

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

May 25, 2020 – 05:31 am BST

PDB ID 5FDH

> Title : CRYSTAL STRUCTURE OF OXA-405 BETA-LACTAMASE

Authors Retailleau, P.; Oueslati, S.; Marchini, L.; Dortet, L.; Naas, T.; Iorga, B.

2015-12-16 Deposited on

2.26 Å(reported) Resolution

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

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

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) Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

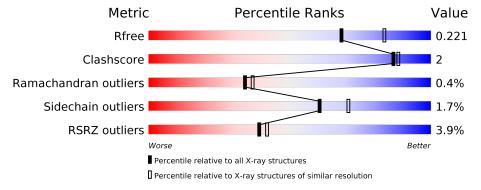
Validation Pipeline (wwPDB-VP) 2.11

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 <=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	250	89%	7% •	
1	В	250	91%	5% • •	



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4482 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 Beta-lactamase.

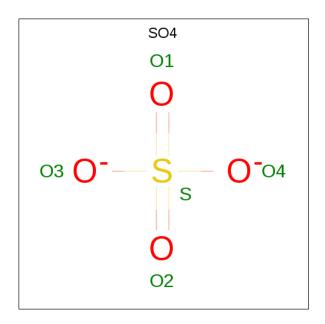
$\mathbf{Mol}$	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	A	242	Total 1985	C 1266	N 349	O 363	S 7	0	1	0
1	В	242	Total 1991	C 1270	Δ.1	O 364	S 7	0	2	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	MET	=	initiating methionine	UNP A0A0F6P2I5
A	266	LEU	=	expression tag	UNP A0A0F6P2I5
A	267	GLU	-	expression tag	UNP A0A0F6P2I5
A	268	HIS	ı	expression tag	UNP A0A0F6P2I5
A	269	HIS	I	expression tag	UNP A0A0F6P2I5
A	270	HIS	1	expression tag	UNP A0A0F6P2I5
A	271	HIS	1	expression tag	UNP A0A0F6P2I5
A	272	HIS	-	expression tag	UNP A0A0F6P2I5
A	273	HIS	-	expression tag	UNP A0A0F6P2I5
A	274	HIS	-	expression tag	UNP A0A0F6P2I5
A	275	HIS	1	expression tag	UNP A0A0F6P2I5
В	22	MET	-	initiating methionine	UNP A0A0F6P2I5
В	266	LEU	1	expression tag	UNP A0A0F6P2I5
В	267	GLU	-	expression tag	UNP A0A0F6P2I5
В	268	HIS	-	expression tag	UNP A0A0F6P2I5
В	269	HIS	-	expression tag	UNP A0A0F6P2I5
В	270	HIS	-	expression tag	UNP A0A0F6P2I5
В	271	HIS	-	expression tag	UNP A0A0F6P2I5
В	272	HIS	=	expression tag	UNP A0A0F6P2I5
В	273	HIS	=	expression tag	UNP A0A0F6P2I5
В	274	HIS	=	expression tag	UNP A0A0F6P2I5
В	275	HIS	-	expression tag	UNP A0A0F6P2I5

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).

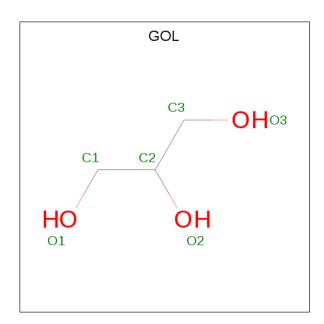




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S	0	0
	11	1	5 4 1	0	U
2	A	1	Total O S	0	0
	11		5 4 1		0
2	A	1	Total O S	0	0
			5 4 1		
2	A	1	Total O S	0	0
			5 4 1		
2	A	1	Total O S	0	0
			5 4 1 Total O S		
2	A	1	Total O S 5 4 1	0	0
			Total O S		
2	A	1	5 4 1	0	0
			Total O S		
2	A	1	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0	0
	D	1	Total O S	0	0
2	В	1	5 4 1	0	0
2	В	1	Total O S	0	0
	Б	1	5 4 1	0	U
2	В	1	Total O S	0	0
	D	1	5 4 1	U	U
$\frac{1}{2}$	В	1	Total O S	0	0
		<u> </u>	5 4 1		

 $\bullet$  Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $\mathrm{C_3H_8O_3}).$ 





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O	0	0
	Α.	7	Total C O	0	0
3	A	1	6 3 3	U	U

## • Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	221	Total O 221 221	0	0
4	В	213	Total O 213 213	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Beta-lactamase

• Molecule 1: Beta-lactamase

• Molecule 1: Beta-lactamase

Chain B:

• Molecule 1: Beta-lactamase



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	90.40Å 90.40Å 172.63Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	13.12 - 2.26	Depositor
resolution (A)	13.12 - 2.26	EDS
% Data completeness	98.0 (13.12-2.26)	Depositor
(in resolution range)	98.4 (13.12-2.26)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$< I/\sigma(I) > 1$	2.05 (at 2.26Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
P. P.	0.175 , $0.213$	Depositor
$R, R_{free}$	0.179 , $0.221$	DCC
$R_{free}$ test set	1671 reflections $(5.00\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.1	Xtriage
Anisotropy	0.611	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 61.9	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4482	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.14% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $< L^2>$  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.

## 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, SO4, KCX

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		
MIOI		RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.51	0/2025	0.66	0/2739	
1	В	0.49	0/2034	0.68	0/2751	
All	All	0.50	0/4059	0.67	0/5490	

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	1985	0	1935	9	0
1	В	1991	0	1943	8	0
2	A	40	0	0	0	0
2	В	20	0	0	0	0
3	A	12	0	16	2	0
4	A	221	0	0	0	0
4	В	213	0	0	2	0
All	All	4482	0	3894	17	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.



The worst 5 of 17 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} & ( ext{Å}) \end{aligned}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ ( ext{Å}) \end{aligned}$
1:A:184:SER:OG	3:A:309:GOL:H32	1.83	0.78
1:B:160:GLY:HA3	4:B:417:HOH:O	1.85	0.77
1:A:186:ARG:HD3	3:A:309:GOL:H31	1.70	0.74
1:B:70:SER:HB3	1:B:73:KCX:HZ	1.72	0.54
1:B:31:TRP:HB2	1:B:57:ASN:HB3	1.91	0.53

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	Perce	$\mathbf{ntiles}$
1	A	$240/250 \ (96\%)$	232 (97%)	7 (3%)	1 (0%)	34	37
1	В	241/250 (96%)	230 (95%)	10 (4%)	1 (0%)	34	37
All	All	481/500 (96%)	462 (96%)	17 (4%)	2 (0%)	34	37

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	A	214	LYS	
1	В	213	PRO	

#### 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	210/218 (96%)	207 (99%)	3 (1%)	67 76		
1	В	211/218 (97%)	207 (98%)	4 (2%)	57 66		
All	All	421/436 (97%)	414 (98%)	7 (2%)	60 71		

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	67	LEU
1	В	158	LEU
1	В	70	SER
1	A	70	SER
1	В	115	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	Tuna	Chain	Res	les Link Bond lengths				В	ond ang	gles
WIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	KCX	A	73	1	7,11,12	0.68	0	4,12,14	0.97	0
1	KCX	В	73	1	7,11,12	0.80	0	4,12,14	1.71	1 (25%)

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	${f Res}$	Link	Chirals	Torsions	Rings
1	KCX	A	73	1	_	1/7/10/12	_
1	KCX	В	73	1	_	0/7/10/12	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

$\mathbf{Mol}$	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^o)$
1	В	73	KCX	CD-CE-NZ	-2.64	104.38	111.49

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	73	KCX	CG-CD-CE-NZ

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	В	73	KCX	1	0

## 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry (i)

14 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	Т	Chain	Res Link		B	ond leng	$\operatorname{gths}$	E	ond ang	gles
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	В	302	_	4,4,4	0.12	0	6,6,6	0.26	0
2	SO4	A	304	-	4,4,4	0.45	0	6,6,6	0.24	0



Mol	Т	Chain	Res	Link	В	ond leng	$\operatorname{gths}$	В	ond ang	gles
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	A	303	_	4,4,4	0.26	0	6,6,6	0.16	0
3	GOL	A	310	-	5,5,5	0.12	0	5, 5, 5	0.24	0
2	SO4	В	301	-	4,4,4	0.26	0	6,6,6	0.29	0
2	SO4	A	301	-	4,4,4	0.35	0	6,6,6	0.69	0
2	SO4	A	305	_	4,4,4	0.21	0	6,6,6	0.15	0
2	SO4	В	304	-	4,4,4	0.11	0	6,6,6	0.13	0
2	SO4	A	302	-	4,4,4	0.42	0	6,6,6	0.44	0
2	SO4	В	303	-	4,4,4	0.19	0	6,6,6	0.15	0
2	SO4	A	306	-	4,4,4	0.18	0	6,6,6	0.17	0
3	GOL	A	309	-	5,5,5	0.16	0	5,5,5	0.43	0
2	SO4	A	308	-	4,4,4	0.31	0	6,6,6	0.11	0
2	SO4	A	307	-	4,4,4	0.15	0	6,6,6	0.11	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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
3	GOL	A	309	-	-	2/4/4/4	-
3	GOL	A	310	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	310	GOL	C1-C2-C3-O3
3	A	309	GOL	O1-C1-C2-C3
3	A	310	GOL	O2-C2-C3-O3
3	A	309	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes		
3	A	309	GOL	2	0		



## 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,  $95^{th}$  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	${f Analysed}$	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB( m \AA^2)$	Q<0.9
1	A	241/250 (96%)	-0.34	11 (4%) 32 35	21, 34, 64, 102	0
1	В	$241/250 \ (96\%)$	-0.34	8 (3%) 46 48	22, 35, 62, 121	0
All	All	482/500 (96%)	-0.34	19 (3%) 39 42	21, 35, 64, 121	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	${f Res}$	Type	RSRZ
1	A	244	SER	5.2
1	В	22	MET	4.4
1	A	242	PRO	4.1
1	A	39	LYS	3.6
1	A	243	THR	3.5

## 6.2 Non-standard residues in protein, DNA, RNA chains (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,  $95^{th}$  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	${f Res}$	Atoms	RSCC	RSR	${f B-factors(\AA^2)}$	Q<0.9
1	KCX	В	73	12/13	0.89	0.17	27,32,53,56	0
1	KCX	A	73	12/13	0.93	0.12	25,30,50,56	0

## 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,  $95^{th}$  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	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
3	GOL	A	310	6/6	0.75	0.20	52,60,60,61	0
2	SO4	A	305	5/5	0.83	0.23	47,50,52,53	5
3	GOL	A	309	6/6	0.86	0.17	50,51,52,52	0
2	SO4	A	306	5/5	0.89	0.16	$61,\!63,\!63,\!63$	5
2	SO4	В	303	5/5	0.89	0.18	44,46,47,47	5
2	SO4	В	304	5/5	0.92	0.14	42,45,45,46	5
2	SO4	В	302	5/5	0.93	0.13	45,47,50,50	4
2	SO4	A	303	5/5	0.93	0.17	37,41,43,49	5
2	SO4	A	302	5/5	0.94	0.21	50,56,59,62	0
2	SO4	A	308	5/5	0.94	0.16	39,43,44,46	5
2	SO4	A	307	5/5	0.95	0.17	49,49,51,52	5
2	SO4	A	304	5/5	0.97	0.13	25,30,32,34	5
2	SO4	В	301	5/5	0.99	0.09	41,44,45,48	0
2	SO4	A	301	5/5	0.99	0.06	24,27,28,29	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

