



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:06 pm BST

PDB ID : 6OVQ
Title : Crystal structure of mithramycin 3-side chain keto-reductase MtmW
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Deposited on : 2019-05-08
Resolution : 1.80 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

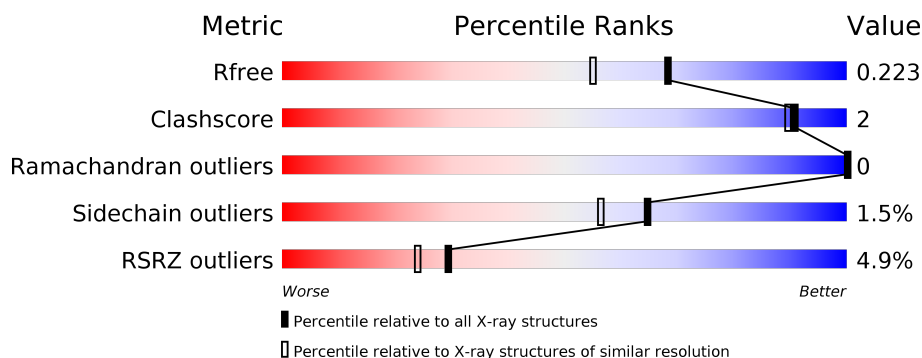
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	333	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	333	<div> <div>7%</div> <div> <div></div> <div>79%</div> <div>6%</div> <div>15%</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4845 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 Putative Side chain reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	302	Total	C	N	O	S	0	1	0
			2306	1456	408	429	13			
1	B	284	Total	C	N	O	S	0	0	0
			2153	1355	381	405	12			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	205	Total 205	O 205	0	0
3	B	169	Total 169	O 169	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	131.10Å 131.10Å 79.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.00 – 1.80 33.09 – 1.79	Depositor EDS
% Data completeness (in resolution range)	97.6 (33.00-1.80) 97.4 (33.09-1.79)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.184 , 0.213 0.194 , 0.223	Depositor DCC
R_{free} test set	3130 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.014 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4845	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL

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	0.66	0/2356	0.74	0/3196
1	B	0.66	0/2188	0.72	0/2966
All	All	0.66	0/4544	0.73	0/6162

There are no bond length outliers.

There are no bond angle outliers.

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	2306	0	2311	7	0
1	B	2153	0	2161	9	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0
3	A	205	0	0	2	0
3	B	169	0	0	1	0
All	All	4845	0	4488	15	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 2.

All (15) 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:101:HIS:HE1	3:A:522:HOH:O	1.87	0.56
1:B:101:HIS:HE1	3:B:542:HOH:O	1.88	0.56
1:B:258:LEU:HD11	1:B:319:LEU:HD11	1.90	0.54
1:A:46:ALA:HB2	1:A:297:LEU:HD23	1.90	0.54
1:A:244:ARG:HD2	3:A:548:HOH:O	2.12	0.49
1:B:188:ALA:N	1:B:189:PRO:HD2	2.28	0.48
1:B:32:PRO:O	1:B:35:VAL:HG12	2.14	0.47
1:A:184:MET:HG2	1:A:276:TRP:CG	2.50	0.46
1:A:309:THR:HG21	1:B:309:THR:HG21	1.97	0.45
1:B:53:THR:HG21	1:B:63:GLU:HG3	1.97	0.45
1:B:46:ALA:HB2	1:B:297:LEU:HD23	1.99	0.44
1:B:314:ARG:O	1:B:318:VAL:HG23	2.18	0.44
1:A:188:ALA:N	1:A:189:PRO:HD2	2.32	0.43
1:B:80:LEU:HD12	1:B:115:VAL:HG11	2.01	0.43

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	297/333 (89%)	291 (98%)	6 (2%)	0	100	100
1	B	276/333 (83%)	271 (98%)	5 (2%)	0	100	100
All	All	573/666 (86%)	562 (98%)	11 (2%)	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	244/268 (91%)	241 (99%)	3 (1%)	71	65
1	B	228/268 (85%)	224 (98%)	4 (2%)	59	48
All	All	472/536 (88%)	465 (98%)	7 (2%)	65	56

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	ARG
1	A	243	ARG
1	A	311	LEU
1	B	59	MET
1	B	121	TYR
1	B	144	ARG
1	B	311	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	HIS
1	A	212	GLN
1	B	101	HIS

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	GOL	B	401	-	5,5,5	0.09	0	5,5,5	0.28	0
2	GOL	A	401	-	5,5,5	0.06	0	5,5,5	0.34	0

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	GOL	B	401	-	-	2/4/4/4	-
2	GOL	A	401	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GOL	O1-C1-C2-C3
2	A	401	GOL	C1-C2-C3-O3
2	A	401	GOL	O1-C1-C2-O2
2	A	401	GOL	O2-C2-C3-O3
2	B	401	GOL	O1-C1-C2-O2
2	B	401	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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 ²)	Q<0.9
1	A	302/333 (90%)	0.05	7 (2%) 60 56	17, 28, 48, 62	0
1	B	284/333 (85%)	0.42	22 (7%) 13 10	19, 31, 60, 92	0
All	All	586/666 (87%)	0.23	29 (4%) 29 24	17, 29, 57, 92	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	90	PHE	4.4
1	B	57	TYR	4.2
1	B	265	ALA	4.0
1	B	259	ARG	3.9
1	B	264	GLU	3.7
1	B	249	ASP	3.6
1	B	248	ASP	3.5
1	B	310	ASP	3.3
1	B	24	LEU	3.3
1	B	266	GLY	3.2
1	A	205	ILE	3.2
1	B	217	GLY	3.2
1	B	250	LYS	3.1
1	B	291	PHE	3.1
1	B	263	GLU	3.0
1	A	59	MET	3.0
1	B	321	ASP	2.9
1	B	35	VAL	2.8
1	A	244	ARG	2.8
1	B	54	ALA	2.7
1	B	314	ARG	2.7
1	B	313	VAL	2.6
1	A	56	VAL	2.4
1	B	261	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	294	GLU	2.4
1	B	125	ARG	2.3
1	B	205	ILE	2.2
1	A	120	VAL	2.1
1	A	240	PRO	2.1

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. The B-factors column lists the minimum, median, 95th 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	B-factors(\AA^2)	Q<0.9
2	GOL	B	401	6/6	0.76	0.17	35,39,42,48	0
2	GOL	A	401	6/6	0.89	0.12	35,37,39,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.