

wwPDB X-ray Structure Validation Summary Report (i)

May 15, 2020 – 05:56 am BST

PDB ID : 5EOE

Title : Crystal structure of extended-spectrum beta-lactamase BEL-1 (orthorhombic

form)

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Deposited on : 2015-11-10

Resolution : 1.60 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 following versions of software and data (see references (1)) 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) oteins) : Engh & Huber (2001

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

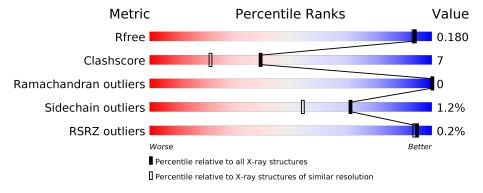
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	263	92%	8%		
1	В	263	90%	9% •		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	1PE	A	304	-	-	X	-
6	IPA	A	305	-	-	X	-
7	MRD	A	306	-	-	X	-
8	PGE	В	304	-	-	X	-



2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 5139 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.

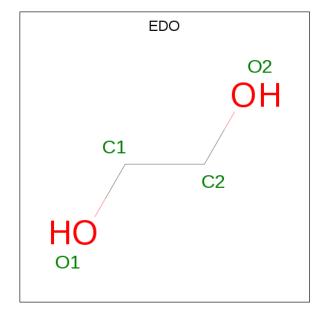
• Molecule 1 is a protein called Beta-lactamase.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	А	263	Total	С	Τ,	О	S	0	20	0
	11	200	2115	1336	362	409	8		20	
1	D	261	Total	С	N	О	S	0	22	0
1	Б	201	2138	1348	378	404	8	U		U

• Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	4	Total Cl 4 4	0	0
2	A	2	Total Cl 2 2	0	0

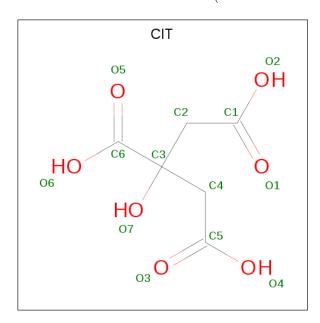
• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0

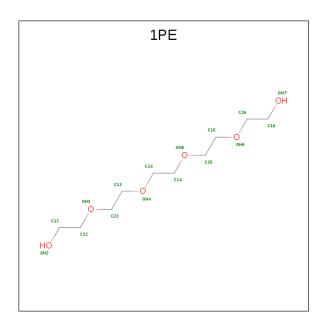
 \bullet Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: $\mathrm{C_6H_8O_7}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 6 7	0	0
4	В	1	Total C O 13 6 7	0	0

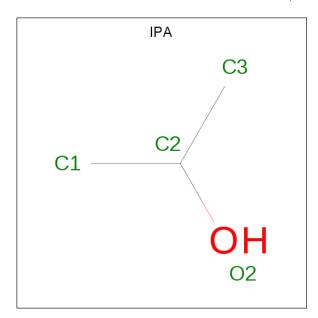
• Molecule 5 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
5	A	1	Total 16	C 10	O 6	0	0

• Molecule 6 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C₃H₈O).

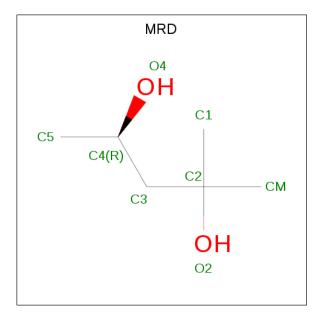


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 3 1	0	0
6	В	1	Total C O 4 3 1	0	0

 \bullet Molecule 7 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula:

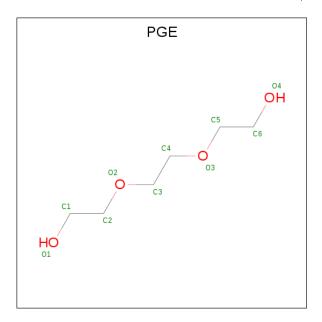


 $C_6H_{14}O_2$).



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

 \bullet Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $\mathrm{C_6H_{14}O_4}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	В	1	Total C O 10 6 4	0	0

• Molecule 9 is water.



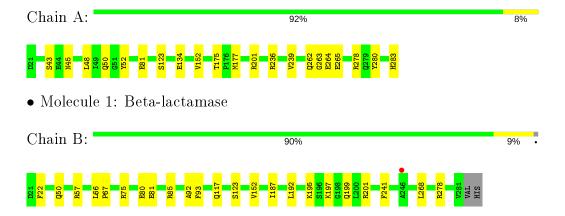
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	381	Total O 381 381	0	0
9	В	419	Total O 419 419	0	0



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





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	100.27Å 120.92Å 53.41Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.25 - 1.60	Depositor
Resolution (A)	28.33 - 1.60	EDS
% Data completeness	99.9 (29.25-1.60)	Depositor
(in resolution range)	99.9 (28.33-1.60)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.48 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.142 , 0.167	Depositor
It, It free	0.156 , 0.180	DCC
R_{free} test set	4328 reflections $(5.01%)$	wwPDB-VP
Wilson B-factor (Å ²)	12.7	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 50.2	EDS
L-test for twinning ²	$ < L >=0.46, < L^2>=0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5139	wwPDB-VP
Average B, all atoms $(Å^2)$	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.86% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: IPA, CL, EDO, 1PE, PGE, CIT, MRD

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		
	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.62	0/2197	0.78	0/2974	
1	В	0.64	0/2215	0.78	0/2991	
All	All	0.63	0/4412	0.78	0/5965	

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	2115	0	2148	21	0
1	В	2138	0	2207	22	0
2	A	2	0	0	1	0
2	В	4	0	0	0	0
3	A	4	0	6	0	0
3	В	8	0	12	3	0
4	A	13	0	5	0	0
4	В	13	0	5	0	0
5	A	16	0	22	8	0
6	A	4	0	8	6	0
6	В	4	0	8	1	0

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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
7	A	8	0	14	10	0
8	В	10	0	14	12	0
9	A	381	0	0	4	0
9	В	419	0	0	14	0
All	All	5139	0	4449	65	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 7.

The worst 5 of 65 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	Clash overlap (Å)
1:B:57[B]:ARG:NH1	9:B:401:HOH:O	1.60	1.29
1:B:92:ALA:O	8:B:304:PGE:H2	1.56	1.04
7:A:306:MRD:C5	7:A:306:MRD:H1C1	1.89	1.03
3:B:306:EDO:H11	9:B:670:HOH:O	1.57	1.02
1:B:93:PHE:HA	8:B:304:PGE:H32	1.51	0.92

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	entiles
1	A	281/263 (107%)	277 (99%)	4 (1%)	0	100	100
1	В	281/263 (107%)	277 (99%)	4 (1%)	0	100	100
All	All	562/526 (107%)	554 (99%)	8 (1%)	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	n Analysed Rotameric Outliers		Percentiles		
1	A	230/214 (108%)	227 (99%)	3 (1%)	69 50	
1	В	233/214 (109%)	230 (99%)	3 (1%)	69 50	
All	All	463/428 (108%)	457 (99%)	6 (1%)	71 50	

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	283	HIS
1	В	123	SER
1	В	117[A]	GLN
1	A	278	ARG
1	В	117[B]	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	${f Res}$	\mathbf{Type}
1	A	279	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.



5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	Tune	Chain	Res	Link	Вс	nd leng	ths	В	ond ang	les
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	В	307	_	3,3,3	0.44	0	2,2,2	0.28	0
7	MRD	A	306	_	7,7,7	0.26	0	9,10,10	0.23	0
4	CIT	В	308	_	3,12,12	1.17	0	3,17,17	0.97	0
8	PGE	В	304	_	9,9,9	0.44	0	8,8,8	0.29	0
5	1PE	A	304	_	15,15,15	0.45	0	14,14,14	0.28	0
3	EDO	В	306	_	3,3,3	0.52	0	2,2,2	0.34	0
6	IPA	A	305	_	3,3,3	0.43	0	3,3,3	1.00	0
6	IPA	В	305	_	3,3,3	0.56	0	3,3,3	0.48	0
4	CIT	A	303	-	3,12,12	1.26	0	3,17,17	1.38	0
3	EDO	A	302	_	3,3,3	0.52	0	2,2,2	0.14	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
7	MRD	A	306	-	-	2/5/5/5	-
4	CIT	В	308	-	-	1/6/16/16	-
8	PGE	В	304	_	-	5/7/7/7	_
5	1PE	A	304	_	-	7/13/13/13	_
3	EDO	В	306	-	-	0/1/1/1	-
3	EDO	В	307	_	-	1/1/1/1	-
4	CIT	A	303	-	-	0/6/16/16	-
3	EDO	A	302	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
7	A	306	MRD	C2-C3-C4-O4
7	A	306	MRD	C2-C3-C4-C5
5	A	304	1PE	OH2-C12-C22-OH3
8	В	304	PGE	O3-C5-C6-O4
5	A	304	1PE	C13-C23-OH3-C22

There are no ring outliers.

6 monomers are involved in 40 short contacts:

Mol	Chain	${f Res}$	Type	Clashes	Symm-Clashes
7	A	306	MRD	10	0
8	В	304	PGE	12	0
5	A	304	1PE	8	0
3	В	306	EDO	3	0
6	A	305	IPA	6	0
6	В	305	IPA	1	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	Analysed	<RSRZ $>$	# RSRZ > 2	$OWAB(\AA^2)$	Q < 0.9
1	A	$263/263 \; (100\%)$	-0.53	0 100 100	8, 12, 21, 42	12 (4%)
1	В	261/263~(99%)	-0.57	1 (0%) 92 92	7, 11, 21, 31	14 (5%)
All	All	524/526~(99%)	-0.55	1 (0%) 95 94	7, 12, 21, 42	26 (4%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	В	246	ALA	2.0	

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, 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	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
5	1PE	A	304	16/16	0.52	0.34	22,31,45,47	16
8	PGE	В	304	10/10	0.62	0.31	10,22,38,42	10
7	MRD	A	306	8/8	0.79	0.21	30,40,44,46	0
6	IPA	В	305	4/4	0.82	0.20	27,32,33,35	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
3	EDO	Α	302	4/4	0.83	0.21	37,40,43,46	0
3	EDO	В	307	4/4	0.86	0.22	35,38,41,48	0
4	CIT	В	308	13/13	0.88	0.14	19,21,25,26	0
4	CIT	A	303	13/13	0.89	0.11	15,17,22,23	0
3	EDO	В	306	4/4	0.93	0.18	18,20,21,21	4
6	IPA	A	305	4/4	0.94	0.11	16,17,19,20	0
2	CL	В	309	1/1	0.95	0.14	37,37,37,37	0
2	CL	В	303	1/1	0.98	0.05	23,23,23,23	0
2	CL	В	301	1/1	0.98	0.04	21,21,21,21	0
2	CL	В	302	1/1	0.99	0.04	14,14,14,14	1
2	CL	A	307	1/1	0.99	0.06	20,20,20,20	0
2	CL	A	301	1/1	0.99	0.06	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.

