



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:40 AM GMT

PDB ID : 4EYB
Title : Crystal structure of NDM-1 bound to hydrolyzed oxacillin
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Deposited on : 2012-05-01
Resolution : 1.16 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

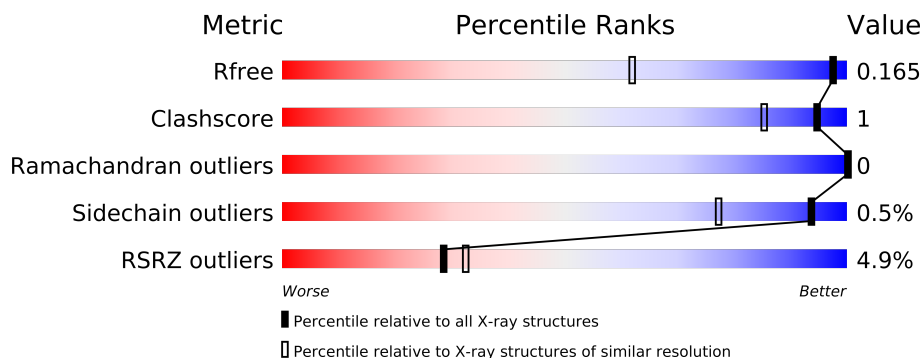
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.16 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}	66092	1042 (1.22-1.10)
Clashscore	79885	1154 (1.22-1.10)
Ramachandran outliers	78287	1097 (1.22-1.10)
Sidechain outliers	78261	1093 (1.22-1.10)
RSRZ outliers	66119	1042 (1.22-1.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	270	
1	B	270	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4076 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

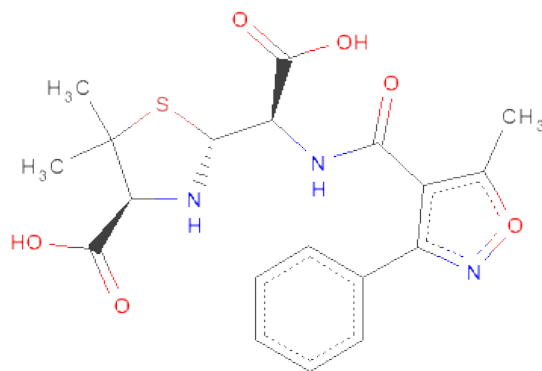
- Molecule 1 is a protein called Beta-lactamase NDM-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	2	0
			1807	1135	321	342	9			
1	B	241	Total	C	N	O	S	0	1	0
			1801	1131	320	341	9			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Zn	0	0
			3	3		
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is (2R,4S)-2-[(R)-CARBOXY{[(5-METHYL-3-PHENYL-1,2-OXAZOL-4-YL) CARBONYL]AMINO}METHYL]-5,5-DIMETHYL-1,3-THIAZOLIDINE-4-CARBOXYLIC ACID (three-letter code: 0WO) (formula: C₁₉H₂₁N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 29	C 19	N 3	O 6	S 1	0	0
3	B	1	Total 29	C 19	N 3	O 6	S 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	217	Total 217	O 217	0	0
4	B	188	Total 188	O 188	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	39.20Å 79.37Å 134.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.42 – 1.16 25.42 – 1.16	Depositor EDS
% Data completeness (in resolution range)	99.5 (25.42-1.16) 99.5 (25.42-1.16)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 1.17Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.135 , 0.164 0.135 , 0.165	Depositor DCC
R_{free} test set	7157 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	9.4	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 43.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 142967 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	4076	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 0WO, ZN

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	0.90	0/1854	1.11	9/2524 (0.4%)
1	B	0.88	1/1845 (0.1%)	1.06	5/2512 (0.2%)
All	All	0.89	1/3699 (0.0%)	1.09	14/5036 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	227	GLU	CG-CD	5.47	1.60	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	85	ARG	NE-CZ-NH2	-10.90	114.85	120.30
1	A	43	ASP	CB-CG-OD1	10.29	127.56	118.30
1	A	211	LYS	CD-CE-NZ	8.69	131.69	111.70
1	A	90	ASP	CB-CG-OD1	8.15	125.64	118.30
1	B	85	ARG	NE-CZ-NH1	7.26	123.93	120.30
1	A	264	ARG	NE-CZ-NH2	-6.83	116.88	120.30
1	B	177	PHE	CB-CG-CD1	6.83	125.58	120.80
1	A	211	LYS	CG-CD-CE	6.52	131.46	111.90
1	A	130	ASP	CB-CG-OD1	6.29	123.96	118.30
1	A	154	MET	CG-SD-CE	5.83	109.52	100.20
1	A	126	MET	CG-SD-CE	5.81	109.49	100.20
1	A	124	ASP	CB-CG-OD2	-5.08	113.73	118.30
1	B	229	TYR	CB-CG-CD2	5.05	124.03	121.00
1	B	260	THR	OG1-CB-CG2	-5.04	98.41	110.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1807	0	0	4	0
1	B	1801	0	0	1	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
3	A	29	0	0	1	0
3	B	29	0	0	0	0
4	A	217	0	0	3	0
4	B	188	0	0	0	0
All	All	4076	0	0	5	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (5) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:35:ILE:CD1	1:B:35:ILE:CD1	2.64	0.74
1:A:216:LYS:NZ	4:A:617:HOH:O	2.22	0.71
1:A:39:MET:SD	4:A:542:HOH:O	2.53	0.65
1:A:152:GLU:CG	4:A:599:HOH:O	2.47	0.62
3:A:303:OWO:CAU	3:A:303:OWO:CAL	2.95	0.42

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	241/270 (89%)	237 (98%)	4 (2%)	0	100	100
1	B	240/270 (89%)	236 (98%)	4 (2%)	0	100	100
All	All	481/540 (89%)	473 (98%)	8 (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	184/204 (90%)	183 (100%)	1 (0%)	94	77
1	B	183/204 (90%)	182 (100%)	1 (0%)	94	77
All	All	367/408 (90%)	365 (100%)	2 (0%)	94	77

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	229	TYR
1	B	229	TYR

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 chains 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

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 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 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
3	OWO	A	303	2	31,31,31	1.34	6 (19%)	44,46,46	2.10	15 (34%)
3	OWO	B	301	2	31,31,31	1.82	6 (19%)	44,46,46	1.98	14 (31%)

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
3	OWO	A	303	2	-	2/21/39/39	0/3/3/3
3	OWO	B	301	2	-	2/21/39/39	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	OWO	OAQ-NAN	6.36	1.47	1.42
3	B	301	OWO	CB-NAP	3.51	1.48	1.45
3	A	303	OWO	CB-NAP	3.13	1.48	1.45
3	B	301	OWO	CAY-CAX	-3.08	1.38	1.41
3	A	303	OWO	CBC-SAR	-3.04	1.79	1.85
3	B	301	OWO	CBC-SAR	-2.58	1.80	1.85
3	B	301	OWO	CA-C	-2.57	1.48	1.52
3	A	303	OWO	CAY-CAX	-2.55	1.39	1.41
3	A	303	OWO	CAY-CAU	-2.55	1.46	1.50
3	B	301	OWO	CAY-CAU	-2.40	1.46	1.50
3	A	303	OWO	OAQ-NAN	2.20	1.44	1.42
3	A	303	OWO	CB-CA	2.03	1.59	1.54

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	301	OWO	CAW-CAX-NAN	5.37	130.29	119.61
3	A	303	OWO	CAW-CAX-NAN	5.14	129.84	119.61
3	A	303	OWO	CBC-CBB-CAT	5.03	119.59	112.55
3	B	301	OWO	CAY-CAX-CAW	-4.76	122.83	127.89
3	B	301	OWO	CAV-OAQ-NAN	4.73	109.20	107.66
3	A	303	OWO	CAL-CAW-CAX	-4.64	113.49	120.56
3	A	303	OWO	OAQ-NAN-CAX	4.24	108.77	105.68
3	A	303	OWO	CAY-CAX-CAW	-4.04	123.59	127.89
3	A	303	OWO	OAQ-CAV-CAA	3.42	124.05	117.16
3	A	303	OWO	CAM-CAW-CAX	3.09	125.26	120.56
3	B	301	OWO	CAX-CAY-CAV	3.05	111.94	106.91
3	B	301	OWO	CBC-CBB-CAT	2.87	116.57	112.55
3	A	303	OWO	CBB-CBC-SAR	-2.69	99.24	104.00
3	B	301	OWO	CAK-CAM-CAW	-2.66	116.91	120.56
3	B	301	OWO	CBB-CBC-SAR	-2.61	99.38	104.00
3	A	303	OWO	CAV-OAQ-NAN	2.53	108.49	107.66
3	B	301	OWO	OAQ-CAV-CAA	2.46	122.13	117.16
3	B	301	OWO	CAC-CBC-SAR	2.41	113.24	109.15
3	A	303	OWO	CB-CA-C	2.36	114.89	110.77
3	B	301	OWO	OAQ-NAN-CAX	2.33	107.38	105.68
3	B	301	OWO	CAM-CAW-CAL	2.31	121.88	117.58
3	B	301	OWO	O-C-OXT	-2.26	118.96	124.07
3	A	303	OWO	CAY-CAX-NAN	-2.26	106.32	111.65
3	A	303	OWO	O-C-OXT	-2.21	119.07	124.07
3	A	303	OWO	CAB-CBC-SAR	2.17	112.83	109.15
3	A	303	OWO	CAX-CAY-CAV	2.04	110.27	106.91
3	B	301	OWO	CAY-CAX-NAN	-2.03	106.85	111.65
3	A	303	OWO	CAK-CAM-CAW	-2.02	117.78	120.56
3	B	301	OWO	CB-CA-N	-2.00	105.23	109.11

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	OWO	CAV-CAY-CAU-N
3	A	303	OWO	OAF-CAU-CAY-CAV
3	B	301	OWO	OAF-CAU-CAY-CAV
3	B	301	OWO	CAV-CAY-CAU-N

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	241/270 (89%)	0.09	12 (4%) 28 31	6, 9, 25, 46	0
1	B	241/270 (89%)	0.10	12 (4%) 28 31	6, 11, 27, 67	0
All	All	482/540 (89%)	0.09	24 (4%) 28 31	6, 10, 26, 67	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	41	THR	7.2
1	A	31	ILE	6.2
1	B	41	THR	6.1
1	A	42	GLY	5.1
1	B	42	GLY	4.3
1	B	31	ILE	4.0
1	A	30	GLU	3.9
1	A	40	GLU	3.9
1	B	68	PRO	3.6
1	B	39	MET	3.6
1	B	30	GLU	3.0
1	A	39	MET	2.8
1	A	68	PRO	2.7
1	A	269	LEU	2.7
1	B	40	GLU	2.6
1	B	32	ARG	2.5
1	B	83	GLY	2.4
1	A	66	ASP	2.4
1	B	33	PRO	2.4
1	B	38	GLN	2.3
1	A	32	ARG	2.3
1	B	36	GLY	2.1
1	A	270	ARG	2.1
1	A	176	ASN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	OWO	A	303	29/29	0.10	0.36	8,11,23,25	0
3	OWO	B	301	29/29	0.08	0.29	8,11,23,25	0
2	ZN	B	304	1/1	0.06	-0.60	12,12,12,12	1
2	ZN	A	301	1/1	0.03	-1.88	7,7,7,7	0
2	ZN	B	303	1/1	0.04	-3.04	7,7,7,7	0
2	ZN	A	302	1/1	0.03	-3.47	7,7,7,7	0
2	ZN	B	302	1/1	0.03	-4.99	7,7,7,7	0

6.5 Other polymers

There are no such residues in this entry.