $C_{62}H_{89}CoN_{13}O_{14}P$ ) (labeled as "Ligand of Interest" by depositor).





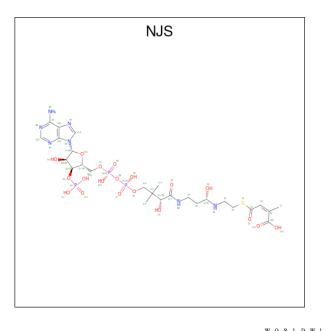
Mol	Chain	Residues		Atoms						ZeroOcc	AltConf
9	٨	1	Total	С	Co	Η	Ν	Ο	Р	0	0
3	А	1	177	62	1	86	13	14	1	0	U

• Molecule 4 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula:  $C_{10}H_{13}N_5O_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
4	٨	1	Total	С	Η	Ν	Ο	0	0
4	A	1	29	10	11	5	3	0	

• Molecule 5 is Itaconyl coenzyme A (three-letter code: NJS) (formula:  $C_{26}H_{42}N_7O_{19}P_3S$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Α	ton	ıs			ZeroOcc	AltConf
5	А	1	Total 56	C 26	N 7	O 19	Р 3	S 1	0	0

• Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total K 1 1	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	555	Total O 555 555	0	0
7	В	565	Total O 565 565	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



# 3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	76.58Å 104.96Å 194.09Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	29.80 - 2.00	Depositor
% Data completeness	97.9 (29.80-2.00)	Depositor
(in resolution range)		-
R <sub>merge</sub>	0.10	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.51 (at 2.00 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
$R, R_{free}$	0.159 , $0.197$	Depositor
Wilson B-factor $(Å^2)$	28.4	Xtriage
Anisotropy	0.320	Xtriage
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	21256	wwPDB-VP
Average B, all atoms $(Å^2)$	35.0	wwPDB-VP

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 4 Model quality (i)

## 4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles (i)

#### 4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 4.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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



Mol	Turne	Chain	Res	Link	Bo	nd lengt	$\mathbf{hs}$	Bond angles		
IVIOI	Type	Chain	res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
4	5AD	А	1001	5	$17,\!20,\!20$	4.45	7 (41%)	15,30,30	3.46	7 (46%)
5	NJS	А	1002	4	48,58,58	2.38	12 (25%)	61,86,86	2.32	14 (22%)
3	B12	А	1000	1	90,101,101	1.39	15 (16%)	137,166,166	2.74	33 (24%)

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).

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
4	5AD	А	1001	5	-	0/0/20/20	0/3/3/3
5	NJS	А	1002	4	-	11/53/75/75	0/3/3/3
3	B12	А	1000	1	-	7/52/223/223	0/3/11/11

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	А	1001	5AD	O4'-C1'	12.29	1.58	1.41
4	А	1001	5AD	C3'-C4'	9.11	1.65	1.52
5	А	1002	NJS	O12-C17	8.52	1.64	1.45
5	А	1002	NJS	C25-C17	-6.65	1.35	1.52
4	А	1001	5AD	C3'-C2'	-6.44	1.35	1.53

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
3	А	1000	B12	C20-C1-C19	-14.32	95.56	109.36
5	А	1002	NJS	C3-C4-S1	11.24	125.27	111.24
3	А	1000	B12	C20-C1-N21	-10.91	92.37	110.27
3	А	1000	B12	C19-C1-N21	8.14	110.50	102.16
5	А	1002	NJS	O1-C4-C3	-7.95	115.74	125.50

There are no chirality outliers.

 $5~{\rm of}~18$  torsion outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms
5	А	1002	NJS	C1-C2-C26-O18

Continued on next page...

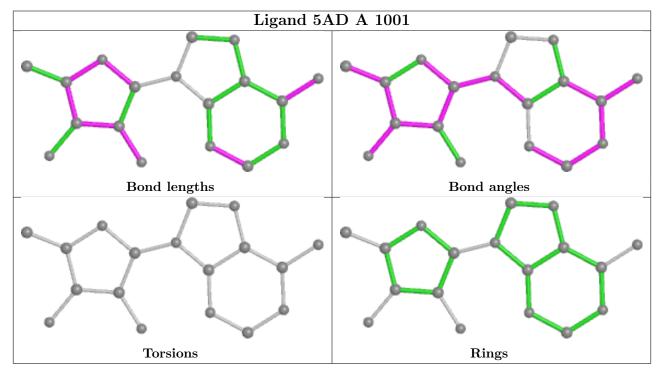
Mol	Chain	Res	Type	Atoms
5	А	1002	NJS	C1-C2-C26-O19
5	А	1002	NJS	C3-C4-S1-C5
5	А	1002	NJS	O1-C4-S1-C5
5	A	1002	NJS	O2-C7-C8-C9

Continued from previous page...

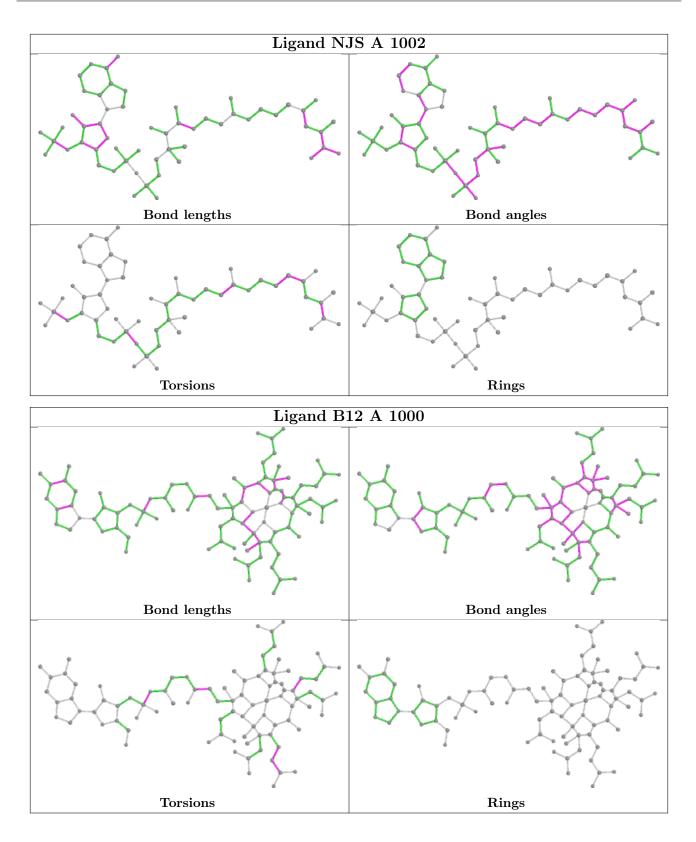
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and sufficient the outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 4.7 Other polymers (i)

There are no such residues in this entry.



## 4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 5 Fit of model and data (i)

## 5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

## 5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

## 5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

### 5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

