



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2023 – 03:49 AM EDT

PDB ID : 6UWW  
Title : Crystal structure of dihydrofolate reductase from Mycobacterium ulcerans with P218 inhibitor  
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2019-11-05  
Resolution : 0.92 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) 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

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 0.92 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

There are 5 unique types of molecules in this entry. The entry contains 1686 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.

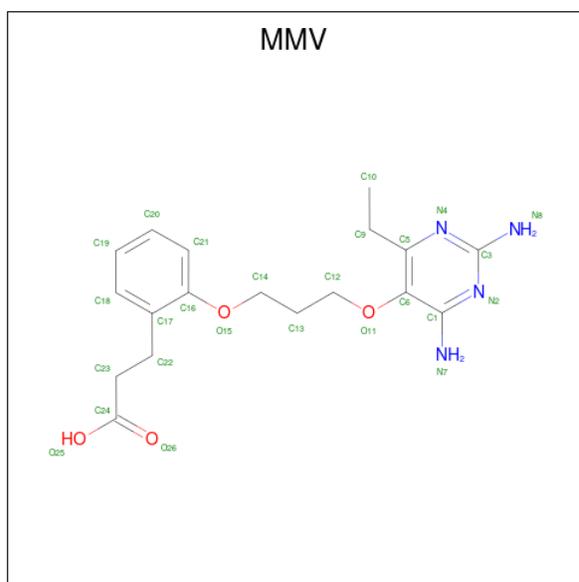
- Molecule 1 is a protein called Dihydrofolate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	163	1331	843	245	239	4	0	14	0

There are 9 discrepancies between the modelled and reference sequences:

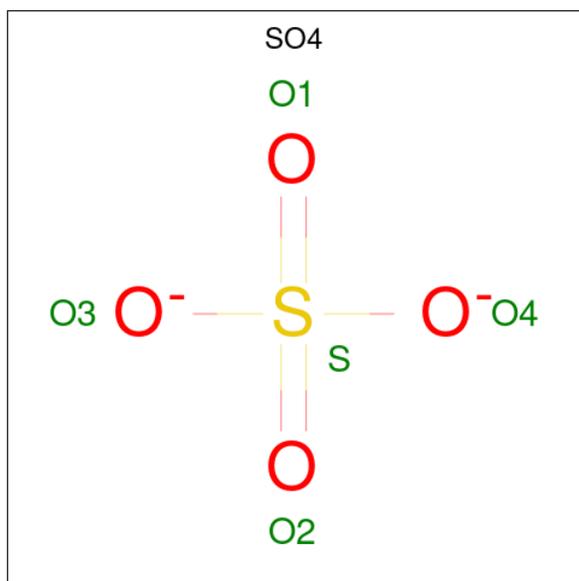
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A0PQG8
A	2	ALA	-	expression tag	UNP A0PQG8
A	3	HIS	-	expression tag	UNP A0PQG8
A	4	HIS	-	expression tag	UNP A0PQG8
A	5	HIS	-	expression tag	UNP A0PQG8
A	6	HIS	-	expression tag	UNP A0PQG8
A	7	HIS	-	expression tag	UNP A0PQG8
A	8	HIS	-	expression tag	UNP A0PQG8
A	97	SER	CYS	conflict	UNP A0PQG8

- Molecule 2 is 3-(2-{3-[(2,4-diamino-6-ethylpyrimidin-5-yl)oxy]propoxy}phenyl)propanoic acid (three-letter code: MMV) (formula: C<sub>18</sub>H<sub>24</sub>N<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	26	18	4	4	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE



### 3 Data and refinement statistics [i](#)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	28.73Å 66.20Å 44.52Å 90.00° 91.61° 90.00°	Depositor
Resolution (Å)	44.50 – 0.92	Depositor
% Data completeness (in resolution range)	98.1 (44.50-0.92)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 0.92Å)	Xtrriage
Refinement program	PHENIX 3423	Depositor
R, $R_{free}$	0.132 , 0.145	Depositor
Wilson B-factor (Å <sup>2</sup> )	8.8	Xtrriage
Anisotropy	0.221	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtrriage
Total number of atoms	1686	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.82% 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.

## 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](#)

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### 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](#)

4 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
4	NAP	A	304	-	45,52,52	2.88	9 (20%)	56,80,80	1.29	7 (12%)
3	SO4	A	302	-	4,4,4	0.13	0	6,6,6	0.05	0
3	SO4	A	303	-	4,4,4	0.14	0	6,6,6	0.05	0
2	MMV	A	301	-	26,27,27	1.12	2 (7%)	32,35,35	1.54	2 (6%)

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	NAP	A	304	-	-	4/31/67/67	0/5/5/5
2	MMV	A	301	-	-	2/15/15/15	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	304	NAP	C2D-C1D	-11.21	1.36	1.53
4	A	304	NAP	O4D-C1D	10.16	1.55	1.41
4	A	304	NAP	O4B-C1B	7.49	1.51	1.41
4	A	304	NAP	O4B-C4B	-4.25	1.35	1.45
4	A	304	NAP	O4D-C4D	-3.37	1.37	1.45
4	A	304	NAP	C7N-N7N	3.22	1.39	1.33
2	A	301	MMV	C3-N8	2.96	1.39	1.33
2	A	301	MMV	C1-N7	2.90	1.41	1.34
4	A	304	NAP	C6A-N6A	2.54	1.43	1.34
4	A	304	NAP	C2A-N1A	2.02	1.37	1.33
4	A	304	NAP	C5A-C4A	-2.01	1.35	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	MMV	C3-N4-C5	6.32	121.51	116.24
4	A	304	NAP	C5A-C6A-N6A	3.83	126.18	120.35
2	A	301	MMV	C6-C5-N4	-3.42	118.22	122.46
4	A	304	NAP	N3A-C2A-N1A	-3.42	123.33	128.68
4	A	304	NAP	O3B-C3B-C2B	2.64	118.67	111.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	304	NAP	C1B-N9A-C4A	-2.53	122.20	126.64
4	A	304	NAP	C3D-C2D-C1D	2.30	104.44	100.98
4	A	304	NAP	C2B-C3B-C4B	-2.28	97.03	101.99
4	A	304	NAP	O4D-C1D-C2D	-2.02	103.98	106.93

There are no chirality outliers.

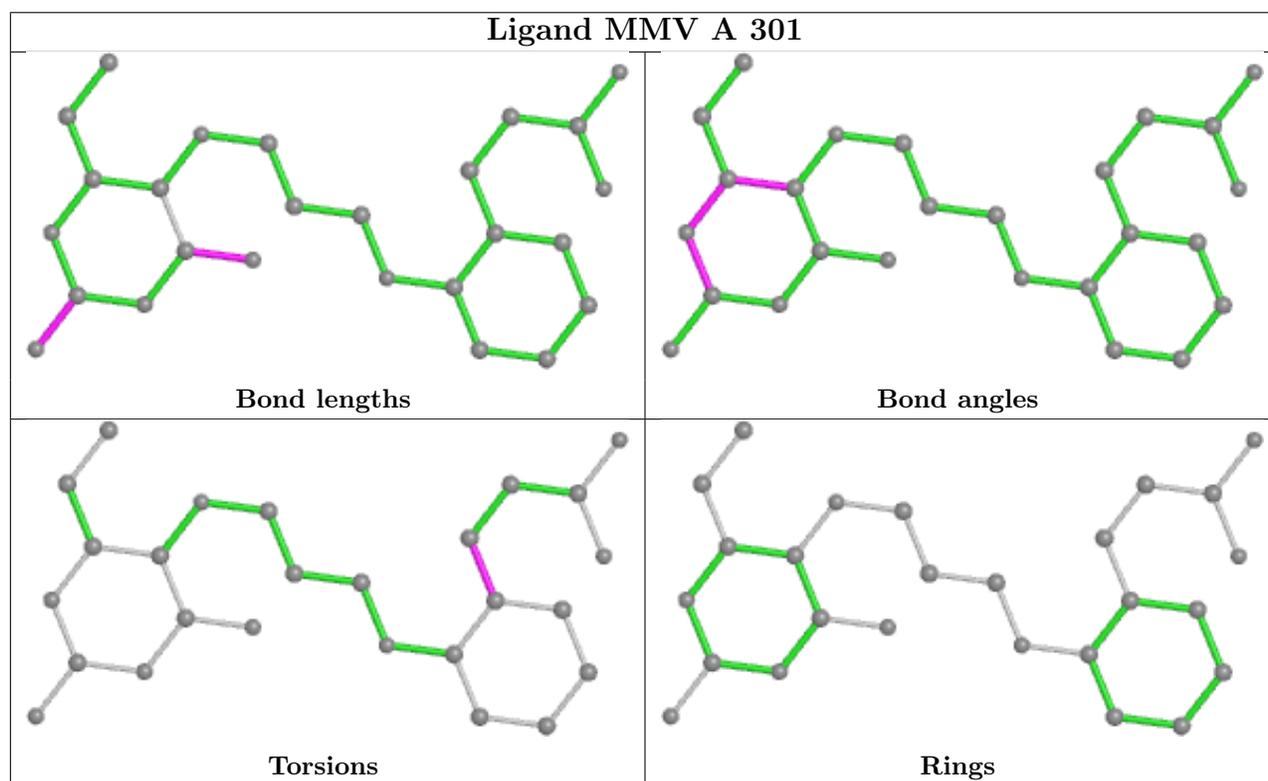
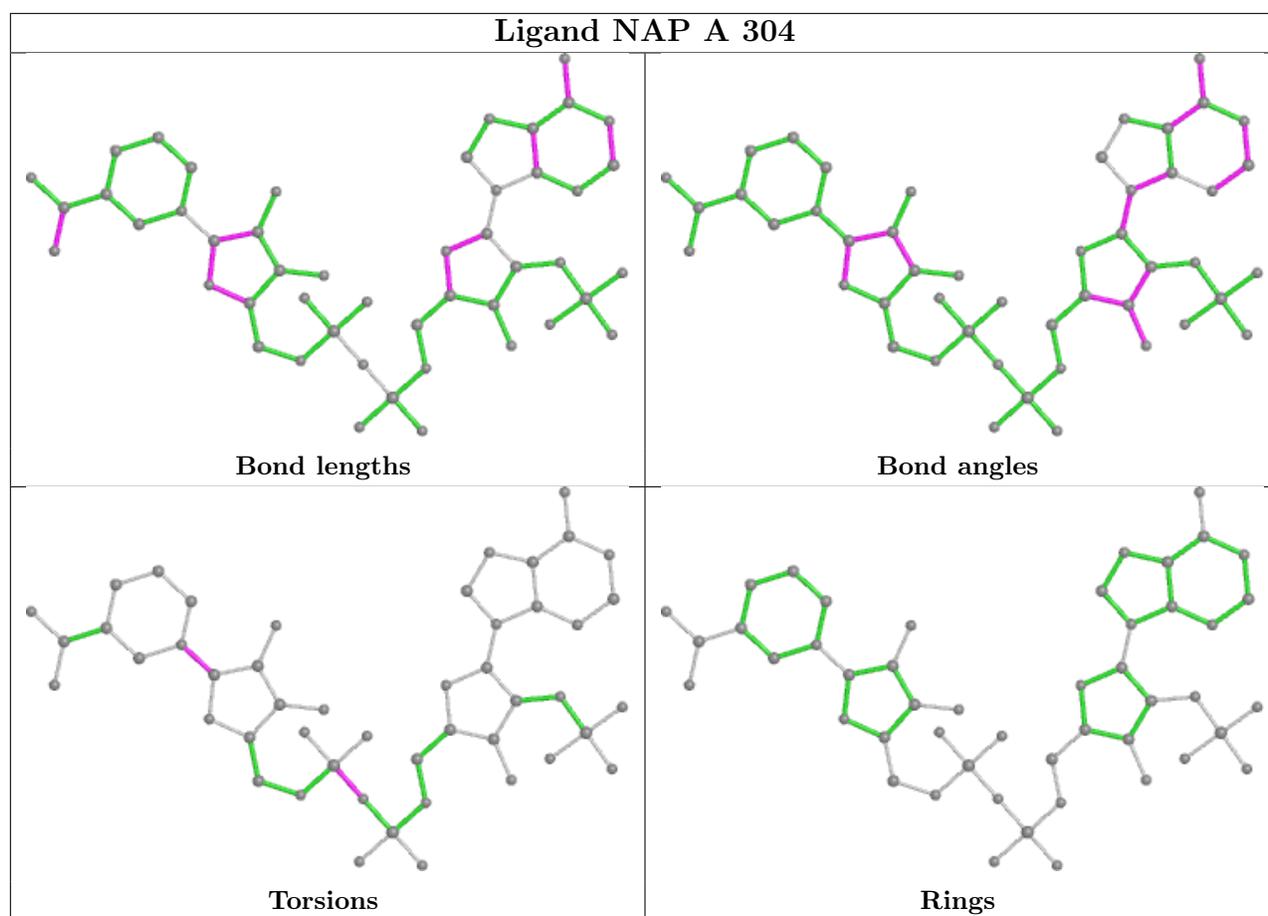
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	304	NAP	O4D-C1D-N1N-C2N
4	A	304	NAP	O4D-C1D-N1N-C6N
2	A	301	MMV	C18-C17-C22-C23
4	A	304	NAP	PA-O3-PN-O5D
2	A	301	MMV	C16-C17-C22-C23
4	A	304	NAP	C2D-C1D-N1N-C2N

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 than 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 any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. 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

### 5.1 Protein, DNA and RNA chains

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

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

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

### 5.3 Carbohydrates

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

### 5.4 Ligands

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

### 5.5 Other polymers

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